



**AGRO-MORPHOLOGICAL VARIABILITY, GENOTYPE BY
ENVIRONMENT INTERACTION, NUTRIENT AND LAND-USE
EFFICIENCY, AND NUTRITIONAL PROFILE OF OAT (*Avena sativa*
L.) GENOTYPES IN ETHIOPIA**

PhD DISSERTATION

GEZAHAGN KEBEDE BUNARE



HAWASSA UNIVERSITY, HAWASSA, ETHIOPIA

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**A THESIS SUBMITTED TO THE
SCHOOL OF PLANT AND HORTICULTURE SCIENCES,
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SCHOOL OF GRADUATE STUDIES,
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The assistance and help received during the course of this investigation have been duly acknowledged. Therefore I recommend that it be accepted as fulfilling the thesis requirements.

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DEDICATION

This dissertation is dedicated to the Almighty God who bestowed me blessings and made all things possible.

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ABBREVIATIONS AND ACRONYMS

AEC	Average Environment Coordinate
AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of Variance
ARDU	Arsi Rural Development Unit
ASV	AMMI Stability Value
BCR	Benefit to Cost Ratio
CADU	Chilalo Agricultural Development Unit
CIMMYT	Maize and Wheat Improvement Center
CSA	Central Statistical Agency
CV	Coefficient of Variation
DMRT	Duncan Multiple Range Test
EAA	Ethiopian Agricultural Authority
ECV	Environmental Coefficient of Variation
EIAR	Ethiopian Institute of Agricultural Research
EMS	Expected Mean Square
FAO	Food and Agricultural Organization for United Nations
FAOSTAT	Food and Agriculture Organization, United Nations Statistical Databases
FDMY	Forage Dry Matter Yield
FDRE	Federal Democratic Republic of Ethiopia
FLDP	Fourth Livestock Development Project
GA	Genetic Advance
GAM	Genetic Advance as Percent of Mean
GCV	Genetic Coefficient of Variation
GDP	Gross Domestic Product
GEA-R	Genotype by Environment Analysis with R
GGE	Genotype plus Genotype by Environment Interaction
GLM	General Linear Model
GTP	Growth and Transformation Plan
GY	Grain Yield
HARC	Holetta Agricultural Research Center
IAR	Institute of Agricultural Research

ABBREVIATIONS AND ACRONYMS (Continued.....)

ILRI	International Livestock Research Institute
IPCA	Interaction Principal Component Analysis
MET	Multi-Environment Trial
MoA	Ministry of Agriculture
MRR	Marginal Rate of Return
MSE	Mean Square of Error
NARS	National Agricultural Research System
NIRS	Near Infra-Red Spectroscopy
PCA	Principal Component Axis
PCs	Principal Components
PCV	Phenotypic Coefficient of Variation
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System
TOL	Tolerance Limit
VIF	Variance Inflation Factor
YSI	Yield Stability Index

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LIST OF JOURNAL MANUSCRIPTS

Experiment	Manuscript	Publisher	Status
I	1. Gezahagn K., Walelign W., Fekede F., & Habte J. 2023. Agro-morphological traits-based genetic diversity assessment on oat (<i>Avena sativa</i> L.) genotypes in the central highlands of Ethiopia. <i>All Life</i> , 16(1):1–17. https://doi.org/10.1080/26895293.2023.2236313 .	Taylor & Francis	Published
	2. Gezahagn K., Walelign W., Fekede F., & Habte J. 2023. Correlation and path coefficient analysis for quantitative traits of oat (<i>Avena sativa</i> L.) genotypes in the central highlands of Ethiopia. <i>Tropical Agriculture</i> (Trinidad), 100(2):68–88.	Trinidad	Published
	3. Gezahagn K., Walelign W., Habte J., & Fekede F. 2023. Multivariate analysis for yield and yield-related traits of oat (<i>Avena sativa</i> L.) genotypes in Ethiopia. <i>Ecological genetics and genomics</i> , 28:1–11. https://doi.org/10.1016/j.egg.2023.100184 .	Elsevier	Published
II	1. Gezahagn K., Walelign W., Fekede F., & Habte J. 2023. Genotype by environment interaction for agro-morphological traits and herbage nutritive values and fodder yield stability in oat (<i>Avena sativa</i> L.) using AMMI analysis in Ethiopia. <i>Journal of Agriculture and Food Research</i> , 14:1–12. https://doi.org/10.1016/j.jafr.2023.100862 .	Elsevier	Published
	2. Gezahagn K., Walelign W., Fekede F., & Habte J. 2023. Genotype by environment interaction and stability analysis for selection of superior fodder yield performing oat (<i>Avena sativa</i> L.) genotypes using GGE biplot in Ethiopia. <i>Ecological genetics and genomics</i> , 28:1–11. https://doi.org/10.1016/j.egg.2023.100192 .	Elsevier	Published
	3. Gezahagn K., Walelign W., Habte J., & Fekede F. 2023. Stability analysis for fodder yield of oat (<i>Avena sativa</i> L.) genotypes using univariate statistical models under diverse environmental conditions in Ethiopia. <i>Ecological genetics and genomics</i> , 29:1–13. https://doi.org/10.1016/j.egg.2023.100202 .	Elsevier	Published
	4. Gezahagn K., Walelign W., Fekede F., & Habte J. 2024. Grain yield stability analysis for oat (<i>Avena sativa</i> L.) genotypes using additive main effects and multiplicative interactions model under different environments in Ethiopia. <i>Ecological Genetics and Genomics</i> , 30:1–13. https://doi.org/10.1016/j.egg.2024.100228 .	Elsevier	Published
	5. Gezahagn K., Walelign W., Habte J., & Fekede F. 2023. GGE biplot analysis of genotype by environment interaction and grain yield stability of oat (<i>Avena sativa</i> L.) in Ethiopia. <i>Agrosystems, Geosciences & environment</i> , pp. 1–16. https://doi.org/10.1002/agg2.20410 .	Wiley	Published
	6. Gezahagn K., Walelign W., Habte J., & Fekede F. 2023. Grain yield stability analysis using parametric and nonparametric statistics in oat (<i>Avena sativa</i> L.) genotypes in Ethiopia. <i>Grassland Research</i> , pp. 1–15. https://doi.org/10.1002/qlr2.12056 .	Wiley	Published

III	1. Gezahagn K., Walelign W., Habte J., & Fekede F. 2024. Grain yield productivity, nutrient uptake and use efficiency and profitability of oat (<i>Avena sativa</i> L.) as influenced by variety and levels of nitrogen and phosphorus fertilizers in the central highlands of Ethiopia. <i>Journal of Crop Science and Biotechnology</i> , pp. 1–26. https://doi.org/10.1007/s12892-023-00230-3 .	Springer	Published
	2. Gezahagn K., Walelign W., Habte J., & Fekede F. 2024. Effects of fertilizer levels and varieties on fodder yield productivity, nutrient use efficiency, and profitability of oat (<i>Avena sativa</i> L.) in the central highlands of Ethiopia. <i>Journal of Agriculture and Food Research</i> , 16:1–19. https://doi.org/10.1016/j.jafr.2024.101161 .	Elsevier	Published
	3. Gezahagn K., Walelign W., Fekede F., & Habte J. Nutritive value of oat (<i>Avena sativa</i> L.) herbage yield as influenced by variety and rate of nitrogen and phosphorus fertilizers in the central highlands of Ethiopia.	Elsevier	Under review
IV	1. Gezahagn K., Walelign W., Fekede F., & Habte J. Forage yield and nutrient use performances of oat (<i>Avena sativa</i> L.) as influenced by fertilizer application under oat/vetch mixed cropping system in the central highlands of Ethiopia.	Elsevier	Under review
	2. Gezahagn K., Walelign W., Habte J., & Fekede F. Herbage yield, biological efficiency, and competitive ability of oat (<i>Avena sativa</i> L.) and economic efficiency of oat/vetch mixtures as influenced by fertilizer rates under mixed cropping system in Ethiopia.	Wiley	Under review
	3. Gezahagn K., Walelign W., Fekede F., & Habte J. Fodder productivity and nutritional quality of oat (<i>Avena sativa</i> L.) and vetch (<i>Vicia villosa</i>) mixtures improved with application of NP fertilizers in Ethiopia.	Wiley	Under review

LIST OF PROCEEDINGS

A. Published papers

- 1 Gezahagn K., Walelign W., Fekede F., Habte J., Mulisa F., Aemiro K., Mesfin D., Diriba G., Getnet A., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genetic diversity assessment of oat (*Avena sativa* L.) genotypes for agro-morphological traits: I. Heritability and genetic gain. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2023. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2022 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 359–379. ISBN: 9789994438631.
- 2 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Aemiro K., Diriba G., Getnet A., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genetic diversity assessment of oat (*Avena sativa* L.) genotypes for agro-morphological traits: II. Correlation and path analyses. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2023. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2022 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 380–400. ISBN: 9789994438631.

- 3 Gezahagn K., Walelign W., Fekede F., Habte J., Aemiro K., Mesfin D., Diriba G., Getnet A., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genetic diversity assessment of oat (*Avena sativa* L.) genotypes for agro-morphological traits: III. Cluster and principal component analyses. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2023. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2022 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 401–423. ISBN: 9789994438631.
- 4 Gezahagn K., Walelign W., Fekede F., Habte J., Mezgeb W., Mesfin D., Aemiro K., Diriba G., Getnet A., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genotype-by-environment interaction for quantitative traits and grain yield stability in oat (*Avena sativa* L.) genotypes: I. AMMI analysis. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2023. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2022 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 424–447. ISBN: 9789994438631.
- 5 Gezahagn K., Walelign W., Fekede F., Habte J., Mezgebu G., Aemiro K., Mesfin D., Diriba G., Getnet A., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genotype-by-environment interaction for quantitative traits and grain yield stability in oat (*Avena sativa* L.) genotypes: II. GGE biplot analysis. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2023. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2022 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 448–469. ISBN: 9789994438631.
- 6 Gezahagn K., Walelign W., Fekede F., Habte J., Tekleyohannes B., Mesfin D., Aemiro K., Diriba G., Getnet A., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genotype-by-environment interaction for quantitative traits and grain yield stability in oat (*Avena sativa* L.) genotypes: III. Parametric and non-parametric analyses. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2023. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2022 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 470–494. ISBN: 9789994438631.
- 7 Gezahagn K., Walelign W., Fekede F., Habte J., Tekleyohannes B., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Fodder yield stability analysis in oat (*Avena sativa* L.) genotypes: I. AMMI analysis. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2024. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2023 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 325–349. ISBN: 9789994439034.
- 8 Gezahagn K., Walelign W., Fekede F., Habte J., Mezgeb W., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Fodder yield stability analysis in oat (*Avena sativa* L.) genotypes: II. GGE biplot analysis. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2024. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2023 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 350–374. ISBN: 9789994439034.
- 9 Gezahagn K., Walelign W., Fekede F., Habte J., Mezgebu G., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Fodder yield stability analysis in oat (*Avena sativa* L.) genotypes: III. Parametric and non-parametric analyses. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2024. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2023 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 375–404. ISBN: 9789994439034.
- 10 Gezahagn K., Walelign W., Fekede F., Habte J., Mulisa F., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Effects of nitrogen and phosphorus fertilizers on the performance of oat (*Avena sativa* L.) varieties: I. Grain yield. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2024. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2023 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 405–440. ISBN: 9789994439034.
- 11 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Effects of nitrogen and phosphorus fertilizers on the performance of oat (*Avena sativa* L.) varieties: II. Fodder yield. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2024. *Livestock Research Proceedings*. Results of Livestock Research Completed during 2023 (Volume I),

Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 441–474. ISBN: 9789994439034.

- 12 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Effects of nitrogen and phosphorus fertilizers on the performance of oat (*Avena sativa* L.) varieties: III. Nutritive value. **In:** Fekede F., Zewdie W., Lamma F., and Temesgen J. (eds.). 2024. Livestock Research Proceedings. Results of Livestock Research Completed during 2023 (Volume I), Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia. pp. 475–512. ISBN: 9789994439034.

B. Under Review Papers

- 1 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Influence of nitrogen and phosphorus fertilizer rates on oat (*Avena sativa* L.) performance under oat/vetch mixed cropping: I. Fodder yield.
- 2 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Influence of nitrogen and phosphorus fertilizer rates on oat (*Avena sativa* L.) performance under oat/vetch mixed cropping: II. Biological efficiency and competitive ability.
- 3 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., & Adegbola T.A. 2024. Influence of nitrogen and phosphorus fertilizer rates on oat (*Avena sativa* L.) performance under oat/vetch mixed cropping: III. Nutritional quality.
- 4 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genetic diversity assessment of oat (*Avena sativa* L.) genotypes for fodder yield and nutritional quality: I. Heritability and genetic gain.
- 5 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genetic diversity assessment of oat (*Avena sativa* L.) genotypes for fodder yield and nutritional quality: II. Correlation and path analyses.
- 6 Gezahagn K., Walelign W., Fekede F., Habte J., Mesfin D., Diriba G., Mengistu A., Mulubrhan B., and Adegbola T.A. 2023. Genetic diversity assessment of oat (*Avena sativa* L.) genotypes for fodder yield and nutritional quality: III. Cluster and principal component analyses.

Thesis Abstract

Agro-morphological variability, genotype by environment interaction, nutrient and land-use efficiency, and nutritional profile of oat (*Avena sativa* L.) genotypes in Ethiopia

Oat (*Avena sativa* L.) is one of the useful annual cereal crops grown at higher altitudes in the tropics and temperate regions. It is a dual-purpose crop cultivated for fodder and grain production in the central highlands of Ethiopia. This crop is mainly cultivated for fodder production and the grain is also used for human food and animal feed in Ethiopia. Oat generally produces high amounts of fodder which has better nutritional quality and it can be used as a green feed and the excess production can be conserved as hay and silage to utilize during the feed scarcity period. Despite its significance, oat production, and productivity are highly influenced by genetics, environments, agronomic management, and their interactions. Therefore, developing high-yielding oat varieties with stable performance under diverse environmental conditions and improving the productivity of oat through various agronomic management are the major research areas for oat improvement in Ethiopia. However, studies on agro-morphological based genetic diversity and yield stability of oat genotypes under diverse environmental conditions and the optimum nutrient requirements of oat for higher yield and nutritional quality under sole and mixed cultures with vetch have not been well studied and properly documented in the country. Thus, the overall aim of this study was to enhance the productivity of oat genotypes through proper exploitation of genetic variability and agronomic management under different environments and management conditions. The first experiment was conducted using 120 oat genotypes using a randomized complete block design with three replications at Holetta and Ada-Berga research stations in the 2020/2021 cropping season. The objectives of this study were to estimate the extent of agro-morphological based genetic variability, heritability, and genetic advance in oat genotypes, to investigate the phenotypic and genotypic relationships between the studied quantitative traits, to determine the direct and indirect effects of measured quantitative traits on fodder and grain yields, and to evaluate the genetic variations using cluster, genetic divergence, and principal component analyses for oat yield improvement. The results revealed that moderately high to very high heritability (62.9–86.4%) coupled with high to moderate genetic advance as percent of mean (16.0–26.1%) were recorded for forage dry matter yield (FDMY), number of leaves at forage harvest (NLFH), stem dry matter yield (SDMY), forage yield production rate (FYPR), grain yield (GY), panicle length at grain harvest (PLGH), number of spikes per panicle (NSPP), and harvest index (HI). This result demonstrated that the selection of oat genotypes based on these traits could be effective for yield improvement. The genotypic and phenotypic correlation and path coefficient analyses indicated that the FYPR had a significant positive association and high direct effect on FDMY and also the biological yield production rate (BYPR) and HI had a significant positive association and high direct effect on GY. This indicated that selection based on FYPR and BYPR/HI would simultaneously improve the FDMY and GY in oat genotypes, respectively. The multivariate analysis revealed that the studied genotypes grouped into four clusters with the intra and inter-cluster genetic distances ranging from 2.3 to 4.3 and 11.7 to 63.2, respectively. The principal component analysis showed that traits such as FYPR, BYPR, PLGH, FDMY, and

number of spikelets per panicle (NSLPP) contributed more for the first component whereas HI, GY, NLFH, and plant height at grain harvest (PHGH) had a high contribution for the second component. The presence of genotype by environment interaction (GEI) complicates the selection of genotypes with high yielding coupled with stable performance across environments. Twenty-four oat genotypes were selected and sown during the 2020/2021 cropping season at Holetta (E1), Ada-Berga (E2), Ginchi (E3), Jeldu (E4), D/Zeit (E5), Kulumsa (E6), Bekoji (E7), Kuyu (E8), and D/Markos (E9) agricultural research stations using a randomized complete block design with three replications. Thus, the second experiment aimed to assess the magnitude of GEI and to evaluate the fodder and grain yield stability performance of oat genotypes using univariate and multivariate statistical models. The additive main effects and multiplicative interaction (AMMI) analysis of variance for fodder yield showed that the total variation was highly contributed by the environment (E) main effect followed by GEI and genotype (G). Moreover, the GGE biplot analysis for fodder yield showed that G6 was the ideal genotype while G2, G3, G10, and G23 were desirable genotypes. Among environments, E7 was an ideal environment whereas E1 and E8 were favorable environments. The results of univariate stability analysis indicated that selection of oat genotypes using genotypic superiority index (P_i), yield stability index (YSI), coefficient of determination (R^2), and coefficient of variation (CV_i) stability parameters would be effective for fodder yield improvement. Similarly, the AMMI analysis of variance for grain yield showed that the E main effect was the highest contributor to the total variation followed by G and GEI. Based on the GGE biplot analysis for grain yield, G19 was an ideal genotype while G8, G11, G12, G14, G17, and G22 were desirable genotypes. Moreover, the ideal environment was E2 whereas E1, E4, and E5 were favorable environments. The univariate stability analysis for grain yield indicated that high grain yield-producing oat genotypes had stable performance using the stability parameters of P_i , the Perkins and Jinks adjusted linear regression coefficient (B_i), and YSI. The yield and nutritional quality of oat can be improved through the application of optimum fertilizer at the right time. Oat can be cultivated using the blanket recommended fertilizer rate in Ethiopia. Thus, the optimum fertilizer rate for fodder and grain production of oat has not been well studied and documented in the country. Therefore, this study aimed to assess the effect of fertilizer rates on agro-morphological traits, nutrient uptake and use efficiency, nutritive value, and economic feasibility of oat varieties at Holetta. The study was carried out during the 2020/2021 and 2021/2022 cropping seasons using a factorial arrangement of eight levels of the blanket recommended fertilizer (0, 25, 50, 75, 100, 125, 150, and 175%) and three oat varieties (CI-8251, SRCPX80Ab2291, and Sorataf) in a randomized complete block design with three replications. The results showed that variety, fertilizer, and year had significant effects on FDMY. The FDMY of oat varieties increased with increasing fertilizer rates and the highest (15.9 t/ha) yield was obtained from the application of 175% (71.8 kg N + 35 kg P/ha) fertilizer. Among oat varieties, the highest FDMY was obtained from CI-8251 (forage type oat) followed by SRCPX80Ab2291 (dual type oat) and Sorataf (grain type). The number of tillers per plant (NTPP), yields of morphological fractions (leaf, stem, and grain), FYPR, nutrient concentration, and uptake had significant positive associations with fertilizer levels and FDMY. However, all the nutrient use efficiencies except agro-physiological efficiency (APE) had inverse associations with fertilizer levels and FDMY. Similar to FDMY, the GY of oat varied significantly for variety, fertilizer, and year effects. Application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate produced the highest GY (6.5 t/ha) and grain nutrient uptake-GNU (141.7 kg/ha) while the lowest GY and GNU were recorded from oat sown without fertilizer application. Sorataf (grain type) variety gave the highest GY, GNU, partial factor

productivity (PFP), and agronomic efficiency (AE) compared to forage and dual-type oat varieties. Oat varieties sown with 25% (10.3 kg N + 5 kg P/ha) fertilizer rate produced the highest PFP (346.6 kg/ha) and AE (164.8 kg/ha) while PFP and AE decreased with increasing fertilizer rates. The nutrient concentration and uptake had positive associations with fertilizer level and GY while nutrient harvest index (NHI) and nutrient use efficiency had inverse associations with fertilizer level and GY. The nutritional quality analysis indicated that digestible yield (DY) and total digestible nutrient yield (TDNY) varied significantly with variety, fertilizer, and year effects. Among oat varieties, CI-8251 gave the highest TDNY while SRCPX80Ab2291 gave the highest DY but the Sorataf variety gave the lowest TDNY and DY. Most of the measured nutritional quality parameters varied for the interaction effect of variety by fertilizer by year effect. Sorataf variety sown with 175% fertilizer rate in 2020 gave the highest crude protein-CP (113.9 g/kg DM), crude protein yield-CPY (1.66 t/ha), and digestible crude protein-DCP (68.2 g/kg DM). Application of fertilizer and FDMY had significant positive associations with CP, CPY, DY, DCP, and TDNY. The combined partial budget analysis for the three oat varieties showed that application of 125% (51.3 kg N + 25 kg P/ha) fertilizer rate produced higher net benefit (83,440 ETB) and marginal rate of return (12,635.6%) from fodder production. On the other hand, the application of 150% fertilizer rate produced the highest net benefit from grain production. Oat can be also cultivated with vetch (annual forage legume) to improve the quantity and quality of feed in the central highlands of Ethiopia. The oat/vetch mixtures are sown with the same blanket recommended fertilizer rate that is used for the production of sole oat in the country. This indicated that the application of fertilizer on oat/vetch mixtures does not depend on the nutrient requirements of oat and vetch for better growth and development under a mixed cropping system. Accordingly, the optimum fertilizer rate for the oat/vetch mixed cropping system has not been well studied and documented in the country. Therefore, this study aimed to investigate the effect of fertilizer rates on agro-morphological traits, nutrient uptake and use efficiency, competitive ability, and economic feasibility of oat under oat/vetch mixed cropping and nutritive value of mixtures at Holetta Agricultural Research Center during the 2020/2021 and 2021/2022 cropping seasons. In this study, the oat/vetch mixture was sown with eight fertilizer rates (0, 25, 50, 75, 100, 125, 150, and 175%) and also sole oat and sole vetch were sown with their recommended fertilizer rate (100%) using a randomized complete block design with three replications. The results showed that fertilizer and year had significant effects on all measured agro-morphological traits, nutrient concentration, and nutrient uptake and use efficiency of oat. Accordingly, all the measured agro-morphological traits increased with increasing fertilizer rates, and the highest values were recorded in the second year. Application of 150% fertilizer rate increased the FDMY of oat/vetch mixtures by 107.4% compared to oat/vetch mixtures sown without fertilizer application. However, the highest nutrient use efficiency was recorded with the application of fertilizer at the rate of 25% while the nutrient use efficiency was the lowest with the highest fertilizer (175%) application rate. The FDMY of oat under oat/vetch mixtures was associated significantly and positively with all measured agro-morphological traits, nutrient concentration, and uptake while it had significant inverse associations with nutrient use efficiencies. The highest net benefit and marginal rate of return were recorded from the application of 150% fertilizer rate. The productivity of oat under oat/vetch mixed cropping was also assessed using different indices. The results showed that over-yielding oat (OYO), land equivalent coefficient (LEC), area-time equivalent ratio (ATER), and land equivalent ratio (LER) were higher in the first year while oat equivalent yield (OEY) and system productivity index (SPI) were higher in the second year. All

the aforementioned biological efficiency indices increased with increasing fertilizer rates and the highest values were recorded from the application of 150% fertilizer rate. Similarly, all the measured competitive indices such as crowding coefficient of oat (KO), actual yield loss of oat (AYLO), intercropping advantages of oat (IAO), and the competitive ratio of oat (CRO) were higher in the first year. All the values of competitive indices except aggressivity of oat (AO) increased with increasing fertilizer rates and the highest values were recorded from the application of 150% fertilizer. The economic efficiency indices of oat/vetch mixtures showed that the higher values of monetary advantages index (MAI), relative value total (RVT), replacement value of intercropping (RVI), and relative net return index (RNRI) were recorded in the first year. All the values of economic efficiency indices increased with increasing fertilizer rates and the highest values were recorded from 150% fertilizer rate. The nutritive values of oat/vetch mixtures also varied with fertilizer application and year of production. All the measured nutritive values except fiber contents (NDF-neutral detergent fiber, ADF-acid detergent fiber, ADL-acid detergent lignin, HC-hemicellulose, and C-cellulose) were higher in the second year. Application of fertilizer at the rate of 150% gave the highest ash, CPY, digestible dry matter (DDM), dry matter intake (DMI), in-vitro dry matter digestibility (IVDMD), DY, total digestible nutrients (TDN), TDNY, relative feed value (RFV), and relative feed quality (RFQ). On the other hand, oat/vetch mixtures sown without fertilizer gave the highest fiber contents. The person correlation analysis indicated that fertilizer application had significant inverse associations with fiber contents while it had significant positive associations with the remaining measured nutritional quality parameters. In conclusion, oat genotypes such as CI-715, CI-1463, SRCPX80Ab2806, A-505, CI-1480, S-122, Bona-bas, and CI-1674 were selected for fodder yield and grain yield improvement. Based on the AMMI, GGE, and univariate stability parameters, G6 (CI-1512), G9 (CI-1629), G10 (C-12), and G23 (CI-8235) were selected for fodder yield improvement while G8 (SRCPX80Ab2267), G17 (SRCPX80Ab2310), and G22 (SRCPX80Ab2691) were selected for grain yield improvement of oat. Application of 125% (51.3 kg N + 25 kg P/ha) fertilizer rate for fodder production and 150% (61.5 kg N + 30 kg P/ha) fertilizer rate for grain production could increase the respective yield and farm profitability in the study area. Similarly, application of 150% fertilizer rate would increase the fodder yield, competitive ability, and economic profitability of oat under oat/vetch mixtures and nutritive value of mixtures. However, the selected genotypes and fertilizer rates should be verified under diverse environments of oat-growing areas in Ethiopia.

Keywords: competitive ability, correlation and path analyses, economic efficiency, genetic diversity, genetic gain, genotype by environment interaction, heritability, mixed cropping, multivariate analysis, nutrient use efficiency, partial budget analysis, yield stability

Chapter I

General Introduction

General Introduction

1.1 Background and Justification

1.1.1 General introduction

Agriculture is the dominant sector of the Ethiopian economy, contributing about 35% to GDP and 68% to employment, and 90% to the export value (FAO, [2019a](#)). Similarly, livestock is an integral part of agriculture, accounting for about 45% of the agricultural GDP, 31 to 48% of the total household income, 10% of the total export earnings of which 69% accounted for live animal exports and supporting the livelihoods of 70% of the rural population (FAO, [2019a](#)). Ethiopia is believed to have the largest livestock population in Africa and has diverse livestock genetic resources and suitable agro-ecologies for different kinds of livestock production. The country has an estimated livestock population of 53.4 million of which 10.7 million are dairy cows, 25.5 million sheep, 22.9 million goats, 6.2 million donkeys, 2 million horses, 1.1 million camels, 49.3 million poultry, and 5.1 million beehives (FAO, [2019b](#)). The report indicated that 98.24% of the total cattle in the country are local breeds with low production and productivity (CSA, [2018](#)) due to poor quality and inadequate quantity of available feed (FAO, [2019a](#)). The remaining are hybrid and exotic breeds that accounted for about 1.54 and 0.22%, respectively. Livestock plays a significant role as a source of food and income in addition to several other important economic and socio-cultural functions. Total production of milk, meat, and eggs estimated to be 5.6 billion liters, 1.1 million tonnes, and 419 million eggs per year, respectively (FAO, [2019a](#)). The respective annual per capita consumption is 56.2 liters, 9 kg, and about 4 pieces and cow milk and cattle beef contribute about 80% of all milk and meat consumption (FAO, [2019a](#)). In 2050, the aggregate consumption of all livestock products will be more than double, and on an annual basis, demand will grow by 2.2% for milk, 3.1% for beef, 3.3% for egg, and 3.2% for poultry in Ethiopia (FAO and Palladium group, [2019](#)). This report also showed that as a response to the growing demand for animal source foods, the livestock sector is expected to make investments that enhance production with annual growth rates of 3.5, 3.0, 4.4, and 4.6% for milk, beef, egg, and poultry, respectively.

The feed resources potential in Ethiopia includes natural pastures, crop residues, and stubble grazing, cultivated forages, agro-industrial byproducts, grain and grain screenings,

compound or formula feeds. The natural pasture grazing accounts for the major share of feed supply (55.96%) followed by crop residues (30.12%) and hay which contribute 6.55% of the total feed (CSA, 2018). Agro-industrial by-products, improved forage crops, and non-conventional feed resources like animal by-products, vegetable and fruit wastes contribute the remaining 1.61, 0.32, and 5.44% of the total feed, respectively. Livestock feeding in Ethiopia mainly depends on natural pasture and crop residue, both of which have low nutritional quality (Adugna *et al.*, 2012a; Alemayehu *et al.*, 2017). The nutritive value of crop residues is variable depending upon the species and variety of the crops, time of harvest, handling and storage conditions. The fibrous agricultural byproducts obtained mainly from cereals and pulses are generally characterized by relatively low nutrient content, high fiber content, low digestibility, and low voluntary intake by animals (Getu, 2019). The grazing land is shrinking from time to time owing to the expansion of arable cropping, urbanization and industrial development as a result it is limited to areas where conditions are adverse for cropping due to topographic, edaphic and climatic limitations which also impose further limitations on the yield and quality of the pasture (Fekede *et al.*, 2015; Alemayehu *et al.*, 2016a). The agro-industrial byproducts produced from flour millings, sugar factories, edible oil processing factories, breweries, and abattoirs are usually less fibrous, rich in energy and/or protein contents, and they have high digestibility and energy values compared with other classes of feed resources (FAO, 2019c). These byproducts play a vital role in the feeding of livestock mainly in urban and peri-urban livestock systems. Their contribution to the total actual feed dry matter (DM), crude protein (CP), and metabolizable energy (ME) availability in Ethiopia are only 1.08, 3.08, and 1.42%, respectively (FAO, 2019c). In general, livestock production is constrained due to poor availability and supply of cultivated forages, supplements, premixes, and feed additives (EIAR, 2017).

There is a substantial loss of energy in the form of methane emission when animals depend on crop residues and other poor quality roughage based diets resulting in reduced efficiency of feed utilization, poor animal performance, and higher greenhouse gas emission per unit of product. The estimated annual greenhouse gas emission (CO₂ equivalent) from the Ethiopian cattle is 192.4 million tons (FAO, 2019a), but the emission level can be reduced through feeding of better quality feeds (Aemiro, 2016). Improved forage crops have diversified functions and play an important role in sustaining the livelihoods of farmers, mainly as a result of their positive effects on livestock production and contribution to economic and environmental sustainability. They sustain the environment by improving soil fertility and

reduce greenhouse gas emission by sequestering more CO₂ and producing a high amount of better quality forage. Improvements in feed quality and feed utilization efficiency will also contribute to the attainment of the climate-resilient green economy development strategy of the government of Ethiopia (FDRE, 2011). Food and nutrition security and climate-resilient green economy can be achieved through the production of improved forage crops. Because animals fed with improved forage crops have better feed conversion efficiency which leads to increase livestock productivity and reduction of greenhouse gas emissions. Therefore, improvement in livestock production and productivity can be achieved through strengthening feed production using improved/ cultivated forage crops in addition to natural pasture and crop residues (Fekede *et al.*, 2015). The utilization of improved forage crops is also increasing due to the reduction of productive pasture lands in the mixed crop-livestock production system (Muluneh *et al.*, 2012). They produce a substantial amount of biomass yield but their productivity varies with species, varieties, soil, weather, and management factors. The overall average productivity of the improved forage crops per unit area has been found to exceed the productivities of seasonally rested and continuously grazed natural pastures by about 3 and 10 folds per single harvest under rainfed condition, respectively (Fekede *et al.*, 2015), but when supplemented with irrigation, multiple harvests could be possible and the potential of herbage yields could be by far higher especially for perennial forage crops. The authors also indicated that the average productivities of improved forage crops relative to natural pasture are found to be about 13, 8, 11, 4, and 1 ton per ha DM yield for grasses, legumes, browse trees, seasonally rested pasture and continuously grazed pasture, respectively.

Over the past five decades, the adaptability and yield performance of different improved forage crops have been tested in areas ranging in altitude from 600-3000 meters above sea level, and many promising species have been selected for high, medium and low altitudes (Getnet and Gezahagn, 2012; Alemayehu *et al.*, 2017). The selected forage crops are generally well adapted to the different agro-ecologies and are high yielding and have better quality compared to natural pasture (Getnet *et al.*, 2012; Fekede *et al.*, 2015). Among the different improved forage crops recommended for various agro-ecological zones of Ethiopia, oat (*Avena sativa* L.) is one of the useful annual forage crops abundantly grown in the central highlands of Ethiopia (Gezahagn *et al.*, 2016). The authors also pointed out that oat is a potential fodder crop for livestock feed and has been growing in the central highlands of Ethiopia for about five decades. It has been well accepted by the farming communities

because of its hardy nature to perform well under stressful conditions such as poor soil fertility, soil acidity, waterlogging, and frost with very minimal managerial inputs (Getnet, 1999; Fekede, 2004; Gezahagn *et al.*, 2016). Generally, it is possible to grow oat under circumstances detrimental to growing other crops. For instance, north Shewa is characterized by most of the stressful conditions mentioned above and this could be one of the reasons why oat has acquired relative importance in the zone. It is used as livestock feed in the form of hay, silage, and grazing or green feed and provides an abundance of excellent forage at a time when other succulent and high-protein feeds are scarce. Its grain also makes part of the staple diet of human beings in some parts of the country most commonly in Selale, Debre-Berhan, Sheno, Arsi, and Gojam (Fekede, 2004; Getnet *et al.*, 2004). Farmers can easily grow it for forage and grain because its production practice is similar to that of other cereals such as barley and wheat. This crop has huge potential to transform the livestock sector which is extensively constrained with a lack of good quality available feeds. However, the livestock production system of the country is affected with inadequate quantity and low quality of feeds which resulted in low production and productivity, and the system generally characterized by a low input-output production system (Getahun, 2019).

1.1.2 Statement of the problem

Ethiopia has a huge livestock population that requires considerable amounts of good quality feed and appropriate feeding systems for increased production, productivity, value addition, and transformation of the livelihood of the farmers. However, inadequate supply of feed for the existing livestock population and poor quality of the available feed resources are the two main factors contributing to the low production and productivity of livestock in Ethiopia (Seyoum *et al.*, 2001; Getnet, 2007; Alemayehu *et al.*, 2017). The livestock master plan of Ethiopia indicated an estimated national annual feed availability of 81.3, 108.5, and 145.2 million ton DM in bad, average, and good weather conditions, respectively (Shapiro *et al.*, 2015). However, the national annual feed requirement is estimated to be 130 million ton DM, indicating positive feed balance of 15.2 million ton DM in good weather conditions while negative feed balance of 21.5 and 48.7 million ton DM are recorded in average and bad weather conditions, respectively (Shapiro *et al.*, 2015). Except during good weather conditions, the livestock feed intake falls short of the required standards of 2.5–3.0 kg per 100 kg live weight, which is the most critical requirement for achieving adequate production levels (Shapiro *et al.*, 2017). The lowland grazing and agro-pastoral production zone produce

the highest feed resources due to 60% of the total land coverage resulting in positive feed balance of 20.6 and 3.6 million ton DM that is estimated in good and average weather conditions, respectively (Shapiro *et al.*, 2015). The authors also estimated a negative feed balance of 13.5 million ton DM in bad weather conditions

The highland mixed crop-livestock agro-ecological zone which is deficient in rainfall and covers 15% of the total land, annually requiring 29 million ton DM but produces 28.1, 19.2, and 15.2 million ton DM in good, average and bad weather conditions, respectively; indicating negative feed balance of 0.9, 9.8 and 13.8 million ton DM for the respective weather conditions (Shapiro *et al.*, 2015). The same authors also pointed out that highland mixed crop-livestock agro-ecological zone which receives sufficient amount of rainfall and covers 25% of the total land, annually produces 48.9, 38.0, and 31.9 million ton DM in good, average, and bad weather conditions, respectively. However, the annual feed requirement estimated in this production zone is 53.4 million ton DM indicating a negative feed balance of 4.5, 15.4, and 21.5 million ton DM in good, average, and bad weather conditions, respectively. Due to the increasing number of livestock in each production system in 2028, the feed requirement will not be met under any climatic conditions without proper policy and technology interventions in the country. The total feed requirements in 2028 will be 55.9, 33.7, and 76.7 million ton DM in lowland grazing and agro-pastoral system, highland mixed crop-livestock system with deficit rainfall, and highland mixed crop-livestock system with sufficient rainfall, respectively (Shapiro *et al.*, 2017). The difference between the availability of feed resources as DM, ME, and CP and the requirements of all animal species (i.e. feed balance) showed that feed deficiency in Ethiopia is 9 % as DM, while ME and CP deficiencies are 45 and 42%, respectively, suggesting lack of good quality feeds (FAO, 2018). But, these feed deficiencies increase to 21% as DM, and 52 and 48% as ME and CP, respectively, after considering the competitive uses of crop residues and export of oilseeds (FAO, 2018).

The government of Ethiopia has set an ambitious target for the livestock sector in terms of increasing production and productivity and thereby contributing to poverty reduction, attainment of better food and nutrition security, national income growth and foreign exchange earnings as outlined in the second growth and transformation plan (GTP II) and livestock master plan (Shapiro *et al.*, 2015). These targets can only be met through securing year-round supplies of good quality feeds and efficient utilization of the available feed

resources through improved feeding management (Seyoum and Dawit, 2012). However, the high cost and low availability of good quality feed is a critical challenge severely limiting livestock productivity. Feed cost accounts for about 60 to 70% of the total cost of livestock production (Adugna *et al.*, 2012b; Fekede, 2013; Seyoum *et al.*, 2018) and it increases to 75-80% during the critical feed shortage period in the country (Demisse, 2017). Feed production and processing industries are not well developed and good quality supplemental feeds are in short supply and very expensive in Ethiopia. Cultivated forage crops have tremendous contribution to boost and sustain the livestock productivity by filling the gap of good quality feed resources available in the country. Cultivation of improved forage crops is highly constrained in the highland crop-livestock mixed farming system due to the competition for land between food and forage crops. However, integration of forage and food crops with different strategies increases the productivity and sustainability of farming systems and improves the quantity and quality of livestock feed (Alemayehu *et al.*, 2016b). Thus, improving the supply and quality of livestock feed through developing appropriate food-feed crops integration strategies is highly important in crop dominated mixed crop-livestock production systems (Muluneh *et al.*, 2014).

Animal feeds and nutrition research strategy was developed to avail feed and nutrition technologies and innovations to enhance livestock production and productivity during the plan period of 2016 to 2030 (EIAR, 2017). The research strategy indicated that development of varieties suitable for different production environments and refining the existing production packages are some of the major envisions of cultivated forage crops research in the country. Generating tangible evidence to show that forage crops are competitive and better enterprise choices to ensure adoption by various target groups is also a research agenda considered in this strategy. So, expanding forage varietal options for various production environments and land-use systems and availing complete packages of production and management of forages are some of the strategic issues of feeds and nutrition research in Ethiopia (EIAR, 2017). Evaluation and varietal development of improved forage crops targeting various production environments and land-use systems and refining the existing production packages and develop environment-specific recommendations for selected forage crops are the main stated strategic interventions to achieve the aforementioned strategic issues of improved forage crops.

Until recently, the focus of research on forage crops in general and oat, in particular, has been limited to evaluation and selection of varieties in terms of adaptation to edaphic and agro-ecological conditions as well as herbage yield potential. However, environmental adaptation and herbage yield alone are not adequate parameters to evaluate and develop a variety for a given purpose. Despite a considerable variation in agronomic and quality traits among oat genotypes under a given environmental condition, the diversified agronomic and nutritional characteristics of oat genotypes have not been thoroughly investigated in Ethiopia. Assessing the extent of agro-morphological based genetic diversity is very essential to exploit the differences in oat genotypes for proper utilization and further improvement. Since oat has dual use as livestock feed and human food, there is a crucial need to further evaluate some potential varieties for other relevant parameters like agro-morphological and nutritional traits under different environment and management conditions. The genotypes of oat which are grown in different environments frequently show significant fluctuations in yield performance. So, understanding the situations of yield performance and yield stability in diverse agro-ecological conditions is very important for oat selection and improvement programs. Farmers usually cultivate oat without any application of fertilizer or with very low fertilizer rate due to high cost of fertilizer and its better performance on relatively less fertile soils. Oats grown with the application of fertilizer on high fertile soils or following legumes or fallow lands are susceptible to lodging and usually requires less fertilizer or do not need any fertilizer. However, application of fertilizers on very poor or less fertile soils could boost the yield. The blanket recommendation of fertilizer for sole oat and oat-vetch mixtures in the highlands is 18/46 kg ha⁻¹ of N/P₂O₅ at sowing and 23 kg ha⁻¹ of N at tillering (Getnet, 1999). So, evaluating the nutrient use efficiency and refining the blanket recommended fertilizer level for sole oat and oat-vetch mixed cropping system are very important to enhance the productivity of oat. Generally, the agro-morphological based genetic diversity, the genotype by environment interaction and yield stability, productivity, nutrient and land-use efficiency, and nutritional profile of oat genotypes under diverse environments and management conditions have not been well studied and documented in the country. Therefore, this study was conducted to enhance the productivity of oat and the conceptual framework of the study is indicated in [Figure 1.1](#).

1.1.3 Research Objectives

1.1.3.1 General objective

The general objective of this study was to enhance the productivity of oat genotypes through proper exploitation of genetic variability and agronomic managements under different environmental and management conditions thereby improves the availability of good quality feed for better livestock production and productivity which contributes towards food security in Ethiopia.

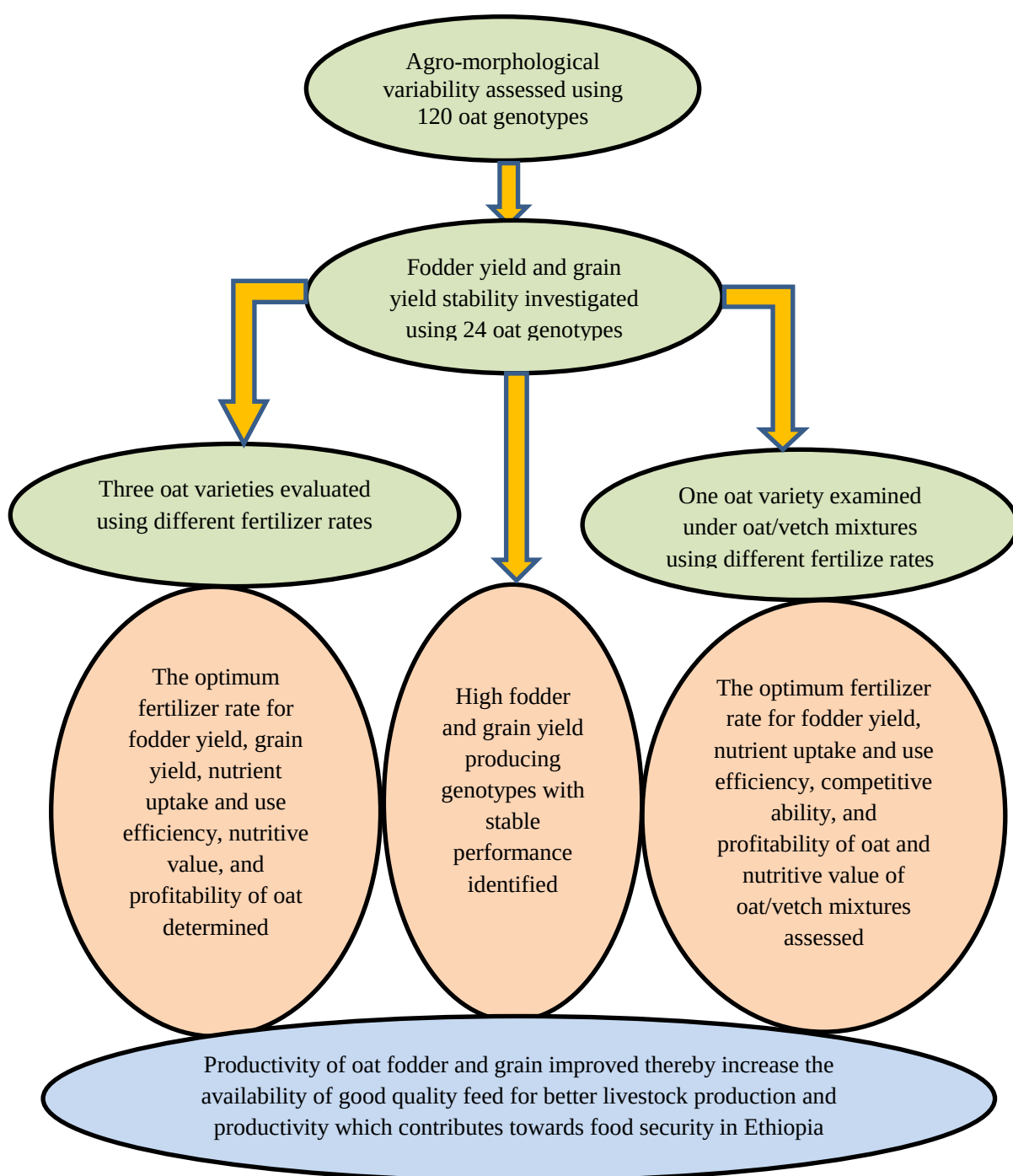


Figure 1.1 Conceptual framework of the study

1.1.3.2 Specific objectives

- i. To evaluate the agro-morphological variability of selected oat genotypes grown in the central highlands.
- ii. To investigate the extent of genotype by environment interaction and stability of oat genotypes grown in different environments.
- iii. To examine the effect of fertilizer levels on the agro-morphological traits, nutrient use efficiency and nutritional value of oat genotypes in pure stand.
- iv. To assess the effect of fertilizer levels on the agro-morphological traits, nutrient, and land-use efficiency and nutritional value of oat in oat/vetch mixed cropping system.

1.1.4 Research hypothesis

- i. Genotypes of oat grown under the same environmental and management conditions would have diversified morphological and agronomical traits.
- ii. Genotypes of oat grown under diverse environmental conditions would have diversified agro-morphological traits and yield performance.
- iii. Genotypes of oat grown under different fertilizer levels would have diversified agro-morphological traits, nutrient uptake and use efficiency and nutritional quality.
- iv. Oat grown in oat/vetch mixed cropping system with different levels of fertilizer would have diversified agro-morphological traits, nutrient uptake and use efficiency, productivity, land-use efficiency and nutritional quality.

1.1.5 Organization of the dissertation

The four specific objectives indicated above were addressed in different chapters that comprise part of this dissertation. The chapters were written as independent papers and somehow inter-related therefore; overlaps are most likely to occur in terms of contents and references among the chapters. The chapters are organized as follows:

Table 1.1 Outline of the dissertation

Chapter	Title
I	General Introduction
II	Literature Review
III	Agro-morphological variability and interrelationships among yield and yield-related attributes of oat (<i>Avena sativa</i> L.) genotypes
IV	Genotype by Environment interaction and yield stability of oat (<i>Avena sativa</i> L.) genotypes
V	Yield, nutrient uptake, nutrient use efficiency and nutritive value of oat (<i>Avena sativa</i> L.) genotypes grown in pure stand under different fertilizer levels
VI	Yield, nutrient uptake, nutrient and land-use efficiency and nutritional value of oat (<i>Avena sativa</i> L.) grown in oat/vetch mixed cropping system under different fertilizer levels
VII	Summary, Conclusions, and Recommendations

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Chapter II

Literature Review

Literature Review

2.1 Literature Review

2.1.1 Biology of oat

2.1.1.1 Taxonomy of oat

Oats belongs to the genus *Avena* and is classified as, Phylum-Spermatophyta, Class-Monocotyledons, Order-Cyperales, Family-Gramineae/Poaceae, and Tribe-Aveneae (Atman, 2017; Fu, 2018). The genus *Avena* is commonly named oat and comprises about 70 species; a few are cultivated (Atman, 2017; Harshita, 2018). The genus *Avena* is very large and diverse and includes diploid, tetraploid, and hexaploid species, with a basic chromosome number of seven (Atman, 2017; Kaur and Kapoor, 2017; Ashenafi, 2018; Harshita, 2018), but the diploid and tetraploid are mostly wild species. Other ploidy levels viz., triploids, pentaploids, octaploids, etc. which are not normally found in nature, can also occur as a result of hybridization and chromosome doubling (Sanjeet, 2018). The two common diploids ($2n=2x=14$) species of the genus *Avena* are *Avena strigosa* and *Avena nuda* (Atman, 2017) having the same genomic (AA) description (Leggett and Thomas, 1995). *A. strigosa*, the bristle-pointed oat or black oat, is used as a winter cover crop and a forage crop in subtropical and temperate climates (Atman, 2017). The diploid *A. strigosa* is hulled, but also has a naked type while *A. nuda* is a non-commonly cultivated and also a diploid naked oat. *A. abyssinica* H. and *A. vaviloviana* M. are examples of tetraploid ($2n=4x=28$) species of the genus *Avena* (Leggett and Thomas, 1995; Ashenafi, 2018) having the same genomic (AABB) designation (Leggett and Thomas, 1995) and they are endemic to Ethiopia (Ladizinsky, 1975; Leggett and Thomas, 1995). *A. abyssinica* is an erect growth habit that can grow up to 1.5m while, *A. vaviloviana* has prostrate to erect growth habit and reaches a height of 1.1m (Ashenafi, 2018). Some of the hexaploid ($2n=6x=42$) species of the genus *Avena* are *A. sativa* L. (common oat/ white oat), *A. sterilis* L. (sterile oat), *A. fatua* L. (wild oat), and *A. byzantina* C. (red oat) (Atman, 2017; Ashenafi, 2018).

All hexaploid oats are inter-fertile and considered as one biological species because they share the same genome (AACCDD) (Ladizinsky and Zohary, 1971; Baum, 1977). But with the advancement of sciences, the hexaploid species of oats have been classified into several taxonomic species (Ashenafi, 2018). *A. sativa* is a self-pollinated hexaploid crop ($2n=6x=42$)

with basic chromosome number $x=7$ having a genomic constitution of AACCCDD (Rines *et al.*, 2006). The cultivated oat (*A. sativa* L.) is more likely evolved from another hexaploid species, *A. sterilis* (Trabut, 1914) instead of *A. fatua* (Thellung, 1912; Zade, 1918). *A. sativa* L. and *A. byzantina* C., are the main oats grown for fodder and grain. They are hexaploids and modern cultivars may contain genetic material from these two species. They are autogamous, allohexaploid, and derived from the natural aggregation of the three ancestral diploid genomes AA, CC, and DD (Rines *et al.*, 2006). The progenitor of A genome is one of the *A. strigosa* species (Nishiyama, 1929) while the C genome is donated by *A. ventricosa* species (Rajhathy, 1966; Thomas, 1970). Though the origin of the D genome has not been precisely known, several research studies indicated that the A and D genomes are very closely related (Leggett and Markhand, 1995; Linares *et al.*, 1996; Linares *et al.*, 1998). Due to the absence of D genome diploid species, A genome diploid species could be the donor of both A and D genomes of hexaploid oat (Rajhathy and Thomas, 1974). Predominantly the two species of oats (*A. sativa* L. and *A. byzantina* C.) are cultivated in the world, however, the common oat (*A. sativa* L.) is the most important, contributing over 80% of the total world acreage (Atman, 2017). The domesticated *A. sativa* is extremely variable and widely distributed as compared to other oat species due to human selection and breeding activities (Ladizinsky, 2012a; Esvelt *et al.*, 2016).

2.1.1.2 Botany of oat

The cultivated oat is a self-pollinated annual grass (Purseglove, 1972; Rines *et al.*, 2006) having the seminal and adventitious root systems. The seminal roots originate during the development of the embryo and they consist of the primary root and two or three lateral roots that arise in the first node. Adventitious roots arise in the nodes of the main stem and the tillers just beneath the surface of the ground. The adventitious roots constitute the major root system of the crop. It has erect and erect to prostrate juvenile growth habit and can reach a height of up to 1.5 to 2 m at the full heading stage (Fekede, 2004). The stem has solid nodes while the elongated internodes of the mature stem are hollow in the center (Fekede, 2004) but during the early vegetative stage of development, the internodes are solid.

The position of the leaf on the oat plant and the types of plant parts produced are similar to those in other grasses. The leaves are solitary, alternate, two-ranked, and sessile (Fekede, 2004). A completely developed oat leaf consists of the terminal portion, the blade, a basal portion, the sheath, and a membranous appendage, the ligule. The blade is elongate, flat,

narrow, and linear. The margin of the blade and its tip is acute. The leaf sheath is an open cylinder. In the young plant, the sheath of the older leaves enclose the stem and younger leaves. At maturity, the leaf sheath encloses all portion of the elongated internode above it. The ligule is a thin membranous appendage that is continuous with the inner margin at the junction of the blade and sheath. The ligule extends upwards and clasps the stem. The lateral branches of the oat plant arise in the axis of the foliage leaves. The plane of the leaves of a tiller is the right angle to that of the parent axis. The leaf is a green or dark grayish-green color in an appearance before or at anthesis (Fekede, 2004).

The inflorescence of cultivated oat is either an equilateral (spreading) or a unilateral (one-sided) panicle is a many-branched, determinate inflorescence. The crop can be distinguished from other temperate cereals by the open spreading panicles bearing large pendulous spikelets, which may or may not be awned (Fekede, 2004). Inflorescence of the oat plant is a panicle composed of a central loose, open rachis with five to seven nodes, from which branches are arise bearing spikelets (Coffman, 1977). Each lateral branch terminates in a single apical spikelet. Another spikelet is born on the second or third-order of branches. Each panicle may have 20 to 50 spikelets. The crop has 2–3 florets per spikelets, non-disarticulates at maturity, and usually has a yellow lemma and awns may be present but reduced in size or absent (Ashenafi, 2018). The flowers are perfect zygomorphic, bracteates, and hypogynous. The flower consists of lemma and palea, two lodicules, three stamens, and one pistil. The oat kernel, also termed caryopsis or groat, is the part after the removal of palea and lemma. The kernel is generally covered with fine, silky hairs and includes the seed coat layers of cells, starchy endosperm, and the embryo.

2.1.2 Origin and domestication of oat

2.1.2.1 Origin of oat

Oat has no well-established center of origin, but most likely its center lies in the western part of the Mediterranean region (Ashenafi, 2018). The common oat (*A. sativa* L.) in its cultivated form is believed to be of Asiatic origin (Gibson and Benson, 2002; Ladizinsky, 2012a; Ankita, 2019). Other investigation indicated that its center of origin in Near East (Vavilov, 1926) but Trabut (1914) and Malzew (1930) also included the Mediterranean region as its center of origin especially for the cultivated red oat (*A. byzantina*). The cultivated oat (*A. sativa* L.) spread like a weed of wheat and barley from the Fertile Crescent

(a region extending from Israel to western Iran) to Europe (Leggett and Thomas, 1995; Ladizinsky, 2012b).

2.1.2.2 Domestication of oat

The production of cultivated oat (*A. sativa*) first appeared on the global agricultural scene probably in the last 4,000 years (Holland, 1997) and it was domesticated next to wheat and barley (Ashenafi, 2018). Oats spread to more temperate areas as weeds of emmer wheat (*Triticum dicoccum*) and, through their greater adaptability, eventually displaced emmer as a cultivated crop (Leggett and Thomas, 1995). The admixture of oat species in samples of emmer wheat from a range of western Asian countries was observed by Vavilov during explorations in 1916 (Jones, 1956). Some of these forms were similar to cultivated oat. Since oats were not cultivated in these regions, Vavilov proposed that their presence in the emmer samples indicated that they had originated in this region but their domestication occurred in more northerly latitudes. Most likely, domestication of oat occurred outside its center of diversity in northern Europe where the man had migrated following the Neolithic revolution (Murphy and Hoffman, 1992). During this migration, northern Europe was probably selected non-shattering grain from the weedy oat present as a contaminant in wheat and barley fields from the Middle East; as these species were introduced and grown as cereal crops (Ashenafi, 2018). The wild oat species *A. fatua* and *A. sterilis* are also distributed throughout these temperate areas as troublesome weeds. The domestication of oats is more generally associated with mid and northern Europe and its origin was dependent on the migration of other cereals (wheat and barley) to more temperate regions (Leggett and Thomas, 1995).

2.1.3 Importance of oat

2.1.3.1 Livestock feed

Oat is a useful annual cereal crop at higher altitudes in the tropics and grown throughout the cooler and wetter parts of the temperate region. It is a dual-purpose crop and is used as both forage and grain worldwide (Fekede, 2004; Suttie and Reynolds, 2004). Two cuttings are possible from a well-grown field of oat, the first cutting often used for feed and the crop then left for grain production (Fekede, 2004). The use of oat as forage or grain crop is a common practice in the world, having an excellent growth habit, quick recovery after cutting, and good quality herbage. Oat has assumed considerable significance as fodder as well as grain for human food and animal feed (Fekede, 2004; Suttie and Reynolds, 2004). It produces an abundance of excellent fodder at the time when other succulent better quality fodders are

scarce and it can be fed green and the surplus converted into hay and silage for use during the scarcity period. The green herbage of oat has adequate soluble carbohydrate as a result it can be easily converted into very good silage, which is preferred by all kinds of livestock. The feeding of livestock with oat forage enables to reduce the quantity of concentrate feeds hence this crop offers a valuable and economical means of maintaining livestock in good condition.

Oat is a decent source of protein, sugar, fiber, nutrients, and minerals, and green fodder contains around 10-12% protein and 30-35% DM (Ruwali and Deo, 2009). The chemical composition of oat on DM basis which harvested at milk stage contains 6.44 % crude protein, 28.72 % fiber, 53.20 % nitrogen-free extract, 2.31 % ether extract, 9.33 % total ash, 0.47 % calcium, 0.22 % phosphorus, 0.22 % magnesium, 0.52 % sodium, and 2.84 % potassium (Monika, 2017). The whole oat forage harvested at the soft dough stage has a mean of 79.0 g/kg DM ash, 60.7 g/kg DM crude protein (CP), 634.7 g/kg DM neutral detergent fiber (NDF), 420.3 g/kg DM acid detergent fiber (ADF), 65.5 g/kg DM acid detergent lignin (ADL), and 529.8 g/kg DM *in-vitro* organic matter digestibility (IVOMD) (Fekede *et al.*, 2008). Oat straw is also used as an animal feed because it is softer and has more digestible organic matter and metabolic energy to livestock than other cereal crops. It is a preferred feed and its straw is soft and superior to wheat and barley. Moreover, the straw is used as bedding material (Fekede, 2004) due to its softness and better absorbent nature.

The nutritional value of oat caryopsis is high as it is rich in protein especially lysine and oil. Oat is nutritious quality fodder for livestock and its grains give high energy when used as animal feed (Ruwali *et al.*, 2013). Moreover, oat grain makes a well-balanced concentrate in the ration for poultry, cattle, sheep, and other animals. Different studies also indicated that oat grain is used as livestock feed (Fekede, 2004; Getnet *et al.*, 2004; Gezahagn *et al.*, 2016; Nikoloudakis, 2016). The presence of the hull, which comprises about 25% of the grain weight, is well tolerated by ruminant animals although it reduces the energy density of the feed. Being a highly nutritious cereal, especially rich in fat, protein, fiber, vitamin B1, phosphorous and iron, it is used for human consumption as well as animals (Butt *et al.*, 2008). The nutritional value of oat is mainly attributed to its composition of protein, lipid, and fiber. Other studies also indicated that oat is a nutritious source of protein, fat, carbohydrate, fiber, vitamins, and mineral as well as antioxidants with beneficial effects on health (Peterson *et al.*, 2005).

2.1.3.2 Human food

The bulk of the oats produced in the world are used extensively as feed for livestock but only 17% of the world grain production is used as human food. Whole oat groat is considered as highly nutritious cereal for human consumption as it is a good source of unsaturated fatty acids, vitamins, dietary fiber, protein, antioxidants, and minerals and also serves as an excellent source of β -glucan (Varma *et al.*, 2016; Premkumar, 2017). For human consumption, oat is considered as the most important cereal crop used as an important source of essential nutrients throughout the world (Boczkowska and Tarczyk, 2013). Health-promoting effects of oat products have been approved by USFDA (1997). Oat is used for human consumption in the form of porridge, oatcakes, and other foods and eating oats and oats bran is a positive direction towards improving the diet since it is nutritionally superior to other cereals such as barley, wheat, maize and rice (Purseglove, 1972). The grain is dehulled before use, whereas husk (hull) after processing may be used in the food industry. Oat groat contains significant amounts of β -glucan that varies between 2.3 and 8.5 g/100 g (Welch *et al.*, 2000). The β -glucan in oat is distributed through the endosperm and is located in the endosperm cell walls constituting about 75% of the endosperm cell walls. Since oats are not suitable for bread making due to lack of gluten therefore often served as porridge, flakes, or breakfast cereals made from crushed or rolled oats. As oat flour or oatmeal, it is utilized in a variety of baked items like composite bread made from a mixture of oatmeal and wheat flour. Oats can be used as a soup thickener and its bran can be spread on salads, soups, and other foods to add fiber (Fekede, 2004).

The grains of oats are superior among other cereal crops due to the relatively high content of health beneficial lipid and protein composition. Increased oat consumption is often enhanced due to nutritional attributes including antioxidants and high soluble fiber (Marmouzi *et al.*, 2016). Oat has adequate soluble carbohydrates and fibers (Peterson *et al.*, 2005) and it provides one of the richest sources of the dietary soluble fiber β -glucan, providing 5.0 g (oatmeal) to 7.2 g (oat bran) per 100 g (Glore *et al.*, 1994). Nutrition experts believe that the β -glucan, the water-soluble fiber present in oat inhibits cholesterol build-up and hence helps in the prevention of heart disease (Whitehead *et al.*, 2014). Oat exerts beneficial effects on plasma glucose and insulin response, which is particularly important for the control of diabetes (Zhu *et al.*, 2016). Moreover, consumption of oat bran is believed to lower down cholesterol and possibly to reduce the risk of heart diseases (Anderson *et al.*, 2009; Satija and Hu, 2012) and it also has high phenolic content and anti-proliferative capacities (Butt *et*

al., 2008). Bran is the edible, outermost layer of the oat kernel and is produced by grinding clean groat or rolled oats and it is not more than 50% of the starting material. It has total β -glucan and dietary fiber not less than 5.5 and 16.0%, respectively with at least one-third of total dietary fiber is soluble fiber (Anonymous, 1989). Like oatmeal, oat bran contains B complex vitamins, protein, fat, minerals, and a heart-healthy soluble fiber called β -glucan. Oat bran contains 17.1% protein, 67.9% carbohydrates, 8.6% fat, 15–22% dietary fiber, 10.4% β -glucan, 1.3 mg niacin, 171 mg magnesium, 6.4 mg iron, 0.17 mg copper, 441 mg potassium and α -tocopherol less than 0.5 mg (Saunders, 1985; Marlett, 1993).

Oat has long been recognized as a good source of protein for human food. The protein concentration is relatively high, and the amino acids are well balanced than most cereal grain (Klose and Arendt, 2012). Oat contains a higher concentration of protein (15–20%) than most other grains when measured in the groat and its protein has a well-balanced amino acid content, which varies little with changes in protein content (Robbins *et al.*, 1971). The amino acid balance of oat protein is also superior to barley, wheat, maize, rice, rye, sorghum, and millet (Kellems and Church, 1998), and this is because of its primary storage protein is a globulin or legume-like protein. Globulins have a higher concentration of lysine and other essential amino acids than do typical cereal storage proteins. However, it is still relatively deficient in methionine, histidine, tryptophan, and lysine (Fekede, 2004). Similarly, starch is the main component of the oat grain and it is made up of amylose and amylopectin. Its content may vary depending upon the variety and growing conditions. The amylose content of oats ranges from 16 to 29 % (Mimoghtadaie *et al.*, 2009), and there are no known waxy. Oat starches have typical gelatinization characteristics, but have high shear susceptibility and tend to behave like waxy starches. They develop unusually high viscosity upon cooling. Cooled oat starches are clearer, less firm, more elastic, and more adhesive than other cereal starches.

Oat grain has a soft kernel and contains higher oil concentration (7%) which distributed throughout the seed, making its milling process more difficult than wheat and maize (Kirk and Sawyer, 1999). For animal feed, higher oil is better, as it is a denser energy source than carbohydrate. However, oat millers prefer low oil concentration for food products, because high oil products are more susceptible to rancidity and as a result shorten product shelf life (Fekede, 2004). Oat oil consists primarily of palmitic (16:0), oleic (18:1), linoleic (18:2), and linolenic (18:3) acids, with variation among genotypes and growing environments in the relative proportions (Zwer, 2010). The high concentration of monounsaturated oleic acid in

oat oil is favorable for its use as food oil. Oat oil contains tocopherols (Vitamin E) mainly α -tocotrienol and α -tocopherol, with trace amounts of other tocopherols (Marmouzi *et al.*, 2016). Tocopherols assist in the protection of cells against oxidation by free radicals and reduce lipid peroxidation (Fardet *et al.*, 2008). Besides the role of antioxidants, tocopherols can reduce serum cholesterol concentration and inhibit the growth of certain cancer cells (Aggarwal *et al.*, 2010). Oat contains primarily α -tocotrienol, in contrast to other grains. Oat is rich in the antioxidants α -tocotrienol, α -tocopherol, and avenanthramides, as well as total dietary fiber including the soluble fiber β -glucan (Oliver *et al.*, 2010). The tocotrienols are stronger free radical scavengers than tocopherols but are not absorbed as readily. Tocopherols are unevenly distributed within the grain, with α -tocotrienol located primarily in the endosperm, whereas α -tocopherol is found in the germ.

Oat Dietary fiber, consisting of cellulose, non-starch and non-cellulosic polysaccharides, and lignin, has been shown to protect against colorectal cancer. Dietary fiber can be divided into two groups based on water solubility. Both water soluble and insoluble fibers are important to health in different ways. Water-soluble fiber composed of polysaccharides, gums, pectin, arabinoxylan, and β -glucan. However, β -glucan is the major component of soluble fiber in oat (Lazaridou and Biliaderis, 2007). The soluble fiber from oatmeal and oat bran is very effective to lower blood cholesterol and normalize blood sugar levels due to the high content of β -glucan (Wood *et al.*, 1990; Wood *et al.*, 1991; Kahlon and Chow, 1997). The insoluble dietary fibers contain lignin, cellulose, and hemicellulose usually has high water holding capacity, which contributes to increased fecal bulk. Oat grain consists of about 1.8-7.9 % of mixed-linked β -glucan as a component of the endosperm cell walls (Saastamoinen *et al.*, 2004). Oat containing β -glucan has also been shown to slow the increase in blood sugar following a meal, an important characteristic for the dietary control of diabetes. The β -glucan is very important for the prevention of constipation, reduction in risk of colorectal cancer, lowering of serum cholesterol, regulation of blood glucose level for diabetic patients, and prevention of infectious disease (Shen *et al.*, 2016; Arena *et al.*, 2017). Oat with high β -glucan concentration is useful for food or as a raw material for fractionation and processing; however, low β -glucan concentration is desirable, particularly for young poultry because high β -glucan reduces the utilization efficiency of the feed. The β -glucan is concentrated in the bran and it is used in many food products. It has many other potential uses in the medical field, such as promoting wound healing, stimulating immune cell function, and protecting

and moisturizing skin. The dietary fiber might have important impacts on mineral balance (Idouraine *et al.*, 1996; Haack *et al.*, 1998).

The mineral content of oat is typical of other cereals, with minerals concentrated in the bran fraction. The major mineral contents of oats are manganese, phosphorus, copper, iron, selenium, magnesium, and zinc (Garg *et al.*, 2005). Manganese is present in the highest concentration, whereas copper is present in a smaller amount. The highest concentration of minerals was found in instant oat bran flakes and the lowest in extruded oat (Skibniewska *et al.*, 2002). Oat contains small but significant quantities of several vitamins such as thiamine, niacin, riboflavin, pyridoxine, folacin, biotin, and pantothenic acid. Oat also contains minor constituents, including tocopherols and avenanthramides that may have antioxidant properties and deliver health benefits to consumers (Fardet *et al.*, 2008). Most of the avenanthramides can be found in the oat groat and bran whereas, in the hull, they are present in limited amounts (Liu *et al.*, 2005). Avenanthramides may be responsible for the anti-irritant properties of oat lotions and relevant creams. Companies produce a colloidal oat extract, which is a complex mixture of phytochemicals including avenanthramides, flavonoids, saponins, and other bioactive compounds. This product protects sunburned skin, which makes it useful for cosmetic and personal care products (Sur *et al.*, 2008; Tiwari and Cummins, 2009). Other substances such as phenols, flavonoids, saponins, lignans, and sterols have antioxidant properties, but their concentrations in the soluble fraction of oat grains are very low compared to the avenanthramides and tocopherols.

2.1.4 Global oat production

Oat requires a cool and moist climate and it is best grown in temperate regions of the world as they are winter hardy in nature. It is also cultivated in subtropical and higher altitude areas of the world. World oat production is generally concentrated between Latitudes 35–65° N and 20–46° S. Oat ranked sixth in the world cereal grain production statistics following wheat, rice, maize, barley and sorghum (FAO, 2012) and ranked first in the world within the fodder production statistics (FAO, 2011). It is one of the most important crops in the world occupying a 9.85 million hectare area with seed production of 23.05 million tonnes and productivity of 2.34 tonnes per hectare during the 2018 cropping season (FAOSTAT, 2018). Continental level, Europe is the largest producer of oat followed by Americans, Asia, Oceania, Australia, and Africa during the 2018 cropping season (FAOSTAT, 2018). The production share of oat by region is dominated by Europe which produces 58.6% of the crop

followed by Americas producing 27.8% and Asia comes in third with just 7.2% during the same cropping season (FAOSTAT, 2018). The largest producer of oat in the world is Russia, which accounts for about 20.5% of the total global production (FAOSTAT, 2018) though it is chiefly a European and North American crop, as these areas have the cool moist climate to which oat is best adapted. During the same cropping season, Canada (14.9%), Spain (6.5%), Australia (5.3%), and Poland (5.1%) are the second, third, fourth, and the fifth-biggest producers of oat, respectively (FAOSTAT, 2018). The first five biggest oat producing countries contribute 52.2% of the world oat production during the 2018 cropping season (FAOSTAT, 2018). The largest oat producing country in Africa was Algeria followed by Ethiopia, South Africa, Morocco and Kenya with the production of 118,018, 45,849, 31,500, 21,424, and 3,633 tonnes, respectively, and they contributed near to 1% of the total world production during the same cropping season (FAOSTAT, 2018).

2.1.5 Oat production in Ethiopia

Among other cultivated forage crops, oat is widely utilized in the highland farming system of Ethiopia. It is best adapted to cool, moist climates and it grows satisfactorily from 1750 to 3000 meters (Fekede, 2004; Getnet *et al.*, 2004) but at lower altitudes, it is less suitable as tillering is limited and no dense canopy is formed (Fekede, 2004). Oat production, area coverage, and productivity varied considerably in Ethiopia (FAOSTAT, 2009-2018).

2.1.6 Oat research in Ethiopia

2.1.6.1 Germplasm introduction/collection and evaluation

Forage research as a national program was formally started with the establishment of the Institute of Agricultural Research (IAR) in the mid-1960s (Alemayehu and Getnet, 2012). Different indigenous forage species have been introduced/ collected by IAR/EIAR from different parts of the country as well as from abroad. Moreover, the International Livestock Research Institute (ILRI) has played a significant role in introducing various forage species in addition to its active involvement in the collection and evaluation of indigenous species, mainly legumes in the past (Fekede *et al.*, 2015). Different temperate and tropical forage species including oat were introduced by the Arsi Rural Development Unit (ARDU)/Chilalo Agricultural Development Unit (CADU) project which was established in 1967 at Asela and made significant contributions to the national agricultural research system in general and the forage and pasture research and development work in particular. Evaluation of oat varieties at Holetta and probably in Ethiopia was started towards the end of the 1960s (Getnet *et al.*,

2004). Nineteen oat genotypes were initially introduced from the USA in 1969 (IAR, 1970) and then 9,054 genotypes of oat were collected from different parts of the world (more than 55 countries) and introduced in the early 1970's through the support of the food and Agricultural Organization (FAO) of the United Nations (IAR, 1973; Astatke, 1976; Lulseged and Alemu, 1985) and 40 gain type oat which are used for food and feed were introduced in the early 1980s through the International Maize and Wheat Improvement Center (CIMMYT) to HARC (IAR, 1982) to broaden the oat genetic base for evaluation and selection of suitable varieties for the diverse agro-ecological conditions of the country.

The focus of oat research efforts over the last five to six decades has been on germplasm introduction/collection, evaluation, selection of promising varieties for the different agro-ecologies, micro-seed multiplication, on-farm demonstrations and promotions to users. The oat varieties introduced/ collected from different sources were evaluated for various desirable characteristics including adaptation to the prevailing climatic and soil conditions, ease of establishment, herbage productivity, seed yield potential, resistance to pests and diseases, forage quality, dual-purpose uses, multi-cut, intercropping with vetch, grown as a precursor to another crop like chickpea, and suitability for integration into the farming system. Different environmental determinants impose limitations on adaptations and overall performance of oat in the highland areas. These include low soil and air temperatures leading to slow establishment and growth, high rainfall, high soil acidity, low soil fertility, drainage problems (waterlogging) especially on vertisols, seasonal frost (October-January), disease (especially rust), and severe competition from weeds. Moreover, high population pressure and land shortage are a critical problem for oat production in the highlands of Ethiopia. To this effect, various adaptable and high yielding oat varieties have been identified and recommended for the high and mid altitudes of the country. Therefore, the evaluation of oat varieties which are producing high yield via adapting the various environmental and socio-economic factors is very important to select promising oat varieties for the diverse conditions of the country.

2.1.6.2 Selection, demonstration, and adoption

After rigorous screening and evaluation work, about six promising oat varieties including CI-8237, Jasari, Lampton, Grey-Algiers, CI-8251, and CI-8235 were selected and recommended for forage production in the highlands of Ethiopia in the mid-1970s and it has been anticipated that the oat which is being owned by smallholder farmers could belong to

either of the aforementioned varieties (Gezahagn *et al.*, 2016). Different oat varieties were tested, selected, and distributed based on their desirable traits, however, survey reports in the central highlands indicated that farmers do not distinguish oat varieties, they just recognized all the varieties as one (Getnet, 1999) and local farmers call oat as "Sinar", "Shalo" and "Shemame" on various localities in the central highlands (Getnet *et al.*, 2004). Although the initial aim of oat introduction to the farmers was for feed production, it has been realized that it is also being extensively grown as a food grain. However, it has been perceived that farmers have no awareness of the existence of different oat varieties with different merits and consequently they grow single variety for multipurpose uses (Getnet, 1999). The grain of oat makes part of the staple diet for humans in some parts of Ethiopia most commonly in Selale, Debre-Berhan, Sheno, Arsi, and Gojam (Lulseged, 1981; Getnet, 1999; Getnet *et al.*, 2004). Different research studies were conducted to generate the grain type oat varieties; accordingly, one-grain type (MoA, 2017) and two dual-purpose type oat varieties (MoA, 2015) have been nationally released. The EIAR and Regional Research Institutes, as the major actors of the National Agricultural Research System (NARS), have been actively involved in oat evaluation and selection. Moreover, other governmental and non-governmental organizations especially ARDU/ CADU and ILRI have also played remarkable roles in supporting the selection process of oat and development efforts.

Even though the feed is one of the major constraints to the livestock sector, improved forage/ oat technologies that were generated by research systems have not been adequately promoted and disseminated due to less focus given by the agricultural extension system and minimal efforts made by national agricultural research systems and private sectors, as a result, both awareness and adoption rates of these technologies have appeared to be very low despite the availability of several options of improved forage/ oat technologies recommended to various parts of the country. Despite this, various promising forage/ oat technologies had been promoted via the Fourth Livestock Development Project (FLDP) and utilized under varying scales in different parts of the country. Moreover, the national agricultural research system, higher learning institutes, Ethiopian seed enterprise, non-governmental organizations, and private sector like Aden field have been directly/ indirectly contributed to oat demonstration and adoption efforts. As there were no formal releasing mechanisms like that of other food crops, oat was demonstrated and seeds were distributed informally to farmers for forage production (Getnet *et al.*, 2004). In 2014 production year, the overall adoption rate of forage crops in Oromiya region is 10% and the highest adoption rate (35%) was recorded for oat-

vetch followed by elephant/Napier grass (15%) and tree lucerne (7%) (Agajie *et al.*, 2016). But the recent adoption study conducted in the same region in 2017 indicated that there is a slight increase in the last 3-4 years and the adoption rate has reached 12% due to extended promotion and dissemination of forage/ oat technologies to the producers through different stakeholders (Agajie *et al.*, 2018).

As the size of farmland increases by one hectare, the likelihood of adopting improved forage technologies including oat increases by 1.6% and the likelihood of adoption of forage technologies including oat increases by 6 and 4% in households with exposure to earlier experience on forage production and training on improved feeding practices, respectively, as compared to those who did not have such an opportunity (Agajie *et al.*, 2016). On the other hand, as a household gets access to credit services; the likelihood of adoption of improved forage technologies including oat declines by 5.6% and it was also noted that the likelihood of adopting forage technologies including oat declines by 6% for households with no exposure to extension services as compared to those who have exposure (Agajie *et al.*, 2016). The adoption intensity of improved forage technologies including oat is positively influenced by the size of cultivated land, training, and experience on forage production. However, it is negatively correlated with access to credit services and household income. For a one hectare increment in farmland, the proportion of improved forage including oat growers will increase by about 2% and the size of land allocated to forage crops will also increase by 0.5% and participation in training enhances improved forage including oat growers by 2.6% and the area allocated to forage production by 0.8%, however, with access to credit, improved forage including oat growers will decline by 3.5% and the area allocated to improved forages will decrease by 1% (Agajie *et al.*, 2016).

2.1.6.3 Varietal registration/ release

The ultimate objective of forage germplasm introduction, collection, and evaluation is to release and/or recommend superior varieties of different species for wider utilization mainly as a source of feed. However, forage research activities have been done without any formal variety releasing mechanisms like other food crops for a long period (Getnet *et al.*, 2004; Fekede *et al.*, 2015). Despite the absence of a formal variety releasing mechanisms in the past, nine forage varieties of various species including one oat variety (CI-8237) which were informally promoted and fairly accepted by the different users were registered in the crop variety register book of the Ministry of Agriculture (Fekede *et al.*, 2015). The variety of

release procedures and guidelines for forage crops have been established and implemented officially since 2009 in the country (Fekede *et al.*, 2015). Seventy-three forage varieties have been released by NARS following the variety release guidelines between 2009 and 2022 years. So far, a total of 82 forage varieties including 12 forage oat varieties have been officially registered in the crop variety register book (EAA, 2022). Moreover, 4 food type oat varieties have been released for acid prone areas (EAA, 2022). The forage yield potential of released oat varieties usually varied from 7.5 to 19.5 t/ha DM with a mean of 11.9 t/ha. Similarly, the seed yield of released oat varieties varied from 1.5 to 4.1 t/ha with a mean of 3.2 t/ha. Besides their forage and seed productivity, all the released fodder oat varieties are also nutritionally superior to that of crop residues and natural pasture which are the dominant feed resources in the country. The released oat varieties with their forage and seed productivity are indicated in Table 2.1.

Table 2.1 Forage and seed productivity of officially released oat varieties

SN	Variety	Mean forage yield (t/ha)	Mean seed yield (t/ha)	Year of release	Breeder/ Maintainer
1	Legend-567	10.3	3.9	2022	HARC
2	FL-720	13.1	4.1	2022	HARC
3	Ezo ote (Acc# ILRI-5527)	12.6	3.6	2022	Arbaminch ARC
4	Enat (Ajay, NZ#: 3107; 2010AFRI core)	-	4.1	2022	Adet ARC
5	Hulegeb (Goslin)	-	3.9	2019	Adet ARC
6	Tena (Souris: ND961161)	-	3.5	2019	Adet ARC
7	Was (CI-1506)	19.5	2.5	2019	HARC
8	Walqaa (SRCPX80Ab2596)	7.5	1.5	2019	HARC
9	Bate (ILRI-5453)	8.6	3.3	2018	BARC
10	Sorataf (79Ab382(TX)80SA94)	10.7	3.2	2017	HARC
11	SRCPX80Ab2806	13.5	3.1	2015	HARC
12	SRCPX80Ab2291	13.8	4.1	2015	HARC
13	CI-8251	12.8	2.9	2013	HARC
14	Bona-bas (IAR-PI. 1660)	10.3	2.1	2011	SARC
15	Bonsa (IAR-PI. 79Ab384)	10.8	2.9	2011	SARC
16	CI-8237	11.5	3.1	1976	HARC
Mean yield		11.9	3.2		

HARC= HOLETTA Agricultural Research Center; **BARC**= Bako Agricultural Research Center; **SARC**= Sinana Agricultural Research Center; **ARC** = Agricultural Research Center. Variety # 4, 5, 6, and 10 are food oat released for acid prone areas while variety # 11 and 12 are dual type oat but other released varieties are forage type oat. (Source: EAA, 2022).

2.1.7 Genetic diversity of oat

2.1.7.1 Genetic variation

Variability is defined as the existence of alterations among individuals due to differences in their genetic composition and/ or the environment in which they are raised (Allad, 1960). All the variability present in the biological systems can be attributed to genotypic and/or

environment (Welsh, 1981). The effectiveness of selection depends upon the variability present among the individuals in a population and the extent to which it is heritable (Singh, 2001). Development in plant breeding depends on variability because superior genotypes can be selected only from heterogeneous populations, but homogeneity is desirable in the final product of breeding outcomes. The amount of variation present in any population is measured and expressed in terms of variance (Falconer and Mackay, 1996). Phenotypic variability, which is observable variation present in a character of a population, includes both genotypic and environmental variation and, as a result, its magnitude varies under different environmental circumstances (Singh, 1993). Genotypic variability, on the other hand, is the component of variation which is due to the genotypic differences among individuals within a population and is the major source of variation in a breeding program (Singh, 2001). If the character expression of two individuals could be measured in the environment identical to both, differences in the expression would result from genetic variation (Welsh, 1981). The occurrence of genetic variability among the individuals due to differences in the genetic composition is very important for rapid and efficient crop improvement through plant breeding because superior genotypes can be selected from the heterogeneous population and proper management of this variation could result in remarkable impact in the performance of the crop (Sharma, 1998).

Estimates of genotypic and phenotypic coefficients of variation are used to study the variability that exists in a given population (Kalloo, 1988). The magnitude of variability can be estimated through determining the phenotypic, genotypic, and environmental coefficient of variations (Singh and Singh, 1975). The selection of plants for the character of interest would be ineffective if the environmental variation is too high because the genetic variation can be highly influenced through this variation. Though some environmental variations can be reduced by proper experimentation, its total elimination is impossible because it includes all the non-genetic variance and much of these are beyond experimental control (Falconer, 1981). The component of genetic parameters such as the genotypic coefficient of variation and phenotypic coefficient of variation is very important to detect the amount of genetic variation exists in the genotypes, however; environmental factors are partially controllable through proper implementation of the research. Generally, the achievement of crop improvement through breeding programs largely relies on the extent of genetic and phenotypic variability existed among individuals in the population and variability can also

be created artificially through hybridization technique by crossing genetically distant parents.

Different research studies conducted in Ethiopia indicated that there is a considerable variation for most measured traits in oat genotypes (Fekede, 2004; Getnet *et al.*, 2004; Gezahagn *et al.*, 2016; Ashenafi, 2018). Getnet *et al.* (2004) studied the variability among twenty-one oat genotypes and found that there were significant variations for forage dry matter yield, plant height, number of days to forage harvesting, leaf proportion, stem proportion, panicle proportion, grain yield, and thousand kernel weights. Twenty oat genotypes were evaluated at Holetta and the genotypes showed a considerable amount of variation in a number of tillers per plant, days to different growth stages (boot, head, milk, soft dough, and grain maturity), vegetative growth period, grain filling period, plant height at different growth stages, leaf, stem and panicle proportions and their yields at different growth stages, total forage dry matter yield, leaf to stem ratio at different growth stages, grain yield, thousand-grain weight, straw yield, harvest index, straw to grain ratio and nutritional qualities (Fekede, 2004). Two forage type and two-grain type oat varieties along with local variety were tested at Girar-Jarso, Wuchale, and Jida woredas of North shewa for two consecutive years and marked differences among genotypes were recorded in plant vigor, plant height at forage harvesting stage, forage dry matter yield, and seed yield (Gezahagn *et al.*, 2016). The quantitative characters measured in eighty-two oat genotypes indicated the presence of significant variations among genotypes for the number of nodes per plant, flag leaf length, length of panicle, plant height, days to maturity, and biological yield (Ashenafi, 2018). Oat genotypes differed significantly in yield, growth, and quality parameters (Bahadur and Choubey, 2008; Shehzad *et al.*, 2011; Khan *et al.*, 2014).

Genetic diversity studied in oat genotypes indicated that there was a significant difference among the genotypes for green fodder yield (Naeem *et al.*, 2007; Ahmed *et al.*, 2011; Arora, 2013; Sofi *et al.*, 2014); the number of tiller per meter row (Naeem *et al.*, 2007; Sofi *et al.*, 2014); seed yield (Ahmed *et al.*, 2011; Sofi *et al.*, 2014); forage dry matter yield (Arora, 2013); plant height (Naeem *et al.*, 2007; Ahmed *et al.*, 2011); and days to 50% flowering, number of spikelet per panicle, panicle length, number of leaves per plant, and leaf stem ratio (Ahmed *et al.*, 2011). High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was recorded in oat genotypes for number of tillers per meter row, green fodder yield and dry matter forage yield (Kumar *et al.*, 2007; Singh and Singh, 2011; Sangwan *et al.*, 2012; Dubey *et al.*, 2014); grain yield per plant and number of grains

per panicle (Kumar *et al.*, 2007; Vishwakarma *et al.*, 2007; Chakraborty *et al.*, 2014; Surje and De, 2014); peduncle length and flag leaf length (Kumar *et al.*, 2007; Chakraborty *et al.*, 2014); the number of leaves per plant, internode length, number of nodes per plant (Kumar *et al.*, 2007); plant height (Vishwakarma *et al.*, 2007; Singh and Singh, 2011); harvest index (Mall *et al.*, 2005; Bind *et al.*, 2016); and thousand-grain weight (Shankar *et al.*, 2002). A significant amount of genetic variation for forage yield, plant height, leaf attributes, growth habit, days to bloom, number of spikelets per panicle, and floral number/ panicle was observed in oat genotypes (Bahuguna and Verma, 2004; Arora *et al.*, 2009).

2.1.7.2 Heritability and genetic advance

Heritability can be defined as the genetic portion of the total phenotypic variability which is transmitted from parent to progeny (Allard, 1960). It is also defined as the measure of the correspondence between breeding values and phenotypic values (Falconer and Mackay, 1996). In general, the degree to which the variability of a character is transmitted to the progeny is referred to as its heritability (Brigges and Krowles, 1967). Heritability represents the ratio between genetic and all factors (including non-genetic ones) that influence the variability (Bernardo, 2002). Allard (1960) defines heritability in a broad sense as the proportion of the total variability that is due to genetic causes, or the ratio of genetic variance to the phenotypic variance. The extent to which a phenotype is determined by its genetic makeup (genotype) is called heritability in the broad sense. At the gene level, broad-sense heritability is the proportion of the total variance that is attributable to the average effects of genes and this is what determines the degree of resemblance between relatives. Heritability expressed as a percentage of an additive component of variance is referred to as narrow-sense heritability. If the genetic variation in a progeny is large about the environmental variation, then heritability will be high; or if the genetic variation is small about the environmental variation, then heritability will be below. Thus, the relative degree of genetic and environmental variation in the population can be determined by estimation of heritability in the broad sense (Marwede *et al.*, 2004; Rafi and Nath, 2004). Heritability of a trait does not depend only on genetic factors, it also depends on the environmental effects to which an individual is subjected (Falconer, 1981). The greater the proportion of the total variability that is due to environment, the more difficult it would be to select for inherited differences due to the masking effect of the environment on the genotypic effects (Singh and Singh, 1975). On the other hand, if environmental variability is small about genotypic differences, the selection will be efficient because the selected character will be transmitted to its

progeny due to a relatively small contribution of the environment to phenotype. However, the yield is greatly influenced by the environment, the heritability of yield itself is low (Hebblethwaite, 1983).

Heritability by itself does not indicate the amount of genetic progress that would result from selecting the best individuals (Johanson *et al.*, 1955). But the estimate of heritability in conjunction with genetic advance can provide the expected genetic gain in the next generation because it is not always necessary that high heritability will be associated with high genetic advance (Johnson *et al.*, 1955; Allard, 1960; Swarup and Chaugale, 1962; Amin *et al.*, 1992; Ramanjinappa *et al.*, 2011). High heritability value would be obtained with genotypes having small/large genetic variance, but genetic progress would be larger with larger genetic variance (Johnson *et al.*, 1955; Allard, 1960). Heritability estimates together with genetic advances are essential to start an efficient breeding program because they give the amount of advance to be expected from selection (Atta *et al.*, 2008). Genetic advance, which is the product of heritability, genetic variability, and selection intensity, can provide the estimate of the expected gain for a particular character through selection (Burton and Devane, 1953; Allard, 1960; Hamdi *et al.*, 2003). Genetic advance under selection measures the difference between the mean genotypic values of the selected population over the mean genotypic value of the original population (Allard, 1960). High estimates of heritability with high genetic advance values can be used as an efficient indicator for the phenotype-based selection (Poehlman and Sleper, 1995; Kebebew *et al.*, 2001). Johnson *et al.* (1955) and Allard (1960) suggested that heritability is not enough in predicting the effectiveness of selection unless otherwise it is considered along with genetic advance.

High heritability along with high genetic advance in oat genotypes were recorded for plant height (Singh, 1999; Bibi *et al.*, 2012); number of leaves per plant and leaf to stem ratio (Singh, 1999); number of tillers per plant (Singh, 1999; Mall *et al.*, 2005; Bibi *et al.*, 2012); days to 50% flowering (Bibi *et al.*, 2012); green and dry forage yield (Singh, 1999; Shankar *et al.*, 2002; Mall *et al.*, 2005; Chakraborty *et al.*, 2014; Krishna *et al.*, 2014; Bind *et al.*, 2016); number of grains per panicle (Mall *et al.*, 2005; Chakraborty *et al.*, 2014; Surje and De, 2014; Bind *et al.*, 2016); seed yield (Mall *et al.*, 2005; Chakraborty *et al.*, 2014; Surje and De, 2014); flag leaf length (Chakraborty *et al.*, 2014; Surje and De, 2014); peduncle length (Chakraborty *et al.*, 2014); panicle length and 1000 grain weight (Krishna *et al.*, 2014); and harvest index (Bind *et al.*, 2016) which revealed that these traits might be under control of additive gene effects and therefore they are more reliable for effective selection

whereas, low heritability coupled with low genetic advance was observed for 1000-grain weight indicating that the environment mostly affected this character (Mall *et al.*, 2005). Pundhir *et al.* (2008) studied the heritability and expected genetic advance in oat genotypes across four environments revealed moderate to high estimates of heritability coupled with high genetic advance for most of the traits. High heritability associated with equally high genetic advance is mainly due to additive gene effect, but if the heritability is due to dominance and epistasis, the genetic advance would be low (Panes, 1957).

2.1.8 Genotype by environment interaction

In studying genotype by environment interaction (GEI), it is important to define the basic components of phenotypic variability, the genotype, the environment, and the interaction of the genotype and the environment. Genotype refers to any of pure-line variety, clone, inbred-line, hybrid variety, open-pollinated variety, composite variety, synthetic variety, elite breeding lines, and others on which the breeder used for investigation. The genotype is a fixed character of the organism as a result it remains constant throughout life and it is unchanged by environmental effects but the phenotype changes continually and the direction of that change is a function of the sequence of environments that individual experiences (Suzuki *et al.*, 1981). Genotype refers to an individual's genetic makeup whereas phenotype refers to the physical appearance of an individual, which may be observable at a physical, morphological, anatomical, or biological level (Kang, 1993). About the comparison of plant material in a set of multi-environment yield trials, the term genotype refers to a cultivar that is genetically homogenous (pure lines or clones) and heterogeneous (open-pollinated populations) rather than to an individual's genetic make-up (FAO, 2002). The phenotype of an individual is determined by both the genotype and the environment, these two effects are not always additive which indicates that genotype by environment interactions are present (Baker, 2002). The phenotype of an individual is determined by both the genotype and the environment; these two effects are not always additive which indicates that GEI, are present. Environment refers to the total conditions surrounding the living organisms that affect the plant growth in the growing season (Kang, 1998) and agricultural context, it is defined as a general term that covers conditions under which plants grow and may encompass locations, years, management practices or all combinations of these factors (Fehr, 1991; Romagoza and Fox, 1993). The GEI refers to the change or modification of genetic factors by environmental factors in which the plants grow (Kang, 1998; Tarakanovas and Ruzgas,

2006; Dia *et al.*, 2016) and it is very important for crop improvement (Eberhart and Russell, 1966).

Genotypes grown over locations react differently to both biotic and abiotic factors (Crossa *et al.*, 1999). An interaction occurs when genotypes differ in their response to a change in environments. Change in ranks of genotypes through environments indicates GEI and lack of stability in the trait under study (Crossa, 1990). The association between the environment and the phenotypic expression of a genotype constitute the GEI. When GEI occurs, factors present in the environment as well as the genetic constitution of an individual, influence the phenotypic expression of a trait (Basford and Cooper, 1998). The GEI results in inconsistent performances among the genotypes across environments due to differences in edaphic, biotic, and abiotic factors (Dixon *et al.*, 1994; Abdurahman, 2009; Gul *et al.*, 2014). Significant GEI results from the changes in the magnitude of differences between genotypes in different environments or changes in the relative ranking of the genotypes (Falconer, 1952; Crossa, 1990; Fernandez, 1991). The presence of GEI complicates the selection of superior and most stable genotypes and it is an important consideration in plant breeding programs because it reduces the progress from the selection in any one environment (Yau, 1995). Information on the adaptation and stability of the genotypes over the years and locations is useful for recommending the genotypes that should be grown under particular environments and predicting the yield expectations of the test genotypes. A Genotype is considered the most stable one if it has a high mean yield, but a low degree of fluctuation in yielding ability when grown over diverse environments (Arshad *et al.*, 2003). Hence, GEI is critical only if it involves significant crossover interactions (Becker and Léon, 1988). The impact of an environmental factor on different genotypes may vary implying that the productivity of plant may also vary from one environment to the next. Therefore, the breeding plans may focus on the GEI to select the best genotype for a target environment (Bondari, 2015). The concepts of genotypic stability are either biological or agronomic (Becker, 1981). Biologically, a genotype with a minimum total variance under different environments is considered to be stable (Hanson, 1970). An agronomically stable genotype has a minimum interaction with environments but responds favorably to the improved environment (Eberhart and Russell, 1966).

There are two possible strategies for developing cultivars with low GEI. The first is partitioning off a heterogeneous area into smaller, more homogenous sub-regions. However, even with this refinement, the level of interaction can remain high because breeding areas do

not reduce the interaction of genotypes with locations on years (Eberhart and Russell, 1966). The second strategy for reducing GEI involves selecting cultivars with better stability across a wide range of environments to better predicted genotypic behavior (Eberhart and Russell, 1966). Multi-location variety trials play a decisive role in the effort to develop high yielding varieties adapted to a wide range of environments. According to Allard and Bradshaw, (1964) environmental variable is categorized into predictable and unpredictable variations. The predictable variations are those, which can be modified by human interference, such as planting time, plant density, rate of nutrient application, etc.; whereas, the unpredictable factors are those fluctuations in weather, such as, amount and distribution of rainfall, relative humidity, and temperature. Under predictable environmental variation, breeders can develop suitable varieties because environmental variation is defined. However, year-to-year fluctuations cannot be predicted in advance as a result breeders can hardly aim their programs to develop varieties suited to particular years (Dabholkar, 1999), so developing genotypes for high genotype by year interaction is more complicated than GEI. The aim of the breeding program should, therefore, be to develop widely adapted genotypes that can withstand unpredictable environmental variations (Dabholkar, 1999) because the predictable variations can be corrected through appropriate management practices.

The information generated through GEI studies may assist crop ecologists, agronomists, and plant breeders to define ecological regions, mega-environments, and ecotypes (Annicchiarico *et al.*, 2011). The GEI has been grouped into crossover and non-crossover interactions (Baker, 1990). The GEI is considered as crossover (qualitative) interaction if it leads to a change in the relative ranking of genotypes in different environments. On the other hand, the non-crossover (quantitative) GEI refers to changes in the magnitude of genotype performance, but rank order of genotypes across environments remains unchanged, i.e., genotypes that are superior in one environment maintains their superiority in other environments. The main feature of crossover interaction is intersecting lines in a graphical representation and if the lines do not intersect, there is no crossover interaction (Kang, 1998). Crossover interaction is more important than non-crossover interaction in plant breeding because it affects the genotypes to be selected in a given environment (Baker, 1990). Such interaction has strong implications for breeding and also suggests that genotypes are specifically adapted to environments (Singh *et al.*, 1999). The non-crossover interaction, on the other hand, influences the nature and magnitude of components of genetic variances and other related parameters like heritability and genetic advance (Alberts, 2004). The non-

crossover interactions indicate that either the genotypes are genetically heterogeneous but test environments are more or less homogeneous or the genotypes are genetically homogeneous but environments are heterogeneous. Understanding the extent of GEI is useful for effective allocation of resources and for the characterization of genotype responses to variable environmental conditions (Mosisa, 1999; Tiruneh, 2000; Mulusew *et al.*, 2008). Moreover, understanding the causes of GEI can be used to establish breeding objectives, to identify ideal test conditions, and to formulate recommendations for areas of optimal cultivar adaptation (Dimakatso, 2006). It can also help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine-tuning the breeding programs (Kang and Magari, 1996). Genotypes that show both low GEI and high yields are desirable for farmers, indicating that the environment has less effect on them and their higher yields are largely due to their genetic composition (Basford and Cooper, 1998). Identification of causal factors of the GEI effect and quantification of unexplained variation is the prime importance for selecting or recommend environmentally specific genotypes (Shaffi *et al.*, 1992; Signor *et al.*, 2001).

Mega-environments are defined as environments with similar “biotic and abiotic stresses, cropping system requirements, consumer preferences, and volume of production” (Braun *et al.*, 1996). A cluster of environments or locations, which constantly share the same best cultivar, is called mega-environments (Yan and Rajcan, 2002). Grouping of the target environments into meaningful mega-environments and using different genotypes for different mega-environments is the only way to utilize positive GEI and avoid negative GEI analysis (Yan *et al.*, 2000). Stability is defined as the ability of a genotype to avoid substantial fluctuation in performance over a range of environments (Eberhart and Russell, 1966). It is a measure of variation between the potential and actual yield of a genotype across changing environments. A genotype is considered to be more adaptive or stable if it has a high mean yield with a low degree of fluctuations in yielding ability when grown under diverse climatic conditions (Muhammad *et al.*, 2003; Tarakanovas and Ruzgas, 2006). Becker and Leon (1988) distinguished two basic concepts of phenotypic stability: the biological/ static concept, which refers to the constant performance of a genotype over a wide range of environments and the agronomic/ dynamic concept, which states that a stable genotype should always give high yield expected at the level of productivity of the respective environments.

To identify stable genotypes, the GEI must be partitioned into stability statistics that are assigned to each genotype evaluated across a range of environments. Different stability indices have allowed researchers to identify widely adapted genotypes for use in breeding programs and to improve recommendations to growers (Yayeh and Bosland, 2000). The additive main effects and multiplicative interaction (AMMI) method combines the additive main effects from analysis of variance and the multiplicative effects from principal components analysis into a unified approach (Gauch, 1988). It clarifies the GEI and summarizes patterns and relationships of genotypes and environments (Zobel *et al.*, 1988; Crossa *et al.*, 1990). The most recent method, the genotype plus GEI (GGE) biplot model, provides a more complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents mean performance and stability, as well as identifying mega-environments (Yan, 2001; Yan and Kang, 2003; Ding *et al.*, 2007). The GGE biplot can be useful to display the which-won-where pattern of the data that may lead to identifying high-yielding and stable cultivars and discriminating and representative test environments (Yan, 2001).

2.1.9 Effect of NP fertilizers on sole oat performances

2.1.9.1 Agro-morphological response of oat to NP fertilizers

The deficiency of N adversely affects the quantity and quality of forage crops. At the same time, excessive quantities of N tends to cause a succulent plant condition, which may increase plant susceptibility to disease and lodging. The level of N influences the green foliage, dry matter yield, nutrient contents, and their uptake by oat crop (Kherawat *et al.*, 2012). Each successive increment in N level up to 150 kg/ha significantly increased yield contributing characters like plant height, tillers per meter row length, and leaf area index of oat (Bali *et al.*, 1998). Rana *et al.* (2002) also observed that plant height, the number of tiller/m row length, and green forage production of forage oat increased significantly with each increment of 40 kg N up to 120 kg N/ha. The maximum plant height, number of tillers/m row length and dry matter accumulation of oat were found with the application of 120 kg N/ha (Malik *et al.*, 2015). Application of N in oat significantly enhanced green and dry forage yields, with every successive increase in levels of N (Joon *et al.*, 1993; Hasan and Shah, 2000). Patel and Rajogopal (1998) reported that the application of N up to 75 kg/ha increased the green and dry matter yields but the significant response was recorded only up to 50 kg/ha. Bali *et al.* (1998) reported that markedly increased green and dry forage yields

of oat with a successive level of N from 0 to 150 kg/ha. They found that the mean green forage yield increased by 31.9% and dry matter yield by 9.6% with each increased level of N between 50 to 100 kg/ha over the control. Midha *et al.* (1999) revealed that the average green forage yield and dry matter yield of oat increased significantly with increased N up to 70 kg/ha, however, the application of 80 kg/ha resulted in a sharp decline in green forage yield. Joon *et al.* (1993) observed that the grain yield of oat increased only up to 80 kg N/ha and decrease thereafter with increasing N up to 160 kg/ha.

Plant height increased significantly with P application (Khan *et al.*, 2005) and the highest plant height was recorded at 75 kg/ha (Bhilare and Joshi, 2007; Jat *et al.*, 2015). Similarly, P application at 75 kg/ha gave better leaf length, leaf width, leaf to stem ratio, leaf area per plant, and leaf area index (Bhilare and Joshi, 2007). An increase in P levels from 0 to 40 kg/ha increased the green fodder yield significantly (Singh *et al.*, 1995; Luikham *et al.*, 2014). Highest green forage yield and yield-related components were found when P was applied at 80 kg/ha (Roy and Khandaker, 2010; Farooq, 2016). The highest dry fodder yield was attained with the application of 40 kg P₂O₅/ha (Luikham *et al.*, 2014) and also it was the highest when P was applied at 60 kg/ha (Malakar *et al.*, 2009). Nakagawa *et al.* (2001) reported that the application of P fertilizer increased the panicle seed number of main culms and number of the tiller. Roy *et al.* (1992) observed that grains per panicle, 1000 grains weight, and grain yield were increased significantly up to 60 kg P₂O₅/ha but straw yield increased significantly only up to 40 kg P₂O₅/ha. Lapa *et al.* (1998) observed that the highest grain yield was obtained with 50 kg P₂O₅/ha. Grain and straw yields significantly increased up to 30 kg P₂O₅/ha (Sharma *et al.*, 2001) and these yields also significantly increased with application up to 40 kg P₂O₅/ha (Khanday *et al.*, 2009). Similarly, Singh *et al.* (1995) also reported that an increase in P levels from 0 to 40 kg/ha increased the grain and straw yields significantly.

Application of 50 kg N/ha and 40 kg P₂O₅/ha gave the highest plant height and number of tillers over the lower doses (Singh *et al.*, 2002). Patel and Rajagopal (1998) indicated that the application of 50 kg N/ha and 40 kg P₂O₅/ha in oat crop is beneficial to get higher forage production. Singh *et al.* (1989) observed that maximum forage production was recorded under combined application of 90 kg N/ha and 50 kg P₂O₅/ha followed by 90 kg N/ha and 25 kg P₂O₅/ha with minimum 30 kg N/ha and 0 kg P₂O₅/ha. Singh *et al.* (2002) also observed that the highest green fodder and dry matter yield were obtained with an application of 80 kg N/ha and 40 kg P₂O₅/ha. Tripathi (1993) reported that application of 90 kg N/ha and 30 kg

P₂O₅/ha in a combined way gave higher total green fodder, dry matter and crude protein yields than 50 kg N/ha and 45 Kg P₂O₅/ha. Sood and Kumar (1994) observed that green forage and dry matter yields increase up to 75 kg N/ha and 75 kg P₂O₅/ha. Moreover, the combined application of fertilizer increased the grain yield and the highest grain yield was obtained with 60 kg N/ha and 45 kg P₂O₅/ha as reported by Kubresh and Bezsilko (1990). Application of fertilizer increases the grain yield and the highest yield was obtained with combined application of 60 kg N/ha and 60 kg P₂O₅/ha (Salmina and Makarova, 1988). Combined application of 60 kg N/ha, 45 kg P₂O₅/ha, and 90 kg K₂O/ha gave the highest grain yield (Kubresh and Bezsilko, 1990). The optimum grain yield was obtained with a combined effect of 40 kg N/ha and 30 kg P₂O₅/ha (Mukherjee *et al.*, 1981).

2.1.9.2 Variation in oat nutrient uptake and use efficiency

The ability of a genotype to give higher yield under nutrients limiting condition may be related to the ability to take up more nutrients from the soil under nutrients limiting condition (uptake efficiency) or the ability to produce higher dry matter and grain yield per unit of nutrients in the plant tissue (utilization efficiency) or a combination of both. Uptake of nutrients by crops in an adequate amount and proportion is very important for producing higher yields. Similarly, the distribution of absorbed or accumulated nutrients in shoot and grain is associated with yield improvement (Fageria and Baligar, 2005a). Nutrient use efficiency can be defined as the maximum economic yield produced per unit of nutrients applied or absorbed by the plant. Nutrient concentration in plant tissue varied with plant tissue analyzed (leaves, shoot, or whole plant), plant age, dry matter or grain yield level, crop species or genotypes within species, crop management practices, and environmental factors (Fageria and Baligar, 2005b; Fageria and Barbosa, 2006). The concentration of nutrients (N and P) is higher in the grain than in the shoot at harvest, indicating translocation of nutrients from shoot to the grain in cereals as well as in legumes. During grain filling, the N and P contents of the non-grain tissue generally decrease while the N and P contents of grain increase (Wilhelm *et al.*, 2002). However, shoot dry weight increased with age advancement up to the flowering growth stage and then decreased (Fageria and Baligar, 2003). The decrease in shoot dry weight at harvest is related to the translocation of assimilates from the shoot to panicle during flowering to maturity growth stages (Fageria *et al.*, 1997).

The application of N fertilizer increased N concentration and its uptake in oat forage yield (Sood and Kumar, 1994). Application of N fertilizer increased the N content of oat grain and

straw up to 100 kg N/ha (Kubresh and Bezsilko, 1990; Sharma *et al.*, 2001). Total uptake of N in oat fodder was highest with the application of 80 kg N/ha as reported by Singh *et al.* (1995). The grain N concentration in oat increased significantly with applied N, on an average of 0.12% per 40 kg N/ha (Chalmers *et al.*, 1998). The highest nitrogen content and uptake in oat were recorded with the application of 120 kg N/ha (Verma, 2003; Devi *et al.*, 2010). Singh *et al.* (1996) observed that the N application increased the P content of the forage. Sood and Kumar (1994) reported that the application of P fertilizers increased P concentration and uptake. Singh *et al.* (1995) revealed that the total P uptake of forage was highest with 80 kg N/ha application. Sharma *et al.* (2001) reported that successively increased in P levels up to 60 kg/ha increased the P content of the forage. Salmina and Makavora (1988) obtained the highest P content in oat grain with a combined application of 60 kg N and 60 kg P₂O₅/ha.

2.1.9.3 Oat nutritional quality response to nutrient application

The nutritive value of oat is affected by genotypes, soil factors, weather conditions, and management conditions which include fertilizer application, seeding rate, cutting stage, and others. Thakuria and Gogoi (2001) reported that the crude protein yield in oat increased with an increase in levels of N. Singh *et al.* (1997) reported that the increase in N levels from 0 to 150 kg/ha in oat produced an increase in crude protein from 7.23 to 10.87%. They found that the crude protein contents of 7.2, 8.8, 10.3 and 10.9% with each application of 0, 50, 100, and 150 kg N/ha, respectively, indicating an increasing trend in crude protein content with increasing levels of N fertilizer. Mandal *et al.* (2000) reported that application of nitrogen above 40 kg/ha increased crude fiber content in oat. Naveen and Sood (1995) reported that the crude fiber content in oat increased with increasing application of N up to 60 kg/ha. Shukla and Lal (1994) observed that increasing N levels up to 75 kg/ha increased the crude protein yield of oat. The crude protein content and crude protein yield of oat significantly increased with each successive increase in N levels from 0 to 80 kg/ha (Das and Sheoran, 1995). Singh *et al.* (1999) reported that crude protein content in fodder yield oat significantly increased with an increase in N level from 60 to 120 kg/ha. Agrawal *et al.* (2000) pointed out that increasing the rate of N application from 50 to 150 kg/ha increased the crude protein yield of oat. Sharma *et al.* (2001) recorded significantly higher N and crude protein contents in oat due to the application of 100 kg N/ha. Kakol *et al.* (2003) reported that increased crude protein and crude fiber contents of oat with increased application of N up to 100 kg/ha

at 55 days after sowing and up to 125 kg/ha at 50% flowering. Raja *et al.* (2003) reported that the crude protein yield of 0.31 t/ha when oat was fertilized by 120 kg N/ha.

Application of 160 kg N/ha in oat produced significantly higher crude protein (19.51 and 11.91%), ash (9.95 and 9.89%), acid detergent fiber (26.50 and 49.21%) and neutral detergent fiber (45.81 and 60.32%) in the first and second cuts, respectively (Bhilare and Joshi, 2007). The highest crude protein (6.32 and 11.70%), crude fiber (28.7 and 25.6%), ether extract (1.85 and 1.37%), total ash (6.10 and 9.70%), and *in-vitro* dry matter digestibility contents (56.2 and 59.7%) were recorded in stems and leaves, respectively (Chaudhary *et al.*, 2007). The maximum crude protein (10.33%) and *in-vitro* dry matter digestibility (51.4%) were found under the 120 kg N/ha (Sheoran and Joshi, 2010). Malik *et al.* (2015) recorded the application of N produced significantly higher crude protein (13.65%) with 120 kg N/ha while maximum *in-vitro* dry matter digestibility (66.12%) in oat were found under 40 kg N/ha. Jehangir *et al.* (2013) reported that the application of N produced significantly higher crude protein (8.90%), crude fiber (22.31%), and ash (9.63%) in fodder oat with 150 kg N/ha. Moreover, the crude protein content in oat fodder increased significantly with increasing P application rates (Rashid *et al.*, 2012). A significant increase in crude protein yield was recorded up to 60 kg P₂O₅/ha (Bali *et al.*, 1998; Sharma *et al.*, 2001). The highest protein content and protein yield were attained with the application of 40 kg P₂O₅/ha (Luikham *et al.*, 2014). Malik *et al.* (2014) reported that P application at four levels (0, 20, 40, and 60 kg P₂O₅/ha) increased the crude protein content in oat fodder with increasing P levels from control up to the highest level. Farooq *et al.* (2016) also revealed that quality traits including crude protein and crude fiber were significantly affected by different P levels. Application of P also increases the crude protein content of oat grain as reported by Nakagawa *et al.* (2001). Combined application of 90 kg N/ha and 30 kg P₂O₅/ha gave the highest crude protein content in oat fodder (Tripathi, 1993), and the highest crude protein in oat grain was recorded with combined application of 60 kg N/ha and 60 kg P₂O₅/ha (Salmina and Makarova, 1988).

2.1.10 Oat-vetch mixed cropping system

2.1.10.1 Effect of oat-vetch mixtures on oat agro-morphological traits

Grass-legume mixed cropping has significant benefits that affect crop yield and has been considered as an important practice in low-input crop production system in the world (Anil *et al.*, 1998; Watson *et al.*, 2002; Knudsen *et al.*, 2004; Ramos *et al.*, 2011). Mixtures of

legumes with cereals are expected to have advantages over pure stands in terms of forage yield and quality. Forage quality and yield of forage from grass and legume mixtures are superior to that of sole grown stands (Daniel, 1990). Cultivation of grass-legume mixture can increase productivity and cause greater stability of yield (Niggli *et al.*, 2008; Doré *et al.*, 2011). Legumes have a positive effect on soil fertility through a symbiosis with rhizobium bacteria and due to a huge amount of crop residue left behind (Staniak *et al.*, 2014). Cereal and legume species that are used in a mixture have different levels of competition and interaction. Yielding of mixtures and crop quality mostly depends on the selection of compatible genotypes and their competition. Competition between component species in a mixture may affect the yield and quality of forage produced. Competition normally reduces the yield of the mixture compared with monoculture, although higher yields have been reported when competition between the two species of a mixture is lower than competition within the same species (Clark, 2007). The seeding rate of each crop in intercrop is adjusted below its full rate to optimize plant density. According to Seran and Brintha (2010), by planting a full rate of each crop neither would yield well because of intense overcrowding. Morgado and Willey (2003) also reported that dry matter yield accumulation of individual maize plants decreased with an increase in the bean plant population. The environmental conditions in addition to the seeding ratios of the selected species are crucial factors affecting the yield and quality of intercropping systems (Caballero *et al.*, 1995; Gierus *et al.*, 2012).

Oat is the most suitable annual forage grass grown with vetch in mixed cropping systems in different parts of the world (Thomson *et al.*, 1992; Johnston *et al.*, 1999; Undersander, 2003; Ross *et al.*, 2004). Legumes as sole crops can be grown alone, but they have some disadvantages compared to legume-grass intercrops. Sole crops of common vetch may often lodge heavily, and this could be prevented by mixed cropping. Vetch is an annual forage legume, belonging to the family fabaceae, which needs a frame due to its climbing growth habit. Most vetch species have a vine growing habit and if sown as mono-crop, they lodge heavily (Caballero *et al.*, 1995), and as a result its forage yield and quality decrease due to the decomposition of herbage. Vetch is usually grown in mixtures with grasses for hay, silage, and green feeding (Anil *et al.*, 1998). In grass-vetch intercropping, grasses provide structural support for vetch growth and improve light absorption for better productivity, whereas vetch in mixtures improves the quality of forage (Caballero *et al.*, 1995; Lithourgidis *et al.*, 2006). The oat-vetch mixture is the most traditionally used and reported

that these species are the most appropriate for the mixture (Lithourgidis *et al.*, 2006). Oat with legumes is effective for reducing diseases, controlling weeds, occupying the greater share of available resources, and improving the nutritive value of the crop compared to oat alone, though dry matter yields are not necessarily improved (Undersander, 2003). Mixtures of oat and vetch have great potential for forage production and higher yields have been documented for intercropping of oat and vetch (Ercoli *et al.*, 1997; Lithourgidis *et al.*, 2006). Oat-vetch mixtures produced more yield per unit area than sole cropping and the highest forage yield was reported at the ratio of 75:25 in oat: vetch seeding rates, respectively (Ansar *et al.*, 2013). Mixtures were more productive than pure vetch sowing and the highest herbage yield was obtained from a mixture of oat and vetch while the lowest herbage yield from pure stands of vetch (Canan and Orak, 2007). Different small grain cereals and vetch have been successfully used in cereal–legume intercropping systems (Dhima *et al.*, 2007; Karagic *et al.*, 2011; Lithourgidis *et al.*, 2011). Generally, green herbage and dry matter yields and percentage of mixture decreased by increasing seed rate of legume in the mixture (Anlarsal and Yücel, 1995).

2.1.10.2 Effect of oat-vetch mixtures on oat nutrient uptake and use efficiency

Intercropping of cereals and legumes is widely used in low-input agriculture because the mixture crop species provide complementarities in the utilization of resources, reduces weed pressure, and sustains productivity (Hauggaard-Nielsen *et al.*, 2003; Vasilakoglou *et al.*, 2005; Jensen *et al.*, 2006). Legumes with effective biological nitrogen fixation (BNF) can be grown with less applied N fertilizer. Appropriate fertilization concerning type, amount, time, and method of fertilizer application can increase the advantage of intercropping (Undie *et al.*, 2012). Due to the rising cost of chemical fertilizers, crop nutrient uptake and utilization must be most efficient to reduce the cost of production and achieving higher profit. Hence, intercropping cereals with legumes is particularly important in countries where the cost of N fertilizer is high and/ or availability of fertilizer is limited. The utilization of inorganic fertilizers is highly limited due to high cost and low fertilizer response of landraces (Rebka *et al.*, 2013), but legumes with effective BNF can be intercropped with cereals with less applied N fertilizer to overcome this problem. Grasses under mixed cropping with legumes can take up more N than those under sole cropping because of the transfer of rhizo-deposited N in the legume to the associated grass (Xiao *et al.*, 2004; Rasmussen *et al.*, 2007). Some pathways of N transfer from the legume to the grass include the death and decay of roots and

root nodules of the legumes (Laidlaw *et al.*, 1996), direct exudation from legume roots (Paynel *et al.*, 2001), and hyphal links formed by arbuscular mycorrhizal fungi between legume and grassroots (He *et al.*, 2009). Of these pathways, the death and decay of roots and root nodules of the legumes could be considered the major source of transferable N in grass-legume mixed cropping system (Laidlaw *et al.*, 1996). The beneficial effect of mixed cropping with a leguminous crop on the growth and nutrient uptake of the associated gramineous crop, especially N transfer from legumes were reported by many researchers (Chu *et al.*, 2004; Xiao *et al.*, 2004; Rasmussen *et al.*, 2007; Li *et al.*, 2009).

Mixing species in cropping systems may lead to a range of benefits that are expressed on various space and time scales, from a short-term increase in crop yield and quality to long-term agro-ecosystem sustainability, up to societal and ecological benefits (Malezieux *et al.*, 2009). Under low-input systems, the soil N level is usually low and legumes have higher interspecific competitive ability relative to the cereal component while cereal crops having higher competitive ability under high N levels (Bedoussac and Justes, 2011; Neugschwandtner and Kaul, 2015; Monti *et al.*, 2016). The soil N pool is maintained because of the use of legumes in the intercropping systems (Hauggaard-Nielsen *et al.*, 2001; Bedoussac and Justes, 2011). As the cereals take up N from the soil under low input system, they force the legume to take up N from N₂ fixation, due to low nitrate (NO₃⁻) concentrations, and symbiotic N₂ fixation is negatively correlated with NO₃⁻ supplied from chemical fertilizers (Hauggaard-Nielsen *et al.*, 2009). Moreover, low N availability promotes nodulation of legumes and improves their N-fixation capacity. Intercrops showed lower nutrient utilization efficiency values than cereal monocultures under high fertilizer application rate, indicating that intercrops with legume required a lower amount of N to produce the same amount of dry matter. This could be attributed to the higher N concentration in the tissues of legume and to the fact that most of the N taken up is derived from N fixation (Fageria and Baligar, 2005a). In some of the mixtures, the nutrient utilization efficiency was lower than the cereal mono-crops (Lithourgidis and Dordas, 2010; Dordas and Lithourgidis, 2011). Intercropping also significantly reduced N fertilizer utilization by 15–50% with the additional benefit of 16–30% higher productivity of wheat under wheat-faba bean intercropping (Xiao *et al.*, 2018). Cereal and legumes in relay intercropping system also promoted higher N fixation, leading to more efficient N utilization (Yong *et al.*, 2018). In oat–pea intercrops a grain N yield advantage in unfertilized treatments could be observed because of the higher grain N concentrations of oat in

intercrops (Neugschwandtner and Kaul, 2015). Moreover, intercropping of oat–pea resulted in higher grain nutrient yields of potassium (K), magnesium (Mg), and phosphorus (P) in N-unfertilized treatments and higher residue nutrients yields of calcium (Ca), K, Mg, and P over several N treatments compared to oat and pea pure stands (Neugschwandtner and Kaul, 2016).

Crop mixtures are extensively grown in traditional agricultural systems of developing countries (Biabani, 2009), and yield advantages have been reported for low soil fertility or low N fertilizer input systems (Bedoussac and Justes, 2011; Neugschwandtner and Kaul, 2015). Intercropping can be considered as an economic method for higher production with lower levels of external inputs (Willey, 1990). More production in intercropping can be attributed to the higher crop growth rate (Watiki *et al.*, 1993; Eskandari *et al.*, 2009b), higher total yield and better land-use efficiency (Dhima *et al.*, 2007; Lithourgidis *et al.*, 2011), higher and more stable yield of the cropping system (Corre-Hellon *et al.*, 2006; Lithourgidis *et al.*, 2006; Jayanta *et al.*, 2018), better utilization of light, water, and nutrients due to differences in resource consumption (Javanmard *et al.*, 2009; Brooker *et al.*, 2015; Sadeghpour, 2015), improved soil conservation (Anil *et al.*, 1998; Dhima *et al.*, 2007), better control of pests and weeds (Vasilakoglou *et al.*, 2008), improve lodging resistance and protein content (Karagic *et al.*, 2011; Bedoussac *et al.*, 2015; Brooker *et al.*, 2015), and complementarity in the use of the available resources (Eskandari, 2012; Varma *et al.*, 2017). Cereal-legume intercropping is among the approaches that induce the productivity of crops (Jensen, 1996; Lauk and Lauk, 2005; Liu *et al.*, 2006). According to the reports on soybean-sorghum (Hayder *et al.*, 2003), cowpea-maize (Eskandari and Ghanbari, 2010), maize-mungbean (Saleem *et al.*, 2015), sorghum-cowpea (Aliyu and Emechebe, 2006) and maize-faba bean (Seran and Brintha, 2010; Tilahun *et al.*, 2012) intercropping systems have higher productivity than the sole cereal systems. Cereal–legume intercropping system has better land-use efficiency compared with the mono-cropping system due to the higher utilization efficiency of limited growth resources (Nyoki and Ndakidemi, 2018). In addition to increased biomass productivity, incorporation of legumes in crop cultivation has been shown to improve plant productivity (Hong *et al.*, 2019). Caballero *et al.* (1995) showed yields of oat-vetch mixtures were 34% higher than pure vetch, they found mixtures yielded 36% less than pure oat.

2.1.10.3 Effect of oat-vetch mixtures on nutritional quality

Mixed cropping of grasses with forage legumes can improve the quality of fodder compared to pure grass crops (Umuna *et al.*, 1995; Mpairwe *et al.*, 2003). Grasses provide high yields in terms of dry weight but they produce forage with low protein. Moreover, the forage quality is generally lower than that required to meet production goals for many classes of livestock (Clark, 2007). Mixtures containing 25-50 % legume produced more quality forage and yield per unit area than those of pure sowings (Qamar *et al.*, 1999; Buyukburc and Karadag, 2002; Alemu *et al.*, 2007; Tuna and Orak, 2007). The incorporation of a legume with grass could be of paramount importance to the nutritive value of the forage mixture and subsequent soil fertility. The inclusion of legumes in intercrops can provide increased protein-rich yields and a more sustainable source of nitrogen; while on the other hand, it saves cost by reducing the requirement for mineral nitrogen application (Anil *et al.*, 1998; Crews and Peoples, 2004), but it depends on the N fixation capacity of the associated legume species. The intake of fodder is relatively low when fed as pure fodders either of legumes or grasses compared with their grass-legume mixtures. Oat forms an excellent combination when fed along with legume crops like berseem, alfalfa, and vetch (Zaman *et al.*, 2006). Increasing on-farm protein production is required to achieve more economically feasible farming systems (Sadeghpour *et al.*, 2014). The crude protein (CP) content is often considered as the most important component of forage quality (Lithourgidis *et al.*, 2007; Cazzato *et al.*, 2012), and CP yield is a valuable measure of the total protein that can be harvested for livestock enterprises (Caballero *et al.*, 1995; Cazzato *et al.*, 2013). Previous studies reported the highest CP content recorded when the legume was grown as a sole crop or formed a high proportion in intercrops with grasses (Lithourgidis *et al.*, 2007; Dhima *et al.*, 2013).

The CP content of forage is one of the most important criteria for forage quality evaluation (Caballero *et al.*, 1995; Getnet and Ledin, 2001). Jannink *et al.* (1996) found that the vetch mixture had much higher CP content than oat alone. Though the CP content of oat-vetch mixtures were below the CP content of sole vetch, mixtures had greater CP content than sole oat (Fantahun, 2016). Research has shown that oat grown with pea can provide high-quality forage and increases CP by 2 to 4% units (Owens *et al.*, 2007). Herbage nutritive value of forage grasses and legumes is negatively related to dry matter accumulation (Bélanger *et al.*, 2001). Thus, increases in herbage dry matter yield are expected to result in a decrease in the nutritive value of mixture than vetch monocultures. Haq *et al.* (2018) reported that the CP

content of the oat-vetch mixture was higher than the oat grown alone, while it was lower than the vetch mono-crop. Important criteria for evaluating forage quality are also acid detergent fiber (ADF) and neutral detergent fiber (NDF), ADF being a better efficient predictor of forage digestibility (Caballero *et al.*, 1995; Lithourgidis *et al.*, 2007; Corleto *et al.*, 2009; Sadeghpour *et al.*, 2014). In fact, as the ADF percentage decrease, the quality and digestibility of forage usually increase (Van Saun, 2015). On the other hand, the NDF content is a good measure of voluntary intake of the feed and it is inversely related to its digestibility or energy density (Sayar *et al.*, 2014). High digestible dry matter contents are required by ruminants to digest the greatest portion of the dry matter in feed intake (Van Saun, 2015).

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Chapter III

Experiment 1: Agro-morphological variability and interrelationships among yield and yield-related attributes of oat (*Avena sativa* L.) genotypes



Agro-morphological variability and interrelationships among yield and yield-related attributes of oat (*Avena sativa* L.) genotypes

Abstract

Oat (*Avena sativa* L.) is an important dual-purpose cereal crop cultivated primarily for fodder and moderately for food grain production in the central highlands of Ethiopia. The degree of available genetic variation influences the effectiveness of breeding programs for improvement. This study was, therefore, designed to determine the extent of oat genetic diversity using markers of agro-morphological traits and to identify suitable genotypes for efficient yield improvement. One hundred twenty oat genotypes, which included nine released varieties, were evaluated at Holetta and Ada-Berga research stations using a randomized complete block design with three replications. The analysis of variance indicated that the mean squares due to locations and genotype $\times$ location interaction varied significantly for some measured traits while that of genotypes varied significantly ($P \leq 0.001$) among all studied traits. The results revealed that very high to moderately high heritability in a broad sense (h^2b) coupled with high to moderate genetic advance as a percent of mean (GAM) were recorded for forage dry matter yield-FDMY ($h^2b = 64.4\%$; GAM = 19.3%), number of leaves at forage harvest-NLFH ($h^2b = 86.4\%$; GAM = 19.9%), stem dry matter yield-SDMY ($h^2b = 62.9\%$; GAM = 18.3%), forage yield production rate-FYPR ($h^2b = 69.7\%$; GAM = 21.7%), grain yield-GY ($h^2b = 64.2\%$; GAM = 26.1%), panicle length at grain harvest-PLGH ($h^2b = 80.9\%$; GAM = 21.9%), number of spikes per panicle-NSPP ($h^2b = 68.8\%$; GAM = 16.0%), and harvest index-HI ($h^2b = 80.9\%$; GAM = 26.0%). The results suggested that these traits are governed more by additive gene action, and selection based on these traits could be effective in achieving the desired genetic gains for improvement. The correlation and path analyses also revealed that the FYPR had a significant positive association with FDMY coupled with a high direct effect on FDMY at phenotypic and genotypic levels. Moreover, the indirect effects of most studied traits on FDMY were positive via FYPR. The biological yield production rate (BYPR) and HI had high direct effects on GY coupled with their significant positive associations with GY at phenotypic and genotypic levels. The indirect effects on GY were high and positive for most studied traits via mainly BYPR. Therefore, breeders should give due attention to FDMY along with FYPR during selection to improve fodder yield and also to GY along with BYPR and HI to increase grain yield productivity in oat genotypes. The result showed that the hierarchical clustering grouped the genotypes into four clusters. High forage yield-producing genotypes were grouped into the second cluster while high grain-producing genotypes were grouped into the third cluster. The intra-cluster genetic distance values ranged from 4.3 (C3) to 2.3 (C1). The minimum inter-cluster genetic distance was 11.7 (between C1 and C2), while the maximum inter-cluster distance was 63.2 (between C3 and C4). Principal component analysis showed that the first four principal components with eigenvalues greater than one contributed 78.3% of the variability among genotypes. The highest contributing traits in the first component were FYPR, BYPR, PLGH, FDMY, and number of spikelets per panicle (NSLPP). The traits with the greatest weight on the second component were HI, GY, NLFH, and plant height at grain harvest (PHGH). Proper selection of best-yield performing genotypes coupled with high-yield contributing traits is very important to yield improvement and future oat breeding programs. Selection based on the traits that had a high contribution to the first two principal components would be effective for yield improvement in oat genotypes. Therefore, high forage dry matter and grain-yielding genotypes along with desirable yield-related traits could be considered for selection in oat genotypes. Accordingly, breeders should give due attention to FDMY along with FYPR during selection to improve fodder yield and also to GY along with BYPR and HI to increase grain yield productivity in oat genotypes. Among the genotypes, CI-715, CI-1463, SRCPX80Ab2806, A-505, CI-1480, S-122, Bona-bas, and CI-1674 produced better fodder and grain yields. Thus, these genotypes could be used as potential parents for improving the genetic gain in oat breeding programs.

Keywords: cluster analysis, correlation, genetic distance, genetic gain, heritability, oat diversity, path coefficient, principal components

3.1 Introduction

The genus *avena* is commonly known as oat and comprises about 70 species; a few are cultivated (Atman, 2017; Harshita, 2018). This genus includes diploid, tetraploid, and hexaploid species, with a basic chromosome number of seven (Kaur and Kapoor, 2017; Ashenafi, 2018; Harshita, 2018), but the diploid and tetraploid are mostly wild species. The common oat (*Avena sativa* L.), which belongs to the genus *avena* and the family *gramineae/poaceae*, is one of the most important dual-purpose cereal crops cultivated for use as fodder and grain worldwide (Stevens *et al.*, 2004; Suttie and Reynolds, 2004; Rines *et al.*, 2006). It is a self-pollinated hexaploid crop ($2n=6x=42$) and more likely evolved from another hexaploid (*Avena sterilis*) oat species (Trabut, 1914). The domestication of oat is more generally associated with mid and northern Europe and its origin was dependent on the migration of other cereals (wheat and barley) to more temperate regions (Leggett and Thomas, 1995). The domesticated common oat is extremely variable and widely distributed as compared to other oat species due to human selection and breeding activities (Ladizinsky, 2012; Esvelt *et al.*, 2016).

Oat is a useful annual cereal crop at higher altitudes in the tropics and grown throughout the cooler wetter parts of the temperate region. It is also widely utilized in the highland farming system of Ethiopia unlike other cultivated forage crops (Getnet *et al.*, 2004). Common oat is an economically important crop and ranks sixth in production among all cereal crops, next to wheat, maize, rice, barley, and sorghum in the world (FAO, 2012). The oat produced in the world is mainly used as feed, and only 17% of its grain production is used for human consumption (Wagh, 2018). The grain of oat has high contribution to human food and also animal feed (Fekede, 2004; Ruwali *et al.*, 2013; Monica *et al.*, 2017). For human consumption, oat is considered a very important cereal crop which is used throughout the world as a source of essential nutrients (Boczkowska and Tarczyk, 2013). Being a highly nutritious cereal, especially rich in fat, protein, carbohydrate, fibre, vitamins, minerals, as well as antioxidants, it is used for human consumption as well as animal feed (Peterson *et al.*, 2005; Butt *et al.*, 2008; Ruwali and Deo, 2009). Moreover, oat is a nutritious quality fodder for livestock and the grains give high energy when used as animal feed (Ruwali *et al.*, 2013). Oat forage harvested at the soft dough stage has a mean of 79 g/kg DM ash, 61 g/kg DM crude protein, and 530 g/kg DM in-vitro organic matter digestibility (Fekede *et al.*, 2008).

Yield is a complex quantitative trait which is governed by a large number of genes and is highly affected by the associations/interactions of various yield attributing traits (Iqbal *et al.*, 2015; Kiranmai *et al.*, 2016). As yield is a complex product of yield-related traits and has low heritability, direct selection only for superior yield may not be adequately effective for improvement (Singh, 2000). Yield-contributing traits, on the other hand, are less complex in inheritance and less influenced by environmental conditions, so selection based on yield components can be effective (Gatti *et al.*, 2005). Thus, selection for high yield could be achieved through indirect selection of traits which have high heritability and high associations with grain yield (Sobhaninan *et al.*, 2019). The feasibility of indirect selection is commonly examined by the associations of traits. The traits, with a high level of phenotypic and genotypic association, can be considered as a selection criterion for yield improvement (Maraisa *et al.*, 2015). However, selection based on genotypic correlation may be more effective than phenotypic correlation under the high influence of environmental conditions because genetic correlation is heritable and contributes more to yield improvement programmes by excluding the environmental influences (Jemal *et al.*, 2020). Moreover, genetic correlation is important to increase selection efficiency by generating indirect gains when the selection is done on low heritability traits and to identify the most desirable yield-contributing traits that can be used as indirect selection tools for yield (Machado *et al.*, 2017).

Genetic variability is defined as the existence of alterations among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allad, 1960). The nature and extent of genetic variability existing in the genotypes is of paramount importance for a successful breeding program because higher genetic variability would allow the selection of promising genotypes (Bhatia *et al.*, 2017). The degree of heritability and genetic advance generally determine the effectiveness of selection (Kumar *et al.*, 2013), while genetic variability is important for continuous genetic improvement (Sandhu *et al.*, 2015). All the variability present in the biological systems can be attributed to genotypic and/or environmental factors (Welsh, 1981). The effectiveness of selection depends upon the variability present among the individuals in a population and the extent to which it is heritable (Singh, 2001). The future of breeding programs mainly depends on the availability of genetic variability to increase productivity and quality (Smith *et al.*, 1991). The occurrence of genetic variability among individuals due to differences in the genetic composition is very important for rapid and efficient crop improvement through plant

breeding because superior genotypes can be selected from the heterogeneous population and proper management of this variation could result in a remarkable impact on the performance of the crop (Sharma, 1998).

Evaluation of oat genotypes, to identify high yielding ones adapted to diverse environmental conditions, is a vital component in oat breeding programs. Oat genotypes for grain purposes have generally been selected for high grain yield and its yield components (Martinez *et al.*, 2010), while high biomass yield, along with its better yield-related traits, is the prerequisite for the selection of fodder cultivars (Stevens *et al.*, 2004). Different research studies in Ethiopia indicated that there is a considerable variation for most measured traits in oat genotypes (Fekede, 2004; Getnet *et al.*, 2004; Ashenafi, 2018). Other studies also indicated that oat genotypes had significant variability in yield, growth, and quality parameters (Shehzad *et al.*, 2011; Khan *et al.*, 2014). So, assessing the extent of genetic diversity using markers of agro-morphological traits is very essential to exploit the existing variations in oat genotypes. Agro-morphological markers, the simplest and the most direct measures of phenotypes, are rapid and inexpensive, allowing large-scale evaluation of genetic diversity (Habte, 2018). Thus, assessing the extent of agro-morphological based genetic diversity is very essential to exploit the differences in oat genotypes for proper utilization and further improvement. Therefore, this research work was conducted using 120 world collection oat genotypes at two locations in the central highlands of Ethiopia aimed to: (i) estimate the extent of agro-morphological based genetic variability, heritability, and expected genetic gain in oat genotypes, (ii) investigate the phenotypic and genotypic relationships between the studied quantitative traits, (iii) determine the direct and indirect effects of measured quantitative traits on fodder and grain yields, (iv) evaluate the genetic variation using cluster, genetic divergence, and principal component analyses in oat genotypes for fodder and grain yields improvement, and (v) identify the best performing oat genotypes for further breeding work in Ethiopia.

3.2 Materials and Methods

3.2.1 Description of the study sites

The field experiment was conducted during the main cropping season (June to January) of 2020/21 under rainfed conditions at Holetta Agricultural Research Center (HARC) and at the Ada-Berga sub-station of HARC (Figure 3.1). The HARC is situated at 09°03'38.14''N latitude, 38°30'03.12''E longitude, and at an altitude of 2400 meters above sea level (masl).

The long term (50-year) average annual rainfall is 1020 mm, and the average maximum and minimum air temperatures are 22.5 and 6.3 °C, respectively. The rainfall in HARC is bimodal and about 85% of the precipitation falls in the period from June to September (the main Meher season), while the remaining 15% falls in the period from March to May (the short Belg season) (Getachew, 2017). Ada-Berga substation of HARC is located at 09°16'09.17''N latitude, 38°22'59.71''E longitude, and at an altitude of 2600 masl. The average annual rainfall of the area is 1225 mm (Direba, 2012), and the average maximum and minimum air temperatures are 25, and 10 °C, respectively (Alemu, 2015). This substation receives most of its rain during the main (Meher) rainy season that extends from June–September. Small Belg rains during March and May also augment the main rains.

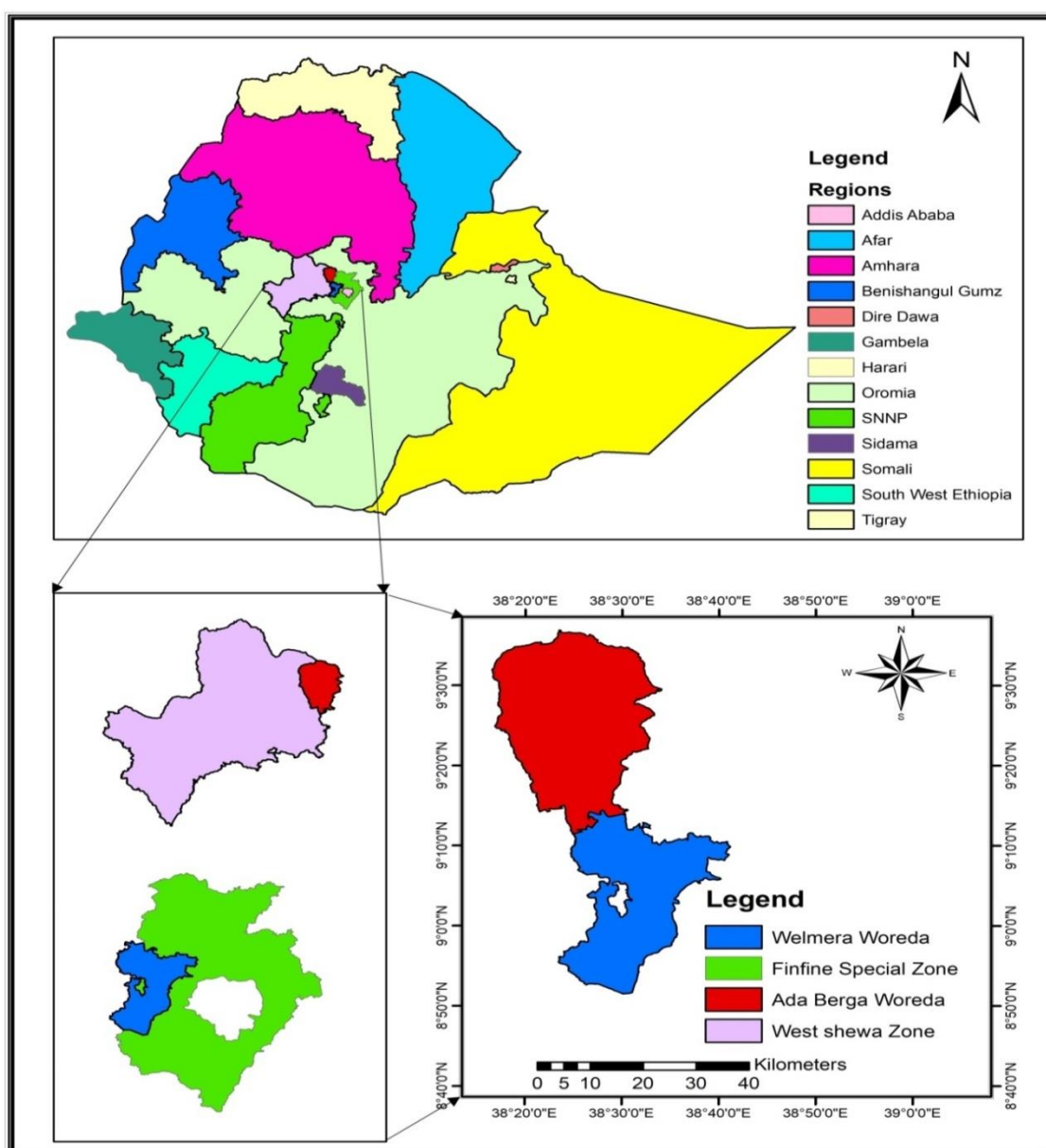


Figure 3.1 Map of the study sites of Holetta and Ada-Berga in Ethiopia

3.2.2 Soil sampling and analysis

Soil samples were collected from 0-20 cm of soil depth at each experimental site prior to planting. The experimental block was divided into two equal parts, and six sampling points were randomly selected within each equally divided experimental block. The organic litter was cleared away from the surface at each sampling point, and samples were collected using a manual auger with a 20 cm core barrel of 6 cm internal diameter. The six samples were combined, making a bulk sample for each equally divided block, and one composite sample per block was prepared, which resulted in three composite samples per site for laboratory analysis. After manual homogenization, the samples were air-dried and ground to pass through a 2-mm sieve. Soil samples were analyzed for pH using a ratio of 2.5 ml water to 1 g soil (McLean, 1982); organic carbon (OC) using the Walkley and Black (1934) method; total nitrogen (TN) content by the Kjeldahl digestion (Nelson and Sommers, 1982); available phosphorus (AP) using the Olsen method (Olsen *et al.*, 1954); and cation exchange capacity (CEC) by ammonium acetate method (Black, 1965) at the soil and plant analysis laboratory of HARC. Moreover, particle size distribution was carried out by Bouyoucos hydrometer method (Bouyoucos, 1996). Based on clay, silt, and sand proportions, soil textural class was identified using the USDA soil textural triangle (Rowell, 1994). The soil type is predominantly acidic Eutric Nitisol at both sites. The soil of the Ada-Berga site had higher OC, TN, C/N ratio, and AP but lower pH, CEC, and clay proportion than Holetta (Table 3.1).

Table 3.1 Description of the test locations for physico-chemical properties of the soils

Parameter	Value		Rating / class		Reference for rating
	Holetta	Ada-Berga	Holetta	Ada-Berga	
pH (1:2.5 H ₂ O)	5.51	4.97	Moderately acidic	Strongly acidic	Tekalign, 1991
OC (%)	1.94	2.17	Moderate	Moderate	Tekalign, 1991
TN (%)	0.18	0.20	Moderate	Moderate	Tekalign, 1991
C/N ratio	10.78	10.85	Low	Low	Newey, 2006
AP (ppm)	7.46	10.40	Moderate	High	Olsen <i>et al.</i> , 1954
CEC (meq/100g)	24.33	15.15	Moderate	Moderate	Hazelton and Murphy, 2007
Sand (%)	13.33	18.33	Low	Low	Hazelton and Murphy, 2007
Silt (%)	29.17	36.67	Moderate	Moderate	Hazelton and Murphy, 2007
Clay (%)	57.50	45.00	Very high	High	Hazelton and Murphy, 2007
Textural class	Clay	Clay	-	-	-

pH = power of hydrogen; **OC** = organic carbon; **TN** = Total nitrogen; **C/N** = carbon to nitrogen ratio; **AP** = Available phosphorus; **CEC** = cation exchange capacity; **ppm** = parts per million; meq = milliequivalent.

3.2.3 Experimental materials

The study was conducted using 120 oat genotypes, which included nine released varieties (8251, Bona-bas, Was, SRCPX80Ab2291, SRCPX80Ab2806, Bonsa, Sorataf, Walqaa, and Dumant 2007 portage) (Table 3.2). The test genotypes were randomly composed of which 98 are world collections which were introduced through the Food and Agricultural Organization (FAO), 20 were introduced via the International Maize and Wheat Improvement Center (CIMMYT), and the remaining 2 were recently introduced from Canada. All the studied genotypes were rejuvenated during the main cropping season of 2019/20 under the same condition at Holetta to minimize the initial variation due to differences in seed age and seed nitrogen as suggested by Liao *et al.* (2008) and Gemechu (2012). The germinating potential of the genotypes was tested prior to sowing and it was above 95% for all genotypes (data not shown).

Table 3.2 List of one hundred twenty oat genotypes used for the study

SN	Genotypes	Source	SN	Genotypes	Source	SN	Genotypes	Source	SN	Genotypes	Source
1	CI-715	FAO	31	CI-1584	FAO	61	CI-1767	FAO	91	S-130	FAO
2	CI-1426	FAO	32	CI-1585	FAO	62	CI-1768	FAO	92	T-19-26-513	FAO
3	CI-1429	FAO	33	CI-1590	FAO	63	CI-1781	FAO	93	Bona-bas	FAO
4	CI-1436	FAO	34	CI-1592	FAO	64	CI-1791	FAO	94	Jassari	FAO
5	CI-1438	FAO	35	CI-1611	FAO	65	CI-1838	FAO	95	Jassari-27639	FAO
6	CI-1446	FAO	36	CI-1623	FAO	66	CI-1842	FAO	96	Jassari-723	FAO
7	CI-1456	FAO	37	CI-1629	FAO	67	CI-1852	FAO	97	Lampton	FAO
8	CI-1463	FAO	38	CI-1646	FAO	68	CI-1853	FAO	98	Was	FAO
9	CI-1466	FAO	39	CI-1652	FAO	69	CI-1864	FAO	99	60MN 16016	CIMMYT
10	CI-1478	FAO	40	CI-1654	FAO	70	CI-2141	FAO	100	Coker SR res 80SA130	CIMMYT
11	CI-1480	FAO	41	CI-1655	FAO	71	CI-5800	FAO	101	MM799883/85	CIMMYT
12	CI-1484	FAO	42	CI-1659	FAO	72	CI-7894	FAO	102	MN79983/85	CIMMYT
13	CI-1485	FAO	43	CI-1664	FAO	73	CI-8235	FAO	103	SRCPX80Ab1751	CIMMYT
14	CI-1488	FAO	44	CI-1671	FAO	74	CI-8251	FAO	104	SRCPX80Ab2035	CIMMYT
15	CI-1495	FAO	45	CI-1672	FAO	75	CI-16016	FAO	105	SRCPX80Ab2050	CIMMYT
16	CI-1496	FAO	46	CI-1674	FAO	76	CI-27830	FAO	106	SRCPX80Ab2267	CIMMYT
17	CI-1497	FAO	47	CI-1677	FAO	77	A-505	FAO	107	SRCPX80Ab2291	CIMMYT
18	CI-1510	FAO	48	CI-1690	FAO	78	B-17	FAO	108	SRCPX80Ab2310	CIMMYT
19	CI-1512	FAO	49	CI-1695	FAO	79	C-2	FAO	109	SRCPX80Ab2475	CIMMYT
20	CI-1528	FAO	50	CI-1704	FAO	80	C-10	FAO	110	SRCPX80Ab2582	CIMMYT
21	CI-1532	FAO	51	CI-1707	FAO	81	C-12	FAO	111	SRCPX80Ab2691	CIMMYT
22	CI-1536	FAO	52	CI-1720	FAO	82	C-16	FAO	112	SRCPX80Ab2754	CIMMYT
23	CI-1538	FAO	53	CI-1746	FAO	83	D-28	FAO	113	SRCPX80Ab2764	CIMMYT
24	CI-1544	FAO	54	CI-1747	FAO	84	E-2	FAO	114	SRCPX80Ab2777	CIMMYT
25	CI-1546	FAO	55	CI-1749	FAO	85	E-15	FAO	115	SRCPX80Ab2806	CIMMYT
26	CI-1547	FAO	56	CI-1750	FAO	86	E-25	FAO	116	Bonsa	CIMMYT
27	CI-1549	FAO	57	CI-1751	FAO	87	F-18	FAO	117	Sorataf	CIMMYT
28	CI-1551	FAO	58	CI-1752	FAO	88	K-2	FAO	118	Walqaa	CIMMYT
29	CI-1567	FAO	59	CI-1759	FAO	89	R-14	FAO	119	Dumant 2007 portage	Canada
30	CI-1577	FAO	60	CI-1765	FAO	90	S-122	FAO	120	Robert 2007 Portage	Canada

The released nine varieties used in this study are: **Bonsa**= 79Ab384(TX)80SA95; **Walqaa** = SRCPX80Ab2596; **Was** = 1506; **Bona-bas** = 1660; **Sorataf** = 79Ab382(TX)80SA94; **8251**; SRCPX80Ab2291; SRCPX80Ab2806; and Dumant 2007 portage.

3.2.4 Experimental design and procedures

A randomized complete block design (RCBD) replicated three times was used for evaluating the genotypes. The genotype randomization was done using PROC PLAN seed procedures

of the SAS general linear model version 9.4 (SAS, 2012). The experimental fields were prepared following the recommended tillage (plowing with a mold-board plow during the short rainy season in March followed by harrowing once using a disc harrow in early May and slight hoeing to loosen the soil) and fine seedbeds were prepared according to the requirement of the crop. A uniform seeding rate of 100 kg/ha was used as per the previous recommendation for a pure stand of oat in the highlands of Ethiopia (Astatke, 1979). The seeds were sown on the 20th of June 2020 at Ada-Berga and the 7th of July 2020 at Holetta. Each genotype was sown to a plot area of 1.6 m² consisting of 2 rows of 4 m length and 0.4 m width with 0.2 m row spacing. The two rows, with a net plot size of 3.8 m by 0.4 m (1.52 m²) were used for data collection. The recommended fertilizer at the rate of 18/46 kg/ha of N/P₂O₅ at sowing and 23 kg/ha of N at tillering (Getnet, 1999; Ashenafi, 2018) was uniformly applied to all experimental plots. The first-hand weeding was done on the 29th of July 2020 at Ada-Berga and the 15th of August 2020 at Holetta, and the second-hand weeding was performed on the 27th of August 2020 at Ada-Berga and the 14th of September 2020 at Holetta to minimize the yield reduction due to weed competition for major growth resources. All other crop management practices such as draining excess water from the plots, maintaining the water drainage canals, protecting the crop at the grain filling stage from bird attacks, and so on were carried out for all genotypes as required.

3.2.5 Data collection and measurements

Data on agro-morphological traits were collected either on a plot basis or from five randomly selected plants per plot. A list of the studied 24 agro-morphological traits with their descriptions and sampling methods is indicated in Table 3.3.

Table 3.3 List of studied agro-morphological traits and their descriptions

SN	Trait	Trait code	Unit	Basis of Sampling	Trait description
1	Number of tillers per plant	NTPP	Number	Plant	Number of tillers counted from five randomly selected plants at tillering stage
2	Tillers dry weight	TDW	g	Plant	Tillers dry weight recorded from five randomly selected plants at tillering stage
3	Number of leaf at forage harvest	NLFH	Number	Plant	Leaf number counted from five randomly selected plants at soft dough stage
4	Largest leaf length at forage harvest	LLFH	cm	Plant	Leaf length measured from the base to the tip of the leaf from five plants at soft dough stage
5	Plant height at forage harvest	PHFH	cm	Plant	Plant height measured from ground level to the tip of five plants at soft dough stage
6	Days to forage harvest	DFH	Days	Plot	Number of days counted from 90% emergence to soft dough stage
7	Leaf dry matter yield	LDMY	t/ha	Plot	The yield estimated by dividing leaf botanical fraction to forage dry matter yield and multiplied by 100
8	Stem dry matter yield	SDMY	t/ha	Plot	The yield estimated by dividing stem botanical fraction to forage dry matter yield and multiplied by 100
9	Panicle dry matter yield	PDMY	t/ha	Plot	The yield estimated by dividing panicle botanical fraction to forage dry matter yield and multiplied by 100
10	Forage yield production rate	FYPR	kg/ha/day	Plot	The rate estimated by dividing forage dry matter yield to days to forage harvest
11	Forage dry matter yield	FDMY	t/ha	Plot	The yield estimated at soft dough stage after oven-drying in 105 °C for 24 hours
12	Plant height at grain harvest	PHGH	cm	Plant	Plant height recorded from ground level to the tip of five plants at grain maturity
13	Panicle length at grain harvest	PLGH	cm	Plant	The length measured from the base to the tip of the panicle from five plants at physiological maturity
14	Days to seed harvest	DSH	Days	Plot	Number of days counted from 90% emergence to physiological maturity
15	Grain filling period	GFP	Days	Plot	Number of days between 50% heading to physiological maturity
16	Number of spikes per panicle	NSPP	Number	Plant	Spikes counted from five randomly selected plants at grain maturity stage
17	Number of spikelets per panicle	NSLPP	Number	Plant	Spikelets counted from five randomly selected plants at grain maturity stage
18	Total biological yield	TBY	t/ha	Plot	Biomass yield determined by summing grain yield and straw yield at grain maturity stage
19	Biological yield production rate	BYPR	kg/ha/day	Plot	The rate estimated by dividing biomass yield to days to seed harvest
20	Grain sink filling rate	GSFR	kg/ha/day	Plot	The rate estimated by dividing grain yield to the number of days from heading to grain maturity
21	Straw yield	SY	t/ha	Plot	The straw yield estimated by adding aftermath and chaff yields at grain maturity stage
22	Thousand seed weight	TSW	g	Plot	The seed weight of 1000 seeds estimated at an adjusted moisture content of 12.5 %
23	Harvest index	HI	%	Plot	The ratio of grain yield to total above-ground biomass yield multiplied by 100
24	Grain yield	GY	t/ha	Plot	The grain yield estimated at an adjusted moisture content of 12.5 %

3.2.6 Data analysis for agro-morphological traits

3.2.6.1 Analysis of variance

The analysis of variance (ANOVA) procedures of the statistical analysis system (SAS) general linear model (GLM) version 9.4 were used for individual locations and combined across location analysis (SAS, 2012). To determine the validity of each location analysis, Bartlett's test for homogeneity of variance was done by the SAS computer packages prior to computing ANOVA. Moreover, the homogeneity of error variance for combined ANOVA was tested using the F-max method of Hartley (1950), which is based on the ratio of the larger mean square of error (MSE) from the separate analysis of variance to the smaller MSE. If the larger MSE is not three-fold larger than the smaller MSE, the error variance is considered homogeneous (Gomez and Gomez, 1984). The combined ANOVA was performed using the PROC GLM procedure of SAS after testing the homogeneity of error variance. A linear random model was used to account for both the genotype and location effects, which were considered random; therefore a linear random model was used. The mean squares of replication, interaction, and residual were combined to test the location effect. Accordingly, the mean square of the location random effect was tested against the sum of replication and interaction mean squares minus the residual mean square as an error term, and the degrees of freedom for these combined mean squares was estimated following Satterthwaite's approximation method. But the genotype random effect was tested against the interaction (genotype x location) mean square while the interaction effect was tested against the residual mean square. A mean comparison between locations was performed using Duncan's Multiple Range Test (DMRT) at a 5% probability level following Gomez and Gomez (1984). Descriptive statistics were also done for the mean, range, standard deviation and standard error of the mean. The location's main effect was tested with a quasi-F test as shown below. The numerator degree of freedom for the location F-test was L-1 while the denominator (combined mean squares) degree of freedom was estimated using Satterthwaite's formula (Satterthwaite, 1946) as indicated below.

$$F_1 = \frac{MS_l}{(MS_r + MS_{gl} - MS_e)} \quad DF_{cms} = \frac{(MS_r + MS_{gl} - MS_e)^2}{\frac{(MS_r)^2}{(r-1)} + \frac{(MS_{gl})^2}{(g-1)(l-1)} + \frac{(MS_e)^2}{(l)(g-1)(r-1)}}$$

where F_1 is F-test for location; MS_l is the mean square of location; MS_r is the mean square of replication; MS_{gl} is the mean square of genotype by location interaction; MS_e is the mean square of error; DF_{cms} is degrees of freedom for combined mean square; r is the number of replication; l is the number of location; and g is the number of genotype.

The statistical models for individual locations and combined across the two locations are presented below. The statistical model of the RCBD design for individual locations is given by:

$$Y_{ij} = \mu + B_i + G_j + \epsilon_{ij}$$

where Y_{ij} is the measured response of genotype j in block i ; μ is the grand mean; B_i is the effect of block i ; G_j is the effect of genotype j ; ϵ_{ij} is the random error effect of genotype j in block i .

The statistical model of the RCBD design for across locations is given by:

$$Y_{ijk} = \mu + (B/L)_{ik} + G_j + L_k + (GL)_{jk} + \epsilon_{ijk}$$

where Y_{ijk} is the measured response of genotypes j in block i nested at location k ; μ is the grand mean; $(B/L)_{ik}$ is the effect of block i within location k ; G_j is the effect of genotype j ; L_k is the effect of location k ; $(GL)_{jk}$ is the interaction effect between genotype j and location k ; and ϵ_{ijk} is the residual or effects of random error.

3.2.6.2 Comparison of selected genotypes with the original population

The 5% best-performing genotypes were selected and their means were independently computed for each trait to compare with the original population. The significance of the difference between the sample mean ($\bar{X}$) and population parameter (μ) was tested using the student t-test table, i.e., when the calculated t-value is greater than the tabulated t-value, the difference is considered significant (Singh, 2001). The absolute t-value was calculated using the student's t-test formula to compare the performance of 5% best-selected genotypes with the base population as:

$$T = \frac{\bar{X} - \mu}{s/\sqrt{n}}$$

where $\bar{X}$ is the mean of selected genotypes, μ is the mean of the base populations, s is the sample standard deviation and n is the number of genotypes selected from the base population for better performance.

3.2.7.2 Estimation of variance components

The total variance components are partitioned into different components using ANOVA by assuming the mean square of each sources of variation is equal to their expected mean

squares (Table 3.4), as suggested by Singh and Chaudhary (1977). The variability present in the population is estimated by the variance components and coefficient of variation. The combined over locations mean squares were computed according to the statistical procedures of SAS and the sources of variations in RCBD design were used to estimate the variance components using the method suggested by Johnson *et al.* (1955) as follows:

$$\begin{aligned}\sigma^2_l &= \frac{(MSl + MSe) - (MSr + MSgl)}{gr} & \sigma^2_r &= \frac{MSr - MSe}{g} & \sigma^2_g &= \frac{MSg - MSgl}{rl} \\ \sigma^2_{gl} &= \frac{MSgl - MSe}{r} & \sigma^2_p &= \sigma^2_g + \frac{\sigma^2_{gl}}{l} + \frac{\sigma^2_e}{rl} & \sigma^2_e &= MSe\end{aligned}$$

where σ^2_l is location variance; MS_l is the mean square of location; MS_{gl} is the mean square of genotype by location interaction; g is the number of genotype; r is the number of replication; σ^2_r is replication variance; MS_r is the mean square of replication; MSe is the mean square of error; σ^2_g is genotypic variance; MS_g is the mean square of genotype; l is the number of location; σ^2_{gl} is genotype by location interaction variance; σ^2_p is phenotypic variance; and σ^2_e is environmental variance.

On the other hand, the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were also calculated according to the formula suggested by Singh and Chaudhary (1977). These estimates of variations were classified as low when values were less than 10%, medium when values were between 10 and 20% and high when values were greater than 20% (Johnson *et al.*, 1955).

$$GCV (\%) = \frac{\sqrt{\sigma^2_g}}{\bar{X}} * 100 \quad PCV (\%) = \frac{\sqrt{\sigma^2_p}}{\bar{X}} * 100 \quad ECV (\%) = \frac{\sqrt{\sigma^2_e}}{\bar{X}} * 100$$

where GCV is the genotypic coefficient of variation; PCV is the phenotypic coefficient of variation; ECV is the environmental coefficient of variation; σ^2_g is genotypic variance; σ^2_p is phenotypic variance; σ^2_e is environmental variance; and $\bar{X}$ is the mean of trait.

3.2.6.4 Estimation of heritability

The estimate of heritability (h^2_b) in the broad sense is expressed as a percentage of the ratio of the genotypic variance to the phenotypic variance as described by Allard (1960) and Falconer (1989). According to Singh (2001), the heritability estimates were classified as low

when the values were less than 40%; values between 40 and 59% were considered medium; values between 60 and 79 were moderately high, and values greater than 80% were reported as very high, and it was calculated as:

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} * 100 \quad \text{Or} \quad h^2 = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{gl}}{l} + \frac{\sigma^2_e}{rl}} * 100$$

where h^2 is heritability; σ^2_g is genotypic variance; σ^2_p is phenotypic variance; σ^2_{gl} is the genotype by location interaction variance; l is the number of location; r is the number of replication; and σ_e^2 is environmental variance.

3.2.6.5 Estimation of genetic advance

The expected genetic advance (GA) for each trait at 5% selection intensity ($k = 2.06$) was estimated using the method illustrated by Allard (1960). Moreover, expected genetic advance as percent of the mean (GAM) was calculated to compare the extent of the predicted advance of different traits under selection, using the formula developed by Comstock and Robinson (1952). According to Johnson *et al.* (1955), the estimated GAM values were classified as low when values were less than 10%; values between 10 and 20% were medium; and values greater than 20% were testified as high.

$$GA = K * (\sqrt{\sigma^2_p} * h^2) \quad \quad \quad GAM = \frac{GA}{\bar{X}} * 100$$

where GA is the genetic advance; K is the standardized selection differential at 5% selection intensity ($k = 2.06$); $\sqrt{\sigma^2_p}$ is the square root of phenotypic variance; h^2 is heritability in broad sense; GAM is the genetic advance as percent mean; and $\bar{X}$ is the mean of the trait population in which selection employed.

Table 3.4 Combined analysis of variance (ANOVA) and expected mean squares for random model of RCBD design

Sources of variation	Degree of freedom	Mean Square (MS)	Expected Mean Square (EMS)	F-test
Location (L)	L-1	MS ₁	$\sigma_e^2 + r\sigma_{gl}^2 + g\sigma_{r(l)}^2 + gr\sigma_l^2$	MS ₁ /(MS ₂ +MS ₄ -MS ₅)
Replication (R) /Location	L(R-1)	MS ₂	$\sigma_e^2 + g\sigma_{r(l)}^2$	MS ₂ /MS ₅
Genotypes (G)	G-1	MS ₃	$\sigma_e^2 + r\sigma_{gl}^2 + rl\sigma_g^2$	MS ₃ /MS ₄
G x L	(G-1)(L-1)	MS ₄	$\sigma_e^2 + r\sigma_{gl}^2$	MS ₄ /MS ₅
Pooled Error	L(G-1)(R-1)	MS ₅	σ_e^2	-

3.2.7 Data analysis for correlation and path analyses

3.2.7.1 Diagnosis of multicollinearity

Multicollinearity (also collinearity) is a situation where two or more predictors are highly and linearly associated and it affects the estimations regarding individual predictors but does not reduce the predictive power of the model. The analysis of multicollinearity between any explanatory traits is one of the assumptions that should be fulfilled for effective and reliable estimation of path coefficients (Bruno *et al.*, 2018). When the traits of interest show low heritability, the collinearity diagnosis is a fundamental phenomenon in plant breeding to make indirect selection more effective for genetic improvement. The estimated coefficients in the presence of moderate to severe multicollinearity problem may show illogical (more than unity) values (Coimbra *et al.*, 2005), and the variances associated with estimators of path coefficients may become inflated and leads to unreliable estimates (Olivoto *et al.*, 2017). So, the presence of multicollinearity for each predictor trait can be detected by examining the correlation matrix or by using variance inflation factor (VIF), tolerance limit (TOL), and eigenvalues. The existence of strong coefficients (close to ± 1) between a pair of explanatory traits in the correlation matrix indicates the possibility of multicollinearity between these traits (Viotto *et al.*, 2020) and it can be checked using VIF, TOL, and eigenvalues. The VIF, TOL, and eigenvalues were performed using the PROC REG with VIF, TOL, and COLLIN procedures of the SAS (SAS, 2012).

The VIF ($VIF = 1/(1 - R_j^2)$, where R_j^2 is the coefficient of determination for the prediction of a j^{th} variable by the predictor variables) measures how much the variance of an estimated regression coefficient is increased due to the effect of the multicollinearity and value exceeds 10 is an indication that the associated regression coefficients are poorly estimated because of multicollinearity (Montgomery, 2001). The TOL is the inverse of VIF and its value greater than 0.1 indicates the occurrence of severe collinearity in the database (Montgomery, 2001). The eigenvalues were used to estimate the condition number (CN) for each trait. The CN can be computed by dividing the largest eigenvalue (λ_{max}) to the successive smaller eigenvalue (λ_{min}) in the correlation matrices as suggested by Montgomery and Peck (1982). According to Montgomery *et al.* (2012), the degree of multicollinearity in the matrices was classified as weak when the estimates of CN were less than 100; estimates between 100 and 1000 were considered moderate, and values greater than 1000 were reported as severe multicollinearity problem. The multicollinearity problem can be also detected via the simultaneous use of eigenvalues and eigenvectors. Accordingly, the traits having low eigenvalue along with high

corresponding eigenvector indicate the existence of a remarkable collinearity problem in the dataset hence, excluding the traits which are responsible for inflating the variance of regression coefficient is crucial unless the trait is our interest for improvement (Olivoto *et al.*, 2017). So, culling the multicollinearity-generating traits from the analysis is a simpler and more effective method to overcome this problem, and it allows estimating the most accurate path coefficients (Olivoto *et al.*, 2017; Bruno *et al.*, 2018; Viotto *et al.*, 2020). Accordingly, the multicollinearity test was performed between the studied traits using the correlation matrices, VIF, TOL, CN, and the eigen-system analysis of the correlation matrix. Based on these multicollinearity diagnosis tests, traits such as days to forage and seed harvests, botanical fractions yields (leaf, stem, and panicle), grain filling period, total biological yield, and straw yield were excluded from the analysis because these traits were highly responsible for multicollinearity in the matrix. The remaining sixteen (about 67%) of the studied traits were considered for analysis due to their low multicollinearity problem.

3.2.7.3 Phenotypic and genotypic correlations

The collected data from the two locations were combined and subjected to correlation and path coefficients analyses. Correlation analysis was performed for all possible combinations of traits after diagnosing the multicollinearity test. Phenotypic correlation, the observable correlation between two explanatory traits, which includes both genotypic and environmental effects, and genotypic correlation, the inherent association between two explanatory traits, were computed from the components of variance and co-variances as described by Singh and Chaudhury (1996). The coefficient of correlation was tested using 'r' tabulated value at n-2 degrees of freedom, at 5, 1, and 0.1% probability level, where n is the number of genotypes.

$$rp_{xy} = \frac{Pcov_{(x,y)}}{\sqrt{\sigma^2 p_x * \sigma^2 p_y}} \quad rg_{xy} = \frac{Gcov_{(x,y)}}{\sqrt{\sigma^2 g_x * \sigma^2 g_y}}$$

where rp and rg are phenotypic and genotypic correlation coefficient between traits x and y, $Pcov_{(x,y)}$ and $Gcov_{(x,y)}$ are phenotypic and genotypic covariance between traits x and y; $\sigma^2 p_x$ and $\sigma^2 p_y$ are phenotypic variance for traits x and y; $\sigma^2 g_x$ and $\sigma^2 g_y$ are genotypic variance for traits x and y, respectively.

3.2.7.3 Path-coefficient analysis

The correlation coefficient was further partitioned into direct and indirect effects using path coefficient analysis as suggested by Dewey and Lu (1959) and developed by Wright (1921).

Path analysis determines whether the cause-and-effect association between two explanatory traits is true and independent of the other traits. In the path coefficient analysis, FDMY and GY were selected as the resultant (dependent) traits and the rest of the traits were used as the causal (predictor) traits. The FDMY was also considered as an independent trait in the path coefficient analysis for GY and vice versa. The direct and indirect effects of the independent traits on FDMY and GY were estimated using the following general formula as applied by Dewey and Lu (1959):

$$r_{ij} = P_{ij} + \sum r_{ik} * P_{kj}$$

where r_{ij} is mutual association between the independent trait (i) and dependent trait (j) as measured by the genotypic and phenotypic correlation coefficients; P_{ij} is components of direct effects of the independent trait (i) on the dependent trait (j) as measured by the genotypic and phenotypic path-coefficients; and $\sum r_{ik} * P_{kj}$ is the summation of components of indirect effects of a given independent trait (i) on a given dependent trait (j) via all other independent trait (k). To determine P_{ij} values, square matrices of the correlation coefficients between independent traits in all possible pairs were inverted and then multiplied by the correlation coefficients between the independent and dependent traits.

Path coefficient analysis was performed based on mean data across the two locations using phenotypic and genotypic correlation matrices set up as $X = Y^{-1} * Z$ for FDMY and GY. In this matrix, vector 'X' represents the phenotypic and genotypic correlation coefficients of dependent traits (FDMY and GY) versus independent quantitative traits. Similarly, vector 'Y' is the inversed value of phenotypic and genotypic correlations for all possible combinations among the studied traits and vector 'Z' is the direct effect of path coefficients. The causal traits of the correlation coefficient matrix which includes reciprocals and autocorrelations were inverted and the inverse of matrix 'Y' was calculated using the matrix inverse (MINVERSE) function of Microsoft Excel 2010. The direct effect of path coefficients was calculated as the product of vector 'X' and each row of vector 'Y' inverse using the matrix multiplication (MMULT) function of Microsoft Excel 2010. The indirect effect of the path coefficient was estimated by multiplying the value of direct effect the path coefficient with the correlation coefficient in the matrix as suggested by Dewey and Lu (1959). The coefficient of determination (R^2) is the summation of the product of direct effect in the path analysis with the corresponding coefficient of a dependent trait in the correlation

analysis via all predictor traits. The contribution of the remaining unknown factor was measured as the residual factor (RF), which was calculated with the following formula;

$$RF = \sqrt{1 - R^2} \quad \text{where } R^2 = (\sum P_{ij} * r_{ij})$$

The magnitude of RF indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1999). That is, if RF value is small (for instance, nearly zero), the dependent trait considered is fully explained by the variability in the predictor traits, whereas higher RF value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent trait.

3.2.8 Data analysis for multivariate analysis

3.2.8.1 Data standardization

The mean data were standardized prior to multivariate analysis (cluster, genetic distance, and principal component analyses) using the Minitab 17.1 software (Minitab, 2013). Accordingly, the mean data measured for each trait was standardized to means of zero and variances of unity before analysis to avoid bias due to differences in measurement scales (Manly, 1986; Martinez-Calvo *et al.*, 2008). Traits that had low eigenvalue along with the highest corresponding eigenvector in absolute value were culled from the analysis unless the trait is our interest for improvement (Olivoto *et al.*, 2017). Excluding these traits is very important for reliable estimates of improvement because these traits contribute little to discriminating between individuals (De Carvalho *et al.*, 2022). Based on this criterion, traits such as days to forage and seed harvests, botanical fractions yields (leaf, stem, and panicle), grain filling period, total biological yield, and straw yield were excluded from the analysis because these traits had little discriminating ability for improvement. The remaining sixteen (about 67%) of the studied traits were considered for multivariate analysis.

3.2.8.2 Cluster analysis

The cluster number for the genotypes was determined by the average linkage method using the PROC cluster procedures of the SAS software version 9.4 (SAS, 2012). The pseudo F and t^2 statistics obtained from the PROC cluster procedure of the SAS were used to determine the number of clusters. Based on these two statistics, points, where a local peak of the pseudo-F statistic joined with a small value of the pseudo t^2 statistic followed by a larger

pseudo t^2 for the next cluster fusion were used to decide the optimum number of clusters (Milligan and Cooper, 1985; Gemechu, 2012). After determining the cluster numbers, the grouping of the genotypes into different clusters was carried out by Ward's agglomerative hierarchical classification with Euclidian distance (Ward, 1963) method as a measure of dissimilarity using the PAST (PAleontological STatistics) software (Hammer *et al.*, 2001). The cut-off line on the dendrogram was then drawn using the average inter-cluster distance value at which the number of genotypes within each cluster was determined. The rectangular tree dendrogram developed by the PAST software (Hammer *et al.*, 2001) was used to construct the polar tree dendrogram using the tree figure drawing (FigTree version 1.4.3) software (Andrew, 2016). Moreover, discriminant function analysis was performed to reassess the clustering of the genotypes using the Minitab 17.1 software (Minitab, 2013).

3.2.8.3 Genetic distance analysis

The relationship among the cluster was assessed by determining the cluster genetic distance using Mahalanobis distance (D^2) statistics (Mahalanobis, 1936). The intra and inter-cluster genetic divergence were estimated by generalized Mahalanobis's D^2 statistics using the PROC discrim procedures of the SAS version 9.4 (SAS, 2012). The D^2 values obtained for pairs of clusters were considered as the calculated chi-square (χ^2) values and these values were tested against the tabulated χ^2 value for 'P' degree of freedom, where P indicates the number of traits considered (Singh and Chaudhary, 1985). Genetic distance between clusters as standardized by Mahalanobis's D^2 statistics was calculated as: $D^2_{ij} = (x_i - x_j)' \text{cov}^{-1} (x_i - x_j)$, where, D^2_{ij} = distance between cases i and j; x_i and x_j = vectors of the values of the variables for cases i and j; and cov^{-1} = the pooled within-groups variance-covariance matrix.

3.2.8.4 Principal component analysis

The principal component analysis (PCA) was used to find out the traits that accounted for most of the total variation. The PCA components with cumulative variability must explain at least 75% of the total variability to have a meaningful dispersion of genotypes (Govindaraj *et al.*, 2020). Principal components (PCs) with eigenvalues greater than unity were used as criteria to determine the number of PCs (Kaiser, 1960; Iezzoni and Pritts, 1991). The sum of the eigenvalues is equal to the number of traits used for the study and these values often decrease progressively with increasing the number of PCs. The eigenvectors of the PCs were compared among the traits to identify the traits that accounted for the highest variation for each PC, and traits that had higher eigenvectors in the absolute value were considered for

selection due to their high contribution to yield improvement (Dhakar *et al.*, 2019). The PCs' eigenvalues and eigenvectors were estimated based on the correlation matrix analysis using the Minitab 17.1 statistical software (Minitab, 2013). Moreover, scree plots and biplot loadings and scatter plot diagrams for the first two PCs were constructed using the Minitab 17.1 statistical software (Minitab, 2013).

3.3 Results

3.3.1 Agro-morphological variability

3.3.1.1 Analysis of variance

The pooled analysis of variance revealed that half of the studied traits were significantly influenced by the test locations (Table 3.5). Among the traits, tillers dry weight (TDW), the largest leaf length at forage harvest (LLFH), days to forage harvest (DFH), panicle length at grain harvest (PLGH), and number of spikelets per panicle (NSLPP) varied ($P \leq 0.0001$) between locations. Likewise, the number of leaves at forage harvest (NLFP), number of spikes per panicle (NSPP), grain sink filling rate (GSFR), and harvest index (HI) differed ($P \leq 0.01$) while differences ($P \leq 0.05$) were also noted for days to seed harvest (DSH), straw yield (SY), and grain yield (GY) between locations. However, forage dry matter yield (FDMY) and its related traits like the number of tillers per plant (NTPP), plant height at forage harvest (PHFH), leaf dry matter yield (LDMY), stem dry matter yield (SDMY), panicle dry matter yield (PDMY), and forage yield production rate (FYPR) and GY related traits such as plant height at grain harvest (PHGH), grain filling period (GFP), total biological yield (TBY), biological yield production rate (BYPR), and thousand seed weight (TSW) did not show significant variations between the test locations. The tested genotypes also showed variation ($P \leq 0.0001$) for all measured traits. Furthermore, the genotype x location interaction effect displayed significant differences for all traits except PDMY and FYPR. The interactions of genotype x location for FDMY and GY were crossover showing the genotypes performed differently with rank change across locations (Figures 3.2a and 3.2b).

Table 3.5 Mean squares from a combined ANOVA for 24 traits of 120 oat genotypes grown at Holetta and Ada-Berga in 2020/21 cropping season

Traits	Mean squares					CV (%)
	Location (L) (df = 1)	Rep(L) (df = 4)	Genotype (G) (df = 119)	GxL (df = 119)	Error (df = 476)	
Number of tillers per plant	1.15 ^{NS}	12.60***	1.20***	0.56*	0.40	25.75
Tillers dry weight (g)	25384.00***	72.79***	71.10***	24.26***	7.90	8.57
Number of leaf at forage harvest	105.65**	1.35***	3.08***	0.42*	0.31	11.64
Largest leaf length at forage harvest (cm)	4428.78***	32.82 ^{NS}	120.40***	61.57***	28.50	13.87
Plant height at forage harvest (cm)	1825.96 ^{NS}	328.15*	823.48***	171.91**	119.16	8.86
Days to forage harvest	28125.00***	15.52*	547.21***	29.06***	5.45	1.82
Leaf dry matter yield (t/ha)	107.65 ^{NS}	33.03***	8.94***	3.61*	2.75	23.28
Stem dry matter yield (t/ha)	251.22 ^{NS}	92.19***	9.45***	3.51*	2.79	21.33
Panicle dry matter yield (t/ha)	42.24 ^{NS}	51.69***	6.49***	2.35 ^{NS}	2.00	25.43
Forage yield production rate (kg/ha/day)	3108.36 ^{NS}	11765.88***	5116.98***	1548.26 ^{NS}	1239.39	21.83
Forage dry matter yield (t/ha)	387.79 ^{NS}	194.59***	70.79***	25.21*	19.86	21.72
Plant height at grain harvest (cm)	8.67 ^{NS}	348.71*	874.79***	167.28***	107.32	8.18
Panicle length at grain harvest (cm)	2447.58***	18.32 ^{NS}	284.38***	54.44***	10.09	7.85
Days to seed harvest	1659.23*	178.86***	687.03***	162.22***	1.68	0.72
Grain filling period (Days)	150.33 ^{NS}	669.97***	475.94***	202.80***	12.56	5.16
Number of spikes per panicle	590.06**	11.43 ^{NS}	62.59***	19.55***	12.15	14.53
Number of spikelets per panicle	12506.67***	117.81 ^{NS}	769.14***	259.22***	58.81	16.63
Total biological yield (t/ha)	2.58 ^{NS}	57.53*	68.32***	38.04***	20.83	19.67
Biological yield production rate (kg/ha/day)	1809.44 ^{NS}	1447.56 ^{NS}	3252.90***	1411.95***	672.53	19.86
Grain sink filling rate (kg/ha/day)	74113.28**	2143.83*	4366.81***	2041.28***	650.90	23.66
Straw yield (t/ha)	197.40*	23.79 ^{NS}	45.26***	20.69***	12.53	22.18
Thousand seed weight (g)	1733.21 ^{NS}	321.68***	99.92***	13.84***	7.93	5.81
Harvest index (%)	5058.85**	205.41***	239.79***	45.81***	26.19	16.33
Grain yield (t/ha)	246.05*	22.29***	16.05***	5.74***	2.74	22.85

df = Degree of freedom; CV = Coefficient of variation; NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively; Rep (L) = Replication nested under location.

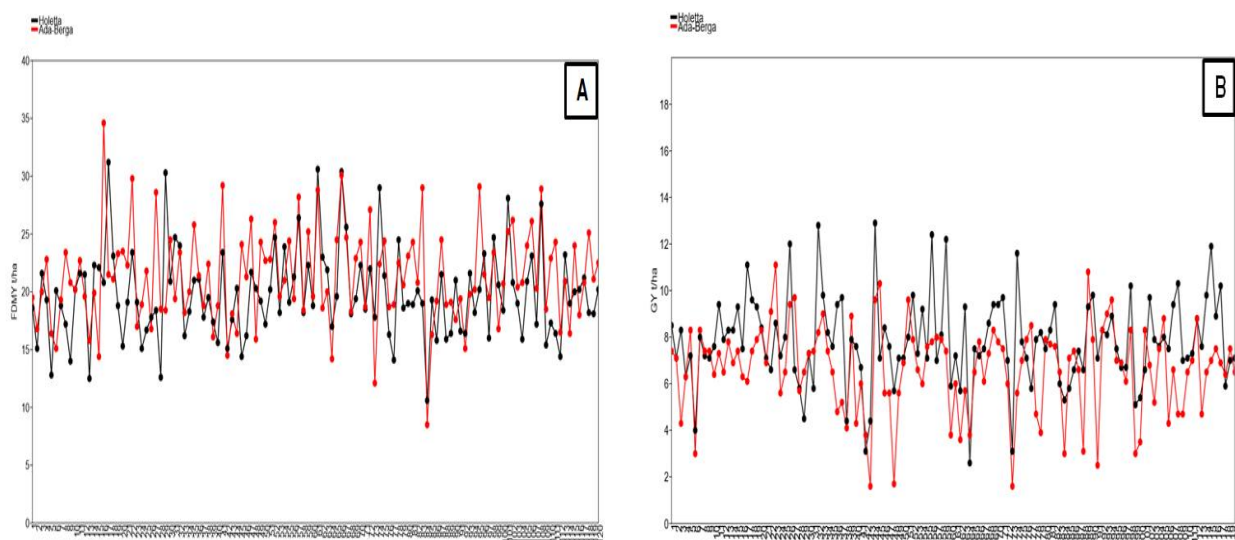


Figure 3.2 Genotype by location interaction (crossover) for (A) forage dry matter yield; and (B) grain yield of 120 oat genotypes grown at two locations in 2020 cropping season

3.3.1.2 Descriptive statistics

The mean, range, standard deviation and standard error of the mean showed remarkable variations among oat genotypes in the studied phenotypic trait (Table 3.6). The result showed that the high yielding-genotype had yield advantages of 367, 219, 180, and 149% over the low-yielding genotype in terms of GY, FDMY, SY and TBV, respectively. The high rate of yield per hectare daily accumulating genotype had 418, 200 and 182% advantages over the low rate of accumulating genotype in GSFR, FYPR and BYPR, respectively. The phenological traits illustrated that early maturing genotype were harvested about 31 and 43 days earlier than late maturing genotype for GY and FDMY, respectively. Forage yield- related traits like PHFH (83%), NLFH (103%), NTPP (147%), SDMY (179%), LDMY (219%), and PDMY (291%) were higher for genotypes which had higher trait performance compared to the corresponding low-performing genotypes for the traits considered. Among the studied traits, FYPR, GSFR, and BYPR had relatively high standard deviations (SD) which were greater than 20. Likewise, PHFH, PHGH, NSLPP, DSH, DFH, and GFP had moderate SD, which were between 10 and 20, while the remaining 15 (about 63%) of the considered traits had low SD, which were less than 10.

Table 3.6 Mean, range, standard deviation, and standard error of mean for 24 traits of 120 oat genotypes grown at Holetta and Ada-Berga in 2020/21 cropping season

Traits	Mean	Range			SD	SEM (±)
		Min.	Max.	Diff.		
Number of tillers per plant	2.5	1.7	4.2	2.5	0.79	0.03
Tillers dry weight (g)	32.8	24.6	44.0	19.4	7.53	0.28
Number of leaf at forage harvest	4.8	3.5	7.1	3.6	0.97	0.04
Largest leaf length at forage harvest (cm)	38.5	26.8	48.1	21.3	7.44	0.28
Plant height at forage harvest (cm)	123.2	85.2	155.7	70.5	15.75	0.59
Days to forage harvest	128.0	115.8	158.7	42.9	11.76	0.44
Leaf dry matter yield (t/ha)	7.1	3.2	10.2	7.0	2.06	0.08
Stem dry matter yield (t/ha)	7.8	4.2	11.7	7.5	2.20	0.08
Panicle dry matter yield (t/ha)	5.6	2.2	8.6	6.4	1.77	0.07
Forage yield production rate (kg/ha/day)	161.3	79.9	239.9	160.0	44.65	1.66
Forage dry matter yield (t/ha)	20.5	9.5	30.3	20.8	5.54	0.21
Plant height at grain harvest (cm)	126.6	85.7	154.3	68.6	15.67	0.58
Panicle length at grain harvest (cm)	40.5	24.0	57.3	33.3	8.14	0.30
Days to seed harvest	179.3	169.0	199.8	30.8	12.04	0.45
Grain filling period (Days)	68.7	49.8	87.7	37.9	11.16	0.42
Number of spikes per panicle	24.0	16.0	33.6	17.6	4.75	0.18
Number of spikelets per panicle	46.1	24.1	82.6	58.5	15.07	0.56
Total biological yield (t/ha)	23.2	11.9	29.6	17.7	5.63	0.21
Biological yield production rate (kg/ha/day)	130.6	62.0	174.9	112.9	35.04	1.31
Grain sink filling rate (kg/ha/day)	107.8	34.5	178.8	144.3	40.08	1.49
Straw yield (t/ha)	16.0	7.8	21.8	14.0	4.43	0.17
Thousand seed weight (g)	48.4	36.8	62.3	25.5	5.32	0.20
Harvest index (%)	31.3	16.0	46.4	30.4	8.53	0.32
Grain yield (t/ha)	7.2	2.4	11.2	8.8	2.43	0.09

Min. = Minimum; **Max.** = Maximum; **Diff.** = Difference between maximum and minimum values; **SD** = Standard deviation; **SEM** (±) = Standard error of the mean.

3.3.1.3 Effect of test locations

The effect of experimental locations on the mean performance of phenotypic trait in oat genotypes is illustrated in Table 3.7. The results indicated that some of the measured traits were significantly influenced by the test locations. Among the traits, NLFH, LLFH, NSPP, NSLPP, GSFR, HI, and GY were significantly higher at Holetta compared to Ada-Berga. On the other hand, the genotypes had significantly higher performances in TDW, PLGH, SY, and longer DFH and DSH at Ada-Berga. The rates of accumulation for GY, FDMY, and TBY were higher by 21, 3, and 3% at Holetta compared to Ada-Berga, respectively. The observed GY and TBY were higher by 16 and 1% at Holetta, whereas FDMY and SY were higher by 8 and 7% at Ada-Berga, respectively. The noted HI and TSW were higher by 19 and 7% at Holetta compared to Ada-Berga, respectively. On the contrary, the traits like NTPP, PHFH, LDMY, SDMY, PDMY, FYPR, FDMY, PHGH, GFP, TBY, BYPR and TSW were less sensitive to changing environments, indicating the low influence of environmental factors on these traits.

Table 3.7 Mean performance of 24 traits in 120 oat genotypes grown at Holetta and Ada-Berga in 2020/21 cropping season

Traits	Location		R ²	P-value
	Holetta	Ada-Berga		
Number of tillers per plant	2.4	2.5	0.57	0.7784
Tillers dry weight (g)	26.9 ^b	38.7 ^a	0.91	<.0001
Number of leaf at forage harvest	5.2 ^a	4.4 ^b	0.78	0.0005
Largest leaf length at forage harvest (cm)	41.0 ^a	36.0 ^b	0.66	<.0001
Plant height at forage harvest (cm)	121.6	124.8	0.68	0.0768
Days to forage harvest	121.8 ^b	134.3 ^a	0.97	<.0001
Leaf dry matter yield (t/ha)	6.7	7.5	0.57	0.1457
Stem dry matter yield (t/ha)	7.2	8.4	0.62	0.1744
Panicle dry matter yield (t/ha)	5.8	5.3	0.58	0.4179
Forage yield production rate (kg/ha/day)	163.3	159.2	0.59	0.6373
Forage dry matter yield (t/ha)	19.8	21.3	0.57	0.2326
Plant height at grain harvest (cm)	126.5	126.7	0.71	0.8894
Panicle length at grain harvest (cm)	38.6 ^b	42.3 ^a	0.90	<.0001
Days to seed harvest	177.8 ^b	180.8 ^a	0.99	0.0442
Grain filling period (Days)	68.3	69.2	0.93	0.6892
Number of spikes per panicle	24.9 ^a	23.1 ^b	0.64	0.0002
Number of spikelets per panicle	50.3 ^a	41.9 ^b	0.83	<.0001
Total biological yield (t/ha)	23.3	23.1	0.57	0.8581
Biological yield production rate (kg/ha/day)	132.2	129.0	0.64	0.3872
Grain sink filling rate (kg/ha/day)	118.0 ^a	97.7 ^b	0.73	0.0009
Straw yield (t/ha)	15.4 ^b	16.5 ^a	0.58	0.0418
Thousand seed weight (g)	50.0	46.9	0.81	0.0806
Harvest index (%)	34.0 ^a	28.7 ^b	0.76	0.0057
Grain yield (t/ha)	7.8 ^a	6.7 ^b	0.69	0.0253

Different superscript letters for each trait between two locations indicate significant variation at $P < 0.05$.

3.3.1.4 Mean performance of genotypes

The numbers of superior and inferior oat genotypes over population mean and mean of nine released varieties based on phenotypic trait performance are depicted in [Figure 3.3](#). The number of superior genotypes showed higher performances in 8 (about 33%) and 14 (about 58%) of the studied traits over the population mean and mean of released varieties, respectively. The numbers of superior genotypes over the population mean were higher for PHFH, PHGH, PLGH, TBY, BYPR, GSFR, SY and GY ([Figure 3.3a](#)). Similarly, the number of superior genotypes over the mean of released varieties was found higher for NTPP, NLFH, LLFH, PHFH, DFH, LDMY, SDMY, PDMY, FDMY, PHGH, PLGH, TBY, BYPR, and SY ([Figure 3.3b](#)). The differences between the number of superior and inferior genotypes over the mean of the population were relatively narrow compared to the mean of released varieties. However, the differences between the number of superior and inferior genotypes over the population mean were relatively wide for NTPP, NLFH, DFH, DSH, NSPP, and BYPR. Moreover, wide variations between the number of superior and inferior

genotypes over the mean of released varieties were observed for TDW, NLFH, LLFH, PHFH, DFH, PHGH, GFP, NSPP, NSLPP, SY, TSW, HI, and GY.

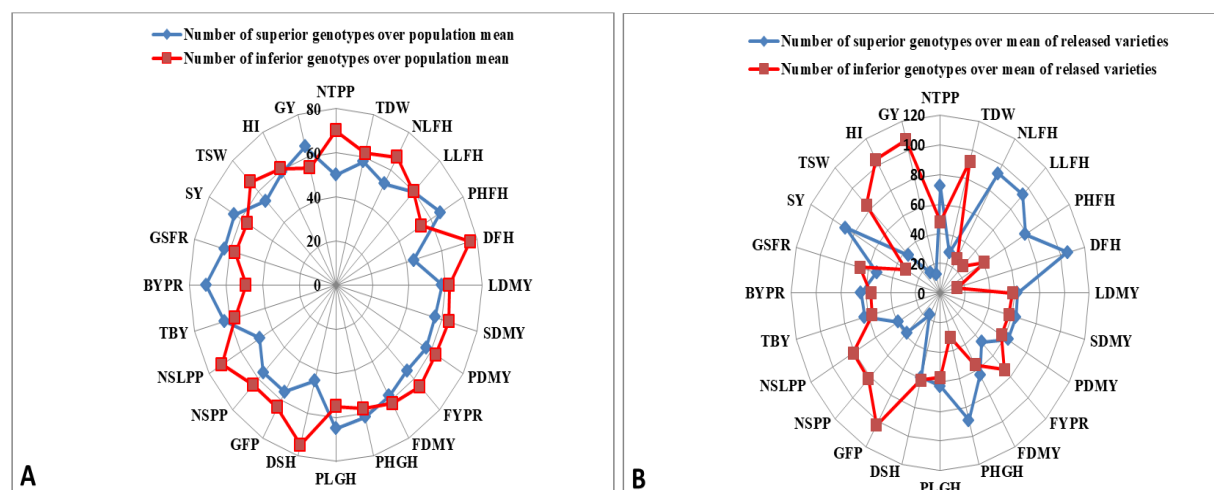


Figure 3.3 Number of superior and inferior genotypes over (A) population mean (B) mean of released varieties grown at Holetta and Ada-Berga in 2020/21 cropping season.
Note: See [Table 3.3](#) for description of abbreviated traits

The mean performance of the top 5% of forage yielder oat genotypes (S-122; T-1926513; CI-1480; CI-1677; Bona-bas; and CI-1674) was compared with the least 5% forage yielder genotypes (SRCPX80Ab1751; CI-1690; SRCPX80Ab2582; SRCPX80Ab2691; SRCPX80Ab2050; and Coker SR res 80SA 130), the mean of the population, and the mean of nine released varieties for studied traits ([Table 3.8](#)). The result revealed that the top forage yielder genotypes were superior over the least forage yielder genotypes, the mean of the population, and the mean of released varieties in NLFH, LLFH, PHFH, LDMY, SDMY, PDMY, FYPR, FDMY, PHGH, PLGH, NSPP, NSLPP, TBY, BYPR, and SY. However, the top forage yielder genotypes were inferior in TDW, GFP, TSW, and HI over the least forage yielder genotypes, the mean of the population, and the mean of released varieties. Similarly, the mean performance of the top 5% of seed yielder oat genotypes (SRCPX80Ab2806; SRCPX80Ab2267; CI-715; CI-1463; SRCPX80Ab2291; and A-505) were compared with the least 5% seed yielder genotypes (CI-1751; CI-1426; SRCPX80Ab2582; CI-1752; CI-1842; and CI-1690), the mean of the population, and the mean of released varieties as explained in [Table 3.8](#). The top seed yielder genotypes in this study were superior in TBY, BYPR, GSFR, TSW, HI, and GY over the least seed yielder genotypes, the mean of the population, and the mean of released varieties. On the contrary, the top seed yielder genotypes were inferior in NLFH, LLFH, PHFH, and PHGH over the least seed yielder genotypes, the mean of the population, and the mean of released varieties.

Table 3.8 Mean comparison of the top 5% forage and seed yielder genotypes with the least 5% genotypes, mean of population and released varieties for 24 traits of oat grown at Holetta and Ada-Berga in 2020/21 cropping season

Traits	High/low forage yielder genotypes							High/low seed yielder genotypes						
	Top	Bottom	MP	MRV	Differences			Top	Bottom	MP	MRV	Differences		
	(A)	(B)	(C)	(D)	(A-B)	(A-C)	(A-D)	(A)	(B)	(C)	(D)	(A-B)	(A-C)	(A-D)
NTPP	2.6	2.8	2.5	2.3	-0.2	0.1	0.3	2.3	3.0	2.5	2.3	-0.7	-0.2	0.0
TDW	32.2	32.5	32.8	35.2	-0.3	-0.6	-3.0	33.6	28.8	32.8	35.2	4.8	0.8	-1.6
NLFH	4.9	4.3	4.8	4.3	0.6	0.1	0.6	4.1	5.7	4.8	4.3	-1.6	-0.7	-0.2
LLFH	38.8	34.9	38.5	35.1	3.9	0.3	3.7	35.0	39.6	38.5	35.1	-4.6	-3.5	-0.1
PHFH	136.8	111.8	123.2	117.7	25.0	13.6	19.1	113.8	118.1	123.2	117.7	-4.3	-9.4	-3.9
DFH	127.3	127.1	128.0	118.5	0.2	-0.7	8.8	119.6	147.6	128.0	118.5	-28.0	-8.4	1.1
LDMY	9.7	4.9	7.1	7.0	4.8	2.6	2.7	6.6	5.8	7.1	7.0	0.8	-0.5	-0.4
SDMY	10.9	5.5	7.8	7.6	5.4	3.1	3.3	7.4	6.4	7.8	7.6	1.0	-0.4	-0.2
PDMY	7.7	3.5	5.6	5.4	4.2	2.1	2.3	5.3	4.3	5.6	5.4	1.0	-0.3	-0.1
FYPR	222.7	110.3	161.3	168.9	112.4	61.4	53.8	161.5	112.2	161.3	168.9	49.3	0.2	-7.4
FDMY	28.3	13.9	20.5	20.0	14.4	7.8	8.3	19.3	16.5	20.5	20.0	2.8	-1.2	-0.7
PHGH	138.8	115.4	126.6	120.4	23.4	12.2	18.4	114.5	126.6	126.6	120.4	-12.1	-12.1	-5.9
PLGH	43.0	32.5	40.5	40.9	10.5	2.5	2.1	39.1	32.1	40.5	40.9	7.0	-1.4	-1.8
DSH	176.4	186.6	179.3	175.6	-10.2	-2.9	0.8	176.1	198.3	179.3	175.6	-22.2	-3.2	0.5
GFP	66.7	78.4	68.7	79.1	-11.7	-2.0	-12.4	77.6	67.3	68.7	79.1	10.3	8.9	-1.5
NSPP	26.9	23.4	24.0	25.4	3.5	2.9	1.5	24.7	20.9	24.0	25.4	3.8	0.7	-0.7
NSLPP	58.1	36.0	46.1	48.8	22.1	12.0	9.3	41.3	34.3	46.1	48.8	7.0	-4.8	-7.5
TBY	26.6	18.4	23.2	23.2	8.2	3.4	3.4	24.6	17.1	23.2	23.2	7.5	1.4	1.4
BYPR	152.2	100.2	130.6	132.5	52.0	21.6	19.7	140.1	86.2	130.6	132.5	53.9	9.5	7.6
GSFR	112.0	74.3	107.8	112.8	37.7	4.2	-0.8	137.8	48.4	107.8	112.8	89.4	30.0	25.0
SY	19.4	12.6	16.0	14.4	6.8	3.4	5.0	14.2	13.8	16.0	14.4	0.4	-1.8	-0.2
TSW	44.0	53.0	48.4	50.0	-9.0	-4.4	-6.0	51.8	46.6	48.4	50.0	5.2	3.4	1.8
HI	27.4	31.1	31.3	38.7	-3.7	-3.9	-11.3	42.4	18.7	31.3	38.7	23.7	11.1	3.7
GY	7.3	5.8	7.2	8.8	1.5	0.1	-1.5	10.4	3.2	7.2	8.8	7.2	3.2	1.6

Top 5% high forage yielder oat genotypes (1st = S-122; 2nd = T-1926513; 3rd = CI-1480; 4th = CI-1677; 5th = Bona-bas; 6th = CI-1674); and 5% low forage yielder oat genotypes (115th = SRCPX80Ab1751; 116th = CI-1690; 117th = SRCPX80Ab2582; 118th = SRCPX80Ab2691; 119th = SRCPX80Ab2050; 120th = Coker SR res 80SA 130); Top 5% high seed yielder oat genotypes (1st = SRCPX80Ab2806; 2nd = SRCPX80Ab2267; 3rd = CI-715; 4th = CI-1463; 5th = SRCPX80Ab2291; 6th = A-505); and 5% low seed yielder oat genotypes (115th = CI-1751; 116th = CI-1426; 117th = SRCPX80Ab2582; 118th = CI-1752; 119th = CI-1842; 120th = CI-1690); MP = Mean of population; MRV = Mean of released varieties; See Table 3.3 for description of abbreviated traits

The performance of the top 5% of forage yielder genotypes for phenotypic trait is elucidated in [Table 3.9](#). The results indicated that the top 5% of forage yielder genotypes had different characteristics in the studied traits. The first top forage yielder genotype (S-122) had higher PHFH, SDMY, PDMY, FYPR, NSLPP, TBY, BYPR, SY, and GY. The genotype (T-1926513) which ranked as the second top forage yielder produced greater LDMY and PLGH, while the third top forage yielder genotype (CI-1480) was superior in GSFR and GY. The attributes of the fourth top forage yielder genotype (CI-1677) were higher in NTPP, NLFH, LLFH, DFH, and TSW. Higher PHGH, NSPP, and GY were the characteristics of the fifth top forage yielder genotype (Bona-bas), while the sixth top forage yielder genotype (CI-1674) showed higher TDW, DSH, GFP, HI, and GY. Except for the second and fourth top forage yielder genotypes, the remaining top 5% forage yielder genotypes produced comparable GY.

The top 5% of seed yielder genotypes for phenotypic trait performance is also displayed in [Table 3.9](#). The result revealed that there was a considerable variation among the top 5% seed yielder genotypes for measured traits. The first top seed yielder genotype (SRCPX80Ab2806) had higher GFP and HI. The second (SRCPX80Ab2267) top seed yielder genotype displayed intermediate characteristics for all traits except NTPP, TDW, LDMY, PDMY, FYPR, and FDMY. These mentioned traits generally showed lower mean values in the second top seed yielder genotypes compared to other top 5% seed yielder genotypes. The genotype (CI-715) which ranked as the third top seed yielder was superior in NLFH, LLFH, PHFH, DFH, LDMY, SDMY, PDMY, FYPR, FDMY, PHGH, PLGH, NSPP, TBY, and GSFR. Likewise, greater TDW, NSLPP, BYPR, and SY were the characteristics of the fourth top seed yielder genotype (CI-1463), while the fifth top seed yielder genotype (SRCPX80Ab2291) produced higher NTPP and DSH. The attributes of the sixth (A-505) top seed yielder genotype were greater in TSW and DSH. The fifth and sixth high seed yielder genotypes require comparable duration for seed maturity and are generally classified as late-maturing genotypes.

The performance of the top 5% of genotypes is compared with the mean of the population and the mean of released varieties based on selected phenotypic trait ([Table 3.10](#)). Although the genotypes differed in their performances, the top 5% of genotypes had better performances in all phenotypic traits compared to the mean of the population and released varieties. The selected genotypes required longer DFH and DSH compared to the mean of the population and released varieties. On average, the top 5% genotypes required 27 and 36

more days for DFH, 20 and 24 more days for DSH and 18 and 8 more days for GFP than the population mean and released varieties, respectively. Likewise, the top 5% genotypes had relative advantages of 40 and 34% in FYPR; 30 and 28% in BYPR; and 53 and 46% in GSFR over the mean of the population and released varieties, respectively. Moreover, FDMY, TBY, SY, and GY obtained from the top 5% of genotypes had relative advantages of 38, 25, 32, and 45% over the mean of the population and had relative advantages of 42, 25, 46, and 18% over the mean of released varieties, respectively.

The student t-test performed between mean of the top 5% of genotypes and mean of population varied ($P \leq 0.0001$) for all measured phenotypic trait ([Table 3.11](#)). The result indicated that the top 5% of genotypes had higher relative advantages in all phenotypic traits which ranged from 11% for days to seed harvest to 62% for NSLPP compared to mean performances of population. The selected genotypes had higher NTPP (44%), NLFH (38%), LLFH (22%), and PHFH (19%) over the mean of the population. Moreover, the botanical fraction yields such as LDMY, SDMY and PDMY had advantages of 38, 40, and 39% over mean of population, respectively. The rates of accumulation noted in GY, FDMY and TBY per hectare of land were higher daily by 53, 40, and 25% in the top 5% of genotypes compared to the mean of the population, respectively. Moreover, the GY, FDMY, SY, and TBY of the top 5% of genotypes had advantages of 44, 38, 32, and 25% over the mean performance of population, respectively.

Table 3.9 Mean performance of the top 5% forage and seed yielder genotypes for 24 traits of oat grown at Holetta and Ada-Berga in 2020/21 cropping season

Traits	Top 5% forage yielder genotypes						Top 5% seed yielder genotypes					
	1 st	2 nd	3 rd	4 th	5 th	6 th	1 st	2 nd	3 rd	4 th	5 th	6 th
Number of tillers per plant	2.5	2.4	2.6	2.9	2.5	2.7	2.3	2.0	2.4	2.3	2.5	2.3
Tillers dry weight (g)	28.7	32.9	34.5	30.1	31.0	35.8	34.1	32.5	32.6	34.7	33.1	34.3
Number of leaf at forage harvest	4.5	4.6	5.1	5.6	4.7	4.7	3.9	3.7	5.1	4.3	3.6	4.1
Largest leaf length at forage harvest (cm)	36.1	41.3	35.9	45.0	33.2	41.5	32.4	36.7	40.2	34.9	33.3	32.3
Plant height at forage harvest (cm)	145.5	140.8	124.3	134.6	143.3	132.2	112.0	109.8	123.4	118.3	101.8	117.5
Days to forage harvest	126.5	127.3	129.7	135.2	119.7	125.2	117.0	118.2	125.0	123.2	116.7	117.7
Leaf dry matter yield (t/ha)	10.0	10.2	9.4	9.5	9.7	9.6	6.1	6.1	8.0	6.8	6.3	6.1
Stem dry matter yield (t/ha)	11.7	11.2	11.4	10.9	10.1	9.9	7.2	6.8	9.1	7.9	6.6	7.0
Panicle dry matter yield (t/ha)	8.6	8.4	7.4	7.4	7.4	7.1	5.0	4.4	6.6	5.7	4.9	5.0
Forage yield production rate (kg/ha/day)	236.9	234.9	218.3	203.8	227.9	214.4	158.2	147.4	190.5	166.3	152.2	154.6
Forage dry matter yield (t/ha)	30.3	29.7	28.2	27.7	27.3	26.7	18.4	17.3	23.7	20.4	17.8	18.1
Plant height at grain harvest (cm)	139.2	144.7	127.0	137.2	147.2	137.2	109.2	109.3	128.2	121.5	105.3	113.2
Panicle length at grain harvest (cm)	41.1	52.9	35.1	37.1	43.0	48.8	41.2	40.6	43.0	39.8	40.0	30.2
Days to seed harvest	171.2	170.5	170.8	184.2	171.2	190.2	179.0	178.3	170.5	170.5	179.2	179.2
Grain filling period (Days)	66.8	57.8	58.2	60.3	74.3	82.8	87.0	84.2	61.5	62.7	85.0	85.0
Number of spikes per panicle	27.0	29.1	20.4	26.3	30.4	28.1	24.3	25.8	26.0	24.2	24.0	23.6
Number of spikelets per panicle	82.6	57.3	39.9	45.1	50.2	73.2	42.7	36.0	45.3	49.2	40.2	34.5
Total biological yield (t/ha)	29.3	28.0	27.8	23.5	27.7	23.5	24.7	24.4	26.6	26.6	22.7	22.5
Biological yield production rate (kg/ha/day)	171.2	164.6	163.1	128.2	161.9	124.0	137.5	136.6	156.3	156.7	127.1	126.3
Grain sink filling rate (kg/ha/day)	113.1	114.8	134.3	117.7	101.1	90.7	129.0	126.9	171.8	162.9	118.7	117.5
Straw yield (t/ha)	21.8	21.4	20.3	16.6	20.2	16.1	13.5	13.6	16.1	16.5	12.6	12.7
Thousand seed weight (g)	36.8	46.4	46.8	50.9	39.7	43.5	50.9	51.0	48.8	46.8	51.1	62.3
Harvest index (%)	25.9	23.8	26.2	29.6	27.0	32.1	45.7	43.4	39.4	37.7	44.3	43.9
Grain yield (t/ha)	7.5	6.6	7.5	6.9	7.5	7.5	11.2	10.7	10.5	10.1	10.0	9.9

Top 5% high forage yielder oat genotypes (1st = S-122; 2nd = T-1926513; 3rd = CI-1480; 4th = CI-1677; 5th = Bona-bas; 6th = CI-1674); 5% high seed yield producing genotypes (1st = SRCPX80Ab2806; 2nd = SRCPX80Ab2267; 3rd = CI-715; 4th = CI-1463; 5th = SRCPX80Ab2291; 6th = A-505).

Table 3.10 Mean performance comparison of the top 5% genotypes with mean of population and released varieties for selected traits of oat grown at Holetta and Ada-Berga in 2020/21 cropping season

Genotype	Mean	Relative advantage (%) over		Genotype	Mean	Relative advantage (%) over	
		MP	MRV			MP	MRV
1/ Days to forage harvest				6/ Total biological yield (t/ha)			
CI-1852	158.7	24.0	33.9	CI-1436	29.6	27.6	27.6
CI-1842	158.2	23.6	33.5	CI-1590	29.4	26.7	26.7
CI-1759	157.3	22.9	32.7	S-122	29.3	26.3	26.3
CI-1426	154.0	20.3	30.0	E-25	28.9	24.6	24.6
CI-1690	149.7	17.0	26.3	CI-1768	28.4	22.4	22.4
CI-1838	148.7	16.2	25.5	C-12	28.3	22.0	22.0
MP	128.0	-	8.0	MP	23.2	-	0.0
MRV	118.5	-7.4	-	MRV	23.2	0.0	-
2/ Forage yield production rate (kg/ha/day)				7/ Biological yield production rate (kg/ha/day)			
S-122	239.9	48.7	42.0	CI-1436	174.9	33.9	32.0
T-1926513	234.9	45.6	39.1	CI-1590	171.6	31.4	29.5
Bona-bas	227.9	41.3	34.9	S-122	171.2	31.1	29.2
CI-1768	222.7	38.1	31.9	E-25	168.8	29.2	27.4
CI-1480	218.3	35.3	29.2	CI-1768	166.3	27.3	25.5
CI-1672	214.9	33.2	27.2	T-1926513	164.6	26.0	24.2
MP	161.3	-	-4.5	MP	130.6	-	-1.4
MRV	168.9	4.7	-	MRV	132.5	1.5	-
3/ Forage dry matter yield (t/ha)				8/ Grain sink filling rate (kg/ha/day)			
S-122	30.3	47.8	51.5	CI-1436	178.8	65.9	58.5
T-1926513	29.7	44.9	48.5	CI-715	171.8	59.4	52.3
CI-1480	28.2	37.6	41.0	CI-1463	162.9	51.1	44.4
CI-1677	27.7	35.1	38.5	Jassari-27639	161.4	49.7	43.1
Bona-bas	27.3	33.2	36.5	CI-1853	156.5	45.2	38.7
CI-1674	26.7	30.2	33.5	CI-1629	155.1	43.9	37.5
MP	20.5	-	2.5	MP	107.8	-	-4.4
MRV	20.0	-2.4	-	MRV	112.8	4.6	-
4/ Days to seed harvest				9/ Straw yield (t/ha)			
CI-1546	199.8	11.4	13.8	S-122	21.8	36.3	51.4
CI-1720	199.7	11.4	13.7	CI-1590	21.6	35.0	50.0
CI-1496	199.5	11.3	13.6	T-1926513	21.4	33.8	48.6
D-28	199.2	11.1	13.4	E-25	20.7	29.4	43.8
CI-1838	199.0	11.0	13.3	MN-79983/85	20.5	28.1	42.4
SRCPX80Ab2582	199.0	11.0	13.3	CI-1768	20.5	28.1	42.4
MP	179.3	-	2.1	MP	16.0	-	11.1
MRV	175.6	-2.1	-	MRV	14.4	-10.0	-
5/ Grain filling period (Days)				10/ Grain yield (t/ha)			
SRCPX80Ab2310	87.7	27.7	10.9	SRCPX80Ab2806	11.2	55.6	27.3
SRCPX80Ab2691	87.5	27.4	10.6	SRCPX80Ab2267	10.7	48.6	21.6
CokerSRres80SA130	87.5	27.4	10.6	CI-715	10.5	45.8	19.3
SRCPX80Ab2806	87.0	26.6	10.0	CI-1463	10.1	40.3	14.8
Sorataf	85.8	24.9	8.5	SRCPX80Ab2291	10.0	38.9	13.6
SRCPX80Ab2475	85.7	24.7	8.3	A-505	9.9	37.5	12.5
MP	68.7	-	-13.1	MP	7.2	-	-18.2
MRV	79.1	15.1	-	MRV	8.8	22.2	

MP = Mean of population; MRV = Mean of released varieties

Table 3.11 Comparison of mean performances of selected top 5% genotypes with population mean performances for 24 traits of oat grown at Holetta and Ada-Berga in 2020/21 cropping season

Traits	Mean of selected genotypes ($\bar{X}$)	Population parameter (μ)	Change through selection ($\bar{X}-\mu$)	Change as % of pop. parameter (μ)	T
Number of tillers per plant	3.6	2.5	1.1	44.0	8.66***
Tillers dry weight (g)	41.1	32.8	8.3	25.3	9.73***
Number of leaf at forage harvest	6.6	4.8	1.8	37.5	14.37***
Largest leaf length at forage harvest (cm)	47.0	38.5	8.5	22.1	27.68***
Plant height at forage harvest (cm)	147.0	123.2	23.8	19.3	12.56***
Days to forage harvest	154.4	128.0	26.4	20.6	14.77***
Leaf dry matter yield (t/ha)	9.8	7.1	2.7	38.0	25.36***
Stem dry matter yield (t/ha)	10.9	7.8	3.1	39.7	12.67***
Panicle dry matter yield (t/ha)	7.8	5.6	2.2	39.3	10.15***
Forage yield production rate (kg/ha/day)	226.4	161.3	65.1	40.4	16.49***
Forage dry matter yield (t/ha)	28.3	20.5	7.8	38.0	13.62***
Plant height at grain harvest (cm)	148.9	126.6	22.3	17.6	17.33***
Panicle length at grain harvest (cm)	53.2	40.5	12.7	31.4	13.76***
Days to seed harvest	199.4	179.3	20.1	11.2	140.34***
Grain filling period (Days)	86.9	68.7	18.2	26.5	49.67***
Number of spikes per panicle	31.6	24.0	7.6	31.7	11.03***
Number of spikelets per panicle	74.6	46.1	28.5	61.8	16.82***
Total biological yield (t/ha)	29.0	23.2	5.8	25.0	26.14***
Biological yield production rate (kg/ha/day)	169.5	130.6	38.9	29.8	25.30***
Grain sink filling rate (kg/ha/day)	164.4	107.8	56.6	52.5	15.09***
Straw yield (t/ha)	21.1	16.0	5.1	31.9	21.30***
Thousand seed weight (g)	58.7	48.4	10.3	21.3	12.16***
Harvest index (%)	44.9	31.3	13.6	43.5	35.71***
Grain yield (t/ha)	10.4	7.2	3.2	44.4	15.74***

T = Student t-test; *** = significantly different at 0.1% probability level; the tabulated t-value at 5 degree of freedom is 6.869 for two-tailed and 5.894 for one-tailed at 0.1% probability.

3.3.1.5 Variance components and coefficient of variation

The magnitudes of variance components for measured traits in oat genotypes are indicated in Table 3.12. The estimates of variance components for the studied traits were highly variable and the values were very sensitive for inter-traits comparison owing to the existence of wide differences in traits measurement scales. The study revealed that the values of phenotypic variance were higher than the corresponding genotypic variance for all studied traits. Furthermore, the values of phenotypic variance were higher than the corresponding genotype x location interaction variance in all traits under consideration. The values of phenotypic variance were also higher than the corresponding environmental variances in TDW, NLFH, PHFH, DFH, PHGH, PLGH, DSH, GFP, NSLPP, GSFR, TSW, and HI. On the other hand, the values of genotypic variance were higher than the corresponding genotype x location interaction variance in all considered traits except LLFH, GFP, TBY, and GSFR. Similarly,

the values of genotypic variance were higher than the corresponding environmental variance in NLFH, DFH, PHGH, PLGH, DSH, GFP, NSLPP, TSW and HI, while 15 (about 63%) of the studied traits had higher environmental variance compared to genotypic variance. Fodder and grain yields were generally controlled by traits of yield components and were more influenced by environmental factors than yield related traits.

The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and environmental coefficient of variation (ECV) in oat genotypes for the studied traits are described in [Table 3.12](#). The result indicated that 16.7, 62.5 and 20.8% of the studied traits showed high, medium, and low PCV, respectively. The PCV values were generally higher than the corresponding GCV values in all measured traits. The highest PCV estimate was recorded for GSFR (25.03%) followed by NSLPP (24.56%), GY (22.72%), and HI (20.20%) while the lowest (5.97%) was recorded for DSH. Furthermore, the PCV values were comparatively higher than the corresponding ECV values in TDW, NLFH, PHFH, DFH, PHGH, PLGH, DSH, GFP, NSLPP, GSFR, TSW, and HI. Likewise, wide variability was observed in GCV and the values ranged from 5.22% for DSH to 20.00% for NSLPP. Among the studied traits, 62.5% of the traits had medium GCV while 37.5% had low GCV. The GCV estimates were relatively higher than the corresponding ECV values in NLFH, DFH, PHGH, PLGH, DSH, GFP, NSLPP, TSW, and HI. But, the observed ECV values ranged from 0.72% to 25.30% for traits studied. The highest ECV estimates were noted in NTPP (25.30%) followed by PDMY (25.25%), GSFR (23.67%), LDMY (23.36%), GY (22.99%), SY (22.12%), FYPR (21.83%), FDMY (21.74%), and SDMY (21.41%), while the lowest (0.72%) was recorded for DSH.

Table 3.12 Components of variance and coefficient of variation for 24 traits of 120 oat genotypes grown at Holetta and Ada-Berga in 2020/21 cropping season

Traits	Variance component						Coefficient of variation		
	σ^2_l	σ^2_r	σ^2_g	σ^2_{gl}	σ^2_e	σ^2_p	GCV	PCV	ECV
Number of tillers per plant	0.000	0.102	0.107	0.053	0.400	0.200	13.06	17.89	25.30
Tillers dry weight (g)	70.263	0.541	7.807	5.453	7.900	11.850	8.52	10.50	8.57
Number of leaf at forage harvest	0.289	0.009	0.443	0.037	0.310	0.513	13.87	14.93	11.60
Largest leaf length at forage harvest (cm)	12.119	0.036	9.805	11.023	28.500	20.067	8.13	11.64	13.87
Plant height at forage harvest (cm)	4.014	1.742	108.595	17.583	119.160	137.247	8.46	9.51	8.86
Days to forage harvest	78.016	0.084	86.358	7.870	5.450	91.202	7.26	7.46	1.82
Leaf dry matter yield (t/ha)	0.205	0.252	0.888	0.287	2.750	1.490	13.27	17.19	23.36
Stem dry matter yield (t/ha)	0.440	0.745	0.990	0.240	2.790	1.575	12.76	16.09	21.41
Panicle dry matter yield (t/ha)	0.000	0.414	0.690	0.117	2.000	1.082	14.83	18.57	25.25
Forage yield production rate (kg/ha/day)	0.000	87.721	594.787	102.957	1239.390	852.830	15.12	18.10	21.83
Forage dry matter yield (t/ha)	0.522	1.456	7.597	1.783	19.860	11.798	13.44	16.76	21.74
Plant height at grain harvest (cm)	0.000	2.012	117.918	19.987	107.320	145.798	8.58	9.54	8.18
Panicle length at grain harvest (cm)	6.625	0.069	38.323	14.783	10.090	47.397	15.29	17.00	7.84
Days to seed harvest	3.666	1.477	87.468	53.513	1.680	114.505	5.22	5.97	0.72
Grain filling period (Days)	0.000	5.478	45.523	63.413	12.560	79.323	9.82	12.96	5.16
Number of spikes per panicle	1.587	0.000	7.173	2.467	12.150	10.432	11.16	13.46	14.52
Number of spikelets per panicle	33.857	0.492	84.987	66.803	58.810	128.190	20.00	24.56	16.64
Total biological yield (t/ha)	0.000	0.306	5.047	5.737	20.830	11.387	9.68	14.54	19.67
Biological yield production rate (kg/ha/day)	0.000	6.459	306.825	246.473	672.530	542.150	13.41	17.83	19.86
Grain sink filling rate (kg/ha/day)	196.053	12.441	387.588	463.460	650.900	727.802	18.26	25.03	23.67
Straw yield (t/ha)	0.460	0.094	4.095	2.720	12.530	7.543	12.65	17.17	22.12
Thousand seed weight (g)	3.905	2.615	14.347	1.970	7.930	16.653	7.83	8.43	5.82
Harvest index (%)	13.427	1.494	32.330	6.540	26.190	39.965	18.17	20.20	16.35
Grain yield (t/ha)	0.613	0.163	1.718	1.000	2.740	2.675	18.21	22.72	22.99

σ^2_l = Location variance; σ^2_r = Replication variance; σ^2_g = Genotypic variance; σ^2_{gl} = Genotypic by location interaction variance; σ^2_e = Error variance; σ^2_p = Phenotypic variance; **PCV** = Phenotypic coefficient of variation; **GCV** = Genotypic coefficient of variation; **ECV** = Environmental coefficient of variation. **Note:** Zero value is reported for negative variance components.

3.3.1.6 Heritability and genetic advance

The estimate of heritability in a broad sense (h^2_b) for the studied agro-morphological traits in oat genotypes is presented in [Figure 3.4](#). The values of heritability varied widely and ranged from 44.3% to 94.7% for considered phenotypic traits. The result revealed that very high heritability (>80%) estimates were recorded for DFH (94.7%), NLFH (86.4%), TSW (86.1%), HI (80.9%), PHGH (80.9%), and PLGH (80.9%). The traits which showed moderately high heritability (60-79%) estimates were PHFH (79.1%), DSH (76.4%), FYPR (69.7%), NSPP (68.8%), NSLPP (66.3%), TDW (65.9%), FDMY (64.4%), GY (64.2%), PDMY (63.8%), and SDMY (62.9%). The remaining eight (about 33%) of the studied traits had medium heritability (40-59%) estimates which ranged from 44.3% for TBY to 59.6% for LDMY.

The genetic advance (GA) for measured phenotypic traits in oat genotypes is highly variable, as indicated in [Figure 3.4](#). Though the estimate of GA values is very sensitive to the scale of measurement, the magnitudes of GA for the studied traits ranged from 0.5 for NTPP to 35.0 kg/ha/day for FYPR. The estimated GA values for FDMY, TBY, SY, and GY were 4.0 t/ha, 3.2 t/ha, 2.9 t/ha, and 1.9 t/ha, respectively. Likewise, the observed GA values were 28.2 kg/ha/day for GSFR, 25.1 kg/ha/day for BYPR, 15.6 cm for PHGH, 14.9 cm for PHFH, 13.4 for DSH, 13.3 for DFH, 9.7 for GFP, 8.2 g for TSW, and 8.2% for HI.

The genetic advance as a percent of the means (GAM) for measured phenotypic traits in oat genotypes is also illustrated in [Figure 3.4](#). The result indicated that medium values of GAM produced traits were higher in number than traits having high GAM estimates. Among the studied traits, seven (about 29.2%) of the studied traits showed high GAM values while sixteen (about 66.7%) and one (about 4.1%) of the studied traits had moderate and low GAM values, respectively. The values of high GAM (>20%) were recorded for NSLPP (28.7%), GSFR (26.2%), GY (26.1%), HI (26.0%), PHGH (21.9%), FYPR (21.7%), and PDMY (21.3%). Similarly, medium GAM (10-20%) values were noted for NLFH (19.9%), FDMY (19.3%), BYPR (19.2%), LDMY (19.0%), NTPP (18.7%), SDMY (18.3%), SY (18.1%), NSPP (16.0%), GFP (14.1%), TBY (13.9%), PHGH (12.3%), TDW (12.2%), PHGH (12.1%), LLFH (11.7%), TSW (11.2%), and DFH (10.4). But, the estimate of GAM reported for DSH was below 10% indicating this trait had low GAM.

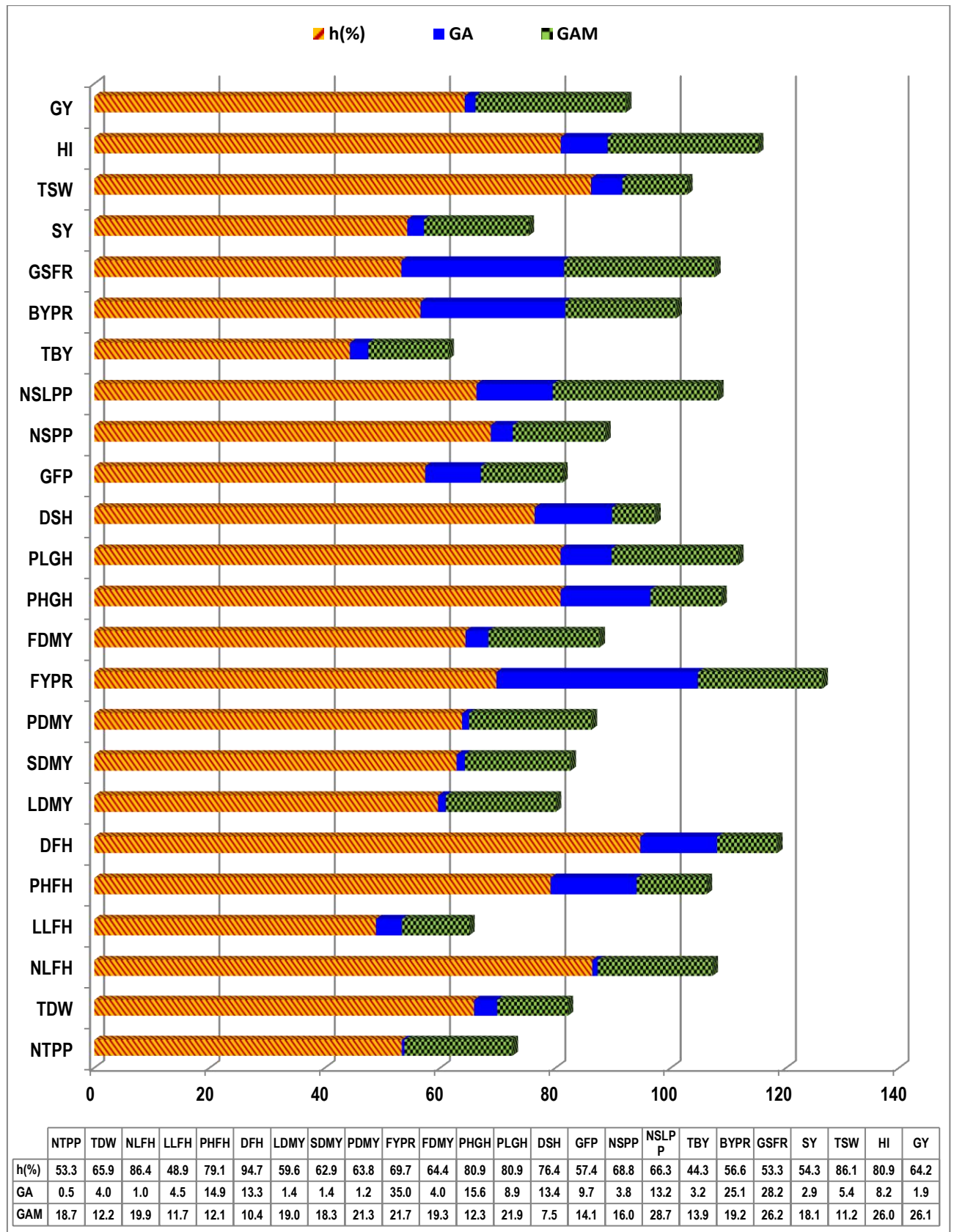


Figure 3.4 Broad sense heritability, genetic advance, and genetic advance as percent of mean for 24 traits of 120 oat genotypes grown at Holetta and Ada-Berga in 2020/21 cropping season. **Note:** h (%) = heritability in percent; GA = Genetic advance; GAM = Genetic advance as percent of mean; See [Table 3.3](#) for description of abbreviated traits

3.3.2 Correlation and path analyses

3.3.2.1 Phenotypic and genotypic correlations of fodder yield with other traits

Out of the tested 15 relations, 13 associations at the phenotypic level and 9 relations at the genotypic level were significant among FDMY and its yield contributing traits (Table 3.13). The results showed that FDMY had very highly significant positive phenotypic correlations with FYPR ($r_p = 0.94$), PHFH ($r_p = 0.62$), BYPR ($r_p = 0.61$), PHGH ($r_p = 0.59$), PLGH ($r_p = 0.44$), NSLPP ($r_p = 0.41$), GSFR ($r_p = 0.34$), and LLFH ($r_p = 0.33$), and highly significant positive phenotypic relation with NSPP ($r_p = 0.25$), and significant positive phenotypic associations with NLFH ($r_p = 0.22$), and GY ($r_p = 0.19$). It also had very highly significant negative phenotypic correlation with TSW ($r_p = -0.39$), and highly significant negative phenotypic association with HI ($r_p = -0.25$). Moreover, FDMY showed very highly significant positive genotypic associations with FYPR ($r_g = 0.99$), BYPR ($r_g = 0.40$), GY ($r_g = 0.32$), GSFR ($r_g = 0.31$), PHFH ($r_g = 0.25$), and PHGH ($r_g = 0.22$). It also had significant positive genotypic associations with PLGH ($r_g = 0.16$), LLFH ($r_g = 0.14$), and NSPP ($r_g = 0.13$).

3.3.2.2 Phenotypic and genotypic correlations of grain yield with other traits

In the present study, out of 15 relationships, 13 relations at the phenotypic level and 8 associations at the genotypic level were significant among GY and its yield contributing traits (Table 3.13). The results showed that GY had very highly significant positive phenotypic associations with GSFR ($r_p = 0.82$), HI ($r_p = 0.77$), BYPR ($r_p = 0.65$), TDW ($r_p = 0.45$), FYPR ($r_p = 0.42$), and NSPP ($r_p = 0.32$). It also had highly significant positive phenotypic correlation with TSW ($r_p = 0.26$), and significant positive phenotypic correlations with PLGH ($r_p = 0.22$), NSLPP ($r_p = 0.20$), and FDMY ($r_p = 0.19$). It also had very highly significant negative phenotypic correlations with NTPP ($r_p = -0.58$), NLFH ($r_p = -0.46$), and highly significant negative phenotypic association with LLFH ($r_p = -0.26$). The GY also showed very highly significant positive genotypic associations with GSFR ($r_g = 0.96$), BYPR ($r_g = 0.77$), HI ($r_g = 0.57$), FYPR ($r_g = 0.34$), and FDMY ($r_g = 0.32$). It also had highly significant positive genotypic association with PHGH ($r_g = 0.18$), and significant positive genotypic association with LLFH ($r_g = 0.15$), and NSPP ($r_g = 0.15$).

3.3.2.3 Phenotypic and genotypic correlation of yield-related traits

The linear pairwise correlations analysis indicated that out of 91 relations, 73 yield-related traits associations were significant at the phenotypic level (Table 3.13). The results revealed that the NTPP had very highly significant positive correlation with NLFH ($r_p = 0.45$) while very highly significant negative associations of NTPP were observed with TDW ($r_p = -0.54$) and FYPR ($r_p = -0.36$). The TDW was found to be very highly significant positive correlations with PLGH ($r_p = 0.48$), NSLPP ($r_p = 0.46$), TSW ($r_p = 0.40$), BYPR ($r_p = 0.39$), HI ($r_p = 0.33$), NSPP ($r_p = 0.31$), and FYPR ($r_p = 0.30$). It also had highly significant positive association with GSFR ($r_p = 0.29$) while very highly significant negative correlation with NLFH ($r_p = -0.31$). The NLFH had very highly significant positive relation with LLFH ($r_p = 0.39$) and highly significant positive association with PHGH ($r_p = 0.24$). It also had significant positive correlation with PHFH ($r_p = 0.22$) while very highly significant negative associations with HI ($r_p = -0.52$) and NSPP ($r_p = -0.44$). This trait also significantly and inversely correlated with BYPR ($r_p = -0.23$), TSW ($r_p = -0.22$), PLGH ($r_p = -0.20$), and GSFR ($r_p = -0.20$). The LLFH had very highly significant positive associations with PHFH ($r_p = 0.45$), PHGH ($r_p = 0.45$) and highly significant positive relation with PLGH ($r_p = 0.29$). It also had very highly significant negative association with HI ($r_p = -0.43$).

Table 3.13 also indicated that the PHFH had very highly significant positive phenotypic correlations with PHGH ($r_p = 0.91$), PLGH ($r_p = 0.63$), FYPR ($r_p = 0.56$), NSLPP ($r_p = 0.49$), BYPR ($r_p = 0.43$), and NSPP ($r_p = 0.32$). It also had very highly significant negative relation with HI ($r_p = -0.41$), and highly significant negative association with TSW ($r_p = -0.28$). The FYPR had very highly significant positive relations with BYPR ($r_p = 0.73$), PHFH ($r_p = 0.56$), PLGH ($r_p = 0.54$), PHGH ($r_p = 0.52$), NSLPP ($r_p = 0.50$), GSFR ($r_p = 0.45$), NSPP ($r_p = 0.42$) while highly significant negative relation with TSW ($r_p = -0.29$). The PHGH showed very highly significant positive associations with PLGH ($r_p = 0.69$), NSLPP ($r_p = 0.52$), BYPR ($r_p = 0.41$), and NSPP ($r_p = 0.37$) while very highly significant negative correlations with HI ($r_p = -0.53$), and TSW ($r_p = -0.38$). The PLGH indicated very highly significant positive associations with NSLPP ($r_p = 0.61$), BYPR ($r_p = 0.55$), and NSPP ($r_p = 0.41$), and significant positive association with GSFR ($r_p = 0.20$). The NSPP showed very highly significant positive correlations with NSLPP ($r_p = 0.67$), and BYPR ($r_p = 0.40$), and significant positive association with GSFR ($r_p = 0.22$). The NSLPP had very highly significant positive correlation with BYPR ($r_p = 0.43$), and significant positive association with GSFR ($r_p = 0.21$) while it had highly significant negative association with TSW ($r_p = -0.29$). The GSFR, HI,

TSW, and BYPR had very highly significant positive associations with BYPR ($r_p = 0.77$), GSFR ($r_p = 0.48$), HI ($r_p = 0.44$), and NSLPP ($r_p = 0.43$), respectively.

The analysis indicated that out of the total 91 relationships, 39 associations were significant at the genotypic level among yield contributing traits (Table 3.13). The results revealed that the NTPP had very highly significant positive association with TSW ($r_g = 0.22$), and had highly significant positive relation with TDW ($r_g = 0.18$). The TDW had significant negative correlation with HI ($r_g = -0.14$) while NLFH had significant positive association with LLFH ($r_g = 0.13$). The LLFH had very highly significant positive associations with PHFH ($r_g = 0.27$), and PHGH ($r_g = 0.22$), and highly significant positive relation with GSFR ($r_g = 0.17$). It had also significant positive associations with FYPR ($r_g = 0.16$), and BYPR ($r_g = 0.13$). The PHFH had very highly significant positive correlation with FYPR ($r_g = 0.24$), and highly significant positive associations with PHGH ($r_g = 0.18$), BYPR ($r_g = 0.18$), and GSFR ($r_g = 0.17$). It had also significant positive relation with TSW ($r_g = 0.14$). The FYPR showed very highly significant positive associations with BYPR ($r_g = 0.41$), GSFR ($r_g = 0.31$), and PHGH ($r_g = 0.24$). It had also significant positive correlations with PLGH ($r_g = 0.16$), and NSPP ($r_g = 0.13$). The PHGH showed very highly significant positive associations with NSLPP ($r_g = 0.47$), NSPP ($r_g = 0.40$), PLGH ($r_g = 0.35$), BYPR ($r_g = 0.27$), and significant positive association with GSFR ($r_g = 0.16$). The PLGH indicated that very highly significant positive correlations were found with NSPP ($r_g = 0.27$), and NSLPP ($r_g = 0.27$) while the significant negative association with HI ($r_g = -0.13$). The NSPP showed very highly significant positive correlation with NSLPP ($r_g = 0.61$), and significant positive association with GSFR ($r_g = 0.14$). The NSLPP and BYPR had significant positive relations with BYPR ($r_g = 0.16$), and TSW ($r_g = 0.13$), respectively. The BYPR and GSFR showed very highly significant positive correlations with GSFR ($r_g = 0.78$), and HI ($r_g = 0.52$), respectively.

Table 3.13 Phenotypic (above diagonal) and genotypic (below diagonal) correlations of 16 agro-morphological traits in 120 oat genotypes grown at Holetta and Ada-Berga

Trait	NTPP	TDW	NLFH	LLFH	PHFH	FYPR	FDMY	PHGH	PLGH	NSPP	NSLPP	BYPR	GSFR	TSW	HI	GY
NTPP		-0.54***	0.45***	0.13 ^{NS}	-0.09 ^{NS}	-0.36***	-0.13 ^{NS}	-0.05 ^{NS}	-0.44***	-0.31***	-0.31***	-0.53***	-0.40***	-0.17 ^{NS}	-0.39***	-0.58***
TDW	0.18**		-0.31***	-0.03 ^{NS}	0.17 ^{NS}	0.30***	0.10 ^{NS}	0.13 ^{NS}	0.48***	0.31***	0.46***	0.39***	0.29**	0.40***	0.33***	0.45***
NLFH	0.04 ^{NS}	-0.03 ^{NS}		0.39***	0.22*	-0.06 ^{NS}	0.22*	0.24**	-0.20*	-0.44***	-0.12 ^{NS}	-0.23*	-0.20*	-0.22*	-0.52***	-0.46***
LLFH	-0.04 ^{NS}	0.08 ^{NS}	0.13*		0.45***	0.14 ^{NS}	0.33***	0.45***	0.29**	-0.09 ^{NS}	0.18 ^{NS}	0.01 ^{NS}	-0.07 ^{NS}	-0.06 ^{NS}	-0.43***	-0.26**
PHFH	-0.09 ^{NS}	-0.06 ^{NS}	0.06 ^{NS}	0.27***		0.56***	0.62***	0.91***	0.63***	0.32***	0.49***	0.43***	0.11 ^{NS}	-0.28**	-0.41***	-0.04 ^{NS}
FYPR	-0.10 ^{NS}	0.00 ^{NS}	0.08 ^{NS}	0.16*	0.24***		0.94***	0.52***	0.54***	0.42***	0.50***	0.73***	0.45***	-0.29**	-0.01 ^{NS}	0.42***
FDMY	-0.10 ^{NS}	0.00 ^{NS}	0.10 ^{NS}	0.14*	0.25***	0.99***		0.59***	0.44***	0.25**	0.41***	0.61***	0.34***	-0.39***	-0.25**	0.19*
PHGH	0.08 ^{NS}	0.08 ^{NS}	0.12 ^{NS}	0.22***	0.18**	0.24***	0.22***		0.69***	0.37***	0.52***	0.41***	0.03 ^{NS}	-0.38***	-0.53***	-0.15 ^{NS}
PLGH	-0.05 ^{NS}	0.07 ^{NS}	-0.02 ^{NS}	-0.08 ^{NS}	-0.06 ^{NS}	0.16*	0.16*	0.35***		0.41***	0.61***	0.55***	0.20*	-0.16 ^{NS}	-0.11 ^{NS}	0.22*
NSPP	-0.01 ^{NS}	0.05 ^{NS}	0.00 ^{NS}	0.12 ^{NS}	-0.01 ^{NS}	0.13*	0.13*	0.40***	0.27***		0.67***	0.40***	0.22*	-0.16 ^{NS}	0.16 ^{NS}	0.32***
NSLPP	0.06 ^{NS}	0.03 ^{NS}	0.09 ^{NS}	0.03 ^{NS}	0.04 ^{NS}	0.06 ^{NS}	0.07 ^{NS}	0.47***	0.27***	0.61***		0.43***	0.21*	-0.29**	-0.04 ^{NS}	0.20*
BYPR	-0.04 ^{NS}	0.08 ^{NS}	-0.06 ^{NS}	0.13*	0.18**	0.41***	0.40***	0.27***	0.08 ^{NS}	0.16*	0.16*		0.77***	-0.14 ^{NS}	0.08 ^{NS}	0.65***
GSFR	-0.06 ^{NS}	0.00 ^{NS}	-0.04 ^{NS}	0.17**	0.17**	0.31***	0.31***	0.16*	0.00 ^{NS}	0.14*	0.12 ^{NS}	0.78***		0.10 ^{NS}	0.48***	0.82***
TSW	0.22***	0.08 ^{NS}	0.00 ^{NS}	-0.02 ^{NS}	0.14*	0.08 ^{NS}	0.08 ^{NS}	0.08 ^{NS}	0.05 ^{NS}	0.03 ^{NS}	0.04 ^{NS}	0.13*	0.08 ^{NS}		0.44***	0.26**
HI	-0.08 ^{NS}	-0.14*	-0.05 ^{NS}	0.00 ^{NS}	-0.04 ^{NS}	-0.03 ^{NS}	-0.04 ^{NS}	-0.11 ^{NS}	-0.13*	0.01 ^{NS}	-0.05 ^{NS}	-0.03 ^{NS}	0.52***	-0.06 ^{NS}		0.77***
GY	-0.11 ^{NS}	-0.03 ^{NS}	-0.06 ^{NS}	0.15*	0.12 ^{NS}	0.34***	0.32***	0.18**	0.00 ^{NS}	0.15*	0.10 ^{NS}	0.77***	0.96***	0.02 ^{NS}	0.57***	

NTPP = Number of tillers per plant; **TDW** = Tillers dry weight; **NLFH** = Number of leaves at forage harvest; **LLFH** = Largest leaf length at forage harvest; **PHFH** = Plant height at forage harvest; **FYPR** = Forage yield production rate; **FDMY** = Forage dry matter yield; **PHGH** = Plant height at grain harvest; **PLGH** = Panicle length at grain harvest; **NSPP** = Number of spikes per panicle; **NSLPP** = Number of spikelets per panicle; **BYPR** = Biological yield production rate; **GSFR** = Grain sink filling rate; **TSW** = Thousand seed weight; **HI** = Harvest index; **GY** = Grain yield. **Note:** The green and yellow colors indicate the strength of correlation; green color is positively correlated; green to light green color indicate strong to weak positive correlation; yellow color is negatively correlated; and yellow to light yellow color indicate strong to weak negative correlation. Above diagonal is phenotypic correlation coefficient while below diagonal is genotypic correlation.

3.3.2.4 Direct and indirect phenotypic and genotypic effects on forage yield

The estimates of direct and indirect phenotypic effects on FDMY in oat genotypes are indicated in [Table 3.14](#). The result revealed that the highest positive direct effect on FDMY was observed for FYPR (0.9970; 81.4%) followed by NLFH (0.1179; 32.1%), and LLFH (0.1040; 28.4%) at the phenotypic level. Other traits which exerted positive direct effects on FDMY were NTPP, BYPR, GSFR, and PHFH. Negative direct effects were exerted on FDMY by GY (-0.1032; 13.7%), TDW (-0.0572; 10.3%), PLGH (-0.0472; 5.9%), and NSPP (-0.0366; 5.5%). Furthermore, negative direct effects on FDMY were exerted by TSW, NSLPP, and PHGH. The indirect effects of the studied traits on FDMY via FYPR were positive except for TSW, NTPP, and NLFH. Moreover, the indirect effects of GY on FDMY via FYPR, BYPR, GSFR, and PHGH were positive. The highest positive indirect effects on FDMY were exerted by BYPR (0.7295; 71.5%) followed by PHFH (0.5544; 73.4%), PLGH (0.5404; 67.3%), PHGH (0.5199; 71.3%), NSLPP (0.5020; 69.6%), GSFR (0.4505; 64.0%), NSPP (0.4215; 63.5%), GY (0.4162; 55.1%), TDW (0.2950; 52.9%), and LLFH (0.1412; 38.6%) via FYPR. The indirect effects of NTPP on FDMY were positive via GY (0.0597; 8.9%), NLFH (0.0532; 7.9%), and TDW (0.0311; 4.6%). Likewise, the positive indirect effects of NLFH were observed on FDMY via GY, LLFH, NTPP, TDW, NSPP, and PLGH.

The magnitudes of direct and indirect genotypic effects of different traits on FDMY in oat genotypes are displayed in [Table 3.15](#). The result showed that the highest direct effects on FDMY were exerted by FYPR (0.9990; 92.9%) followed by GSFR (0.0915; 17.8%), NLFH (0.0183; 16.4%), and TDW (0.0045; 27.5%). Likewise, NSLPP, PHFH, and BYPR also had positive direct effects on FDMY. On the contrary, negative direct effects on FDMY were exerted by GY (-0.1019; 19.0%), LLFH (-0.0198; 9.1%), and TSW (-0.0089; 8.6%). Furthermore, negative direct effects on FDMY were exerted by NTPP, PLGH, PHGH, and NSPP. Despite a high positive direct effect of FYPR on FDMY, the indirect effects of NTPP and TDW via FYPR were negative. The highest positive indirect effects on FDMY via FYPR were exerted by BYPR (0.4135; 71.6%) followed by GY (0.3358; 62.6%), GSFR (0.3145; 61.0%), PHFH (0.2431; 83.4%), PHGH (0.2384; 79.2%), PLGH (0.1647; 89.9%), LLFH (0.1576; 72.4%), NSPP (0.1344; 74.5%), NLFH (0.0777; 69.9%), and NSLPP (0.0643; 59.7%). Similarly, the indirect effects of TDW via GY (0.0033; 20.3%) and GY (0.0878; 16.4%), BYPR (0.0709; 12.3%), NSLPP (0.0110; 10.2%), NSPP (0.0131; 7.3%), LLFH (0.0153; 7.0%), and TSW (0.0069; 6.6%) via GSFR were also positive on FDMY. However, NTPP (-0.0987) exerted the highest negative indirect effect on FDMY via FYPR.

Table 3.14 Estimate of direct and indirect phenotypic effects of 14 traits on forage yield in 120 oat genotypes at Holetta and Ada-Berga

Traits		NTPP	TDW	NLFH	LLFH	PHFH	FYPR	PHGH	PLGH	NSPP	NSLPP	BYPR	GSFR	TSW	GY
Direct effect		0.0708	-0.0572	0.1179	0.1040	0.0249	0.9970	-0.0027	-0.0472	-0.0366	-0.0192	0.0526	0.0275	-0.0132	-0.1032
Indirect effect via															
Path coefficients	NTPP		0.0311	0.0532	0.0133	-0.0023	-0.3620	0.0001	0.0206	0.0113	0.0059	-0.0279	-0.0111	0.0022	0.0597
	TDW	-0.0384		-0.0365	-0.0033	0.0042	0.2950	-0.0004	-0.0225	-0.0112	-0.0088	0.0205	0.0079	-0.0053	-0.0466
	NLFH	0.0319	0.0177		0.0410	0.0055	-0.0563	-0.0007	0.0093	0.0162	0.0023	-0.0123	-0.0054	0.0029	0.0476
	LLFH	0.0091	0.0018	0.0464		0.0111	0.1412	-0.0012	-0.0135	0.0034	-0.0034	0.0005	-0.0019	0.0008	0.0273
	PHFH	-0.0065	-0.0097	0.0260	0.0464		0.5544	-0.0025	-0.0299	-0.0117	-0.0095	0.0228	0.0030	0.0037	0.0043
	FYPR	-0.0257	-0.0169	-0.0067	0.0147	0.0139		-0.0014	-0.0256	-0.0155	-0.0097	0.0385	0.0124	0.0039	-0.0431
	PHGH	-0.0034	-0.0076	0.0280	0.0465	0.0228	0.5199		-0.0323	-0.0134	-0.0100	0.0214	0.0008	0.0050	0.0155
	PLGH	-0.0310	-0.0273	-0.0232	0.0298	0.0158	0.5404	-0.0019		-0.0149	-0.0117	0.0289	0.0055	0.0021	-0.0231
	NSPP	-0.0219	-0.0175	-0.0523	-0.0098	0.0080	0.4215	-0.0010	-0.0193		-0.0128	0.0210	0.0061	0.0021	-0.0334
	NSLPP	-0.0218	-0.0261	-0.0142	0.0186	0.0123	0.5020	-0.0014	-0.0288	-0.0244		0.0227	0.0057	0.0038	-0.0202
	BYPR	-0.0375	-0.0223	-0.0275	0.0009	0.0108	0.7295	-0.0011	-0.0259	-0.0146	-0.0083		0.0210	0.0018	-0.0667
	GSFR	-0.0286	-0.0165	-0.0231	-0.0072	0.0028	0.4505	-0.0001	-0.0095	-0.0082	-0.0040	0.0403		-0.0013	-0.0848
	TSW	-0.0118	-0.0228	-0.0254	-0.0065	-0.0070	-0.2931	0.0010	0.0075	0.0058	0.0055	-0.0071	0.0028		-0.0266
	GY	-0.0409	-0.0258	-0.0544	-0.0275	-0.0010	0.4162	0.0004	-0.0105	-0.0118	-0.0038	0.0340	0.0226	-0.0034	
Direct effect		10.5	10.3	32.1	28.4	3.3	81.4	0.4	5.9	5.5	2.7	5.2	3.9	3.0	13.7
Indirect effect via															
Percent path coefficients	NTPP		4.6	7.9	2.0	0.3	53.9	0.0	3.1	1.7	0.9	4.1	1.7	0.3	8.9
	TDW	6.9		6.5	0.6	0.8	52.9	0.1	4.0	2.0	1.6	3.7	1.4	0.9	8.3
	NLFH	8.7	4.8		11.2	1.5	15.4	0.2	2.5	4.4	0.6	3.3	1.5	0.8	13.0
	LLFH	2.5	0.5	12.7		3.0	38.6	0.3	3.7	0.9	0.9	0.1	0.5	0.2	7.5
	PHFH	0.9	1.3	3.4	6.1		73.4	0.3	4.0	1.6	1.3	3.0	0.4	0.5	0.6
	FYPR	2.1	1.4	0.5	1.2	1.1		0.1	2.1	1.3	0.8	3.1	1.0	0.3	3.5
	PHGH	0.5	1.0	3.8	6.4	3.1	71.3		4.4	1.8	1.4	2.9	0.1	0.7	2.1
	PLGH	3.9	3.4	2.9	3.7	2.0	67.3	0.2		1.9	1.5	3.6	0.7	0.3	2.9
	NSPP	3.3	2.6	7.9	1.5	1.2	63.5	0.2	2.9		1.9	3.2	0.9	0.3	5.0
	NSLPP	3.0	3.6	2.0	2.6	1.7	69.6	0.2	4.0	3.4		3.2	0.8	0.5	2.8
	BYPR	3.7	2.2	2.7	0.1	1.1	71.5	0.1	2.5	1.4	0.8		2.1	0.2	6.5
	GSFR	4.1	2.3	3.3	1.0	0.4	64.0	0.0	1.3	1.2	0.6	5.7		0.2	12.0
	TSW	2.7	5.2	5.8	1.5	1.6	67.2	0.2	1.7	1.3	1.3	1.6	0.6		6.1
	GY	5.4	3.4	7.2	3.6	0.1	55.1	0.1	1.4	1.6	0.5	4.5	3.0	0.5	

$R^2 = 0.9802$; Residual factor = 0.1406; **NTPP** = Number of tillers per plant; **TDW** = Tillers dry weight; **NLFH** = Number of leaves at forage harvest; **LLFH** = Largest leaf length at forage harvest; **PHFH** = Plant height at forage harvest; **FYPR** = Forage yield production rate; **PHGH** = Plant height at grain harvest; **PLGH** = Panicle length at grain harvest; **NSPP** = Number of spikes per panicle; **NSLPP** = Number of spikelets per panicle; **BYPR** = Biological yield production rate; **GSFR** = Grain sink filling rate; **TSW** = Thousand seed weight; **GY** = Grain yield.

Table 3.15 Estimate of direct and indirect genotypic effects of 14 traits on forage yield in 120 oat genotypes at Holetta and Ada-Berga

	Traits	NTPP	TDW	NLFH	LLFH	PHFH	FYPR	PHGH	PLGH	NSPP	NSLPP	BYPR	GSFR	TSW	GY
Path coefficients	Direct effect	-0.00486	0.00449	0.01828	-0.01984	0.00874	0.99900	-0.01125	-0.00702	-0.00240	0.00941	0.00227	0.09152	-0.00891	-0.10189
	Indirect effect via														
	NTPP		0.00079	0.00070	0.00071	-0.00077	-0.09870	-0.00091	0.00037	0.00002	0.00056	-0.00008	-0.00566	-0.00197	0.01091
	TDW	-0.00085		-0.00049	-0.00158	-0.00048	-0.00210	-0.00086	-0.00046	-0.00011	0.00027	0.00018	-0.00045	-0.00067	0.00331
	NLFH	-0.00019	-0.00012		-0.00256	0.00048	0.07772	-0.00139	0.00015	-0.00001	0.00088	-0.00015	-0.00361	0.00001	0.00569
	LLFH	0.00017	0.00036	0.00235		0.00239	0.15764	-0.00247	0.00055	-0.00028	0.00027	0.00029	0.01527	0.00015	-0.01575
	PHFH	0.00043	-0.00025	0.00101	-0.00542		0.24306	-0.00199	0.00043	0.00003	0.00042	0.00041	0.01549	-0.00122	-0.01273
	FYPR	0.00048	-0.00001	0.00142	-0.00313	0.00213		-0.00268	-0.00116	-0.00032	0.00061	0.00094	0.02881	-0.00073	-0.03425
	PHGH	-0.00039	0.00034	0.00225	-0.00436	0.00154	0.23836		-0.00246	-0.00095	0.00445	0.00062	0.01506	-0.00070	-0.01832
	PLGH	0.00025	0.00029	-0.00039	0.00155	-0.00054	0.16473	-0.00394		-0.00065	0.00256	0.00019	-0.00016	-0.00049	-0.00050
	NSPP	0.00003	0.00021	0.00008	-0.00232	-0.00011	0.13436	-0.00447	-0.00189		0.00578	0.00035	0.01309	-0.00023	-0.01509
	NSLPP	-0.00029	0.00013	0.00170	-0.00057	0.00039	0.06434	-0.00532	-0.00191	-0.00147		0.00036	0.01095	-0.00036	-0.01055
	BYPR	0.00018	0.00036	-0.00117	-0.00256	0.00157	0.41348	-0.00308	-0.00059	-0.00037	0.00151		0.07093	-0.00116	-0.07817
	GSFR	0.00030	-0.00002	-0.00072	-0.00331	0.00148	0.31448	-0.00185	0.00001	-0.00034	0.00112	0.00176		-0.00067	-0.09776
	TSW	-0.00108	0.00034	-0.00003	0.00034	0.00119	0.08152	-0.00088	-0.00039	-0.00006	0.00038	0.00029	0.00692		-0.00174
	GY	0.00052	-0.00015	-0.00102	-0.00307	0.00109	0.33576	-0.00202	-0.00003	-0.00036	0.00097	0.00174	0.08780	-0.00015	
Percent path coefficients	Direct effect	3.8	27.5	16.4	9.1	3.0	92.9	3.7	3.8	1.3	8.7	0.4	17.8	8.6	19.0
	Indirect effect via														
	NTPP		0.6	0.5	0.6	0.6	77.7	0.7	0.3	0.0	0.4	0.1	4.5	1.6	8.6
	TDW	5.2		3.0	9.7	3.0	12.9	5.3	2.8	0.7	1.7	1.1	2.7	4.1	20.3
	NLFH	0.2	0.1		2.3	0.4	69.9	1.2	0.1	0.0	0.8	0.1	3.2	0.0	5.1
	LLFH	0.1	0.2	1.1		1.1	72.4	1.1	0.3	0.1	0.1	0.1	7.0	0.1	7.2
	PHFH	0.1	0.1	0.3	1.9		83.4	0.7	0.1	0.0	0.1	0.1	5.3	0.4	4.4
	FYPR	0.0	0.0	0.1	0.3	0.2		0.2	0.1	0.0	0.1	0.1	2.7	0.1	3.2
	PHGH	0.1	0.1	0.7	1.4	0.5	79.2		0.8	0.3	1.5	0.2	5.0	0.2	6.1
	PLGH	0.1	0.2	0.2	0.8	0.3	89.9	2.2		0.4	1.4	0.1	0.1	0.3	0.3
	NSPP	0.0	0.1	0.0	1.3	0.1	74.5	2.5	1.0		3.2	0.2	7.3	0.1	8.4
	NSLPP	0.3	0.1	1.6	0.5	0.4	59.7	4.9	1.8	1.4		0.3	10.2	0.3	9.8
	BYPR	0.0	0.1	0.2	0.4	0.3	71.6	0.5	0.1	0.1	0.3		12.3	0.2	13.5
	GSFR	0.1	0.0	0.1	0.6	0.3	61.0	0.4	0.0	0.1	0.2	0.3		0.1	19.0
	TSW	1.0	0.3	0.0	0.3	1.1	78.3	0.8	0.4	0.1	0.4	0.3	6.6		1.7
	GY	0.1	0.0	0.2	0.6	0.2	62.6	0.4	0.0	0.1	0.2	0.3	16.4	0.0	

$R^2 = 0.9841$; Residual factor = 0.1261; **NTPP** = Number of tillers per plant; **TDW** = Tillers dry weight; **NLFH** = Number of leaves at forage harvest; **LLFH** = Largest leaf length at forage harvest; **PHFH** = Plant height at forage harvest; **FYPR** = Forage yield production rate; **PHGH** = Plant height at grain harvest; **PLGH** = Panicle length at grain harvest; **NSPP** = Number of spikes per panicle; **NSLPP** = Number of spikelets per panicle; **BYPR** = Biological yield production rate; **GSFR** = Grain sink filling rate; **TSW** = Thousand seed weight; **GY** = Grain yield.

3.3.2.5 Direct and indirect phenotypic and genotypic effects on grain yield

The phenotypic direct and indirect effects of measured traits on GY are indicated in [Table 3.16](#). The results indicated that HI (0.8037; 81.8%) exerted the highest positive direct effects on GY followed by BYPR (0.6814; 78.0%), NLFH (0.0937; 12.5%), LLFH (0.0633; 12.9%), NSPP (0.0351; 6.3%), NTPP (0.0193; 2.4%), and PLGH (0.0063; 1.0%). The negative direct effects on GY were also exerted by NSLPP (-0.0615; 13.1%), GSFR (-0.0387; 3.8%), FDMY (-0.0236; 3.1%), PHFH (-0.0171; 2.3%), PHGH (-0.0052; 0.6%), TDW (-0.0034; 0.5%), and TSW (-0.0011; 0.2%). Despite the high positive direct effects of HI on GY, its indirect effects via NLFH, LLFH, GSFR, NTPP, TDW, PLGH, and, TSW were negative. The HI which exerted the highest positive direct effect on GY also had positive indirect effects via BYPR, PHFH, FDMY, NSPP, PHGH, and NSLPP. The positive direct effect on GY was exerted by BYPR which also had positive indirect effects via HI, NSPP, PLGH, LLFH, and TSW. The highest positive indirect effects via BYPR were recorded for GSFR (0.5216; 51.8%) followed by FDMY (0.4176; 55.6%), PLGH (0.3739; 62.1%), PHFH (0.2953; 38.8%), NSLPP (0.2942; 62.5%), PHGH (0.2769; 33.0%), NSPP (0.2726; 48.8%), and TDW (0.2650; 41.9%), and also GSFR (0.3842; 38.1%) and TSW (0.3576; 68.2%) gave high and positive indirect effects via HI. On the other hand, the highest negative indirect effects through HI were observed for PHGH followed by NLFH, LLFH, PHFH, NTPP, and FDMY, and also high and negative indirect effects were observed via BYPR in NTPP and NLFH.

The direct and indirect genotypic effects of the studied traits on GY are presented in [Table 3.17](#). The highest positive direct effect on GY was exerted by BYPR (0.4613; 56.5%) followed by GSFR (0.3968; 40.6%), HI (0.3757; 61.6%), PHGH (0.0305; 10.2%), LLFH (0.0252; 14.6%), FDMY (0.0210; 5.7%), NSPP (0.0104; 5.9%), PLGH (0.0086; 6.7%), and NLFH (0.0029; 3.6%). On the contrary, the highest negative direct effect on GY was exerted by TSW (-0.0438; 25.4%) followed by NTPP (-0.0236; 20.3%), PHFH (-0.0225; 10.4%), NSLPP (-0.0190; 10.0%), and TDW (-0.0140; 11.6%). Despite a high positive direct effect of HI on GY, its indirect effects via BYPR, PHGH, PLGH, FDMY, NLFH, and LLFH were negative. The positive direct effects of BYPR on GY also had negative indirect effects via HI, TSW, PHFH, NSLPP, TDW, and NLFH. The GSFR exerted a positive direct effect on GY and also this trait had negative indirect effects on GY via PHFH, TSW, NSLPP, NLFH, and PLGH. The highest positive indirect effects via BYPR were recorded for GSFR (0.3575; 36.5%), FDMY (0.1860; 50.4%), PHGH (0.1261; 42.1%), PHFH (0.0830; 38.4%), NSLPP

(0.0739; 38.8%), NSPP (0.0718; 41.8%), TSW (0.0599; 34.8%), LLFH (0.0595; 34.4%), PLGH (0.0384; 30.0%), and TDW (0.0372; 31.0%). Likewise, high and positive indirect effects through GSFR were observed for BYPR (0.3075; 37.6%), HI (0.2070; 33.9%), FDMY (0.1214; 32.9%), PHFH (0.0671; 31.0%), LLFH (0.0662; 38.3%), PHGH (0.0653; 21.8%), NSPP (0.0567; 32.4%), and NSLPP (0.0475; 24.9%) while GSFR (0.1960; 20.0%) exerted through HI. On the contrary, the highest negative indirect effects via HI were observed in TDW, PLGH, PHGH, NTPP, TSW, NSLPP, and NLFH. Moreover, NLFH via BYPR and NTPP via GSFR had negative indirect effects on GY.

Table 3.16 Estimate of direct and indirect phenotypic effects of 14 traits on grain yield in 120 oat genotypes at Holetta and Ada-Berga

	Traits	NTPP	TDW	NLFH	LLFH	PHFH	FDMY	PHGH	PLGH	NSPP	NSLPP	BYPR	GSFR	TSW	HI
	Direct effect	0.0193	-0.0034	0.0937	0.0633	-0.0171	-0.0236	-0.0052	0.0063	0.0351	-0.0615	0.6814	-0.0387	-0.0011	0.8037
	Indirect effect via														
Path coefficients	NTPP		0.0018	0.0423	0.0081	0.0016	0.0032	0.0003	-0.0028	-0.0109	0.0189	-0.3607	0.0156	0.0002	-0.3155
	TDW	-0.0105		-0.0290	-0.0020	-0.0029	-0.0023	-0.0007	0.0030	0.0107	-0.0280	0.2650	-0.0111	-0.0004	0.2627
	NLFH	0.0087	0.0010		0.0249	-0.0038	-0.0051	-0.0012	-0.0012	-0.0156	0.0074	-0.1589	0.0076	0.0002	-0.4188
	LLFH	0.0025	0.0001	0.0369		-0.0077	-0.0077	-0.0023	0.0018	-0.0033	-0.0110	0.0060	0.0027	0.0001	-0.3461
	PHFH	-0.0018	-0.0006	0.0207	0.0283		-0.0145	-0.0048	0.0040	0.0113	-0.0303	0.2953	-0.0043	0.0003	-0.3281
	FDMY	-0.0026	-0.0003	0.0204	0.0206	-0.0106		-0.0031	0.0028	0.0089	-0.0251	0.4176	-0.0131	0.0004	-0.2016
	PHGH	-0.0009	-0.0004	0.0223	0.0283	-0.0157	-0.0139		0.0043	0.0129	-0.0319	0.2769	-0.0012	0.0004	-0.4259
	PLGH	-0.0084	-0.0016	-0.0185	0.0181	-0.0109	-0.0104	-0.0036		0.0143	-0.0375	0.3739	-0.0078	0.0002	-0.0908
	NSPP	-0.0060	-0.0010	-0.0416	-0.0059	-0.0055	-0.0060	-0.0019	0.0026		-0.0410	0.2726	-0.0087	0.0002	0.1309
	NSLPP	-0.0059	-0.0015	-0.0113	0.0113	-0.0085	-0.0096	-0.0027	0.0039	0.0234		0.2942	-0.0080	0.0003	-0.0282
	BYPR	-0.0102	-0.0013	-0.0218	0.0006	-0.0074	-0.0144	-0.0021	0.0035	0.0140	-0.0265		-0.0296	0.0001	0.0606
	GSFR	-0.0078	-0.0010	-0.0183	-0.0044	-0.0019	-0.0080	-0.0002	0.0013	0.0079	-0.0127	0.5216		-0.0001	0.3842
	TSW	-0.0032	-0.0013	-0.0202	-0.0040	0.0048	0.0092	0.0020	-0.0010	-0.0056	0.0175	-0.0925	-0.0039		0.3576
	HI	-0.0076	-0.0011	-0.0488	-0.0273	0.0070	0.0059	0.0028	-0.0007	0.0057	0.0022	0.0514	-0.0185	-0.0005	
	Direct effect	2.4	0.5	12.5	12.9	2.3	3.1	0.6	1.0	6.3	13.1	78.0	3.8	0.2	81.8
	Indirect effect via														
Percent path coefficients	NTPP		0.2	5.3	1.0	0.2	0.4	0.0	0.3	1.4	2.4	45.0	2.0	0.0	39.4
	TDW	1.7		4.6	0.3	0.5	0.4	0.1	0.5	1.7	4.4	41.9	1.8	0.1	41.6
	NLFH	1.2	0.1		3.3	0.5	0.7	0.2	0.2	2.1	1.0	21.2	1.0	0.0	56.0
	LLFH	0.5	0.0	7.5		1.6	1.6	0.5	0.4	0.7	2.2	1.2	0.5	0.0	70.4
	PHFH	0.2	0.1	2.7	3.7		1.9	0.6	0.5	1.5	4.0	38.8	0.6	0.0	43.1
	FDMY	0.3	0.0	2.7	2.7	1.4		0.4	0.4	1.2	3.3	55.6	1.7	0.1	26.9
	PHGH	0.1	0.1	2.7	3.4	1.9	1.7		0.5	1.5	3.8	33.0	0.1	0.0	50.7
	PLGH	1.4	0.3	3.1	3.0	1.8	1.7	0.6		2.4	6.2	62.1	1.3	0.0	15.1
	NSPP	1.1	0.2	7.4	1.1	1.0	1.1	0.3	0.5		7.3	48.8	1.5	0.0	23.4
	NSLPP	1.3	0.3	2.4	2.4	1.8	2.0	0.6	0.8	5.0		62.5	1.7	0.1	6.0
	BYPR	1.2	0.2	2.5	0.1	0.9	1.7	0.2	0.4	1.6	3.0		3.4	0.0	6.9
	GSFR	0.8	0.1	1.8	0.4	0.2	0.8	0.0	0.1	0.8	1.3	51.8		0.0	38.1
	TSW	0.6	0.3	3.9	0.8	0.9	1.8	0.4	0.2	1.1	3.3	17.7	0.7		68.2
	HI	0.8	0.1	5.0	2.8	0.7	0.6	0.3	0.1	0.6	0.2	5.2	1.9	0.0	

$R^2 = 0.9559$; Residual factor = 0.2099; **NTPP** = Number of tillers per plant; **TDW** = Tillers dry weight; **NLFH** = Number of leaves at forage harvest; **LLFH** = Largest leaf length at forage harvest; **PHFH** = Plant height at forage harvest; **FDMY** = Forage dry matter yield; **PHGH** = Plant height at grain harvest; **PLGH** = Panicle length at grain harvest; **NSPP** = Number of spikes per panicle; **NSLPP** = Number of spikelets per panicle; **BYPR** = Biological yield production rate; **GSFR** = Grain sink filling rate; **TSW** = Thousand seed weight; **HI** = Harvest index.

Table 3.17 Estimate of direct and indirect genotypic effects of 14 traits on grain yield in 120 oat genotypes at Holetta and Ada-Berga

	Traits	NTPP	TDW	NLFH	LLFH	PHFH	FDMY	PHGH	PLGH	NSPP	NSLPP	BYPR	GSFR	TSW	HI
Path coefficients	Direct effect	-0.023622	-0.013991	0.002886	0.025154	-0.022487	0.020970	0.030493	0.008623	0.010361	-0.019020	0.461275	0.396828	-0.043771	0.375690
	Indirect effect via														
	NTPP		-0.002454	0.000110	-0.000900	0.001977	-0.002074	0.002464	-0.000448	-0.000069	-0.001132	-0.016652	-0.024524	-0.009682	-0.030093
	TDW	-0.004143		-0.000077	0.002002	0.001237	0.000004	0.002339	0.000567	0.000486	-0.000550	0.037225	-0.001944	-0.003283	-0.052371
	NLFH	-0.000900	0.000374		0.003240	-0.001237	0.001996	0.003760	-0.000184	0.000048	-0.001773	-0.029614	-0.015635	0.000061	-0.018822
	LLFH	0.000846	-0.001114	0.000372		-0.006146	0.002959	0.006696	-0.000674	0.001213	-0.000544	0.059504	0.066191	0.000744	-0.000601
	PHFH	0.002076	0.000770	0.000159	0.006875		0.005209	0.005379	-0.000528	-0.000126	-0.000841	0.082983	0.067143	-0.005970	-0.015741
	FDMY	0.002336	-0.000003	0.000275	0.003549	-0.005586		0.006836	0.001344	0.001320	-0.001271	0.185986	0.121429	-0.003410	-0.014577
	PHGH	-0.001909	-0.001073	0.000356	0.005524	-0.003967	0.004701		0.003022	0.004115	-0.008995	0.126066	0.065318	-0.003427	-0.040424
	PLGH	0.001228	-0.000919	-0.000061	-0.001967	0.001376	0.003269	0.010688		0.002789	-0.005172	0.038424	-0.000675	-0.002399	-0.050305
	NSPP	0.000158	-0.000656	0.000013	0.002946	0.000274	0.002672	0.012109	0.002321		-0.011684	0.071774	0.056746	-0.001151	0.002217
	NSLPP	-0.001405	-0.000404	0.000269	0.000719	-0.000994	0.001401	0.014420	0.002345	0.006365		0.073896	0.047461	-0.001790	-0.019761
	BYPR	0.000853	-0.001129	-0.000185	0.003245	-0.004045	0.008455	0.008334	0.000718	0.001612	-0.003047		0.307542	-0.005681	-0.010745
	GSFR	0.001460	0.000069	-0.000114	0.004196	-0.003805	0.006417	0.005019	-0.000015	0.001482	-0.002275	0.357488		-0.003309	0.195960
	TSW	-0.005225	-0.001049	-0.000004	-0.000428	-0.003067	0.001634	0.002388	0.000473	0.000273	-0.000778	0.059874	0.030000		-0.023218
	HI	0.001892	0.001950	-0.000145	-0.000040	0.000942	-0.000814	-0.003281	-0.001155	0.000061	0.001001	-0.013192	0.206985	0.002705	
Percent path coefficients	Direct effect	20.3	11.6	3.6	14.6	10.4	5.7	10.2	6.7	5.9	10.0	56.5	40.6	25.4	61.6
	Indirect effect via														
	NTPP		2.1	0.1	0.8	1.7	1.8	2.1	0.4	0.1	1.0	14.3	21.1	8.3	25.9
	TDW	3.4		0.1	1.7	1.0	0.0	1.9	0.5	0.4	0.5	31.0	1.6	2.7	43.6
	NLFH	1.1	0.5		4.0	1.5	2.5	4.7	0.2	0.1	2.2	36.8	19.4	0.1	23.4
	LLFH	0.5	0.6	0.2		3.6	1.7	3.9	0.4	0.7	0.3	34.4	38.3	0.4	0.3
	PHFH	1.0	0.4	0.1	3.2		2.4	2.5	0.2	0.1	0.4	38.4	31.0	2.8	7.3
	FDMY	0.6	0.0	0.1	1.0	1.5		1.9	0.4	0.4	0.3	50.4	32.9	0.9	4.0
	PHGH	0.6	0.4	0.1	1.8	1.3	1.6		1.0	1.4	3.0	42.1	21.8	1.1	13.5
	PLGH	1.0	0.7	0.0	1.5	1.1	2.6	8.4		2.2	4.0	30.0	0.5	1.9	39.3
	NSPP	0.1	0.4	0.0	1.7	0.2	1.5	6.9	1.3		6.7	41.0	32.4	0.7	1.3
	NSLPP	0.7	0.2	0.1	0.4	0.5	0.7	7.6	1.2	3.3		38.8	24.9	0.9	10.4
	BYPR	0.1	0.1	0.0	0.4	0.5	1.0	1.0	0.1	0.2	0.4		37.6	0.7	1.3
	GSFR	0.1	0.0	0.0	0.4	0.4	0.7	0.5	0.0	0.2	0.2	36.5		0.3	20.0
	TSW	3.0	0.6	0.0	0.2	1.8	0.9	1.4	0.3	0.2	0.5	34.8	17.4		13.5
	HI	0.3	0.3	0.0	0.0	0.2	0.1	0.5	0.2	0.0	0.2	2.2	33.9	0.4	

$R^2 = 0.9647$; Residual factor = 0.1880; **NTPP** = Number of tillers per plant; **TDW** = Tillers dry weight; **NLFH** = Number of leaves at forage harvest; **LLFH** = Largest leaf length at forage harvest; **PHFH** = Plant height at forage harvest; **FDMY** = Forage dry matter yield; **PHGH** = Plant height at grain harvest; **PLGH** = Panicle length at grain harvest; **NSPP** = Number of spikes per panicle; **NSLPP** = Number of spikelets per panicle; **BYPR** = Biological yield production rate; **GSFR** = Grain sink filling rate; **TSW** = Thousand seed weight; **HI** = Harvest index.

3.3.3 Multivariate analysis

3.3.3.1 Clustering of oat genotypes

The 120 oat genotypes were grouped primarily into four hierarchical clusters using the mean of 16 agro-morphological traits following Ward's method of classification based on the Euclidean distance (Table 3.18 and Figure 3.5). The dendrogram performed based on the Euclidean distance had two major groups at a linkage distance of 67.87 (Figure not shown). The first group had three clusters (C1, C2, and C3) at a linkage distance of 33.93 and each cluster was further partitioned into two sub-clusters at a linkage distance of 25.0. The second group had one cluster at a linkage distance of 33.93 and this cluster was further subdivided into two sub-clusters at a linkage distance of 25.0.

The number of genotypes varied from cluster to cluster due to differences in measured agro-morphological traits (Table 3.18 and Figure 3.5). The highest number of genotypes was observed in cluster one (C1) followed by cluster two (C2) and cluster four (C4) while the lowest was observed in cluster three (C3). The first cluster (C1, n=38) contributed 31.7% of the total studied genotypes of which 31 genotypes were introduced via the Food and Agricultural Organization (FAO) while the remaining 5 and 2 genotypes were introduced via the International Maize and Wheat Improvement Center (CIMMYT) and Canada, respectively. The second cluster (C2, n=35) comprised 29.2% of the total genotypes under consideration of which 32 genotypes were introduced via the FAO while 3 genotypes were introduced via the CIMMYT. The third cluster (C3, n=14) consisted of 11.7% of the total genotypes of which 10 genotypes were introduced via the CIMMYT while 4 genotypes were from the FAO introduction. The fourth cluster (C4, n=33) comprised 27.5% of the total genotypes of which 31 genotypes were introduced via the FAO and other 2 genotypes were introduced via the CIMMYT. The accuracy of the identified groups produced was reassessed using discriminant function analysis (Table 3.19). The results indicated that the 3rd cluster (100%) discriminated correctly followed by the 2nd (97.1%) and the 4th cluster (97.0%) while the 1st cluster had the lowest proportion of correct placement, with only 34 of 38 genotypes, or 89.5%, correctly placed into that cluster.

Table 3.18 Grouping of 120 oat genotypes into five clusters based on the mean performance of 16 agro-morphological traits

Cluster number	Number of genotypes	Proportion (%)	List of oat genotypes
C1	38	31.67	(3)=CI-1704; (7)=CI-1853; (14)=CI-1532; (15)=Bonsa; (17)=CI-1672; (18)=R-14; (20)=CI-1659; (24)=CI-1707; (25)=CI-2141; (32)=CI-715; (34)=CI-1590; (45)=SRCPX80Ab2764; (55)=E-2; (56)=CI-1463; (58)=SRCPX80Ab2035; (59)=CI-1549; (68)=CI-1485; (70)=B-17; (71)=CI-1749; (74)=CI-1646; (80)=CI-16016; (81)=CI-1652; (82)=CI-1765; (90)=Jassari-27639; (93)=CI-1584; (98)=C-12; (102)=CI-1629; (103)=CI-1664; (104)=CI-1654; (105)=SRCPX80Ab2475; (108)=CI-1480; (110)=CI-1495; (114)=CI-8235; (115)=CI-1436; (116)=Robert2007Portage; (117)=Dumant2007Portage; (119)= 60MN16016; and (120)=CI-1478
C2	35	29.17	(1)=CI-1538; (8)=CI-1456; (9)=CI-1488; (11)=MM799883/85; (12)=CI-1864; (19)=Walqaa; (21)=CI-1510; (22)=CI-1768; (27)=E-25; (31)=Jassari-723; (36)=CI-1767; (37)=CI-1484; (41)=CI-1747; (47)=CI-1429; (49)=CI-1611; (51)=CI-1781; (52)=Lampton; (54)=CI-1536; (57)=Bonabas; (61)=T-1926513; (63)=CI-1577; (66)=S-122; (67)=CI-1512; (69)=CI-8251; (72)=MN79983/85; (78)=CI-5800; (79)=CI-7894; (86)=CI-1655; (87)=CI-1438; (95)=C-2; (97)=CI-1466; (101)=CI-1674; (107)=CI-1547; (111)=CI-1528; and (113)=CI-1750
C3	14	11.67	(2)=Sorataf; (5)=SRCPX80Ab2691; (13)=SRCPX80Ab2050; (23)=A-505; (26)=SRCPX80Ab2267; (33)=SRCPX80Ab2777; (39)=Jassari; (44)=SRCPX80Ab2806; (76)=SRCPX80Ab2310; (77)=CI-1695; (89)=SRCPX80Ab2291; (92)=SRCPX80Ab2754; (94)=Was; and (112)=SRCPX80Ab1751
C4	33	27.50	(4)=CI-1592; (6)=CI-1426; (10)=CI-1497; (16)=CI-1677; (28)=C-16; (29)=CI-1551; (30)=CI-1791; (35)=E-15; (38)=CI-1585; (40)=CI-1746; (42)=SRCPX80Ab2582; (43)=CI-1842; (46)=K-2; (48)=CI-1751; (50)=C-10; (53)=CI-1496; (60)=CI-1544; (62)=CI-1567; (64)=CI-1752; (65)=CI-1446; (73)=CI-1690; (75)=S-130; (83)=CI-1546; (84)=CokerSRres80SA130; (85)=CI-1852; (88)=CI-1838; (91)=D-28; (96)=CI-1623; (99)=CI-1759; (100)=CI-27830; (106)=F-18; (109)=CI-1671; and (118)=CI-1720

Note: Number in parenthesis indicates the genotype code used for dendrogram (Figure 3.5).

3.3.3.2 Performance of genotypes under different clusters

Inter-cluster mean performances indicated the presence of remarkable variations among the clusters for the traits considered as illustrated in Table 3.20. Each cluster had peculiar characteristics in terms of the traits under consideration. The first cluster (C1) had the highest mean values for TDW and GSFR while the remaining fourteen traits had intermediate mean values. The second cluster (C2) was characterized by high mean values for PHFH, FYPR, FDMY, PHGH, PLGH, NSPP, NSLPP, and BYPR while NTPP, TDW,

NLFH, LLFH, GSFR, HI, and GY had intermediate mean values and the lowest mean value was recorded for TSW. The third cluster (C3) had the highest mean values for TSW, HI, and GY while TDW, FYPR, BYPR, and GSFR had intermediate mean values and the remaining nine traits (NTPP, NLFH, LLFH, PHFH, FDMY, PHGH, PLGH, NSPP, and NSLPP) indicated the lowest mean performances. The fourth cluster (C4) exhibited the highest mean values for NTPP, NLFH, and LLFH while PHFH, FDMY, PHGH, PLGH, NSPP, NSLPP, and TSW had intermediate mean values and the lowest mean performances were recorded from TDW, FYPR, BYPR, GSFR, HI, and GY. The highest number of traits with maximum performance was recorded in the second cluster (C2, n=8 traits) followed by the third and fourth clusters (C3 and C4, n=3 traits) while the first cluster (C1, n=2 traits) had the lowest number of traits with maximum performance. On the contrary, the fourth cluster (C4, n=9 traits) had the highest number of traits which consisted of the minimum performances followed by the third cluster (C3, n=6 traits) while the second cluster (C2, n=2 traits) had the lowest number of traits having the minimum performances.

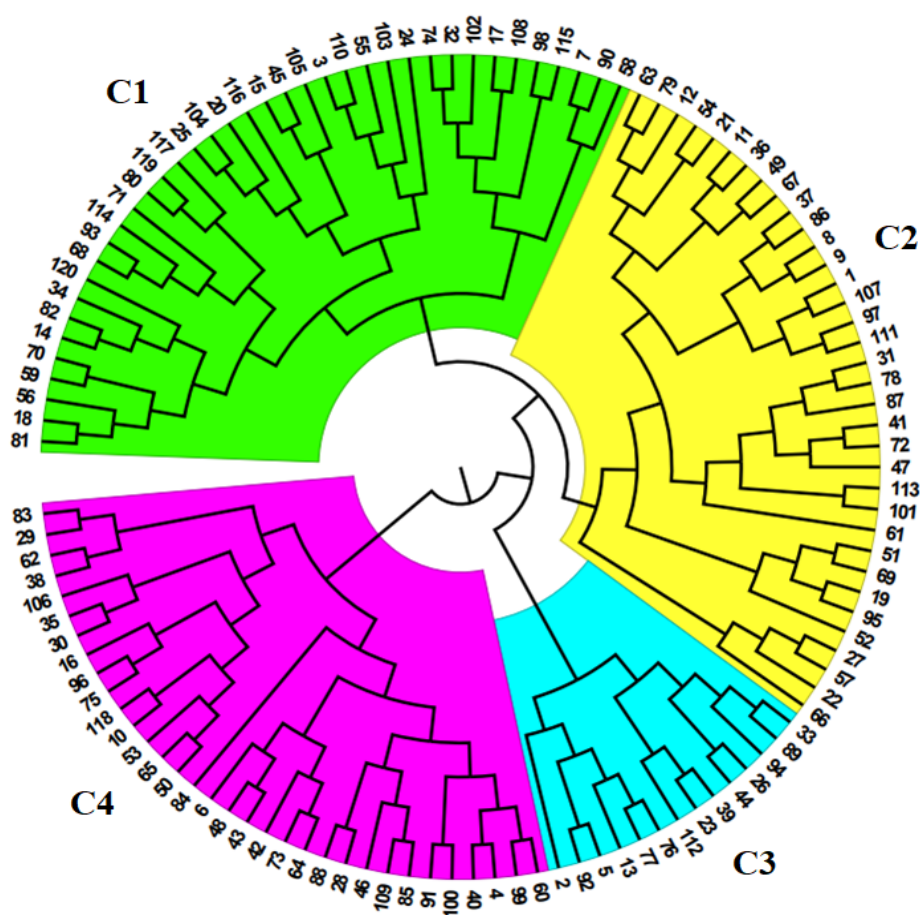


Figure 3.5 Cluster dendrogram developed by Ward's agglomerative hierarchical classification method based on Euclidian distance for 16 agro-morphological traits of 120 oat genotypes. **Note:** See [Table 3.18](#) for genotypes description.

Table 3.19 Determination of clustering accuracy using discriminant function analysis

Cluster analysis group	Predicted group membership							
	Cluster 1		Cluster 2		Cluster 3		Cluster 4	
	Count	%	Count	%	Count	%	Count	%
C1	34	89.5	1	2.9	0	0	1	3.0
C2	1	2.6	34	97.1	0	0	0	0
C3	3	7.9	0	0	14	100	0	0
C4	0	0	0	0	0	0	32	97.0
Total N	38		35		14		33	
N correct	34		34		14		32	
Proportion	0.895		0.971		1.000		0.970	

C1 = cluster 1; C2 = cluster 2; C3 = cluster 3; C4 = cluster 4; 95.0% of the cluster analysis was correctly classified

Table 3.20 Intra-cluster means and range for 16 agro-morphological traits of 120 oat genotypes grown at Holetta and Ada-Berga in 2020/21

Traits	C1			C2			C3			C4			Grand mean
	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	
NTPP	1.8	3.3	2.3	1.7	2.7	2.3	1.7	2.6	2.2	2.2	4.2	3.0	2.5
TDW	26.1	41.0	34.2	28.7	44.0	33.9	30.2	37.4	33.6	24.6	36.2	29.8	32.8
NLFH	3.9	5.5	4.7	3.7	5.3	4.5	3.5	4.6	3.9	3.9	7.1	5.6	4.8
LLFH	29.6	45.0	37.7	27.5	47.1	39.6	26.8	36.7	32.8	35.8	48.1	40.6	38.5
PHFH	107.9	136.6	120.4	123.5	155.7	133.9	85.2	119.7	105.1	108.2	142.2	122.8	123.2
FYPR	134.2	218.3	168.3	138.6	239.9	181.6	117.6	162.9	142.5	80.0	203.8	139.7	161.3
FDMY	17.0	28.3	21.0	17.4	30.3	22.5	14.1	19.2	16.8	9.6	27.7	19.6	20.5
PHGH	112.0	140.7	124.3	125.2	154.3	138.3	85.7	120.2	104.8	112.7	137.2	125.9	126.6
PLGH	28.2	49.9	40.7	41.1	57.3	47.5	24.0	41.2	34.0	28.0	45.7	35.4	40.5
NSPP	19.4	32.9	24.5	21.1	33.6	26.2	20.2	25.9	23.2	16.0	26.8	21.5	24.0
NSLPP	29.3	74.1	48.1	37.3	82.6	55.0	28.6	43.8	35.6	24.1	47.6	38.9	46.1
BYPR	119.0	174.9	143.3	124.1	171.2	145.0	90.0	152.1	119.2	62.1	147.2	105.5	130.6
GSFR	97.5	178.9	128.1	85.5	131.1	108.8	83.4	129.0	108.2	34.5	141.3	83.4	107.9
TSW	42.1	56.0	49.1	36.8	55.8	46.3	46.0	62.3	53.7	43.7	57.6	47.8	48.5
HI	26.2	40.5	33.4	23.8	36.0	29.2	32.6	46.4	42.3	16.0	35.8	26.6	31.4
GY	6.3	10.5	8.2	6.0	8.9	7.3	7.1	11.3	8.9	2.4	7.4	5.5	7.3

NTPP = Number of tillers per plant; **TDW** = Tillers dry weight (g); **NLFH** = Number of leaves at forage harvest; **LLFH** = Largest leaf length at forage harvest (cm); **PHFH** = Plant height at forage harvest (cm); **FYPR** = Forage yield production rate (kg/ha/day); **FDMY** = Forage dry matter yield (t/ha); **PHGH** = Plant height at grain harvest (cm); **PLGH** = Panicle length at grain harvest (cm); **NSPP** = Number of spikes per panicle; **NSLPP** = Number of spikelets per panicle; **BYPR** = Biological yield production rate (kg/ha/day); **GSFR** = Grain sink filling rate (kg/ha/day); **TSW** = Thousand seed weight (g); **HI** = Harvest index (%); **GY** = Grain yield (t/ha).

3.3.3.3 Genetic divergence

The genetic distances as measured by the pairwise generalized Mahalanobis's D^2 statistics between each cluster showed high genetic distances among clusters (Table 3.21). The intra-cluster genetic distance was non-significant for all clusters. The highest intra-cluster genetic distance was observed in cluster C3 ($D^2=4.3$) followed by cluster C4 ($D^2=2.6$) and cluster C2 ($D^2=2.5$) while cluster C1 ($D^2=2.3$) was the least divergent. On the other hand, the inter-cluster genetic distance values ranged from 11.7 to 63.2 and these distances were significant between different clusters except between clusters C1 and C2. The maximum and most

significant genetic divergence were found between clusters C3 and C4 ($D^2=63.2$) followed by clusters C2 and C3 ($D^2=52.2$), and clusters C2 and C4 ($D^2=37.7$). The inter-cluster genetic distances were significant and intermediate between clusters C1 and C4 ($D^2=36.5$), and between clusters C1 and C3 ($D^2=26.8$) while the least non-significant genetic divergence was found between clusters C1 and C2 ($D^2=11.7$). The highest mean inter-cluster genetic distance was observed in cluster C3 ($D^2= 47.4$) followed by cluster C4 ($D^2=45.8$) and cluster C2 ($D^2=33.9$) while the least mean genetic distance was recorded from cluster C1 ($D^2= 25.0$).

Table 3.21 Pair-wise generalized square distance (D^2) among four clusters of 120 oat genotypes based on 16 agro-morphological traits and mean distance of each cluster from other clusters

Cluster	C1	C2	C3	C4	Mean distance
C1	2.3^{NS}	11.7 ^{NS}	26.8*	36.5**	25.0
C2		2.5^{NS}	52.2***	37.7**	33.9
C3			4.3^{NS}	63.2***	47.4
C4				2.6^{NS}	45.8
Overall mean					38.0

* = significant at $P < 0.05$, ** = highly significant at $P < 0.01$, and *** = very highly significant at $P < 0.001$; NS = non-significant at $P > 0.05$. Chi-Square (χ^2) 16 DF = 26.296 at $P < 0.05$; 32.000 at $P < 0.01$, and 39.252 at $P < 0.001$; Inter-cluster is off-diagonal; and intra-cluster is diagonal bold.

3.3.3.4 Principal component analysis

Principal component analysis (PCA) indicated that the first eight principal components (PCs) with eigenvalues greater than 0.5 accounted for 92.6% of the total variation among the 120 oat genotypes studied for the sixteen agro-morphological traits (data not shown). Of these, the first four PCs with eigenvalues greater than unity accounted for 78.3% of the total variation in oat genotypes (Table 3.22). The scree plot also showed that the first four PCs were important to exploit the variation in oat genotypes (Figure 3.6). The first PC axis accounted for 35.6% of the total variation and differentiated the population based on FYPR (0.358), BYPR (0.355), PLGH (0.328), FDMY (0.306), NSLPP (0.304), PHFH (0.286), PHGH (0.277), and NSPP (0.258). Among the studied traits, GSFR, NTPP, GY, and TDW had intermediate while TSW, NLFH, LLFH, and HI had the lowest contribution for the total variation in the first PC. The second PC axis explained 25.2% of the total variation and had higher magnitudes of positive loadings in respect of traits of HI (0.444), GY (0.375), and TSW (0.271) and negative loadings for NLFH (-0.332), PHGH (-0.317), LLFH (-0.285), PHFH (-0.275), and NTPP (-0.253).

Table 3.22 Eigenvalue, proportion of variance and factor loadings (eigenvectors) contributed by four principal components in 120 oat genotypes based on 16 agro-morphological traits

Parameter	Principal Components (PCs)			
	PC ₁	PC ₂	PC ₃	PC ₄
Eigenvalue	5.69	4.03	1.52	1.28
Variance (%)	35.6	25.2	9.5	8.0
Cumulative variance (%)	35.6	60.8	70.3	78.3
Traits	-----Factor loading-----			
Number of tillers per plant	-0.230	-0.253	0.127	-0.108
Tillers dry weight (g)	0.218	0.203	-0.327	0.355
Number of leaves at forage harvest	-0.086	-0.332	0.297	0.269
The largest leaf length at forage harvest (cm)	0.081	-0.285	-0.012	0.466
Plant height at forage harvest (cm)	0.286	-0.275	-0.072	0.133
Forage yield production rate (kg/ha/day)	0.358	-0.050	0.249	-0.083
Forage dry matter yield (t/ha)	0.306	-0.186	0.345	-0.025
Plant height at grain harvest (cm)	0.277	-0.317	-0.133	0.055
Panicle length at grain harvest (cm)	0.328	-0.075	-0.277	0.122
Number of spikes per panicle	0.258	0.071	-0.312	-0.404
Number of spikelets per panicle	0.304	-0.056	-0.305	-0.160
Biological yield production rate (kg/ha/day)	0.355	0.091	0.250	-0.005
Grain sink filling rate (kg/ha/day)	0.237	0.240	0.418	0.093
Thousand seed weight (g)	-0.087	0.271	-0.153	0.575
Harvest index (%)	0.020	0.444	0.052	0.005
Grain yield (t/ha)	0.221	0.375	0.233	0.045

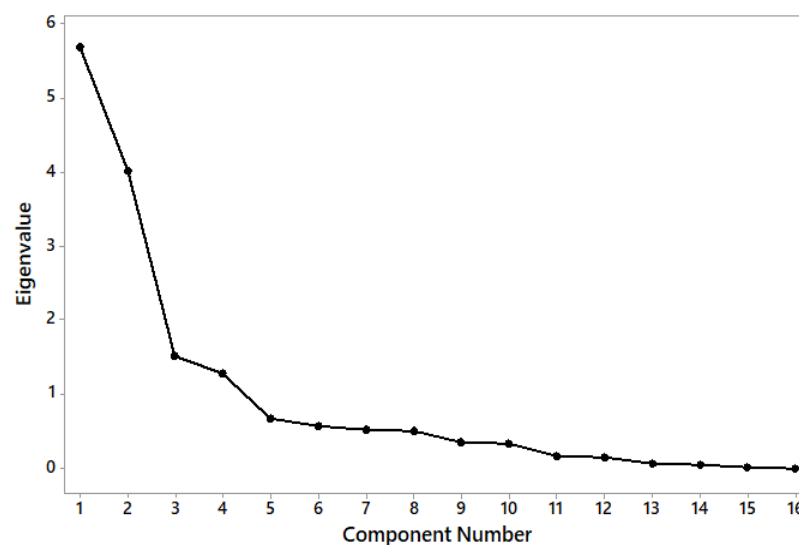


Figure 3.6 Scree plot showing eigenvalues in response to number of principal components for 16 agro-morphological traits of 120 oat genotypes

On the other hand, the contribution of variation observed in the second PC from GSFR, TDW and FDMY were intermediate while the lowest values were recorded from BYPR, PLGH, NSPP, NSLPP, and FYPR. Eigenvectors of the third PC axis accounted for 9.5% of the total phenotypic variation and had high positive contributing factor loadings from GSFR (0.418), FDMY (0.345), NLFH (0.297), and BYPR (0.250) and that of high negative factor loadings from TDW (-0.327), NSPP (-0.312), NSLPP (-0.305), and PLGH (-0.277). However, FYPR, GY, TSW, PHGH, and NTPP had intermediate while the remaining traits had the least contribution to the total variation in the third PC. The fourth PC axis explained 8.0% of the total variation due to high positive eigenvector values of TSW (0.575), LLFH (0.466), TDW (0.355), and NLFH (0.269) and the high negative values of NSPP (-0.404) while the remaining traits had a lower contribution to the total variability.

The biplot loadings for the first two PCs of the 16 agro-morphological traits in oat genotypes were displayed in [Figure 3.7](#). The results indicated that the studied traits were classified into four groups based on the length, direction, and proximity among the vector lines. The first group comprised BYPR which had positive eigenvectors for both PCs while positive PC1 and negative PC2 values were observed for FYPR, NSLP, PLGH, FDMY, PHFH, and PHGH. The second group consisted of four traits (GY, GSFR, TDW, and NSPP) that had positive factor loadings for both PCs. The third group was formed by two traits (HI and TSW) which had positive PC2 values but the PC1 value was positive for HI and it was negative for TSW. The fourth group was characterized by NTPP, NLFH, and LLFH of which NTPP and NLFH had negative eigenvectors for both PCs but LLFH had positive values for PC1 and negative values of PC2. The scatter plot for the first two PCs also grouped the studied genotypes into four clusters based on the studied agro-morphological traits ([Figure 3.8](#)). The result indicated that the first, second and fourth groups were close to each other and were located near to the center of the plot while the third group was located relatively far from the center of the plot.

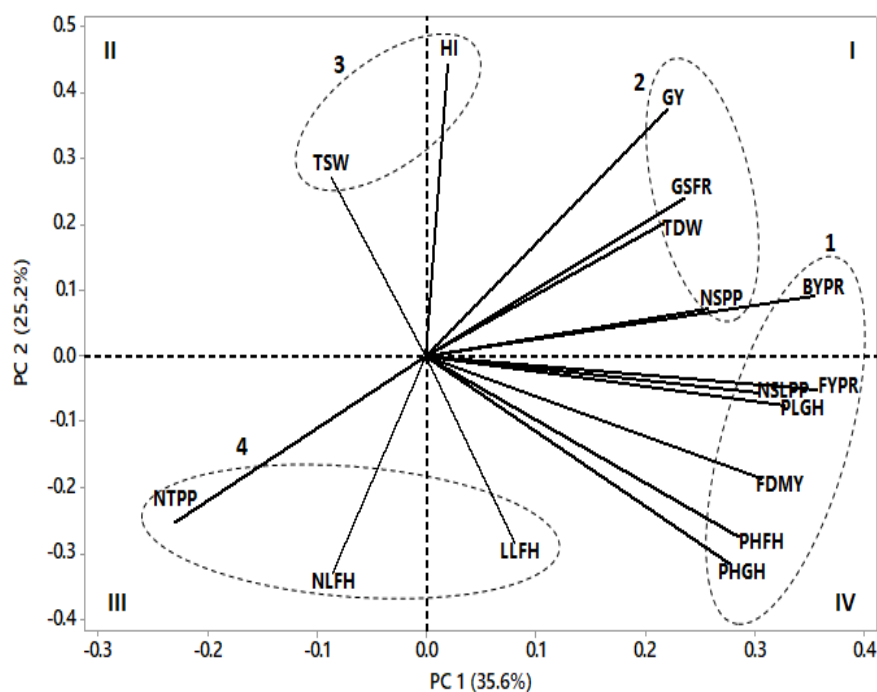


Figure 3.7 Biplot loadings of the first two principal components (PC1 and PC2) showing the association of 16 agro-morphological traits in 120 oat genotypes.

Note: NTPP = Number of tillers per plant; TDW = Tillers dry weight (g); NLFH = Number of leaves at forage harvest; LLFH = Largest leaf length at forage harvest (cm); PHFH = Plant height at forage harvest (cm); FYPR = Forage yield production rate (kg/ha/day); FDMY = Forage dry matter yield (t/ha); PHGH = Plant height at grain harvest (cm); PLGH = Panicle length at grain harvest (cm); NSPP = Number of spikelets per panicle; BYPR = Biological yield production rate (kg/ha/day); GSFR = Grain sink filling rate (kg/ha/day); TSW = Thousand seed weight (g); HI = Harvest index (%); GY = Grain yield (t/ha).

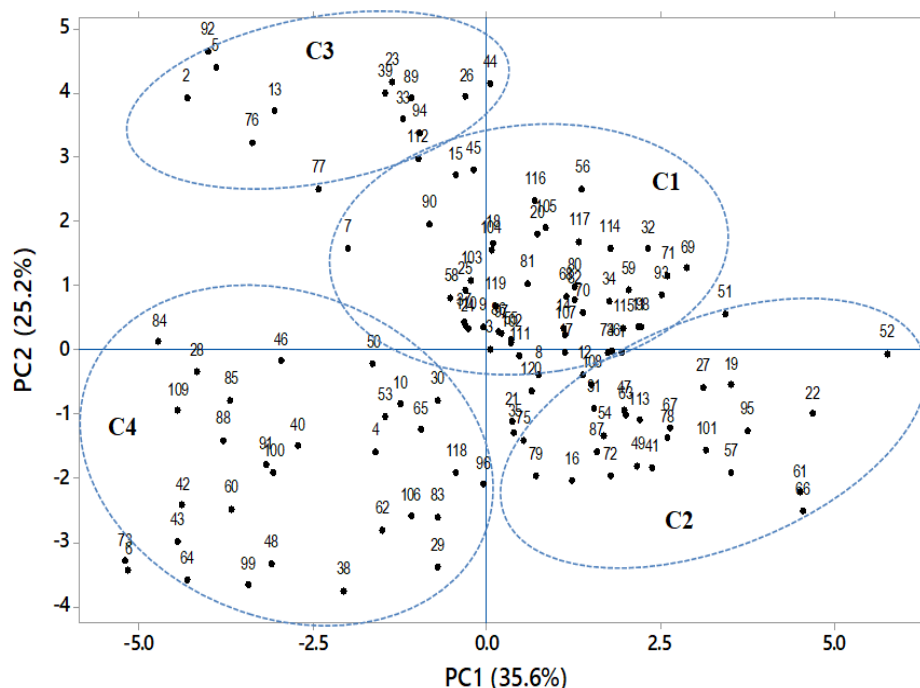


Figure 3.8 Scatter plot diagram of the first two principal components (PC1 and PC2) showing the grouping of 120 oat genotypes into four clusters.

Note: See Table 3.18 for genotypes description. C1 = 1st cluster; C2 = 2nd cluster; C3 = 3rd cluster; and C4 = 4th cluster.

3.4 Discussion

3.4.1 Agro-morphological variability

3.4.1.2 Effect of location, genotype, and their interactions

The extents of significant variations in this study were variable among locations, genotypes, and genotype x location interaction for all or some of the measured traits. The test locations influenced some of the studied traits significantly in oat genotypes. This might be attributed to the presence of significant variations in biotic, edaphic and climatic conditions between the two locations. The effect of locations on the performance of oat genotypes was also reported (Ashenafi, 2018; Gezahagn *et al.*, 2021). The mean squares of genotypes from the analysis of variance also indicated that there was a wide variation among the genotypes for measured traits. The great variations observed among the studied genotypes indicate the presence of remarkable inherent variability among oat genotypes for the traits studied. The existence of substantial variations was also reported in oat genotypes by different scholars (Fekede, 2004; Tanvi, 2016; Atman, 2017; Ashenafi, 2018; Wagh, 2018; Gezahagn *et al.*, 2021).

The genotype x location interactions were found to be significant for traits TDW, NLFH, LLFH, DSH, PLGH, DSH, NSPP, NSLPP, GSFR, SY, HI, and GY. This is due to both the differential response of genotypes to the test locations and the influence of the test locations on the genotypes differently. However, the observed significant interactions for the remaining ten (about 45%) of the studied traits were only due to the differential response of genotypes to the test locations. The performance of a genotype is generally expected to vary under diverse environments due to variations in growing conditions (Gemechu, 2012; Mussa, 2017; Habte, 2018; Wondimu *et al.*, 2022). The observed crossover interactions in FDMY and GY were owing to variations in genotypic performance with changing environments. The crossover interaction indicates the change in the rank order of genotypes across environments, and it can be managed either by selecting the best-performing genotypes for each environment or avoiding them by identifying high-yielding and relatively stable genotypes across environments (Caccarelli, 1989; Moghaddam and Pourdad, 2009). When genotypes are tested under various environments, the performance of genotypes fluctuates frequently, and genotypes that perform best in a particular environment may perform poorly under diverse environmental conditions (Caccarelli, 1997; Gemechu, 2012; Temesgen *et al.*, 2022; Wondimu *et al.*, 2022).

3.4.1.2 Performance of genotypes

Plant height is one of the important traits, which has a significant contribution for forage yield improvement, and it generally varies among oat genotypes (Fekede, 2004; Ashenafi, 2018). The observed taller plant heights in the top 5% of forage yielder genotypes might be due to the inherent genetic variation, strong light competition, and partitioning of more assimilates for stem elongation. This result is also in close conformity with the findings of Steiner (1986); Ballare *et al.* (1990); and Irfan *et al.* (2016). The higher FDMY and GY revealed in the top 5% of forage yielder genotypes might be due to better radiation-use efficiency, greater accumulation of dry matter, and better nutrient uptake and use efficiency. The existence of better yield attributes in the top 5% of forage yielder genotypes generally leads to greater FDMY and GY, which is mainly due to better source-sink relationship, and this result is also in agreement with that of Siloriya *et al.* (2014).

The contribution of NTPP for forage yield in the top 5% of forage yielder genotypes was moderately lower than the least 5% of forage yielder genotypes. The reason might be related to the genotypes being small-seeded, which is reflected by the small weight of TSW that may use large numbers of seed per unit area of land at planting. This high population density can hamper the tillering performance of genotypes owing to high intra and inter-tillers competition for growth resources. Fekede (2004) reported that oat genotypes may express their tillering performances under low plant population, which may be possible by considering TSW to establish the seeding rate for each genotype. Higher NLFH and LLFH in the top 5% of forage yielder genotypes provide better canopy cover at the early growth stage, which results in the efficient interception of photosynthetically active radiation for photosynthesis. Differences in the number of leaves (Wang, 2018; Tessema and Getinet, 2020) and leaf length (Tanvi, 2016; Atman, 2017) were also reported in oat genotypes.

Tillering performance of oat genotypes varies with cultivars, environmental and management conditions. Low tillering performance in the top 5% of seed yielder genotypes could be mainly due to the existence of low inherent tillering potential in the genotypes. Although the NTPP were relatively higher in the least 5% of seed yielder genotypes, the GY performances in these genotypes were lower. This might be due to the production of a high number of non-panicle-bearing tillers, which leads to a decrease in grain yield. Early canopy cover associated with rapidly attaining the optimum leaf area index and maintaining it for a longer time would be helpful to enhance grain yield by creating favorable conditions for

spikelet and floret formation and a longer grain filling period (Peltonen-Sainio, 1999). The plant height varied among genotypes, and a shorter plant height was recorded in the top seed yielder genotypes. The research findings also indicated that high grain producing genotypes had generally shorter plant heights (Lynch and Frey, 1993; Reynolds *et al.*, 2009; Tao *et al.*, 2021). The observed seed yield in the top 5% of seed yielder genotypes was relatively higher, which might be related to better use of growth resources for photosynthesis and efficient translocation of synthesized assimilates and mobilization of stored food to the grain during the grain filling period. A shorter growth period during vegetative growth ensures more growth resources are reserved for the reproductive phase, which leads to higher GY due to the efficient utilization of growth resources for yield formation (Tao *et al.*, 2021). Variations in HI between the top and least 5% of seed yielder genotypes were due to the differences in GY and TBY, and this result is also supported by Dreccer *et al.* (2009); and Siloriya *et al.* (2014). Higher yield performances (forage, grain, straw and biological yields) were observed in the top 5% of genotypes, which generally indicates the presence of a high level of oat improvements through selection.

3.4.1.3 Phenotypic and genotypic coefficient of variations

In the current study, the magnitudes of phenotypic variances were comparatively higher than the corresponding genotypic and the interaction of genotype x location variances for all studied agro-morphological traits. This indicates that the extent of environmental influence is relatively high on the expression of these traits. This result is also in line with the findings of Ashenafi (2018), who reported that the phenotypic variance in all studied traits is higher than the genotypic and interaction variances in oat genotypes. The magnitudes of genotype x location interaction variances were relatively higher than the respective genotypic variances in LLFH, GFP, TBY and GSFR. This suggests that location effect caused a substantial variation in the aforementioned traits compared to other traits. When the interaction variance for a trait is greater than the genotypic variance, selection of the best genotypes based on this trait should be performed depending on target environment (Tahmasebi *et al.*, 2014). The values of genotypic variances in nine (about 38%) of the studied traits were relatively higher than the corresponding environmental variances, indicating that the contribution of the environment to the expression of these traits was relatively lower when compared to the remaining studied traits.

The observed wider variability on phenotypic and genotypic coefficients of variation generally indicates the existence of substantial variability in the studied traits. The study illustrated that 20.8 and 37.5% of the studied traits had lower PCV and GCV estimates, respectively; suggesting selection based on these traits may not be effective. However, 79.2 and 62.5% of the studied traits had high to moderate values of PCV and GCV, respectively; indicating that the larger proportion of variability was contributed by the genetic component but less by the environment. Thus, selection may be effective based on the phenotypic performance of these traits. Among the studied traits, NSLPP, GSFR, GY, and HI had high PCV values, but these respective traits gave moderate GCV values. Similarly, Singh and Singh (2011); Bind *et al.* (2016); Atman (2017); and Harshita (2018) have reported low PCV and GCV values for DFH and DSH in oat. The PCV values for all measured traits were comparatively higher than the corresponding GCV values, indicating the greater influence of the environment on the expression of these traits. Similar results were also reported on various traits in oat genotypes by different scholars (Singh and Singh, 2011; Bind *et al.*, 2016; Kumar *et al.*, 2016; Atman, 2017; Ashenafi, 2018). The estimates of ECV were relatively low for eight (about 33%) of the studied traits, showing these traits were less sensitive to environmental factors. The higher PCV values for forage dry matter yield was also reported for grass grown under non-stress and drought stress conditions (Shariatipour *et al.*, 2022). On the contrary, the influence of environment in nine (about 38%) of the studied traits exhibited high (>20%) estimates of ECV. The influence of environment on yield traits (FDMY, TBY, SY, and GY) and botanical fractions yields (LDMY, SDMY, and PDMY) was higher compared to other traits. The observed moderate to high PCV and moderate GCV, accompanied by the corresponding low to moderate ECV estimates for NLFH, PLGH, NSPP, and HI, indicated that improvement in these traits could be achieved through selection. The estimates of PCV and GCV are always high when the population has considerable genetic variability, and their high values provide a wide scope of selection based on the phenotypic performance of these traits for improvement (Yadav, 2000; Khan *et al.*, 2009; Habte *et al.*, 2015).

Although the estimates of PCV were greater than GCV, the differences between high to moderate PCV and the respective moderate GCV were relatively lower in magnitude for NLFH (1.06%), PLGH (1.71%), HI (2.03%), and NSPP (2.30%). The lower values indicated that these traits had relatively high exploitable inherent genetic variability and the phenotypic performance was less influenced by environmental factors. Therefore, selection

based on phenotypic performance would be an effective way to bring about considerable improvement in these traits. This result is also in agreement with the findings of Singh (1999) and Surje and De (2014). On the contrary, slightly wider ranges between high to moderate PCV and the corresponding moderate GCV were observed for GSFR (6.73%) and NTPP (4.83%), suggesting that the influence of the environment on these traits is high and selection based on the phenotypic performance of these traits may not be effective for genetic improvement.

3.4.1.4 Heritability and genetic gains

The study revealed that the estimated heritability, in a broad sense, generally exhibited considerable variability for measured phenotypic traits. This wide range of variability in the studied traits indicated the possibility of high genetic improvement of traits under consideration because the extent of wide variability virtually offers better scope for selection. The tested oat genotypes had a very high degree of heritability in DFH, NLFH, TSW, PHGH, PLGH, and HI, while moderately high heritability estimates were recorded for PHFH, DSH, FYPR, NSPP, NSLPP, TDW, FDMY, GY, PDMY, and SDMY. This indicates the influence of environmental factors on the expression of these traits was relatively small. Consequently, the expressed phenotypic performance was manifested mainly due to the substantial effect of the genetic factor. Hence, significant attention should be given to these particular transmissible traits to make selection effective for oat improvement. The high heritability estimates observed in this study were also supported by Atman (2016) and Bind *et al.* (2016), who observed high heritability estimates in one or more of their studied traits in oat genotypes. The phenotypic based selection could be effective for yield improvement when the traits have moderate to high heritability (Shariatipour *et al.*, 2022). The influence of environmental factors on the phenotypes is relatively low for traits having a very high degree of heritability, and selection based on these traits might be effective due to the presence of high additive gene action on the expression of these traits (Rosmaina *et al.*, 2016). The estimates of heritability were medium for LDMY, GFP, BYPR, SY, GSFR, NTPP, LLFH, and TBY. This medium heritability of traits indicated that the environmental effect was relatively high on the expression of these traits, and selection based on the phenotypic performance of these traits may not be effective for improvement. Singh (1993) also reported that estimates of medium to low heritability make selection considerably difficult due to the significant masking effect of the environment on the genotypic effects. The heritability estimates in this study were generally lower than those reported from a

single environment (Tanvi, 2016; Atman, 2017; Harshita, 2018; Wagh, 2018). The observed low heritability estimates in the current study might be mainly due to the presences of significant genotype x location interactions in 22 (about 92%) of the studied traits. Ashenafi (2018) also reported lower estimates of heritability in oat genotypes tested at two locations and for two cropping seasons in Ethiopia. The existence of high genotype by year interaction for grain yield could be one of the reasons for low heritability of grain yield compared to other traits (Sobhaninan *et al.*, 2019). Shariatipour *et al.* (2022) also pointed out that the heritability estimates for forage dry matter yield under non-stress condition is relatively higher than drought stress condition, indicating the effects of environments are remarkable on the heritability of the trait. The heritability of grain yield reduced under drought stress conditions compared to optimum growing condition (Sobhaninan *et al.*, 2019).

The estimates of GA and GAM in the present study had wide variations among the observed traits, suggesting the existence of considerable expected genetic gain in oat genotypes for improvement. Based on the estimation of genetic gain in the current study, whenever we select the best 5% of high yielding genotypes as parents, the mean performance of the offspring is expected to be improved. Accordingly, the genotypic performance of the new population (progeny) is expected to be improved from 20.5 to 24.5 t/ha for FDMY; 16.0 to 18.9 t/ha for SY; 23.2 to 26.4 t/ha for TBY; and 7.2 to 9.1 t/ha for GY. Similarly, improvement in FYPR (161.3 to 196.3 kg/ha/day), BYPR (130.6 to 155.7 kg/ha/day), GSFR (107.8 to 136.0 kg/ha/day), PHFH (123.2 to 138.1 cm), TSW (48.4 to 56.6 g), and HI (31.3 to 39.5%) could be expected. All the studied traits had high to medium GAM estimates, except for DSH and this is in line with that of Atman (2017) and Harshita (2018), who reported high to medium GAM, in one or more their considered traits in oat. High expected genetic advance confirmed the relatively greater involvement of the additive gene action component indicating that selection based on phenotypic performance might be effective for improvement.

3.4.1.5 Selection of traits for yield improvement

Selection based on broad sense heritability alone may not be predictive, since the broad sense heritability is based on the total genetic variation, which involves additive, dominance, and epistatic variances. Thus, estimates of heritability coupled with genetic advance are more effective in predicting the genetic gain under selection than heritability alone (Singh, 1999; Bicer and Sakar, 2004; Singh and Singh, 2009; Kapoor *et al.*, 2011; Chakraborty *et*

al., 2014; Charupriya and Singh, 2019). Traits showing high heritability might not necessarily lead to high genetic gain (Johnson *et al.*, 1955). Estimates of very high to moderately high heritability accompanied by high GAM were found in HI, PLGH, FYPR, PDMY, NSLPP, and GY. Traits with such high heritability in conjunction with high genetic advance are dominated with additive gene effects thereby selection based on the phenotypic performance of these traits would be promising for improvement. Higher heritability in combination with high genetic advance resulted in better genetic gain, implying that phenotypic selection can be an effective approach for improving of traits under consideration (Johnson *et al.*, 1955). On the other hand, very high to moderately high heritability estimates associated with medium GAM were observed in DFH, NLFH, PHGH, TDW, PHFH, SDMY, FDMY, NSPP, and TSW. These traits are most likely governed by both comparable additive and non-additive gene actions for the manifestation of phenotypic performance. The trait DSH had moderately high heritability along with low GAM indicating greater influence of the environment on the expression of this trait. This is due to the predominant nature of the non-additive gene action and hence selection based on phenotypic performance of this trait may not be effective for improving the genetic gain in oat genotypes. The traits which had very high to moderately high heritability in combination with high to medium GAM estimates in the present study suggest the extent of genetic gain through phenotypic selection would be reliable and effective for genetic improvement (Burton, 1952; Burton and Devane, 1953; Johnson *et al.*, 1955).

3.4.2 Correlation and path analyses

3.4.2.1 Associations between fodder yield and yield-related traits

The presence of a strong positive relationship between yield attributing traits and yields (FDMY and GY) helps to identify traits that could be used for indirect selection for the improvement of FDMY and GY in oat genotypes. The correlation analysis indicated that the LLFH, PHFH, FYPR, PHGH, PLGH, NSPP, BYPR, GSFR, and GY associated significantly and positively with FDMY both at phenotypic and genotypic levels. This indicated that these traits were the major yield contributing traits to be given more attention for improving FDMY in oat genotypes. Positive correlations of FDMY with LLFH, PHFH, PLGH, and GY were also observed in other studies (Bahadur and Choubey, 2008; Krishna *et al.*, 2014; Atman, 2017). The genotypic correlation of PHFH with NLFH was positive, suggesting that taller plants produce more leaves which results in increased FDMY (Mushtaq *et al.*, 2013). The NLFH and NSLPP had significant positive associations with FDMY only at the

phenotypic level. On the other hand, TSW and HI correlated significantly but negatively with FDMY at the phenotypic level while NTPP had a non-significant and inverse relation with FDMY both at phenotypic and genotypic levels suggesting that selection through NTPP, TSW, and HI would not be effective for FDMY improvement in oat genotypes. These results are in line with the findings of Mayank *et al.* (2020), who reported that higher NTPP would decrease the FDMY in oat genotypes both at the phenotypic and genotypic levels. However, the results opposes the findings of Bhandari *et al.* (2003); Surendra (2006), and Mushtaq *et al.* (2013), who reported that the NTPP had positive genotypic correlation with FDMY in oat genotypes. The correlation estimates are dependent upon the genetic constitution evaluated and upon the environment in which the study is conducted (Claudir *et al.*, 2006). The positive correlations between yields and yield contributing traits generally indicate the possibility of improving oat genotypes through the selection of those multiple traits.

3.4.2.2 Associations between grain yield and yield-related traits

Correlation studies revealed that the GY had a significant positive correlation with FYPR, FDMY, NSPP, BYPR, GSFR, and HI both at phenotypic and genotypic levels, suggesting that these traits could be used as an appropriate selection criterion for GY improvement in oat genotypes. Furthermore, TDW, PLGH, NSLPP, and TSW showed significant positive associations with GY at the phenotypic level while GY had a significant positive correlation with LLFH and PHGH at the genotypic level. Significant positive genotypic associations of GY with NSPP and TSW were also reported by Mushtaq *et al.* (2013). Other studies also indicated that GY had positive association with PLGH, NSLPP, and FDMY (Vaisi *et al.*, 2013; Atman, 2017). The PHFH had a non-significant positive correlation with GY at the genotypic level but its association with GY was a non-significant negative at the phenotypic level. On the contrary, the phenotypic associations of NTPP, NLFH, and LLFH with GY were significant but negative while GY had a non-significant inverse association with NTPP and NLFH at genotypic level. This indicates that selection based on NTPP, NLFH, and LLFH would not be effective for the improvement of GY in oat genotypes. Thus, selections for high NTPP, NLFH, and LLFH do not necessarily ensure high GY in oat genotypes. The negative association between NTPP and GY is also reported at the phenotypic as well as genotypic levels in oat genotypes (Kapoor *et al.*, 2011). The phenotypic correlation coefficients were generally higher than the genotypic correlation coefficient, which indicate that the inherent associations among various studied traits were influenced by environmental

factors and this result was also in close conformity with other study done on oat genotypes (Mayank *et al.*, 2020). But other studies indicated that genotypic correlation coefficients are higher than the corresponding phenotypic ones indicating a strong inherent association between two correlated traits as well as low masking effect of environment in their studied oat genotype (Bibi *et al.*, 2012; Atman, 2017).

3.4.2.3 Associations between yield attributing traits

The phenotypic correlation analysis indicated that the NTPP was associated significantly and positively with NLFH which also correlated significantly and positively with LLFH, PHFH, and PHGH. Other research findings also showed that the NTPP had significant positive association with NLFH and also significant positive associations of NLFH with LLFH and PHFH were reported at the phenotypic level (Kapoor *et al.*, 2011). On the other hand, the NTPP was associated significantly but negatively with TDW, FYPR, PLGH, NSPP, NSLPP, BYPR, and GSFR, which indicated that genotypes having high NTPP had low contribution to the improvement of these traits. These results are in line with the findings of Nirmalakumari *et al.* (2013); and Harshita *et al.* (2019), who reported that the NTPP had an inverse phenotypic relationship with PLGH in oat genotypes. The TDW associated significantly and positively with FYPR, PLGH, NSPP, NSLPP, BYPR, GSFR, TSW, and HI indicating that genotypes having high vigorous growth at the early stage contributed more to the improvement of these yield-related traits. Moreover, the LLFH had significant positive phenotypic association with PHFH, PHGH, and PLGH. This indicates that genotypes having high LLFH could produce higher plant height at both phenological stages and higher panicle length at physiological maturity was also shown by Anjani *et al.* (2017) and Atman (2017). The phenotypic associations of TDW with NLFH and also NLFH with PLGH, NSPP, BYPR, and GSFR were significant but negative, suggesting that the increase in TDW could reduce the NLFH which in turn negatively influences the performance of PLGH, NSPP, BYPR, and GSFR. The observed phenotypic associations of PHFH with FYPR, PHGH, PLGH, NSPP, NSLPP, and BYPR and also FYPR with PHGH, PLGH, NSPP, NSLPP, BYPR, and GSFR were significant and positive. This showed that the genotypes having higher PHFH and FYPR could contribute more to the improvement of the above respective correlated traits. Surje and De (2014) and Atman (2017) also reported that PHFH had positive association with NSLPP in oat genotypes. The PHGH and PLGH had significant positive phenotypic association with NSPP, NSLPP, and BYPR, indicating that genotypes having high PHGH and PLGH could produce higher NSPP, NSLPP, and

BYPR. The phenotypic associations of TSW with NLFH, PHFH, FYPR, PHGH, and NSLPP and also HI with NTPP, NLFH, LLFH, PHFH, and PHGH were significant but negative showing selection based on TSW and HI could lead to a decrease in the performance of the corresponding correlated traits. This result is in line with the results of Kumar *et al.* (2004) and Krishna *et al.* (2014), who reported that TSW had an inverse association with PHFH in oat genotypes.

The genotypic correlation among yield-attributing traits indicated that the NTPP had a significant positive association with TDW and TSW while a significant but an inverse association was also observed between TDW and HI. The genotypic associations of NLFH with LLFH and also LLFH with PHFH, FYPR, PHGH, BYPR, and GSFR were significant and positive. Kapoor *et al.* (2011) also reported that the genotypic correlation between NLFH and LLFH, as well as between LLFH and PHFH in oat genotypes were significant and positive. The observed genotypic correlation of PHFH with FYPR, PHGH, BYPR, GSFR, and TSW and also FYPR with PHGH, PLGH, NSPP, BYPR, and GSFR were significant and positive indicating the possibility of selection of one of the above component traits would result in the improvement of other traits (Mayank *et al.*, 2020). The PHGH had significant positive genotypic correlations with PLGH, NSPP, NSLPP, BYPR, and GSFR and also PLGH had significant positive genotypic correlations with NSPP and NSLPP while PLGH was associated significantly but negatively with HI. This indicates that selection based on a higher PHGH could lead to higher respective correlated traits, which is similar to the findings of Bahadur and Choubey (2008); Ahmed *et al.* (2013) and Atman (2017), who reported that oat genotypes having higher plant height had higher PLGH and NSLPP. The genotypic associations of NSPP with NSLPP, BYPR, and GSFR and also NSLPP with BYPR were significant and positive. Furthermore, the BYPR had significant positive genotypic correlations with GSFR and TSW and also significant positive genotypic association was observed between GSFR and HI. The correlations of FYPR with PHGH, NSPP, BYPR and GSFR were significant and positive at the genotypic level, demonstrating that the improvement of these traits would simultaneously improve the performance of the respective associated traits.

3.4.2.4 Effects of yield contributing traits on fodder yield

The phenotypic and genotypic correlation coefficients of various yield contributing traits for FDMY and GY were further partitioned into direct and indirect effects. The results indicated

that the NLFH, PHFH, FYPR, BYPR, and GSFR had positive direct effects on FDMY both at phenotypic and genotypic levels. This indicates selection based on these traits could be effective for the improvement of FDMY in oat genotypes. These results are also in agreement with the findings of Krishna *et al.* (2014) and Mayank *et al.* (2020), who reported that PHFH had positive direct effects on FDMY in oat genotypes. On the other hand, the highest negative direct effects contributing towards FDMY were observed due to PHGH, PLGH, NSPP, TSW, and GY both at phenotypic and genotypic levels indicating that direct selection of these traits could not be effective for the improvement of FDMY in oat genotypes. The PLGH had negative direct effect on FDMY in oat genotypes (Atman, 2017; Harshita *et al.*, 2019), which is in line with the current findings. However, high indirect effects of PHGH, PLGH, NSPP, GY, LLFH, and NSLPP via mainly FYPR suggested that indirect selection of these traits via FYPR may also increase FDMY in oat genotypes. The direct effects of NTPP and LLFH on FDMY were positive only at the phenotypic level while TDW and NSLPP had positive direct effects on FDMY at the genotypic level. The residual effects were estimated to determine the unaccounted variability of the dependent factors (FDMY and GY). The residual effects of 0.1406 and 0.1261 indicated that the traits which were included in the phenotypic and genotype path coefficients analysis explained 85.9 and 87.4% of the total variation in FDMY, respectively. These indicate that the independent traits considered in this study adequately captured the variation of FDMY in oat genotypes. However, there were other contributors (at phenotypic level 14.1% and genotypic level 12.6%) which were responsible for variations in FDMY but were not taken into consideration in the current study.

3.4.2.5 Effects of yield contributing traits on grain yield

The results of a path analysis revealed that NLFH, LLFH, PLGH, NSPP, BYPR, and HI were identified as important traits for direct selection as these traits had high positive direct effects on GY both at phenotypic and genotypic levels. This indicates that selection based on these traits could be effective for the improvement of GY in oat genotypes. On the other hand, TDW, PHFH, NSLPP, and TSW had negative direct effects at both phenotypic and genotypic levels indicating that direct selection based on these traits could not improve the GY in oat genotypes. The results were in agreement with the findings of Fevzi (2022), who reported that TSW had negative direct effect on GY in oat genotypes while Ziya *et al.* (2012), Nirmalakumari *et al.* (2013) and Rukoo *et al.* (2021) found that TSW in oat genotypes had positive direct effect on GY. The direct selection of TDW, PHFH, NSLPP,

and TSW at both phenotypic and genotypic levels would decrease the GY; however, their indirect selection via mainly BYPR may improve the GY in oat genotypes. The direct effect of NTPP on GY was negative only at the genotypic level while FDMY, PHGH, and GSFR had positive direct effect on GY only at the genotypic level. The results of other studies also indicated that the NTPP had negative direct effect on GY in oat genotypes (Shankar *et al.*, 2002; Kapoor *et al.*, 2011). So, indirect selection of FDMY, PHGH, and GSFR via mainly BYPR could improve the GY at the phenotypic level. The residual effects were estimated to determine the unaccounted variability of the dependent factor (grain yield). The residual values of 0.2099 and 0.1880 indicated that the traits which are included in the phenotypic and genotypic path coefficients analysis explained 79.0 and 81.2% of the total variation in grain yield, respectively. These indicate that the independent traits considered in this study adequately captured the variation of grain yield in oat genotypes. However, some more traits that are contributing towards grain yield should be considered to capture the entire variability of grain yield in oat genotypes.

3.4.2.6 Selection of traits using correlation and path coefficients

Correlation coefficients are coupled with path coefficients provide more reliable information which can be effectively utilized in crop improvement programs (Sahu and Tiwari, 2020). The results showed that FYPR, PHFH, BYPR, and GSFR had positive direct effects on FDMY coupled with significant positive association with FDMY both at phenotypic and genotypic levels, indicating that selection based on phenotypic expression of these traits could be effective for FDMY improvement in oat genotypes. Although PHGH, PLGH, NSPP, and GY had significant positive phenotypic and genotypic correlations with FDMY, these traits showed negative direct effects on FDMY both at phenotypic and genotypic levels. The occurrence of significant positive phenotypic and genotypic associations, along with inverse direct effects between FDMY and these traits, could be due to the high positive counterbalancing potential of the phenotypic and genotypic indirect effects exerted by these traits via mainly FYPR. The TSW had significant negative phenotypic association with FDMY and this trait also had negative phenotypic direct effect and high negative phenotypic indirect effect via mainly FYPR. This indicates that direct selection of TSW and indirect selection of this trait via all studied traits may not be effective for improving FDMY in oat genotypes. Despite the non-significant positive genotypic association of TSW with FDMY, its genotypic direct effect on FDMY was negative indicating that the positive genotypic association between these traits was due to the high and positive neutralizing genotypic

indirect effect of this trait via mainly FYPR. Despite the positive phenotypic direct effect of NTPP on FDMY, its negative phenotypic association with FDMY could be due to the positive phenotypic direct effect of NTPP being neutralized by its high negative phenotypic indirect effect via primarily FYPR. The genotypic relationship between NTPP and FDMY was non-significant negative accompanied by negative genotypic direct effect and high negative genotypic indirect effect via mainly FYPR. This indicates that the NTPP and FDMY had negative true relationship, which suggests that direct selection based on NTPP and its indirect selection through all studied traits, may not be effective to improve FDMY in oat genotypes.

The HI, BYPR, and NSPP had positive phenotypic and genotypic direct effects on GY along with significant positive associations with GY both at phenotypic and genotypic levels, indicating that selection based on phenotypic expression of these traits could be effective for GY improvement in oat genotypes. Furthermore, GSFR, PHGH, LLFH, and FDMY had positive genotypic direct effects coupled with significant positive genotypic associations with GY suggesting that genotypic selection based on phenotypic expression of these traits could be reliable for GY improvement in oat genotypes. This is in line with the findings of Nirmalakumari *et al.* (2013), who reported that HI and FDMY had direct positive effects on GY along with the corresponding positive associations with GY. Despite the phenotypic and genotypic direct effects of NLFH on GY being positive, its associations with GY were negative both at phenotypic and genotypic levels, which could be due to high and negative neutralizing potential of the indirect effects exerted by NLFH via mainly BYPR and HI. The phenotypic and genotypic direct effects of NSLPP and TSW were negative but their associations with GY were positive both at phenotypic and genotypic levels. This was due to the high and positive neutralizing potential of the phenotypic and genotypic indirect effects exerted by both traits via mainly BYPR and/or HI. The phenotypic (PHFH and PHGH) and genotypic (NTPP and TDW) direct effects on GY and their respective associations with GY were negative indicating that the GY improvement based on the selection of these traits may not be effective in oat genotypes.

3.4.3 Multivariate analysis

3.4.3.1 Clustering of genotypes

The studied 120 oat genotypes were grouped into four different clusters based on the mean performance of 16 agro-morphological traits. Grouping many genotypes into different

clusters based on their mean performance is one of the most efficient methods to exploit genetic variation for yield improvement. The total success rate of the discriminant function analysis was 95.0%, which implies that it was successful in discriminating different groups. Different genotypes grouped within a cluster are anticipated to be more closely associated in terms of the traits under consideration with each other than those genotypes in different clusters (Singh and Chaudhary, 1985). This study indicated that the 120 oat genotypes were grouped into four clusters. However, the number of clusters reported by different scholars was highly variable due to differences in the number of genotypes, genetic variation, and methods of analysis. Prasad *et al.* (2003) grouped 247 oat genotypes into XVI clusters. Fekede (2004) grouped 20 oat genotypes into VIII clusters. Kumar *et al.* (2005) grouped 100 oat genotypes into IX clusters. Singh and Singh (2010) grouped 70 oat genotypes into VII clusters. Krishna *et al.* (2014) grouped 50 oat genotypes into X clusters. Ashenafi (2018) grouped 73 oat (*Avena sativa* L.) genotypes into III clusters and 176 oat genotypes which comprised five *Avena* species were also grouped into III clusters. The results of the current study indicated that the numbers of oat genotypes included in each cluster were generally variable due to their genetic variation and origin of introduction. The third cluster (C3) in this study mostly consisted of genotypes introduced via the CIMMYT, while C1, C2, and C4 comprised mainly genotypes introduced via the FAO. This indicates the clustering of the genotypes is mostly performed based on their origin of introduction. However, some of the CIMMYT and FAO introduced genotypes were distributed into different clusters, suggesting the existence of genetic variability with their origin of introduction. This result is also in line with the findings of Gemechu (2012), Habte (2018), Sonia *et al.* (2020), and Mohammad *et al.* (2021), who reported that genotypes from the same origin could be grouped into different clusters.

3.4.3.2 Performance of genotypes under different clusters

The first and second clusters were generally characterized by high forage yield-producing clusters while the third cluster was a high grain yield-producing cluster and high tillers, leaf number, and leaf size was the characteristics of the fourth cluster. The genotypes grouped in the second cluster had higher mean performances in PHFH, FYPR, FDMY, PHGH, PLGH, NSPP, NSLPP, and BYPR. This cluster also included the top-performing genotypes in terms of the above-mentioned traits and the mean values of these traits were also higher than the grand mean of the respective trait averaged over all clusters. Despite high grain yield-related traits (especially PLGH, NSPP, and NSLPP) being observed in the second cluster, the GY

produced by the genotypes under this cluster was intermediate. This might be due to the seed size (TSW) produced by the genotypes in this cluster being too small which could significantly influence the GY per unit area. The research findings also indicated that TSW remarkably influences the GY in oat genotypes (Ahmed *et al.*, 2013; Krishna *et al.*, 2014). The genotypes classified in the third cluster had higher mean performances, top-performing genotypes, and higher mean values than the grand mean in terms of TSW, HI, and GY. However, the genotypes included in the third cluster had the lowest mean values of NTPP, NLFH, LLFH, PHFH, PHGH, and PLGH. This result indicated that high GY-producing genotypes had shorter plant height and panicle length and low tillering performance. Different scholars reported that modern cultivars (high grain yielders) had short plant heights as compared to landraces which produce low grain yield (Reynolds *et al.*, 2009; Tao *et al.*, 2021).

3.4.3.3 Genetic divergence

The pairwise generalized square distance (D^2) in this study generally showed the existence of significant ($P < 0.05$) inter-cluster genetic distance among the clusters except between clusters C1 and C2. The observed intra-cluster genetic distance was smaller than the inter-cluster genetic distance indicating the genotypes grouped within a cluster had narrow genetic variation due to their similar performance for the studied traits. This result is also in line with the results of Ahmed *et al.* (2011), Krishna *et al.* (2014), Kumar *et al.* (2016), and Harshita (2018), who reported that the intra-cluster genetic distance was generally lower than the inter-cluster genetic distance in oat genotypes. The intra-cluster genetic distance was relatively high for cluster C3, indicating the genotypes in this cluster was more diverse than any other cluster. On the other hand, the intra-cluster genetic distance for cluster C1 was comparatively low, suggesting the genotypes in this cluster were more homogenous than those in other clusters and these genotypes could be used for backcross breeding programs. To select a genotype that showed better performance in the selected cluster, intra and inter-cluster genetic distances as well as cluster means were considered for effective yield improvement in oat genotypes.

The inter-cluster genetic distance was the lowest and non-significant ($P > 0.05$) between clusters C1 and C2, which indicated that the genotypes grouped in these clusters had a close relationship than the genotypes grouped in other clusters. The diverse and desirable genotypes were identified based on the selection of the cluster that showed the maximum

inter-cluster distance. The genotypes in different clusters with non-significant inter-cluster genetic distance were expected to have closer relationships with each other than those genotypes grouped in significantly distant clusters (Singh and Chaudhary, 1985). The inter-cluster genetic distances were the highest and most significant ($P < 0.05$) between clusters C3 and C4 followed by clusters C2 and C3. This indicates the existence of remarkable genetic variations between these clusters and yield improvement could be achieved through the selection of genotypes based on the purpose of production from these clusters. The highest genetic divergence between these clusters is assumed to yield maximum genetic recombination and difference in the crossing of parents selected from these genetically distant clusters. However, the selection of parents from these distant clusters should be based on the peculiar characteristics of each cluster and the performance of each genotype within each cluster considered depending on the specific purposes of crossing or hybridization (Singh, 1990). Since maximum genetic recombination and variation in the subsequent generation is expected from crosses of parents grouped in divergent clusters, the crossing of the genotypes located in cluster C3 with C4 and also genotypes located in cluster C2 with C3 are expected to provide relatively better genetic recombination and segregation in their progenies. So crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in oat improvement (Ahmed *et al.*, 2011; Krishna *et al.*, 2014). Maximum genetic recombination and variation in the subsequent generation are expected from crosses that involve parents from the clusters characterized by maximum distances (Sawarkar *et al.*, 2015; Tanvi, 2016). Parents with one or more of the desired traits can be selected from each cluster based on both group performance and the performances of individual genotypes for specific traits (Singh, 2002). Genotypes grouped in various clusters were heterogeneous and can be used for a hybridization program to give a high heterotic effect in the first generation and a broad spectrum of variability in segregating generations (Verma *et al.*, 2012; Ayenew *et al.*, 2020). So, genotypes grouped in clusters C2, C3, and C4 can be used as potential parents for heterosis breeding.

3.4.3.4 Principal component analysis

The result of PCA elucidated the existence of substantial genetic diversity in oat genotypes. Despite the various PCs contributing differently to the total variation, the first two PCs had a higher contribution than the remaining PCs. The first two PCs in this study accounted for 60.8% of the total variation but the third (9.5%) and fourth (8.0%) PCs contributed less to the total variation. Chahal and Gosal (2002) also reported that the first few PCs generally

contributed more to the total variation. Ahmed *et al.* (2011) reported that the first four PCs (98.3%) accounted for more of the total variation in oat genotypes. The report of Krishna *et al.* (2014) also revealed that the first six PCs accounted for 84.9% of the variance in oat genotypes. According to the criterion of Raji (2002), traits with an absolute value of eigenvectors greater than 0.3 contributed more to the total variation in that particular PC, while traits with values less than 0.3 were less considered due to their slight contribution to the total variation. The observed variation in the first PC was mainly due to FYPR, BYPR, PLGH, FDMY, and NSLPP, while HI, GY, NLFH, and PHGH had a high contribution to the total variation in the second PC, because the eigenvectors of these traits were higher than the cut-off limit as suggested by Raji (2002). On the other hand, it was generally supposed that traits with relatively larger absolute values of eigenvector closer to unity within the first PC influence the clustering more than those with lower absolute values closer to zero (Chahal and Gosal, 2002). In this study, however, all the studied traits individually contributed less (0.020–0.358) to the total variation in the first PC and, therefore, the differentiation of the genotypes into different clusters was rather dictated by the cumulative effects of the traits under consideration. Gemechu (2012) also reported that the cumulative effects of the traits had a high contribution to the groupings of genotypes into different clusters when the traits considered had lower values of the eigenvector in the first PC. The eigenvector sign indicates the association of traits with PCs. A negative eigenvector for a given trait indicates a negative correlation between that trait and the given PC and vice versa. Accordingly, NTPP, NLFH, and TSW had a negative association with the first PC while the remaining traits had a positive correlation with this PC.

To examine the contribution of the traits to the total genetic variation among the genotypes, a biplot analysis was performed using the first two PCs. The length of the trait vector arising from the origin of the two-dimensional plot indicates the importance of a given trait to the total variation in that particular PC. Sonia *et al.* (2020) also reported that traits displayed closer to the center on the biplot played the least role in the total variation than traits displayed further away from the center. The length of vector lines and their closeness to the axis are generally proportional to the magnitude of the vector loadings in the biplot analysis. For vector lines that are longer and closer to the X-axis in the first two PCs, the contribution of this trait to the total variation in the first PC is much higher than the contribution of traits that had shorter and longer vector lines with a narrow and wide distance of the vector trait from the axis, respectively. For instance, traits of FYPR and BYPR had longer vector lines

which are closer to the X-axis as compared to those of HI, which also had longer vector lines but the line was far from the X-axis. This indicates the contribution of FYPR and BYPR to the total variation was higher in the first PC as compared to HI. However, HI had a longer vector line which is very close to the Y-axis indicating that the contribution of this trait to the second PC was higher as compared to other traits. Generally, the cosine of the angle between a vector and an axis indicates the importance of the contribution of the corresponding trait to the PC, and hence, the FYPR in the first PC and HI in the second PC had a remarkable contribution to the total variation due to the small cosine of the angle between the traits and the respective PC.

The cosine of the angle between pairs of vectors also indicates a correlation between the corresponding traits. This is in line with the findings of Zinhle *et al.* (2018); Maxwell *et al.* (2019) and Sonia *et al.* (2020), who reported that smaller angles between vectors in the same direction showed the presence of a high correlation between the traits. The narrow cosine of the angle between vectors that point in similar directions had a high correlation while uncorrelated traits were nearly perpendicular to each other. Accordingly, the biplot loadings showed that GY, GSFR, TDW, and NSPP were grouped indicating the existence of a strong positive association among these traits. The acute angles ($<90^\circ$) between the vector line of NSPP from the second group and TSW from the third group, and also GY from the second group with PHFH and PHGH from the first group indicate the existence of non-significant positive association with these respective traits. Moreover, a high obtuse angle ($>90^\circ$) formed between the vector line of FDMY which was located in the first group with traits of the third group (HI and TSW), and also between GY located in the second group with traits of the fourth group (NTPP, NLFH, and LLFH), indicates the presence of a significant negative association between these respective traits. Generally, the biplot loadings of the first two PCs were determined according to the phenotypic correlation values observed among the traits (data not shown).

A pattern analysis based on scatter plots of the genotypes using the first two PCs accounted for 60.8% of the total variation and the results of the scatter plots were more strongly supported by the cluster analysis. The first, second, and fourth clusters were distributed closer to each other around the center of the PC plane, while cluster C3 was spatially situated relatively far apart from other clusters. This indicates genotypes under clusters C1, C2, and C4 had more or less similar performances in measured traits, and these clusters had relatively lower inter-cluster genetic distances when compared to cluster C3. Moreover,

cluster C3 was far from clusters C2 and C4 indicating the inter-cluster genetic distance between clusters C3 and C2 and clusters C3 and C4 were relatively higher and the mean performance of the genotypes in cluster C3 for most measured traits were lower compared to other clusters. Abdollah *et al.* (2011) reported that the scatter plot showed genetic distances among the species that reflect their relationships. The pattern of the scatter plot in the first two PCs was generally consistent with the result of cluster analysis. Abdollah *et al.* (2011); Zinhle *et al.* (2018), and Mohammed *et al.* (2022) also reported that the results of the scatter plot confirmed the results of cluster analysis. Points those are close to each other in the biplot represent observations/genotypes with similar performances in measured traits. In the genotype-vector biplot, a cluster of the genotypes which was closer to the vectors indicates the clustering of the genotypes mainly characterized by those vector loadings. Accordingly, the genotype-trait biplot analysis in this study indicated that GY, GSFR, TDW, and NSPP had a high contribution to the first cluster while the second cluster was highly contributed by BYPR, FYPR, NSLPP, PLGH, FDMY, PHFH, and PHGH (figure not shown). Similarly, the third cluster had more contribution from HI and TSW, while NTPP, NLFH, and LLFH had a high contribution to the fourth cluster. Sonia *et al.* (2020) also reported that the biplot provides a visual representation of the grouping of genotypes and the major traits associated with the genotypes.

3.5 Conclusion

The results of this study revealed the presence of substantial variation among 120 oat genotypes for measured agro-morphological traits. Based on variability, heritability, and genetic advance, selection of oat genotypes using FDMY, NLFH, SDMY, FYPR, GY, NSPP, PLGH, and HI could be reliable for improvement. Selection of genotypes based on high FDMY coupled with better NLFH, SDMY, and FYPR could be effective for fodder yield improvement while selection based on high GY along with better HI, PLGH, and NSPP could be effective for grain yield improvement in oat genotypes. The correlation and path analyses also indicated that FYPR was the most important trait and selection of oat genotypes using this trait would improve the FDMY in oat genotypes. Similarly, selection based on BYPR, HI, and GSFR will ultimately improve the GY in oat genotypes. The principal component analysis also showed that selection based on FYPR, BYPR, PLGH, FDMY, NSLPP, HI, GY, NLFH, and PHGH traits could be effective for yield improvement in oat genotypes. Out of the studied oat genotypes, CI-715, CI-1463, SRCPX80Ab2806, A-505, CI-1480, S-122, Bona-bas, and CI-1674 produced better fodder and grain yields.

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Chapter IV

Experiment 2: Genotype by Environment interaction and yield stability of oat (*Avena sativa* L.) genotypes



Genotype by Environment interaction and yield stability of oat (*Avena sativa* L.) genotypes

Abstract

The fodder dry matter yield and grain yield performances of oat genotypes usually vary across environments and the existence of genotype by environment interaction (GEI) complicates the selection process. Twenty-four oat genotypes were sown during the 2020/2021 cropping season at Holetta (E1), Ada-Berga (E2), Ginchi (E3), Jeldu (E4), D/Zeit (E5), Kulumsa (E6), Bekoji (E7), Kuyu (E8), and D/Markos (E9) using a randomized complete block design with three replications. The study aimed to evaluate the magnitude of GEI and determine the stability of oat genotypes for fodder dry matter yield and grain yield using univariate and multivariate statistical models. The additive main effects and multiplicative interaction (AMMI) analysis of variance for fodder yield showed significant variation ($p < 0.0001$) for genotype (G), environment (E), and GEI. The main effect of the E had the highest contribution for the total variation (67.45%) followed by GEI (22.73%) and G (9.82%). The first (44.11%) and the second (26.79%) interaction principal component axes (IPCA) were significant and cumulatively accounted for 70.91% of the total interaction variance. The AMMI analysis indicated that G6, G7, G9, G10, and G23, were high-yielding and stable genotypes. Based on the G plus GEI (GGE) biplot analysis for fodder yield, the ideal genotype which is located at the center of the concentric circles was G6 while the desirable genotypes were G10, G3, G23, and G2 which is located relatively closer to the ideal genotype. Among the environments, E7 was an ideal environment which had higher discriminating ability and representativeness whereas E1 and E8 were favorable environments. Based on the GGE biplot analysis, G6, G9, G10, and G23 had high yields and stable performance. The results of univariate stability analysis showed that high fodder yield-producing genotypes had stable performance using the stability parameters of genotypic superiority index (P_i), yield stability index (YSI), coefficient of determination (R^2), and coefficient of variability (CV_i), demonstrating that selection of oat genotypes using these stability parameters would be effective for fodder yield improvement. Moreover, Spearman's rank correlation coefficients indicated that the stability parameters of P_i , YSI, R^2 , and CV_i had significant positive associations with fodder dry matter yield. The stable and high-yielding genotypes using the stability parameters of P_i , YSI, R^2 , and CV_i were G6, G7, G9, G10, and G23. Similarly, the AMMI analysis of variance for grain yield showed significant variation for G, E, and GEI effects and the E main effect was a predominant source of variation (44.62%) followed by G (28.84%) and GEI (26.54%). The first two IPCAs of AMMI were significant and cumulatively explained 63.96% of the total GEI variance. Based on AMMI analysis, G8, G17, and G22 had high yield and stable performance under diverse environments. The GGE biplot analysis showed that G19 was an ideal genotype which located at the center of the concentric circles whereas G14, G8, G11, G12, G17, and G22 were the desirable genotypes. Among the environments, E2 was an ideal test environment, whereas E5, E1, and E4 were identified as favorable environments. Excluding the released varieties, G8, G17, and G22 were the best-adapted genotypes to wider environments. The results of univariate stability analysis indicated that genotypes with superior grain yield had stable performances based on the stability parameters of P_i , the Perkins and Jinks adjusted linear regression coefficient (B_j), and YSI. This indicated that selection using these stability parameters would be efficient for grain yield improvement in oat genotypes. Moreover, Spearman's rank correlation coefficients showed that the stability parameters of P_i , B_j , and YSI had significant positive associations with grain yield. Accordingly, G8, G16, G17, and G22 showed high yield and stable performance based on P_i , B_j , and YSI. Therefore, G6, G9, G10, and G23 were selected using AMMI, GGE, and univariate stability parameters for fodder yield improvement whereas G8, G17, and G22 were selected and recommended for grain yield improvement of oat in Ethiopia.

Keywords: AMMI analysis, fodder yield, GE interaction, GGE biplot, grain yield, oat genotypes, univariate stability, yield stability

4.1 Introduction

The performances of fodder and grain yields of oat (*Avena sativa* L.) genotypes generally vary with changing environmental conditions. Yield is a complex quantitative trait that is governed by many genes and it is influenced by the actions and interactions of different traits as well as the effects of genotype, environment, and their interactions (Tonk *et al.*, 2011; Nowsad *et al.*, 2016). Multi-environment trials (METs) are usually conducted to select high-yielding and stable genotypes across environments (Yan *et al.*, 2000; Wondimu *et al.*, 2022). In METs, genotype by environment interaction (GEI) is a common phenomenon which complicates the selection of superior genotypes under diverse environmental conditions (Ceccarelli *et al.*, 2006; Waki and Birte, 2018; Goksoy *et al.*, 2019). The GEI is the result of changes in the genotype's relative performance across environments and/or due to differential responses of genotypes to growing environments and it influences the process of genotype selection in yield improvement programs (Mehari *et al.*, 2015; Satoto and Widyastuti, 2016; Sharifi *et al.*, 2017). The phenotypic performance of a genotype is a combined effect of genotype, environment, and GEI and it may not be consistent across environments (Yan *et al.*, 2007; Goksoy *et al.*, 2019; Hossein *et al.*, 2020). The existence of GEI complicates the selection of high-yielding genotypes for a range of environments and calls for the evaluation of genotypes under diverse environmental conditions to define their true genetic potential (Gauch and Zobel, 1996; Ebdon and Gauch, 2002). Therefore, assessing the degree of GEI observed in MET is useful in breeding programs to select genotypes for all environments or to identify genotypes for specific target environments and to identify the best environments (Abakemal *et al.*, 2016; Goksoy *et al.*, 2019).

Genotypes that perform consistently across environments have small environmental variances and are considered stable while genotypes showing significant GEI effects are not suited for a wide range of environments and substantially affect the selection of high-yielding genotypes with stable performance across environments (Gezahagn *et al.*, 2023a). Genotypes showed either crossover (rank changes) or non-crossover (change in magnitude of performance but no rank changes) type of GEI due to the differential response of genotypes across environments (Kang, 1998). The GEI is important only when it is significant and causes a significant change in genotype ranks (crossover-interaction) in diverse environmental conditions (Crossa, 1990; Yan, 2019). Selection of a high-yielding and highly stable genotype is highly desirable for the cultivation of wider environments and high-yielding but low-stability performance is also desirable for specific environment

selection. However, the selection of a genotype for low yield and low stability is desirable for special breeding purposes (e.g. drought tolerance selection) while a genotype with low yield and high stability is the most undesirable for selection. Breeders often evaluate various genotypes across environments prior to a new improved variety being released for production (Gezahagn *et al.*, 2023b). The main target of the breeder is to develop varieties with high yield and stable performance across environments, however, the breeding activities become much more complicated with GEI and the selection of stable genotypes becomes more difficult (Gauch *et al.*, 2008; Mohammadi *et al.*, 2012a; Erdemci, 2018). The development of resilient varieties for edaphic, biotic, and abiotic factors through a breeding program is vital for yield improvement (Gezahagn *et al.*, 2024). Thus, understanding the extent of GEI is important in plant breeding programs because its significant effect can extremely affect the selection of superior genotypes (Yan and Racjan, 2002; Li *et al.*, 2017).

The GEI requires more advanced statistical methods than the analysis of variance (ANOVA). The ANOVA is an additive model that describes the main effects effectively but it does not give an insight into the patterns of GEI (Samonte *et al.*, 2005). The ANOVA model partitions the total sum of squares into the components of environment, genotype, and GEI without further partitioning the GEI. Thus, many statistical methods have been developed to study the pattern of GEI (Cooper *et al.*, 2001; Naveed *et al.*, 2007). These statistical methods can be divided into two major groups, univariate and multivariate stability parameters (Annicchiarico, 2002; Kang, 2002; Sabaghnia *et al.*, 2008). Among the multivariate methods, the additive main effects and multiplicative interaction (AMMI) model is one of the popular extensions of ANOVA used to analyze multi-environment varietal trials effectively and efficiently (Yuksel *et al.*, 2002; Samonte *et al.*, 2005; Annicchiarico *et al.*, 2010). The AMMI model is a hybrid model that combines ANOVA for additive main effects and uses principal component analysis (PCA) to partition the multiplicative structure of the GEI (Gauch and Zobel, 1996; Gauch, 2007). The model separates the additive variance from the multiplicative variance and then applies PCA to the interaction portion to a new set of coordinate axes that explains in more detail the interaction pattern (Thillainathan and Fernandez, 2001). The AMMI biplot analysis is also an effective tool to diagnose GEI patterns graphically (Mukherjee *et al.*, 2013). Hence, the AMMI model is widely used to analyze the GEI in different crops (Sayyed *et al.*, 2012; Daba and Dawit, 2021).

The yield data obtained from multi-environment trials (MET) is too large and so difficult to understand the general pattern of the data without some graphical biplot techniques (Gabriel, 1971). Various statistical methods for describing GEI have been developed or used by several researchers (Gabriel, 1971; Gauch, 2006; Yan and Tinker, 2006; Yan *et al.*, 2007). The stability analysis can be performed using univariate and multivariate stability methods. However, the GEI can be explained more using multivariate analysis (Crossa *et al.*, 1990a). The most recent method, the genotype plus GEI (GGE) biplot model, provides a more complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents mean performance and stability, as well as identifying mega environments (Yan, 2001; Yan and Kang, 2003; Ding *et al.*, 2007). The GGE biplot can be useful to display the which-won-where pattern of the data that may lead to identifying high-yielding and stable cultivars and discriminating and representative test environments (Yan, 2001). Like the AMMI analysis model, the GGE biplot is a hybrid model that requires a two-way data matrix and it combines the additive main effects from the analysis of variance and the multiplicative effects from the principal components analysis of GEI (Gauch and Zobel, 1996; Gauch, 2006). The GGE biplot analysis model was often used for GEI studies of METs in different crops (Tamene and Tadesse, 2014; Fentaw *et al.*, 2015; Mare *et al.*, 2017; Irfan, 2018; Wondimu *et al.*, 2022).

The univariate stability parameters, which are classified as parametric and nonparametric statistics, are the most important statistical techniques used to study the yield stability performance of genotypes under different environmental conditions. The univariate stability concept can be divided into two groups, static/biological and dynamic/agronomic stability (Becker and Leon, 1988). The effect of GEI can be studied using parametric and nonparametric statistical models (Hussein *et al.*, 2000; Mohammadi *et al.*, 2010). Explaining the performance of adaptability and stability of genotypes in different environments is difficult with a single statistical method (Dehghani *et al.*, 2006). Several stability studies have been carried out using various univariate and multivariate stability parameters on different crops in Ethiopia (Legesse *et al.*, 2015; Kassaye *et al.*, 2017; Tadele *et al.*, 2018; Wondimu *et al.*, 2022). The extent of correlation between yield and different stability parameters is also used to select one or more stability statistics for reliable prediction of responses in different environments. According to Duarte and Zimmermann (1995), this association can help breeders choose the stability statistics that better obey the concept of stability.

The AMMI analysis (Anandan *et al.*, 2009; Sayyed *et al.*, 2012; Daba and Dawit, 2021), GGE biplot analysis (Tamene and Tadesse, 2014; Massaine *et al.*, 2018; Wondimu *et al.*, 2022), and univariate stability analysis (Tamene *et al.*, 2015; Cubukcu *et al.*, 2021; Erdogdu and Esendal, 2021) are often used for GEI studies of METs in different crops. However, information on the extent and pattern of GEI and stability for fodder dry matter yield and grain yield performances of oat genotypes using AMMI, GGE, and univariate (parametric and nonparametric) stability models is scanty and not properly documented in Ethiopia. Therefore, this study was undertaken with the objectives (i) to assess the effect of GEI on quantitative traits of oat genotypes under diverse environments, (ii) to evaluate the stability performances for fodder and grain yields of oat genotypes using various stability parameters, (iii) to determine the association of fodder yield and grain yield of oat genotypes with various univariate (parametric and nonparametric) stability parameters, (iv) to examine the relative importance of each univariate (parametric and nonparametric) stability parameter to select oat genotypes for yields of fodder and grain improvement, and (v) to identify genotypes with high yields (fodder and grain) and stable performance under diverse environmental conditions of Ethiopia.

4.2 Materials and Methods

4.2.1 Description of the study sites

The field experiment was conducted during the 2020/21 main cropping season in nine oat-growing environments in the central highlands of Ethiopia. The study was done at agricultural research stations of Holetta (E1), Ada-Berga (E2), Ginchi (E3), Jeldu (E4), D/Zeit (E5), Kulumsa (E6), Bekoji (E7), Kuyu (E8) and D/Markos (E9) (Figure 4.1). These environments are among the major oat growing areas and are generally characterized by a crop-livestock mixed production system. The physicochemical properties of the soils for the study environments were also determined following the standard soil analysis procedures. A description of the study environments is presented in Table 4.1.

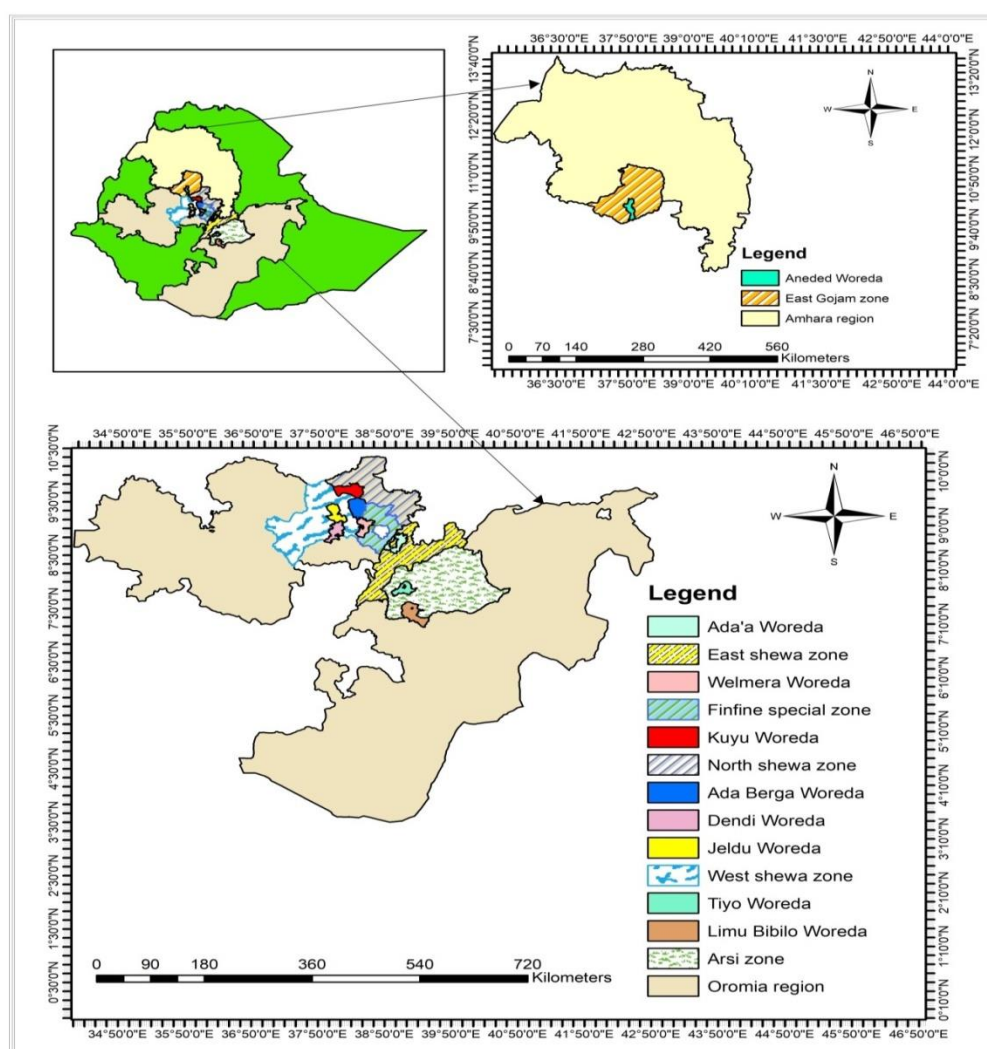


Figure 4.1 Map of study areas of Holetta (Welmera Woreda), Ada-Berga (Ada Berga Woreda), Ginchi (Dendi Woreda), Jeldu (Jeldu Woreda), D/Zeit (Ada'a Woreda), Kulumsa (Limu Bibilo Woreda), Bekoji (Tiyo Woreda), Kuyu (Kuyu Woreda), and D/Markos (Aneded Woreda) in Ethiopia

Table 4.1 Description of testing environments for evaluation of oat genotypes in Ethiopia

Parameter	Environment								
	E1	E2	E3	E4	E5	E6	E7	E8	E9
Altitude (masl)	2400	2600	2200	2865	1850	2183	2800	2530	2470
Latitude (N)	09°03'40"	09°16'09"	09°01'21"	09°16'13"	08°03'04"	08°01'17"	07°34'59"	09°48'20"	10°16'01"
Longitude (E)	38°30'02"	38°22'59"	38°10'45"	38°05'35"	39°03'30"	39°09'26"	39°09'60"	38°26'44"	37°46'31"
ARF (mm)	1055	1225	1095	1200	850	820	1020	1228	1350
Min. Temp. (°C)	6.1	10.0	8.4	2.1	8.9	10.5	8.0	7.0	7.5
Max. Temp. (°C)	22.2	25.0	24.6	16.9	28.3	22.7	20.0	23.0	27.0
Soil pH	5.50	5.32	6.88	5.23	7.43	6.16	5.54	5.31	5.29
OC (%)	2.11	2.21	1.13	2.73	1.10	2.30	2.47	1.06	2.02
TN (%)	0.21	0.22	0.08	0.29	0.08	0.17	0.21	0.12	0.18
C/N ratio	9.99	9.87	14.67	9.61	13.34	13.69	11.80	8.88	10.95
AP (ppm)	23.86	17.46	9.33	12.26	37.71	14.00	10.66	13.06	10.93
CEC (meq/100 g)	23.47	20.05	48.73	19.20	36.67	26.35	22.36	18.86	18.48
Textural class	Clay	Clay	Clay	Clay	Clay	Clay	Clay	Clay	Clay
Sand (%)	5.83	13.33	8.17	14.17	15.00	12.50	10.83	19.67	5.00
Silt (%)	40.00	27.50	30.18	33.33	28.33	21.67	27.50	26.50	20.83
Clay (%)	54.17	59.17	61.67	52.50	56.67	65.83	61.67	53.83	74.17

Key: masl = meters above sea level; N = north; E = east; ARF = annual rainfall; mm = millimeter; ppm = parts per million; meq = milliequivalent; pH = power of hydrogen; OC = organic carbon; TN = total nitrogen; C/N = carbon to nitrogen ratio; AP = available phosphorus; CEC = cation exchange capacity; E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos

4.2.2 Experimental treatments

The study was conducted using 24 oat genotypes including eight released varieties (Table 4.2). The released varieties considered in this study were Walqaa, Bona-bas, 8251, Sorataf, SRCPX80Ab2806, SRCPX80Ab2291, Was, and Bonsa. Among the studied genotypes, 14 genotypes are world collections which were introduced through the Food and Agricultural Organization (FAO), and 10 genotypes were introduced via the International Maize and Wheat Improvement Center (CIMMYT). The genotypes were selected from a preliminary screening trial conducted at Holetta Agricultural Research Center (HARC). All the studied genotypes were rejuvenated during the main cropping season of 2019/20 under similar conditions at HARC.

Table 4.2 List of twenty-four oat genotypes with their origins for the experiment

Genotype code	Genotype	Source	Genotype code	Genotype	Source
G1	CI-1646	FAO	G13	CI-1510	FAO
G2	Walqaa	CIMMYT	G14	Was	FAO
G3	Bona-bas	FAO	G15	CI-1652	FAO
G4	CI-8251	FAO	G16	Jassari	FAO
G5	Sorataf	CIMMYT	G17	SRCPX80Ab2310	CIMMYT
G6	CI-1512	FAO	G18	CI-1623	FAO
G7	MM799883/85	CIMMYT	G19	Bonsa	CIMMYT
G8	SRCPX80Ab2267	CIMMYT	G20	SRCPX80Ab2582	CIMMYT
G9	CI-1629	FAO	G21	Lampton	FAO
G10	C-12	FAO	G22	SRCPX80Ab2691	CIMMYT
G11	SRCPX80Ab2806	CIMMYT	G23	CI-8235	FAO
G12	SRCPX80Ab2291	CIMMYT	G24	CI-1759	FAO

Key: Walqaa = SRCPX80Ab2596; Bona-bas = CI-1660; Sorataf = 79Ab382(TX)80SA94; Was = CI-1506; Bonsa = 79Ab384(TX)80SA95; CI-8251; SRCPX80Ab2291 and SRCPX80Ab2806 are the released oat varieties; CIMMYT = International Maize and Wheat Improvement Center; FAO = Food and Agricultural Organization

4.2.3 Experimental design and management

The experimental fields were prepared following the recommended tillage (plowing with a mold-board plow during the short rainy season in March followed by harrowing once using a disc harrow in early May and slight hoeing to loosen the soil) and a fine seedbed was prepared according to the requirement of the crop and seeds were sown in June at all testing sites. A randomized complete block design (RCBD) replicated three times was used for the evaluation of oat genotypes. The treatment randomization was done using PROC PLAN seed procedures of SAS general linear model version 9.4 (SAS, 2012). The genotypes were assigned randomly within a block. The sowing time ranged from the 16th of June 2020 at Fiche (E8) to the 14th of July 2020 at D/Zeit (E5). Each genotype was sown on a plot area of 4 m² consisting of 5 rows of 4 m length and 1 m width with 0.2 m row spacing. The spacing between plots and blocks was 0.5 m and 1.5 m, respectively. One outermost row at both

sides was left as guard rows to avoid the border effects for each plot. Thus, three rows with a net plot size of 3.8 m by 0.6 m (2.28 m²) were used for data collection. The recommended seeding rate of 100 kg/ha was used at sowing (Astatke, 1979). The recommended fertilizer at the rate of 18/46 kg/ha of N/P₂O₅ at sowing and 23 kg/ha of N at tillering (Getnet, 1999; Ashenafi, 2018) was uniformly applied to all experimental plots. Hand weeding was done twice at all testing environments to minimize yield reduction due to weed competition for major growth resources. All other crop management practices such as draining excess water from the plots, maintaining the water drainage canals, protecting the crop from animal attack etc., were uniformly applied to all genotypes as required.

4.2.4 Data collection and measurements

4.2.4.1 Forage dry matter yield

Data on 10 agro-morphological traits were collected either on a plot basis or from five randomly selected plants per plot following the standard procedures (For detail see [Table 3.3](#); [Chapter 3](#)). Data on number of tillers per plant (NTPP), number of leaves at forage harvest (NLFH), leaf length at forage harvest (LLFH), and plant height at forage harvest (PHFH) were collected from five randomly selected plants per plot. Moreover, data on days to forage harvest (DFH), forage dry matter yield (FDMY), forage yield production rate (FYPR), leaf dry matter yield (LDMY), stem dry matter yield (SDMY), and panicle dry matter yield (PDMY) were also collected on a plot basis. At the recommended forage harvesting stage (soft dough stage) of oat, the forage biomass was clipped and the total biomass yield for each genotype was determined. About 500 g of forage sample biomass was taken from each experimental plot and then oven-dried for 72 hours at a temperature of 65 °C. The oven-dried samples were weighed to determine FDMY and then used for laboratory analysis to determine the chemical composition and in-vitro dry matter digestibility.

4.2.4.2 Herbage nutritive value analysis

The oven-dried samples were ground to pass through a 1 mm sieve size for laboratory analysis. Before scanning, the samples were dried at 60 °C overnight in an oven to standardize the moisture and then 3 g of each sample was scanned by the Near Infra-Red Spectroscopy (NIRS) machine for analysis. The samples were analyzed in percent dry matter basis for ash, crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), and in-vitro dry matter digestibility (IVDMD) using a calibrated NIRS (Foss 5000 apparatus and Win ISI II software). The crude protein yield and

digestible yield in t/ha were calculated by multiplying forage dry matter yield with CP and IVDMD then dividing by 100, respectively.

4.2.4.3 Grain yield and yield components

Data on 14 quantitative traits were collected either on a plot basis or from five randomly selected plants per plot following the standard procedures (For detail see [Table 3.3](#); [Chapter 3](#)). Data on flag leaf length at forage harvest (FLFH), plant height at grain harvest (PHGH), panicle length at grain harvest (PLGH), number of spikes per panicle (NSPP), and number of spikelets per panicle (NSLPP) were collected from five randomly selected plants per plot. Moreover, data on days to seed harvest (DSH), grain filling period (GFP), total biological yield (TBY), biological yield production rate (BYPR), grain sink filling rate (GSFR), thousand seed weight (TSW), harvest index (HI), straw yield (SY), and grain yield (GY) were also collected on a plot basis.

4.2.5 Data analysis

4.2.5.1 Analysis of variance

The analysis of variance (ANOVA) procedures of the statistical analysis system (SAS) general linear model (GLM) version 9.4 was used for individual environments and combined across environments (SAS, [2012](#)). The validity of assumptions of ANOVA for each environment using Bartlett's test and the homogeneity of error variance for combined data ANOVA using F-max method of Hartley were computed (For detail see subsection [3.2.6.1](#); [Chapter 3](#)). The genotype was fixed and the environment/location was considered random, therefore a linear mixed model was used for data analysis. The genotype was tested against the genotype by environment (GxE) interaction mean square while the environment and the interaction effects were tested against the replication mean square and residuals, respectively ([Table 4.3](#)). Mean comparison was done using Duncan's Multiple Range Test (DMRT) at a 5% probability level following the procedures suggested by Gomez and Gomez ([1984](#)). The statistical model for combined analysis of variance of the RCBD design across environments is given by:

$$Y_{ijk} = \mu + B_i(k) + G_j + E_k + (GE)_{jk} + \epsilon_{ijk}$$

where Y_{ijk} is the measured response of genotypes j in block i nested at location k ; μ is the grand mean; $B_i(k)$ is the effect of block i within location k ; G_j is the effect of genotype j ; E_k is the effect of environment k ; $(GE)_{jk}$ is the interaction effect between genotype j and environment k ; and ϵ_{ijk} is the residual or effects of random error.

Table 4.3 Combined analysis of variance (ANOVA) and expected mean squares for the mixed model of RCBD design

Sources of variation	Degree of freedom	Mean square (MS)	Expected mean square (EMS)	F-test
Environment (E)	E - 1	MS ₁	$\sigma_e^2 + g\sigma_{r(l)}^2 + rg\sigma_1^2$	MS ₁ /MS ₂
Replication (R)/Environment	E(R - 1)	MS ₂	$\sigma_e^2 + g\sigma_{r(l)}^2$	MS ₂ /MS ₅
Genotype (G)	(G - 1)	MS ₃	$\sigma_e^2 + r\sigma_{gl}^2 + rl\theta_g^2$	MS ₃ /MS ₄
G x E interaction	(G - 1)(E - 1)	MS ₄	$\sigma_e^2 + r\sigma_{gl}^2$	MS ₄ /MS ₅
Pooled error	E(G - 1)(R - 1)	MS ₅	σ_e^2	-

Environment is random effect while genotype is fixed effect; σ^2 is used for random effect while θ^2 for fixed effect.

4.2.5.2 AMMI analysis for forage and grain yields

Additive main effects and multiplicative interaction (AMMI) is one of the most widely used models to explain the genotype by environment interaction (GEI) of a multi-environment trial and categorizing the genotypes into wider or specific adaptation (Crossa *et al.*, 1990b). The AMMI analysis of variance was computed using Gollob's F-test procedure (Gollob, 1968). The AMMI analysis was performed using the Genotype by Environment Analysis with R (GEA-R) version 4.0 (Pacheco *et al.*, 2016).

4.2.5.3 Biplot analysis for forage and grain yields

Genotype plus genotype-by-environment (GGE) biplot was used to visually analyze the genotypes in different environments (Yan *et al.*, 2000; Yan *et al.*, 2001). The first two principal components were used to construct a biplot using the model "GH" (column metric preserving) method of singular value partitioning (SVP), "tester-centered G+GE" and "no scaling". The GGE biplot analysis was performed using the Genotype by Environment Analysis with R (GEA-R) version 4.0 (Pacheco *et al.*, 2016).

4.2.5.4 Parametric and nonparametric analyses for forage and grain yields

The two environmental variances ($S^{(1)}_i$ and $S^{(2)}_i$) are nonparametric, while the remaining 12 parameters included in this study are parametric. The stability analysis for forage and grain yields of oat genotypes evaluated across environments was determined using the standard deviation (SD), coefficient of variability (CV_i), Eberhart and Russell linear regression coefficient (b_i), Eberhart and Russell deviation from regression (S_{di}^2), coefficient of determination (R^2), Shukla's stability variance (σ_i^2), Hernandez desirability index (D_{ji}), Perkins and Jinks adjusted linear regression coefficient (B_i), Wricke's ecovalence (W_i), Lin and Binns's genotypic superiority index (P_i), and environmental variances ($S^{(1)}_i$ and $S^{(2)}_i$) (Table 4.4). These stability parameters were performed using the Genotype by Environment

Analysis with R (GEA-R) version 4.0 software (Pacheco *et al.*, 2016). Moreover, the AMMI stability value (ASV) was calculated based on the AMMI model's interaction principal component axis (IPCA1 and IPCA2 values) for each genotype and each environment as suggested by Purchase (1997) using Microsoft Excel 2010. The ASV was calculated using the following formula:

$$ASV = \sqrt{\left[\frac{IPCA1 \text{ sum of square}}{IPCA2 \text{ sum of square}} (IPCA1 \text{ score})\right]^2 + [IPCA2 \text{ score}]^2}$$

Table 4.4 Parametric and non-parametric stability parameters used for data analysis

Type of stability	Stability parameter	Symbol of stability parameter	Stability indication	Reference
Parametric	Standard deviation	SD	Small values	-
	Coefficient of variability	CV_i	Small values	Francis and Kannenberg's (1978)
	Eberhart and Russell linear regression coefficient	b_i	Values close to one	Eberhart and Russell's' (1966)
	Eberhart and Russell deviation from regression	S_{di}^2	Small values	Eberhart and Russell's' (1966)
	Coefficient of determination	R^2	Big values	Pinthus (1973)
	Shukla's stability variance	σ_i^2	Small values	Shukla's (1972)
	Perkins and Jinks adjusted linear regression coefficient	B_i	Values close to one	Perkins and Jinks (1968)
	Hernandez desirability index	D_{ji}	Small values	Hernandez <i>et al.</i> (1993)
	Wricke's ecovalence	W_i	Small values	Wricke's (1962)
	Lin and Binns's genotypic superiority index	P_i	Small values	Lin and Binns's (1988)
	AMMI stability value	ASV	Small values	Purchase (1997)
	Yield stability index	YSI	Small values	Kang (1993)
Non-Parametric	Average absolute rank difference of genotype on the environment	$S^{(1)}_i$	Small values	Huehn (1979)
	Variance ranges of environments	$S^{(2)}_i$	Small values	Huehn (1979)

The yield stability index (YSI) was also used to measure the stability of genotypes based on the rank of mean yield of genotypes across environments and the rank of AMMI stability value (Farshadfar *et al.*, 2011a). The YSI incorporates both yield and stability index in single criteria. It was calculated by $YSI_i = RASV_i + RY_i$; where YSI_i is the forage and grain yield stability index of genotype i ; $RASV_i$ is the rank of AMMI stability value of genotype i ; and

RY_i is the rank of mean forage and grain yield of genotype i . The values of stability parameters can be interpreted based on the principle of each stability parameter. Accordingly, the largest values of R^2 and values closer to unity for b_i and B_i indicate high stability of genotype across environments. Moreover, the smallest values of the remaining stability parameters indicate the high stability of the genotype in different environments. Based on the criteria of stability parameters, the highest stable genotype was ranked first while the lowest stable genotype was ranked last.

4.2.5.5 Correlation and principal component analyses

Spearman's rank correlation coefficient analysis was performed based on the ranking procedures for yield and stability parameters using the CORR procedures of the SAS version 9.4 statistical software (SAS, 2012). Moreover, the principal component analysis based on the rank correlation matrix was performed using the Minitab 17.1 statistical software (Minitab, 2013) and a biplot of the first two principal components was displayed for a better understanding of the relationship among the stability parameters used for determination of forage and grain yields stability in oat genotypes.

4.3 Results

4.3.1 Forage yield, yield components, and nutritive values of oat genotypes

4.3.1.1 Analysis of variance

The pooled analysis of variance for fodder dry matter yield of twenty-four oat genotypes tested in nine environments is indicated in Table 4.5. The result revealed that the genotype, environment, and their interaction effects showed variation ($P < 0.001$) for fodder dry matter yield. However, the genotype, environment, and their interaction effects had different contributions to the total variance ($G + E + GE$) in fodder dry matter yield. Consequently, the environment main effect had the highest (67.45%) contribution to the total variance in fodder yield followed by the interaction effect (22.73%) while the genotypic effect had the lowest (9.82%) contribution to the total variance in oat fodder yield.

Table 4.5 Combined analysis of variance for fodder dry matter yield of 24 oat genotypes tested across nine environments during the 2020/21 cropping season

Source of variation	df	SS	MS	Explained SS (%)	F
Model	233	10913.8	46.84		8.3***
Replication/Environment	18	515.3	28.63		5.1***
Environment (E)	8	7013.9	876.74	67.45	30.6***
Genotype (G)	23	1020.8	44.38	9.82	3.5***
G x E interaction	184	2363.9	12.85	22.73	2.3***
Error	414	2327.0	5.62		

df = Degree of freedom; SS = sum of square; MS = mean square; *** = significantly different at $p < 0.001$.

The combined analysis of variance for fodder dry matter yield, its yield-related traits, and herbage nutritive values of 24 oat genotypes evaluated across nine environments is indicated in Table 4.6. The result disclosed that all the studied agro-morphological traits and herbage nutritive values were influenced ($P < 0.001$) by the testing environments. Moreover, significant ($P < 0.05$) variation was observed among the studied oat genotypes for all measured agro-morphological traits and nutritive values except herbage ash content. The genotype by environment interaction effect was also varied ($P < 0.001$) for all agro-morphological traits and nutritive values. The genotypes showed a crossover type of interaction for fodder dry matter yield (Figure 4.2).

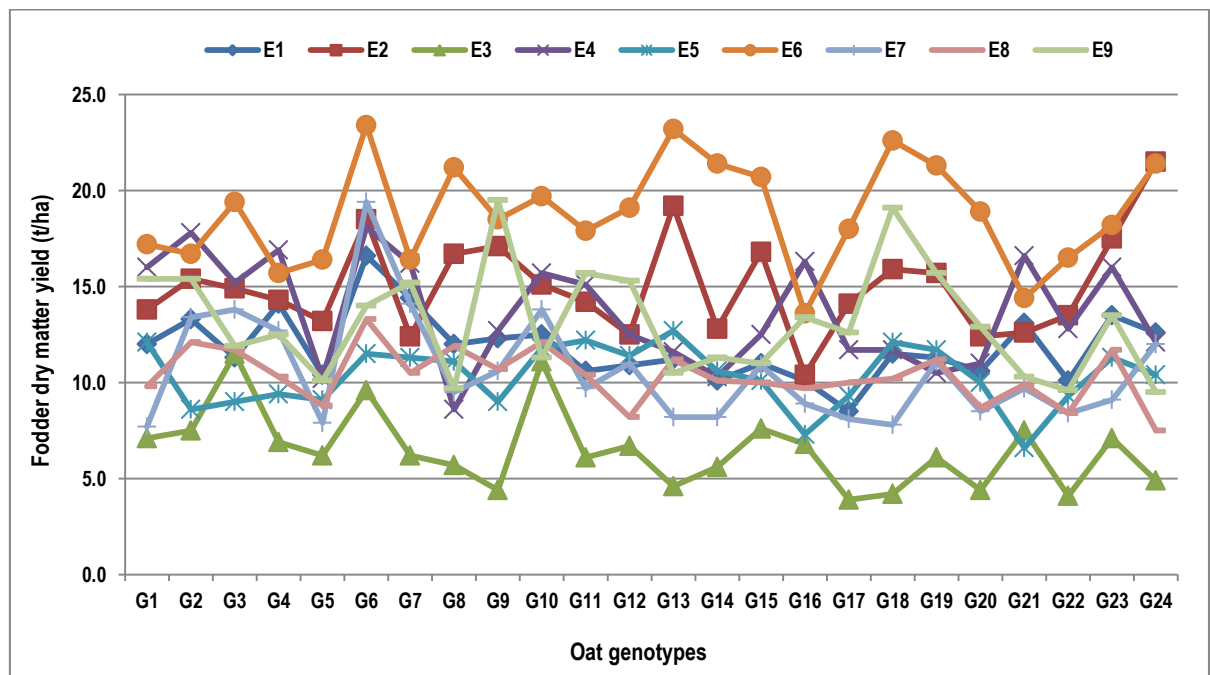


Figure 4.2 Genotype by location interaction (crossover) for fodder yield of 24 oat genotypes grown at nine environments in 2020/21 cropping season

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos; G1 = CI-1646; G2 = Walqaa; G3 = Bona-bas; G4 = CI-8251; G5 = Sorataf; G6 = CI-1512; G7 = MM799883/85; G8 = SRCPX80Ab2267; G9 = CI-1629; G10 = C-12; G11 = SRCPX80Ab2806; G12 = SRCPX80Ab2291; G13 = CI-1510; G14 = Was; G15 = CI-1652; G16 = Jassari; G17 = SRCPX80Ab2310; G18 = CI-1623; G19 = Bonsa; G20 = SRCPX80Ab2582; G21 = Lampton; G22 = SRCPX80Ab2691; G23 = CI-8235; G24 = CI-1759.

Table 4.6 Combined analysis of variance for agro-morphological traits and nutritive values of 24 oat genotypes tested in nine environments during the 2020/21 cropping season

Traits	Mean squares					CV	R ²
	Environment (E) (df = 8)	Rep (R)/E (df = 18)	Genotype (G) (df = 23)	G*L (df = 184)	Error (df = 414)		
NTPP	64.24***	2.34***	13.91***	1.12**	0.81	23.83	0.76
NLFH	34.95***	1.20***	11.36***	0.65***	0.25	10.48	0.87
LLFH	762.46***	36.09**	502.08***	48.07***	15.00	11.16	0.81
PHFH	15457.47***	776.71***	7547.79***	300.64***	110.23	8.71	0.89
DFH	11660.58***	39.19***	2388.37***	91.06***	11.52	2.77	0.97
FDMY	876.73***	28.63***	44.38***	12.85***	5.62	19.35	0.82
FYPR	66580.13***	1863.07***	3289.08***	849.85***	385.52	19.43	0.83
LDMY	105.59***	2.87***	7.95***	1.49***	0.78	22.34	0.81
SDMY	127.70***	4.67***	7.86***	2.19***	0.96	22.26	0.81
PDMY	87.53***	3.33***	3.87*	2.41***	0.91	24.52	0.77
CPY	8.08***	0.15***	0.10*	0.06***	0.03	21.87	0.86
Ash	2460.17***	384.28***	208.25 ^{NS}	164.71***	32.00	8.34	0.82
CP	13816.50***	159.83***	1103.29***	139.00***	24.79	7.48	0.94
NDF	75381.30***	1105.74***	16232.89**	2290.13***	327.35	2.72	0.91
ADF	60071.04***	1855.09***	12396.41****	1505.95***	207.98	4.21	0.93
ADL	2061.09***	40.51***	583.27***	55.02***	7.46	5.18	0.93
IVDMD	26955.99***	1057.48***	5196.23***	711.17***	100.39	1.66	0.92
DY	295.72***	8.67***	13.57***	4.65***	2.04	19.48	0.81

df = degree of freedom; Rep/E = replication nested under environment; CV = coefficient of variation; R² = coefficient of determination; DM = dry matter; NTPP = number of tillers per plant; NLFH = number of leaves at forage harvest; LLFH = leaf length at forage harvest (cm); PHFH = plant height at forage harvest (cm); DFH = days to forage harvest (days); FDMY = forage dry matter yield (t/ha); FYPR = forage yield production rate (kg/ha/day); LDMY = leaf dry matter yield (t/ha); SDMY = stem dry matter yield (t/ha); PDMY = panicle dry matter yield (t/ha); CP = crude protein (g/kg DM); NDF = neutral detergent fiber (g/kg DM); ADF = acid detergent fiber (g/kg DM); ADL = acid detergent lignin (g/kg DM); IVDMD = in-vitro dry matter digestibility (g/kg DM); CPY = crude protein yield (t/ha); DY = digestible yield (t/ha); NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively.

4.3.1.2 Effect of environments on oat performance

The mean performances of oat genotypes for agro-morphological traits and nutritive values at each testing environment are presented in Table 4.7. The result indicated that the NTPP, NLFH, LLFH, PHFH, FDMY, FYPR, LDMY, SDMY, and PDMY were significantly higher at E6. The studied genotypes showed early maturity for fodder yield at E5, E3, and E6 while the genotypes at E7, E9, E4, and E2 mature late for fodder yield. Significantly the lowest FYPR, FDMY, and botanical fraction yields (LDMY, SDMY, and PDMY) were recorded at E3. The herbage nutritional analysis revealed that significantly the highest ash content was observed at E9 followed by E5. Significantly the highest CP and IVDMD and the lowest fiber contents (NDF, ADF, and ADL) were recorded at E5. However, significantly the highest CPY and DY were observed at E6.

Table 4.7 Mean performance for agro-morphological traits and nutritive values of 24 oat genotypes evaluated in nine environments during the 2020/21 cropping season

Traits	E1	E2	E3	E4	E5	E6	E7	E8	E9	Mean	P-value
NTPP	2.9 ^f	4.0 ^c	4.6 ^b	2.8 ^f	3.2 ^e	5.8 ^a	3.8 ^{cd}	3.3 ^e	3.7 ^d	3.8	<.0001
NLFH	4.6 ^e	4.1 ^f	5.1 ^b	5.0 ^{bc}	4.8 ^d	5.9 ^a	4.9 ^{cd}	3.4 ^g	5.1 ^b	4.8	<.0001
LLFH	34.6 ^b	38.2 ^a	34.3 ^b	37.9 ^a	34.3 ^b	38.5 ^a	31.2 ^c	28.7 ^d	34.6 ^b	34.7	<.0001
PHFH	129.9 ^b	129.4 ^b	104.5 ^e	119.4 ^d	98.2 ^f	136.4 ^a	136.6 ^a	104.5 ^e	125.7 ^c	120.5	<.0001
DFH	117.4 ^e	129.6 ^c	108.2 ^g	131.5 ^b	102.5 ^h	112.4 ^f	140.3 ^a	127.2 ^d	132.2 ^b	122.4	<.0001
FDMY	11.8 ^d	15.0 ^b	6.5 ^f	13.7 ^c	10.3 ^e	18.8 ^a	10.6 ^e	10.4 ^e	13.1 ^c	12.3	<.0001
FYPR	101.3 ^c	115.9 ^b	60.4 ^e	104.6 ^c	100.8 ^c	168.3 ^a	76.1 ^d	81.8 ^d	100.2 ^c	101.0	<.0001
LDMY	3.8 ^c	4.7 ^b	2.2 ^f	4.8 ^b	3.6 ^c	6.4 ^a	3.0 ^e	3.3 ^d	3.8 ^c	4.0	<.0001
SDMY	4.2 ^d	5.4 ^b	2.2 ^f	4.9 ^c	3.8 ^e	7.1 ^a	4.2 ^d	3.5 ^e	4.2 ^d	4.4	<.0001
PDMY	3.8 ^{cd}	4.9 ^b	2.0 ^g	4.1 ^c	2.9 ^f	5.4 ^a	3.4 ^e	3.5 ^{de}	5.2 ^{ab}	3.9	<.0001
CPY	0.64 ^f	1.15 ^b	0.39 ^h	0.79 ^d	0.95 ^c	1.50 ^a	0.53 ^g	0.71 ^e	0.73 ^{de}	0.8	<.0001
Ash	63.3 ^e	60.2 ^f	71.1 ^{bc}	59.4 ^f	74.1 ^a	71.3 ^b	66.6 ^d	69.3 ^c	75.4 ^a	67.8	0.0005
CP	53.9 ^h	76.9 ^c	62.2 ^e	58.5 ^f	92.0 ^a	79.9 ^b	50.6 ⁱ	68.8 ^d	56.4 ^g	66.6	<.0001
NDF	710.9 ^a	704.0 ^b	657.9 ^e	680.2 ^c	610.4 ^g	660.8 ^e	627.8 ^f	662.0 ^e	673.2 ^d	665.2	<.0001
ADF	387.0 ^a	384.8 ^a	346.6 ^c	336.6 ^d	306.1 ^h	355.2 ^b	313.7 ^g	328.9 ^e	323.7 ^f	342.5	<.0001
ADL	56.3 ^b	59.2 ^a	46.8 ^e	47.2 ^e	43.8 ^f	53.7 ^d	54.7 ^c	56.3 ^b	56.1 ^b	52.7	<.0001
IVDMD	569.8 ^g	576.5 ^f	599.5 ^d	611.6 ^c	628.3 ^a	592.3 ^e	616.6 ^b	611.4 ^c	612.9 ^c	602.1	<.0001
DY	6.7 ^d	8.7 ^b	3.8 ^e	8.3 ^{bc}	6.5 ^d	11.2 ^a	6.5 ^d	6.3 ^d	8.0 ^c	7.3	<.0001

NTPP = number of tillers per plant; NLFH = number of leaves at forage harvest; LLFH = leaf length at forage harvest (cm); PHFH = plant height at forage harvest (cm); DFH = days to forage harvest (days); FDMY = forage dry matter yield (t/ha); FYPR = forage yield production rate (kg/ha/day); LDMY = leaf dry matter yield (t/ha); SDMY = stem dry matter yield (t/ha); PDMY = panicle dry matter yield (t/ha); CP = crude protein (g/kg DM); NDF = neutral detergent fiber (g/kg DM); ADF = acid detergent fiber (g/kg DM); ADL = acid detergent lignin (g/kg DM); IVDMD = in-vitro dry matter digestibility (g/kg DM); CPY = crude protein yield (t/ha); DY = digestible yield (t/ha); E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos; Means followed by a common superscript letter with in a row are not significantly different from each other at $P < 0.05$.

4.3.1.3 Mean performance of oat genotypes

The mean performances of oat genotypes for measured agro-morphological traits and herbage nutritive values were significant ($P < 0.05$) except for herbage ash content (Table 4.8). The result revealed that the highest NTPP, LLFH, and PHFH were observed for G20, G2, and G21, respectively. The lowest NLFH, DFH, FYPR, CPY, and NTPP were recorded for G5, G17, G20, G1, and G2, respectively. The shortest PHFH and the lowest NLFH producing genotype (G5) had the highest CP content. The highest FDMY producing genotype (G6) had the highest FYPR, botanical fraction yields (i.e., LDMY, SDMY, and PDMY), CPY, and DY. The highest fiber (NDF, ADF, and ADL) contents having genotype (G3) had the lowest LLFH, CP, and IVDMD while the lowest fiber producing genotype (G24) had the highest NLFH, IVDMD, and longer DFH.

The mean performance of genotypes for forage dry matter yield was significant for combined analysis and individual environment analysis except at E5 and E8 as indicated in Table 4.9. The combined analysis revealed that the fodder dry matter yield was above the grand mean for G6, G10, G23, G7, G9, G18, G13, G1, G24, G15, G2, G3, G19, G4, and G11. Among these listed genotypes, the first ten genotypes have not been released. The highest fodder yield at E1, E4, E6, E7, and E8 was recorded from G6. Similarly, the highest

fodder yielder at E2, E3, E9, and E5 were G24, G3, G9, and G13, respectively. On the other hand, G1 at E7; G8 at E4; G16 at E2 and E6; G17 at E1 and E3; G21 at E5; and G24 at E8 and E9 were produced the lowest fodder yield.

Table 4.8 Mean performance of 24 oat genotypes based on measured agro-morphological traits and nutritive values during the 2020/21 cropping season

Traits	Genotype											
	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12
NTPP	4.4 ^{bc}	2.5 ^f	4.0 ^c	3.2 ^{de}	4.0 ^c	4.1 ^c	3.0 ^{d-f}	4.4 ^{bc}	4.4 ^{bc}	3.0 ^{d-f}	3.4 ^d	4.0 ^c
NLFH	5.7 ^b	5.1 ^{c-e}	4.9 ^{ef}	5.1 ^{c-e}	3.7 ⁱ	4.6 ^{fg}	4.6 ^{fg}	3.9 ^{hi}	4.9 ^{de}	5.3 ^c	4.9 ^{ef}	4.0 ^h
LLFH	37.0 ^{cd}	41.8 ^a	26.9 ⁱ	39.7 ^{ab}	30.8 ^{gh}	38.4 ^{b-d}	37.1 ^{cd}	32.0 ^g	31.8 ^g	40.0 ^{ab}	31.8 ^g	32.7 ^{fg}
PHFH	105.8 ^{h-l}	146.2 ^{ab}	144.9 ^{ab}	142.9 ^{a-c}	91.3 ^m	134.8 ^{de}	140.6 ^{b-d}	109.3 ^{ij}	107.9 ^{ij}	129.5 ^{ef}	119.3 ^{gh}	111.7 ⁱ
DFH	130.2 ^d	119.6 ^{ij}	116.8 ^{kl}	121.0 ^{g-i}	114.7 ^{mn}	124.1 ^f	120.7 ^{hi}	115.6 ^{lm}	129.9 ^d	122.9 ^{fg}	114.7 ^{mn}	113.9 ^{mn}
FYPR	96.0 ^{fj}	110.8 ^{b-d}	113.6 ^b	103.5 ^{b-h}	89.5 ^l	129.1 ^a	106.9 ^{b-g}	103.0 ^{b-h}	97.6 ^{e-j}	112.3 ^{bc}	108.9 ^{b-e}	106.2 ^{b-g}
LDMY	4.5 ^{bc}	4.3 ^{b-d}	4.1 ^{b-e}	4.0 ^{c-g}	3.0 ^j	5.3 ^a	4.0 ^{b-f}	3.5 ^{fj}	4.2 ^{b-d}	4.6 ^b	3.8 ^{d-h}	3.8 ^{d-h}
SDMY	4.5 ^{c-g}	4.8 ^{bc}	5.2 ^{ab}	4.6 ^{c-f}	3.5 ^j	5.6 ^a	4.9 ^{bc}	4.1 ^{d-i}	4.5 ^{c-g}	4.9 ^{bc}	4.5 ^{c-g}	4.3 ^{c-h}
PDMY	3.4 ^{ef}	4.2 ^b	3.8 ^{b-f}	4.0 ^{b-e}	3.8 ^{b-f}	5.1 ^a	4.0 ^{b-d}	4.2 ^{bc}	4.0 ^{b-d}	4.2 ^b	4.2 ^b	3.9 ^{b-f}
CPY	0.73 ^e	0.83 ^{a-e}	0.74 ^e	0.80 ^{b-e}	0.83 ^{b-e}	0.94 ^a	0.76 ^{de}	0.90 ^{ab}	0.82 ^{b-e}	0.78 ^{b-e}	0.88 ^{a-d}	0.89 ^{ab}
Ash	66.7	65.4	60.5	67.2	68.5	68.6	67.4	69.9	69.0	69.8	67.2	64.8
CP	57.1 ^{lm}	63.1 ^{jk}	55.7 ^m	64.2 ^{jk}	79.7 ^a	59.4 ^l	58.5 ^{lm}	73.8 ^{bc}	65.5 ^{ij}	56.9 ^{lm}	69.3 ^{e-h}	73.5 ^{b-d}
NDF	652.5 ^{ij}	688.4 ^{b-d}	725.3 ^a	674.0 ^{ef}	641.0 ^k	693.1 ^{bc}	698.0 ^b	669.1 ^{e-g}	664.2 ^{f-h}	685.1 ^{cd}	665.3 ^{f-h}	656.7 ^{hj}
ADF	338.1 ^{h-j}	366.1 ^{bc}	391.0 ^a	346.4 ^{f-h}	317.1 ^m	368.0 ^{bc}	372.3 ^b	334.4 ^{i-k}	342.3 ^{g-j}	355.2 ^{de}	348.0 ^{e-g}	335.0 ^{i-k}
ADL	46.5 ⁱ	56.7 ^{bc}	63.8 ^a	54.0 ^{d-f}	52.9 ^{f-h}	53.8 ^{ef}	54.8 ^{de}	51.7 ^{hi}	48.6 ^k	53.8 ^{ef}	56.5 ^{bc}	55.5 ^{cd}
IVDMD	611.1 ^d	592.0 ⁱ	568.7 ^k	599.9 ^{f-h}	617.8 ^c	585.6 ^j	585.6 ^j	600.9 ^{fg}	604.2 ^{ef}	596.2 ^{g-i}	599.2 ^{f-h}	603.9 ^{ef}
DY	7.5 ^{b-f}	7.9 ^{bc}	7.5 ^{b-f}	7.5 ^{b-f}	6.3 ^h	9.4 ^a	7.6 ^{b-e}	7.1 ^{c-h}	7.6 ^{b-e}	8.1 ^b	7.4 ^{b-f}	7.2 ^{b-g}

Traits	Genotype											
	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24
NTPP	3.9 ^c	4.2 ^{bc}	4.2 ^{bc}	2.6 ^{ef}	4.4 ^{bc}	4.2 ^{bc}	3.0 ^{d-f}	5.3 ^a	2.9 ^{d-f}	4.0 ^c	3.1 ^{de}	4.7 ^b
NLFH	5.2 ^{cd}	3.9 ^{hi}	4.8 ^{ef}	4.4 ^g	3.9 ^{hi}	5.7 ^b	4.4 ^g	5.0 ^{c-e}	5.1 ^{c-e}	3.8 ^{hi}	5.0 ^{c-e}	6.0 ^a
LLFH	38.8 ^{bc}	30.7 ^{gh}	34.3 ^{ef}	36.2 ^{de}	28.1 ⁱ	37.2 ^{cd}	30.4 ^{gh}	32.4 ^{fg}	39.9 ^{ab}	28.7 ^{hi}	38.4 ^{b-d}	37.9 ^{b-d}
PHFH	124.3 ^{fg}	110.5 ^{ij}	123.0 ^{gh}	108.5 ^{ij}	104.9 ^{j-l}	117.6 ^h	125.2 ^{fg}	107.1 ^{i-k}	148.2 ^a	99.8 ^l	137.3 ^{cd}	101.6 ^{kl}
DFH	127.2 ^e	114.5 ^{mn}	121.5 ^{g-i}	118.5 ^{jk}	113.0 ⁿ	136.3 ^c	114.2 ^{mn}	139.1 ^b	118.6 ^{jk}	115.6 ^{lm}	122.5 ^{f-h}	151.5 ^a
FYPR	100.5 ^{c-j}	98.5 ^{d-j}	102.7 ^{b-i}	90.5 ^l	95.3 ^{fj}	94.6 ^{g-k}	112.1 ^{bc}	79.5 ^l	94.2 ^{h-k}	89.8 ^l	107.3 ^{b-f}	82.8 ^{kl}
LDMY	4.6 ^b	3.3 ^{h-j}	3.8 ^{d-h}	3.5 ^{g-j}	3.2 ^{ij}	4.2 ^{b-d}	4.0 ^{c-g}	3.6 ^{e-i}	3.7 ^{e-i}	3.2 ^{ij}	4.4 ^{bc}	4.3 ^{b-d}
SDMY	4.4 ^{c-g}	4.0 ^{fj}	4.5 ^{c-g}	3.8 ^{h-j}	3.5 ^j	4.6 ^{b-e}	4.6 ^{c-f}	3.9 ^{g-j}	4.0 ^{e-j}	3.6 ^{ij}	4.7 ^{b-d}	4.7 ^{b-d}
PDMY	3.5 ^{d-f}	3.9 ^{b-f}	4.0 ^{b-e}	3.5 ^{d-f}	4.0 ^{b-d}	4.0 ^{b-e}	4.2 ^b	3.3 ^f	3.5 ^{d-f}	3.5 ^{c-f}	3.9 ^{b-f}	3.5 ^{d-f}
CPY	0.81 ^{b-e}	0.83 ^{a-e}	0.77 ^{c-e}	0.74 ^e	0.84 ^{a-e}	0.82 ^{b-e}	0.90 ^{ab}	0.80 ^{b-e}	0.75 ^e	0.75 ^e	0.89 ^{ab}	0.88 ^{a-c}
Ash	68.3	66.6	68.5	67.5	62.6	67.6	72.5	71.4	67.2	69.8	68.4	73.0
CP	62.3 ^k	72.0 ^{c-e}	63.2 ^{jk}	68.9 ^{f-h}	75.1 ^b	62.8 ^{jk}	68.4 ^{gh}	71.5 ^{c-f}	67.5 ^{hi}	70.7 ^{d-g}	67.3 ^{hi}	71.7 ^{c-f}
NDF	668.6 ^{e-g}	647.1 ^{jk}	656.3 ^{h-j}	678.5 ^{de}	655.9 ^{h-j}	661.4 ^{g-i}	664.5 ^{f-h}	617.8 ^l	674.3 ^{ef}	657.3 ^{h-j}	664.7 ^{f-h}	606.6 ^m
ADF	351.6 ^{ef}	324.9 ^l	336.4 ^{ij}	352.0 ^{ef}	327.6 ^{kl}	331.1 ^{j-l}	345.2 ^{f-h}	303.9 ⁿ	362.2 ^{cd}	333.8 ^{i-k}	342.3 ^{g-i}	294.7 ^o
ADL	50.4 ^{ij}	53.3 ^{e-g}	49.9 ^{jk}	57.3 ^b	54.6 ^{d-f}	47.0 ^l	53.7 ^{ef}	44.1 ^m	57.1 ^b	53.7 ^{ef}	51.9 ^{g-i}	42.5 ⁿ
IVDMD	596.3 ^{g-i}	612.1 ^d	611.1 ^d	594.5 ^{hi}	602.1 ^{fg}	608.6 ^{de}	598.0 ^{f-i}	629.5 ^b	594.1 ^{hi}	601.6 ^{fg}	601.3 ^{fg}	635.8 ^a
DY	7.4 ^{b-f}	6.8 ^{d-i}	7.5 ^{b-f}	6.3 ^{hi}	6.5 ^{g-i}	7.7 ^{b-d}	7.6 ^{b-e}	6.8 ^{e-i}	6.6 ^{f-i}	6.2 ⁱ	7.8 ^{bc}	7.8 ^{bc}

NTPP = number of tillers per plant; NLFH = number of leaves at forage harvest; LLFH = leaf length at forage harvest (cm); PHFH = plant height at forage harvest (cm); DFH = days to forage harvest (days); FYPR = forage yield production rate (kg/ha/day); LDMY = leaf dry matter yield (t/ha); SDMY = stem dry matter yield (t/ha); PDMY = panicle dry matter yield (t/ha); CP = crude protein (g/kg DM); NDF = neutral detergent fiber (g/kg DM); ADF = acid detergent fiber (g/kg DM); ADL = acid detergent lignin (g/kg DM); IVDMD = in-vitro dry matter digestibility (g/kg DM); CPY = crude protein yield (t/ha); DY = digestible yield (t/ha); Means followed by a common superscript letter with in a row are not significantly different from each other at $P < 0.05$. See Table 4.2 for genotypes description.

Table 4.9 Mean fodder dry matter yield (t/ha) of 24 oat genotypes tested at nine environments during the 2020/21 cropping season

SN	Genotype	Environment									Mean
		E1	E2	E3	E4	E5	E6	E7	E8	E9	
1	G1	12.0 ^{b-e}	13.8 ^{b-e}	7.1 ^{bc}	16.0 ^{a-d}	12.1	17.2 ^{c-g}	7.7 ^f	9.8	15.4 ^{a-c}	12.4 ^{b-d}
2	G2	13.3 ^{a-d}	15.4 ^{b-e}	7.5 ^{bc}	17.8 ^a	8.6	16.7 ^{c-g}	13.4 ^{b-e}	12.1	15.4 ^{a-c}	13.4 ^{bc}
3	G3	11.3 ^{b-e}	14.9 ^{b-e}	11.5 ^a	15.2 ^{a-f}	9.0	19.4 ^{a-f}	13.8 ^{b-d}	11.7	11.9 ^{b-d}	13.2 ^{bc}
4	G4	14.1 ^{a-c}	14.3 ^{b-e}	6.9 ^{bc}	16.9 ^{ab}	9.4	15.7 ^{e-g}	12.7 ^{b-f}	10.3	12.5 ^{b-d}	12.5 ^{b-d}
5	G5	10.4 ^{c-e}	13.2 ^{c-e}	6.2 ^{bc}	10.2 ^{gh}	9.1	16.4 ^{c-g}	7.9 ^{ef}	8.8	10.1 ^d	10.3 ^f
6	G6	16.6 ^a	18.5 ^{a-c}	9.6 ^{ab}	18.1 ^a	11.5	23.4 ^a	19.4 ^a	13.3	14.0 ^{b-d}	16.0 ^a
7	G7	14.4 ^{ab}	12.4 ^{de}	6.2 ^{bc}	16.2 ^{a-d}	11.3	16.4 ^{d-g}	14.1 ^b	10.5	15.2 ^{a-c}	12.9 ^{bc}
8	G8	12.0 ^{b-e}	16.7 ^{a-d}	5.7 ^c	8.6 ^h	11.1	21.2 ^{a-d}	9.5 ^{b-f}	11.9	9.7 ^d	11.8 ^{c-e}
9	G9	12.3 ^{b-d}	17.1 ^{a-d}	4.4 ^c	12.7 ^{b-h}	9.0	18.5 ^{a-g}	10.6 ^{b-f}	10.7	19.5 ^a	12.8 ^{bc}
10	G10	12.5 ^{b-d}	15.1 ^{b-e}	11.1 ^a	15.7 ^{a-e}	11.8	19.7 ^{a-e}	13.8 ^{bc}	12.1	11.3 ^{b-d}	13.7 ^b
11	G11	10.6 ^{b-e}	14.2 ^{b-e}	6.1 ^{bc}	15.1 ^{a-g}	12.2	17.9 ^{b-f}	9.7 ^{b-f}	10.4	15.7 ^{ab}	12.4 ^{b-d}
12	G12	10.9 ^{b-e}	12.5 ^{de}	6.7 ^{bc}	12.5 ^{b-h}	11.4	19.1 ^{a-f}	11.0 ^{b-f}	8.2	15.3 ^{a-c}	12.0 ^{c-e}
13	G13	11.2 ^{b-e}	19.2 ^{ab}	4.6 ^c	11.6 ^{e-h}	12.7	23.2 ^a	8.2 ^{d-f}	11.2	10.5 ^d	12.5 ^{b-d}
14	G14	10.1 ^{de}	12.8 ^{c-e}	5.6 ^c	10.3 ^{f-h}	10.6	21.4 ^{a-d}	8.2 ^{d-f}	10.1	11.3 ^{b-d}	11.2 ^{d-f}
15	G15	11.0 ^{b-e}	16.8 ^{a-d}	7.6 ^{bc}	12.5 ^{b-h}	10.1	20.7 ^{a-e}	10.9 ^{b-f}	10.0	11.0 ^{cd}	12.3 ^{b-d}
16	G16	10.1 ^{de}	10.4 ^e	6.8 ^{bc}	16.3 ^{a-d}	7.3	13.6 ^g	8.9 ^{b-f}	9.7	13.4 ^{b-d}	10.7 ^{ef}
17	G17	8.5 ^e	14.1 ^{b-e}	3.9 ^c	11.7 ^{c-h}	9.3	18.0 ^{b-g}	8.1 ^{ef}	10.0	12.6 ^{b-d}	10.7 ^{ef}
18	G18	11.5 ^{b-e}	15.9 ^{a-e}	4.2 ^c	11.7 ^{c-h}	12.1	22.6 ^{ab}	7.8 ^{ef}	10.2	19.1 ^a	12.8 ^{bc}
19	G19	11.3 ^{b-e}	15.7 ^{b-e}	6.1 ^{bc}	10.5 ^{f-h}	11.7	21.3 ^{a-d}	11.1 ^{b-f}	11.2	15.7 ^{ab}	12.7 ^{bc}
20	G20	10.6 ^{b-e}	12.4 ^{de}	4.4 ^c	11.0 ^{e-h}	10.0	18.9 ^{a-f}	8.5 ^{b-f}	8.7	12.9 ^{b-d}	10.8 ^{ef}
21	G21	13.1 ^{a-d}	12.6 ^{de}	7.5 ^{bc}	16.6 ^{a-c}	6.6	14.4 ^{fg}	9.7 ^{b-f}	9.9	10.3 ^d	11.2 ^{d-f}
22	G22	10.1 ^{de}	13.5 ^{b-e}	4.1 ^c	12.8 ^{b-h}	9.3	16.5 ^{c-g}	8.4 ^{c-f}	8.4	9.6 ^d	10.3 ^f
23	G23	13.5 ^{a-d}	17.5 ^{a-d}	7.1 ^{bc}	16.0 ^{a-e}	11.3	18.2 ^{b-g}	9.1 ^{b-f}	11.7	13.5 ^{b-d}	13.1 ^{bc}
24	G24	12.6 ^{b-d}	21.5 ^a	4.9 ^c	12.1 ^{b-h}	10.4	21.4 ^{a-c}	12.0 ^{b-f}	7.5	9.5 ^d	12.4 ^{b-d}
Mean		11.8	15.0	6.5	13.7	10.3	18.8	10.6	10.4	13.1	12.3
P-value		0.0046	0.0091	0.0002	0.0001	0.0513	0.0002	0.0007	0.1597	<.0001	

E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos; Means followed by a common superscript letter within a column are not significantly different from each other at $P < 0.05$. See Table 4.2 for genotypes description.

4.3.1.4 AMMI analysis of variance for fodder dry matter yield

The AMMI model of analysis of variance revealed that the environment, genotype, and GEI had very highly significant effects on fodder dry matter yield (Table 4.10). The environment's main effect accounted for 67.45% of the total variation ($G + E + GEI$), while genotype and GEI accounted for 9.82 and 22.73% of the total variance, respectively. The GEI effect was further partitioned into various AMMI interaction principal component axes. Accordingly, the mean squares of the first two AMMI interaction principal component axes (AMMI-IPCA1 and AMMI-IPCA2) were very highly significant and explained 44.11 and 26.79% of the total variance of GEI, respectively. The cumulative percentage of the first two IPCAs accounted for 70.91% of the total GEI variance. However, the remaining IPCAs were non-significant and cumulatively accounted for 29.09% of the total GEI sum of squares.

The genotypes such as G6, G10, G2, G3, and G23 were the first top five mean fodder dry matter yield performing genotypes across environments (see Table 4.9). The AMMI analysis model also indicated the first four best fodder dry matter yield-producing genotypes in each

environment (Table 4.11). For instance, the first four top fodder-producing genotypes at E1 were G6, G7, G4, and G23. Based on the AMMI model analysis, the first top fodder yield performing genotype (G6) was selected as the 1st best genotype at five environments (E1, E4, E6, E7, and E8) and the 3rd best genotype at two environments (E2 and E3) while the second top fodder yield producing genotype (G10) was also selected as the 2nd best genotype at E3 environment and the 3rd best genotype at two environments (E7 and E8). Similarly, the third top fodder yield performing genotype (G2) was selected as the second best genotype at E4 and E8 environments while the fourth high fodder yield producing genotype (G3) was selected as the 1st best genotype at the E3 environment, and the 4th best genotype at E7 environment. Furthermore, the fifth high fodder yield performing genotype (G23) was selected as the 4th best genotype at E1 and E2 environments.

Table 4.10 Additive main effects and multiplicative interaction (AMMI) analysis of variance for fodder dry matter yield of 24 oat genotypes evaluated in nine environments during the 2020/21 cropping season

Source of variation	df	SS	MS	Explained SS (%)			F
				Factor	GEI	Cumulative	
Environment (E)	8	7013.9	876.7	67.45		67.45	133.3***
Genotype (G)	23	1020.8	44.4	9.82		77.27	6.8***
GEI	184	2363.9	12.8	22.73		100.00	2.0***
AMMI-PC1	30	1042.8	34.8		44.11	44.11	5.4***
AMMI-PC2	28	633.4	22.6		26.79	70.91	3.5***
AMMI-PC3	26	239.8	9.2		10.14	81.05	1.4 ^{NS}
AMMI-PC4	24	207.4	8.6		8.77	89.83	1.3 ^{NS}
AMMI-PC5	22	94.4	4.3		3.99	93.82	0.7 ^{NS}
AMMI-PC6	20	67.4	3.4		2.85	96.67	0.5 ^{NS}
AMMI-PC7	18	44.9	2.5		1.90	98.57	0.4 ^{NS}
AMMI-PC8	16	33.8	2.1		1.43	100.00	0.3 ^{NS}
Residuals	432	2842.3	6.6				

df = degree of freedom; SS = sum of squares; MS = mean square; GEI = genotype by environment interaction; NS = non-significant; *** = significantly different at $P < 0.001$.

Table 4.11 The first four best oat genotypes selected for fodder dry matter yield (t/ha) by AMMI model per environment

Environment	Code	Mean yield	IPCA1 score	Best genotypes			
				1	2	3	4
Holetta	E1	11.8	-0.165	G6	G7	G4	G23
Ada-Berga	E2	15.0	0.527	G24	G13	G6	G23
Ginchi	E3	6.5	-0.319	G3	G10	G6	G15
Jeldu	E4	13.7	-0.744	G6	G2	G4	G21
D/Zeit	E5	10.3	0.335	G13	G11	G1	G18
Kulumsa	E6	18.8	0.769	G6	G13	G18	G24
Bekoji	E7	10.6	-0.312	G6	G7	G10	G3
Kuyu/Gebre Guracha	E8	10.4	-0.021	G6	G2	G10	G8
D/Markos	E9	13.1	-0.070	G9	G18	G11	G19
Grand mean		12.3					

IPCA1 = the first interaction principal component axis

4.3.1.5 AMMI-1 biplot for forage dry yield

In the AMMI-1 biplot analysis, the genotypes and environment's main effects and the IPCA-1 scores are plotted against each other (Figure 4.3). The IPCA-1 of the AMMI-1 explained 44.11% of the interaction's total variance. The result showed that E9, E1, and E8 were located closer to the biplot origin. On the contrary, E6, E3, E4, and E2 were located far from the biplot origin while E5 and E7 had intermediate distance from the center of the biplot. Like the environments, the genotypes also scattered on the biplot and the genotypes located closer to zero IPCA-1 score (abscissa line) were G12, G11, G23, G9, G5, G22, G1, G10, G17, and G20. On the other hand, G13, G8, G24, G18, G16, and G21 were located far from zero IPCA-1 score while G15, G3, G6, G14, G19, G7, G4, and G2 had intermediate distance from the IPCA-1. The genotypes G16, G21, G4, G7, G2, G3, G10, G6, G1, G11, G23, G12, and G22 and the environments E4, E3, E7, E1, E9, and E8 had negative IPCA-1 scores while the remaining genotypes and environments which located in the opposite side had positive IPCA-1 scores. Similarly, G13, G24, G18, G19, G15, and G9 with E2 and E6 had positive IPCA-1 scores while G12, G22, G21, and G16 with E3, E7, and E1 which located in the opposite side had negative IPCA-1 scores.

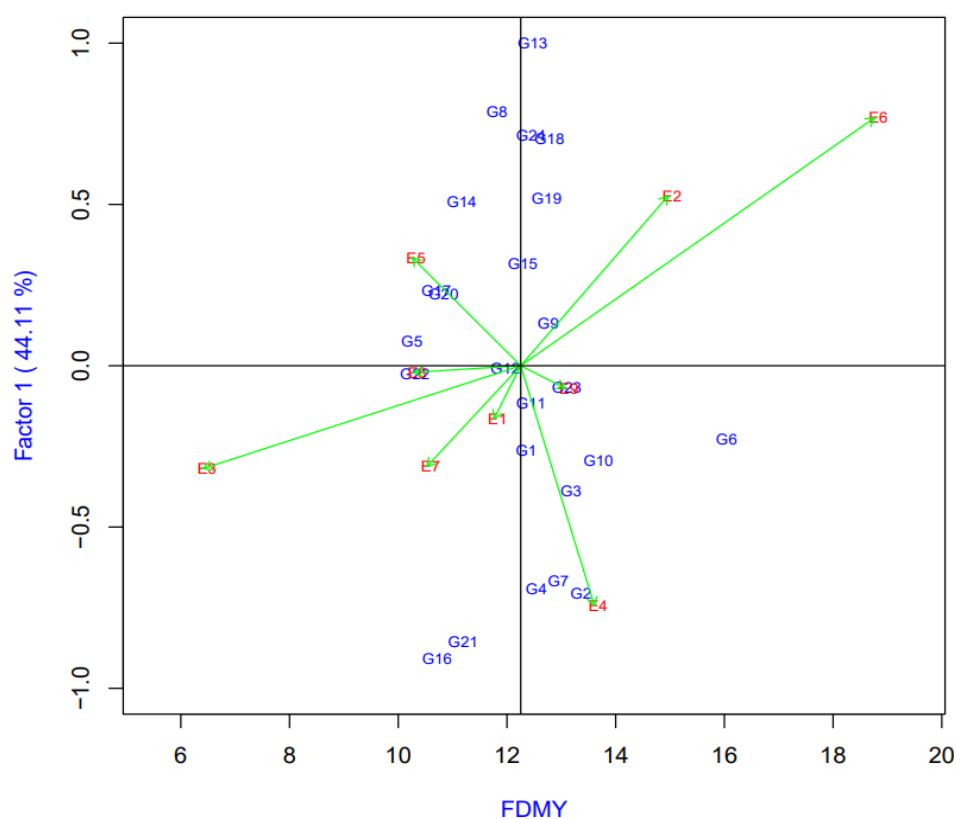


Figure 4.3 AMMI-1 biplot of stability (IPCA-1) plotted against the mean fodder dry matter yield of 24 oat genotypes tested across nine environments.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.1.6 AMMI-2 biplot for forage dry yield

The AMMI-2 biplot analysis indicated that the first interaction principal component scores for both the genotypes and environments were plotted against the second interaction principal component scores for the genotypes and environments (Figure 4.4). The first and the second IPCAs of the AMMI-2 biplot captured 44.11% and 26.79% of the total interaction variance, respectively. Thus, the first two IPCAs together explained 70.91% of the total interaction variance. The environments located far from the biplot origin were E9, E4, E6, E2, and E7. On the contrary, E8 and E1 were located closer to the biplot origin while E3 and E5 had a relatively intermediate distance from the center of the biplot origin. The AMMI-2 biplot also showed the distribution of genotypes on the biplot. Accordingly, G18, G16, G21, G24, and G8 were located far from the biplot origin. On the other hand, G23, G22, G5, G20, G17, G14, and G12 were located closer to the origin while G1, G11, G19, G15, G4, G2, G7, G3, G10, G6, G13, and G9 had relatively intermediate distance from the center of the biplot. The first two IPCAs were positive for E5 environment and for G9, G18, G20, G17, and G19 genotypes while G22, G6, G10, G3, G4, and G21 with E8, E1, E3, E7, and E4 had negative scores for the first two IPCAs. On the contrary, G2, G7, G16, G22, G12, G11, and G1 with E9 were positive for the second IPCAs and negative for the first IPCAs while the inverse is true for the remaining genotypes which were located at the opposite side.

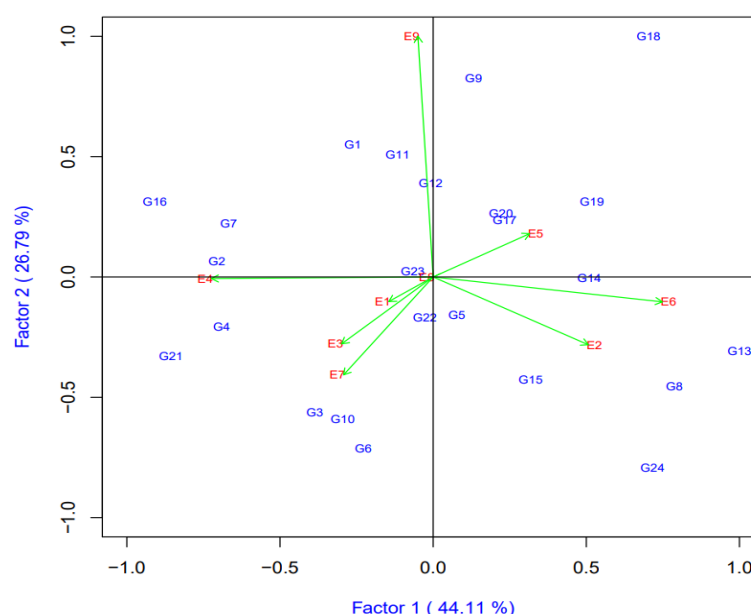


Figure 4.4 AMMI-2 biplot of IPCA-1 against IPCA-2 for mean fodder dry matter yield of 24 oat genotypes tested across nine environments.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.1.7 Genotype evaluation for fodder yield based on GGE biplot

4.3.1.7.1 Mean performance and stability of genotypes

The mean fodder dry matter yield of oat genotypes is plotted against the stability of genotypes using the GGE biplot analysis (Figure 4.5). The ordinate line of the average-environment coordinate (AEC) passed through the origin of the biplot and divided the genotypes into two parts based on the performance of genotypes for fodder yield across environments. Accordingly, genotypes located on the left side of the AEC ordinate were G6, G10, G3, G2, G7, G4, G23, G24, G15, G19, G13, and G9 while the remaining genotypes were located on the right side of this ordinate. On the other hand, the arrowed line of the AEC abscissa also passed through the biplot origin. The result indicated that the vector of each genotype had a different projection length which originated from the arrowed AEC abscissa and was parallel to the AEC ordinate. Consequently, the longer vector projections of genotypes for fodder yield were observed for G13, G24, G8, G21, and G16. On the contrary, the shorter vector projections from the arrowed AEC abscissa were recorded for G6, G10, G3, G23, G9, G15, G11, G12, G1, G20, G7, G5, and G22 while the remaining genotypes had intermediate projections from this abscissa.

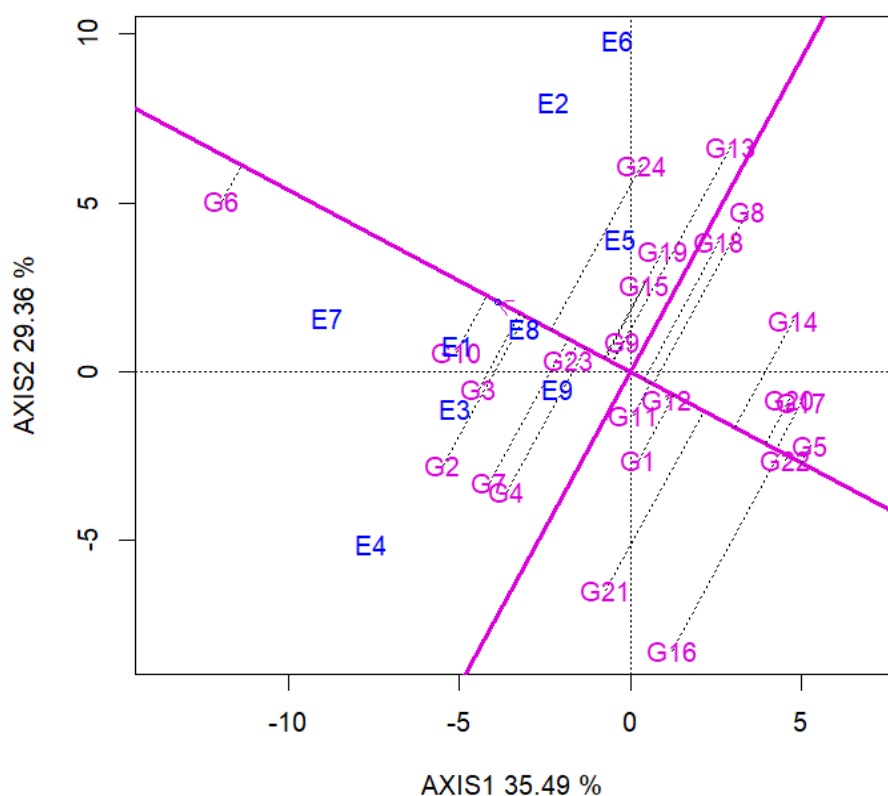


Figure 4.5 Average-environment coordination (AEC) view to show the mean fodder yield performance and stability of 24 oat genotypes using GGE biplot analysis.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.1.7.2 Ranking of genotypes relative to the ideal genotype

The performance of oat genotypes for fodder dry matter yield is ranked relative to the ideal genotype using the arrowed AEC abscissa and different concentric circles of the GGE biplot analysis (Figure 4.6). Among the genotypes, G6 was located at the center of the concentric circles while the remaining genotypes were located out of the concentric circles. However, high fodder-yielding genotypes were relatively closer to the center of the concentric circles compared to low fodder-yielding genotypes. Accordingly, G10, G3, G23, and G2 were located relatively closer to the center of the concentric circles while G5, G22, G16, G17, and G20 were located very far from the center of the concentric circles. The remaining genotypes had intermediate distances from the center of the concentric circles.

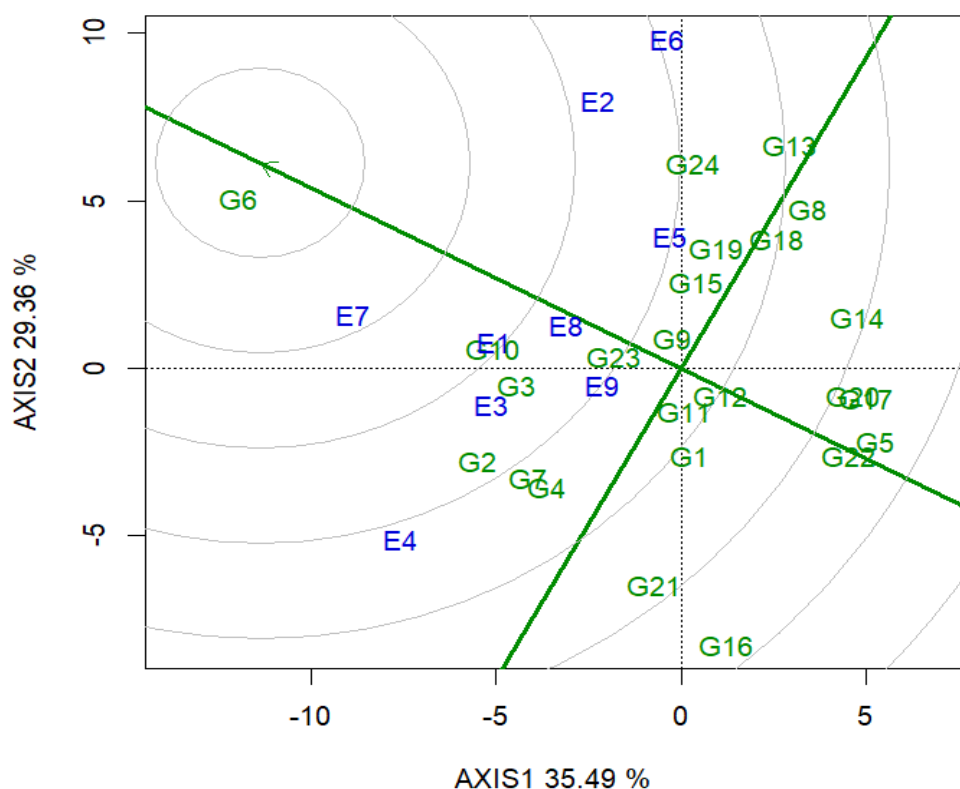


Figure 4.6 Average-environment coordination (AEC) view to rank genotypes' fodder yield performance relative to an ideal genotype using GGE biplot analysis.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.1.7.3 Which-won-where and mega environment identification

The best fodder dry matter yield performing genotypes at each environment and group of environments are illustrated using the 'which-won-where' or polygon view of the GGE biplot analysis (Figure 4.7). The genotypes which located very far from the biplot origin

were used for polygon formation. Thus, these oat genotypes were connected to form a six sides polygon and the remaining genotypes were located inside the polygon. Accordingly, the genotypes located very far from the biplot origin that used to construct the polygon are considered vertex genotypes. Thus, the vertex genotypes were G6, G13, G14, G5, G16, and G2. The six lines which originated from the biplot origin were perpendicular to the sides of the polygon and divided the polygon into different sectors/sections. Accordingly, the genotypes were grouped into six sectors while the environments were grouped into two sectors.

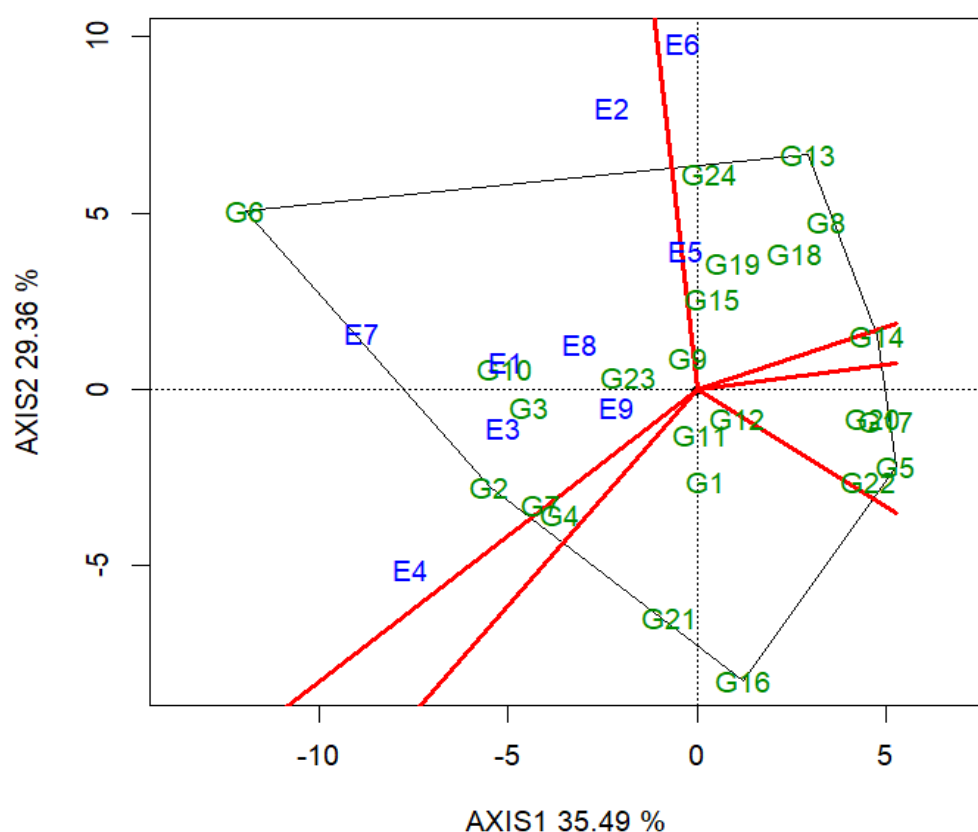


Figure 4.7 Which-Won-Where view of the GGE biplot to show which genotypes performed best in which environment/s using GGE biplot analysis.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

The target environment is further divided into various sub-regions (mega-environments) using the polygon view of the GGE biplot analysis (Figure 4.7). Accordingly, the target environment was classified into two mega-environments (MEs). The first mega-environment (ME-1) included E7, E1, E8, E3, E9, E2, and E4 while the environments which included in the second mega-environment (ME-2) were E5 and E6. The vertex genotypes for ME-1 were G6 and G2 while G13 was the vertex genotype for ME-2. On the contrary, the remaining three vertex genotypes such as G16, G5, and G14 were not included in any of the two

identified MEs. The genotypes grouped in the ME-1 were G6, G10, G3, G2, G7, G23, and G9. Similarly, the genotypes categorized in the ME-2 were G13, G24, G8, G18, G19, and G15. However, the remaining eleven genotypes which were grouped into four sectors were not included in the two MEs.

4.3.1.8 Environment evaluation based on GGE biplot for fodder yield

4.3.1.8.1 Relationships among test environments

The relationships among the testing environments are displayed using the vector view of the GGE biplot (Figure 4.8). The vectors of environments which connect the biplot origin with the markers of the environments had variable distances among the environmental vectors. The result revealed that the narrower vector distances were observed between vectors of E5 and E6; between E1 and E7; and between E3 and E9. Similarly, E2 was relatively closer to E5 and E6 while E3 was located closer to E9, E1, E4, E7, and E8. Moreover, E2 had an intermediate distance from E3 and E9. On the contrary, E6, E5, and E2 had relatively wider distance from E4, E9, and E3. Generally, the widest vector distance was observed between E6 and E4 followed by between E5 and E4 and between E2 and E4.

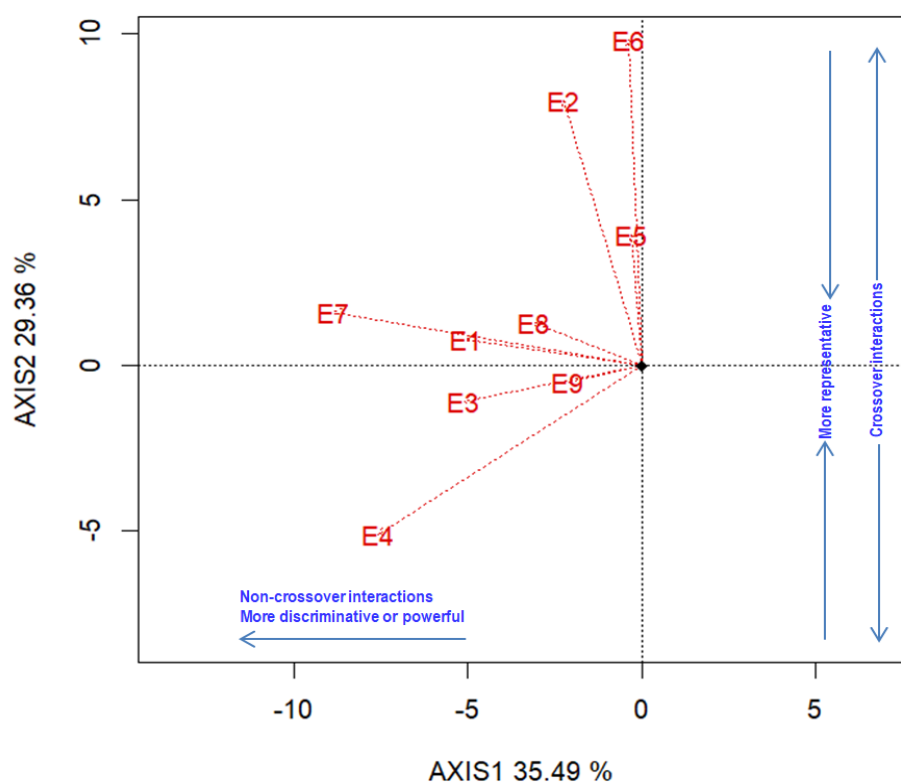


Figure 4.8 GGE biplot showing the relationship among the test environments.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos.

4.3.1.8.2 Discriminativeness and representativeness of test environments

The discriminating ability and representativeness of the test environments are presented using the GGE biplot analysis (Figure 4.9). The discriminating ability of the test environments was explained using the vector length while the representativeness of the test environments was defined using the angle between the vectors and the arrowed AEC abscissa. The average coordinates of all test environments (average environment) are represented by the small circle at the end of the pointed arrow on the AEC abscissa which passed through the biplot origin. Accordingly, the environments which had vector lengths above the average environment were E6, E2, E7, E4, E1, and E3 while E5, E8, and E9 had vector lengths below the average environment. The longer vector lengths were observed for E7, E4, E2, E6, E1, and E3 while the shorter vector lengths were observed for E9, E8, and E5. Among the environments, E8, E7, and E1 had shorter distances from the arrowed AEC abscissa while E3 and E9 had intermediate distances. On the contrary, E6, E5, E2, and E4 had wider distances from the arrowed AEC abscissa.

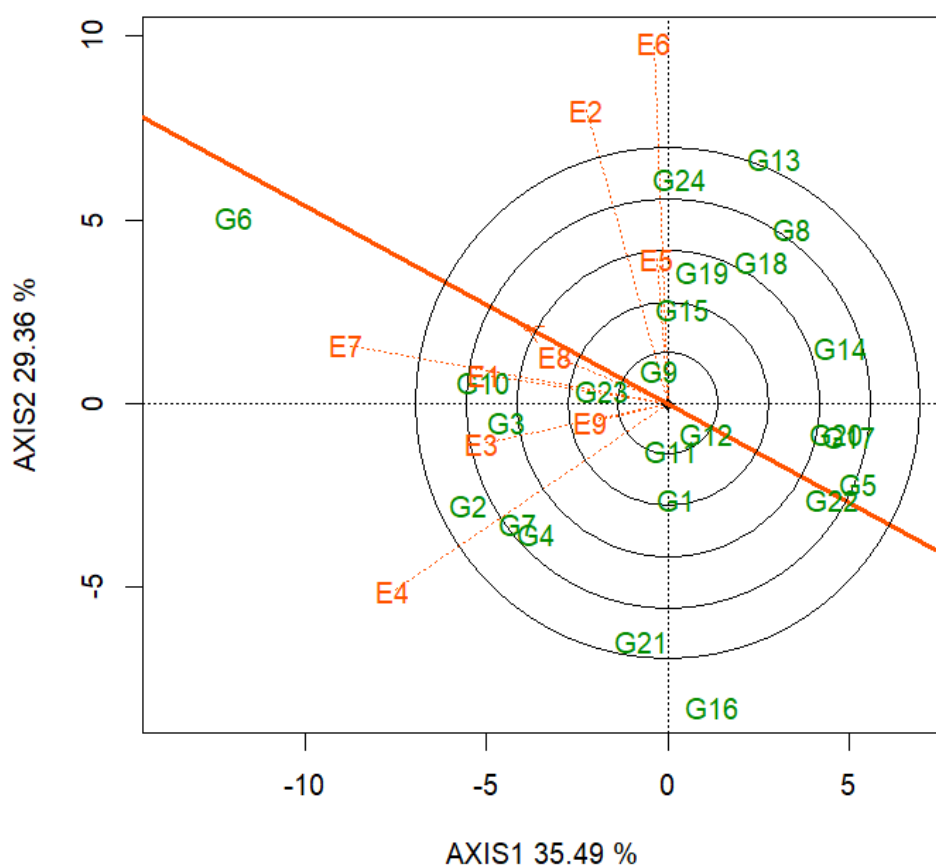


Figure 4.9 Discrimination and representativeness view of the GGE biplot to show the discriminating ability and representativeness of the test environments.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.1.8.3 Ranking environments based on discriminating and representativeness

The discriminating ability and representativeness of the testing environments are also ranked using the GGE biplot (Figure 4.10). The test environment which is located at the center or closer to the center of the concentric circles is considered an ideal test environment. Consequently, the ideal test environment is generally characterized by smaller PC2 scores and relatively higher PC1 scores compared to other environments. The environment E7 was located closer to the center of the concentric circles while E1 and E8 were relatively closer to E7. On the other hand, E6 and E4 were located very far from the center of the concentric circles while E3, E2, E9, and E5 had intermediate distances from the concentric circles.

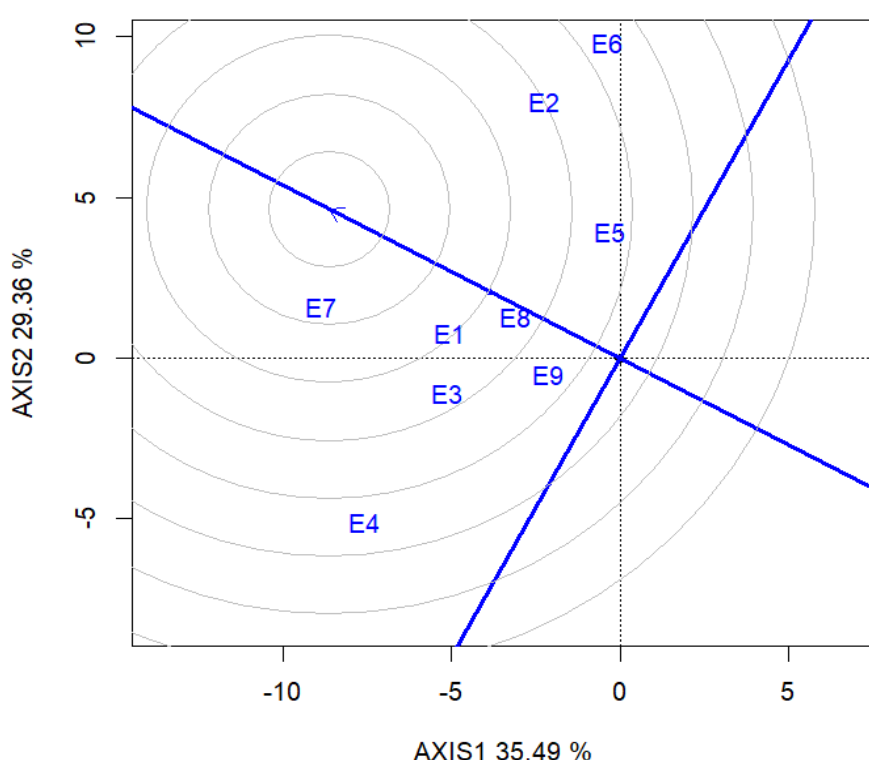


Figure 4.10 Discrimination and representativeness view of the GGE biplot to rank test environments relative to an ideal test environment.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos.

4.3.1.9 Genotype stability for fodder yield based on univariate analysis

The genotypes' stability and their rankings for fodder dry matter yield of oat genotypes using the mean fodder yield and 14 stability parameters are indicated in Table 4.12. The result revealed that the mean performance of oat genotypes varied ($P < 0.05$) for fodder dry matter yield across environments. Among the genotypes, G1, G2, G3, G4, G6, G7, G9, G10, G11, G13, G15, G18, G19, G23, and G24 produced fodder dry matter yield above the grand mean.

The genotypes changed their rank order of stability performance with changing stability parameters. Among the first ten high stability rank orders for each stability parameter, the first top fodder yielder genotype (G6) had stable performance using the stability parameters of CV_i , R^2 , P_i , $S^{(1)}_i$, $S^{(2)}_i$, and ASV. Similarly, the second top fodder yielder genotype (G10) showed stable performance in terms of SD, CV_i , S_{di}^2 , R^2 , B_i , D_{ji} , P_i , $S^{(2)}_i$, ASV, and YSI. Furthermore, the third (G2) and fourth (G3) top fodder yielder genotypes showed stable performance in SD, CV_i , R^2 , and P_i . Moreover, G3 was stable in the B_i stability parameter. The fifth top fodder-yielding genotype (G23) had stable performance using the stability parameters of CV_i , b_i , S_{di}^2 , σ_i^2 , D_{ji} , W_i , P_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI. Among high fodder yielding genotypes, G11 (SD, CV_i , b_i , S_{di}^2 , σ_i^2 , D_{ji} , W_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI) and G23 (CV_i , b_i , S_{di}^2 , σ_i^2 , D_{ji} , W_i , P_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI) had stable performances in 11 stability parameters while G10 and G15 (b_i , S_{di}^2 , σ_i^2 , D_{ji} , W_i , P_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI) had stable performances in 10 stability parameters. Moreover, G3 and G4 (SD, CV_i , R^2 , B_i , P_i , and YSI), G6 and G19 (S_{di}^2 , σ_i^2 , D_{ji} , W_i , P_i , and $S^{(1)}_i$) had stable performance in 6 stability parameters; G1 (SD, b_i , R^2 , ASV), G2, and G7 (CV_i , R^2 , B_i , P_i) were stable in 4 stability parameters; G9 was stable in 3 stability (B_i , P_i , and YSI) parameters; G18 was stable in 2 stability (B_i and YSI) parameters; while G13 and G24 were stable only in B_i stability parameter.

The genotypes were categorized into four clusters (I, II, III, and IV as indicated in parentheses) based on the mean stability values and fodder yield performance across nine environments (Table 4.12). The first (I) and second (II) group contained high fodder yield performing genotypes. However, group I contained widely adaptable (stable) genotypes unlike group II contained unstable (specifically adaptable) genotypes. On the other hand, group III was characterized by low fodder yield performing genotypes with stable performance contrary to group IV which were low yielding genotypes with unstable performance. Among the genotypes, G11 and G23 showed characteristics of group I using 13 stability parameters while G13 and G24 showed characteristics of group I using only 2 stability parameters. The first top fodder-yielding genotype (G6) showed characteristics of group I in CV_i , b_i , P_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI stability parameters while the second top-yielding genotype (G10) showed characteristics of group I in all stability parameters except b_i and R^2 . Similarly, the third top fodder-yielding genotype (G2) had group I characteristics in SD, CV_i , b_i , D_{ji} , P_i , and YSI stability parameters while the fourth top yielder genotype (G3) had group I characteristics in SD, CV_i , S_{di}^2 , B_i , D_{ji} , P_i , $S^{(2)}_i$, ASV, and YSI stability

parameters. Furthermore, the fifth top yielder genotype (G23) had group I characteristics in all stability parameters except B_i . On the contrary, G8, G16, and G21 genotypes had group IV characteristics in S_{di}^2 , R^2 , σ_i^2 , D_{ji} , W_i , P_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI. Moreover, G5 had group IV characteristics in stability parameters of B_i and P_i ; G12 in B_i and $S^{(1)}_i$; G14 in SD, CV_i , b_i , B_i , P_i , and YSI; G17 in SD, CV_i , B_i , and P_i ; G20 in CV_i , B_i , and P_i ; G22 in CV_i , B_i , and P_i stability parameters.

Table 4.12 Stability of 24 oat genotypes for fodder yield and their rankings based on the mean fodder yield performance and stability parameters

GEN	Mean	Rank	SD	Rank	CV_i	Rank	b_i	Rank	S_{di}^2	Rank	R^2	Rank	σ_i^2	Rank	B_i	Rank
G1	12.4 ^{b-d}	11	3.62	9 (I)	29.32	12 (I)	0.90	8 (I)	1.82	13 (I)	0.75	8 (II)	3.47	11 (I)	-0.10	17 (II)
G2	13.4 ^{bc}	3	3.51	7 (I)	26.25	5 (I)	0.84	13 (I)	2.48	15 (II)	0.69	5 (II)	4.32	14 (II)	-0.17	12 (II)
G3	13.2 ^{bc}	4	3.04	3 (I)	23.09	2 (I)	0.70	18 (II)	1.93	14 (I)	0.64	4 (II)	4.64	15 (II)	-0.30	7 (I)
G4	12.5 ^{b-d}	9	3.18	5 (I)	25.39	4 (I)	0.76	16 (II)	1.73	12 (I)	0.69	5 (II)	4.03	13 (I)	-0.24	9 (I)
G5	10.3 ^f	18	3.00	2 (III)	29.28	11 (III)	0.83	14 (III)	-1.13	8 (III)	0.93	17 (III)	0.90	2 (III)	-0.17	11 (IV)
G6	16.0 ^a	1	4.34	17 (II)	27.04	6 (I)	1.05	5 (I)	4.30	19 (II)	0.71	6 (II)	5.73	17 (II)	0.05	20 (II)
G7	12.9 ^{bc}	6	3.27	6 (I)	25.27	3 (I)	0.74	17 (II)	2.72	16 (II)	0.62	3 (II)	5.09	16 (II)	-0.26	8 (I)
G8	11.8 ^{c-e}	14	4.62	18 (IV)	39.10	21 (IV)	1.12	10 (III)	4.92	23 (IV)	0.72	7 (IV)	6.49	18 (IV)	0.12	15 (IV)
G9	12.8 ^{bc}	7	4.89	19 (II)	38.31	19 (II)	1.22	15 (II)	4.63	21 (II)	0.76	9 (II)	6.67	21 (II)	0.22	10 (I)
G10	13.7 ^b	2	2.79	1 (I)	20.41	1 (I)	0.68	20 (II)	0.64	4 (I)	0.72	7 (II)	3.58	12 (I)	-0.32	5 (I)
G11	12.4 ^{b-d}	10	3.64	10 (I)	29.22	10 (I)	0.96	3 (I)	0.34	3 (I)	0.85	14 (I)	1.94	7 (I)	-0.04	22 (II)
G12	12.0 ^{c-e}	13	3.65	11 (III)	30.46	13 (III)	0.95	4 (III)	0.69	5 (III)	0.83	13 (III)	2.29	8 (III)	-0.05	21 (IV)
G13	12.5 ^{b-d}	9	5.58	20 (II)	44.76	23 (II)	1.45	23 (II)	4.41	20 (II)	0.82	12 (I)	8.51	22 (II)	0.45	2 (I)
G14	11.2 ^{d-f}	15	4.34	17 (IV)	38.88	20 (IV)	1.15	12 (IV)	1.42	11 (III)	0.85	14 (III)	3.23	10 (III)	0.15	13 (IV)
G15	12.3 ^{b-d}	12	4.02	14 (II)	32.69	14 (II)	1.09	6 (I)	0.11	2 (I)	0.89	16 (I)	1.80	6 (I)	0.09	19 (II)
G16	10.7 ^{ef}	17	3.12	4 (III)	29.16	8 (III)	0.64	21 (IV)	3.50	17 (IV)	0.52	1 (IV)	6.61	20 (IV)	-0.36	4 (III)
G17	10.7 ^{ef}	17	4.04	15 (IV)	37.77	18 (IV)	1.12	9 (III)	-0.76	7 (III)	0.94	18 (III)	1.07	4 (III)	0.12	16 (IV)
G18	12.8 ^{bc}	7	5.66	21 (II)	44.25	22 (II)	1.46	24 (II)	4.90	22 (II)	0.81	11 (I)	9.12	23 (II)	0.46	1 (I)
G19	12.7 ^{bc}	8	4.31	16 (II)	33.90	15 (II)	1.14	11 (I)	1.41	10 (I)	0.85	14 (I)	3.19	9 (I)	0.14	14 (II)
G20	10.8 ^{ef}	16	3.94	13 (III)	36.32	17 (IV)	1.09	7 (III)	-0.73	6 (III)	0.94	18 (III)	1.00	3 (III)	0.09	18 (IV)
G21	11.2 ^{d-f}	15	3.27	6 (III)	29.20	9 (III)	0.68	19 (IV)	3.84	18 (IV)	0.53	2 (IV)	6.59	19 (IV)	-0.32	6 (III)
G22	10.3 ^f	18	3.59	8 (III)	34.79	16 (IV)	1.00	1 (III)	-1.14	9 (III)	0.95	19 (III)	0.51	1 (III)	0.00	24 (IV)
G23	13.1 ^{bc}	5	3.71	12 (I)	28.37	7 (I)	1.00	2 (I)	0.10	1 (I)	0.87	15 (I)	1.69	5 (I)	0.00	23 (II)
G24	12.4 ^{b-d}	10	5.67	22 (II)	45.59	24 (II)	1.43	22 (II)	6.60	24 (II)	0.77	10 (II)	10.30	24 (II)	0.43	3 (I)
Mean	12.3	-	3.95	-	32.45	-	1.00	-	2.34	-	0.78	-	4.28	-	0.19	-
GEN	D_{ji}	Rank	W_i	Rank	P_i	Rank	$S^{(1)}_i$	Rank	$S^{(2)}_i$	Rank	IPCA1	IPCA2	ASV	Rank	YSI	Rank
G1	3.70	13 (I)	26.84	11 (I)	17.07	15 (I)	1.58	13 (II)	46.78	17 (II)	-0.26	0.55	0.70	8 (I)	18	4 (I)
G2	4.35	15 (I)	33.12	14 (II)	9.95	3 (I)	1.50	12 (II)	49.28	18 (II)	-0.71	0.07	1.16	16 (II)	19	5 (I)
G3	3.80	14 (I)	35.49	15 (II)	11.23	4 (I)	1.68	15 (II)	36.91	13 (I)	-0.39	-0.56	0.85	12 (I)	16	3 (I)
G4	3.60	12 (I)	30.96	13 (I)	14.09	9 (I)	1.75	16 (II)	39.62	14 (II)	-0.69	-0.21	1.15	15 (II)	24	8 (II)
G5	0.74	2 (III)	8.06	2 (III)	27.84	24 (IV)	0.81	3 (III)	10.25	2 (III)	0.08	-0.16	0.20	3 (III)	20	6 (III)
G6	6.17	19 (II)	43.44	17 (II)	2.46	1 (I)	0.67	1 (I)	9.00	1 (I)	-0.23	-0.71	0.80	10 (I)	11	2 (I)
G7	4.60	16 (II)	38.74	16 (II)	12.56	6 (I)	2.25	20 (II)	54.28	20 (II)	-0.67	0.22	1.12	14 (II)	20	6 (I)
G8	6.79	23 (IV)	49.05	18 (IV)	20.64	17 (IV)	2.03	18 (IV)	46.62	16 (IV)	0.79	-0.45	1.37	17 (IV)	30	12 (IV)
G9	6.51	21 (II)	50.37	21 (II)	13.23	7 (I)	1.50	12 (II)	41.62	15 (II)	0.13	0.83	0.85	12 (I)	19	5 (I)
G10	2.51	8 (I)	27.65	12 (I)	9.92	2 (I)	1.36	11 (I)	24.38	7 (I)	-0.30	-0.59	0.76	9 (I)	11	2 (I)
G11	2.22	7 (I)	15.66	7 (I)	15.21	11 (I)	1.19	9 (I)	30.00	10 (I)	-0.12	0.51	0.54	6 (I)	16	3 (I)
G12	2.57	9 (III)	18.20	8 (III)	16.66	14 (III)	1.61	14 (IV)	33.25	12 (III)	-0.01	0.39	0.39	4 (III)	16	3 (III)
G13	6.28	20 (II)	63.84	22 (II)	18.71	16 (II)	2.56	21 (II)	70.75	23 (II)	1.00	-0.31	1.67	21 (II)	30	12 (II)
G14	3.30	11 (III)	25.12	10 (III)	23.51	19 (IV)	1.31	10 (III)	27.62	9 (III)	0.51	-0.01	0.84	11 (III)	25	9 (IV)
G15	1.98	6 (I)	14.62	6 (I)	14.94	10 (I)	1.11	7 (I)	25.12	8 (I)	0.32	-0.43	0.68	7 (I)	18	4 (I)
G16	5.37	17 (IV)	49.90	20 (IV)	26.46	22 (IV)	1.61	14 (IV)	50.50	19 (IV)	-0.91	0.31	1.53	20 (IV)	36	14 (IV)
G17	1.12	3 (III)	9.29	4 (III)	24.67	21 (IV)	1.14	8 (III)	16.66	6 (III)	0.23	0.23	0.45	5 (III)	21	7 (III)
G18	6.77	22 (II)	68.28	23 (II)	16.47	13 (I)	2.17	19 (II)	64.53	22 (II)	0.70	1.00	1.53	20 (II)	27	10 (II)
G19	3.28	10 (I)	24.79	9 (I)	13.42	8 (I)	1.07	6 (I)	31.03	11 (I)	0.52	0.31	0.91	13 (II)	21	7 (I)
G20	1.14	4 (III)	8.79	3 (III)	23.81	20 (IV)	0.92	4 (III)	14.91	4 (III)	0.22	0.26	0.45	5 (III)	20	6 (III)
G21	5.71	18 (IV)	49.77	19 (IV)	23.21	18 (IV)	1.94	17 (IV)	62.53	21 (IV)	-0.86	-0.33	1.45	19 (IV)	33	13 (IV)
G22	0.74	1 (III)	5.16	1 (III)	27.24	23 (IV)	0.97	5 (III)	13.28	3 (III)	-0.03	-0.17	0.18	2 (III)	19	5 (III)
G23	1.98	5 (I)	13.84	5 (I)	12.42	5 (I)	0.72	2 (I)	16.50	5 (I)	-0.07	0.02	0.11	1 (I)	6	1 (I)
G24	8.47	24 (II)	76.99	24 (II)	16.21	12 (I)	1.58	13 (II)	71.62	24 (II)	0.72	-0.79	1.42	18 (II)	28	11 (II)
Mean	3.90	-	32.83	-	17.16	-	1.46	-	36.96	-	-	-	0.88	-	21	-

FDMY = Fodder dry matter yield; SD = standard deviation; CV_i = Francis and Kannenberg's (1978) coefficient of variability; b_i = Eberhart and Russell's (1966) regression coefficient; S_{di}^2 = Eberhart and Russell's (1966) deviation from regression; R^2 = Pinthus (1973) coefficient of determination; σ_i^2 = Shukla's (1972) stability variance; B_i = Perkins and Jinks (1968) adjusted linear regression coefficient; D_{ji} = Hernandez *et al.* (1993) desirability index; W_i = Wricke's (1962) ecovalence; P_i = Lin and Binns's (1988) genotypic superiority index; $S^{(1)}_i$ = average absolute rank difference of genotype on the environment; $S^{(2)}_i$ = Variance ranges of environments; ASV = AMMI stability value; YSI = yield stability index; the number in parenthesis indicate the stability group (I = high yield and stable; II = high yield and unstable; III = low yield and stable; IV = low yield and unstable). Means followed by the different common superscript letters within column differently significant at $P < 0.05$.

Among the genotypes, G24 had group II characteristics in SD, CV_i , b_i , S_{di}^2 , R^2 , σ_i^2 , D_{ji} , W_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI stability parameters. Similarly, G13 had group II characteristics in the stability parameters of SD, CV_i , b_i , S_{di}^2 , σ_i^2 , D_{ji} , W_i , P_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI. Furthermore, G18 had group II characteristics in SD, CV_i , b_i , S_{di}^2 , σ_i^2 , D_{ji} , W_i , $S^{(1)}_i$, $S^{(2)}_i$, ASV, and YSI. The genotypes (G2 and G7) also had group II characteristics in stability parameters of S_{di}^2 , R^2 , σ_i^2 , W_i , $S^{(1)}_i$, $S^{(2)}_i$, and ASV. Among the genotypes, G5 and G12 had group III characteristics in stability parameters of SD, CV_i , b_i , S_{di}^2 , R^2 , σ_i^2 , D_{ij} , W_i , $S^{(2)}_i$, ASV, and YSI. Similarly, G14, G17, G20, and G22 had group III characteristics in S_{di}^2 , R^2 , σ_i^2 , D_{ij} , W_i , $S^{(1)}_i$, $S^{(2)}_i$, and ASV stability parameters. Furthermore, G16 and G21 had group III characteristics in stability parameters of SD, CV_i , and B_i .

4.3.1.10 Associations among fodder yield stability parameters

The Spearman rank correlation of 12 parametric and 2 nonparametric stability parameters with fodder dry matter yield of oat genotypes is indicated in Table 4.13. The result revealed that fodder dry matter yield had significant positive Spearman rank correlation coefficients with P_i ($r = 0.96$), YSI ($r = 0.47$), R^2 ($r = 0.44$), and CV_i ($r = 0.43$). However, the fodder yield had a non-significant ($p > 0.05$) positive association with B_i while it had non-significant negative associations with σ_i^2 , W_i , D_{ji} , b_i , $S^{(1)}_i$, ASV, $S^{(2)}_i$, and S_{di}^2 stability parameters. The correlation analysis observed between σ_i^2 and W_i was perfectly positive unlike the association between b_i and B_i was perfectly negative. The W_i stability parameter had significant positive associations with D_{ji} ($r = 0.97$), ASV ($r = 0.89$), S_{di}^2 ($r = 0.87$), $S^{(2)}_i$ ($r = 0.81$), b_i ($r = 0.75$), $S^{(1)}_i$ ($r = 0.70$), and YSI ($r = 0.47$) while it had significant negative association with R^2 ($r = -0.72$). The correlation coefficients between W_i and the remaining stability parameters were similar to the coefficients between the respective stability parameters and σ_i^2 stability parameter. The B_i stability parameter had a significant positive association with R^2 ($r = 0.56$) while it had significant negative associations with ASV ($r = -0.80$), σ_i^2 ($r = -0.75$), W_i ($r = -0.75$), $S^{(2)}_i$ ($r = -0.70$), $S^{(1)}_i$ ($r = -0.67$), S_{di}^2 ($r = -0.62$), D_{ji} ($r = -0.62$), and YSI ($r = -0.59$). The coefficients of correlation between B_i and all other stability parameters were similar but had inverse associations with the coefficients between the corresponding stability parameters and the b_i stability parameter.

Table 4.13 Spearman's correlation coefficients among ranks of forage dry matter yield and stability parameters for 24 oat genotypes tested in nine environments

Parameters	FDMY	SD	CV _i	b _i	S _{di} ²	R ²	σ _i ²	B _i	D _{ji}	W _i	P _i	S ⁽¹⁾ _i	S ⁽²⁾ _i	ASV	YSI
FDMY	1.00	-0.05 ^{NS}	0.43*	-0.19 ^{NS}	-0.16 ^{NS}	0.44*	-0.40 ^{NS}	0.19 ^{NS}	-0.38 ^{NS}	-0.40 ^{NS}	0.96***	-0.12 ^{NS}	-0.16 ^{NS}	-0.23 ^{NS}	0.47*
SD		1.00	0.83***	-0.01 ^{NS}	0.41*	0.31 ^{NS}	0.34 ^{NS}	0.01 ^{NS}	0.44*	0.34 ^{NS}	0.03 ^{NS}	0.03 ^{NS}	0.21 ^{NS}	0.23 ^{NS}	0.26 ^{NS}
CV _i			1.00	0.06 ^{NS}	0.33 ^{NS}	0.50*	0.16 ^{NS}	-0.06 ^{NS}	0.23 ^{NS}	0.16 ^{NS}	0.52**	0.08 ^{NS}	0.21 ^{NS}	0.16 ^{NS}	0.51*
b _i				1.00	0.62**	-0.56**	0.75***	-1.00***	0.62**	0.75***	-0.04 ^{NS}	0.67***	0.70***	0.80***	0.59**
S _{di} ²					1.00	-0.56**	0.87***	-0.62**	0.91***	0.87***	-0.01 ^{NS}	0.59**	0.69***	0.80***	0.59**
R ²						1.00	-0.72***	0.56**	-0.68***	-0.72***	0.41*	-0.63**	-0.60**	-0.68***	-0.20 ^{NS}
σ _i ²							1.00	-0.75***	0.97***	1.00***	-0.26 ^{NS}	0.70***	0.81***	0.89***	0.47*
B _i								1.00	-0.62**	-0.75***	0.04 ^{NS}	-0.67***	-0.70***	-0.80***	-0.59**
D _{ji}									1.00	0.97***	-0.26 ^{NS}	0.66***	0.77***	0.85***	0.45*
W _i										1.00	-0.26 ^{NS}	0.70***	0.81***	0.89***	0.47*
P _i											1.00	0.00 ^{NS}	-0.04 ^{NS}	-0.10 ^{NS}	0.57**
S ⁽¹⁾ _i												1.00	0.87***	0.75***	0.53**
S ⁽²⁾ _i													1.00	0.84***	0.59**
ASV														1.00	0.70***
YSI															1.00

Note: The green, orange, and yellow colors indicate the strength of correlation; green color is positively correlated; green to light green color indicate strong to weak positive correlation; orange color is negatively correlated; orange to light orange color indicate strong to weak negative correlation; and yellow color is positively and negatively correlated; yellow to light yellow color indicate no correlation to very weak correlation.

Abbreviations: FDMY = Fodder dry matter yield; SD = Standard deviation; CV_i = Francis and Kannenberg's (1978) coefficient of variability; b_i = Eberhart and Russell's (1966) regression coefficient; S_{di}² = Eberhart and Russell's (1966) deviation from regression; R² = Pinthus (1973) coefficient of determination; σ_i² = Shukla's (1972) stability variance; B_i = Perkins and Jinks (1968) adjusted linear regression coefficient; D_{ji} = Hernandez *et al.* (1993) desirability index; W_i = Wricke's (1962) ecovalence; P_i = Lin and Binns's (1988) genotypic superiority index; S⁽¹⁾_i = average absolute rank difference of genotype on the environment; S⁽²⁾_i = Variance ranges of environments; ASV = AMMI stability value; YSI = yield stability index; NS = non-significant ($p > 0.05$); * = $p < 0.05$; ** = $p < 0.01$; and *** = $p < 0.001$.

4.3.1.11 Principal component analysis (PCA) of the rank correlation

The principal component analysis (PCA) of the univariate stability parameters revealed that the first three PCs with eigenvalues greater than unity explained 88.8% of the total stability variation in oat genotypes. Of these, the first two PCs accounted for 76.8% of the total stability variation in oat genotypes. The biplot analysis of the univariate stability parameters for the first two PCs is displayed in Figure 4.11. The result revealed that the stability parameters were categorized into three clusters. The first cluster consisted of σ_i², W_i, D_{ji}, b_i, S⁽¹⁾_i, ASV, S⁽²⁾_i, and S_{di}² stability parameters. Of these, the first four stability parameters had positive factor loadings for both PCs while the remaining four stability parameters had negative PC2 and positive PC1 factor loadings. The second cluster was a solitary cluster that consisted of the B_i stability parameter which had negative factor loadings for both PCs. The third cluster consisted of FDMY and five stability parameters (R², P_i, CV_i, SD, and YSI). Among the stability parameters in the third cluster, P_i and R² with FDMY had negative factor loadings for both PCs while CV_i, SD, and YSI had negative PC1 and positive PC2 factor loadings. The stability parameters in the first and second clusters had static/biological stability patterns while the third cluster which associated positively with FDMY had dynamic/agronomic stability patterns. The contribution of S_{di}², σ_i², D_{ji}, W_i, S⁽²⁾_i and ASV

stability parameters was high for the first PC while the second PC contributed more by CV_i , R^2 , P_i , and YSI stability parameters.

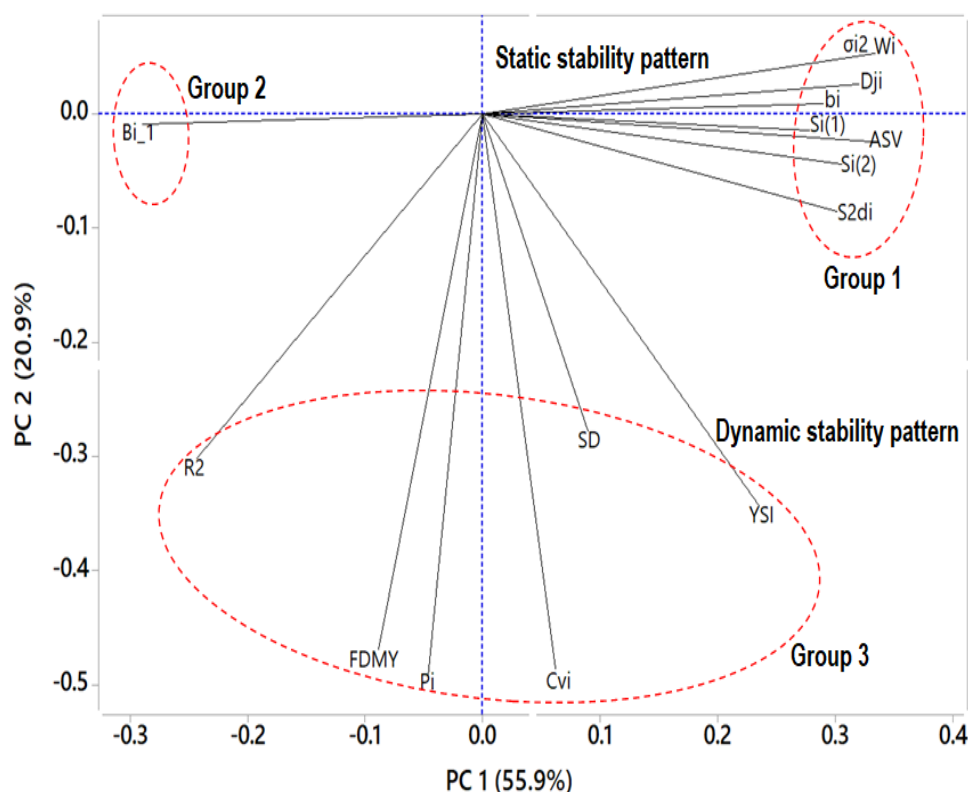


Figure 4.11 Biplot analysis for the spearman's rank correlation matrix of parametric and non-parametric stability statistics and fodder yield of oat genotypes across nine environments

Abbreviations: FDMY = Fodder dry matter yield; SD = Standard deviation; CV_i = Francis and Kannenberg's (1978) coefficient of variability; b_i = Eberhart and Russell's (1966) regression coefficient; S_{di}^2 = Eberhart and Russell's (1966) deviation from regression; R^2 = Pinthus (1973) coefficient of determination; σ_i^2 = Shukla's (1972) stability variance; B_i = Perkins and Jinks (1968) adjusted linear regression coefficient; D_{ji} = Hernandez *et al.* (1993) desirability index; W_i = Wricke's (1962) ecovalence; P_i = Lin and Binns's (1988) genotypic superiority index; $S^{(2)}_i$ = average absolute rank difference of genotype on the environment; $S^{(2)}_i$ = Variance ranges of environments; ASV = AMMI stability value; YSI = yield stability index.

4.3.2 Grain yield and yield components

4.3.2.1 Analysis of variance

The combined analysis of variance for grain yield of twenty-four oat genotypes evaluated across nine environments is disclosed in Table 4.14. The result showed that the genotype (G) and environment (E) main effects and their interaction (GE) effects had very highly significant variations ($P < 0.0001$) for grain yield. Of the total variance of grain yield, the environment's main effect accounted for 44.62% while the genotype and their interaction effects explained 28.84 and 26.54% of the total variation (G + E + GE), respectively.

Table 4.14 Combined analysis of variance for grain yield of 24 oat genotypes tested across nine environments during 2020/21 cropping season

Source of variation	df	SS	MS	Explained SS (%)	F
Model	233	1600.7	6.87		10.5***
Replication/Environment	18	44.4	2.47		3.8***
Environment (E)	8	694.5	86.81	44.62	35.2***
Genotype (G)	23	448.8	19.51	28.84	8.7***
G x E interaction	184	413.0	2.24	26.54	3.4***
Error	414	270.8	0.65		

df = Degree of freedom; SS = sum of square; MS = mean square; *** = significantly different at $p < 0.001$.

The pooled analysis of variance for grain yield and its yield-related traits of 24 oat genotypes across nine environments is presented in Table 4.15. The result revealed that the testing environments ($P < 0.0001$) influenced the performance of all the studied traits. The tested genotypes also showed variation ($P < 0.0001$) for all measured traits except GFP. Furthermore, the genotype by environment interaction effect revealed ($P < 0.0001$) variations for all measured traits. The interaction of genotype by the environment for grain yield was crossover showing the genotypes performed inconsistently under diverse environments (Figure 4.12).

Table 4.15 Combined analysis of variance for quantitative traits of 24 oat genotypes tested in 9 environments during 2020/21 cropping season

SN	Traits	Mean square					CV	R ²
		Environment (E) (df = 8)	Rep(L) (df = 18)	Genotype (G) (df = 23)	G*E (df = 184)	Error (df = 414)		
1	FLFH	550.83***	31.83***	446.30***	33.29***	12.86	15.21	0.80
2	PHGH	15470.81***	578.57***	7392.21***	307.42***	65.49	6.30	0.93
3	PLGH	2162.81***	29.87*	925.46***	54.34***	17.56	10.41	0.87
4	NSPP	900.95***	68.97***	146.60***	15.63***	9.14	12.26	0.80
5	NSLPP	60.12***	2.09NS	56.91***	3.09***	1.64	22.20	0.78
6	DSH	27834.60***	41.68***	3322.97***	310.82***	7.07	1.55	0.99
7	GFP	16203.79***	29.10*	344.47NS	314.34***	16.06	6.03	0.97
8	TBY	652.93***	37.86***	27.62***	10.42***	4.66	16.41	0.81
9	BYPR	24030.03***	1161.92***	1699.03***	423.60***	165.14	16.44	0.83
10	GSFR	16108.63***	709.92***	4797.20***	1020.22***	187.02	22.28	0.85
11	TSW	8259.16***	20.25**	440.20***	29.28***	8.55	6.35	0.96
12	HI	1330.02***	28.00NS	1217.83***	57.97***	20.25	15.21	0.86
13	SY	334.33***	22.41***	43.17***	6.26***	2.81	18.05	0.82
14	GY	86.81***	2.47***	19.51***	2.24***	0.65	20.90	0.86

FLFH = flag leaf length at forage harvest (cm); PHGH = plant height at grain harvest (cm); PLGH = panicle length at grain harvest (cm); NSPP = number of spikes per panicle; NSLPP = number of spikelets per panicle; DSH = days to seed harvest; GFP = grain filling period (days); TBY = total biological yield (t/ha); BYPR = biological yield production rate (kg/ha/day); GSFR = grain sink filling rate (kg/ha/day); TSW = thousand seed weight (g); HI = harvest index (%); SY = straw yield (t/ha); GY = grain yield (t/ha); df = degree of freedom; NS = non-significant; *, **, and *** = significantly different at $P < 0.05$, $P < 0.01$, and $P < 0.001$, respectively.

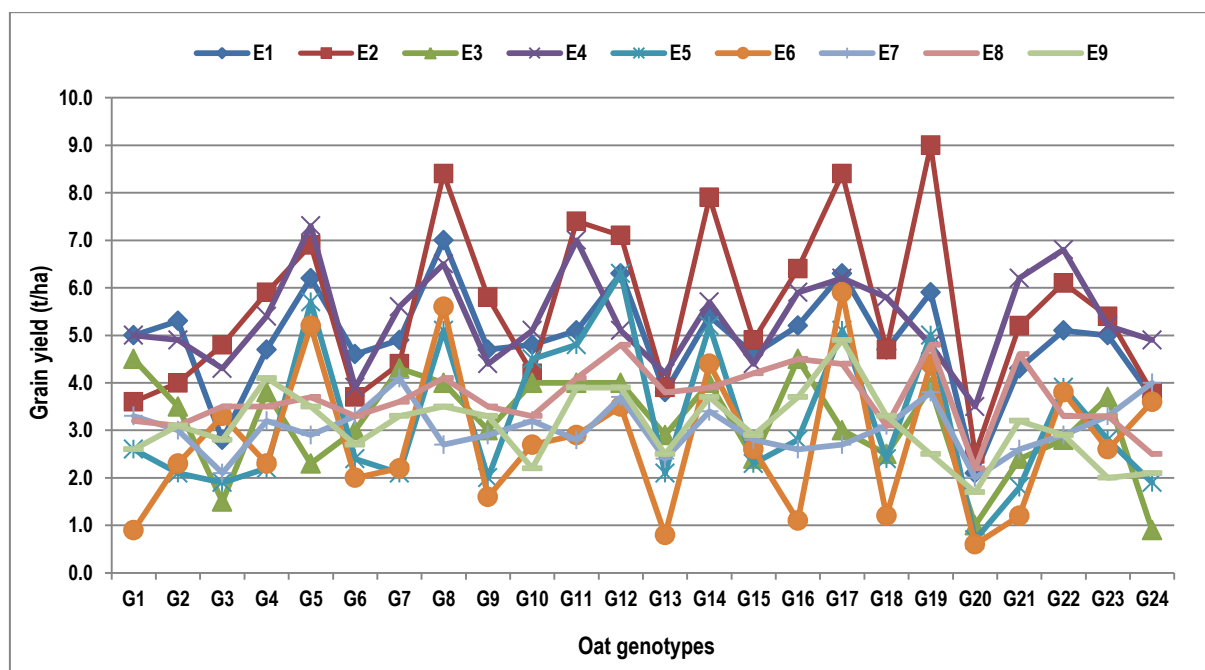


Figure 4.12 Genotype by location interaction (crossover) for grain yield of 24 oat genotypes grown at nine environments in 2020/21 cropping season

E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos; G1 = CI-1646; G2 = Walqaa; G3 = Bona-bas; G4 = CI-8251; G5 = Sorataf; G6 = CI-1512; G7 = MM799883/85; G8 = SRCPX80Ab2267; G9 = CI-1629; G10 = C-12; G11 = SRCPX80Ab2806; G12 = SRCPX80Ab2291; G13 = CI-1510; G14 = Was; G15 = CI-1652; G16 = Jassari; G17 = SRCPX80Ab2310; G18 = CI-1623; G19 = Bona; G20 = SRCPX80Ab2582; G21 = Lampton; G22 = SRCPX80Ab2691; G23 = CI-8235; G24 = CI-1759.

4.3.2.2 Effect of environments on oat performance

All the measured traits varied ($P < 0.0001$) across the testing environments (Table 4.16). The result indicated that all the values of the measured traits were above the grand mean at E4. At E2, the values of all measured traits were also above the grand mean except the NSLPP. Furthermore, nine (about 64%) of the studied traits at E1 had higher values compared to the grand mean. The studied genotypes had longer DSH and GFP at E2, E3, E4, and E7 compared to other environments. On the contrary, E5, E6, and E9 had shorter DSH and GFP. The GY, TBY, and SY were higher at E2 and E4. Moreover, GY and TBY at E1, and TBY and SY at E6 were above the grand mean. The BYPR and GSFR were higher at E1, E2, E4, E5, and E6 while E3 and E7 had the lowest rates compared to other environments.

Table 4.16 Mean performance for quantitative traits of 24 oat genotypes evaluated in 9 environments during 2020/21 cropping season

SN	Traits	E1	E2	E3	E4	E5	E6	E7	E8	E9	Mean	P-value
1	FLFH	23.1 ^c	29.7 ^a	23.5 ^c	24.9 ^b	23.1 ^c	24.7 ^b	20.3 ^e	21.7 ^d	21.2 ^{de}	23.6	<.0001
2	PHGH	134.9 ^b	136.8 ^b	117.3 ^d	135.0 ^b	105.0 ^e	143.2 ^a	143.5 ^a	107.5 ^e	132.0 ^c	128.4	<.0001
3	PLGH	38.2 ^c	44.5 ^b	38.5 ^c	43.1 ^b	31.6 ^e	35.1 ^d	49.6 ^a	43.8 ^b	37.9 ^c	40.3	<.0001
4	NSPP	27.1 ^{bc}	26.2 ^c	28.0 ^{ab}	28.7 ^a	24.1 ^d	19.6 ^e	25.1 ^d	24.5 ^d	18.5 ^f	24.6	<.0001
5	NSLPP	6.7 ^b	5.6 ^c	5.8 ^c	7.3 ^a	5.6 ^c	6.3 ^b	5.5 ^c	4.5 ^d	4.5 ^d	5.8	<.0001
6	DSH	164.1 ^f	176.5 ^d	184.7 ^c	201.1 ^a	150.4 ^h	142.2 ⁱ	191.1 ^b	174.0 ^e	155.0 ^g	171.0	<.0001
7	GFP	63.0 ^e	71.6 ^d	87.5 ^a	86.0 ^b	58.9 ^f	45.0 ⁱ	77.3 ^c	56.9 ^g	51.9 ^h	66.5	<.0001
8	TBY	14.1 ^c	18.6 ^a	10.3 ^e	16.9 ^b	11.6 ^d	13.7 ^c	9.6 ^e	11.5 ^d	12.0 ^d	13.2	<.0001
9	BYPR	87.6 ^c	105.8 ^a	55.8 ^f	84.1 ^c	78.5 ^d	97.1 ^b	50.0 ^g	66.8 ^e	77.7 ^d	78.2	<.0001
10	GSFR	80.3 ^a	77.9 ^a	35.9 ^d	62.1 ^c	62.3 ^c	64.3 ^{bc}	40.1 ^d	68.1 ^b	61.1 ^c	61.4	<.0001
11	TSW	52.5 ^a	51.2 ^b	49.3 ^c	51.9 ^{ab}	52.1 ^{ab}	22.7 ^e	33.0 ^d	52.4 ^a	49.2 ^c	46.0	<.0001
12	HI	34.5 ^a	30.0 ^c	30.2 ^c	31.8 ^b	27.7 ^d	20.6 ^f	33.3 ^{ab}	32.2 ^b	26.0 ^e	29.6	<.0001
13	SY	9.2 ^d	13.0 ^a	7.1 ^g	11.6 ^b	8.3 ^{ef}	11.0 ^c	6.5 ^h	7.9 ^f	8.9 ^{de}	9.3	<.0001
14	GY	4.9 ^b	5.6 ^a	3.2 ^d	5.3 ^a	3.2 ^d	2.8 ^e	3.0 ^{de}	3.7 ^c	3.1 ^d	3.9	<.0001

FLFH = flag leaf length at forage harvest (cm); PHGH = plant height at grain harvest (cm); PLGH = panicle length at grain harvest (cm); NSPP = number of spikes per panicle; NSLPP = number of spikelets per panicle; DSH = days to seed harvest; GFP = grain filling period (days); TBY = total biological yield (t/ha); BYPR = biological yield production rate (kg/ha/day); GSFR = grain sink filling rate (kg/ha/day); TSW = thousand seed weight (g); HI = harvest index (%); SY = straw yield (t/ha); GY = grain yield (t/ha); E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos; Means followed by a common superscript letter within a row are not significantly different from each other at $P < 0.05$.

4.3.2.3 Mean performance of oat genotypes

The mean performance of oat genotypes for measured traits is indicated in Table 4.17. The result showed that all measured traits varied significantly except GFP. Among the genotypes, G1 (1646), G20 (SRCPX80Ab2582), and G18 (1623) were late maturing for DSH while G5 (Sorataf) G17 (SRCPX80Ab2310), and G19 (Bonsa) were early maturing types. The highest TBY and SY were recorded for G6 (1512), and G13 (1510). The BYPR was the highest for G19 (Bonsa), G6 (1512), and G3 (Bona-bas) while the lowest was recorded for G20 (SRCPX80Ab2582), and G24 (1759). Similarly, the highest GSFR was observed for G17 (SRCPX80Ab2310), followed by G5 (Sorataf), and G8 (SRCPX80Ab2267) while G20 (SRCPX80Ab2582) and G3 (Bona-bas) had the lowest values.

The mean GY performance of oat genotypes across nine testing environments is indicated in Table 4.18. The result revealed that the GY of oat genotypes varied significantly in each environment except at E7 and E8. The mean GY observed for G8 (SRCPX80Ab2267), G17 (SRCPX80Ab2310), G12 (SRCPX80Ab2291), G19 (Bonsa), G5 (Sorataf), G14 (Was), G11 (SRCPX80Ab2806), G22 (SRCPX80Ab2691), G16 (Jassari), and G4 (8251) was high as compared to other genotypes. On the other hand, the mean GY recorded for G20 (SRCPX80Ab2582), G13 (1510), G3 (Bona-bas), G24 (1759), and G6 (1512) were generally low.

Table 4.17 Mean performance of 24 oat genotypes based on quantitative traits during 2020/21 cropping season

Genotype	FLFH	PHGH	PLGH	NSPP	NSLP		GFP	TBY	BYPR	GSFR	TSW	HI	SY
					P	DSH							
G1	29.8 ^a	116.7 ^{ij}	34.9 ^f	23.8 ^{ef}	4.7 ^{i-l}	180.4 ^f	61.3	13.4 ^{b-e}	74.9 ^{c-h}	57.1 ^{e-h}	45.7 ^f	25.7 ^{ef}	10.0 ^{c-f}
G2	26.9 ^{bc}	151.8 ^{a-c}	45.9 ^b	26.5 ^{bc}	7.3 ^{de}	165.7 ^k	64.7	12.3 ^{e-i}	74.7 ^{d-h}	56.3 ^{e-h}	46.3 ^{ef}	28.0 ^{de}	8.8 ^{g-j}
G3	14.1 ^l	153.1 ^{ab}	44.8 ^b	30.4 ^a	8.3 ^{ab}	163.4 ^{mn}	68.1	14.0 ^{a-c}	86.9 ^{ab}	46.7 ⁱ	33.9 ^l	21.2 ^h	11.0 ^{a-c}
G4	25.2 ^{c-e}	147.8 ^{cd}	45.3 ^b	26.1 ^{b-d}	7.4 ^{cd}	167.7 ^{ij}	66.1	13.5 ^{b-e}	82.0 ^{a-e}	62.2 ^{d-f}	48.3 ^{cd}	28.7 ^d	9.6 ^{e-g}
G5	22.2 ^{f-h}	97.2 ^m	28.2 ^h	26.7 ^{b-c}	5.3 ^{hi}	159.7 ^p	66.0	11.8 ^{g-i}	75.5 ^{c-h}	80.5 ^a	43.2 ^{h-j}	40.2 ^a	7.0 ^m
G6	26.9 ^{bc}	148.6 ^{b-d}	53.6 ^a	27.1 ^b	6.6 ^{ef}	170.2 ^h	62.7	15.1 ^a	89.6 ^a	53.4 ^{g-i}	44.9 ^{f-h}	21.5 ^h	11.9 ^a
G7	24.1 ^{d-f}	148.2 ^{cd}	44.3 ^{bc}	25.0 ^{c-e}	8.7 ^a	165.4 ^{kl}	63.5	14.1 ^{a-c}	85.0 ^{ab}	60.5 ^{d-g}	45.0 ^{f-h}	27.5 ^{de}	10.2 ^{c-e}
G8	22.5 ^{fg}	117.6 ^{h-j}	44.1 ^{bc}	26.9 ^b	4.4 ^{j-l}	163.0 ^{mn}	68.4	13.5 ^{b-e}	84.5 ^{ab}	79.9 ^a	48.1 ^d	40.0 ^a	8.2 ^{i-l}
G9	19.3 ^{ij}	118.2 ^{hi}	38.1 ^e	23.2 ^{e-g}	4.6 ^{i-l}	184.2 ^d	70.3	12.8 ^{c-h}	70.1 ^{hi}	53.0 ^{g-i}	44.7 ^{f-i}	27.3 ^{de}	9.3 ^{e-h}
G10	30.4 ^a	134.0 ^{ef}	44.8 ^b	21.0 ^h	6.7 ^{d-f}	167.8 ^{ij}	60.4	13.7 ^{b-d}	82.7 ^{a-c}	66.6 ^{cd}	43.7 ^{g-j}	27.9 ^{de}	9.9 ^{d-f}
G11	20.6 ^{g-i}	130.1 ^f	39.9 ^{de}	26.2 ^{b-d}	5.6 ^h	163.9 ^{mn}	68.0	13.8 ^{a-d}	84.6 ^{ab}	70.7 ^{bc}	50.0 ^{bc}	34.2 ^c	9.1 ^{f-i}
G12	25.9 ^{b-d}	122.2 ^{gh}	40.9 ^d	24.2 ^{ef}	5.3 ^h	163.0 ^{mn}	68.9	13.3 ^{b-f}	83.6 ^{ab}	76.1 ^{ab}	49.2 ^{b-d}	37.2 ^b	8.4 ^{h-k}
G13	27.8 ^b	135.7 ^e	41.9 ^{cd}	24.0 ^{ef}	6.4 ^{fg}	182.4 ^e	66.6	14.3 ^{ab}	79.6 ^{b-g}	49.0 ^{hi}	41.3 ^k	22.0 ^{gh}	11.4 ^{ab}
G14	24.3 ^{d-f}	118.4 ^{hi}	40.2 ^{de}	24.5 ^{d-f}	5.4 ^{hi}	163.1 ^{mn}	67.3	13.6 ^{b-e}	84.4 ^{ab}	74.9 ^{ab}	47.5 ^{ed}	35.7 ^{bc}	8.7 ^{g-j}
G15	27.7 ^b	132.0 ^{ef}	45.4 ^b	23.5 ^{ef}	5.1 ^{h-j}	174.7 ^g	71.1	12.3 ^{e-i}	71.8 ^{g-i}	54.8 ^{f-i}	44.6 ^{f-i}	28.1 ^{de}	8.8 ^{g-j}
G16	25.9 ^{b-d}	114.2 ^{i-k}	35.5 ^f	23.3 ^{e-g}	5.8 ^{gh}	163.1 ^{mn}	61.9	11.9 ^{g-i}	73.1 ^{f-i}	66.2 ^{cd}	53.3 ^a	33.5 ^c	7.9 ^{j-m}
G17	16.7 ^k	112.9 ^{j-l}	31.5 ^g	23.0 ^{fg}	4.1 ^{k-m}	161.0 ^{op}	68.8	12.5 ^{d-h}	80.2 ^{b-f}	80.7 ^a	49.2 ^{b-d}	41.6 ^a	7.3 ^{lm}
G18	23.6 ^{ef}	123.9 ^g	35.1 ^f	21.0 ^h	4.2 ^{k-m}	191.1 ^c	69.1	14.1 ^{a-c}	74.4 ^{e-i}	51.9 ^{hi}	45.1 ^{fg}	24.3 ^{fg}	10.7 ^{b-d}
G19	20.3 ^{h-j}	130.4 ^f	40.0 ^{de}	26.1 ^{b-d}	5.3 ^{hi}	162.4 ^{no}	67.6	14.3 ^{ab}	89.7 ^a	76.4 ^{ab}	50.4 ^b	34.4 ^c	9.4 ^{e-h}
G20	20.0 ^{ij}	108.8 ^l	34.3 ^f	23.4 ^{ef}	3.6 ^m	194.8 ^b	75.1	11.0 ^j	57.0 ^j	23.8 ^j	42.1 ^{jk}	16.5 ⁱ	9.2 ^{e-i}
G21	25.2 ^{e-e}	153.6 ^a	45.6 ^b	26.1 ^{b-d}	6.9 ^{d-f}	167.3 ^j	67.2	12.0 ^{f-i}	71.4 ^{hi}	51.8 ^{hi}	50.2 ^b	28.1 ^{de}	8.5 ^{g-j}
G22	18.2 ^{jk}	109.1 ^l	34.3 ^f	21.1 ^h	3.9 ^{lm}	164.2 ^{lm}	68.0	11.6 ^{hi}	71.2 ^{hi}	63.6 ^{c-e}	50.7 ^b	36.1 ^{bc}	7.5 ^{k-m}
G23	23.5 ^{ef}	144.4 ^d	43.4 ^{bc}	26.8 ^{bc}	8.0 ^{bc}	169.1 ^{hi}	62.2	13.7 ^{b-d}	82.4 ^{a-d}	62.3 ^{d-f}	44.6 ^{f-i}	27.5 ^{de}	10.0 ^{c-f}
G24	24.8 ^{c-e}	111.7 ^{kl}	34.1 ^f	21.5 ^{gh}	4.8 ^{l-k}	196.4 ^a	61.7	13.1 ^{b-g}	10.0 ^{c-f}	66.6 ⁱ	54.4 ^{f-i}	43.0 ^{l-k}	22.9 ^{gh}

FLFH = flag leaf length at forage harvest (cm); PHGH = plant height at grain harvest (cm); PLGH = panicle length at grain harvest (cm); NSPP = number of spikes per panicle; NSLPP = number of spikelets per panicle; DSH = days to seed harvest; GFP = grain filling period (days); TBY = total biological yield (t/ha); BYPR = biological yield production rate (kg/ha/day); GSFR = grain sink filling rate (kg/ha/day); TSW = thousand seed weight (g); HI = harvest index (%); and SY = straw yield (t/ha); Means followed by a common superscript letter within a column are not significantly different from each other at $P < 0.05$. See Table 4.2 for genotypes description.

4.3.2.4 AMMI analysis of variance for grain yield

The AMMI model of analysis of variance (ANOVA) for GY across nine environments is indicated in Table 4.19. The results of the AMMI analysis showed variation ($P < 0.0001$) for genotype, environment, and GEI. From the total treatment sum of the square of the model, 44.62% accounted for environmental effects and the rest for genotypic effects (28.84%) and the GEI (26.54%). The GEI component of the AMMI model was further partitioned into various interaction principal component axes (IPCAs) and significant variations were observed for the first four IPCAs. The first four IPCAs accounted for 86.20% of the total GEI variance while the remaining IPCAs contributed to 13.80% of the GEI sum of squares. The partitioned GEI was significantly explained by IPCA-1 (46.43%) followed by IPCA-2 (17.53%), IPCA-3 (13.12%), and IPCA-4 (9.12%). The first two IPCAs generally accounted for 63.96% of the total GEI sum of squares.

The first top five mean grain yield producing genotypes across environments were G8, G17, G12, G19, and G5 (see Table 4.16). The AMMI analysis model also indicated the first four

best grain yield performing genotypes at each environment (Table 4.20). Among the top grain yielding genotypes, G8 was the first top grain yield producing genotype identified by AMMI model and this genotype was selected as the 1st, 2nd, and 3rd best genotype at E1, E6, and E2 environment, respectively, and as the 4th best genotype at E3, E4, and E5 environments. Similarly, the second top grain yielder genotype (G17) was selected as the 1st best genotype at E6 and E9 and the 2nd and 3rd best genotype at E2 and E1, respectively. The third top grain yield producing genotype (G12) was selected as the 1st best genotype at E5; the 2nd best genotype at E1 and E8; and the 4th best genotype at E7 and E9. Furthermore, the fourth top grain yielding genotype (G19) was selected as the 1st best genotype at E2 and E8 and the 3rd best genotype at E7 while the fifth top grain yield producing genotype (G5) was selected as the 1st, 2nd, 3rd, and 4th best genotype at E4, E5, E6, and E1, respectively.

Table 4.18 Mean grain yield (t/ha) of 24 oat genotypes tested at 9 locations during 2020/21 cropping season

Genotype	Environment									Mean
	E1	E2	E3	E4	E5	E6	E7	E8	E9	
G1	5.0 ^{b-f}	3.6 ^{lm}	4.5 ^a	5.0 ^{c-g}	2.6 ^f	0.9 ^{j-l}	3.3	3.2	2.6 ^{d-h}	3.4 ^{d-f}
G2	5.3 ^{b-e}	4.0 ^{j-m}	3.5 ^{a-f}	4.9 ^{c-g}	2.1 ^f	2.3 ^{e-i}	3.0	3.1	3.1 ^{b-g}	3.5 ^{d-f}
G3	2.8 ^{gh}	4.8 ^{g-l}	1.5 ^{g-i}	4.3 ^{d-g}	1.9 ^f	3.3 ^{c-g}	2.1	3.5	2.8 ^{c-h}	3.0 ^{fg}
G4	4.7 ^{d-f}	5.9 ^{d-i}	3.8 ^{a-f}	5.4 ^{a-g}	2.2 ^f	2.3 ^{e-i}	3.2	3.5	4.1 ^{ab}	3.9 ^{cd}
G5	6.2 ^{a-c}	6.9 ^{b-f}	2.3 ^{f-i}	7.3 ^a	5.7 ^{ab}	5.2 ^{ab}	2.9	3.7	3.5 ^{b-e}	4.9 ^{ab}
G6	4.6 ^{d-f}	3.7 ^{k-m}	3.0 ^{a-g}	3.9 ^{fg}	2.4 ^f	2.0 ^{g-k}	3.3	3.3	2.7 ^{c-h}	3.2 ^{e-g}
G7	4.9 ^{b-f}	4.4 ^{h-l}	4.3 ^{ab}	5.6 ^{a-f}	2.1 ^f	2.2 ^{f-j}	4.1	3.6	3.3 ^{b-f}	3.8 ^{cd}
G8	7.0 ^a	8.4 ^{ab}	4.0 ^{a-c}	6.5 ^{a-c}	5.1 ^{bc}	5.6 ^{ab}	2.7	4.1	3.5 ^{b-e}	5.2 ^a
G9	4.7 ^{d-f}	5.8 ^{d-j}	3.0 ^{a-g}	4.4 ^{a-g}	2.0 ^f	1.6 ^{h-l}	2.9	3.5	3.3 ^{b-f}	3.5 ^{d-f}
G10	4.8 ^{c-f}	4.2 ^{i-m}	4.0 ^{a-c}	5.1 ^{b-g}	4.5 ^{cd}	2.7 ^{d-h}	3.2	3.3	2.2 ^{f-h}	3.8 ^{cd}
G11	5.1 ^{b-f}	7.4 ^{a-d}	4.0 ^{a-d}	7.0 ^{ab}	4.8 ^{b-d}	2.9 ^{d-h}	2.8	4.1	3.9 ^{a-c}	4.7 ^b
G12	6.3 ^{ab}	7.1 ^{b-e}	4.0 ^{a-c}	5.1 ^{b-g}	6.3 ^a	3.5 ^{c-f}	3.7	4.8	3.9 ^{a-c}	5.0 ^{ab}
G13	3.8 ^{fg}	3.9 ^{k-m}	2.9 ^{b-g}	4.2 ^{e-g}	2.1 ^f	0.8 ^{kl}	2.4	3.8	2.5 ^{e-h}	2.9 ^g
G14	5.4 ^{b-e}	7.9 ^{a-c}	3.9 ^{a-d}	5.7 ^{a-f}	5.2 ^{bc}	4.4 ^{bc}	3.4	3.9	3.7 ^{b-e}	4.8 ^{ab}
G15	4.6 ^{d-f}	4.9 ^{g-l}	2.4 ^{d-h}	4.4 ^{d-g}	2.3 ^f	2.6 ^{d-h}	2.8	4.2	2.9 ^{b-h}	3.5 ^{d-f}
G16	5.2 ^{b-f}	6.4 ^{c-g}	4.5 ^a	5.9 ^{a-e}	2.8 ^{ef}	1.1 ^{i-l}	2.6	4.5	3.7 ^{b-d}	4.1 ^c
G17	6.3 ^{ab}	8.4 ^{ab}	3.0 ^{a-g}	6.2 ^{a-d}	5.1 ^{bc}	5.9 ^a	2.7	4.4	4.9 ^a	5.2 ^a
G18	4.7 ^{d-f}	4.7 ^{g-l}	2.5 ^{c-h}	5.8 ^{a-f}	2.4 ^f	1.2 ^{i-l}	3.1	3.1	3.3 ^{b-f}	3.4 ^{d-f}
G19	5.9 ^{a-d}	9.0 ^a	3.9 ^{a-e}	4.8 ^{c-f}	5.0 ^{bc}	4.4 ^{bc}	3.8	4.8	2.5 ^{d-h}	4.9 ^{ab}
G20	2.1 ^h	2.5 ^m	1.0 ^{hi}	3.5 ^g	0.7 ^g	0.6 ^l	2.0	2.2	1.7 ^h	1.8 ^h
G21	4.3 ^{ef}	5.2 ^{f-l}	2.4 ^{e-h}	6.2 ^{a-d}	1.8 ^f	1.2 ^{i-l}	2.6	4.6	3.2 ^{b-f}	3.5 ^{d-f}
G22	5.1 ^{b-f}	6.1 ^{d-h}	2.8 ^{b-g}	6.8 ^{a-c}	3.9 ^{ed}	3.8 ^{cd}	2.9	3.3	2.9 ^{b-h}	4.2 ^c
G23	5.0 ^{b-f}	5.4 ^{e-k}	3.7 ^{a-f}	5.2 ^{b-g}	2.8 ^{ef}	2.6 ^{d-h}	3.3	3.3	2.0 ^{gh}	3.7 ^{c-e}
G24	3.7 ^{fg}	3.8 ^{k-m}	0.9 ⁱ	4.9 ^{c-g}	1.9 ^f	3.6 ^{c-e}	4.0	2.5	2.1 ^{gh}	3.1 ^{fg}
Mean	4.9	5.6	3.2	5.3	3.2	2.8	3.0	3.7	3.1	3.9
P-value	<.0001	<.0001	<.0001	0.0007	<.0001	<.0001	0.1277	0.1612	<.0001	<.0001

E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. Means followed by a common superscript letter within a column are not significantly different from each other at P < 0.05. See Table 4.2 for genotypes description.

Table 4.19 Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield of 24 oat genotypes evaluated in 9 environments during 2020/21 cropping season

Source of variation	df	SS	MS	Explained SS (%)			F
				Factor	GEI	Cumulative	
Environment (E)	8	694.5	86.8	44.62		44.62	119.0***
Genotype (G)	23	448.8	19.5	28.84		73.46	26.7***
GEI	184	413.0	2.2	26.54		100	3.1***
AMMI-PC1	30	191.8	6.4		46.43	46.43	8.8***
AMMI-PC2	28	72.4	2.6		17.53	63.96	3.6***
AMMI-PC3	26	54.2	2.1		13.12	77.08	2.9***
AMMI-PC4	24	37.7	1.6		9.12	86.20	2.2**
AMMI-PC5	22	21.3	1.0		5.16	91.36	1.3 ^{NS}
AMMI-PC6	20	15.7	0.8		3.81	95.17	1.1 ^{NS}
AMMI-PC7	18	11.0	0.6		2.67	97.84	0.8 ^{NS}
AMMI-PC8	16	8.9	0.6		2.16	100	0.8 ^{NS}
Residuals	432	315.2	0.7				

df = degree of freedom; SS = sum of squares; MS = mean square; GEI = genotype by environment interaction; NS = non-significant; ** and *** = significantly different at $P < 0.01$, and $P < 0.001$, respectively.

Table 4.20 The first four best oat genotypes selected for grain yield (t/ha) by AMMI model per environment

Environment	Code	Mean yield	IPCA1 score	Best genotypes			
				1	2	3	4
Holetta	E1	4.9	-0.039	G8	G12	G17	G5
Ada-Berga	E2	5.6	1.000	G19	G17	G8	G14
Ginchi	E3	3.2	-0.789	G1	G16	G7	G8
Jeldu	E4	5.3	-0.201	G5	G11	G22	G8
D/Zeit	E5	3.2	0.723	G12	G5	G14	G8
Kulumsa	E6	2.8	0.948	G17	G8	G5	G14
Bekoji	E7	3.0	-0.780	G7	G24	G19	G12
Kuyu/Gebre Guracha	E8	3.7	-0.439	G19	G12	G21	G16
D/Markos	E9	3.1	-0.423	G17	G4	G11	G12
Grand mean		3.9					

IPCA1 = the first interaction principal component axis

4.3.2.5 AMMI-1 biplot for grain yield

The AMMI-1 biplot of 24 oat genotypes evaluated at nine testing environments was generated using genotype and environmental mean grain yield plotted against the first IPCA scores (Figure 4.13). The first IPCA of the AMMI-1 accounted for 46.43% of the sum of squares of GEI. The result indicated that E2, E6, E5, E3, and E7 were far from the biplot origin while E1, E4, E8, and E9 were relatively closer to the center of the biplot. The AMMI-1 analysis also indicated that the studied genotypes scattered on the biplot and genotypes located far from the origin were G17, G8, G5, G19, G14, G20, G7, and G1 while

G23, G10, G15, G9, G24, G4, and G3 were relatively closer to the biplot origin. Among the studied genotypes, G17, G8, G5, G19, G14, G12, G11, G22, G3, and G24 and the environments such as E2, E5, and E6 had positive signs on the IPCA-1 scores while the remaining genotypes and environments had negative IPCA-1 scores. Similarly, G1, G7, G20, G13, G6, G15, G21, G2, G9, G15, G23, G10, G24, and G3 and the environments E3, E7, E8, E9, E5, and E6 had negative IPCA-1 scores while the remaining genotypes and environments located at the opposite side had positive IPCA-1 scores.

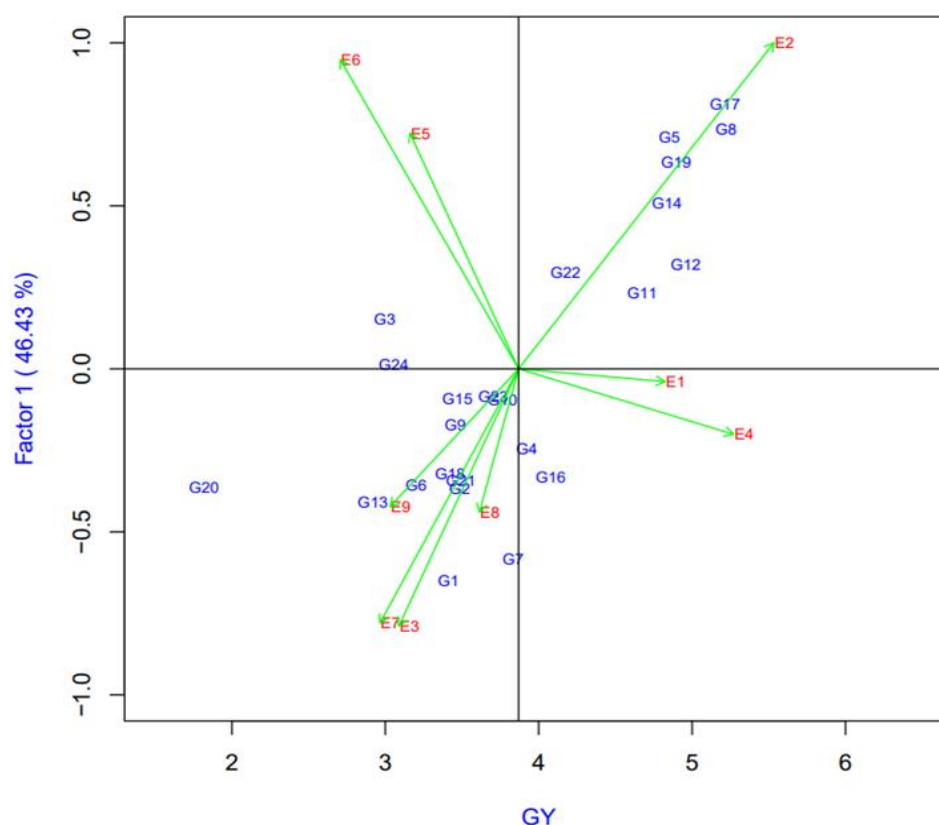


Figure 4.13 AMMI-1 biplot of IPCA-1 against the mean grain yield of 24 oat genotypes tested across nine environments.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.2.6 AMMI-2 biplot for grain yield

The AMMI-2 biplot analysis based on the mean grain yield of 24 oat genotypes tested at nine environments was generated using the first two interaction principal component (IPCA-1 and IPCA-2) scores (Figure 4.14). The first and the second IPCAs of the AMMI-2 biplot explained 46.43% and 17.53% sum of squares of GEI, respectively. Both principal components together accounted for 63.96% of the sum of squares of GEI. The environments located far from the biplot origin were E6, E3, E2, E7, and E5 while E1, E4, E8, and E9

were relatively closer to the center of the biplot. The AMMI-2 analysis also showed that the genotypes distributed on the biplot and genotypes located far from the origin were G24, G16, G19, and G5 while G10, G23, G15, G4, G9, G13, G21, G18, G2, and G6 were relatively closer to the biplot origin. Among the studied genotypes, G3, G22, G5, G17, and G24 and the environment E6 had positive signs of the first two IPCAs scores while G21, G10, G23, G9, G4, G13, G1, and G16 and the environments such as E1, E8, and E3 had negative signs of the first two IPCAs scores. On the other hand, G8, G14, G19, G12, and G1 and E2 and E5 had negative IPCA-2 and positive IPCA-1 while the inverse is true for the remaining genotypes and environments.

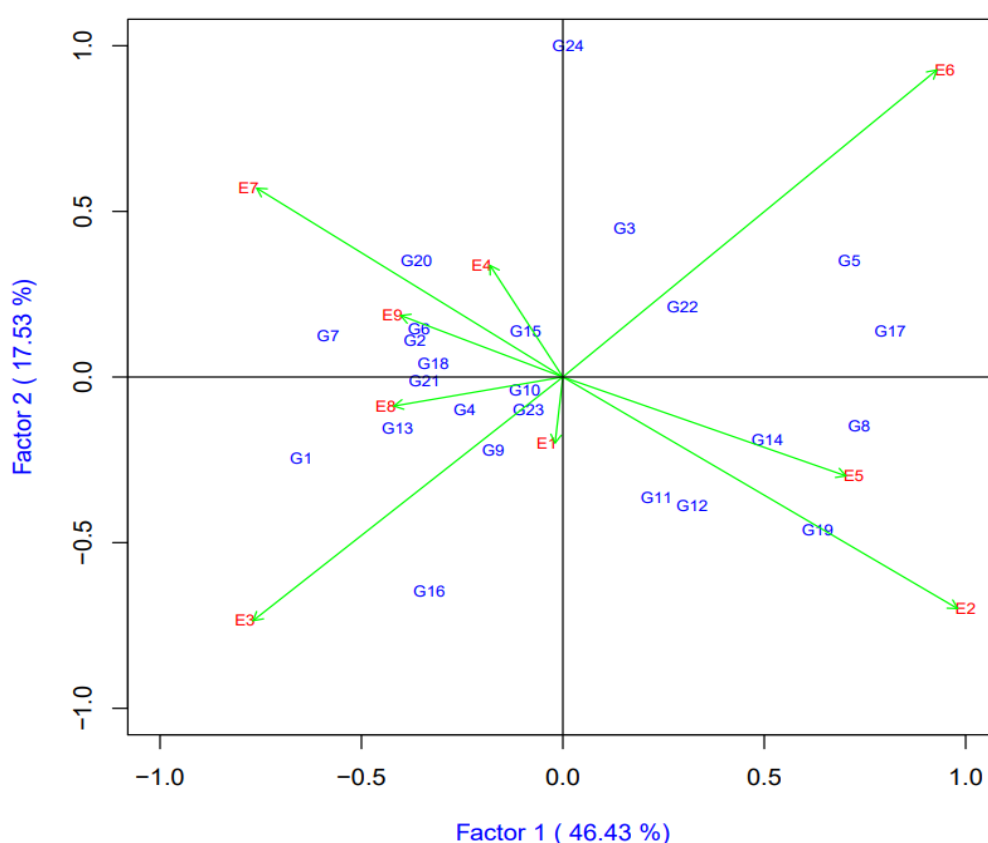


Figure 4.14 AMMI-2 biplot of IPCA-1 against IPCA-2 for mean grain yield of 24 oat genotypes tested across nine environments.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.2.7 Genotype evaluation for grain yield based on GGE biplot

4.3.2.7.1 Mean performance and stability of genotypes

The GGE biplot analysis indicated the performance of oat genotypes based on the first two principal components (PCs) as shown in Figure 4.15. The first and the second PCs of the

GGE biplot explained 68.46% and 11.84% of the total variation in GEI, respectively. The first two PCs together accounted for 80.30% of the total variation in GEI. Among the genotypes, G8, G17, G5, G14, G19, G22, G12, G11, G4, and G16, which were located on the left side of the ordinate (y-axis) had grain yield above the grand mean. The remaining 14 genotypes, which were located at the right side of the ordinate, on the other hand, had grain yield below the grand mean. The GGE biplot also showed the distribution of the genotypes and the genotypes located far from the abscissa (x-axis) line were G24, G3, G20, G16, and G1, whereas the remaining 19 genotypes were relatively located closer to the abscissa line.

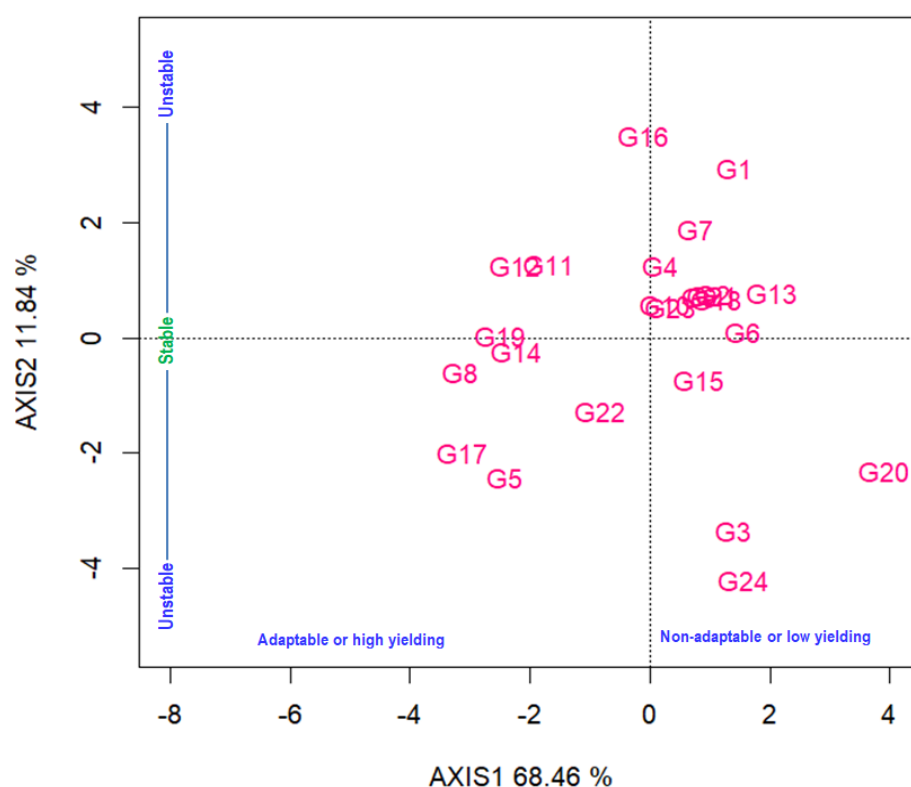


Figure 4.15 Mean grain yield performance and stability of 24 oat genotypes based on GGE biplot analysis.

See Table 4.2 for genotypes description.

The mean grain yield versus stability of oat genotypes based on the GGE biplot is presented in Figure 4.16. The result revealed that the average-environment coordinate (AEC) or the average tester coordinate (ATC) ordinate that passed through the origin of the GGE biplot separated the genotypes into two parts based on the grain yield performance of the genotypes across environments. Genotypes such as, G8, G17, G5, G14, G19, G22, G12, G11, G4, and G16, were located on the left side of the AEC/ATC ordinate, whereas others were located on the right side of this ordinate. The AEC/ATC abscissa arrowed line, which passed through

the biplot origin, had a different length of genotype projections that are perpendicular to the AEC/ATC abscissa or parallel to the ordinate. The genotype that had the longest vector/projection line was G24 followed by G16, G3, and G1 whereas G19, G14, G8, G11, G12, G17, and G22 had high grain yield with short projection vectors as compared to the other genotypes.

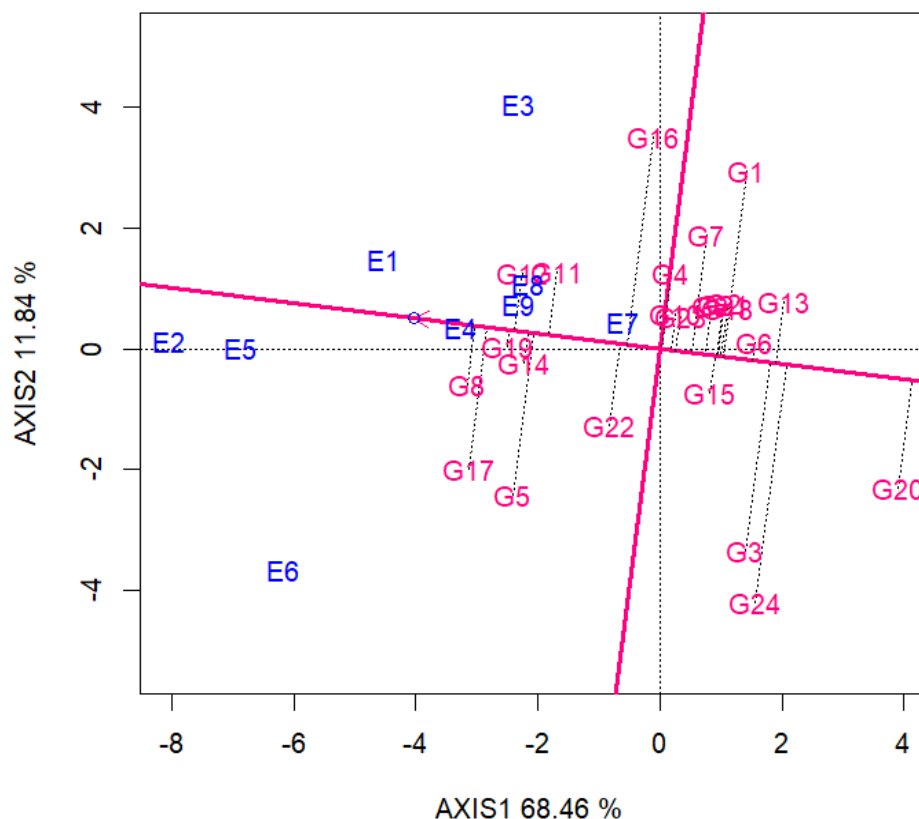


Figure 4.16 Average-environment coordination (AEC) view to show the mean grain yield performance and stability of 24 oat genotypes using GGE biplot analysis.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.2.7.2 Ranking of genotypes relative to the ideal genotype

The rank of the genotypes relative to ideal genotypes based on the arrowed AEC/ATC abscissa and various concentric circles of the GGE biplot is illustrated in Figure 4.17. The result indicated that some of the genotypes were closer to the center of the concentric circles, whereas others were relatively far from the origin of the concentric circles. Among the genotypes, G19 was located near the center of the concentric circles followed by G14, G8, G12, G11, G17, and G22. On the other hand, G24, G3, G20, G16, and G1 were far from the center of the concentric circles, whereas other genotypes had intermediate distances from the center of the concentric circles.

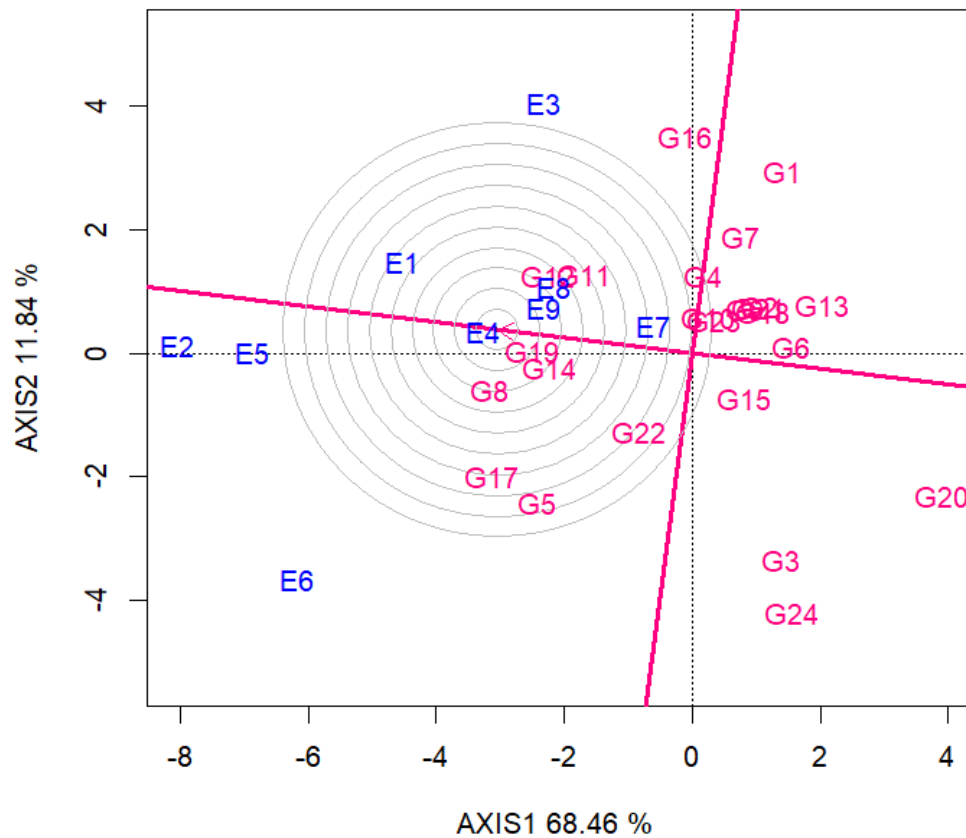


Figure 4.17 Average-environment coordination (AEC) view to rank genotypes grain yield performance relative to an ideal genotype using GGE biplot analysis.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.2.7.3 Which-won-where and mega environment identification

The 'which-won-where' or polygon view of the GGE biplot indicated the best grain yield performing genotype(s) for each environment and group of environments (Figure 4.18). In this study, a polygon with seven sides is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are encircled by the polygon. The genotypes that occupied the peaks of the polygon were used to connect the polygon and represent the vertex genotype. Thus, the vertex genotypes were G16, G1, G20, G24, G17, G8, and G12. The rays, in the polygon view of the GGE biplot, are lines that are perpendicular to the sides of the polygon or extended, and these eight rays separated a biplot into eight sectors in which genotypes and environments fell into seven and four sectors, respectively.

The polygon view of the GGE biplot subdivides the target environment into sub-regions (mega-environments) and is used for mega-environment identification. Hence, the polygon view of the GGE biplot classified the environment markers into four mega-environments.

The first sector formed by mega-environment (ME-1) was E3; the second (ME-2) by E7 and E8; the third (ME-3) by E1, E2, E4, E5, and E9; and the fourth (ME-4) by E6. The genotypes, such as G16 in ME-1, G12 in ME-2, and G8 and G17 in ME-4 were located at the vertices of the polygon, whereas ME-3 had no vertex genotype. The vertex genotype (G1) that was located closer to the first ME also produced the highest yield in this ME. However, the two vertex genotypes, G20, and G24, had not produced the highest yield in any of the environments.

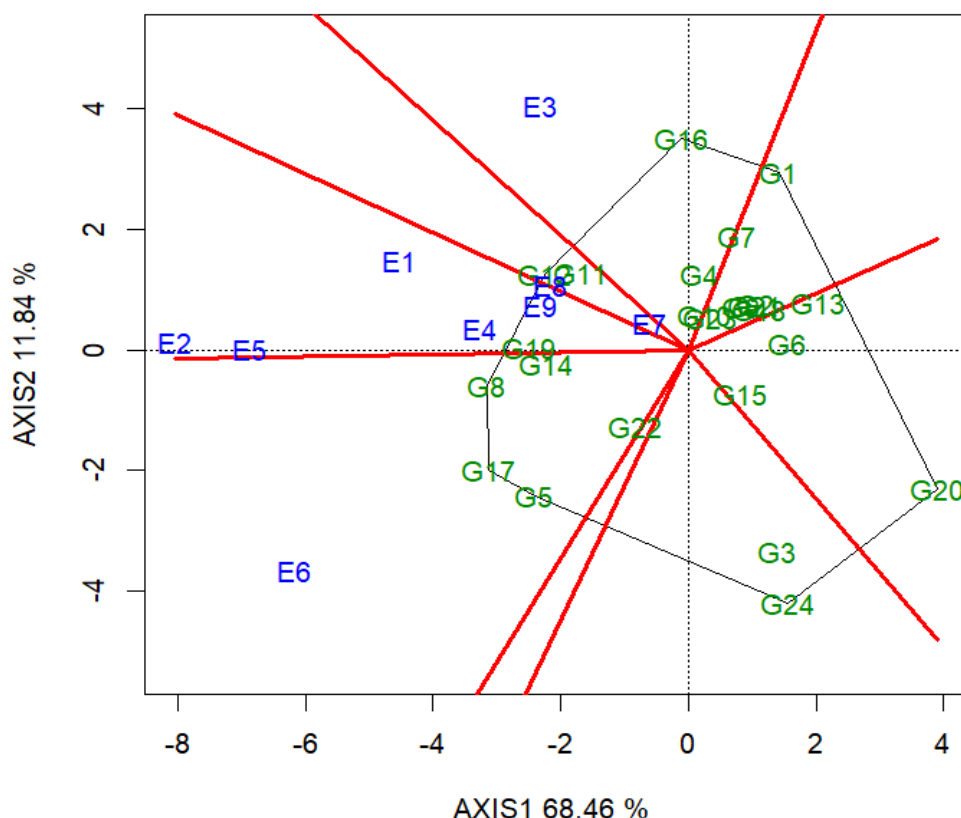


Figure 4.18 Which-Won-Where view of the GGE biplot to show which genotypes performed best in which environment/s using GGE biplot analysis.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.2.8 Environment evaluation based on GGE biplot for grain yield

4.3.2.8.1 Relationships among the test environments

The vector view of the GGE biplot provides a summary of the associations among the environments (Figure 4.19). The vectors of environments, which connect the biplot origin and the markers for the environments, had different distances between the vectors of environments. The result indicated that the vectors of environments had a narrow distance between E2 and E5; E1 and E9; and E7 and E8 when compared to other vectors of environments. The vector distance of E4 was also relatively closer to E1, E2, E5, and E9

than other vectors. Moreover, the vector distance of E8 was closer to E1, E7, and E9 than other vectors of environments. On the other hand, the vector distance for environments observed between E3 and E6 was relatively wide compared to other vectors of environments.

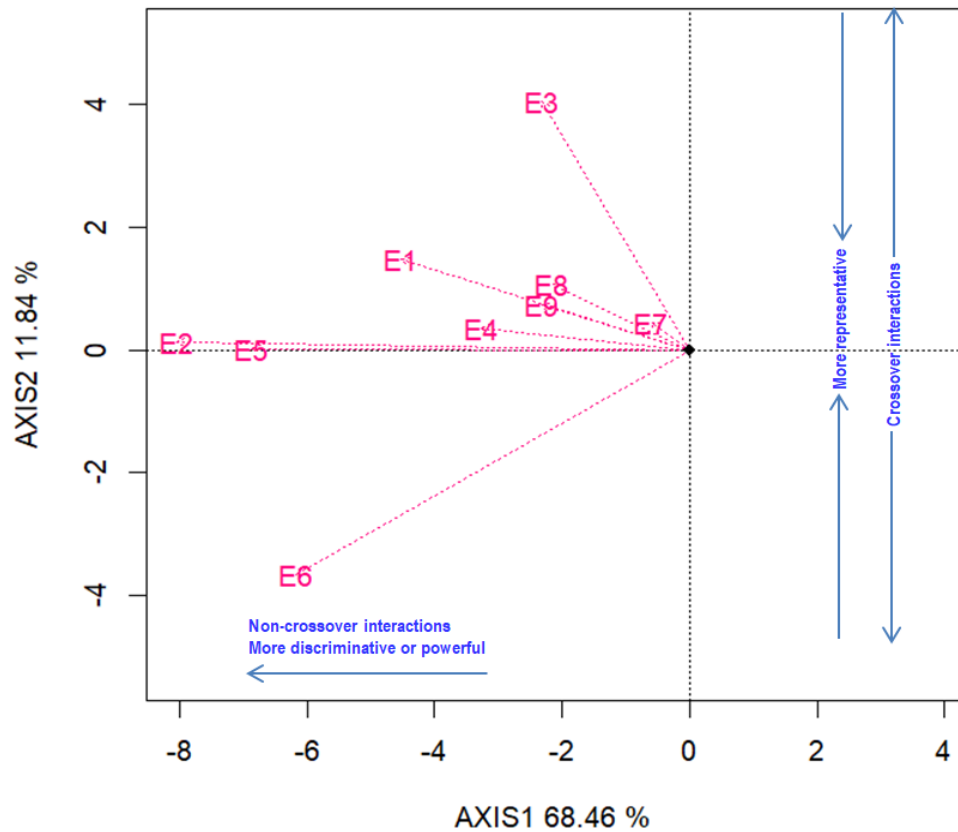


Figure 4.19 GGE biplot showing the relationship among the test environments.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos.

4.3.2.8.2 Discriminativeness and representativeness of test environments

The view of the GGE biplot shows the discriminating ability and representativeness of the test environments (Figure 4.20). The length of the vectors indicates the discriminating ability of the test environments, whereas the angle between the vectors and the AEC abscissa (or AEA) indicates the representativeness of the test environments. The average environment, which is represented by the small circle at the end of the arrow on the AEA line that passes through the average environment and the biplot origin, has the average coordinates of all test environments. The environments that had vectors length above the average coordinates of all test environments were E2, E5, E6, E3, and E1 while E7, E8, E9, and E4 had vectors length below the average coordinates of all test environments. Among the environments, E2, E5, E6, E3, E1, and E4 had longer vectors lengths, whereas E7, E8, and E9 had short vectors

lengths. Furthermore, E2, E5, E1, E4, E9, E7, and E8 vectors were located very close to the AEA, whereas E6 and E3 vectors were relatively located far from the AEA line.

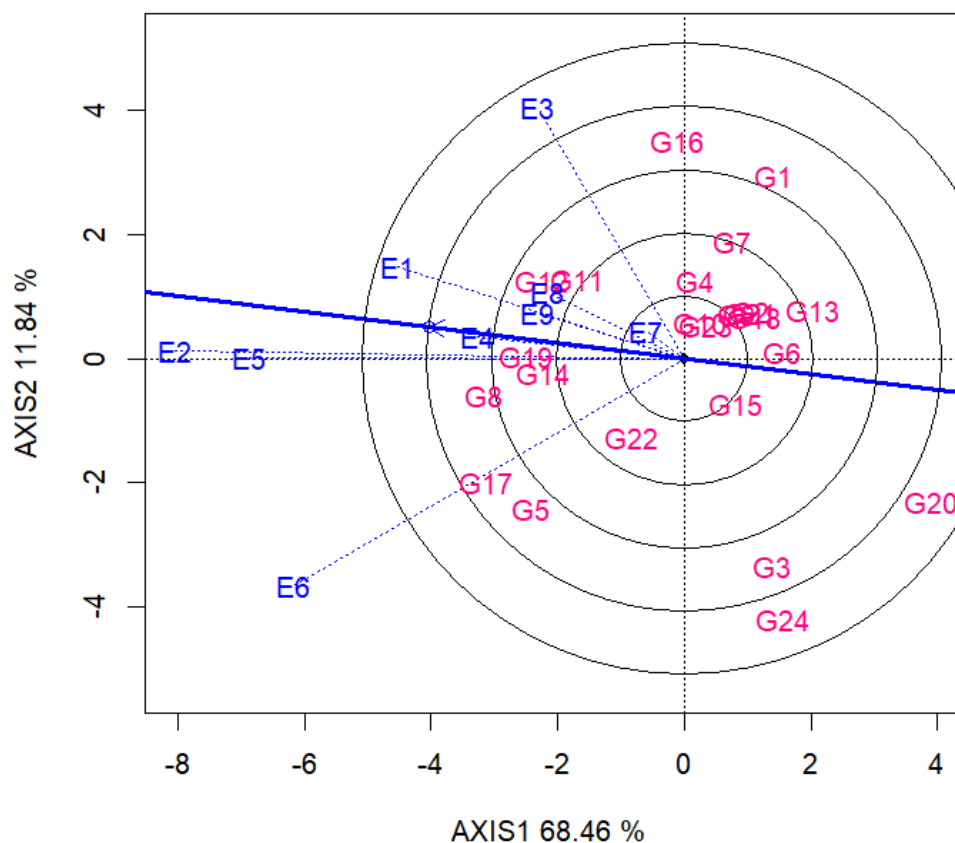


Figure 4.20 Discrimination and representativeness view of the GGE biplot to show the discriminating ability and representativeness of the test environments.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos. See Table 4.2 for genotypes description.

4.3.2.8.3 Ranking environments based on discriminating and representativeness

The view of the GGE biplot also ranks the testing environments based on their discriminating ability and representativeness (Figure 4.21). The ideal test environment that is represented by an arrow pointing to it at the center of the concentric circles should have large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments). Among the testing environments, E2 was located at the center of the concentric circles, whereas E5, E1, and E4 were closer to the center of the concentric circles. On the other hand, E7, E3, E8, E9, and E6 were relatively far from the center of the concentric circles.

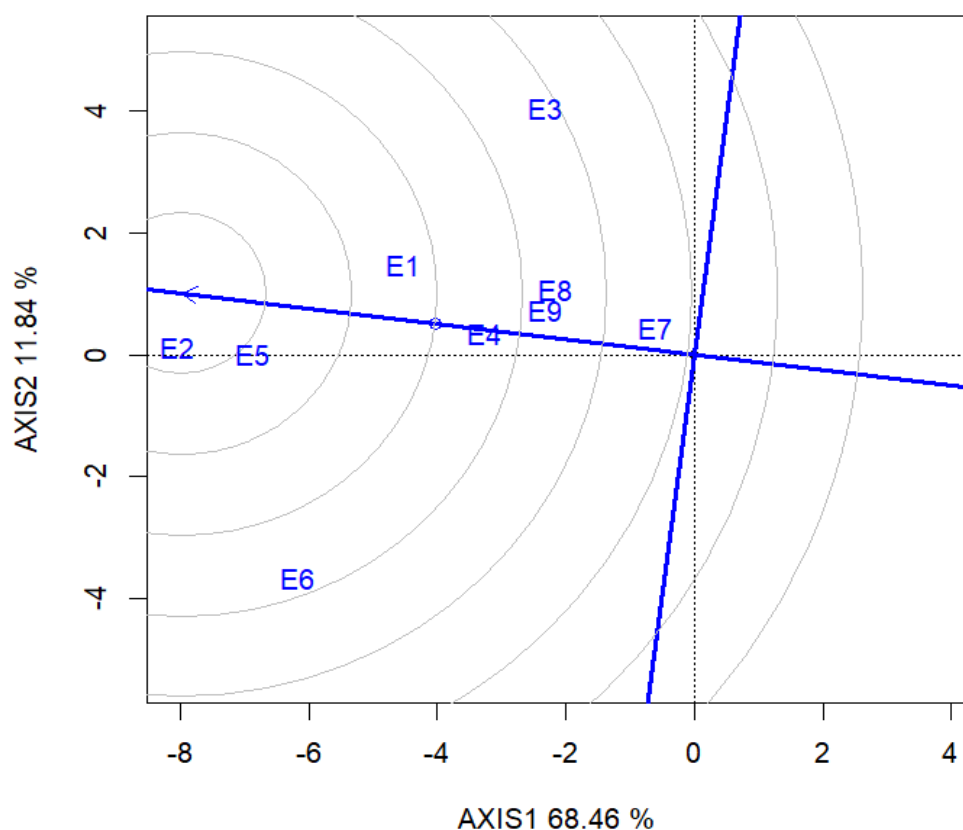


Figure 4.21 Discrimination and representativeness view of the GGE biplot to rank test environments relative to an ideal test environment.

Note: E1 = Holetta; E2 = Ada-Berga; E3 = Ginchi; E4 = Jeldu; E5 = D/Zeit; E6 = Kulumsa; E7 = Bekoji; E8 = Kuyu/Gebre Guracha; E9 = D/Markos.

4.3.2.9 Genotype stability for grain yield based on univariate analysis

The stability of grain yield and ranking of oat genotypes using the grain yield and 14 stability parameters (12 parametric and 2 nonparametric) are summarized in Table 4.21. The results indicated that the stability of grain yield tested using different stability parameters was highly variable among the studied oat genotypes. According to the stability parameters of SD, the first top four genotypes such as G6, G10, G15, and G20 were stable and low-grain-yielding genotypes, while G9, G10, G15, and G23 were found to perform consistently in different environments based on the stability parameter of ASV. The σ_i^2 and W_i stability parameters yielded similar rank orders, and the first four stable genotypes using these stability parameters were G15, G23, G9, and G4. Similarly, S_{di}^2 and D_{ji} stability parameters had also similar rank orders, and the first four stable genotypes using these two stability parameters were G15, G23, G6, and G9. On the contrary, high-grain-yielding genotypes showed relatively stable performance based on the stability parameters of P_i , B_i , and YSI. Thus, the stable genotypes based on the stability parameter of P_i were G8, G17, G14, G5, G12, G19, G11, G22, and G16. Likewise, G8, G11, G16, G5, G19, G22, G17, G14, and G12

were stable based on B_i stability parameter, while G11, G12, G22, G4, G8, G14, G16, G19, G5, and G17 were stable based on the stability parameter of YSI.

The genotypes were divided into four major groups using the stability and grain yield performance and the number in parentheses indicates the degree of grain yield compared to the grand mean stability value (Table 4.21). Genotype that was closer to unity for B_i and b_i stability parameters; above the mean value for R^2 ; and below mean values for the remaining stability parameters were considered adaptable genotype in all nine environments. Accordingly, a genotype that had a mean grain yield above the grand mean coupled with stable performance was assigned to group I, while a genotype with a mean grain yield that exceeded the grand mean along with unstable performance was assigned to group II. Furthermore, a genotype that had a mean grain yield below the grand mean coupled with wide adaptation in all nine environments was assigned to group III, while a genotype with a mean grain yield below the grand mean in combination with specific environment adaptation was assigned to group IV. Genotypes (G4, G5, G8, G11, G12, G14, G16, G17, G19, and G22) that produced grain yield above the grand mean had stable performance in three (G19) to thirteen (G4) stability parameters were assigned to group I. These genotypes were also assigned to group II on the basis of some of the stability parameters studied. The remaining oat genotypes that produced a mean grain yield below the grand mean were assigned to either group III or group IV.

A genotype with a mean grain yield above the grand mean of yield and stability parameter above the grand mean of stability value based on the stability criteria was considered a stable genotype. Accordingly, G4, which had a mean grain yield above the grand mean, also showed consistent performance based on all the studied stability parameters, except B_i . A high grain yielding genotype (G11) was also considered a stable genotype based on all the studied parameters of stability, except SD and b_i , and G14 was also a high-yielding and stable genotype based on all the parameters of stability, except SD, B_i , and ASV. A genotype (G22) that produced a high mean grain yield was also considered a stable genotype based on all the studied stability parameters, except SD, b_i , B_i , and $S_i^{(1)}$. Similarly, G12 was a high grain yielder and stable genotype based on SD, b_i , $S_i^{(1)}$, ASV, CV_i , P_i , $S_i^{(2)}$, and YSI stability parameters. Furthermore, G8 was a high grain yielder and stable genotype based on CV_i , B_i , P_i , $S_i^{(1)}$, $S_i^{(2)}$, YSI, and R^2 , while G16 was a high yielder and stable genotype based on R^2 , B_i , P_i , $S_i^{(1)}$, and YSI. Moreover, G19, G17, and G5 were high grain yielders and stable

genotypes based on B_i , P_i , and YSI; CV_i and P_i ; and B_i and P_i stability parameters, respectively.

Table 4.21 Ranking and stability of the 24 oat genotypes by mean grain yield and stability parameters

GEN	GY	Rank	SD	Rank	CV_i	Rank	b_i	Rank	$S_{d_i}^2$	Rank	R^2	Rank	σ_i^2	Rank	B_i	Rank
G1	3.4 ^{d-f}	19	1.32	12 (III)	38.66	19 (IV)	0.78	11 (III)	0.93	19 (IV)	0.42	23 (IV)	1.12	19 (IV)	-0.22	18 (IV)
G2	3.5 ^{d-f}	15	1.09	6 (III)	31.34	7 (III)	0.81	9 (III)	0.24	11 (III)	0.66	13 (III)	0.45	8 (III)	-0.19	17 (IV)
G3	3.0 ^{fg}	22	1.09	5 (III)	36.33	14 (IV)	0.73	16 (IV)	0.41	13 (III)	0.54	20 (IV)	0.67	13 (III)	-0.28	20 (III)
G4	3.9 ^{cd}	10	1.27	10 (I)	32.43	8 (I)	1.03	1 (I)	0.18	7 (I)	0.78	7 (I)	0.35	4 (I)	0.03	13 (II)
G5	4.9 ^{ab}	5	1.81	23 (II)	37.25	16 (II)	1.27	15 (II)	1.28	22 (II)	0.60	16 (II)	1.50	22 (II)	0.27	5 (I)
G6	3.2 ^{e-g}	20	0.80	1 (III)	24.99	1 (III)	0.57	24 (IV)	0.06	3 (III)	0.61	15 (IV)	0.48	10 (III)	-0.43	24 (III)
G7	3.8 ^{cd}	11	1.18	8 (III)	30.65	6 (III)	0.77	12 (III)	0.54	16 (IV)	0.52	21 (IV)	0.76	15 (IV)	-0.23	19 (IV)
G8	5.2 ^a	1	1.83	24 (II)	34.99	12 (I)	1.38	23 (II)	0.97	20 (II)	0.69	11 (I)	1.29	20 (II)	0.38	1 (I)
G9	3.5 ^{d-f}	17	1.32	14 (III)	38.32	18 (IV)	1.10	4 (IV)	0.12	4 (III)	0.83	5 (III)	0.30	3 (III)	0.10	10 (IV)
G10	3.8 ^{cd}	12	0.99	3 (III)	26.42	2 (III)	0.63	22 (IV)	0.37	12 (III)	0.48	22 (IV)	0.71	14 (IV)	-0.37	23 (III)
G11	4.7 ^b	7	1.62	18 (II)	34.69	11 (I)	1.37	21 (II)	0.20	8 (I)	0.86	1 (I)	0.55	11 (I)	0.37	2 (I)
G12	5.0 ^{ab}	3	1.32	13 (I)	26.63	3 (I)	0.90	5 (I)	0.67	18 (II)	0.56	18 (II)	0.83	16 (II)	-0.10	14 (II)
G13	2.9 ^g	23	1.10	7 (III)	37.66	17 (IV)	0.82	8 (III)	0.24	10 (III)	0.67	12 (III)	0.44	7 (III)	-0.18	16 (IV)
G14	4.8 ^{ab}	6	1.40	15 (II)	29.03	4 (I)	1.06	3 (I)	0.47	14 (I)	0.69	10 (I)	0.63	12 (I)	0.07	11 (II)
G15	3.5 ^{d-f}	16	1.05	4 (III)	30.31	5 (III)	0.87	6 (III)	-0.01	1 (III)	0.83	4 (III)	0.19	1 (III)	-0.13	15 (IV)
G16	4.1 ^c	9	1.71	20 (II)	41.87	21 (II)	1.36	20 (II)	0.56	17 (II)	0.77	8 (I)	0.88	18 (II)	0.36	3 (I)
G17	5.2 ^a	2	1.77	21 (II)	34.01	10 (I)	1.20	10 (I)	1.41	24 (II)	0.55	19 (II)	1.57	23 (II)	0.20	8 (II)
G18	3.4 ^{d-f}	18	1.44	16 (IV)	42.01	22 (IV)	1.18	7 (IV)	0.23	9 (III)	0.81	6 (III)	0.43	6 (III)	0.18	9 (IV)
G19	4.9 ^{ab}	4	1.80	22 (II)	36.85	15 (II)	1.24	14 (II)	1.39	23 (II)	0.57	17 (II)	1.58	24 (II)	0.24	6 (I)
G20	1.8 ^h	24	0.94	2 (III)	51.90	24 (IV)	0.68	17 (IV)	0.17	5 (III)	0.62	14 (IV)	0.47	9 (III)	-0.32	21 (III)
G21	3.5 ^{d-f}	14	1.67	19 (IV)	47.77	23 (IV)	1.33	18 (IV)	0.54	15 (IV)	0.76	9 (III)	0.83	17 (IV)	0.33	4 (III)
G22	4.2 ^c	8	1.47	17 (II)	35.31	13 (I)	1.23	13 (II)	0.18	6 (I)	0.84	3 (I)	0.41	5 (I)	0.23	7 (II)
G23	3.7 ^{c-e}	13	1.23	9 (III)	33.33	9 (III)	1.04	2 (III)	0.04	2 (III)	0.85	2 (III)	0.21	2 (III)	0.04	12 (IV)
G24	3.1 ^{fg}	21	1.28	11 (III)	41.77	20 (IV)	0.66	19 (IV)	1.04	21 (IV)	0.32	24 (IV)	1.32	21 (IV)	-0.34	22 (III)
Mean	3.9	-	1.35	-	35.61	-	1.00	-	0.51	-	0.66	-	0.75	-	0.24	-
GEN	D_{ji}	Rank	W_i	Rank	P_i	Rank	$S^{(1)}_i$	Rank	$S^{(2)}_i$	Rank	IPCA1	IPCA2	ASV	Rank	YSI	Rank
G1	1.15	19 (IV)	8.49	19 (IV)	4.77	19 (IV)	2.44	23 (IV)	50.41	23 (IV)	-0.65	-0.25	1.74	20 (IV)	39	13 (IV)
G2	0.46	11 (III)	3.58	8 (III)	4.03	16 (IV)	1.33	13 (IV)	18.88	8 (III)	-0.37	0.11	0.98	13 (III)	28	9 (IV)
G3	0.63	13 (III)	5.13	13 (III)	4.99	21 (IV)	1.47	15 (IV)	24.25	12 (III)	0.15	0.45	0.60	5 (III)	27	8 (IV)
G4	0.40	7 (I)	2.79	4 (I)	2.83	9 (I)	0.93	6 (I)	18.16	7 (I)	-0.24	-0.10	0.65	6 (I)	16	2 (I)
G5	1.50	22 (II)	11.23	22 (II)	0.86	4 (I)	1.50	16 (II)	41.25	19 (II)	0.71	0.35	1.92	22 (II)	27	8 (II)
G6	0.28	3 (III)	3.76	10 (III)	4.82	20 (IV)	1.56	18 (IV)	26.25	14 (III)	-0.36	0.14	0.96	12 (III)	32	11 (IV)
G7	0.76	16 (IV)	5.79	15 (III)	3.57	13 (IV)	1.78	21 (IV)	35.50	17 (IV)	-0.58	0.13	1.55	19 (IV)	30	10 (IV)
G8	1.19	20 (II)	9.72	20 (II)	0.39	1 (I)	0.92	5 (I)	25.94	13 (I)	0.74	-0.15	1.95	23 (II)	24	5 (I)
G9	0.34	4 (III)	2.47	3 (III)	3.85	15 (IV)	0.69	3 (III)	13.00	3 (III)	-0.17	-0.22	0.51	4 (III)	21	4 (III)
G10	0.58	12 (III)	5.42	14 (III)	3.21	12 (IV)	1.25	12 (III)	26.84	16 (III)	-0.09	-0.04	0.25	2 (III)	14	1 (III)
G11	0.42	8 (I)	4.26	11 (I)	1.15	7 (I)	1.12	9 (I)	19.09	9 (I)	0.23	-0.36	0.72	7 (I)	14	1 (I)
G12	0.89	18 (II)	6.30	16 (II)	0.89	5 (I)	1.08	8 (I)	14.62	4 (I)	0.32	-0.39	0.94	11 (I)	14	1 (I)
G13	0.46	10 (III)	3.50	7 (III)	5.70	23 (IV)	1.19	10 (III)	16.38	5 (III)	-0.41	-0.16	1.10	17 (IV)	40	15 (IV)
G14	0.69	14 (I)	4.88	12 (I)	0.72	3 (I)	0.61	2 (I)	4.780	2 (I)	0.51	-0.19	1.36	18 (II)	24	5 (I)
G15	0.21	1 (III)	1.64	1 (III)	3.75	14 (IV)	1.07	7 (III)	16.66	6 (III)	-0.09	0.14	0.28	3 (III)	19	3 (III)
G16	0.77	17 (II)	6.68	18 (II)	2.84	10 (I)	1.22	11 (I)	47.72	21 (II)	-0.33	-0.65	1.09	16 (II)	25	6 (I)
G17	1.63	24 (II)	11.75	23 (II)	0.43	2 (I)	1.71	20 (II)	39.44	18 (II)	0.81	0.14	2.16	24 (II)	26	7 (II)
G18	0.44	9 (III)	3.42	6 (III)	4.11	17 (IV)	1.54	17 (IV)	20.78	11 (III)	-0.32	0.04	0.85	9 (III)	27	8 (IV)
G19	1.61	23 (II)	11.81	24 (II)	0.99	6 (I)	1.56	18 (II)	45.75	20 (II)	0.63	-0.46	1.74	21 (II)	25	6 (I)
G20	0.39	5 (III)	3.69	9 (III)	9.62	24 (IV)	0.06	1 (III)	0.12	1 (III)	-0.36	0.35	1.02	15 (III)	39	14 (IV)
G21	0.75	15 (IV)	6.31	17 (IV)	4.20	18 (IV)	2.14	22 (IV)	49.78	22 (IV)	-0.34	-0.01	0.91	10 (III)	24	5 (III)
G22	0.40	6 (I)	3.29	5 (I)	1.83	8 (I)	1.35	14 (II)	26.44	15 (I)	0.30	0.21	0.82	8 (I)	16	2 (I)
G23	0.26	2 (III)	1.82	2 (III)	3.14	11 (IV)	0.78	4 (III)	19.78	10 (III)	-0.09	-0.10	0.25	1 (III)	14	1 (III)
G24	1.26	21 (IV)	9.94	21 (IV)	5.23	22 (IV)	1.67	19 (IV)	62.38	24 (IV)	0.01	1.00	1.00	14 (III)	35	12 (IV)
Mean	0.73	-	5.74	-	3.25	-	1.29	-	27.68	-	0.37	0.26	1.06	-	25	-

GY = grain yield; SD = standard deviation; CV_i = Francis and Kannenberg's (1978) coefficient of variability; b_i = Eberhart and Russell's (1966) regression coefficient; $S_{d_i}^2$ = Eberhart and Russell's (1966) deviation from regression; R^2 = Pinthus (1973) coefficient of determination; σ_i^2 = Shukla's (1972) stability variance; B_i = Perkins and Jinks (1968) adjusted linear regression coefficient; D_{ji} = Hernandez *et al.* (1993) desirability index; W_i = Wricke's (1962) ecovalence; P_i = Lin and Binns's (1988) genotypic superiority index; $S^{(1)}_i$ = average absolute rank difference of genotype on the environment; $S^{(2)}_i$ = Variance ranges of environments; IPCA1 = interaction principal component axis 1; IPCA2 = interaction principal component axis 2; ASV = AMMI stability value; YSI = yield stability index; the number in parenthesis indicate the stability group (I = high yield and stable; II = high yield and unstable; III = low yield and stable; IV = low yield and unstable).

4.3.2.10 Associations among grain yield stability parameters

A correlation analysis was performed based on parametric and nonparametric stability statistics using Spearman's rank coefficient for each oat genotype (Table 4.22). The result indicated that the grain yield had a remarkable variation and positive association with P_i ($r = 0.98$), B_i ($r = 0.67$), and YSI ($r = 0.57$). However, the grain yield was significantly but

inversely correlated with SD ($r = -0.72$), S_{di}^2 and D_{ji} ($r = -0.48$), and σ_i^2 and W_i ($r = -0.42$) stability parameters. The associations between S_{di}^2 and D_{ji} and also between σ_i^2 and W_i were perfectly positive. The correlations of S_{di}^2 with σ_i^2 , W_i , ASV, and R^2 and also the relations of R^2 with σ_i^2 , W_i , and D_{ji} were very highly significant and positive. The observed associations of ASV with D_{ji} , σ_i^2 , and W_i and also $S^{(2)}_i$ with $S^{(1)}_i$, σ_i^2 , and W_i were very highly significant and positive. Positive and very highly significant associations were also observed between P_i and B_i and also D_{ji} with W_i and σ_i^2 . On the other hand, SD had very highly significant but inverse relations with B_i and P_i stability parameters.

Table 4.22 Spearman's correlation coefficients among ranks of grain yield and stability parameters for 24 oat genotypes tested in nine environments

Parameter	GY	SD	CV _i	b _i	S _{di} ²	R ²	σ _i ²	B _i	D _{ji}	W _i	P _i	S ⁽¹⁾ _i	S ⁽²⁾ _i	ASV	YSI
GY	1.00														
SD	-0.72***	1.00													
CV _i	0.35 ^{NS}	0.34 ^{NS}	1.00												
b _i	0.03 ^{NS}	0.08 ^{NS}	0.16 ^{NS}	1.00											
S _{di} ²	-0.48*	0.60**	0.18 ^{NS}	0.26 ^{NS}	1.00										
R ²	0.11 ^{NS}	-0.18 ^{NS}	-0.06 ^{NS}	0.30 ^{NS}	0.64***	1.00									
σ _i ²	-0.42*	0.53**	0.18 ^{NS}	0.50*	0.94***	0.67***	1.00								
B _i	0.67***	-0.90***	-0.29 ^{NS}	-0.01 ^{NS}	-0.26 ^{NS}	0.55**	-0.20 ^{NS}	1.00							
D _{ji}	-0.48*	0.60**	0.18 ^{NS}	0.26 ^{NS}	1.00***	0.64***	0.94***	-0.26 ^{NS}	1.00						
W _i	-0.42*	0.53**	0.18 ^{NS}	0.50*	0.94***	0.67***	1.00***	-0.20 ^{NS}	0.94***	1.00					
P _i	0.98***	-0.68***	0.39 ^{NS}	0.12 ^{NS}	-0.38 ^{NS}	0.19 ^{NS}	-0.30 ^{NS}	0.65***	-0.38 ^{NS}	-0.30 ^{NS}	1.00				
S ⁽¹⁾ _i	0.07 ^{NS}	0.16 ^{NS}	0.17 ^{NS}	0.33 ^{NS}	0.51*	0.54**	0.54**	0.10 ^{NS}	0.51*	0.54**	0.19 ^{NS}	1.00			
S ⁽²⁾ _i	-0.13 ^{NS}	0.38 ^{NS}	0.28 ^{NS}	0.52**	0.61**	0.44*	0.69***	-0.13 ^{NS}	0.61**	0.69***	-0.02 ^{NS}	0.82***	1.00		
ASV	-0.34 ^{NS}	0.48*	0.20 ^{NS}	0.21 ^{NS}	0.75***	0.46*	0.73***	-0.23 ^{NS}	0.75***	0.73***	-0.28 ^{NS}	0.34 ^{NS}	0.35 ^{NS}	1.00	
YSI	0.57**	-0.23 ^{NS}	0.42*	0.20 ^{NS}	0.23 ^{NS}	0.51*	0.26 ^{NS}	0.41*	0.23 ^{NS}	0.26 ^{NS}	0.60**	0.42*	0.21 ^{NS}	0.56**	1.00

GY = grain yield; SD = standard deviation; CV_i = Francis and Kannenberg's (1978) coefficient of variability; b_i = Eberhart and Russell's (1966) regression coefficient; S_{di}² = Eberhart and Russell's (1966) deviation from regression; R² = Pinthus (1973) coefficient of determination; σ_i² = Shukla's (1972) stability variance; B_i = Perkins and Jinks (1968) adjusted linear regression coefficient; D_{ji} = Hernandez *et al.* (1993) desirability index; W_i = Wricke's (1962) ecovalence; P_i = Lin and Binns's (1988) genotypic superiority index; S⁽¹⁾_i = average absolute rank difference of genotype on the environment; S⁽²⁾_i = Variance ranges of environments; IPCA1 = interaction principal component axis 1; IPCA2 = interaction principal component axis 2; ASV = AMMI stability value; YSI = yield stability index. *, **, and *** indicate significance at $P < 0.05$; $P < 0.01$; and $P < 0.001$, respectively. Note: The green, orange, and yellow colors indicate the strength of correlation; green color is positively correlated; green to light green color indicate strong to weak positive correlation; orange color is negatively correlated; orange to light orange color indicate strong to weak negative correlation; and yellow color is positively and negatively correlated; yellow to light yellow color indicate no correlation to very weak correlation.

4.3.2.11 Principal component analysis of the stability parameters

Principal component analysis (PCA) indicated that the first four principal components (PCs) with eigenvalues higher than unity accounted for 90.1% of the overall variation among 24 oat genotypes studied for 14 stability parameters. Of these, the first two PCs explained 71.0% of the entire variation in stability parameters. The biplot for the first two PCs of 14 stability parameters in oat genotypes is shown in Figure 4.22. The results indicated that the studied stability parameters were divided into three major groups using the length, direction, and proximity among the vector lines. The first group comprised SD, which had positive eigenvectors for both PCs, while negative PC2 and positive PC1 values were observed for

S_{di}^2 , D_{ji} , W_i , σ_i^2 , ASV, and $S^{(2)}_i$. The second group had negative PC2 and positive PC1 values for b_i , $S^{(1)}_i$, R^2 , and CV_i . The third group consisted of grain yield and three stability parameters (P_i , B_i , and YSI) that had negative factor loadings (GY, P_i , and B_i) for both PCs, while YSI was negative for the second PC and positive for the first PC. Based on the first two PCs, all the studied parameters of stability had factor loadings above 30%, except CV_i , b_i , $S^{(1)}_i$, and $S^{(2)}_i$. The contribution of σ_i^2 , W_i , S_{di}^2 , and D_{ji} stability parameters was high for the first PC, while P_i , GY, YSI, B_i , R^2 , and SD had a high contribution for the second PC. The stability parameters in the first and second groups, which did not have a strong association with the mean grain yield, had static/biological stability, while the stability parameters in the third group, which were strongly correlated with grain yield, had dynamic/agronomic stability.

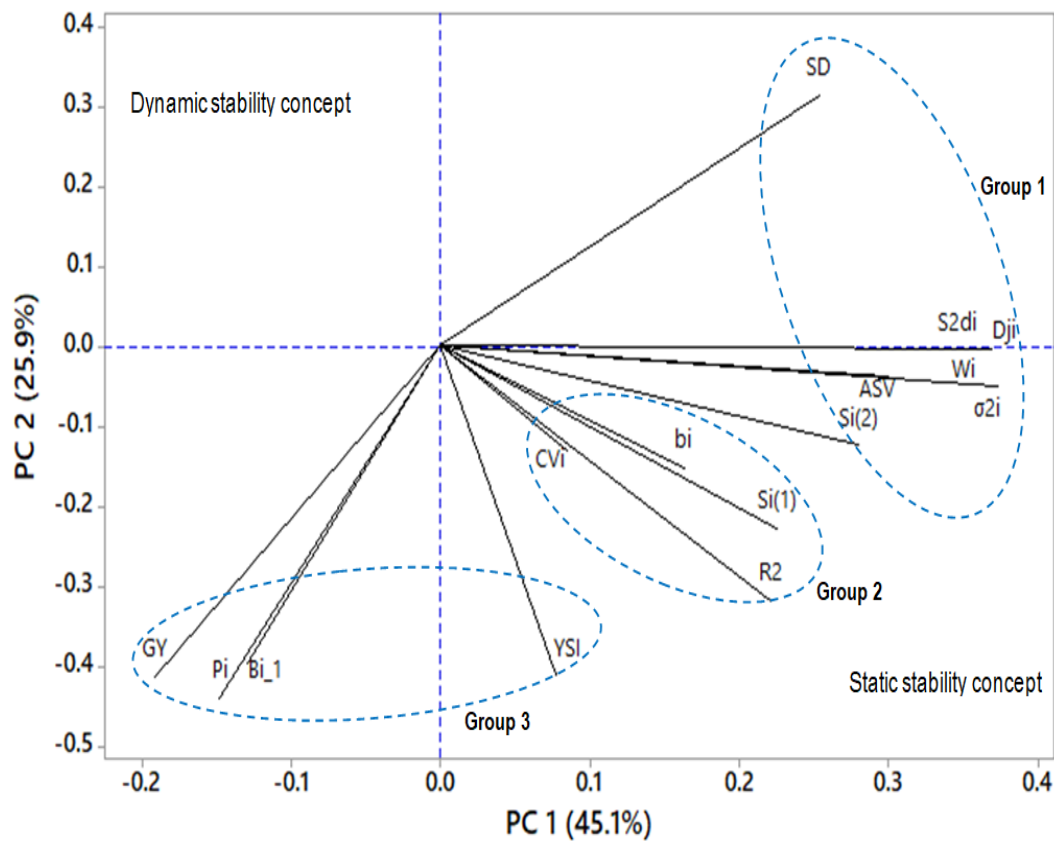


Figure 4.22 Biplot of PC1 and PC2 of the spearman's rank correlation matrix of the 14 stability parameters with grain yield

Note: GY = grain yield; SD = standard deviation; CV_i = Francis and Kannenberg's (1978) coefficient of variability; b_i = Eberhart and Russell's (1966) regression coefficient; S_{di}^2 = Eberhart and Russell's (1966) deviation from regression; R^2 = Pinthus (1973) coefficient of determination; σ_i^2 = Shukla's (1972) stability variance; B_i = Perkins and Jinks (1968) adjusted linear regression coefficient; D_{ji} = Hernandez *et al.* (1993) desirability index; W_i = Wricke's (1962) ecovalence; P_i = Lin and Binns's (1988) genotypic superiority index; $S^{(1)}_i$ = average absolute rank difference of genotype on the environment; $S^{(2)}_i$ = Variance ranges of environments; **IPCA1** = interaction principal component axis 1; **IPCA2** = interaction principal component axis 2; ASV = AMMI stability value; YSI = yield stability index.

4.4 Discussion

4.4.1 Genotypes for forage yield, yield components, and nutritive value

4.4.1.1 Analysis of variance and genotypic performance

The pooled data analysis of variance indicated that genotype (G), environment (E), and their interaction (GEI) effects were significant for fodder yield, all measured agro-morphological traits and fodder nutritional qualities except ash content of the genotypic main effect. The difference in fodder yield among oat genotypes might be associated with the existence of inherent genetic variability among genotypes. The variations in fodder dry matter yield among oat genotypes have been also reported by different scholars (Fekede, 2004; Getnet *et al.*, 2004; Ashenafi, 2018; Tessema and Getinet, 2020; Gezahagn *et al.*, 2021). Due to the presence of inherent genetic variability among the genotypes, the performance of oat genotypes varied significantly for measured traits. The result of significant variations among oat genotypes in this study is also in line with the findings of Getnet *et al.* (2004), Amanullah and Stewart (2013), Ashenafi (2018), Tessema and Getinet (2020), Gezahagn *et al.* (2021), who reported that oat genotypes varied with fodder dry matter yield.

The performance of genotypes for measured traits and nutritive values were so variable across environments indicating that the environments are diverse due to variations in edaphic, biotic, and abiotic factors. For instance, due to the presence of wide altitudinal variation (1850-2800 meters above sea level) among the environments, the amount and distribution of annual precipitation as well as the minimum and maximum temperatures of the study areas were so different. Furthermore, the edaphic factors such as soil pH, organic carbon, total nitrogen, available phosphorus, cation exchange capacity, and proportions of soil particles (sand, silt, and clay contents) were variable among environments. Accordingly, the effect of environment on the performance of oat genotypes for fodder yield was the highest followed by the interaction (GEI) and genotype effects. The contribution of the environment to the total fodder yield variation was about seven times higher than the genotypic main effect in oat genotypes, indicating that the variations in environmental factors were so diverse. Similarly, large environmental effects followed by GEI and genotype effects have been reported on different crops (Mehari *et al.*, 2015; Melkamu *et al.*, 2015; Al-Naggar *et al.*, 2018; Irfan, 2018; Amare *et al.*, 2019; Zamalotshwa *et al.*, 2019; Atinkut *et al.*, 2022). The observed variation in fodder dry matter yield among the tested oat genotypes across environments is in close conformity with the findings of Ashenafi (2018)

and Gezahagn *et al.* (2021). Moreover, the effect of environmental variations on many crops has also been reported by many scholars (Gauch and Zobel, 1997; Kaya *et al.*, 2006; Legesse *et al.*, 2015; Aklilu *et al.*, 2021; Gezahagn *et al.*, 2021).

The GEI effect varied significantly for the fodder yield performance of oat genotypes. The magnitude of the GEI sum of squares was twice larger than the genotype sum of squares, indicating that the fodder yield performance of oat genotypes differed across environments. Significant GEI for fodder dry matter yield was also reported in sorghum (Rakshit *et al.*, 2012; Aklilu *et al.*, 2021), and in oat (Abuye *et al.*, 2020; Gezahagn *et al.*, 2021). Due to the existence of significant GEI, the genotypes are changing their rank order for fodder yield performance under changing environmental conditions. The rank order change of the genotypes for fodder yield across environments could be attributed due to the differential influence of environment on oat fodder yield and/or the differential response of oat genotypes for various growing environmental conditions. Different research studies also indicated that a large proportion of variations attributed to environment followed by GEI and genotype effects in different crops (Melkamu *et al.*, 2015; Kadhem and Baktash, 2016; Mekonnen *et al.*, 2017; Irfan, 2018). The type of interaction observed in this study was cross-over type because the genotypes changed their rank order under different environments. When the genotypes changed their rank order for yield performance across environments due to the presence of significant GEI, the selection of top yielding with widely adaptable genotypes is very difficult (Ebdon and Gauch, 2002; Matus *et al.*, 2003; Gauch, 2006; Kaya *et al.*, 2006). Significant GEI indicates the differential response of genotypes across environments and the selection process is more complicated under its presence. In the presence of significant GEI, the target environments may need to be classified into mega-environments (Ayalew *et al.*, 2018) and the selection of superior genotypes for each clustered environment is very important to improve yield (Romagosa and Fox, 1993). The existence of a higher magnitude of GEI causes unstable performance of genotypes across environments and complicates the selection and recommendation of genotypes in a specified environment. The stability analysis using different stability statistics is very important when the GEI effect is significant and the crossover type of interaction (Bose *et al.*, 2014a; Legesse *et al.*, 2015; Parimala *et al.*, 2019).

4.4.1.2 Performance of genotypes across environments

Significant variation was observed among oat genotypes for all measured agro-morphological traits. The top fodder dry matter yield-producing genotypes (15 genotypes)

had mean advantages of 21.4% for NLFH, 11.4% for LLFH, 15.1% for PHFH, 5.7% for DFH, and 11.8% for FYPR over the low-fodder producing genotypes (9 genotypes). Furthermore, the LDMY for the top fodder yielder genotypes had mean advantages of 26.5% while the SDMY and PDMY had 23.7 and 8.1% advantages over the low-fodder yielder genotypes, respectively. On the contrary, the NTPP for low-fodder yielder genotypes had a mean advantage of 7.5% over the top fodder yielder genotypes. Oat genotypes with taller PHFH, late maturity for DFH, and a high NLFH in this study could produce better fodder dry matter yield. This might be associated with better utilization of growth resources (Amanullah *et al.*, 2004; Lodhi *et al.*, 2009). The cultivation of late-maturing genotypes under optimum growing conditions gives more time to utilize the growth resources efficiently for the production of maximum yield. The NTPP in this study contributed less to fodder yield which could be attributed to high intra and inter tillers competition for growth resources. Significant variations in oat genotypes were also reported for the number of leaves (Naeem *et al.*, 2005; Khan *et al.*, 2014; Gebremedhn *et al.*, 2015), for the number of tillers per plant (Arif *et al.*, 2002; Fekede, 2004; Khan *et al.*, 2014), for plant height at forage harvest (Hussain *et al.*, 2005; Naeem *et al.*, 2006; Ayub *et al.*, 2011; Dawit and Mulusew, 2017), and for days to forage harvest (Fekede, 2004; Tessema and Getinet, 2020).

The herbage nutritive values of oat genotypes were significant for all measured quality traits except the ash content of the fodder yield. High fodder dry matter yield-producing genotypes had better mean CPY, DY, and ash content compared to the mean of low-fodder yield-producing genotypes. On the other hand, low-fodder yield-producing genotypes had better mean CP, IVDMD, and low mean fiber contents (NDF and ADF) while the ADL was higher compared to high fodder yield producing genotypes. The occurrence of low mean CP content in high fodder dry matter yield-producing genotypes might be associated with dilution effects. The mean IVDMD of high fodder dry matter yield-producing genotypes was low compared to low fodder yield-producing genotypes. This might be associated with the presence of high fiber contents (NDF and ADF) and low CP in high fodder-producing genotypes. Fekede *et al.* (2007) reported that shorter and early maturing oat varieties have higher CP content when compared to longer and late maturing varieties. Aklilu *et al.* (2021) also reported that early maturing fodder sorghum varieties accumulated low dry matter yield and less dilution of the CP concentration due to hastened growth and development which resulted in higher CP content. The CP concentration of fodder is directly proportional to earliness in maturity and low concentration of dry matter yield to reduce the dilution process

(Bhattarai *et al.*, 2019). The result of this study showed that late maturing, tall growing, and high fodder yield producing oat genotypes had low CP and IVDMD while higher NDF and ADF contents compared to early maturing, short growing, and low fodder yield producing genotypes. This result is also in line with the findings of Prakash *et al.* (2010) in sorghum, Govintharaj *et al.* (2018) in pearl millet, and Aklilu *et al.* (2021) in forage sorghum varieties, who reported that the NDF content is lower in low dry matter yield producing varieties which had short plant height and early maturity. The higher IVDMD in low fodder dry matter producing genotypes might be associated with high CP and lower fiber contents (NDF and ADF). This result is also confirmed by other reports (Govintharaj *et al.*, 2018; Aklilu *et al.*, 2021). Generally, due to the dilution effects, higher fodder yield-producing genotypes usually have lower CP concentration. So, the animals fed with high fodder yield-producing genotypes should be supplemented by high nutritional quality feed (i.e. agro-industrial byproducts) to satisfy their nutritional requirements for better growth and productivity.

4.4.1.3 Genotypes evaluation for fodder yield based on AMMI

4.4.1.3.1 Evaluation of genotypes for fodder yield based on AMMI

The genotype, environment and GEI effects of the AMMI analysis of variance also revealed significant variation for fodder dry matter yield. The environment's main effect had a predominant contribution to the total variation and it accounted for 67.45% while the genotype and GEI effects explained 9.82 and 22.73% of the total variation, respectively. The higher contribution of the environment on the total variation of fodder dry matter yield indicates the presence of wide variability among the testing environments. The magnitude GEI sum of squares was more than two-fold than that of the genotype main effect indicating that there were remarkable variations in genotypic response for fodder yield across environments. High fodder yield difference explained by environment followed by GEI indicated that the environments were diverse, with remarkable variations among environments causing most of the difference in fodder yield. Furthermore, significant variation of genotype indicates differential fodder yield performance among genotypes tested across environments. Various studies also indicated that a large proportion of the variations attributed to environments followed by GEI and genotype effects in different crops (Tamene *et al.*, 2013; Kadhem and Baktash, 2016; Irfan, 2018; Mizan *et al.*, 2019; Wondimu *et al.*, 2022). The GEI effect was further partitioned into different AMMI-IPCA's and the result disclosed that only the first two components contributed more to fodder yield differences in

oat genotypes. This indicates that the first two AMMI-IPCA's had a remarkable contribution to the total variation of the GEI effect (Legesse *et al.*, 2015; Esayas *et al.*, 2019; Hassan *et al.*, 2022). According to Gauch *et al.* (2008), the AMMI model with the first two IPCA's is sufficient for cross-validation of the yield variation explained by GEI. Wondimu *et al.* (2022) also stated that the first two IPCA's are adequate to describe the two-dimensional AMMI biplot for further analysis of genotype stability.

The testing environments are categorized into favorable and unfavorable environments for oat fodder production using the AMMI model analysis. According to Miriam *et al.* (2019) and Yirga *et al.* (2021), a favorable environment is the one which gives the mean yield of the environment exceeds the grand mean of the environment while unfavorable environment has less mean value compared to the grand mean of the environments. Thus, E2, E4, E6, and E9 environments were considered favorable environments while E1, E3, E5, E7, and E8 were unfavorable environments to cultivate the studied oat genotypes for fodder production. Among the environments, E3 was the most unfavorable environment which produced about 47.2% less fodder yield compared to the grand mean of the environments. The higher fodder yield reductions at E3 might be associated with the heavy vertisol nature of the soil which could hamper the growth and development of the crop due to the high waterlogging problem. Among the first top four selected genotypes for fodder yield using the AMMI model, G6, G2, and G23 were selected for cultivation both in favorable and unfavorable environments. On the contrary, G3, G10, and G7 were promising genotypes in unfavorable environments while G9 performed better in favorable environments.

4.4.1.3.2 Evaluation of genotypes for fodder yield based on AMMI-1

In the AMMI-1 biplot analysis, the fodder dry matter yield for the genotype and environment was plotted against the first IPCA scores of the genotypes and environments to visualize the GEI interaction pattern graphically (Kaya *et al.*, 2002). The vertical line (ordinate) that passed through the biplot origin was the grand mean of the genotypes while the horizontal line (abscissa) that passed through zero IPCA-1 score indicates the interaction pattern. Genotypes and environments located on the right side of the ordinate (y-axis) have higher yields while their corresponding low yielding counterparts were located at the left side of the ordinate (Ngeve and Bouwkamp, 1993; Banik *et al.*, 2010; Irfan, 2018; Ahmed *et al.*, 2021). In this study, G13, G24, G18, G19, G15, G9, G23, G11, G1, G10, G6, G3, G4, G7, and G2 genotypes and E2 and E6 environments were located at the right side of the ordinate

indicating both these genotypes and environments had superior performance in fodder dry matter yield compared to the remaining genotypes and environments which were located at the left side of the ordinate. In the AMMI-1 biplot model, the genotypes and environments located on the same parallel line, relative to the ordinate, have similar yield performance while genotypes and environments located on the same parallel line, relative to the abscissa, have similar interaction pattern (Alberts, 2004; Kilic, 2014; Wondimu *et al.*, 2022). For instance, G13, G24, G15, G11, and G1 were located on the same ordinate line indicating these genotypes had similar fodder yield performance while each group of G24 and G18; G1 and G6; and G4, G7, and G2 were located on the same abscissa line indicating that these grouped genotypes had similar intra group but different inter-group interaction patterns.

Genotypes and environments which have similar signs of the first IPCA scores interact positively and these environments are favorable for genotypes having similar signs of the first IPCA scores with environments (Esnart *et al.*, 2021). Accordingly, high fodder-yielding genotypes such as G13, G24, G18, G19, G15, and G9 had positive IPCA-1 scores and interact positively with E2 and E6 environments indicating that both these environments were more favorable for the above genotypes while E1, E3, E7, and E8 environments which located at the opposite side were unfavorable for these genotypes. On the other hand, the remaining high fodder-yielding genotypes like G23, G11, G1, G4, G7, G2, G3, G10, and G6 had negative IPCA-1 scores with E4 and E9 environments indicating that these genotypes and environments were interact positively and both these environments were more favorable for the above genotypes while E5 which located at the opposite side was unfavorable for these genotypes. Among the studied genotypes, G6 was located relatively far from the grand mean while the remaining genotypes were located near the grand mean indicating that the genotypes had less contribution to the total variation (Mizan *et al.*, 2019). However, the environments were relatively scattered on the biplot indicating that the contribution of environment for the total variation was higher compared to the genotype.

The stability of genotypes should be considered simultaneously with yield performance during the selection of genotypes (Naroui *et al.*, 2013; Hossein *et al.*, 2020). The extent of the genotypes' IPCA-1 scores on the biplot indicates the relative contributions of genotypes to the total GEI variance (Kilic, 2014). Genotypes located closer to zero IPCA-1 scores on either side of the abscissa had low contribution to the total GEI variation and these genotypes had stable performance. On the contrary, genotypes with high IPCA-1 scores on either side of the abscissa had high contribution to the total variance of GEI and these

genotypes were unstable across environments. Ebdon and Gauch (2002) also stated that genotypes with IPCA-1 scores closer to zero indicated wide adaptation while genotypes with high IPCA-1 scores had specific adaptation. The genotypes viz. G11, G23, G9, G1, and G10 produced fodder yield above the grand mean and had low scores for the first IPCA indicating that these genotypes contributed less to the total GEI variance and perform consistently across environments while G12, G5, G22, G17, and G20 produced low yield with stable performance. Furthermore, low-yielding genotypes like G14 and high-yielding genotypes such as G15, G3, G6, G19, G7, G4, and G2 had intermediate IPCA-1 scores suggesting that these genotypes had relatively stable performance across environments. However, high-yielding genotypes (G13, G24, and G18) and low-yielding genotypes (G8, G16, and G21) had high IPCA-1 scores indicating that these genotypes had high contribution to the total GEI variation and inconsistency in fodder yield performance across environments. The genotypes had positive IPCA-1 scores and attained the maximum fodder yield at E6 followed by E2 while the lowest yield was attained in E3 which had a negative IPCA-1 score suggesting that all the genotypes performed poorly under this environment. The contribution of environments for the total GEI variance is so different and the magnitude of contribution was assessed using the vector length of the environment (Wondimu *et al.*, 2022). Accordingly, E6, E4, E2, and E3 had longer vectors suggesting these environments had high discriminating power with better contribution for the total GEI variance while E5 and E7 had intermediate discriminating ability and moderate contribution to GEI. On the other hand, E1, E8, and E9 had shorter vectors indicating that these environments had low discriminating ability on genotypes performance for fodder yield and low contribution to the total variation of GEI.

4.4.1.3.3 Evaluation of genotypes for fodder yield based on AMMI-2

In the AMMI-2 biplot analysis, the first IPCA scores of genotypes and environments were plotted against the second IPCA scores of genotypes and environments to demonstrate the magnitude of the GEI. The genotypes' distance from the biplot origin indicates the stability of genotypes. Thus, genotypes located closer to the biplot origin are more stable and less interactive with environments and vice versa (Purchase, 1997). The genotypes located closer to the biplot origin were G23, G22, G5, G20, G17, G14, and G12 indicating better stability while G18, G16, G21, G24, and G8 located far from the biplot origin suggested inconsistent performance across environments. On the other hand, G1, G11, G19, G15, G4, G2, G7, G3, G10, G6, G13, and G9 had intermediate distances from the biplot origin indicating average

stability. Genotypes and environments located closer to each other have similar interaction patterns while genotypes and environments located far away from each other have different interaction patterns. Hossein *et al.* (2020) also stated that any genotypes that are close to the environment have specific stability in that environment. Accordingly, G9, G20, G17, G19, and G18 had similar interaction patterns with E5 indicating that these genotypes performed better in this environment while these genotypes performed less at E8, E4, E1, E3, and E7 which were located on the opposite side and had different interaction pattern. Similarly, G14, G5, G15, G24, G8, and G13 had also similar interaction patterns with E2 and E6 suggesting that these genotypes had better performance in these environments while the performance of these genotypes at E9 which was located on the opposite side was poor due to different interaction between E9 and the above genotypes.

The stability performances of the genotypes and environments were variable for AMMI-1 and AMMI-2 biplot analysis. For instance, G11, G1, G9, and G10 were high with better stability performance in AMMI-1 but these high-yielding genotypes were relatively stable in AMMI-2 while the relatively stable genotype (G14) in AMMI-1 had better stability performance in AMMI-2. This indicates that AMMI-2 is more stringent and accurate than AMMI-1 because AMMI-2 is explained by high total variation of GEI than AMMI-1 (Oliveira *et al.*, 2014; Wondimu *et al.*, 2022). The length of the vectors for environments indicates the discriminating ability of the environments. Accordingly, E9, E4, E6, E2, and E7 had longer vector distances from the biplot origin indicating the discriminating ability on the performance of genotypes for fodder dry matter yield was higher compared to others. On the contrary, E8 and E1 were located very close to the biplot origin indicating that these environments had low discriminating power on genotypes for fodder dry matter yield. However, E3 and E5 had intermediate distances from the biplot origin and had average discriminating ability on the genotype performance for fodder yield. Genotypes and environments have similar interaction patterns and interact positively when both have the same sign of IPCA-1 and IPCA-2 scores while genotypes have different signs for the first two IPCA scores with the environments then the genotypes and the environments have different interaction patterns and one interacts negatively with the other. For instance, G9, G18, G20, G17, and G19 interact positively with E5 while E4, E1, E8, E3, and E7 which located on the opposite side of the biplot had different interaction patterns and negatively interact with the above genotypes.

4.4.1.4 Genotypes evaluation for fodder yield based on GGE biplot

4.4.1.4.1 Mean performance and stability of genotypes

The mean fodder dry matter yield performances of oat genotypes grown under different environments were defined using the AEC ordinate of the GGE biplot. Accordingly, the genotypes located on the left side of this ordinate had higher fodder yield while genotypes located on the right side of this ordinate produced a lower fodder yield. Based on the AEC ordinate of the GGE biplot, high fodder-yielding genotypes which located on the left side were G6, G10, G3, G2, G24, G7, G4, G23, G19, G13, G15, and G9. On the other hand, G5 and G22 which were located very far from the right side of the AEC ordinate produced the lowest fodder dry matter yield compared to other genotypes located at the right side of this ordinate. Yan (2001) also reported that the genotypes located closer to the oval (the positive end of the AEC abscissa) have the highest yield while the genotypes located far from this oval on the opposite side have the lowest yield. According to Bhartiya *et al.* (2017), the mean performance of the genotype is measured by AEC abscissa while the stability is represented by AEC ordinate. The lines parallel to the AEC ordinate would help to rank the genotype's stability and genotypes with lower variability or higher stability have a smaller absolute length of projection in either direction from the AEC abscissa and vice versa (Yan *et al.*, 2000; Yan, 2001; Kaya *et al.*, 2006; Farshadfar and Sadeghi, 2014). Accordingly, the projection from the AEC abscissa provides the stability performances of oat genotypes across environments. The longer projection of the genotypes from this abscissa showed a lower stability while genotypes with shorter projections from this abscissa had better stability performance across environments. Consequently, G6, G10, G3, G23, and G9 genotypes that produced higher fodder yield had stable performance. Among high fodder-yielding genotypes, G13 and G24 were the most unstable while G15, G19, G2, G7, and G4 genotypes which produced higher fodder yield had moderate stability. The genotypes located far from the biplot origin are either the best or the poorest or the most unstable. Accordingly, G6 was the best-performing genotype; G5 and G22 were the poorest while G16 was the most unstable genotype.

4.4.1.4.2 Ranking of genotypes relative to the ideal genotype

In the GGE biplot analysis, the fodder dry matter yield performance of oat genotypes was ranked relative to the ideal genotype using the AEC abscissa and various concentric circles. In genotype selection, the stability parameter should be associated with a high mean yield

performance (Yan and Tinker, 2006; Farshadfar *et al.*, 2012a). An ideal genotype has the highest yield and is stable across environments (Yan and Kang, 2003; Kaya *et al.*, 2006; Farshadfar *et al.*, 2012a). According to Yan (2001), an ideal genotype is located at the center of the concentric circles and has the longest vector of all genotypes' projection on the AEC abscissa (the most discriminating) and zero projection on the AEC ordinate (the most representative). The center of the concentric circles was pointed using the arrowed AEC abscissa and the genotype located at the center of the concentric circles or closer to this point is considered an ideal genotype and the performance of the remaining genotypes are ranked relative to this ideal genotype. Consequently, G6 was located at the center of the concentric circles and considered an ideal genotype compared to other genotypes. The genotypes which located closer to the ideal genotype were G10, G3, G2, G23, and G24. These genotypes were considered the most desirable while G16, G5, G22, G17, and G20 were located far from the ideal genotype and considered the least desirable genotypes. An ideal genotype should have both high mean yield performance and high stability across environments and genotypes located closer to the ideal genotype are more desirable than others (Kaya *et al.*, 2006; Yan and Tinker, 2006; Mitrovic *et al.*, 2012; Rakshit *et al.*, 2012; Mesfin and Abush, 2019). On the other hand, genotypes located far from the ideal genotype can be rejected in early breeding cycles while genotypes that are close to the ideal genotype can be considered in further tests (Yang *et al.*, 2009; Esnart *et al.*, 2021).

4.4.1.4.3 Which-won-where and mega environment identification

The studied genotypes and testing environments were classified using the GGE biplot analysis based on the fodder yield performance of oat genotypes and the influence of environments on fodder yield. Based on the 'which-won-where' pattern of the GGE biplot, the vertex genotypes which located far from the biplot origin were G6, G13, G14, G5, G16, and G2. These vertex genotypes constructed a six side polygon while the remaining genotypes were contained within this polygon. The genotypes located at the vertices of the polygon were the most superior or the most inferior in some or all of the environments because they were located farthest from the biplot origin (Yan and Kang, 2003). The genotypes located at the vertices of the polygon generally have the highest fodder dry matter yield at least in one or all testing environments found in the sector. The which-won-where pattern in various studies also indicated that the genotypes located at the vertices of a polygon have better responses to variable environments compared to other genotypes which

contained within a polygon (Gauch and Zobel, 1997; Yan and Tinker, 2006). On the other hand, genotypes located closer to the biplot origin have little contribution to both genotype and GEI while genotypes located far from the biplot origin have large contributions to either genotype or GEI or both (Yan and Tinker, 2006). According to Voltas *et al.* (2002), genotypes located near to the biplot origin are less responsive than the vertex genotypes indicating the general adaptability of genotypes to all environments.

The lines which originated from the center of the GGE biplot are perpendicular to the lines connecting the vertices of the genotypes and classify the genotypes and environments into different sectors (Yan, 2001; Yan and Tinker, 2006; Irfan, 2018; Tazebachew and Cherinet, 2018; Esnart *et al.*, 2021). Accordingly, the studied oat genotypes were grouped into six sectors while the testing environments were clustered into two mega-environments. Based on the which-won-where pattern of the GGE biplot, the target environments were classified into two sectors and the first ME contained E7, E1, E8, E3, E9, E2, and E4 environments. On the other hand, the second ME had E5 and E6 environments. The vertex genotypes in the first ME were G6 and G2 indicating that both genotypes had the highest fodder dry matter yield performance in all or some members of environments in this mega-environment. Similarly, the vertex genotype in the second ME was G13 suggesting that this genotype produced the highest fodder dry matter yield in both testing environments (ME-2). On the other hand, the remaining vertex genotypes (G14, G5, and G16) which did not exist in both MEs and located on the opposite side of these MEs were generally produced the lowest fodder dry matter yield in all or some testing environments. However, to determine the reliable mega-environments for oat fodder production, the identified mega-environments should be verified by repeating the same experiment over years. Kaya *et al.* (2006); Yan and Tinker (2006) also reported that the mega-environment identification should require multi-year data to see the reputability of information over years.

4.4.1.5 Environment evaluation based on GGE biplot

4.4.1.5.1 Relationships among the test environments

The association between the testing environments can be explained using the vector view of the GGE biplot. The cosine of the angle between the vectors of two environments indicates the approximate correlation between environments (Yan 2001; Kaya *et al.*, 2006; Yan and Tinker, 2006; Dehghani *et al.*, 2009; Yan and Holland, 2010; Kendal, 2016). The cosine of the angles between the vectors of the environments in the current study was so variable

suggesting that the correlation among the testing environments was different. According to Yan and Kang (2003), the coefficient of correlation between environments is significantly positive when the cosine of the angles between vectors of the environments is acute ($<90^\circ$) while significant and negative correlation is observed between vectors of environments for obtuse angle ($>90^\circ$). However, a very weak or no correlation is observed between two environments when the vectors of the environments have a right angle (90°) or closer to the right angle (Yan and Tinker, 2006) angle. Based on the correlation analysis, the number of testing environments can be reduced to minimize the cost of experimentation. Before reducing the testing environments, the association among environments should be confirmed over years. The testing cost can be reduced when the environments have close association over years and one or more highly associated environments can be dropped without loss of much information about the genotypes (Yan and Tinker, 2006; Glaz and Kang, 2008; Choukan, 2010; Farshadfar *et al.*, 2011b; Tukamuhabwa *et al.*, 2012; Gupta *et al.*, 2013).

The result showed that the cosine of the angle between the environment vectors of E6 and E5; E1 and E7; and E3 and E9 were very small suggesting that the correlation between these paired environments was very strong and positive. Furthermore, E2 had a strong positive association with E5 and E6 while the correlation among the environmental vectors of E1, E3, E7, E8, and E9 was also significant and positive. On the other hand, the cosine of the angle between E4 and E6 vectors of the environments was very large followed by between E4 and E5 environmental vectors indicating that these paired environments had relatively strong negative associations compared to other environments. However, E2 had a closer to right angle with the environment vectors of E3 and E9 showing that the environment E2 had no association with E3 and E9 environments. Thus, if two environments are positively correlated, the best-yielding genotype in one environment can perform best in the other while if two environments are negatively correlated, the best-yielding genotypes in one environment perform the least in the other environment and vice versa (Yan, 2002; Yan and Kang, 2003).

4.4.1.5.2 Discriminativeness and representativeness of test environments

The vector view of the GGE biplot also indicates the discriminating power and representativeness of the test environments. The longer the vector distance between the marker of the environment and the biplot origin indicates the more discriminating ability of the environment while the longer the absolute length of the projection from the marker of the

environment onto the AEC ordinate shows the less representative the environment (Yan, 2001; Placide *et al.*, 2020). Testing environments with longer vectors and higher PC2 scores have a high discriminating ability on the fodder yield performance of oat genotypes while environments with either longer or shorter vectors coupled with lower PC1 scores or the vectors have a smaller angle with the AEC abscissa indicate the representativeness of the environments. Among the testing environments, E6, E2, E7, E4, E1, and E3 had longer vectors indicating that the discriminating ability of these environments was higher compared to other environments. On the contrary, the discriminating ability of E9 was the least while E8 and E5 had intermediate discriminating ability. Among the testing environments, the most representing environment for fodder yield production of oat genotypes was E8 followed by E7 and E1. On the other hand, the least representative environments were E6, E4, E5, and E2 while E3 and E9 environments were moderately representing the test environments. According to Placide *et al.* (2020), highly discriminative test environments are useful for early-generation variety evaluation and selection. Test environments that are consistently discriminating (informative) provide better information on the performance of genotypes while consistently non-discriminating (non-informative) test environments should not be used as test environments because they provide little information on the performance of genotypes (Yan and Tinker, 2006; Yan *et al.*, 2007).

The smaller angle between the vector of the environments and the AEC abscissa indicates a higher representativeness of the test environments and vice versa (Yan and Tinker, 2006; Asnake *et al.*, 2013; Esnart *et al.*, 2021). The longer projection from the AEC abscissa shows a lower stability or higher variability of the genotypes while highly stable genotypes have a shorter projection from the AEC abscissa (Yan and Kang, 2003; Yan *et al.*, 2007). Among the testing environments, E6, E2, and E4 had longer vectors coupled with larger angles with the AEC abscissa. This indicates that these environments were mainly used to select specifically adapted oat genotypes. However, E7, E1, and E3 environments had longer vectors coupled with smaller angles with the AEC abscissa suggesting that these environments were used to select a high fodder yielding with consistently performing genotypes across environments. On the contrary, the environments such as E9, E5, and E8 had short vectors regardless of the angle with the AEC abscissa suggesting that these environments provide little information on the performance of genotypes or the fodder yield performance of oat genotypes was less discriminated in these environments. When the environments provide little information about the genotypes, some of these testing

environments should be excluded after checking their consistency over years to reduce the cost of genotype evaluation. The discriminating and representative test environments are useful to select generally adapted genotypes while discriminating but non-representative test environments are useful to select specifically adapted genotypes when the environments are divided into different mega-environments (Yan and Tinker, 2006).

The type of genotype by environment interaction can be explained using the scores of the first two principal components (PCs). The result indicated that the first PC had both positive and negative scores while the second PC had only negative scores. The type of interaction is a crossover (qualitative) when the environments have larger PC1 scores with opposite signs. However, environments with large PC2 scores which are either positive or negative scores indicate the non-crossover (quantitative) type of the genotype by environment interaction. The result of this study showed that the environments such as E7 and E4 had higher PC2 scores with similar signs (negative) suggesting that the proportional yield differences across environments, which lead to a non-crossover type of interaction (Yan *et al.*, 2000; Kaya *et al.*, 2006). On the contrary, E6 and E4 had the highest PC1 scores with opposite signs. This indicates that these environments had a strong crossover type of interaction, leading to disproportionate the genotypes yield differences across environments (Yan *et al.*, 2000; Kaya *et al.*, 2006). Among the testing environments, E7 was the most discriminating and representative environment to identify the best oat genotypes for fodder yield production.

4.4.1.5.3 Ranking environments based on discriminating and representativeness

The GGE biplot is used to rank the environments based on the discriminating ability and representativeness of the test environments. The ideal environment which is located at the center of the concentric circles or closer to this point has the largest PC2 score but smaller PC1 score. This indicates that the ideal environment has a high discriminating ability of the genotypes for fodder dry matter yield and represents other testing environments. According to Yan (2001); Yan and Tinker (2006), an ideal environment is located at the center of the concentric circles and has the longest vector of all environments projection on the AEC abscissa (the most discriminating power) and its projection on the AEC ordinate are zero, meaning that it is representative of the average environment. Among the environments, E7 was located closer to the center of the concentric circles and considered an ideal environment to select superior fodder yield with consistently performing genotypes. The environments such as E1 and E8 were closer to the ideal environment and considered the most favorable

environments for oat fodder production compared to other environments while the environment such as E6 and E4 were located far from the ideal test environment and used to select specifically adapted oat genotypes for fodder yield. According to Sharma *et al.* (2009); Naroui *et al.* (2013); Yusuff *et al.* (2017), an environment is more favorable and discriminating when located closer to the center of the concentric circles or an ideal environment. However, the ideal test environment should be confirmed with multi-year data (Yan and Tinker, 2006).

4.4.1.6 Genotypes stability for forage yield based on univariate stability parameters

4.4.1.6.1 Stability performance of genotypes for fodder yield

Various parametric and non-parametric stability parameters were used to assess the stability of oat genotypes for fodder yield. Different non-parametric stability statistics were used to evaluate the yield stability of genotypes (Scapim *et al.*, 2000; Solomon *et al.*, 2007; Kan *et al.*, 2010). Two univariate nonparametric stability statistics were used in this study to determine the stability of oat genotypes. The stable genotypes have lower environmental variances ($S^{(1)}_i$ and $S^{(2)}_i$) compared to unstable genotypes. According to Huehn (1979) criteria of $S^{(1)}_i$ and $S^{(2)}_i$ stability parameters, high-yielding and stable genotypes were G6, G11, G15, and G23 while low-yielding genotypes such as G5, G14, G17, G20, and G22 also showed stable performance based on these stability parameters. On the other hand, genotypes with lower values of the SD stability parameter have a stable performance than genotypes with higher values of the SD stability parameter (Gezahagn *et al.*, 2023b). Accordingly, G1, G2, G3, G4, G5, G7, G10, and G11 had higher yields with stable performance while low-yielding genotypes which showed stable performance across environments were G16 and G22.

The fodder yield stability of oat genotypes was also assessed using 12 parametric stability parameters. The stability parameters of Wricke ecovalence (W_i) and Shukla stability variance (σ_i^2) were used to determine the fodder yield stability of oat genotypes. Genotypes with the lowest W_i have stable performance across environments (Wricke, 1962). Similarly, genotypes with the lowest σ_i^2 perform consistently under changing environmental conditions (Shukla, 1972). Based on the stability parameters of σ_i^2 and W_i , the low-yielding genotypes that perform consistently under a wide range of environmental conditions were G5, G12, G14, G17, G20, and G22. Similarly, the high-yielding genotypes which performed under wider environmental conditions using σ_i^2 and W_i stability parameters were G11, G15, G19,

and G23. The σ_i^2 and W_i stability parameters had similar genotypes ranking which is also confirmed by the presence of a perfect positive Spearman rank correlation between these stability parameters. Becker and Leon (1988); Bhargava *et al.* (2005); Tamene *et al.* (2015); Erdogdu and Esendal (2021) also stated that σ_i^2 and W_i stability measures give similar ranking of genotypes.

The AMMI stability value (ASV) was also used to determine the stability of oat genotypes for fodder yield. The smaller values of ASV indicate a higher stability performance of the genotypes across environments while the larger values of ASV indicate adaptation of genotypes in specific environments (Purchase, 1997). The lower-yielding genotypes that had stable performance using the stability parameter of ASV across environments were G5, G12, G17, and G22. Similarly, G1, G6, G10, G11, G15, and G23 produced higher fodder yield with stable performance using ASV stability parameter across environments. The stability of oat genotypes was also determined using the Hernandez desirability index (D_{ji}) measure of stability. The genotype with the lowest value of D_{ji} has higher stability under varying environmental conditions while the highest D_{ji} value shows a specific adaptation of the genotype (Hernandez *et al.*, 1993). According to the stability criteria of Hernandez *et al.* (1993), G5, G12, G17, G20, and G22 which produced a lower fodder yield had wide adaptation. Similarly, high fodder-yielding genotypes such as G10, G11, G12, G15, G19, and G23 showed stable performance across environments based on the D_{ji} stability parameter.

The stability of genotypes can be also determined using regression coefficient (b_i) and deviation from regression (S_{di}^2) stability parameters. Eberhart and Russell's (1966) model considers both linear (b_i) and non-linear (S_{di}^2) components of GEI in determining the stability of genotypes. The unity of b_i value coupled with zero value of deviation from regression indicates yield stability (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). According to the yield stability criteria of Becker and Leon (1988); Finlay and Wilkinson (1963); Eberhart and Russell (1966), an ideal genotype has a higher mean yield, b_i value equal or closer to unity ($b_i = 1$), and S_{di}^2 value closer or equal to zero (S_{di}^2). The genotypes with higher or medium fodder yield coupled with the value of the b_i stability parameter closer to unity ($b_i = 1$) are considered widely adaptable genotypes. On the other hand, the genotypes are more responsive to favorable and unfavorable environments when the values of b_i stability parameters are greater than unity ($b_i > 1$) or lower than unity ($b_i < 1$), respectively (Mut *et al.*, 2010; Morsy *et al.*, 2015). Among the genotypes, G10, G11,

G15, and G23 had mean fodder yield above the grand mean, b_i values closer to unity ($b_i = 1$), and S_{di}^2 values near zero ($S_{di}^2 = 0$) indicating that these genotypes had stable performance across environments.

Genotypes that had average or higher fodder yield coupled with b_i values higher than unity ($b_i > 1$) were G6, G9, G13, G18, G19, and G24. These genotypes were less stable under wider environmental conditions (above average stability) but desirable under favorable environments. Lotan *et al.* (2012); El-Hashash and El-Absy (2013); and Kurt (2020) also confirmed that these genotypes are highly sensitive to environmental changes and under an intensive production system, these genotypes produce maximum yield while the yield remarkably declines under poor management and growing conditions. On the other hand, genotypes such as G1, G2, G3, G4, and G7 which had medium or higher yield coupled with b_i values below unity ($b_i < 1$) were resistant to environmental variations (above average stability) but desirable under unfavorable environments. Mut *et al.* (2010); Topal and Yildiz (2011); and Lotan *et al.* (2012) also stated that the response of genotypes to environmental change is very minimal or remains steady under poor growing conditions and the improvement of the environment cannot be exploited by these genotypes. The genotypes (G8, G12, G14, and G21) which adapted moderately to all environments had closer mean fodder yield coupled with b_i values closer to unity ($b_i = 1$) and this result is in line with the findings of other scholars (Hossain *et al.*, 2003; Morsy *et al.*, 2015; Cubukcu *et al.*, 2021). On the other hand, G5, G16, G17, G20, and G22 had fodder yield below the grand mean coupled with b_i values closer to unity ($b_i = 1$) indicating these genotypes performed poorly under all tested environments and this result is in close conformity with the findings of Oliveira *et al.* (2012); El-Refaey *et al.* (2013); Cubukcu *et al.* (2021). The genotype stability was also assessed using the Perkins and Jinks adjusted linear regression coefficient (B_i) stability parameter. Genotypes with higher yield coupled with adjusted linear regression coefficient values closer to unity ($B_i = 1$) indicate stable performance across environments (Perkins and Jinks, 1968). The higher-yielding genotypes that performed consistently across environments using the B_i stability parameter were G3, G4, G7, G9, G10, G13, G18, and G24 while G16 and G21 had lower yield with stable performance across environments.

The stability of oat genotypes for fodder dry matter yield was also assessed using R^2 , P_i , CV_i , and YSI stability parameters. According to the stability parameter of coefficient of determination (R^2), genotypes with higher yield coupled with R^2 values closer to unity ($R^2 = 1$) are considered stable (Pinthus, 1973). Based on the Pinthus's (1973) stability criteria, G2,

G3, G6, G7, and G10 genotypes had high fodder yield coupled with stable performance. Genotypes are considered stable when the genotypes have lower values of the genotypic superiority index (P_i) coupled with higher yield (Lin and Binns, 1988). Accordingly, G2, G3, G6, G7, G9, G10, and G23 genotypes had high fodder yield coupled with low P_i values indicating these genotypes were stable performance across environments. The higher mean fodder yield coupled with a lower coefficient of variation (CV_i) indicates better stability (Francis and Kannenberg, 1978). According to Francis and Kannenberg's (1978) stability criteria of CV_i , the stable genotypes were G2, G3, G6, G7, G10, and G23. High-yielding genotypes coupled with lower values of YSI are considered stable genotypes across environments (Kang, 1993). According to the stability criteria of YSI, G2, G3, G6, G9, G10, and G23 were considered stable genotypes. Generally, based on the stability parameters of R^2 , P_i , CV_i , and YSI, G2, G3, G6, G7, G9, G10, and G23 had better stability performance and selection of oat genotypes for fodder yield using these stability parameters could be effective for genetic gain and yield improvement.

4.4.1.6.2 Association among fodder yield stability parameters

According to Steel and Torrie (1980), all pairwise comparisons of stability parameters and yield were computed using Spearman's rank correlation coefficients. Oliveira *et al.* (2012) stated that the rank correlation coefficient between the estimates of stability parameters is very useful in predicting the stability of genotypes across environments. Among the stability parameters, R^2 , P_i , CV_i , and YSI had significant positive associations with fodder dry matter yield (FDMY), indicating that the selection of oat genotypes using these stability parameters would lead to the development of high fodder-yielding genotypes with stable performance across environments. Different research studies also indicated the existence of significant positive associations of yield with YSI (Kang and Magari, 1995; Flores *et al.*, 1998; Segherloo *et al.*, 2008; Farshadfar *et al.*, 2012b; Mohammadi and Amri, 2008; Yusuff *et al.*, 2017) and with P_i (Abdurahman, 2009; Tamene *et al.*, 2015; Lemi, 2016; Afework, 2017; Mesfin, 2017) in different crops. However, FDMY had non-significant negative associations with σ_i^2 , W_i , D_{ji} , b_i , $S^{(1)}_i$, ASV, $S^{(2)}_i$, and S_{di}^2 stability parameters. This indicated that the selection of oat genotypes using these stability parameters favors low fodder-yielding genotypes over high fodder-yielding genotypes. Tegegn (2019) also reported that yield had non-significant negative associations with W_i , σ_i^2 , ASV, and S_{di}^2 stability parameters. The YSI which associated significantly and positively with FDMY also had significant positive associations with σ_i^2 , W_i , D_{ji} , b_i , $S^{(1)}_i$, ASV, $S^{(2)}_i$, and S_{di}^2 stability parameters. The research

finding also indicated that YSI had significant positive associations with W_i , σ_i^2 , ASV, and P_i stability parameters (Tegegn, 2019). The association between FDMY and B_i was non-significant positive, indicating selection of oat genotypes using the B_i stability parameter is less effective for fodder yield improvement. The stability parameters which correlated non-significantly with mean yield generally allow the identification of genotypes adapted to unfavorable growing conditions (Farshadfar *et al.*, 2012b).

The rank correlation coefficients between all pairs of σ_i^2 , W_i , D_{ji} , b_i , $S^{(1)}_i$, ASV, $S^{(2)}_i$ and S_{di}^2 stability parameters were significant and positive, indicating the possibility of using these stability parameters interchangeably for fodder yield stability of oat genotypes. Hence, it is possible to use only one of them as a measure of stability (Akcura *et al.*, 2006). Cubukcu *et al.* (2021) also reported that the paired correlation coefficients between W_i , S_{di}^2 , $S^{(1)}_i$, and $S^{(2)}_i$ stability parameters were significantly positive, indicating their close relationship with each other. A significant positive association was also observed between $S^{(1)}_i$ and $S^{(2)}_i$ stability parameters (Flores *et al.*, 1998; Scapim *et al.*, 2000). However, the B_i stability parameter had a significant negative association with σ_i^2 , W_i , D_{ji} , b_i , $S^{(1)}_i$, ASV, $S^{(2)}_i$, S_{di}^2 , and YSI stability parameters while it had a significant positive association with R^2 stability parameter. This indicated that the selection of oat genotypes for fodder yield using the stability parameter of B_i coupled with either one or all of the stability parameters (σ_i^2 , W_i , D_{ji} , b_i , $S^{(1)}_i$, ASV, $S^{(2)}_i$, S_{di}^2 , and YSI) would not be effective for yield improvement. On the other hand, the rank correlation coefficient between σ_i^2 and W_i was perfect positive, indicating that both stability parameters have equivalent genotype ranking ability. Thus, oat genotype selection using either of these two stability parameters could be effective for fodder yield improvement. The perfect positive associations between σ_i^2 and W_i in this study are in line with the findings of other scholars in different crops (Tamene *et al.*, 2015; Afework, 2017; Mesfin, 2017; Yusuff *et al.*, 2017; Wakuma, 2019; Cubukcu *et al.*, 2021; Erdogdu and Esendal, 2021). However, the correlation coefficient between the b_i and B_i was perfect negative, indicating that these two stability parameters provide different genotype rankings for fodder yield in oat genotypes. Thus, these two stability parameters had inverse genotypes ranking for fodder yield and thus, the top stable genotypes in the b_i stability parameter were the least stable in the B_i stability parameter and vice versa. However, Erdogdu and Esendal (2021) reported that the b_i stability parameter had a perfect positive association with B_i stability parameter.

4.4.1.6.3 Principal component analysis of fodder yield stability parameters

Principal component analysis (PCA) based on the rank correlation matrix was used for a better understanding of the associations among yield with parametric and nonparametric univariate stability parameters (Farshadfar *et al.*, 2012b). The relationships among various parametric and nonparametric univariate stability parameters are graphically displayed in a biplot of the first two principal component axes (Mohammadi *et al.*, 2012a; Tamene *et al.*, 2015; Kaya and Turkoz, 2016; Gezahagn *et al.*, 2023b). Accordingly, the cosine of the angle between vectors of two stability parameters indicates the approximate correlation coefficient between any two stability parameters. Thus, the rank correlation coefficient between two stability parameters is significantly positive when the cosine of the angles between vectors of the stability parameters is acute ($<90^\circ$) while the parameters have a significant negative association when the angles between the stability parameters are obtuse ($>90^\circ$). However, a very weak or no correlation is observed between two stability parameters when the vectors of stability parameters have a right angle (90°) or closer to the right angle. On the other hand, the stability parameters have perfect positive and perfect negative relationships when the cosine of the angle between two stability parameters are zero (0°) and straight-line (180°), respectively. The biplot of the first two principal components based on the rank correlation matrix of the stability parameters was more or less consistent with Spearman's rank correlation coefficients for the stability parameters (Farshadfar *et al.*, 2012b; Tamene *et al.*, 2015; Gezahagn *et al.*, 2023b). However, some inconsistencies are expected because the biplot of the first two PCs did not explain 100% of the total variation (Yan, 2002).

Based on the biplot of the first two PCs, the stability parameters were clustered into three groups. Various studies also indicated that the stability parameters grouped into three clusters (Farshadfar *et al.*, 2011b; Kaya and Turkoz, 2016; Gezahagn *et al.*, 2023b) and four clusters (Tamene *et al.*, 2015). The first group, which is located on the right side of the PC1 and closer to the PC2, comprised σ_i^2 , W_i , D_{ji} , b_i , $S^{(1)}_i$, ASV, $S^{(2)}_i$, and S_{di}^2 stability parameters. The cosine of the angle among the first group stability parameters is acute ($<90^\circ$), indicating significant positive associations between them and suggesting the use of B_i and one of the stability parameters from the first group simultaneously to determine the stability of oat fodder yield. The vector of the σ_i^2 stability parameter overlapped on the W_i stability parameters. This indicated that the cosine of the angle between σ_i^2 and W_i was zero (0°) which showed a perfect positive association between them and suggested the use of either of the stability parameters due to the similarity of both stability parameters in genotypes

ranking for fodder yield. The cosine of the angle between B_i and any of the stability parameters contained in the first group was obtuse ($>90^\circ$), indicating significant negative associations between them and suggesting the use of B_i and one of the stability parameters from the first group simultaneously to determine the stability of oat fodder yield. The cosine of the angle between B_i and b_i was straight-line (180°), indicating perfect negative associations between them and suggesting the inverse ranking ability of these stability parameters. The first and second group of stability parameters had static/biological stability patterns, indicating that low fodder-yielding genotypes are more stable than high fodder-yielding genotypes. The result of this study is also in line with the findings of Tamene *et al.* (2015), who reported that b_i , S_{di}^2 , D_{ji} , W_i , σ_i^2 , ASV, and $S^{(2)}_i$ stability parameters have static stability patterns. Nassar and Huehn (1987); Sabaghnia *et al.* (2006); and Kaya and Turkoz (2016) also pointed out that environmental variances such as $S^{(1)}_i$ and $S^{(2)}_i$ have static stability patterns which is in line with the result of this study. Akcura *et al.* (2009) reported that the static stability statistics could be used as compromise methods to select genotypes with moderate yield and high stability. According to Becker (1981), the static (biological) stability concept is not acceptable to breeders and agronomists because they prefer high-yielding genotypes that have better potential to respond to agronomic management and better environmental conditions.

The third group of stability parameters which had negative PC1 scores and located below the PC2 abscissa comprised R^2 , P_i , CV_i , SD, and YSI stability parameters with fodder dry matter yield (FDMY). The cosine of the angle between members of the third group stability parameters was acute ($<90^\circ$), indicating a significant positive association between these stability parameters and fodder yield. However, the Spearman's rank correlation indicated that SD was significantly and positively correlated with the CV_i stability parameter while it had a non-significant positive association with the third group of stability parameters (R^2 , P_i , and YSI) and a non-significant inverse association with FDMY. Thus, from the third group of stability parameters, the selection of oat genotypes using the R^2 , P_i , CV_i , and YSI stability parameters would lead to the selection of high fodder-yielding genotypes that perform consistently across environments. The third group of stability parameters had a dynamic (agronomic) stability pattern, indicating that high fodder-yielding oat genotypes are more stable compared to low fodder-yielding genotypes. The result of this study is in line with the findings of Kang and Magari (1995); Flores *et al.* (1998); and Kaya and Turkoz (2016), who reported that YSI has a dynamic (agronomic) stability pattern due to significant positive

association with yield. The result of this study is also in line with the findings of Tamene *et al.* (2015), who reported that the P_i stability parameter has a dynamic (agronomic) stability pattern. In the dynamic concept of stability, breeders and agronomists prefer genotypes with high yield and responsiveness to agricultural inputs or better agricultural conditions (Becker and Leon, 1988). Although the static or biological concept of stability is not acceptable by breeders and agronomists, it may be more useful than dynamic stability in developing countries (Simmonds, 1991).

4.4.1.7 Genotypes performance for grain yield and yield components

4.4.1.7.1 Analysis of variance and genotypic performance

A very highly significant difference was observed among the genotype, environment and genotype by environment interaction (GEI) for grain yield and all yield-related traits considered in this study except grain filling period for genotype main effects. The differences in grain yield of oat genotypes might be attributed to inherent genetic variation among oat genotypes, the differential response of genotypes to the environment, and the differential influence of environment on genotype. The significant difference among the genotypes is indicating the presence of variability in the inherent genetic constituents of the genotypes. Genetic variation among oat genotypes was also reported (Naeem *et al.*, 2002; Fekede, 2004; Getnet *et al.*, 2004; Ashenafi, 2018; Gezahagn *et al.*, 2021). Gezahagn *et al.* (2021) also reported that the genetic difference and their differential response to the growing environments are the major reasons for grain yield variations in oat genotypes. The studied oat genotypes had a differential response for grain yield performance with rank order changes across environments. This indicates that genotypes may not express the same phenotypic performance across environments or different genotypes may respond differently to a specific environment. The existence of substantial genetic variations and the influence of the environment on the performance of oat genotypes were also reported (Ashenafi, 2018; Gezahagn *et al.*, 2021).

Grain yield is a multi-gene-controlled trait and is highly affected by genetic, environmental, and interaction factors (Sahin *et al.*, 2016; Aydogan *et al.*, 2020). Thus, the percentage of total variation attributed to the environment component was higher than the component of genotype for grain yield compared to yield-related traits (Epinat-Le Signor *et al.*, 2001). However, yield-related traits are generally less influenced by the environment because they are governed by few genes compared to grain yield (Ethridge and Hequet, 2000). The

significant difference observed among environments indicated that the mean grain yield performance of genotypes differed from one environment to another due to variations in edaphic, biotic, and abiotic factors among environments. Fehr (1993) also reported that environmental factors have a remarkable potential to cause differential performances in genotypes. The percentages of the total sum of squares explained by the main effects of genotype and environment and their interaction effects have been used as an indicator of the total variation attributed to each component (Kerby *et al.*, 2000).

The existence of very highly significant GEI suggested that the studied oat genotypes varied across the tested environments for measured traits. This result revealed that there was a differential response of oat genotypes for the studied quantitative traits across testing environments. Significant GEI indicates the differential response of genotypes across environments and genotypes that perform well in one environment may perform poorly in another (Fox *et al.*, 1996). The effect of GEI was significant for grain yield, indicating that the genotypes had a different response to environmental changes and complicates the selection of superior genotypes (Yan and Kang, 2003). The inconsistent performance of genotypes from one environment to other indicates the existence of a crossover type of interaction and this result is confirmed by others (Cross, 1990; Matus *et al.*, 2003; Akcura *et al.*, 2006). The genotypes change their rank order from one environment to the other due to the crossover type of interaction. Tariku *et al.* (2013) and Gezahagn *et al.* (2017) also stated that the rank order changes of the genotypes could occur in the presence of GEI. When the ranking of genotypes remains constant in diverse environments and the interaction due to the change in magnitude of genotype response is significant, the type of interaction is a non-crossover (Kang, 2017). Therefore, the existence of inconsistent genotypic variation across the environment indicates the importance of performing stability analysis (Legesse *et al.*, 2015; Morsy *et al.*, 2015; Parimala *et al.*, 2019). Hence, the genotypes should be tested over years before selection and recommendation of consistently performing genotypes across environments. Generally, GEI can be exploited either by selecting the best-performing genotypes for each specific target environment or avoided by choosing stable genotypes across environments (Wondimu *et al.*, 2022).

4.4.1.7.2 Performance of genotypes across environments

The mean performance of oat genotypes across testing environments varied significantly for all measured traits except GFP. High grain yield producing oat genotypes had relatively

shorter DSH, GFP, and higher BYPR, GSFR, TSW, and HI compared to low grain-yielding genotypes. Among high GY producing oat genotypes, G5 required shorter DSH followed by G17 and G19 while G20, G24, and G18 produced GY below the grand mean and required longer DSH. The GFP was shorter for G10, G1, and G24 while G20, G15, and G9 had longer GFP. The GSFR was high for top grain yield-producing genotypes (G17, G5, and G8) while genotypes such as G20, G3, and G13 produced GY below the grand mean and the lowest GSFR. According to Peltonen-Sainio (1992), shorter GFP and higher GSFR have high contribution to GY improvement in oat genotypes. The observed low GY in late maturing and longer GFP genotypes might be related to the existence of terminal moisture stress which could affect florets and spikelets formation and finally leads to GY reduction. However, a shorter growth period coupled with high growth rate during vegetative growth stage and longer growth period during grain filling stage under optimal growth conditions leads to efficient utilization of growth resources for yield formation (Tao *et al.*, 2021). The highest HI was observed for high grain yield-producing genotypes (G17, G5, and G8) while the lowest was recorded for G20, G3, and G6 which produced GY below the grand mean. Different research findings also indicated that the GY of crops increased with increasing HI (Salman and Brinkman, 1992; Hay, 1995; Siloriya *et al.*, 2014; Tao *et al.*, 2021).

4.4.1.8 Genotypes evaluation for grain yield based on AMMI

4.4.1.8.1 Evaluation of genotypes for grain yield based on AMMI

The AMMI analysis of variance showed significant variation for genotype, environment and their interaction effects. The highest grain yield variation was explained by the environment main effect (44.62%) followed by genotype main effect (28.84%) and GEI (26.54%) effect revealing that the testing environments were diverse and contributed more to grain yield variation in the studied oat genotypes. This result is also in line with the findings of Agyeman *et al.* (2015); Tazebachew and Cherinet (2018); and Ahmed *et al.* (2021), who reported that a large proportion of grain yield variation attributed to environment followed by genotype and GEI in different crops. The highly significant environment effect could be attributed to large differences among the test environments in altitude, soil types, temperature and differences in both amount and distribution of annual rainfall and other agro-climatic factors, which are partly observed in our test environments. In the presence of GEI, a genotype does not exhibit a similar response under diverse test environments and various genotypes respond differently to a specific environment (Fox *et al.*, 1996; Mustamu

et al., 2018; Ruswandi *et al.*, 2020; Wicaksana *et al.*, 2022). The existence of significant GEI requires stability analysis to determine the stable oat genotypes across environments.

The GEI was further partitioned into different IPCAs and the result showed that the first four components had a significant contribution to grain yield variation in oat genotypes. The first two AMMI-IPCAs accounted for 63.96% of the GEI sum of squares. Other research findings also indicated that the first two IPCAs explained 61.1% of the interaction sum of squares in barely (Hasan, 2014), 48.9% in lentil (Yadav *et al.*, 2016), 36.3% in soybean (Bhartiya *et al.*, 2017), 61.2% in maize (Ahmed *et al.*, 2021), and 58.1% in cowpea (Yasin *et al.*, 2022) in which some are lower while others are comparable to that reported in this study. On the other hand, greater values such as 79.1% in maize (Zerihun, 2011), 87.1% (Legesse *et al.*, 2015) and 69.2% (Irfan, 2018) in chickpea, 72.5% in tef (Habte *et al.*, 2019), and 70.1% in barley (Wondimu *et al.*, 2022), and 81.7% in sweet corn (Ruswandi *et al.*, 2020) were also observed. The reported differences in the explained interaction variance of the first two IPCAs might be due to variations in test environments, crop type, and GEI effect.

The AMMI model is also used for the identification of the best environment for grain yield production and thus, the testing environments are classified into favorable and unfavorable environments. The environment is said to be favorable when the mean grain yield of the environment is greater than the grand mean of environments while the opposite is true for the unfavorable environment (Miriam *et al.*, 2019; Yirga *et al.*, 2021). Accordingly, E1, E2, and E4 were considered favorable environments while E3, E5, E6, E7, E8, and E9 were unfavorable environments. Based on the first four superior genotypes selection using the AMMI model, G8 was selected at three favorable (E1, E2, and E4) and also three unfavorable (E3, E5, and E6) environments whereas, G17 and G5 were selected at two favorable (E1 and E2 for G17 and E1 and E4 for G5) and also at two unfavorable environments (E6 and E9 for G17 and E5 and E6 for G5). Similarly, G12 and G19 were selected at one favorable environment (E1 for G12 and E2 for G19) and also at four (E5, E8, E7, and E9 for G15) and at two (E7 and E8 for G19) unfavorable environments. The first top five grain yield producing genotypes (G8, G17, G12, G19, and G5) were selected both at favorable and unfavorable environments, suggesting that these genotypes are desirable for cultivation at both environments.

4.4.1.8.2 Evaluation of genotypes for grain yield based on AMMI-1

The AMMI-1 biplot analysis is an effective tool, graphically showing mean values of grain yield on the abscissa and the first IPCA scores as the ordinate (Crossa *et al.*, 1990b). This biplot analysis generally provides information on the mean grain yield and stability of genotypes using the first IPCA scores of both genotypes and environments against the main effects of genotypes. Genotypes and environments that appear on a vertical line have similar yield performances and those that appear on a horizontal line have similar interaction patterns (Bose *et al.*, 2014b; Wondimu *et al.*, 2022). Similar signs of the first IPCA scores for both environments and genotypes suggest positive interaction, and these environments were considered favorable for genotypes which had similar signs of the first IPCA scores with these environments. However, opposite signs of the first IPCA scores for genotypes and environments indicate negative interaction and these environments were considered unfavorable for these genotypes. Accordingly, G22, G11, G12, G14, G19, G5, G8, and G17 had positive IPCA-1 scores with E2 indicating that this favorable environment interacts positively with these genotypes while E3, E7, E8, and E9 and the above genotypes (G22, G11, G12, G14, G19, G5, G8, and G17) had the opposite sign of the IPCA-1 scores suggesting that these environments were unfavorable for the above genotypes. Similarly, G4 and G16 had positive IPCA-1 scores with E1 and E4 demonstrating that these favorable environments had positive interactions with these genotypes while E5 and E6 and the above both genotypes (G4 and G16) had negative IPCA-1 scores implying that these environments were unfavorable for G4 and G16. The result of the AMMI-1 biplot analysis in this study illustrated that the scores of the environment effect were more scattered on the biplot than the scores of the genotype effect signifying the existence of variation among environments is higher compared to genetic variability among genotypes. This result is also in line with the findings of Wondimu *et al.* (2022), who reported that the environments scattered more on the biplot than the genotypes in barley.

The contribution of genotypes to the interaction variance depends on the position of the genotypes on the biplot. Hence, the genotypes located closer to the first IPCA contributed less than the genotypes located farther away from either side of the ordinate. Among the studied genotypes, G23, G10, G15, G9, G24, G4, and G3 located near the first IPCA indicating these genotypes had a low contribution to GEI compared to G17, G8, G5, G19, G14, G20, G7, and G1 genotypes which located far from the first IPCA. Genotypes located near the first IPCA had wide adaptation but low contribution to GEI while genotypes located

far from the first IPCA had high contribution to GEI, and these genotypes adapted to specific environment(s). Genotypes; G22, G11, G12, G4, and G16 that were characterized by mean grain yield above the grand mean and the first IPCA scores closer to zero were considered adaptable to all environments while G14, G19, G5, G8, and G17 genotypes with high mean grain yield and high scores of the first IPCA were considered as adaptable to specific environment(s). Moreover, G22, G11, G12, G14, G19, G5, G8, G17, G4, and G16 genotypes and E1, E2, and E4 environments located on the right side of the ordinate had higher grain yield than those on the left side and this result is also in agreement with others (Nassir and Ariyo, 2011; Lemi *et al.*, 2018). On the other hand, E2, E6, E5, E3, and E7 environments had longer vectors indicating high discriminating ability and contributed more to GEI while E1, E4, E8, and E9 had shorter vectors suggesting less discriminating power and low contribution to GEI.

4.4.1.8.3 Evaluation of genotypes for grain yield based on AMMI-2

Unlike AMMI-1, the performance of genotypes and environments in AMMI-2 can be determined using the first two IPCAs. The AMMI-2 biplot presents the first two IPCAs scores of genotype and environment and helps for visual interpretation of the GEI patterns (Vargas and Crossa, 2000). As the second IPCA scores also have a significant role in explaining the GEI, the first IPCA scores were plotted against the second IPCA scores to further explore adaptation. Genotypes which are very close to the biplot origin are more stable and less interactive with environments than those away from the origin (Purchase, 1997). Consequently, G10, G23, G15, G4, G9, G13, G21, G18, G2, G22, and G6 were stable genotypes though they had below-average grain yield performance except for G4 and G22. Among high-grain yield-producing genotypes, G4, G22, G11, G12, G14, G8, and G17 were relatively closer to the biplot origin suggesting that these genotypes also perform consistently across environments. According to Samonte *et al.* (2005), genotypes located closer to the biplot origin are less sensitive to the environment's interactive forces and those far from the origin have high interactions. The stable genotypes which have nearly zero scores for the first two IPCAs can show general adaptation across testing environments while genotypes are more responsive or unstable when the genotypes located farther away from the biplot origin (Wondimu *et al.*, 2022). Genotypes and environments that are closer to each other have similar interaction patterns while genotypes and environments located far away from each other have different interaction patterns.

The stability information obtained from the first two AMMI analyses was variable for some genotypes and environments. Among high grain yielding and stable genotypes of the AMMI-1 biplot, G16 become unstable under AMMI-2 biplot but G14, G8, and G17 become stable under AMMI-2 indicating the stability information obtained from AMMI-2 is more accurate than AMMI-1 biplot as AMMI-2 provides information from the first two IPCAs (Oliveira *et al.*, 2014; Wondimu *et al.*, 2022). The existence of a longer vector of environments compared to genotypes explains the sum of squares of environments was higher as compared to the sum of squares of the genotypes. Environments such as E6, E3, E2, E7, and E5 were located far from the biplot origin implying these environments had a higher contribution to the environment sum of square while E1, E4, E8, and E9 had low contribution because they located closer to the origin. The vector length of environments indicates the discriminating (informative) ability of the environment on the studied genotypes. Thus, a longer vector length of the environment from the biplot origin indicates a high discriminating ability of the environment on genotypes while a shorter vector length of the environment had non-discriminating (non-informative) ability and low interaction with genotypes. The first two IPCAs had positive scores for E6 environment and for G24, G3, G22, G5, and G17 indicating both these genotypes and E6 environment were interacting positively while E1, E3, and E8 environments and G16, G1, G13, G4, G9, G23, G10, and G21 had negative scores for the first two IPCAs indicating the existence of positive interaction among them but they interact negatively with genotypes and environments which were located at the opposite side. On the other hand, E2 and E5 had negative IPCA-1 and positive IPCA-2 scores with G19, G8, G14, G11, and G12 implying these environments and genotypes interact positively while these genotypes and environments interact negatively with genotypes and environments which were located at the opposite side (positive IPCA-1 and negative IPCA-2).

4.4.1.9 Genotypes evaluation for grain yield based on GGE biplot

4.4.1.9.1 Mean performance and stability of genotypes

The GGE biplot analysis showed the existence of wide variations in grain yield performance across the testing environments. Thus, G8, G17, G5, G14, G19, G22, G12, G11, G4, and G16 located at the left side of the ordinate were considered adaptable or high grain-yielding genotypes, whereas those genotypes located at the right side of the ordinate were non-adaptable or low grain-yielding ones. On the other hand, the genotypes located far from the second PC ordinate in either direction were unstable, whereas those closer to the ordinate in

either direction were stable (Kaya *et al.*, 2006). Thus, from the high grain-yielding genotypes listed above, G19, G14, G8, G11, G12, G17, and G22 were relatively stable, whereas G16 and G5 were unstable genotypes.

The AEC ordinate line passed through the origin of the GGE biplot, and genotypes that had grain yield above the grand mean were located at the left side of the AEC ordinate, whereas low grain-yielding genotypes were located at the right side of the AEC ordinate. The vector projections for the genotypes, which are parallel to the AEC ordinate or perpendicular to the AEC abscissa in either direction, indicate the extent of genotypic stability across testing environments (Yan, 2001; Yan and Hunt, 2001; Kaya *et al.*, 2006). Among the high grain-yielding genotypes, G19, G14, G8, G11, G12, G17, and G22 were considered stable genotypes. G24, G3, and G1 from the low grain-yielding genotypes and G16 and G5 from the high grain-yielding genotypes had longer projections from AEC abscissa indicating that these genotypes have inconsistent performance across environments.

4.4.1.9.2 Ranking of genotypes relative to the ideal genotype

The GGE biplot ranks the genotypes relative to the ideal genotype using AEC abscissa and different concentric circles (Yan *et al.*, 2000). The arrow located on AEC abscissa pointed to the center of the concentric circles and the genotype located in the center of the concentric circles or closer to this center was considered an ideal genotype, and the remaining studied genotypes were ranked relative to this ideal genotype (Yan, 2001). Accordingly, G19 was very close to the center of the concentric circles and hence considered an ideal genotype. Similarly, G14, G8, G11, G12, G17, and G22, which were relatively closer to the ideal genotype (G19), were considered desirable genotypes. Among the low grain yielding genotypes, G24, G3, and G20 were located very far from the ideal genotype (G19) and were considered to be the most undesirable for production in the testing environments.

4.4.1.9.3 Which-Won-Where and mega environment identification

The GGE biplot analysis supports the classification of the studied genotypes and environments based on the performance of genotypes and the response of the growing environments (Gauch and Zobel, 1997; Yan *et al.*, 2000; Wondimu *et al.*, 2022). According to Yan (2001), Kaya *et al.* (2006), and Yan and Tinker (2006), the GGE biplot shows the “whichwon-where” pattern of genotype by the environment. The vertex genotypes (G16, G1, G20, G24, G17, G8, and G12) located far from the biplot origin created a polygon, and genotypes located at the vertices of a polygon had the highest grain yield in one or all

environments that fell in the sector. This result is in agreement with the findings of Yan (2002), Yan *et al.* (2010), Zerihun (2011), and Wondimu *et al.* (2022). The genotypes contained within the sector of a polygon were less responsive than the vertex genotypes in that sector, and vertex genotypes located on the opposite side of the mega-environments had the poorest performance in all environments. Based on the GGE biplot classification, genotypes and environments were classified into different groups using the lines coming from the biplot origin, which are perpendicular to the line connecting the furthest genotypes (Zerihun, 2011). Thus, the nine test environments were grouped into four mega-environments, whereas the genotypes were grouped into five genotypic groups.

The results showed that the selection of superior genotypes should be done for each mega-environment to enhance oat productivity. Accordingly, the first mega-environment was E3, and the vertex genotype for this sector was G16 suggesting that this genotype was the best yielder in this environment. The second mega-environment consisted of E7 and E8, and the winning genotype in this sector was G12. Similarly, the third mega-environment consisted of E1, E2, E4, E5, and E9, and this sector had no vertex genotype, whereas the fourth mega-environment was E6, and the vertex genotypes in this sector were G8 and G17. These winner genotypes were also the top mean grain yielders across environments, but they were the best at E6. The three vertex genotypes, G1, G20, and G24, had no corresponding environment indicating that these genotypes were the poorest in some or all of the testing environments. Yan and Tinker (2006) and Alidu *et al.* (2017) also stated that genotypes located on the vertices of the polygon perform either the best or the poorest in one or more environments. Generally, the identified mega-environments would not be consistent over the years that may vary depending on the climatic conditions of the areas. So, it is pertinent to conduct a multiyear experiment to determine the reliable mega-environments for oat production in the central highlands of Ethiopia. Kaya *et al.* (2006) and Zerihun (2011) also noted that the identification of mega-environment should be verified through multiyear experimental trials conducted in the target environments.

4.4.1.10 Environment evaluation based on GGE biplot

4.4.1.10.1 Relationship among the test environments

The vector view of the GGE biplot shows the interrelationships among the test environments. The result indicated that the cosine of the angles between the vectors of the environment was different indicating that the associations among the testing environments

were variable. The cosine of the angle between vectors of the environments indicates the associations between the vectors (Yan, 2000; Yan, 2002; Yan *et al.*, 2007). The highly correlated environments have smaller angles with AEC abscissa (Yan and Kang, 2003). When the cosine of the angle between vectors of the environments is acute ($< 90^\circ$), the association between the vectors is significantly positive while the angle between the vectors is obtuse ($> 90^\circ$), and the association is significantly negative (Yan and Tinker, 2006). On the other hand, the vectors do not have an association when the angle between the vectors is right angle (90°) or closer to right angle. Alidu *et al.* (2017) also reported that shorter environment vectors are associated weakly with test environments with longer vectors.

In this study, the cosine of the angle between environment vectors of E1, E2, E4, E5, E7, E8, and E9 was very small ($< 90^\circ$) as compared to the angle between E3 and E6. The strongly associated testing environments can produce similar information on the performance of the genotypes. According to Yan and Tinker (2006) and Yan *et al.* (2007), some of the strongly correlated testing environments can be avoided without affecting the validity of the information. Thus, the experimental cost can be reduced and efficiency improved by using a minimum set of test environments, but the selection of the test environments should be supported by multiyear data (Yan *et al.*, 2007). On the other hand, the angle between E3 and E6 was very closer to the right angle indicating that the association between these environments is very weak, which signifies independent genotypic performance in those environments. Generally, the vector view of the GGE biplot of the first two PCs was in line with the results of most correlation coefficients observed among the testing environments (data not shown). However, some inconsistencies are expected because the biplot did not explain 100% of the GGE variation (Yan, 2002).

4.4.1.10.2 Discriminativeness and representativeness of test environments

The discriminating ability and representativeness of the test environments were visualized using the vector view of the GGE biplot. Environments with both longer vectors and larger PC2 scores have high discriminating power, whereas those with longer/shorter vector lengths coupled with smaller angle between the AEC abscissa and vectors indicate the representativeness of the environments (Yan, 2001; Yan and Tinker, 2006; Yan *et al.*, 2007). Among the environments, E2, E5, E6, E1, E3, and E4 had longer vectors, and also all these environments had larger PC2 scores except E3. Thus, the discriminating ability of E2, E5, E6, E1, and E4 was higher compared to other environments. On the other hand, E7 had the

shortest vector length coupled with the smallest PC2 score followed by E8 indicating that this environment was the least in discriminating ability. The environments, such as E2, E5, E1, E4, E9, E7, and E8, had smaller angles with the AEC abscissa or smaller PC1 scores indicating these environments were more representative of other environments. On the contrary, E3 and E6 had large deviations from AEC abscissa, and these environments had larger PC1 scores compared to others implying the least representativeness of these testing environments.

Test environments (E3 and E6) with longer vectors and larger angles with the AEC abscissa cannot be used in selecting superior genotypes but are useful for selecting specifically adapted genotypes, whereas test environments (E1, E2, E4, E5, and E9) with longer vectors and smaller angles with the AEC abscissa are ideal for selecting superior genotypes (Alidu *et al.*, 2017; Yan and Tinker, 2006; Yan *et al.*, 2007; Yan *et al.*, 2010). On the other hand, environments (E7 and E8) with short vectors regardless of the angles with the AEC abscissa should not be used as test environments because they provide little or no discriminating information about the genotypes (Yan and Tinker, 2006; Yan *et al.*, 2007). Environments with longer vectors offer more information about the genotypes, whereas environments (E7 and E8) with shorter vectors offer little or no information about the genotypes; hence, to reduce the cost of assessment, one of the later environments could be excluded without the loss of much information about the genotypes when the association between these environments was consistent over years (Yan and Tinker, 2006; Yan *et al.*, 2007). Accordingly, E3 and E6 had longer vectors and larger angles with the AEC abscissa signifying that they may not be used in selecting superior genotypes but may be used in identifying specifically adapted genotypes. However, E2 and E5 had longer vectors and smaller angles with the AEC abscissa suggesting that they are ideal environments to select high-yielding genotypes.

The absolute values of the first two PC scores also indicate the type of GEI. The first PC scores had positive and negative scores, whereas the second PC had only negative scores. Environments with larger PC1 scores, which are opposite in signs, indicate the presence of the crossover (qualitative) type of GEI, whereas the larger PC2 scores of the environments with a similar sign of PC2 scores indicate the non-crossover (quantitative) type of the GEI (Kaya *et al.*, 2006). Accordingly, E2 and E5 had the largest PC2 scores and similar signs (negative) of PC2 scores indicating proportional genotype yield differences across environments, which lead to a non-crossover type of interaction (Yan *et al.*, 2000). In

contrast to environmental PC2, PC1 gives the crossover GEI because it had both positive and negative scores. Thus, the PC1 scores of E3 and E6 were the highest, but opposite signs imply that these environments had a strong crossover type of interaction, leading to disproportionate genotype yield differences across environments (Yan *et al.*, 2000). In general, the vector view of the GGE biplot indicated that E2 was the most discriminating and representative environment to select the best genotypes for production in the target environments. The most discriminating and representative environments could be considered the best testing environments for the selection of high-yielding genotypes (Yan and Tinker, 2006).

4.4.1.10.3 Ranking environments based on discriminating and representativeness

The environments were ranked based on the discriminating power and representativeness of the overall environments using the GGE biplot analysis (Yan *et al.*, 2000; Yan and Kang, 2003; Naroui *et al.*, 2013). The ideal environment that is located at the center of the concentric circles has the largest PC2 and smaller PC1 scores indicating more power to discriminate the genotypes and representative of other environments (Yan, 2001; Yan and Rajcan, 2002; Kaya *et al.*, 2006; Yan *et al.*, 2007). Accordingly, E2, which is located at the center of the concentric circles, was considered an ideal test environment for the selection of high-yielding genotypes. The environments that are closer to the center of the concentric circles or ideal test environment (E2) are classified as favorable environments, whereas the environments located far away from the center of the concentric circles or ideal test environments (E2) are considered unfavorable environments (Kaya *et al.*, 2006). Thus, E5, E1, and E4 were closer to the ideal test environment (E2) indicating that these environments were favorable, whereas E7 was relatively far from the ideal test environment (E2) and was considered the most unfavorable environment for the selection of high yielding oat genotypes.

4.4.1.11 Genotypes stability for grain yield based on univariate stability parameters

4.4.1.11.1 Stability performance of genotypes for grain yield

The stability of oat genotypes in terms of the mean grain yield was assessed using different parameters of stability. The stability parameters consisting of SD, environmental variances ($S^{(1)}_i$ and $S^{(2)}_i$), coefficient of variation (CV_i), and coefficient of determination (R^2) showed “static” stability, whereby low-yielding genotypes had more favorable values of these stability parameters than high-yielding genotypes. The small values of SD, $S^{(1)}_i$, $S^{(2)}_i$, and

CV_i , and the large value of R^2 indicate that genotypes perform consistently across environments. According to Francis and Kannenberg's (1978) criteria of CV_i , the stable genotypes were, in rank order of most stable first, G2, G3, G6, G7, G10, G13, G15, and G23, and these genotypes including G20 were also stable based on the stability parameter of SD. The genotypes with R^2 values closer to unity are considered stable (Pinthus, 1973), and a low value of this stability parameter indicates high dispersion of the data (Freiria *et al.*, 2018). According to Pinthus's (1973) stability parameter, the stable genotypes were G2, G9, G13, G15, G18, G20, G21, and G23. The genotypes G2, G3, G9, G10, G13, G15, G20, and G23 had low values of $S^{(1)}_i$ and $S^{(2)}_i$, indicating better performance across environments. However, high-grain-yielding genotypes such as G4, G8, G11, and G14 were moderately stable based on CV_i , R^2 , $S^{(1)}_i$, and $S^{(2)}_i$ stability parameters.

The contribution of a genotype to the GEI can be measured using stability parameters of ecovalence (W_i), which was first proposed by Wricke. According to Wricke (1962), the genotypes with the lowest W_i have lower yield variation across a wider range of environmental conditions and are considered to be more stable than others. Shukla (1972) also suggested that the stability variance (σ_i^2) indicates the amount of G×E variance associated with genotypes. Genotypes with the lowest σ_i^2 are more stable across environments than other genotypes. Although the values of the stability parameters W_i and σ_i^2 were very different, the stability rankings of W_i and σ_i^2 in this study were similar, which is confirmed by the existence of a perfect correlation between them. This result is also in line with the findings of Tamene *et al.* (2015), Cubukcu *et al.* (2021), and Erdogdu and Esendal (2021). Thus, using either of the two stability parameters can lead to similar stability results in the oat selection program. Based on these two stability parameters, the first three most consistently performing genotypes were G9, G15, and G23, which produced a mean grain yield below the grand mean, indicating that the low-yielding genotypes were more favored and genotype selection using these parameters may not be effective for grain yield improvement in oat genotypes. Among high-yielding genotypes, G4, G11, G14, and G22 were moderately stable (below the grand mean stability value) in terms of the stability parameters W_i and σ_i^2 .

It is emphasized that deviation from regression or the nonlinear (S_{di}^2) component of GEI is necessary for judging the stability of a genotype across environments and a value of zero indicates excellent stability of genotypes (Eberhart and Russell, 1966). According to the desirability index (D_{ji}) of Hernandez *et al.* (1993), stable genotypes with wide adaptability to

all environments would have a zero value, while unstable genotypes would have high values of this stability parameter. Like W_i and σ^2_i , the stability parameters S_{di}^2 and D_{ji} had similar values of genotype rankings, suggesting that both stability parameters yield the same stability result, so that the use of either of the two stability parameters would be enough for grain yield stability assessment. The stability parameters S_{di}^2 and D_{ji} had static or biological stability properties, indicating that low-yielding genotypes were more favored than high-yielding genotypes. Thus, the top five performing oat genotypes for consistency, using the stability parameters S_{di}^2 and D_{ji} , were G6, G9, G15, G20, and G23. Among high-grain-yielding genotypes, G4, G11, G14, and G22 were moderately stable (below the grand mean stability value) across diverse environments based on the stability parameters S_{di}^2 and D_{ji} .

The regression coefficient (b_i) approximating one coupled with deviation from regression (S_{di}^2) of zero values indicates average yield stability (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963). According to Becker and Leon (1988), Finlay and Wilkinson (1963), and Eberhart and Russell (1966), the ideal genotype has a high average yield, b_i equal to unity ($b_i = 1$) and S_{di}^2 closer to zero ($S_{di}^2 = 0$). The genotypes with medium or higher grain yield are considered adaptable to all environments when the b_i is closer to unity, whereas b_i values that are greater than unity ($b_i > 1$) or lower than unity ($b_i < 1$) indicate that the genotypes are more responsive to high and low-yielding environments, respectively (Zeki *et al.*, 2010; Morsy *et al.*, 2015). Genotypes G4, G12, and G14 had b_i near to unity ($b_i = 1$), S_{di}^2 closer to zero ($S_{di}^2 = 0$), and their mean grain yields were greater than the grand mean, showing that these genotypes have consistent yield performance across environments. However, genotypes G5, G8, G11, G16, G17, G19, and G22 had medium or higher grain yield and b_i above unity ($b_i > 1$), indicating that these genotypes show variations in yields under different environments (below average stability) and were suitable for growing under optimal environmental conditions. On the other hand, G6, G10, and G24 had medium grain yield coupled with b_i below unity ($b_i < 1$), so these genotypes were resistant to changing environmental conditions (above average stability) and suitable for cultivation under suboptimal environmental conditions. Genotypes G9, G18, G21, and G23 had near average grain yield coupled with b_i closer to unity ($b_i = 1$), indicating that these genotypes adapted moderately to all environments, while G1, G2, G3, G7, G13, G15, and G20 produced grain yield below the grand mean in conjunction with b_i closer to unity ($b_i = 1$), showing that these genotypes adapted poorly across all environments.

The larger the ASV, the more specifically adapted a genotype is to certain environments, while a smaller value implies greater stability performance across different environments (Purchase, 1997). The ASV in this study showed that low-grain-yield-producing genotypes were more stable compared to high-grain-yield-performing genotypes, indicating that this stability parameter had an inverse association with grain yield and it had static (biological) stability. This result is also in line with the findings of Tamene *et al.* (2015), who reported that ASV had static stability and it was associated negatively with grain yield in faba bean genotypes tested across environments. The five most stable genotypes based on ASV were G3, G9, G10, G15, and G23. However, G4, G11, G12, and G22, which produced mean grain yields above the grand mean, had ASV below the grand mean indicating that these genotypes were moderately stable compared to other high-yielding genotypes, and were assigned to the first group (high yield along with stability below the grand mean).

The genotypic superiority index (P_i), the Perkins and Jinks adjusted linear regression coefficient (B_i), and the YSI had dynamic (agronomic) stability, and superior genotypes were favored more by these stability parameters compared to low-yielding ones. The genotype with the lowest P_i value should be considered a superior genotype (Lin and Binns, 1988). Consequently, genotypes G5, G8, G11, G12, G14, G16, G17, G19, and G22 had high grain yield coupled with low P_i values and were found to be widely adapted genotypes. The B_i stability parameters indicated that G4, G5, G8, G11, G12, G14, G16, G17, G19, and G22 had grain yield above the grand mean along with adjusted linear regression coefficient values closer to unity ($B_i = 1$), indicating stable performance across environments as suggested by Perkins and Jinks (1968). The YSI is used to identify high-yielding and stable genotypes based on a combined measure of yield and stability of a genotype (Kang, 1993). Selection of genotypes based on a stability parameter alone may not be effective (Mohammadi and Amri, 2008), but considering both mean yield and stability parameters simultaneously would be effective for yield improvement (Farshadfar, 2008). According to this stability parameter, G4, G5, G8, G11, G12, G14, G16, G17, G19, and G22 had mean grain yields above the grand mean, coupled with comparatively low YSI values, indicating high stability of genotypes in diverse growing environments. According to stability parameters of P_i , B_i , and YSI, genotypes such as G5, G8, G11, G12, G14, G16, G17, G19, and G22 performed consistently across environments, and selection of genotypes using these stability parameters could be efficient to improve the grain yield in oat genotypes.

4.4.1.11.2 Association among grain yield stability parameters

Spearman's coefficient of rank correlation was computed for each of the possible pairwise comparisons of the various stability parameters and mean grain yield (Steel and Torrie, 1980). The stability parameter that is correlated positively with the mean grain yield supports selection of both superior and consistently performing genotypes. The mean grain yield had significant positive rank correlation coefficients with B_i , P_i , and YSI, while it had non-significant positive associations with CV_i , b_i , R^2 , and $S^{(1)}_i$. Therefore, selection of oat genotypes using B_i , P_i , and YSI would lead to development of superior and consistently performing genotypes. Other studies also indicated the presence of significant positive correlations of grain yield with P_i (Kilic *et al.*, 2010; Zeki *et al.*, 2010; Tamene *et al.*, 2015; Yirga, 2016) and with YSI (Mohammadi *et al.*, 2008; Segherloo *et al.*, 2008; Lemi, 2016; Afework, 2017) in different crops. However, all pairwise correlations of SD, S_{di}^2 , σ_i^2 , D_{ji} , and W_i stability parameters were significant and positive, but these parameters had significant negative rank correlations with grain yield, indicating that inferior genotypes were more stable than superior genotypes. Therefore, selection of oat genotypes using these stability parameters would not lead to higher grain yields in oat genotypes. These stability parameters are grouped under static stability, which favors low-yielding genotypes compared to high-yielding ones (Karimizadeh *et al.*, 2012; Tamene *et al.*, 2015). The static stability pattern is more helpful than dynamic stability for resource-poor farmers because these farmers prefer to select genotypes that can produce low yields with stable performance under minimal external inputs and management conditions (De Boef *et al.*, 1996). On the other hand, breeders and agronomists would prefer the dynamic stability pattern to select genotypes with high yield and better response for optimum management conditions (Becker and Léon, 1988). Accordingly, B_i , P_i , and YSI stability parameters would be preferred to identify genotypes that would fulfill the dynamic model of stability.

The observed correlation coefficients between all pairs of S_{di}^2 , σ_i^2 , D_{ji} , W_i , $S^{(1)}_i$, and $S^{(2)}_i$ were positive and significant. The stability parameters among these rank correlation coefficients ranged from $r = 0.51$ to 1.00 , indicating the possibility of using these stability parameters interchangeably in grain yield stability of oat genotypes. Likewise, all possible pairs of ASV, S_{di}^2 , σ_i^2 , D_{ji} , and W_i stability parameters also showed significant positive rank correlation coefficients that ranged from $r = 0.73$ for S_{di}^2 and ASV to $r = 1.00$ for D_{ji} and S_{di}^2 or W_i and σ_i^2 , indicating that these parameters can evaluate genotypes to some degree similarly and a possibility of not necessarily using all these stability parameters simultaneously in oat

genotype selection. A significant positive correlation between these stability parameters indicates the existence of similarity in the ranking of genotypes based on these stability parameters (Kilic, 2012). According to Tamene *et al.* (2015), when the stability parameters have a positive association with each other, they can be used interchangeably because they can provide a similar pattern in the genotype ranking. The observed correlation coefficients between D_{ji} and S_{di}^2 and also between W_i and σ_i^2 were perfect positive, indicating that these pairs of stability parameters are similar in genotype ranking and thus, selection using one of each pair of stability parameters is enough for oat genotype selection. The existence of a positive correlation between W_i and σ_i^2 was also reported by various scholars (Akram *et al.*, 2012; Tamene *et al.*, 2015; Afework, 2017; Mesfin, 2017). Among the measured stability parameters, CV_i had a non-significant correlation with all stability parameters, except YSI, indicating that this stability parameter had unique characteristics in the genotype ranking.

4.4.1.11.3 Principal component analysis among yield stability parameters

The PC analysis aids understanding of the associations among parametric and nonparametric stability parameters. The biplot of the first two PCs classified the stability parameters into two stability patterns (Mohammadi *et al.*, 2012b; Tamene *et al.*, 2015), and the stability parameters considered in this study were clustered into three major groups. The stability parameters in the first and second groups (SD , CV_i , b_i , S_{di}^2 , R^2 , σ_i^2 , D_{ji} , W_i , ASV , $S^{(1)}_i$, and $S^{(2)}_i$) were not related to the grain yield, indicating that the estimates of stability using these parameters are independent and had static (biological) stability. However, the stability parameters of the third group (B_i , P_i , and YSI), which had dynamic (agronomic) stability, were significantly associated with grain yield, suggesting that breeders or agronomists can simultaneously select the genotypes for high grain yield and stability. In this study, the stability parameters on the lower left side of the biplot analysis corresponded with dynamic (agronomic) stability, which implies that the response of a genotype under changing environmental conditions is variable. Lin *et al.* (1986) and Becker and Leon (1988) reported that under dynamic stability conditions, a genotype can adjust its yield according to the environmental conditions. Sabaghnia *et al.* (2014) also reported that genotypes with dynamic stability respond differently to different environments and can yield above or below average yield across environments. The stability parameters in the third group included P_i , B_i , and YSI, and these parameters show the dynamic stability pattern. By contrast, the stability parameters on the upper right side of the biplot correspond to the static (biological) stability pattern, which indicates that a genotype shows small variance with changing environments.

This stability pattern includes the remaining 11 stability parameters, in two subgroups. The stability parameters included in the first group were SD , S_{di}^2 , D_{ji} , W_i , σ_i^2 , ASV , and $S^{(2)}_i$, while CV_i , b_i , R^2 , and $S^{(1)}_i$ were included in the second group. The biplot of the first two PCs based on the rank correlation matrix was more consistent with Spearman's coefficient of rank correlation, and this result is also in line with the findings of Tamene *et al.* (2015).

Among the stability parameters included in the first group, SD , S_{di}^2 , D_{ji} , W_i , and σ_i^2 had significant negative correlations with grain yield, while ASV and $S^{(2)}_i$ had non-significant negative correlations with grain yield. The stability parameters in the first group had static or biological stability, and based on the stability parameters of this group, low-grain-yielding genotypes were more adaptive under wider environmental conditions. Thus, selection of oat genotypes using these stability parameters may not be appropriate because these parameters measured only the extent of stability without considering the grain yield simultaneously. However, breeders, agronomists, and farmers prefer to select high-yielding genotypes that perform consistently across environments (Tamene *et al.*, 2015). The stability parameters in the second group also showed static stability, and these parameters could be used as substitute parameters to select superior genotypes with better stability. Based on the second group stability parameters, high-grain-yielding genotypes were adapted to specific environments. All the third-group stability parameters (P_i , B_i , and YSI) were strongly correlated with the grain yield of oat genotypes. Thus, genotypes with superior grain yield and widely adaptable performance could be selected through P_i , B_i , and YSI . Becker and Leon (1988) also reported that the genotypic response to changes in environmental conditions may not necessarily be equal for all genotypes. Therefore, P_i , B_i , and YSI could be used to select superior oat genotypes that perform well under wider environmental conditions in Ethiopia. However, the selection of stable genotypes based on P_i , B_i , and YSI may lead to the culling of genotypes that produce low grain yield with wide adaptation and also high grain yield with adaptability in a specific environment or environments (Roostaei *et al.*, 2014).

4.5 Conclusion

The agro-morphological traits and fodder nutritive values of oat genotypes were significantly influenced by genotype, environment, and their interaction. The environment had the highest influence on $FDMY$ followed by GEI and genotypic effects. Due to the considerable effect of GEI on the $FDMY$ performance of oat genotypes, stability analysis was done using

AMMI, GGE, and univariate analysis models. Using these statistical models, G6 and G23 had higher FDMY and performed consistently across environments. Similarly, the GY performance of these oat genotypes was significantly influenced by environment followed by genotype and their interaction. Due to the presence of significant GEI, stability analysis was also done for the GY performance of oat genotypes using AMMI, GGE, and univariate statistical models. Based on these models, G8 and G17 produced higher GY and performed consistently across environments. Therefore, G6 and G23 for FDMY; and G8 and G17 for GY were selected to verify their yield and stability performance for FDMY and GY improvements, respectively.

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Chapter V

Experiment 3: Yield, nutrient uptake, nutrient use efficiency and nutritive value of oat (*Avena sativa* L.) genotypes grown in pure stand under different fertilizer levels



Yield, nutrient uptake, nutrient use efficiency and nutritive value of oat (*Avena sativa* L.) genotypes grown in pure stand under different fertilizer levels

Abstract

The study aimed to assess the effect of fertilizer rates on agro-morphological traits, nutrient uptake and use efficiency, nutritive value, and economic feasibility of oat (*Avena sativa* L.) varieties at Holetta during the 2020/2021 and 2021/2022 cropping seasons. The study was carried out using a factorial arrangement of eight fertilizer rates (0, 25, 50, 75, 100, 125, 150, and 175%) and three oat varieties (CI-8251, SRCPX80Ab2291, and Sorataf) in a randomized complete block design with three replications. The results obtained from forage dry matter yield (FDMY) analysis revealed that variety, fertilizer, and year had significant effects on FDMY. The FDMY increased with increasing levels of fertilizer up to 175% of the blanket recommended fertilizer and application of 100, 125, 150, and 175% produced FDMY of 14.0, 15.6, 15.8, and 15.9 t/ha, respectively. The fodder type oat (CI-8251) and dual type oat (SRCPX80Ab2291) variety had 15.4 and 10.6% FDMY advantages over grain type oat (Sorataf), respectively. Moreover, the interaction effect of variety by fertilizer by year was significant for fodder nitrogen and phosphorus concentrations, nitrogen and total nutrient uptake, partial factor productivity (PFP), internal utilization efficiency (IUE), agronomic efficiency (AE), and agro-physiological efficiency (APE). The Pearson correlation analysis indicated that the number of tillers per plant, yields of morphological fractions (leaf, stem, and panicle), forage yield production rate, nutrient concentration, and uptake had significant positive associations with fertilizer levels and FDMY. In contrast, all nutrient use efficiency except APE had inverse associations with fertilizer levels and FDMY. The results obtained from grain yield (GY) analysis also revealed that fertilizer level, variety, and year had significant effects on GY, grain nutrient uptake (GNU), PFP, and AE. The highest GY (6.5 t/ha) and GNU (141.7 kg/ha) were recorded from a fertilizer level of 150% while unfertilized treatment produced the least. Among varieties, Sorataf produced the highest GY (5.7 t/ha) and GNU (129.3 kg/ha). On the other hand, the highest PFP (346.6 kg/ha) and AE (164.8 kg/ha) were observed from 25% fertilizer while the lowest PFP (59.4 kg/ha) and AE (33.4 kg/ha) were recorded from 175% fertilizer level. Sorataf exhibited the highest PFP (143.3 kg/ha) and AE (74.9 kg/ha). The Pearson correlation analysis indicated that the nutrient concentration and uptake had a positive association with fertilizer level and GY while nutrient harvest index and nutrient use efficiency had an inverse correlation with fertilizer level and GY. The results of the nutritional analysis showed that variety, fertilizer, and year had significant effects on digestible yield (DY) and total digestible nutrient yield (TDNY). Application of 175% fertilizer rate had advantages of 92.5, and 25.3% over unfertilized treatment in DY and TDNY, respectively. Among oat varieties, CI-8251 had advantages of 14.1% over the Sorataf variety in TDNY. Moreover, a 6.3% advantage in DY was recorded for SRCPX80Ab2291 over the Sorataf variety. The interaction of variety by fertilizer by year also had a significant effect on crude protein (CP), crude protein yield (CPY), digestible crude protein (DCP), in-vitro dry matter digestibility (IVDMD), total digestible nutrient (TDN), and digestible dry matter (DDM). Accordingly, the interaction effect of the Sorataf variety sown with 175% fertilizer in 2020 gave the highest CP (113.9 g/kg DM), CPY (1.66 g/kg DM), and DCP (68.2 g/kg DM). Similarly, the highest IVDMD (697.2 g/kg DM) was recorded for the interaction effect of the Sorataf variety sown with 50% fertilizer in the 2021 cropping season. Moreover, the highest TDN (704.6 g/kg DM) and DDM (707.2 g/kg DM) were observed from the interaction effect of the Sorataf variety sown with 100% fertilizer rate in the 2021 cropping season. The Pearson correlation analysis also indicated that the CP, CPY, DY, DCP, and TDNY had positive and significant associations with fertilizer application and FDMY. The combined partial budget analysis for the three oat varieties showed that the application of 125% fertilizer rate produced a higher net benefit (83,440 ETB) and marginal rate of return (12,635.6%) from fodder production. On the other hand, the application of 150% fertilizer rate produced the highest net benefit from grain production. Therefore, the application of 125% (51.3 kg N + 25 kg P/ha) fertilizer rate for fodder production and 150% (61.5 kg N + 30 kg P/ha) fertilizer rate for grain production could increase the respective yield and farm profitability in the study area.

Keywords: agro-morphological traits, economic feasibility, fertilizer application, fodder yield, grain yield, nutrient uptake, nutrient use efficiency, nutritional quality

5.1 Introduction

Soils in the highlands of Ethiopia usually have low levels of essential plant nutrients for crop production (Assefa *et al.*, 2017). However, yield response to fertilizer application varies and depends on the environment, time and frequency of harvest, and growing season precipitation (Muir *et al.*, 2001; Guretzky *et al.*, 2011). Soil fertility depletion due to limited fertilizer application, low inherent soil fertility, high rate of nitrogen (N) leaching, high fixation of phosphorus (P) in acidic soil, removal of crop residues from the field, limited application of organic manures, and soil erosion is one of the major factors that account low productivity of the crop. Hailelassie *et al.* (2006) also reported that the fertility of the soil declined due to continuous and intensive cultivation of lands without restoration of soil fertility to produce enough food for the rapidly growing population in Ethiopia. The application of optimal NP fertilizer is very important to overcome the declining soil fertility status thereby improving crop productivity (Gezahagn *et al.*, 2024). The use of inorganic fertilizers to maintain soil fertility and increase fodder and grain yields of oat is very low. Accordingly, high levels of nutrient mining due to sub-optimal fertilizer application causes severe nutrient deficiency in the Ethiopian soils which leads to high yield reduction (Assefa *et al.*, 2013; Getachew *et al.*, 2016). Therefore, adequate mineral fertilizer application is considered to be one of the most important requirements for better yield and quality (Parashar *et al.*, 2020).

The N and P nutrients are highly deficient in soils of sub-Saharan Africa (Mafongoya *et al.*, 2000). Moreover, both nutrients are most limiting for plant growth and development in most Ethiopian soils (Tadesse, 2001). N is a macronutrient also known as a vegetative nutrient and is mostly used to increase grain yield (Kamara *et al.*, 2011). It is an essential plant mineral for cell division and elongation, formation of nucleotides and enzymes resulted in higher photosynthesis activity which leads to more accumulation of photosynthates and higher fodder yield (Soheir El-Sherbeny *et al.*, 2012; Corkran *et al.*, 2015). This mineral is also responsible for the dark green color of stems and leaves, vigorous growth, branching, tillering, leaf production, size enlargement, and yield formation. N is a highly mobile nutrient in the soil system and plants absorb N either as the nitrate ion (NO_3^-) or the ammonium ion (NH_4^+) (Fageria and Baligar, 2005a). However, the availability of N is highly affected by soil acidity, and a large amount of N is lost through leaching, runoff, denitrification, volatilization, and removal by crops (Acquaah, 2002). P is also a macronutrient and it is an essential part of metabolic processes that occur within the plant,

such as photosynthesis, the synthesis and breakdown of carbohydrates, and energy transfer. Singh and Verma (2023) also pointed out that P is an integral part of nucleic acid and is essential for cellular respiration and metabolic activity. P also improves seeding vigor, encourages early growth, encourages root development, influences flowering and fruiting habits, hastens maturity, increases grain production, strengthens stalk and straw, and improves crop quality. Crops generally require an adequate amount of P fertilizer at early growth stages for optimum crop production (Colomb *et al.*, 2000; Grant *et al.*, 2005). P is absorbed as the orthophosphate ion which is either as H_2PO_4^- or HPO_4^{2-} depending on soil pH and as the soil pH increases, the relative proportion of H_2PO_4^- decreases while that of HPO_4^{2-} and PO_4^{3-} increases (Mengel *et al.*, 2001). However, its availability critically reduces under acidic soil conditions due to its reaction with aluminum and iron which form insoluble phosphate and it reacts with calcium and magnesium under alkaline soil conditions (Kamprath, 1984).

Despite the tremendous increase in fertilizer use in Ethiopia, the average fertilizer application rate is below 20 kg/ha (FAO, 2004) mainly due to the high cost of fertilizer, lack of availability and accessibility of fertilizer, low response of problematic soils (acidic, alkaline, saline soils and waterlogging in vertisols) for fertilizer application, lack of awareness on fertilizer use, and traditional farm management practices which significantly reduce yield. Increasing the use of applied fertilizer (use efficiency) through the application of fertilizer at the proper time is very important to reduce the costs of fertilizer, optimize nutrient uptake, and minimize the loss of nutrients from the soil. Thus, the application of fertilizer at the rapid growth phase is essential to increase nutrient uptake which optimizes yield and quality (Scharf and Lory, 2006). Farmers usually cultivate oat in Ethiopia with very low or without any application of fertilizer due to its better yield performance on low fertile soils compared to food crops. Oat grown with the application of fertilizer on fertile soils is susceptible to lodging and usually does not need a high amount of fertilizer. However, application of optimum fertilizer on very low fertile soil could boost the fodder and grain yields of oat.

Yield production and productivity of forage crops in general and oat (*Avena sativa* L.) crop, in particular, are highly influenced by the limited application of fertilization and loss of soil fertility in Ethiopia. So, the use of fertilizer is one of the most important agronomic practices for various forage crops and its optimum rate for higher fodder and grain productivity generally depends on crop, climate, soil, and management factors. Joshi *et al.* (2015) also

reported that the vegetative growth and yield of fodder crops depend upon the amount, type, and time of nutrient application, and capacity of the soil to supply the nutrients to the crop, and the capacity of the plant uptake and use of the applied nutrient during the growing period. The application of essential nutrients at the early growth stage is highly important to increase fodder yield. Different research studies indicated that fertilizer application generally improves the fodder yield in oat (Dubey *et al.*, 1995; Bali *et al.*, 1998; Hasan and Shah, 2000; Kumar and Ramawat, 2006; Rawat and Aggarwal, 2010; Godara *et al.*, 2016). Moreover, different scholars also reported that the application of fertilizer improves the fodder nutritional qualities in oat (Tripathi, 1993; Bhilare and Joshi, 2007; Sheoran and Joshi, 2010; Jehangir *et al.*, 2013a; Luikham *et al.*, 2014; Malik *et al.*, 2015). The deficiency of NP fertilizers adversely affects the performance of fodder and grain yields of different forage crops. Moreover, excessive application of N for fodder crops leads to succulent plant conditions, which may increase plant susceptibility to lodging and different diseases.

The ability of a genotype to give higher yield under nutrient-limiting conditions may be related to the ability to take up more nutrients from the soil under nutrient-limiting conditions (uptake efficiency) or the ability to produce higher dry matter yield per unit of nutrients in the plant tissue (utilization efficiency) or a combination of both. Uptake of adequate amount and proportion of nutrients by fodder crops is very important to produce higher yield. Similarly, the distribution of absorbed or accumulated nutrients in the shoot and grain is associated with yield improvement (Fageria and Baligar, 2005a). Nutrient use efficiency can be defined as the maximum economic yield produced per unit of nutrients applied or absorbed by the plant. Nutrient concentration in plant tissue varied with plant tissue analyzed (leaves, shoot, or whole plant), plant age, dry matter or grain yield level, crop species or genotypes within species, crop management practices, and environmental factors (Fageria and Baligar, 2005b). The application of N fertilizer increased N concentration and its uptake in oat forage yield (Sood and Kumar, 1994). The total uptake of N in oat fodder was highest with the application of 80 kg N/ha as reported by Singh *et al.* (1995a). The highest N content and uptake in oat were also recorded with the application of 120 kg N/ha (Verma, 2003; Devi *et al.*, 2010). Singh *et al.* (1996) also observed that the N application increased the P content of the forage. Sood and Kumar (1994) reported that the application of P fertilizers increased P concentration and its uptake. The total P uptake of forage was highest with 80 kg N/ha application (Singh *et al.*, 1995a).

Among management conditions, the application of essential nutrients at the right amount and time significantly improves yield and nutritional quality. Thus, optimum application of N and P fertilizers is very important for yield and quality improvement in oat. However, the recommended fertilizer rate for most forage species in Ethiopia is blanket and the recommendation doesn't depend on the physiological requirements of the crop and factors of soil, climate, and management conditions. So, the optimum fertilizer rate for higher yield and better herbage nutritional quality of oat has not been well studied and documented in Ethiopia. Accordingly, determining the optimum rate of fertilizer for higher fodder and grain yields and better nutritional quality is very important for oat improvement. Moreover, the optimum rate of fertilizer for higher fodder and grain yields should be economical and acceptable to smallholder farmers in the study area. Thus, assessing the performance of fodder and grain yields, the fodder and grain nutrient uptake, and the use efficiency, and nutritive value of oat varieties under different rates of fertilizer application is very crucial to improve yield and quality. Therefore, the objectives of this study were to (i) assess the effect of fertilizer rates on agro-morphological traits of oat varieties; (ii) evaluate the fodder and grain nutrient uptake and use efficiency of oat varieties under different fertilizer levels; (iii) investigate the effect of fertilizer application on fodder nutritive value of oat varieties (iv) determine the association coefficients between the studied parameters of oat varieties under different fertilizer levels; and (v) estimate the economic profitability of fodder and grain production from oat varieties under different fertilizer levels in the study area.

5.2 Materials and Methods

5.2.1 Description of the study area

The experiment was conducted under rainfed conditions during the main cropping seasons of 2020/2021 and 2021/2022 at Holetta Agricultural Research Center (HARC) in the central highlands of Ethiopia ([Figure 5.1](#)). The center is located at 09°03'42"N latitude, 38°29'59"E longitude, and at an altitude of 2400 meters above sea level. It is located 34 km west of Addis Ababa and is characterized by a 50-year (1970–2019) average annual rainfall of 1019.6 mm, average minimum and maximum air temperatures of 6.3 and 22.5°C, respectively. The annual precipitation of the study area during the 2020/2021 and 2021/2022 cropping seasons were 1248.9 mm and 1289.6 mm, respectively. The respective minimum temperatures of the study area were 7.1 and 8.7°C while the maximum temperatures were 23.4 and 23.9 °C, respectively ([Figure 5.2](#)). The soil type of the area is predominantly acidic Eutric Nitosol. Prior to planting, soil samples were collected from 0 to 20 cm of soil depth at

both cropping seasons and the samples were analyzed following the standard soil analysis procedures at the soil and plant analysis laboratory of HARC. The physicochemical properties of soils of the study area are indicated in [Table 5.1](#).

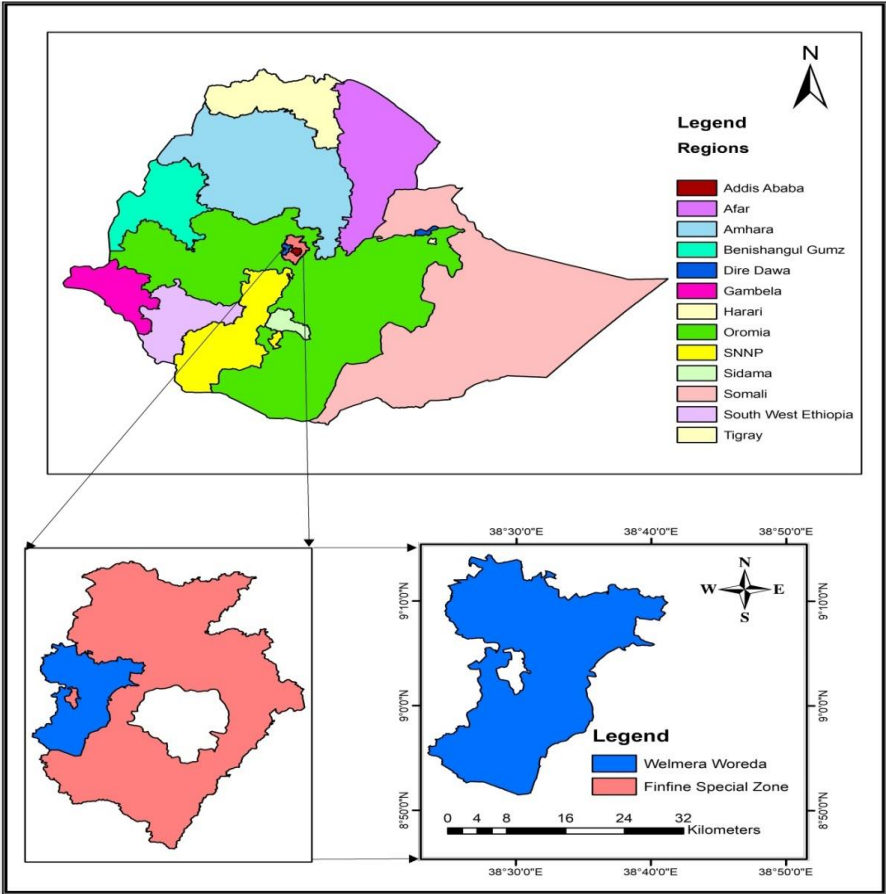


Figure 5.1 Map of the study area Holetta (Welmera Woreda)

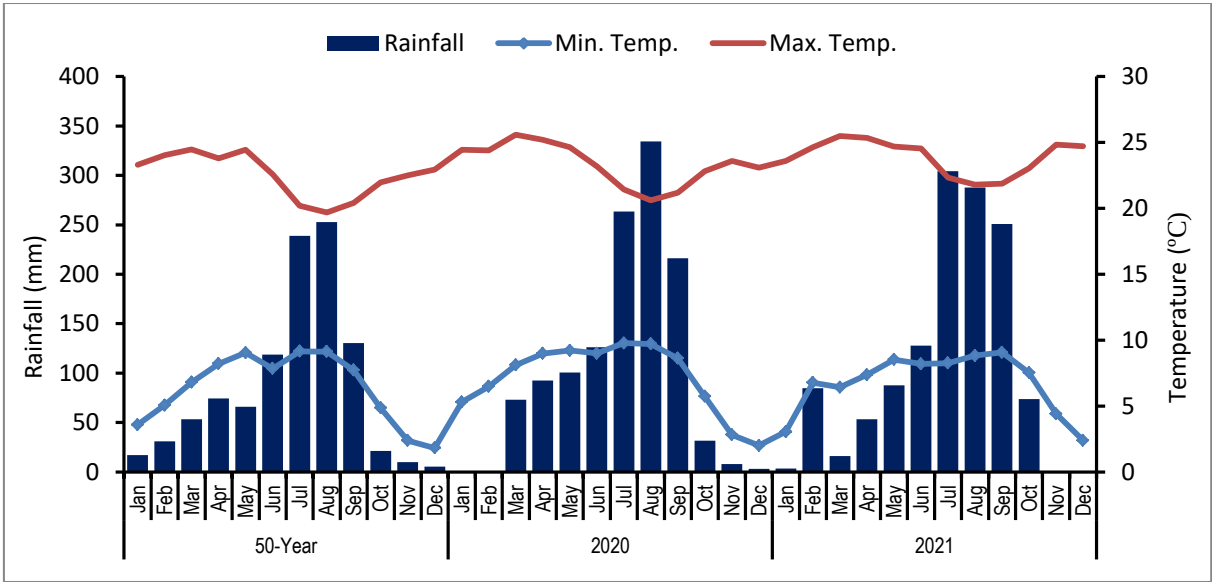


Figure 5.2 Monthly total rainfall and average minimum and maximum temperatures during the cropping seasons and 50-year (1970–2019) at Holetta

Table 5.1 Description of the test location for physico-chemical properties of the soils

Parameter	Value		Rating / class		Reference for rating
	2020	2021	2020	2021	
pH (1:2.5 H ₂ O)	5.34	5.04	Moderately acidic	Strongly acidic	Tekalign, 1991
OC (%)	1.47	1.78	Low	Moderate	Tekalign, 1991
TN (%)	0.14	0.18	Moderate	Moderate	Tekalign, 1991
C/N ratio	10.50	10.85	Low	Low	Newey, 2006
AP (ppm)	11.86	11.60	High	High	Olsen <i>et al.</i> , 1954
CEC (meq/100g)	20.61	19.82	Moderate	Moderate	Hazelton and Murphy, 2007
Sand (%)	8.33	12.67	Very low	Low	Hazelton and Murphy, 2007
Silt (%)	19.17	23.00	Low	Low	Hazelton and Murphy, 2007
Clay (%)	72.50	64.33	Very high	Very high	Hazelton and Murphy, 2007
Textural class	Clay	Clay	-	-	-

pH = power of hydrogen; **OC** = organic carbon; **TN** = Total nitrogen; **C/N** = carbon to nitrogen ratio; **AP** = Available phosphorus; **CEC** = cation exchange capacity; **ppm** = parts per million; **meq** = milliequivalent.

5.2.2 Experimental treatments and design

The study was conducted using three released oat varieties (forage type oat, dual purpose oat, and grain type oat) and eight levels of fertilizer (0, 25, 50, 75, 100, 125, 150, and 175% of the blanket recommended 100 kg/ha DAP at sowing and 50 kg/ha urea at tillering). A randomized complete block design (RCBD) replicated three times in a factorial arrangements was used for the experiment. The three oat varieties were combined with eight fertilizer levels to produce 24 treatment combinations ([Table 5.2](#)). The treatment randomization was done using PROC PLAN seed procedures of SAS general linear model version 9.4 (SAS, [2012](#)). A fine seedbed was prepared and the recommended seeding rate of 100 kg/ha was used at sowing (Astatke, [1979](#)). Each treatment was sown to a plot area of 4 m² consisting of 5 rows of 4 m long and 1 m wide with 0.2 m row spacing. The spacing between plots and blocks was 0.5 m and 1.5 m, respectively. One outermost row at both sides and 0.10 m row length from both sides of row endings were left as guard rows to avoid the border effects for each treatment. Thus, three rows with a net plot size of 3.8 m by 0.6 m (2.28 m²) were used for data collection. The blanket recommended fertilizer for oat was 18/46 kg/ha of N/P₂O₅ at sowing and 23 kg/ha of N at tillering (Getnet, [1999](#); Ashenafi, [2018](#)). The first-hand weeding was done 30 days after 90% seedling emergence (40 days after sowing) and the second hand weeding was performed 30 days after the first weeding in both cropping seasons.

Table 5.2 List of twenty-four treatments combinations used for the study

SN	Treatment combination	SN	Treatment combination
1	CI-8251 + 0/0 kg/ha DAP/Urea	13	SRCPX80Ab2291 + 100/50 kg/ha DAP/Urea
2	CI-8251 + 25/12.5 kg/ha DAP/Urea	14	SRCPX80Ab2291 + 125/62.5 kg/ha DAP/Urea
3	CI-8251 + 50/25 kg/ha DAP/Urea	15	SRCPX80Ab2291 + 150/75 kg/ha DAP/Urea
4	CI-8251 + 75/37.5 kg/ha DAP/Urea	16	SRCPX80Ab2291 + 175/87.5 kg/ha DAP/Urea
5	CI-8251 + 100/50 kg/ha DAP/Urea	17	Sorataf + 0/0 kg/ha DAP/Urea
6	CI-8251 + 125/62.5 kg/ha DAP/Urea	18	Sorataf + 25/12.5 kg/ha DAP/Urea
7	CI-8251 + 150/75 kg/ha DAP/Urea	19	Sorataf + 50/25 kg/ha DAP/Urea
8	CI-8251 + 175/87.5 kg/ha DAP/Urea	20	Sorataf + 75/37.5 kg/ha DAP/Urea
9	SRCPX80Ab2291 + 0/0 kg/ha DAP/Urea	21	Sorataf + 100/50 kg/ha DAP/Urea
10	SRCPX80Ab2291 + 25/12.5 kg/ha DAP/Urea	22	Sorataf + 125/62.5 kg/ha DAP/Urea
11	SRCPX80Ab2291 + 50/25 kg/ha DAP/Urea	23	Sorataf + 150/75 kg/ha DAP/Urea
12	SRCPX80Ab2291 + 75/37.5 kg/ha DAP/Urea	24	Sorataf + 175/87.5 kg/ha DAP/Urea

CI-8251 = forage type oat; SRCPX80Ab2291 = dual type oat; Sorataf (79Ab382 (TX) 80SA94) = grain type oat; **DAP** = diammonium phosphate (100 kg DAP = 18/46 kg N/P₂O₅ or 18/20 N/P); 100 kg Urea = 46 kg N; 0% = 0/0kg/ha DAP/Urea; **25%** = 25/12.5 kg/ha DAP/Urea; **50%** = 50/25 kg/ha DAP/Urea; **75%** = 75/37.5 kg/ha DAP/Urea; **100%** = 100/50 kg/ha DAP/Urea; **125%** = 125/62.5 kg/ha DAP/Urea; **150%** = 150/75 kg/ha DAP/Urea; **175%** = 175/87.5 kg/ha DAP/Urea.

5.2.3 Data collection

5.2.3.1 Fodder yield and its yield related traits

Data on agro-morphological traits were collected either on a plot basis or from randomly selected five plants per plot. Data collected on a plant basis were the number of tillers per plant (NTPP), tillers dry weight (TDW), number of leaves at forage harvest (NLFH), leaf length at forage harvest (LLFH), and plant height at forage harvest (PHFH). Similarly, the plot basis data were also collected on days to forage harvest (DFH), leaf dry matter yield (LDMY), stem dry matter yield (SDMY), panicle dry matter yield (PDMY), leaf to stem ratio (LSR), forage yield production rate (FYPR), and fodder dry matter yield (FDMY). These data were collected following the standard procedures (For detail see [Table 3.3](#); [Chapter 3](#)).

5.2.3.2 Grain yield and its yield related traits

Data on agro-morphological traits were collected either on a plot basis or from five randomly selected plants per plot. Data were collected on a plant basis were flag leaf length at grain harvest (FLLGH), plant height at grain harvest (PHGH), panicle length at grain harvest (PLGH), number of spikes per panicle (NSPP), and number of spikelets per panicle (NSLPP). Similarly, the plot basis data were also collected on days to seed harvest (DSH), grain filling period (GFP), biological yield production rate (BYPR), grain sink filling rate (GSFR), thousand seed weight (TSW), harvest index (HI), straw yield (SY), total biological

yield (TBY), and grain yield (GY). These grain yield and yield related data were collected following the standard procedures (For detail see [Table 3.3; Chapter 3](#)).

5.2.3.3 Nutrient uptake and use efficiency for fodder yield

The plants were harvested at the forage harvesting stage (soft dough stage) to determine the nitrogen (N) and phosphorus (P) contents. About 500 g of herbage samples were taken from each treatment and oven-dried at 65°C for 72 hours and then ground to pass a 1 mm sieve for nutrients (N and P) analysis. The forage N concentration (FNC) was determined by Kjeldahl digestion (Nelson and Sommers, [1982](#)), while the forage P concentration (FPC) was estimated photometrically in the same digest using the molybdenum blue method (Mills and Jones, [1996](#)). The fodder nutrient uptake (FNU) was calculated by multiplying the fodder yield with N and P concentrations and then dividing by 100. The fodder total nutrient uptake (FTNU) is the sum of fodder nitrogen uptake (FNU) and fodder phosphorus uptake (FPU). Moreover, the nutrient use efficiencies were calculated according to Fageria and Barbosa ([2007](#)); Getachew *et al.* ([2016](#)); and Niaz *et al.* ([2016](#)). Accordingly, the nutrient use efficiencies were calculated for partial factor productivity (PFP), partial nutrient balance (PNB), internal utilization efficiency (IUE), Agronomic efficiency (AE), and agro-physiological efficiency (APE) as indicated in [Table 5.3](#).

5.2.3.4 Nutrient uptake and use efficiency for grain yield

The plants were clipped at their base during the 90% physiological maturity for the determination of N and P contents. About 500 g of grain and 500 g of straw samples were taken and oven-dried at 65 °C for 72 hours and then ground to pass a 1 mm sieve for analysis of N and P nutrients. The total N and P concentrations for grain yield were determined following the same standard procedures as indicated above. The grain nutrient uptake (GNU) and straw nutrient uptake (SNU) were calculated by multiplying grain yield and straw yield with the respective N and P concentrations and then dividing by 100. Total nutrient uptake (TNU) is the sum of GNU and SNU. The nutrient harvest index (NHI) of grain yield was computed as follows:

$$NHI_{GY} (\%) = \frac{GNU}{TNU} * 100$$

where NHIGY = nutrient harvest index of grain yield; GNU=grain nutrient uptake; TNU=total nutrient uptake.

Similar to fodder yield, the nutrient use efficiencies for grain yield were also calculated for PFP, PNB, IUE, AE, and PE using the same equations by replacing the fodder yield by grain yield (refer Table 5.3). Moreover, the agro-physiological efficiency (APE) which refers to the economic (grain yield) production obtained per unit of nutrient uptake by biological yield (grain + straw) was calculated for grain yield as follows:

$$APE_{GY} (kg\ kg^{-1}) = \frac{GY_F - GY_U}{NuBY_F - NuBY_U}$$

where APE_{GY} = agro-physiological efficiency of grain yield; GY_F and GY_U = grain yield of the fertilized and unfertilized plot, respectively; and $NuBY_U$ and $NuBY_U$ = the nutrient uptake by the biological yield of the fertilized and unfertilized plot, respectively.

Table 5.3 Equation and its description for nutrient use efficiency parameters used for fodder yield analysis

Parameter	Definition	Equation	Equation description
Partial Factor Productivity (PFP)	The amount of fodder produced per nutrient uptake by fodder yield	$PFP_{FY} (kg\ kg^{-1}) = \frac{FY_F}{N_A}$	PFP_{FY} = partial factor productivity of fodder yield; FY_F = fodder yield in the fertilized plot; and N_A = quantity of nutrients applied as fertilizer.
Partial nutrient balance (PNB)	The nutrient exported per nutrient applied	$PNB_{FY} (kg\ kg^{-1}) = \frac{NuFY}{N_A}$	PNB_{FY} = partial nutrient balance of fodder yield; $NuFY$ = nutrient uptake by fodder yield; and N_A = the amount of applied nutrients.
Internal utilization efficiency (IUE)	The yield produced per nutrient uptake	$IUE_{FY} (kg\ kg^{-1}) = \frac{FY}{NuFY}$	IUE_{FY} = internal utilization efficiency of fodder yield; FY = fodder yield; $NuFY$ = nutrient uptake by fodder yield.
Agronomic efficiency (AE)	The economic fodder yield obtained per unit of nutrient applied	$AE_{FY} (kg\ kg^{-1}) = \frac{FY_F - FY_U}{N_A}$	AE_{FY} = agronomic efficiency of fodder yield; FY_F = fodder yield of the fertilized plot; FY_U = fodder yield of the unfertilized plot; and N_A = quantity of nutrients applied as fertilizer.
Agro-physiological efficiency (APE)	The economic (fodder yield) production obtained per unit of nutrient uptake by fodder yield	$APE_{FY} (kg\ kg^{-1}) = \frac{FY_F - FY_U}{NuFY_F - NuFY_U}$	APE_{FY} = agro-physiological efficiency of fodder yield; FY_F and FY_U = fodder yield of the fertilized and unfertilized plot, respectively; and $NuFY_U$ and $NuFY_U$ = the nutrient uptake by fodder yield of the fertilized and unfertilized plot, respectively.

5.2.3.5 Estimation of fodder nutritive values

At the recommended forage harvesting stage of oat (soft dough stage), the fodder was clipped and 500 g of forage sample was taken from each experimental unit and then oven-dried for 72 hours at a temperature of 65 °C to determine the nutritive value of the fodder oat. The oven-dried samples were ground to pass through a 1 mm sieve size for laboratory analysis. The samples were analyzed in percent dry matter basis for ash, crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), and in-vitro dry matter digestibility (IVDMD) following the standard procedures. The remaining parameters of nutritive value were also estimated using various equations as indicated in [Table 5.4](#).

Table 5.4 List of parameters of nutritive value with their methods and equations

Parameter	Abbreviation	Method/equation	Reference
Ash (g/kg DM)	Ash	Complete burning of the feed	AOAC, 1990
Neutral detergent fiber (g/kg DM)	NDF	Detergent extraction method	Goering and Van Soest, 1970
Acid detergent fiber (g/kg DM)	ADF	Detergent extraction method	Goering and Van Soest, 1970
Acid detergent lignin (g/kg DM)	ADL	Detergent extraction method	Goering and Van Soest, 1970
Hemicellulose (g/kg DM)	HC	$NDF - ADF$	Greg, 2018
Cellulose (g/kg DM)	C	$ADF - ADL$	Greg, 2018
Crude protein (g/kg DM)	CP	Kjeldahl method	Nelson and Sommers, 1982
Crude protein yield (t/ha)	CPY	$[CP (\%) \times \text{Forage yield (t/ha)}] / 100$	Akim et al., 2019
Digestible crude protein (g/kg DM)	DCP	$(CP (\%) \times 0.929) - 3.52$	Demarquilly and Weiss, 1970
In-vitro dry matter digestibility (g/kg DM)	IVDMD	In-vitro fermentation techniques	Tilley and Terry, 1963
Total digestible nutrients (g/kg DM)	TDN	$88.9 - (ADF (\%) \times 0.79)$	Greg, 2018
Digestible dry matter (g/kg DM)	DDM	$88.9 - (ADF (\%) \times 0.779)$	Greg, 2018
Digestible yield (t/ha)	DY	$[IVDMD (\%) \times \text{Forage yield (t/ha)}] / 100$	Mulisa et al., 2022
Total digestible nutrients yield (t/ha)	TDNY	$[TDN (\%) \times \text{Forage yield (t/ha)}] / 100$	Akim et al., 2019
Dry matter intake (% BW)	DMI	$120 / NDF (\%)$	Greg, 2018
Relative feed value	RFV	$[DDM (\%) \times DMI (\%)] / 1.29$	Greg, 2018
Relative feed quality	RFQ	$[TDN (\%) \times DMI (\%)] / 1.23$	Greg, 2018
Digestible energy (MJ/kg DM)	DE	$(TDN (\%) \times 0.04409) \times 4.184$	NRC, 2001
Metabolizable energy (MJ/kg DM)	ME	$DE \times 0.82$	Weiss, 1993
Net energy for lactation (MJ/kg DM)	NEl	$[(TDN (\%) \times 0.01114) - 0.054] \times 9.224149$	Gökhan and Ayşe, 2021
Net energy for maintenance (MJ/kg DM)	NE _m	$[(TDN (\%) \times 0.01318) - 0.132] \times 9.224149$	Gökhan and Ayşe, 2021
Net energy for gain (MJ/kg DM)	NE _g	$[(TDN (\%) \times 0.01318) - 0.459] \times 9.224149$	Gökhan and Ayşe, 2021

5.2.4 Data analysis

Analysis of variance (ANOVA) procedures of the SAS general linear model (GLM) version 9.4 was used to compare treatment means (SAS, 2012). The validity of assumptions of ANOVA for each year and over years was computed using the Bartlett test and F-max method of Hartley, respectively (For detail see subsection 3.2.6.1; Chapter 3). After testing the homogeneity of error variance using the F-max method of Hartley, combined analyses of variance was performed using the PROC GLM procedure where variety, fertilizer, and year effects were fixed, therefore a linear fixed model was used for data analysis. Accordingly, all factors were tested against the last mean square error (residuals). The statistical significance was determined using the F-test and mean comparisons were done using Duncan's Multiple

Range Test at 5% probability levels (Gomez and Gomez, 1984). The statistical model for combined analysis over years is presented below.

$$Y_{ijkl} = \mu + (B/Y)_{il} + V_j + F_k + Y_l + (VF)_{jk} + (VY)_{jl} + (FY)_{kl} + (VFY)_{jkl} + \epsilon_{ijkl}$$

where Y_{ijkl} = measured response of variety j in fertilizer k in block i (at year) l ; μ = grand mean; $(B/Y)_{il}$ = the effect of block i (within year l); V_j = effect of variety j ; F_k = effect of fertilizer k ; Y_l = effect of year l ; $(VF)_{jk}$ = interaction effect between variety j and fertilizer k ; $(VY)_{jl}$ = interaction effect between variety j and year l ; $(FY)_{kl}$ = interaction effect between fertilizer k and year l ; $(VFY)_{jkl}$ = interaction effect among variety j , fertilizer k and year l ; and ϵ_{ijkl} = residual or effect of random error.

Moreover, the Pearson correlation analysis of measured parameters with fertilizer levels and yields (fodder and grain) was performed following the SAS CORR procedure of version 9.4 (SAS, 2012). Correlation analysis was also performed between some measured plant and nutrient parameters for both fodder and grain yields.

5.2.5 Economic analysis

The economic analysis was performed to investigate the economic feasibility of the treatments by using a partial budget analysis (CIMMYT, 1988). Total cost is the sum of costs of input (seeds and fertilizers) and labor for different field activities and it was recorded as a total cost (TC) during the experimental period. Labor cost for each activity was taken based on the local daily wage per person to perform the activity. The fodder selling price was determined based on the average price of natural pasture hay obtained from the local market (Holetta) at harvest. Moreover, the grain and straw selling prices were obtained from Holetta market at harvest. The gross benefits (GB) for fodder and grain yields were calculated by multiplying the fodder and grain plus straw yields (kg/ha) by their respective average open market price (birr/kg fodder and grain plus straw yields). In the economic analysis, the average fodder and grain plus straw yields were adjusted downwards by 10%, taking into consideration that farmers could obtain 10% less than the experiment yield (CIMMYT, 1988). The net benefits (NB) for fodder and grain plus straw were calculated as the amount of money left when the TC was deducted from the GB. The net benefit-to-cost ratio (BCR) for fodder and grain plus straw yields was estimated by dividing NB by TC. The marginal rate of return (MRR) is used to assess the relative profitability among alternative treatments. It measures the percentage increase in NB and the 100% rate of return is

considered as a minimum value upon which farmers could be willing to invest (CIMMYT, 1988). The MRR was calculated as the change in NB divided by the change in TC of the successive NB and TC levels and a treatment that is non-dominated having a MRR greater than 100% and having the highest NB is said to be economically profitable (CIMMYT, 1988).

$$\text{MRR (\%)} = \frac{\Delta \text{NB}}{\Delta \text{TC}} * 100$$

where MRR = marginal rate of return; ΔNB and ΔTC = change in net benefit and total cost, respectively.

To perform dominance analysis, the treatments were arranged in order of increasing TC. Accordingly, treatment is said to be dominated which denoted by "D", if its TC is higher than the preceding treatment but its net benefit is lower (CIMMYT, 1988). Moreover, sensitivity analysis was performed due to the ever-increasing of market prices (input and labor costs). So, it was estimated that a 100% increase (20% per annum) of TC over the next five years starting from 2023.

5.3 Results

5.3.1 Fodder yield and yield related traits

5.3.1.1 Analysis of variance

The pooled analysis of variance for measured 22 parameters is indicated in Table 5.5. The results showed that the varietal effect was significant for all measured parameters except TDW, PDMY, and PNB. Similarly, the fertilizer effect had a significant influence on all measured parameters except DFH, LSR, and PNB. The production year also had a significant effect on all measured parameters except TDW, NLFH, LLFH, LDMY, PFP, IUE, and AE. The interaction effect of variety and fertilizer was significant for TDW, LSR, FPC, and FNC. Similarly, the interaction effect of variety and year was also significant for TDW, NLFH, DFH, LDMY, PDMY, and FPC. Moreover, the interaction effect of fertilizer and year was significant for LLFH, LSR, FPC, FNC, FPU, and APE. The three-way interaction of variety by fertilizer by year effect was significant for NLFH, FPC, FNC, FNU, TFNU, PFP, IUE, AE, and APE.

Table 5.5 Analysis of variance for 22 parameters of three oat varieties sown with eight fertilizer levels in 2020/2021 and 2021/2022 cropping seasons at Holetta

Parameter	Mean squares									Mean
	R	V	F	Y	V x F	V x Y	F x Y	V x F x Y	Error	
NTPP	4.87***	1.89*	1.38**	13.81***	0.23 ^{NS}	1.19 ^{NS}	0.44 ^{NS}	0.24 ^{NS}	0.45	2.99
TDW	21.88*	17.99 ^{NS}	24.41***	23.36 ^{NS}	11.12*	20.81*	10.70 ^{NS}	4.22 ^{NS}	4.22	25.32
NLFH	0.20 ^{NS}	10.60***	1.96***	0.06 ^{NS}	0.12 ^{NS}	1.45***	1.45 ^{NS}	0.21*	0.11	4.77
LLFH	11.18 ^{NS}	2803.73***	144.94***	42.47 ^{NS}	10.45 ^{NS}	25.61 ^{NS}	41.64*	10.89 ^{NS}	15.59	42.91
PHFH	104.31 ^{NS}	26233.53***	257.96*	620.43*	145.52 ^{NS}	71.44 ^{NS}	8.98 ^{NS}	137.17 ^{NS}	111.83	138.07
DFH	2.08 ^{NS}	2472.27***	12.08 ^{NS}	396.67***	5.17 ^{NS}	175.34***	3.91 ^{NS}	4.84 ^{NS}	5.74	111.15
LDMY	0.20 ^{NS}	9.11***	10.08***	0.06 ^{NS}	0.45 ^{NS}	2.77*	0.63 ^{NS}	0.70 ^{NS}	0.76	4.19
SDMY	0.03 ^{NS}	14.57***	19.64***	40.32***	0.67 ^{NS}	2.48 ^{NS}	1.58 ^{NS}	1.09 ^{NS}	1.09	5.27
PDMY	0.34 ^{NS}	1.36 ^{NS}	11.63***	3.48*	0.75 ^{NS}	3.23*	1.18 ^{NS}	0.99 ^{NS}	0.72	3.91
LSR	0.02 ^{NS}	0.10*	0.03 ^{NS}	0.97***	0.05*	0.02 ^{NS}	0.08*	0.05 ^{NS}	0.03	0.82
FYPR	13.34 ^{NS}	2047.30**	10132.07***	3705.77**	156.26 ^{NS}	73.61 ^{NS}	109.09 ^{NS}	300.48 ^{NS}	330.14	120.63
FDMY	0.46 ^{NS}	45.04***	118.06***	18.35*	1.61 ^{NS}	2.27 ^{NS}	1.41 ^{NS}	4.08 ^{NS}	3.98	13.38
FPC	0.00 ^{NS}	0.03***	0.01***	0.33***	0.002***	0.002*	0.002***	0.002***	0.0004	0.20
FNC	0.01 ^{NS}	0.86***	0.28***	0.61***	0.05**	0.03 ^{NS}	0.04*	0.09***	0.02	1.04
FPU	19.21 ^{NS}	200.39***	911.72***	4751.80***	32.67 ^{NS}	44.49 ^{NS}	97.44***	38.92 ^{NS}	23.81	26.37
FNU	218.58 ^{NS}	3422.94*	27066.92***	20549.22***	1522.70 ^{NS}	525.24 ^{NS}	1013.45 ^{NS}	2285.35**	2285.35	141.72
FTNU	366.09 ^{NS}	4978.60*	37653.89***	5552.73*	1728.10 ^{NS}	658.55 ^{NS}	999.54 ^{NS}	2409.65*	1240.40	168.09
PFPHY	960.30 ^{NS}	15377.01*	820221.02***	13037.74 ^{NS}	1415.31 ^{NS}	4026.68 ^{NS}	2346.90 ^{NS}	10048.00**	3931.12	317.20
PNBFY	0.39 ^{NS}	3.29 ^{NS}	111.45 ^{NS}	4.73*	0.93 ^{NS}	0.96 ^{NS}	1.29 ^{NS}	0.97 ^{NS}	1.08	3.99
IUEFY	12.74 ^{NS}	4201.88***	215.73**	139.13 ^{NS}	105.25 ^{NS}	64.25 ^{NS}	84.32 ^{NS}	243.11***	53.55	79.86
AEFY	1138.19 ^{NS}	11354.53*	38865.45***	5208.43 ^{NS}	2412.39 ^{NS}	1897.20 ^{NS}	1402.19 ^{NS}	8064.40*	3554.39	111.87
APEFY	196.13 ^{NS}	2299.70***	707.58**	760.24*	267.61 ^{NS}	278.91 ^{NS}	589.00**	1547.99***	174.11	65.47

NTPP = number of tillers per plant (number); TDW = tillers dry weight (g); NLFH = number of leaves at forage harvest (number); LLFH = leaf length at forage harvest (cm); PHFH = plant height at forage harvest (cm); DFH = days to forage harvest (days); LDMY = leaf dry matter yield (t/ha); SDMY = stem dry matter yield (t/ha); PDMY = panicle dry matter yield (t/ha); LSR = leaf to stem ratio; FYPR = forage yield production rate (kg/ha/day); FDMY = fodder dry matter yield (t/ha); FPC = fodder phosphorus concentration (%); FNC = fodder nitrogen concentration (%); FPU = fodder phosphorus uptake (kg/ha); FNU = fodder nitrogen uptake (kg/ha); FTNU = fodder total nutrient uptake (kg/ha); PFPHY = partial factor productivity of fodder yield (kg/kg); PNBFY = partial nutrient balance of fodder yield (kg/kg); IUEFY = internal utilization efficiency of fodder yield (kg/kg); AEFY = agronomic efficiency of fodder yield (kg/kg); APEFY = agro-physiological efficiency of fodder yield (kg/kg); R = replication; V = variety; F = fertilizer level; Y = year; V x F = variety by fertilizer level interaction; V x Y = variety by year interaction; F x Y = fertilizer level by year interaction; V x F x Y = variety by fertilizer level by year interaction; NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively.

5.3.1.2 Main and interaction effects on agro-morphological traits

The NTPP was significantly influenced by fertilizer, variety, and year effects (Table 5.6). The NTPP increased with increasing levels of fertilizer up to the application of 125% (51.3 kg N + 25 kg P/ha) of the recommended fertilizer rate. Among oat varieties, the grain type oat (Sorataf) gave the highest NTPP (3.2) while the forage type oat (CI-8251) gave the lowest (2.8). The NTPP was higher (3.3) in 2021 than in 2020 (2.7) cropping season. The TDW was influenced significantly by the interaction effects of variety by fertilizer (Table 5.7) and variety by year (Figure 5.3 top left). Accordingly, the highest TDW (28.7 g) was recorded from the interaction effect of the Sorataf variety with the application of 125% of the recommended fertilizer. In contrast, the lowest TDW (22.8 g) was obtained from the interaction effect of the CI-8251 variety with the application of 25% (10.3 kg N + 5 kg P/ha)

of the recommended fertilizer rate. The interaction effect of the CI-8251 variety with the 2020 cropping season gave the highest TDW (26.1 g) while the lowest (23.6 g) was recorded from the interaction effect of Sorataf variety with the 2020 cropping season.

Table 5.6 Effects of fertilizer, variety and year on number of tillers per plant, plant height at forage harvest, stem dry matter yield, and fodder yield production rate of oat at Holetta

Parameter	Traits			
	NTPP	PHFH	SDMY	FYPR
Percent of the recommended fertilizer rate				
0%	2.6 ^c	132.0 ^c	3.3 ^e	75.3 ^d
25%	2.7 ^{bc}	134.4 ^{bc}	4.5 ^d	103.4 ^c
50%	2.8 ^{bc}	136.1 ^{a-c}	5.1 ^{cd}	115.1 ^{bc}
75%	3.1 ^{ab}	139.1 ^{a-c}	5.0 ^{cd}	116.3 ^b
100%	3.2 ^{ab}	140.6 ^{ab}	5.6 ^{bc}	125.4 ^b
125%	3.4 ^a	143.5 ^a	6.0 ^{ab}	142.7 ^a
150%	2.9 ^{a-c}	141.0 ^{ab}	6.2 ^{ab}	143.2 ^a
175%	3.2 ^{ab}	138.0 ^{a-c}	6.4 ^a	143.5 ^a
<i>P-value</i>	0.0060	0.0325	<.0001	<.0001
Variety				
CI-8251	2.8 ^b	162.5 ^a	5.8 ^a	119.2 ^b
SRCPX80Ab2291	2.9 ^b	135.8 ^b	5.4 ^a	127.8 ^a
Sorataf	3.2 ^a	115.9 ^c	4.7 ^b	114.9 ^b
<i>P-value</i>	0.0183	<.0001	<.0001	0.0030
Year				
2020	2.7 ^b	136.0 ^b	4.7 ^b	115.6 ^b
2021	3.3 ^a	140.1 ^a	5.8 ^a	125.7 ^a
<i>P-value</i>	<.0001	0.0206	<.0001	0.0012

NTPP = number of tillers per plant (numbers); PHFH = plant height at forage harvest (cm); SDMY = stem dry matter yield (t/ha); FYPR = fodder yield production rate (kg/ha/day); Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

The PHFH is influenced by fertilizer, variety, and year effects (Table 5.6). The highest PHFH (143.5 cm) was recorded from the application of 125% (51.3 kg N + 25 kg P/ha) of the recommended fertilizer rate while unfertilized treatment gave the lowest (132.0 cm). Among oat varieties, CI-8251 had the highest PHFH (162.5 cm) while Sorataf gave the lowest (115.9 cm). The second year of production gave higher PHFH (140.1 cm) compared to the first year of production (136.0 cm). The FYPR was also influenced significantly by the effects of fertilizer, variety, and year (Table 5.6). The FYPR increased with the increasing rate of fertilizer. Accordingly, the highest FYPR (143.5 kg/ha/day) was recorded from the application of 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate while unfertilized treatment had the lowest (75.3 kg/ha/day). The dual-type oat (SRCPX80Ab2291) variety had the highest FYPR (127.8 kg/ha/day) while the grain type (Sorataf) had the lowest (114.9 kg/ha/day). The FYPR was higher (125.7 kg/ha/day) in 2021 compared to 2020 (115.6 kg/ha/day) cropping season.

Table 5.7 Interaction effect of fertilizer by variety for tillers dry weight and leaf to stem ratio of oat at Holetta

Traits	Percent of fertilizer level	Variety		
		CI-8251	SRCPX80Ab2291	Sorataf
TDW	0%	24.1 ^{d-f}	23.7 ^{d-f}	23.2 ^{ef}
	25%	22.8 ^f	25.2 ^{a-f}	24.7 ^{b-f}
	50%	26.7 ^{a-e}	25.4 ^{a-f}	23.0 ^f
	75%	27.7 ^{a-c}	25.8 ^{a-f}	24.0 ^{d-f}
	100%	25.9 ^{a-f}	27.9 ^{ab}	25.7 ^{a-f}
	125%	26.8 ^{a-d}	26.2 ^{a-f}	28.7 ^a
	150%	25.9 ^{a-f}	25.2 ^{a-f}	23.2 ^{ef}
	175%	27.0 ^{a-d}	24.2 ^{c-f}	24.8 ^{b-f}
LSR	0%	0.82 ^{a-c}	0.90 ^{a-c}	0.87 ^{a-c}
	25%	1.07 ^a	0.70 ^c	0.75 ^{bc}
	50%	0.82 ^{a-c}	0.73 ^{bc}	0.80 ^{a-c}
	75%	1.00 ^{ab}	0.80 ^{a-c}	0.82 ^{a-c}
	100%	0.80 ^{a-c}	0.75 ^{bc}	0.93 ^{a-c}
	125%	0.98 ^{a-c}	0.80 ^{a-c}	0.80 ^{a-c}
	150%	0.77 ^{bc}	0.75 ^{bc}	0.82 ^{a-c}
	175%	0.72 ^{bc}	0.80 ^{a-c}	0.78 ^{a-c}

TDW = tillers dry weight (g); LSR = leaf to stem ratio; Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$.

The LSR varied significantly for the interaction effect of variety by fertilizer (Table 5.7). The highest LSR (1.07) was recorded for the interaction effect of the CI-8251 variety with 25% (10.3 kg N + 5 kg P/ha) of the recommended fertilizer rate while the lowest (0.70) was obtained from the interaction effect of SRCPX80Ab2291 variety with 25% fertilizer rate. Moreover, the LSR was significant for the interaction effect of fertilizer by year (Table 5.9). The result showed that the interaction effect of 25% fertilizer with 2020 and 2021 cropping seasons produced the highest (1.02) and the lowest (0.66) LSR, respectively. The SDMY was significant for fertilizer, variety, and year effects (Table 5.6). The DFH was influenced significantly by the interaction effect of variety by year (Figure 5.3 top right). The interaction effect of the CI-8251 variety with the 2021 cropping season requires a longer DFH (119.6) while a shorter DFH (102.9) was recorded for the interaction effect of the SRCPX80Ab2291 variety with the 2021 cropping season. The highest SDMY (6.4 t/ha) was recorded for 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate while unfertilized treatment produced the lowest (3.3 t/ha). Among oat varieties, CI-8251 produced the highest SDMY (5.8 t/ha) while the lowest (4.7 t/ha) was recorded from the Sorataf variety. The SDMY was higher (5.8 t/ha) in 2021 compared to 2020 (4.7 t/ha) cropping season (Table 5.6).

The LDMY and PDMY were significant for the interaction effect of variety by year (Figure 5.3 bottom left and right). Accordingly, the highest LDMY (4.8 t/ha) and SDMY (4.2 t/ha) were recorded for the interaction effects of the CI-8251 variety with 2021 and CI-8251 variety with 2020 cropping season, respectively. On the other hand, the lowest LDMY (3.7 t/ha) and SDMY (3.4 t/ha) were recorded for the interaction effect of Sorataf with the 2020 cropping season and the interaction effect of CI-8251 variety with the 2021 cropping season, respectively. The LDMY was also significantly influenced by fertilizer (Figure 5.4 right). Accordingly, the LDMY increased with increasing rate of fertilizer application up to 125% (51.3 kg N + 25 kg P/ha) of the recommended fertilizer rate. The result indicated that the highest LDMY (5.1 t/ha) was recorded from the application of 125% fertilizer rate while unfertilized treatment produced the lowest (2.8 t/ha).

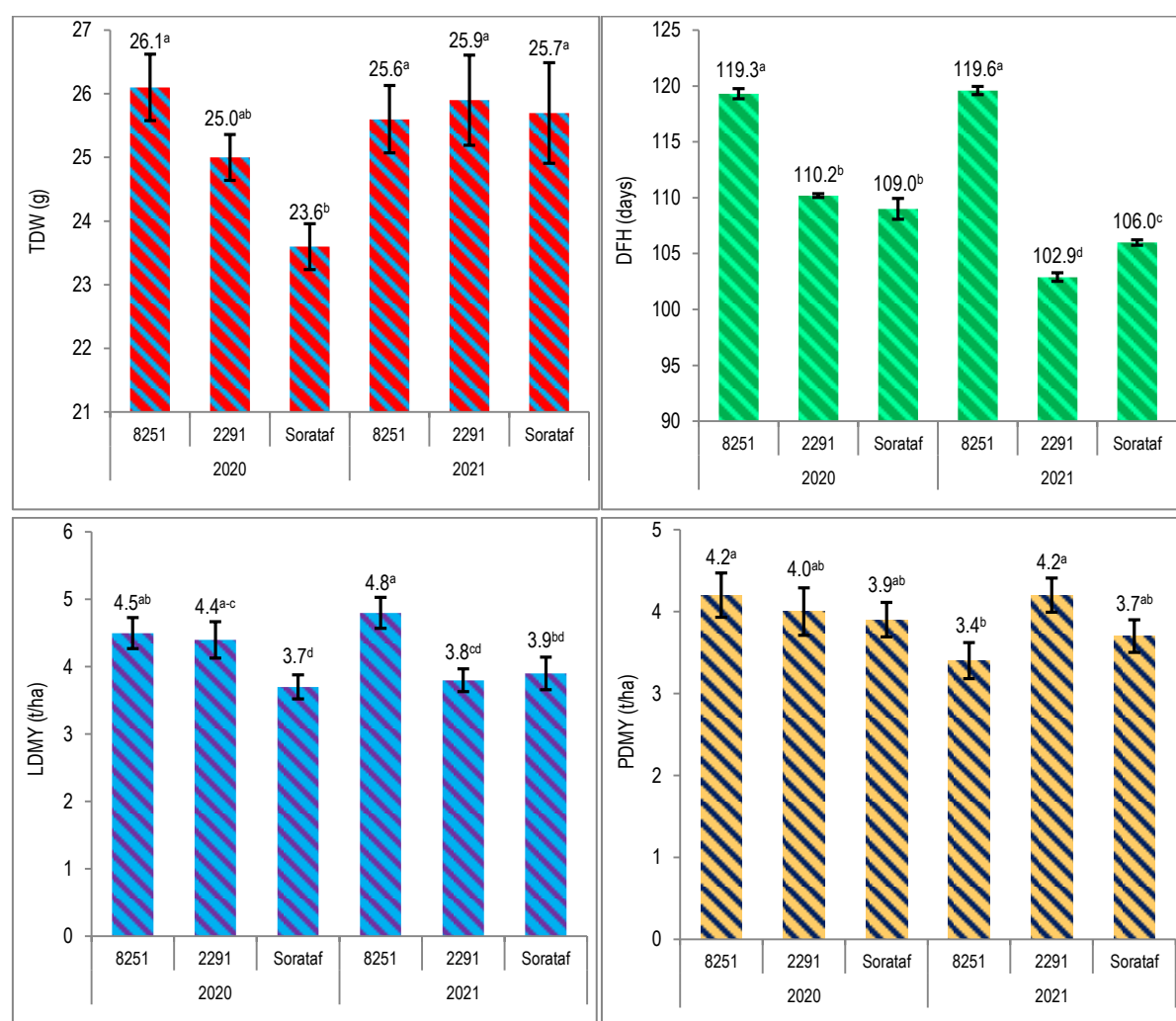


Figure 5.3 Interaction effect of variety by year on tillers dry weight (TDW), days to forage harvest (DFH), leaf dry matter yield (LDMY), and panicle dry matter yield (PDMY) of oat at Holetta

Table 5.8 Interaction effect of variety by fertilizer by year on the mean performance of number of leaves at forage harvest (NLFH) of oat at Holetta

Trait	Percent of fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
NLFH	0%	5.6 ^{ab}	4.5 ^{h-l}	3.9 ^{lm}	5.0 ^{b-h}	4.3 ^{i-m}	4.7 ^{f-j}
	25%	5.4 ^{a-d}	4.3 ^{i-m}	4.4 ^{h-l}	5.3 ^{a-g}	4.4 ^{h-l}	4.7 ^{g-j}
	50%	5.0 ^{b-h}	4.6 ^{g-k}	4.6 ^{g-k}	5.2 ^{a-g}	4.7 ^{e-j}	4.6 ^{g-k}
	75%	5.7 ^a	4.4 ^{h-l}	4.5 ^{h-l}	4.9 ^{c-i}	4.9 ^{c-i}	4.8 ^{d-j}
	100%	5.7 ^a	4.8 ^{d-i}	4.7 ^{f-j}	5.7 ^a	4.7 ^{f-j}	4.8 ^{d-i}
	125%	5.8 ^a	5.0 ^{b-h}	5.0 ^{b-h}	5.7 ^a	5.0 ^{b-h}	5.4 ^{a-e}
	150%	5.3 ^{a-f}	4.0 ^{k-m}	4.0 ^{k-m}	4.9 ^{d-i}	3.7 ^m	4.1 ^{j-m}
	175%	5.5 ^{a-c}	4.3 ^{i-m}	3.9 ^{lm}	4.3 ^{i-m}	3.9 ^{lm}	4.3 ^{i-m}

NLFH = number of leaves at forage harvest (numbers); Means followed by a common superscript letter within a column and row are not significantly different from each other at $P < 0.05$.

Table 5.9 Interaction effect of fertilizer by year on the mean performance of leaf length at forage harvest (LLFH) and leaf to stem ratio (LSR) of oat at Holetta

Traits	Percent of fertilizer level	Year	
		2020	2021
LLFH	0%	40.0 ^{bc}	40.1 ^{bc}
	25%	40.5 ^{bc}	41.2 ^{bc}
	50%	41.6 ^{a-c}	43.4 ^{a-c}
	75%	42.4 ^{a-c}	44.2 ^{a-c}
	100%	45.2 ^{a-c}	45.3 ^{a-c}
	125%	49.9 ^a	47.4 ^{ab}
	150%	43.4 ^{a-c}	39.6 ^{bc}
	175%	44.6 ^{a-c}	37.8 ^c
LSR	0%	0.86 ^{a-c}	0.87 ^{a-e}
	25%	1.02 ^a	0.66 ^d
	50%	0.90 ^{ab}	0.67 ^{dc}
	75%	0.89 ^{ab}	0.86 ^{a-c}
	100%	0.87 ^{a-c}	0.79 ^{b-d}
	125%	0.91 ^{ab}	0.81 ^{b-d}
	150%	0.91 ^{ab}	0.64 ^d
	175%	0.89 ^{ab}	0.64 ^d

LLFH = leaf length at forage harvest (cm); LSR = leaf to stem ratio; Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$.

The interaction effect of variety by fertilizer by year was significant for the NLFH (Table 5.8). The result indicated that the CI-8251 variety sown with the application of 125% of the recommended fertilizer rate in the 2020 cropping season gave the highest NLFH (5.8). In contrast, the lowest NLFH (3.7) was recorded for the SRCPX80Ab2291 variety sown with the application of 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate in the 2021 cropping season. The LLFH showed significant variation in the interaction effect of fertilizer by year (Table 5.9). The highest LLFH (49.9 cm) was recorded for the interaction effect of 125% (51.3 kg N + 25 kg P/ha) of the recommended fertilizer rate during the 2020 cropping season. In contrast, the interaction effect of 175% (71.8 kg N + 35 kg P/ha) of the

recommended fertilizer rate during the 2021 cropping season produced the lowest LLFH (37.8 cm). Moreover, the LLFH varied significantly among oat varieties (Figure 5.4 left). The result showed that the highest LLFH (51.8 cm) was recorded for the CI-8251 variety while the lowest (38.3 cm) was recorded for the SRCPX80Ab2291 variety.

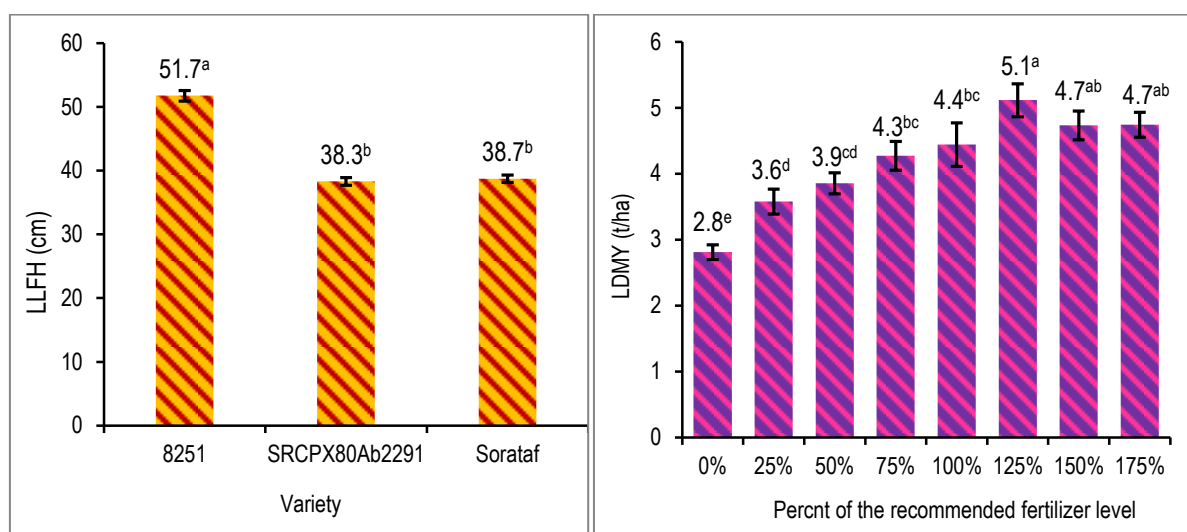


Figure 5.4 Effect of variety on leaf length at forage harvest (left) and fertilizer on leaf dry matter yield (right) at Holetta. **Note:** LLFH = leaf length at forage harvest; LDMY = leaf dry matter yield

The FDMY varied significantly for the effects of fertilizer, variety, and year (Figure 5.5). The FDMY increased with increasing levels of fertilizer (Figure 5.5 top). Accordingly, application of 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer gave the highest FDMY (15.9 t/ha) followed by 150% (61.5 kg N + 30 kg P/ha), 125% (51.3 kg N + 25 kg P/ha), 100% (41.0 kg N + 20 kg P/ha), and 75% (30.8 kg N + 15 kg P/ha) of fertilizer which produced FDMY of 15.8, 15.6, 14.0, and 13.0 t/ha, respectively. In contrast, the unfertilized treatment produced the lowest FDMY (8.4 t/ha). The box and whisker plot also showed the variability of FDMY for each fertilizer rate. The highest inter-quintile range (IQR) was observed for 25% (10.3 kg N + 5 kg P/ha) of the recommended fertilizer rate followed by 100% and 125% of fertilizer while the lowest IQR was recorded from unfertilized treatment. The range of FDMY was the highest for 150% fertilizer rate while unfertilized treatment had the lowest range. The shortest lower whisker was observed for the application of 25% fertilizer rate while 150% fertilizer rate had the longest upper whisker which showed narrow and wide variability in the 25% of the lower and higher data set, respectively. The FDMY varied among oat varieties (Figure 5.5 bottom left). The highest FDMY (14.2 t/ha) was recorded for forage type oat (CI-8251) followed by dual type oat (SRCPX80Ab2291) and grain type oat (Sorataf) which produced 13.6 and 12.3 t/ha, respectively. The 2021 cropping

season gave the highest FDMY (13.7 t/ha) compared to the 2020 (13.0 t/ha) cropping season (Figure 5.5 bottom right).

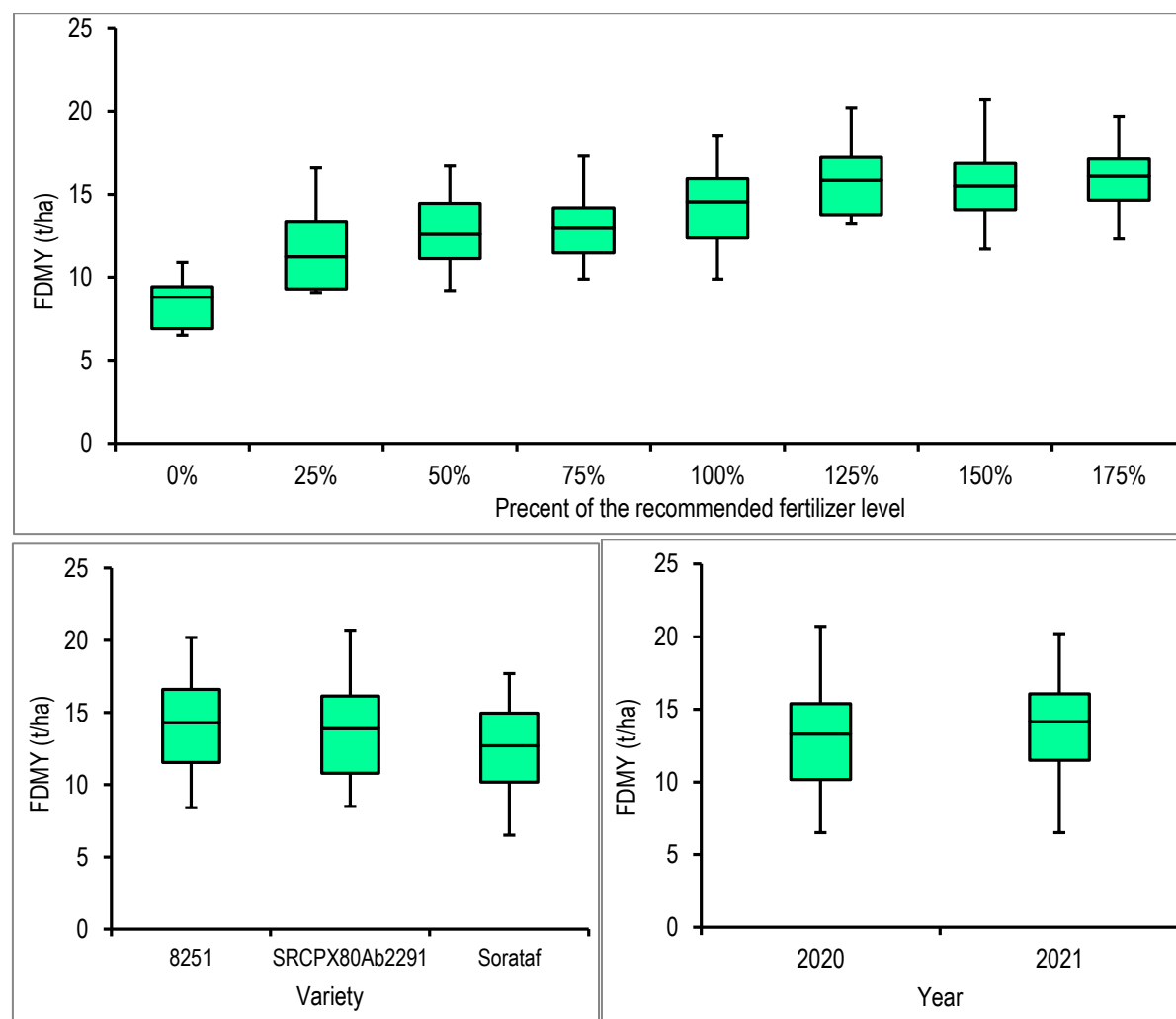


Figure 5.5 Box and whisker plot for oat fodder yield as influenced by levels of fertilizer, variety and year at Holetta. **Note:** FDMY = forage dry matter yield

5.3.1.3 Main and interaction effects on nutrient content, uptake and use efficiency

The FPC varied significantly for the interaction effect of variety by fertilizer by year (Table 5.10). The results showed that the Sorataf variety which received 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate in the 2020 cropping season produced the highest FPC (0.32%). In contrast, the CI-8251 variety sown without fertilizer in the 2021 cropping season gave the lowest FPC (0.10%). Similarly, the highest FNC (1.78%) was observed for the Sorataf variety sown with the application of 175% fertilizer rate in the 2020 cropping season while the lowest FNC (0.66%) was observed for the CI-8251 variety sown without fertilizer in 2020 cropping season. Moreover, the highest FNU (264.8 kg/ha) and FTNU (313.4 kg/ha) was recorded for the Sorataf variety sown with 175% fertilizer rate in 2020

cropping season. The lowest FNU (52.0 kg/ha) and TFNU (61.7 kg/ha) were observed for the Sorataf variety sown without fertilizer in 2020 cropping season. The FPU was influenced significantly by the interaction effect of fertilizer by year (Table 5.11). The result showed that the highest FPU (43.2 kg/ha) was observed for 175% fertilizer rate in the 2020 cropping season. In contrast, the lowest FPU (10.0 kg/ha) was observed for unfertilized treatment in the 2021 cropping season. The FPU also varied significantly among oat varieties (Figure 5.6 bottom left). The highest FPU (27.6 kg/ha) was recorded for the SRCPX80Ab2291 variety while the CI-8251 had the lowest FPU (24.0 kg/ha).

Table 5.10 Interaction effect of variety by fertilizer by year for fodder phosphorus and nitrogen concentrations, fodder nitrogen uptake, and fodder total nutrient uptake performance of oat at Holetta

Parameter	Recommended fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
FPC	0%	0.11 ^{xw}	0.20 ^{k-m}	0.14 ^{r-w}	0.10 ^x	0.12 ^{u-x}	0.13 ^{s-x}
	25%	0.25 ^{f-j}	0.27 ^{d-g}	0.29 ^{a-e}	0.13 ^{t-x}	0.15 ^{o-w}	0.16 ^{m-u}
	50%	0.19 ^{l-n}	0.28 ^{b-f}	0.30 ^{a-d}	0.14 ^{s-x}	0.15 ^{n-v}	0.19 ^{l-p}
	75%	0.27 ^{c-f}	0.25 ^{e-i}	0.22 ^{j-l}	0.13 ^{u-x}	0.15 ^{n-v}	0.19 ^{l-o}
	100%	0.17 ^{m-t}	0.26 ^{e-i}	0.31 ^{a-c}	0.13 ^{s-x}	0.17 ^{m-t}	0.17 ^{m-t}
	125%	0.23 ^{i-k}	0.26 ^{e-i}	0.31 ^{ab}	0.13 ^{s-x}	0.16 ^{n-v}	0.18 ^{l-r}
	150%	0.23 ^{h-k}	0.26 ^{e-i}	0.25 ^{f-j}	0.12 ^{v-x}	0.14 ^{q-w}	0.17 ^{m-s}
	175%	0.23 ^{g-k}	0.27 ^{d-h}	0.32 ^a	0.15 ^{p-w}	0.16 ^{n-u}	0.18 ^{l-q}
FNC	0%	0.66 ^o	0.66 ^o	0.76 ^{m-o}	0.74 ^{no}	0.81 ^{l-o}	1.03 ^{e-m}
	25%	0.80 ^{l-o}	0.85 ^{j-o}	1.00 ^{g-n}	0.89 ^{i-o}	1.07 ^{c-l}	1.31 ^{bc}
	50%	0.89 ^{i-o}	1.07 ^{c-l}	1.09 ^{c-j}	1.14 ^{c-i}	0.96 ^{g-n}	1.43 ^b
	75%	0.74 ^{no}	0.98 ^{g-n}	1.13 ^{c-i}	1.01 ^{f-m}	1.19 ^{b-h}	1.15 ^{c-i}
	100%	1.30 ^{b-d}	1.14 ^{c-i}	1.04 ^{d-l}	0.94 ^{h-n}	1.09 ^{c-j}	1.33 ^{bc}
	125%	0.92 ^{h-n}	0.93 ^{h-n}	1.08 ^{c-k}	0.92 ^{h-n}	1.28 ^{b-f}	1.33 ^{bc}
	150%	0.97 ^{g-n}	0.98 ^{g-n}	0.92 ^{h-n}	1.02 ^{f-m}	1.11 ^{c-j}	1.32 ^{bc}
	175%	0.82 ^{k-o}	0.98 ^{g-n}	1.78 ^a	1.03 ^{e-m}	1.23 ^{b-g}	1.29 ^{b-e}
FNU	0%	57.5 ^{pq}	60.3 ^{o-q}	52.0 ^q	73.6 ^{m-q}	73.2 ^{m-q}	69.5 ^{n-q}
	25%	80.2 ^{l-q}	107.7 ^{j-q}	103.3 ^{j-q}	125.1 ^{g-n}	118.4 ^{i-o}	147.4 ^{c-k}
	50%	125.6 ^{f-n}	113.0 ^{i-p}	130.6 ^{e-n}	149.6 ^{b-k}	133.7 ^{d-m}	186.1 ^{b-g}
	75%	98.9 ^{k-q}	133.0 ^{e-m}	139.6 ^{c-l}	132.0 ^{e-m}	166.5 ^{b-j}	136.6 ^{c-l}
	100%	190.6 ^{b-e}	158.0 ^{b-k}	121.1 ^{h-n}	143.7 ^{c-k}	157.5 ^{b-k}	189.1 ^{b-f}
	125%	149.3 ^{b-k}	142.4 ^{c-l}	146.0 ^{c-k}	158.3 ^{b-k}	198.4 ^{bc}	210.5 ^b
	150%	163.1 ^{b-j}	161.3 ^{b-k}	121.5 ^{h-n}	174.2 ^{b-i}	183.6 ^{b-h}	197.1 ^{b-d}
	175%	130.3 ^{e-n}	164.4 ^{b-j}	264.8 ^a	185.6 ^{b-g}	186.0 ^{b-g}	192.2 ^{b-e}
FTNU	0%	67.0 ^j	78.6 ^{ij}	61.7 ^j	83.3 ^{h-j}	84.5 ^{h-j}	78.5 ^{ij}
	25%	105.1 ^{g-j}	142.1 ^{e-i}	133.3 ^{f-i}	143.0 ^{e-i}	134.6 ^{f-i}	165.8 ^{c-g}
	50%	152.6 ^{c-g}	142.3 ^{e-i}	166.4 ^{c-g}	167.6 ^{c-g}	155.1 ^{c-g}	210.3 ^{b-e}
	75%	135.4 ^{f-i}	167.4 ^{c-g}	165.6 ^{c-g}	148.2 ^{d-h}	187.7 ^{b-f}	158.7 ^{c-g}
	100%	215.2 ^{b-d}	191.0 ^{b-f}	156.9 ^{c-g}	164.0 ^{c-g}	181.7 ^{b-f}	213.0 ^{b-e}
	125%	185.9 ^{b-f}	182.7 ^{b-f}	188.1 ^{b-f}	180.3 ^{b-f}	222.5 ^{bc}	239.2 ^b
	150%	201.4 ^{b-f}	203.1 ^{b-f}	154.3 ^{c-g}	193.9 ^{b-f}	207.4 ^{b-e}	222.5 ^{bc}
	175%	166.9 ^{c-g}	208.7 ^{b-e}	313.4 ^a	212.0 ^{b-e}	209.9 ^{b-e}	219.5 ^{b-d}

FPC = fodder phosphorus concentration (%); **FNC** = fodder nitrogen concentration (%); **FNU** = fodder nitrogen uptake (kg/ha); **FTNU** = fodder total nutrient uptake (kg/ha); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$.

Table 5.11 Interaction effect of fertilizer by year on the mean performance of fodder phosphorus uptake of oat at Holetta

Parameter	Percent of fertilizer level	Year	
		2020	2021
FPU	0%	12.5 ^{ij}	10.0 ^j
	25%	29.8 ^{c-e}	17.5 ^{hi}
	50%	30.7 ^{cd}	21.2 ^{f-h}
	75%	32.3 ^c	19.9 ^{gh}
	100%	31.2 ^{cd}	22.8 ^{f-h}
	125%	39.7 ^{ab}	24.9 ^{e-g}
	150%	37.6 ^b	23.0 ^{f-h}
	175%	43.2 ^a	25.8 ^{d-f}

FPU = fodder phosphorus uptake (kg/ha); Means followed by a common superscript letter within a column and row are not significantly different from each other at $P < 0.05$.

The PNB varied significantly for the effect of fertilizer (Figure 5.6 top). The result showed that the PNB decreased with increasing rates of fertilizer. The highest PNB (9.0 kg/ha) was recorded for the application of 25% (10.3 kg N + 5 kg P/ha) of the recommended fertilizer rate followed by 50% (20.5 kg N + 10 kg P/ha), 75% (30.8 kg N + 15 kg P/ha), and 100% (41.0 kg N + 20 kg P/ha) of fertilizer while application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rate had the lowest PNB (2.1 kg/ha). The variation among oat varieties for PNB was non-significant while the PNB varied significantly between the two production years (Figure 5.6 bottom right). Despite the variations among oat varieties being non-significant for PNB, the grain type oat (Sorataf) variety had numerically higher PNB (4.3 kg/ha) while the lowest (3.7 kg/ha) was recorded for forage type oat (CI-8251). However, significantly the highest PNB (4.2 kg/ha) was recorded for the 2021 cropping season compared to the 2020 (3.8 kg/ha) cropping season.

The PFP, IUE, AE, and APE were significant for the interaction effect of variety by fertilizer by year (Table 5.12). Accordingly, the highest PFP (915.6 kg/kg) was observed for forage type oat (CI-8251) variety sown with 25 % (10.3 kg N + 5 kg P/ha) of the recommended fertilizer rate in the 2021 cropping season. In contrast, the lowest PFP (138.3 kg/kg) was recorded for grain type oat (Sorataf) variety sown with 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate in the 2021 cropping season. Similarly, the forage type oat (CI-8251) variety sown with 75% (30.8 kg N + 15 kg P/ha) fertilizer rate in the 2020 cropping season gave the highest IUE (98.9 kg/kg) while the grain type oat (Sorataf) variety which received 175% of fertilizer rate in 2020 gave the lowest IUE (50.5 kg/kg). The grain type oat (Sorataf) variety sown with 25% fertilizer rate in the 2021 cropping season gave the highest AE (289.6 kg/kg). In contrast, the lowest AE (47.8 kg/kg) was observed for the dual-type oat

(SRCPX80Ab2291) variety sown with 50% (20.5 kg N + 10 kg P/ha) of the recommended fertilizer rate in the 2020 cropping season. The highest APE (109.5 kg/kg) was observed for forage type oat (CI-8251) variety sown with 75% of the recommended fertilizer rate in the 2020 cropping season. The lowest APE (23.9 kg/kg) was observed for the dual-type oat (SRCPX80Ab2291) variety sown with 50% fertilizer rate in the 2020 cropping season.

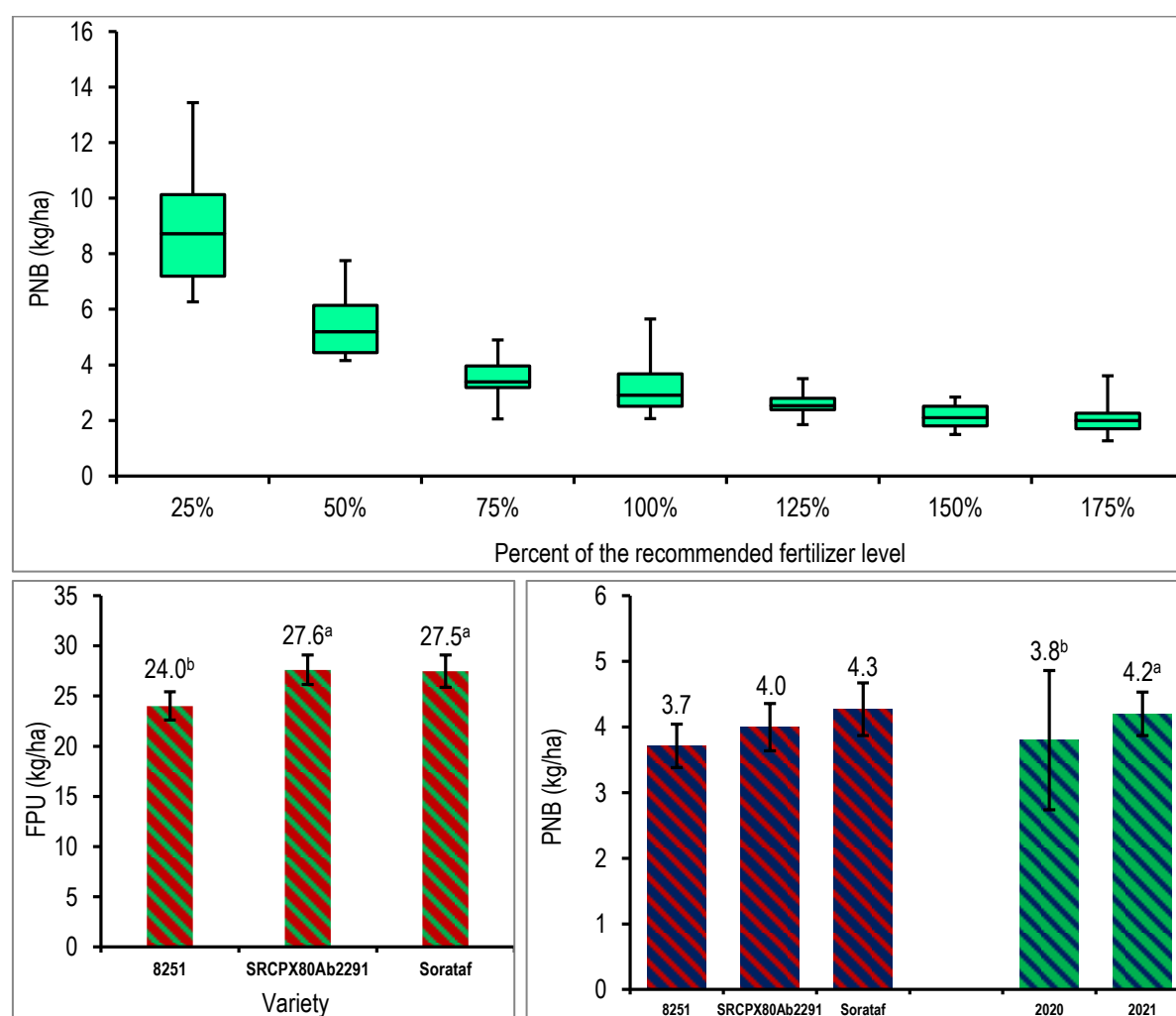


Figure 5.6 Effects of fertilizer levels on partial nutrient balance (top), variety on fodder phosphorus uptake (left bottom), and variety and year on partial nutrient balance (right bottom) at Holetta. **Note:** PNB = partial nutrient balance; FPU = fodder phosphorus uptake

5.3.1.4 Correlation analysis

The Pearson correlation analysis of measured parameters with fertilizer rates and fodder dry matter yield is displayed in Table 5.13. The results revealed that the NTPP ($r = 0.76^{**}$), LDMY ($r = 0.91^{**}$), SDMY ($r = 0.95^{***}$), PDMY ($r = 0.93^{**}$), FYPR ($r = 0.94^{***}$), and FDMY ($r = 0.95^{***}$) were significantly and positively correlated with levels of fertilizer.

Moreover, the FNC ($r = 0.76^*$), FPU ($r = 0.89^{**}$), FNU ($r = 0.93^{***}$), FTNU ($r = 0.92^{***}$), and APE ($r = 0.76^*$) were associated significantly and positively with fertilizer rates. However, the partial factor productivity PFP ($r = -0.87^*$), PNB ($r = -0.88^{**}$), and AE ($r = -0.88^{**}$) had significant inverse associations with fertilizer rates.

Table 5.12 Interaction effect of variety by fertilizer by year for partial factor productivity, internal utilization efficiency, agronomic efficiency, and agro-physiological efficiency performance of oat at Holetta

Parameter	Recommended fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
PFPFY	25%	660.1 ^b	842.0 ^a	677.8 ^b	915.6 ^a	711.7 ^b	733.3 ^b
	50%	463.0 ^c	348.3 ^{c-e}	384.6 ^{cd}	436.3 ^c	455.5 ^c	426.9 ^c
	75%	292.7 ^{d-g}	293.9 ^{d-g}	268.9 ^{d-i}	280.0 ^{d-h}	306.9 ^{d-f}	258.8 ^{e-j}
	100%	244.9 ^{e-j}	238.7 ^{e-j}	190.5 ^{f-j}	252.0 ^{e-j}	250.8 ^{e-j}	233.2 ^{e-j}
	125%	212.4 ^{f-j}	201.6 ^{f-j}	177.1 ^{g-j}	224.4 ^{f-j}	203.8 ^{f-j}	207.4 ^{f-j}
	150%	181.5 ^{g-j}	179.0 ^{g-j}	144.7 ^{ij}	185.3 ^{f-j}	180.7 ^{g-j}	162.8 ^{h-j}
	175%	149.1 ^{ij}	156.1 ^{h-j}	140.6 ^j	169.4 ^{g-j}	141.7 ^j	138.3 ^j
IUEFY	25%	95.8 ^{ab}	90.3 ^{a-d}	77.5 ^{d-i}	98.6 ^a	83.8 ^{a-h}	68.4 ^{ij}
	50%	93.2 ^{a-c}	74.6 ^{e-j}	72.2 ^{g-j}	79.8 ^{c-i}	89.6 ^{a-e}	61.8 ^{jk}
	75%	98.9 ^a	80.9 ^{b-i}	74.3 ^{f-j}	89.3 ^{a-f}	74.8 ^{e-j}	74.6 ^{e-j}
	100%	73.4 ^{g-i}	72.0 ^{g-j}	74.2 ^{f-j}	93.7 ^{a-c}	79.5 ^{c-i}	67.1 ^{ij}
	125%	87.2 ^{a-g}	84.1 ^{a-h}	72.1 ^{g-j}	95.1 ^{ab}	70.1 ^{h-j}	66.5 ^{ij}
	150%	84.5 ^{a-h}	80.8 ^{b-i}	86.0 ^{a-g}	88.8 ^{a-f}	79.9 ^{c-i}	67.0 ^{ij}
	175%	96.6 ^a	80.0 ^{c-i}	50.5 ^k	85.6 ^{a-g}	72.6 ^{g-j}	68.3 ^{ij}
AEFY	25%	83.1 ^{ef}	240.9 ^{ab}	227.5 ^{a-c}	264.3 ^{ab}	117.1 ^{c-f}	289.6 ^a
	50%	174.4 ^{b-e}	47.8 ^f	159.5 ^{b-f}	110.6 ^{d-f}	158.2 ^{b-f}	205.0 ^{a-d}
	75%	100.3 ^{d-f}	93.4 ^{d-f}	118.8 ^{c-f}	62.9 ^{ef}	108.7 ^{d-f}	110.9 ^{d-f}
	100%	100.6 ^{d-f}	77.8 ^{ef}	77.9 ^{e-f}	89.2 ^{d-f}	92.8 ^{d-f}	122.3 ^{c-f}
	125%	97.0 ^{d-f}	81.4 ^{ef}	87.0 ^{d-f}	94.2 ^{d-f}	84.8 ^{ef}	118.6 ^{c-f}
	150%	85.4 ^{ef}	78.8 ^{ef}	69.6 ^{ef}	76.7 ^{ef}	81.6 ^{ef}	88.9 ^{d-f}
	175%	66.6 ^{ef}	70.2 ^{ef}	76.3 ^{ef}	76.3 ^{ef}	56.8 ^{ef}	74.9 ^{ef}
APEFY	25%	51.1 ^{g-l}	78.5 ^{b-f}	66.3 ^{c-j}	75.9 ^{c-g}	34.1 ^{lm}	58.1 ^{e-l}
	50%	77.0 ^{b-g}	23.9 ^m	62.4 ^{d-k}	46.3 ^{h-m}	80.4 ^{b-e}	52.9 ^{f-l}
	75%	109.5 ^a	55.2 ^{e-l}	62.4 ^{d-k}	44.8 ^{i-m}	52.6 ^{f-l}	75.6 ^{c-g}
	100%	52.9 ^{f-l}	38.8 ^{k-m}	65.1 ^{d-k}	77.2 ^{b-g}	62.6 ^{d-k}	63.2 ^{d-k}
	125%	80.5 ^{b-e}	75.6 ^{c-g}	70.7 ^{c-i}	85.6 ^{b-d}	51.7 ^{g-l}	64.7 ^{d-k}
	150%	77.3 ^{b-g}	70.5 ^{c-i}	91.5 ^{a-c}	70.4 ^{c-i}	67.6 ^{c-j}	63.7 ^{d-k}
	175%	101.8 ^{ab}	72.4 ^{c-h}	43.0 ^{j-m}	73.9 ^{c-g}	53.9 ^{e-l}	68.0 ^{c-j}

PFPFY = partial factor productivity of fodder yield (kg/kg); IUEFY = internal utilization efficiency of fodder yield (kg/kg); AEFY = agronomic efficiency of fodder yield (kg/kg); and APEFY = Agro-physiological efficiency of fodder yield (kg/kg); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$.

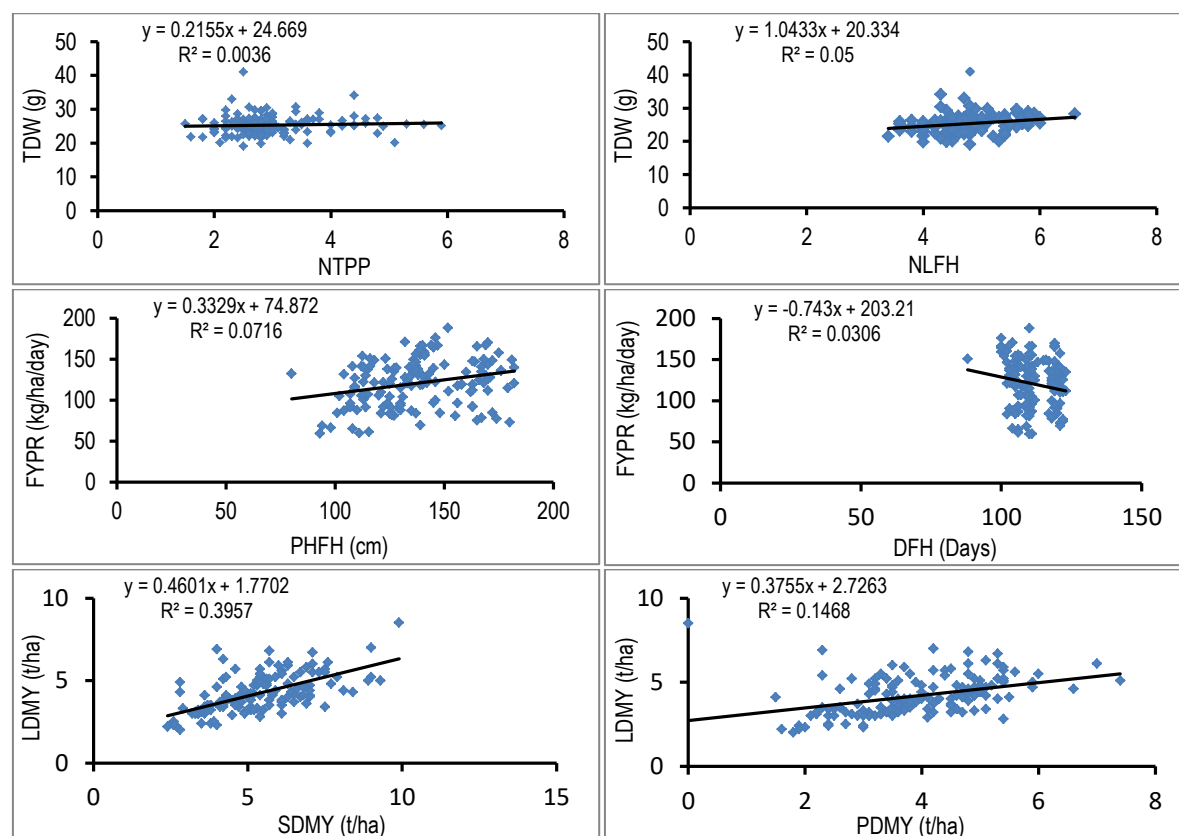
The association of FDMY with NTPP ($r = 0.82^*$), PHFH ($r = 0.74^*$), LDMY ($r = 0.97^{***}$), SDMY ($r = 0.99^{***}$), PDMY ($r = 0.99^{***}$), FYPR ($r = 0.99^{***}$), FPC ($r = 0.77^*$), FNC ($r = 0.86^{**}$), FPU ($r = 0.97^{***}$), FNU ($r = 0.98^{***}$), FTNU ($r = 0.98^{***}$), and APE ($r = 0.79^*$) were significant and positive. In contrast, the association of FDMY with PFP ($r = -0.87^*$), PNB ($r = -0.88^{**}$), IUE ($r = -0.86^{**}$), and AE ($r = -0.86^{**}$) were significant and negative. The associations between some of the selected parameters are presented in [Figure 5.7](#). The result revealed that TDW had a positive association with NTPP and the NLFH. The association of FYPR with PHFH was positive while DFH had an inverse association with

FYPR. The association of LDMY with SDMY and PDMY was positive. The FNC and FNU had a positive association with FPC and FPU, respectively. The association between FPU and FTNU was positive and also the AE had a positive association with APE. Moreover, the correlation of PFP with PNB and IUE was positive.

Table 5.13 Relationships of measured parameters with fertilizer levels and fodder dry matter yield of oat varieties grown at Holetta

Parameter	With RFL	With FDMY	Parameter	With RFL	With FDMY
NTPP	0.76*	0.82*	FDMY	0.95***	—
TDW	0.53 ^{NS}	0.65 ^{NS}	FPC	0.59 ^{NS}	0.77*
NLFH	-0.19 ^{NS}	-0.01 ^{NS}	FNC	0.76*	0.86**
LLFH	0.33 ^{NS}	0.48 ^{NS}	FPU	0.89**	0.97***
PHFH	0.64 ^{NS}	0.74*	FNU	0.93***	0.98***
DFH	-0.60 ^{NS}	-0.67 ^{NS}	FTNU	0.92***	0.98***
LDMY	0.91**	0.97***	PFPFY	-0.87*	-0.87*
SDMY	0.95***	0.99***	PNBFY	-0.88**	-0.88**
PDMY	0.93***	0.99***	IUEFY	-0.69 ^{NS}	-0.86**
LSR	-0.54 ^{NS}	-0.50 ^{NS}	AEFY	-0.88**	-0.86**
FYPR	0.94***	0.99***	APEFY	0.76*	0.79*

NTPP = number of tillers per plant (number); TDW = tillers dry weight (g); NLFH = number of leaves at forage harvest (number); LLFH = leaf length at forage harvest (cm); PHFH = plant height at forage harvest (cm); DFH = days to forage harvest (days); LDMY = leaf dry matter yield (t/ha); SDMY = stem dry matter yield (t/ha); PDMY = panicle dry matter yield (t/ha); LSR = leaf to stem ratio; FYPR = forage yield production rate (kg/ha/day); FDMY = fodder dry matter yield (t/ha); FPC = fodder phosphorus concentration (%); FNC = fodder nitrogen concentration (%); FPU = fodder phosphorus uptake (kg/ha); FNU = fodder nitrogen uptake (kg/ha); FTNU = fodder total nutrient uptake (kg/ha); PFPFY = partial factor productivity of fodder yield (kg/kg); PNBFY = partial nutrient balance of fodder yield (kg/kg); IUEFY = internal utilization efficiency of fodder yield (kg/kg); AEFY = agronomic efficiency of fodder yield (kg/kg); APEFY = agro-physiological efficiency of fodder yield (kg/kg); RFL = recommended fertilizer level; NS = non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively.



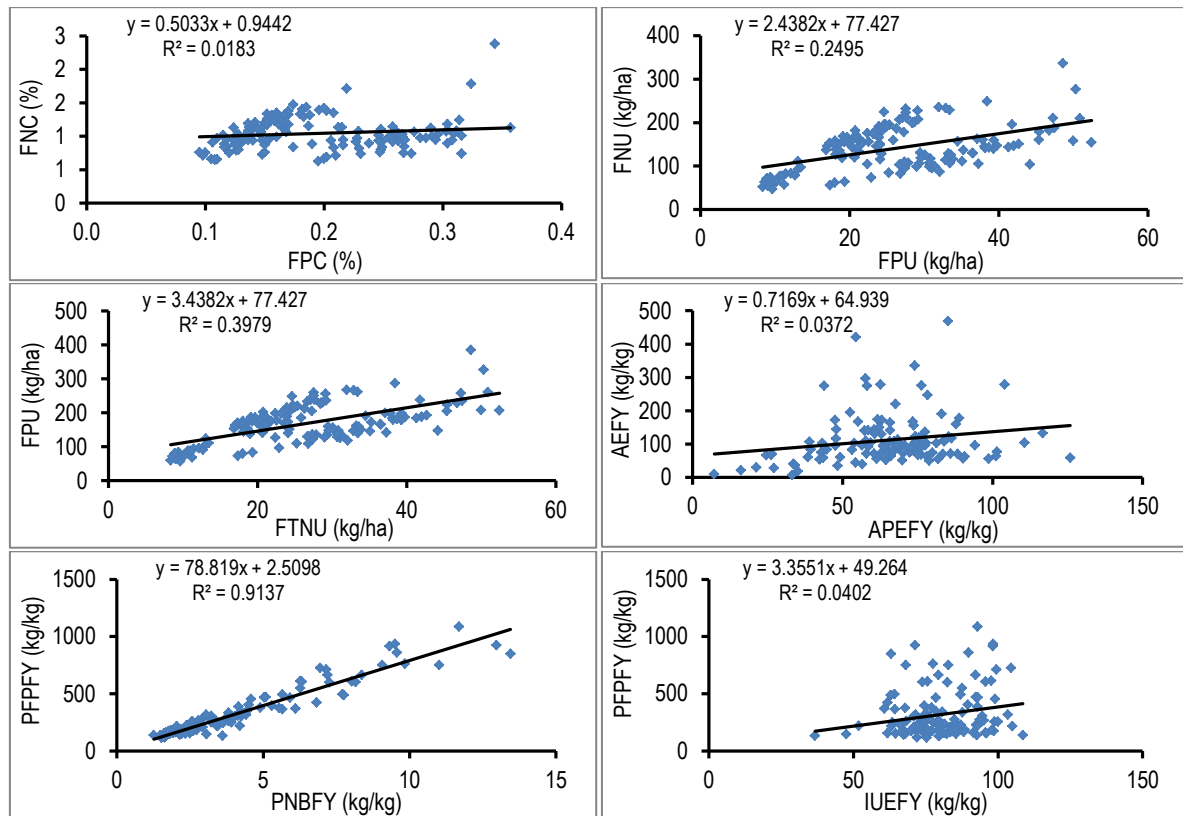


Figure 5.7 Relationships between selected plant parameters, nutrient uptake and use efficiency of three oat varieties sown with eight fertilizer levels at Holetta

Note: TDW = tillers dry weight (g); NTTP = number of tillers per plant (numbers); NLFH = numbers of leaves at forage harvest (numbers); PYPR = forage yield production rate (kg/ha/day); PHFH = plant height at forage harvest (cm); DFH = days to forage harvest (days); LDMY = leaf dry matter yield (t/ha); SDMY = stem dry matter yield (t/ha); PDMY = panicle dry matter yield (t/ha); FNC = forage nitrogen concentration (%); FPC = forage phosphorus concentration (%); FNU = forage nitrogen uptake (kg/ha); FPU = forage phosphorus uptake (kg/ha); FTNU = forage total nutrient uptake (kg/ha); AEGY = agronomic efficiency of fodder yield (kg fodder/kg nutrient applied); APEGY = agro-physiological efficiency of fodder yield (kg fodder/kg nutrient uptake by fodder yield); PPFY = partial factor productivity of fodder yield (kg fodder/kg nutrient applied); PNBFY = partial nutrient balance of fodder yield (kg nutrient uptake by fodder/kg nutrient applied); IUEFY = internal utilization efficiency of fodder yield (kg fodder/kg nutrient uptake by fodder).

5.3.1.5 Economic analysis

The partial budget analysis for each oat variety and combined oat varieties over the years is presented in Table 5.14. The results showed that the forage type oat (CI-8251) variety had the highest net benefit (90,697 ETB/ha) with the application of 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer. Similarly, the dual-type oat (SRCPX80Ab2291) variety produced the highest net benefit of 89,101 ETB/ha using the application of 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate. In addition, the grain type oat (Sorataf) variety sown with the application of 125% (51.3 kg N + 25 kg P/ha) of the recommended fertilizer gave the highest net benefit (77,875 ETB/ha). The combined analysis of oat varieties over the years produced the highest net benefit of 83,933 ETB/ha with the application of 150% of the recommended fertilizer followed by the application of 125% which gave a net benefit of 83,440 ETB/ha.

Table 5.14 Partial budget analysis on the effect of fertilizer application in oat fodder at Holetta

Variety	RFL	Adj. FDMY	FDMYR	TC	NB	MNB	MTC	NBCR	MRR
CI-8251	25%	10.8	82620	20090	62530	—	—	3.1	—
	0%	8.4	64260	20639	43621	-18909	549	2.1	D
	50%	12.4	94860	21625	73235	29614	986	3.4	3002
	75%	11.8	90270	23768	66502	-6732	2142	2.8	D
	100%	13.6	104040	24434	79606	13103	667	3.3	1965
	125%	15	114750	25709	89041	9436	1274	3.5	741
	150%	15.1	115515	25855	89660	619	146	3.5	424
	175%	15.3	117045	26348	90697	1037	493	3.4	210
SRCPX80Ab2291	25%	10.7	81855	21306	60549	—	—	2.8	—
	0%	8.2	62730	21941	40789	-19760	635	1.9	D
	125%	13.9	106335	22931	83404	42615	990	3.6	4305
	50%	11.0	84150	23101	61049	-22355	170	2.6	D
	75%	12.4	94860	23160	71700	10651	59	3.1	18053
	150%	14.8	113220	24119	89101	17401	959	3.7	1815
	100%	12.5	95625	24955	70670	-18432	837	2.8	D
	175%	14.3	109395	26869	82526	11857	1914	3.1	620
Sorataf	50%	11.1	84915	21104	63811	—	—	3.0	—
	25%	9.7	74205	22000	52205	-11606	896	2.4	D
	0%	6.1	46665	22028	24637	-27568	28	1.1	D
	100%	11.6	88740	22091	66649	42012	63	3.0	66898
	75%	10.9	83385	22986	60399	-6251	896	2.6	D
	125%	13.2	100980	23105	77875	17477	118	3.4	14786
	150%	12.7	97155	24119	73036	-4839	1014	3.0	D
	175%	13.4	102510	26088	76423	3386	1969	2.9	172
Combined	25%	10.4	79560	21132	58428	—	—	2.8	—
	0%	7.6	57885	21536	36349	-22079	404	1.7	D
	50%	11.5	87975	21944	66031	29682	408	3.0	7280
	75%	11.7	89505	23305	66200	169	1361	2.8	12
	100%	12.6	96135	23827	72308	6108	522	3.0	1170
	125%	14.0	107355	23915	83440	11132	88	3.5	12636
	150%	14.2	108630	24697	83933	492	783	3.4	63
	175%	14.3	109650	26435	83215	-717	1737	3.1	D

RFL = recommended fertilizer level; Adj. FDMY = adjusted fodder dry matter yield; FDMYR = fodder dry matter yield revenue; GB = gross benefit; TC = total cost; NB = net benefit; MNB = marginal net benefit; MTC = marginal total cost; NBCR = net benefit to cost ratio; MRR = marginal rate of return; D = dominated suggesting treatment has a lower NB with higher TC compared to the preceding treatment NB and TC; 1kg DAP = 13.5 ETB in May, 2020 and 15.5 ETB in May, 2021 with a mean of 14.5 ETB; 1kg Urea = 16.2 ETB in May, 2020 and 18.6 ETB in May, 2021 with a mean of 17.4 ETB; 1kg natural pasture hay = 7.30 ETB in January 01, 2021 and 8.00 ETB in January 01, 2022 with a mean of 7.65 ETB; ETB = Ethiopian birr; Except fertilizer cost, land preparation (4000.0 ETB), planting (1822.9 ETB), weeding (8854.2 ETB), harvesting (3472.2 ETB), and Seed (2750.0 ETB) costs are the same for all treatments per hectare; The sum of the total cost except fertilizer cost is 20,899.3 ETB for all treatments; January 01, 2021 exchange rate (\$ 1 USD = 39.55 ETB) and January 01, 2022 exchange rate (\$ 1 USD = 49.15 ETB) and mean of the two years exchange rate (\$ 1 USD = 44.35 ETB).

5.3.2 Grain yield and yield related traits

5.3.2.1 Analysis of variance

The combined analysis of variance for 28 parameters is indicated in Table 5.15. The results revealed that all the measured 14 agro-morphological traits had significant ($P < 0.0001$) variation among oat varieties. Moreover, except SPC, SNC and TNU, all the measured nutrient concentrations, nutrient uptake, and nutrient use efficiency varied significantly among varieties. All the measured parameters except DSH, TSW, HI, IUE, PE, and APE had significant variation for application of different fertilizer levels. The three-way interaction (V x F x Y) was non-significant ($P > 0.05$) for all measured parameters except SPC, SNC, GPC,

GNC, and NHI. The fertilizer by year interaction (F x Y) was significant for PLGH, GFP, HI, and GPC. Moreover, the variety by year interaction (V x Y) was significant for DSH, FLLGH, PHGH, GFP, NSPP, NSLPP, HI, GPC, and GNC. Furthermore, the interaction effect of variety by fertilizer (V x F) was significant for PHGH, SY, TBY, SPC, SNC, GPC, SNU, TNU, NHI, PNB, IUE, and APE.

Table 5.15 Analysis of variance for 28 parameters of three oat varieties sown with eight fertilizer levels in 2020/2021 and 2021/2022 cropping seasons at Holetta

Parameter	Mean squares								Error	Mean
	R	V	F	Y	V x F	V x Y	F x Y	V x F x Y		
DSH	9.19 ^{NS}	2405.63***	9.96 ^{NS}	6710.34***	13.73 ^{NS}	286.92***	21.98 ^{NS}	12.37 ^{NS}	12.92	160.12
FLLGH	38.90**	253.47***	145.16***	170.09***	10.43 ^{NS}	124.40***	7.99 ^{NS}	3.489 ^{NS}	7.41	29.46
PHGH	19.04 ^{NS}	40751.89***	822.00***	8.75 ^{NS}	84.42***	202.22***	39.72 ^{NS}	32.76 ^{NS}	26.15	140.56
PLGH	21.23 ^{NS}	5163.93***	111.01***	1704.31***	4.45 ^{NS}	13.13 ^{NS}	33.33**	4.26 ^{NS}	8.66	38.03
GFP	5.15 ^{NS}	1602.52***	32.90*	15047.11***	11.39 ^{NS}	316.67***	30.52*	15.11 ^{NS}	12.73	64.63
NSPP	11.85 ^{NS}	147.74***	71.83***	84.03***	9.68 ^{NS}	18.75*	7.71 ^{NS}	2.35 ^{NS}	5.75	31.08
NSLPP	14.09 ^{NS}	3155.45***	522.49***	1416.27***	28.70 ^{NS}	809.71***	24.80 ^{NS}	34.92 ^{NS}	19.99	71.63
BYPR	162.20 ^{NS}	3881.76***	6932.18***	712.00 ^{NS}	371.82 ^{NS}	580.73 ^{NS}	212.65 ^{NS}	96.34 ^{NS}	210.89	92.13
GSFR	89.19 ^{NS}	326.27***	909.13***	3.52 ^{NS}	47.38 ^{NS}	14.84 ^{NS}	33.60 ^{NS}	18.52 ^{NS}	34.10	33.48
TSW	3.57 ^{NS}	229.58***	10.51 ^{NS}	384.49***	10.85 ^{NS}	7.21 ^{NS}	11.23 ^{NS}	7.82 ^{NS}	11.77	53.50
HI	16.13 ^{NS}	1625.49***	7.28 ^{NS}	128.82***	13.03 ^{NS}	42.09*	23.28*	17.25 ^{NS}	10.80	36.84
SY	0.80 ^{NS}	175.43***	75.52***	1.12 ^{NS}	5.86*	7.81 ^{NS}	3.31 ^{NS}	2.65 ^{NS}	2.60	9.38
TBY	5.00 ^{NS}	121.97***	182.71***	12.48 ^{NS}	9.75*	11.40 ^{NS}	6.52 ^{NS}	3.02 ^{NS}	5.12	14.73
GY	2.23 ^{NS}	5.55***	23.72***	5.33 ^{NS}	1.16 ^{NS}	0.53 ^{NS}	0.88 ^{NS}	0.52 ^{NS}	0.81	5.35
SPC	0.0007*	0.00 ^{NS}	0.001***	0.00 ^{NS}	0.0003***	0.00 ^{NS}	0.00 ^{NS}	0.0003***	0.00	0.05
SNC	0.00 ^{NS}	0.01 ^{NS}	0.04***	0.79***	0.01**	0.01 ^{NS}	0.01 ^{NS}	0.01**	0.00	0.39
GPC	0.01***	0.01***	0.01***	0.02***	0.0007*	0.001*	0.002***	0.0008**	0.00	0.27
GNC	0.01 ^{NS}	0.06**	0.30***	0.03 ^{NS}	0.03 ^{NS}	0.04***	0.01 ^{NS}	0.02*	0.01	1.82
GNU	2016.02*	4494.73***	15230.54***	4486.77**	766.83 ^{NS}	360.25 ^{NS}	615.64 ^{NS}	312.38 ^{NS}	473.31	113.33
SNU	140.30 ^{NS}	2895.81***	2721.03***	8097.00***	359.89**	61.81 ^{NS}	221.47 ^{NS}	216.87 ^{NS}	128.47	41.69
TNU	3108.16*	586.16 ^{NS}	30579.61***	24638.53***	1569.06*	717.60 ^{NS}	1142.18 ^{NS}	581.95 ^{NS}	850.13	155.02
NHI	11.00 ^{NS}	1166.41***	41.23*	721.37***	38.30**	25.90 ^{NS}	23.04 ^{NS}	32.54*	15.67	73.66
PPPGY	1365.81 ^{NS}	3175.39*	184876.59***	7105.51**	1398.86 ^{NS}	195.13 ^{NS}	1589.51 ^{NS}	300.13 ^{NS}	780.96	133.45
PNBGY	1.01 ^{NS}	2.77**	81.78***	5.37***	0.96*	0.48 ^{NS}	1.12 ^{NS}	0.41 ^{NS}	0.41	2.84
IUEGY	16.86 ^{NS}	50.77**	11.52 ^{NS}	25.16 ^{NS}	17.89**	9.52 ^{NS}	8.63 ^{NS}	12.60 ^{NS}	6.78	47.06
AEGY	2054.50 ^{NS}	3649.67*	38762.00***	3433.09*	1288.30 ^{NS}	451.13 ^{NS}	1036.20 ^{NS}	226.97 ^{NS}	833.70	65.96
PEBY	150.06 ^{NS}	4660.95***	222.78 ^{NS}	105.33 ^{NS}	240.96 ^{NS}	159.96 ^{NS}	149.50 ^{NS}	142.83 ^{NS}	218.79	79.33
APEGY	40.58 ^{NS}	85.63*	8.45 ^{NS}	208.03**	49.14*	28.42 ^{NS}	25.42 ^{NS}	38.31 ^{NS}	22.77	27.90

DSH = days to seed harvest (days); FLLGH = flag leaf length at grain harvest (cm); PHGH = plant height at grain harvest (cm); PLGH = panicle length at grain harvest (cm); GFP = grain filling period (days); NSPP = number of spikes per panicle (number); NSLPP = number of spikelets per panicle (number); BYPR = biological yield production rate (kg/ha/day); GSFR = grain sink filling rate (kg/ha/day); TSW = thousand-grain weight (g); HI = harvest index (%); SY = straw yield (t/ha); TBY = total biological yield (t/ha); GY = grain yield (t/ha); SPC = straw phosphorus concentration (%); SNC = straw nitrogen concentration (%); GPC = grain phosphorus concentration (%); GNC = grain nitrogen concentration (%); GNU = grain nutrient uptake (kg/ha); SNU = straw nutrient uptake (kg/ha); TNU = total nutrient uptake (kg/ha); NHI = nutrient harvest index (%); PPPGY = partial factor productivity of grain yield (kg/kg); PNBGY = partial nutrient balance of grain yield (kg/kg); IUEGY = internal utilization efficiency of grain yield (kg/ha); AEGY = agronomic efficiency of grain yield (kg/kg); PEBY = physiological efficiency of grain yield (kg/kg); APEGY = agro-physiological efficiency of grain yield (kg/ha); R = replication; V = variety; F = fertilizer level; Y = year; V x F = variety by fertilizer level interaction; V x Y = variety by year interaction; F x Y = fertilizer level by year interaction; V x F x Y = variety by fertilizer level by year interaction; NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively

5.3.2.2 Main and interaction effects on agro-morphological traits

The FLLGH had a significant variation for fertilizer levels (Figure 5.8 left top). The result revealed that the blanket recommended fertilizer of 125% (51.3 kg N + 25 kg P/ha) produced the highest FLLGH (33.1 cm) while the varieties produced the lowest (23.9 cm) for unfertilized treatment. The interaction effect of variety by year was also significant for FLLGH (Table 5.16). The highest FLLGH was observed for the interaction effect of CI-8251 variety by the 2020 cropping season while the interaction of Sorataf variety by the 2021 cropping season produced the lowest. The NSPP and NSLPP showed significant variation for fertilizer levels (Figure 5.8 right top and left bottom). The highest NSPP (34.2) and NSLPP (78.3) were recorded for a fertilizer level of 125% while the varieties produced

the least NSPP (27.6) and NSLPP (60.6) without fertilizer application. The interaction of variety by year was also significant for NSPP and NSLPP (Table 5.16). The NSPP and NSLPP showed the highest interaction for Sorataf and CI-8251 varieties with the same cropping season (2020), respectively. The PLGH varied significantly among oat varieties (Figure 5.8 right bottom). The highest PLGH (47.9 cm) was recorded for CI-8251 followed by SRCPX80Ab2291 (39.0 cm) while Sorataf (27.2 cm) produced the lowest. The interaction of fertilizer by year was also significant for PLGH (Table 5.17). The interaction effect of 125% fertilizer by the 2020 cropping season produced the highest PLGH (45.5 cm) while the least (32.6 cm) was observed for the interaction effect of unfertilized treatment by the 2020 cropping season.

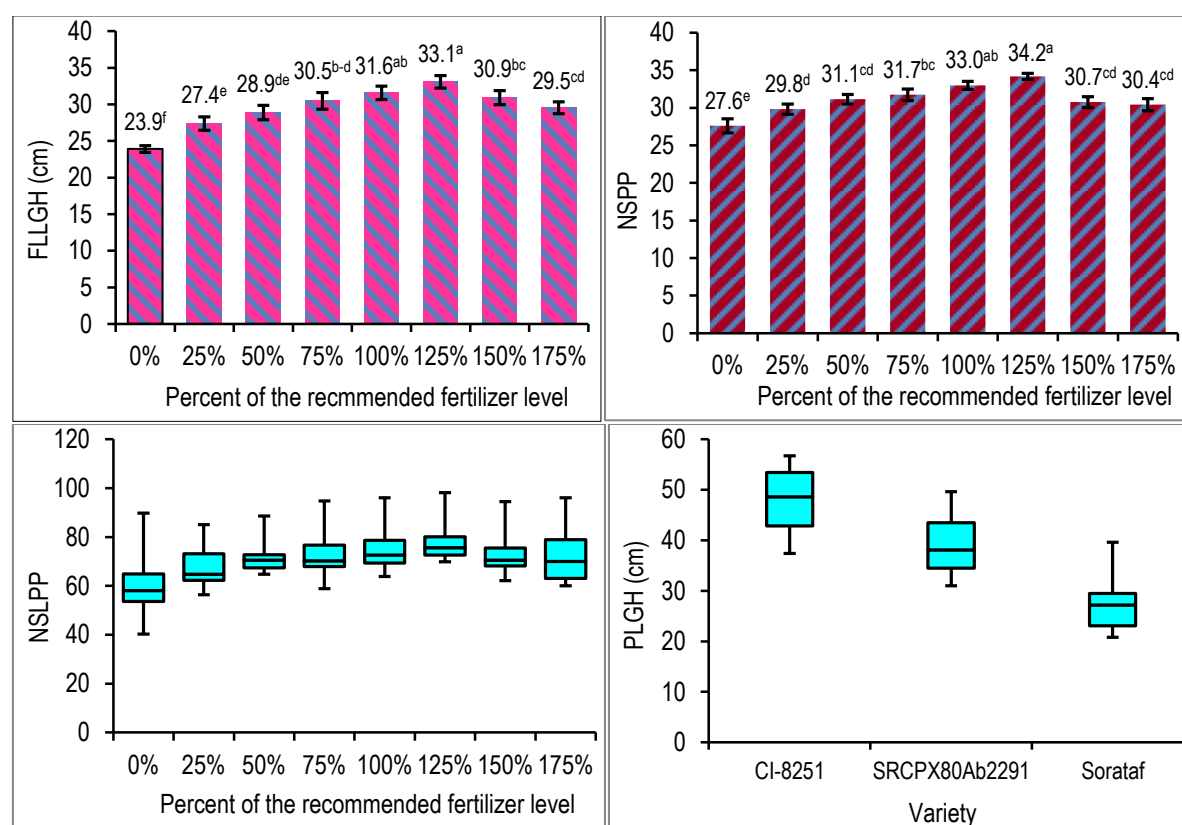


Figure 5.8 Mean of flag leaf length at grain harvest (FLLGH), number of spikes per panicle (NSPP), and number of spikelets per panicle (NSLPP) as influenced by levels of fertilizer and effect of variety on panicle length at grain harvest (PLGH) in oat at Holetta

The interaction of variety by year showed significant variation for days to seed harvest (DSH) as indicated in Table 5.16. Accordingly, the highest DSH (174.3 days) was observed for the interaction of the CI-8251 variety by the 2021 cropping season while the interaction of the SRCPX80Ab2291 variety by the 2020 cropping season produced the least (144.9 days). The interaction effect of variety by year was significant for plant height at

grain harvest (PHGH) as indicated in Table 5.16. The result revealed that the highest PHGH (172.9 cm) was exhibited by the interaction effect of CI-8251 variety with the 2020 cropping season while the least (112.0 cm) was observed from the interaction effect of Sorataf variety by the 2020 cropping season. Moreover, the interaction of variety by fertilizer showed significant variation for PHGH (Table 5.18). The interaction effect of CI-8251 variety with the blanket recommended fertilizer level of 175% (71.8 kg N + 35 kg P/ha) produced the maximum PHGH (178.0 cm) while the interaction effect of Sorataf variety with unfertilized treatment produced the minimum (102.1 cm).

Table 5.16 Interaction effect of variety by year on the performance of agro-morphological traits of oat at Holetta

Variety	Year	Parameter						
		PHGH	FLLGH	DSH	GFP	NSPP	NSLPP	HI
CI-8251	2020	172.9 ^a	34.4 ^a	156.2 ^d	51.3 ^e	32.3 ^a	88.8 ^a	29.7 ^e
	2021	168.8 ^a	29.5 ^b	174.3 ^a	70.3 ^c	29.2 ^b	73.1 ^b	31.9 ^d
SRCPX80Ab2291	2020	136.1 ^b	28.4 ^b	144.9 ^e	48.8 ^f	30.1 ^b	67.1 ^c	35.5 ^c
	2021	140.1 ^b	29.8 ^b	159.2 ^c	74.9 ^b	28.9 ^b	64.8 ^c	39.0 ^b
Sorataf	2020	112.0 ^c	28.9 ^b	158.8 ^c	63.2 ^d	33.2 ^a	68.4 ^c	42.5 ^a
	2021	113.5 ^c	25.9 ^c	167.3 ^b	79.3 ^a	32.7 ^a	67.6 ^c	42.4 ^a

PHGH = plant height at grain harvest (cm); FLLGH = flag leaf length at grain harvest (cm); DSH = days to seed harvest (days); GFP = grain filling period (days); NSPP = number of spikes per plant (number); NSLPP = number of spikelets per panicle (number); HI = harvest index (%); Means followed by a common superscript letter within a column are not significantly different from each other at $P < 0.05$.

The interaction effect of variety by year also showed significant variation for GFP and HI as indicated in Table 5.16. The result revealed that the longest GFP was exhibited by the interaction effect of Sorataf variety by the 2021 cropping season while the shortest was recorded from the interaction effect of SRCPX80Ab2291 variety by the 2020 cropping season. The highest HI (42.5%) was recorded due to the interaction effect of Sorataf variety by the 2020 cropping season while the least (29.7%) was observed from the interaction effect of CI-8251 variety by the 2020 cropping season. The interaction effect fertilizer by year also showed significant variation for GFP and HI (Table 5.17). The result revealed that the longest GFP (75.7 days) was recorded from the interaction effect of the blanket recommended fertilizer level of 150% (61.5 kg N + 30 kg P/ha) by the 2021 cropping season while the shortest was recorded from the interaction effect of the 2020 cropping season with unfertilized treatment. The interaction effect of the 2021 and 2020 cropping seasons with unfertilized treatment produced the highest (41.2%) and the lowest (34.2%) HI, respectively. The interaction effect of variety by fertilizer also showed significant variation for SY and TBY as indicated in Table 5.18. The result revealed that the highest SY (13.9 t/ha) and TBY

(20.1 t/ha) were recorded from the interaction effect of CI-8251 variety by the blanket recommended fertilizer level of 150%. On the other hand, the lowest SY (3.8 t/ha) and TBY (6.6 t/ha) were observed for the interaction effect of Sorataf variety with unfertilized treatment.

Table 5.17 Interaction effect of fertilizer by year on the mean performance of panicle length at grain harvest (PLGH), grain filling period (GFP), and harvest index (HI) of oat at Holetta

Percent of fertilizer level	Year	Parameter		
		PLGH	GFP	HI
0%	2020	33.9 ^{bc}	49.9 ^c	34.2 ^b
	2021	32.6 ^c	75.2 ^a	41.2 ^a
25%	2020	39.3 ^{a-c}	52.3 ^{bc}	35.7 ^{ab}
	2021	33.6 ^{bc}	74.1 ^a	38.4 ^{ab}
50%	2020	41.8 ^{a-c}	53.1 ^{bc}	35.0 ^{ab}
	2021	35.2 ^{a-c}	74.4 ^a	36.7 ^{ab}
75%	2020	42.6 ^{a-c}	57.2 ^b	35.7 ^{ab}
	2021	35.9 ^{a-c}	74.2 ^a	37.5 ^{ab}
100%	2020	43.7 ^{ab}	53.4 ^{bc}	36.2 ^{ab}
	2021	36.6 ^{a-c}	75.0 ^a	37.5 ^{ab}
125%	2020	45.5 ^a	56.2 ^{bc}	36.6 ^{ab}
	2021	37.1 ^{a-c}	75.1 ^a	37.1 ^{ab}
150%	2020	43.7 ^{ab}	56.4 ^{bc}	37.4 ^{ab}
	2021	32.9 ^c	75.7 ^a	37.9 ^{ab}
175%	2020	41.1 ^{a-c}	56.6 ^{bc}	36.4 ^{ab}
	2021	33.0 ^c	75.0 ^a	36.0 ^{ab}
<i>P-value</i>		0.0010	0.0266	0.0452

PLGH = panicle length at grain harvest (cm); **GFP** = grain filling period (days); **HI** = harvest index (%); Means followed by a common superscript letter within a column are not significantly different from each other at $P < 0.05$.

The GY was significantly influenced by the effects of fertilizer level, variety, and year of production (Figure 5.9 top). The results revealed that the highest GY (6.5 t/ha) was obtained from application of the blanket recommended fertilizer of 150% (61.5 kg N + 30 kg P/ha) followed by the application of 175% (71.8 kg N + 35 kg P/ha), 125% (51.3 kg N + 25 kg P/ha) and 100% (41.0 kg N + 20 kg P/ha) which produced GY of 6.3, 5.9, and 5.5 t/ha, respectively. On the other hand, the least GY (2.8 t/ha) was obtained from unfertilized treatment. The box and whisker plot also indicates the variability of oat for GY. Accordingly, the varieties had wider GY variability at the application of 100% fertilizer rate followed by 75% (30.8 kg N + 15 kg P/ha) fertilizer rate while unfertilized treatment had the least variability. The inter quintile range (IQR) of the box plot also showed the variability of 50% data set. Thus, the highest IQR was recorded from the application of 75% fertilizer rate followed by the application of 175% fertilizer rate while the lowest IQR was observed from unfertilized treatment. Among oat varieties, the highest GY (5.7 t/ha) was obtained from

Sorataf variety followed by SRCPX80Ab2291 (5.3 t/ha) while CI-8251 (5.0 t/ha) produced the least (Figure 5.9 bottom left). The varieties also produced higher GY (5.5 t/ha) in the 2021 cropping season than in the 2020 cropping season (5.2 t/ha) under different levels of fertilizer application (Figure 5.9 bottom right).

Table 5.18 Interaction effect of fertilizer by variety for plant height at grain harvest (PHGH), straw yield (SY), and total biological yield (TBY) performance of oat at Holetta

Trait	Percent of fertilizer level	Variety		
		CI-8251	SRCPX80Ab2291	Sorataf
PHGH	0%	146.4 ^c	130.0 ^f	102.1 ⁱ
	25%	165.3 ^b	132.7 ^{ef}	108.6 ^h
	50%	171.4 ^{ab}	136.7 ^{de}	113.4 ^{gh}
	75%	174.1 ^a	138.2 ^{de}	114.2 ^{gh}
	100%	176.0 ^a	139.4 ^{c-e}	115.0 ^{gh}
	125%	177.9 ^a	142.0 ^{dc}	117.3 ^g
	150%	177.9 ^a	143.5 ^{dc}	114.9 ^{gh}
	175%	178.0 ^a	142.4 ^{dc}	116.3 ^g
SY	0%	5.3 ^g	5.0 ^g	3.8 ^g
	25%	10.7 ^{b-e}	8.9 ^{ef}	7.6 ^f
	50%	13.7 ^a	8.4 ^f	7.7 ^f
	75%	10.7 ^{b-e}	9.4 ^{c-f}	7.6 ^f
	100%	12.3 ^{ab}	8.6 ^{ef}	8.0 ^f
	125%	11.5 ^{bc}	10.7 ^{b-e}	8.5 ^{ef}
	150%	13.9 ^a	9.3 ^{c-f}	9.6 ^{c-f}
	175%	13.8 ^a	11.2 ^{b-d}	9.2 ^{d-f}
TBY	0%	7.8 ⁱ	8.1 ⁱ	6.6 ⁱ
	25%	15.4 ^{c-h}	14.3 ^{e-h}	13.5 ^{f-h}
	50%	19.4 ^{ab}	12.9 ^h	13.2 ^{gh}
	75%	16.0 ^{c-g}	14.5 ^{d-h}	12.9 ^{gh}
	100%	17.5 ^{a-d}	13.8 ^{fg}	14.1 ^{e-h}
	125%	16.4 ^{c-f}	17.1 ^{b-e}	14.9 ^{c-h}
	150%	20.1 ^a	15.7 ^{c-h}	16.4 ^{c-f}
	175%	19.5 ^{ab}	17.7 ^{a-c}	16.0 ^{c-h}

PHGH = plant height at grain harvest (cm); **SY** = straw yield (t/ha); **TBY** = total biological yield (t/ha); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$.

The BYPR and GSFR showed significant variation for the application of different fertilizer levels (Table 5.19). The results showed that the highest BYPR (110.6 kg/ha/day) was recorded for the blanket recommended fertilizer of 175% (71.8 kg N + 35 kg P/ha) while the least BYPR (47.5 kg/ ha/day) was recorded from unfertilized treatment. Similarly, the GSFR was the highest for the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate while unfertilized treatment produced the least (17.5 kg/ha/day). Moreover, the BYPR, GSFR, and TSW varied significantly among oat varieties (Table 5.19). The result showed that the highest BYPR (100.0 kg/ha/day) was obtained from CI-8251 variety followed by SRCPX80Ab2291 (94.0 kg/ ha/day) while Sorataf produced the least (82.3 kg/ha/day). The lowest GSFR (30.5 kg/ha/day) and TSW (51.0 g) were recorded from CI-8251 and Sorataf varieties, respectively. Significantly the highest TSW (55.1 g) was obtained in the 2021 cropping season (Table 5.19).

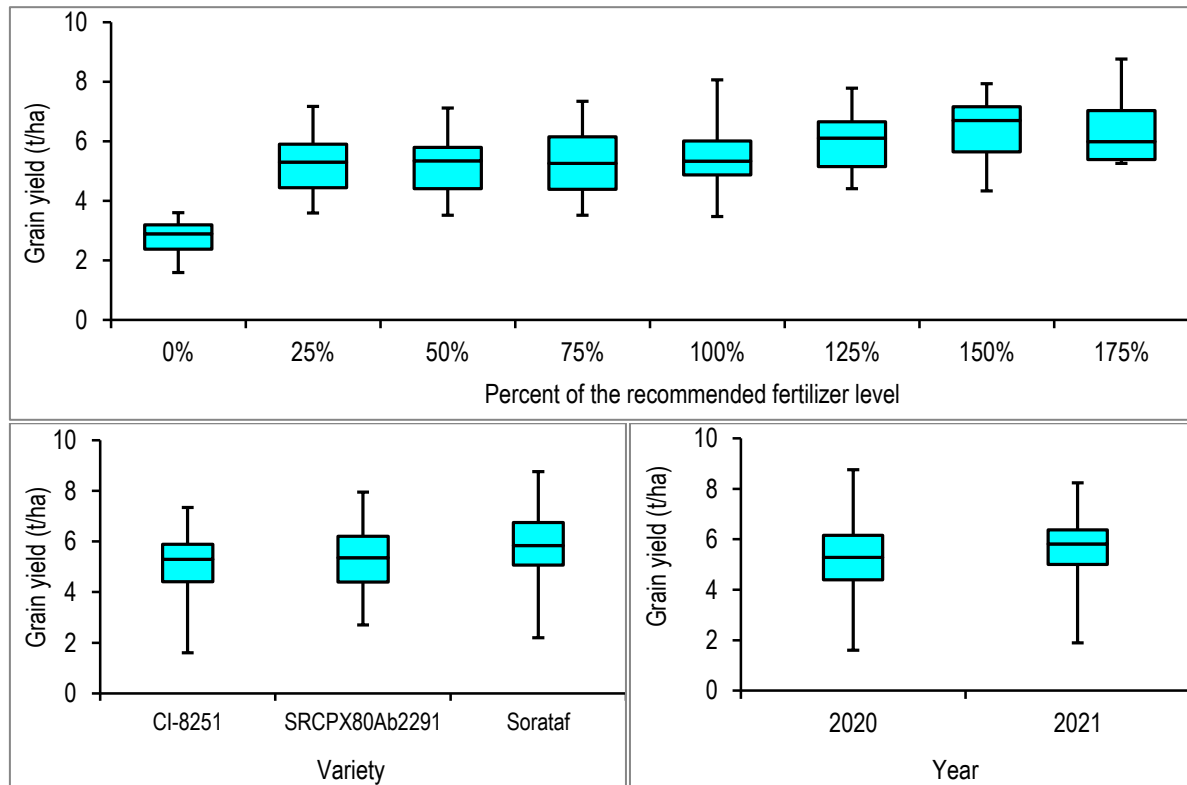


Figure 5.9 Box and whisker plot of oat grain yield as influenced by levels of fertilizer, variety and year at Holetta

Table 5.19 Effects of fertilizer, variety and year on the performance of biological yield production rate, grain sink filling rate, and thousand seed weight of oat at Holetta

Parameter	Parameter		
	BYPR	GSFR	TSW
Percent of the recommended fertilizer rate			
0%	47.5 ^d	17.5 ^d	54.8
25%	90.3 ^c	33.2 ^{bc}	53.0
50%	94.8 ^{bc}	33.1 ^{bc}	54.1
75%	90.1 ^c	32.7 ^c	52.9
100%	94.3 ^{bc}	34.3 ^{bc}	54.1
125%	100.9 ^{ba}	37.0 ^{ab}	53.3
150%	108.5 ^a	40.4 ^a	53.4
175%	110.6 ^a	39.6 ^a	52.5
<i>P-value</i>	<.0001	<.0001	0.5154
Variety			
CI-8251	100.0 ^a	30.5 ^b	54.3 ^a
SRCPX80Ab2291	94.0 ^b	35.0 ^a	55.2 ^a
Sorataf	82.3 ^c	35.0 ^a	51.0 ^b
<i>P-value</i>	<.0001	0.0002	<.0001
Year			
2020	94.4	33.6	51.9 ^b
2021	89.9	33.3	55.1 ^a
<i>P-value</i>	0.0693	0.7489	<.0001

BYPR = biological yield production rate (kg/ha/day); GSFR = grain sink filling rate (kg/ha/day); TSW = thousand seed weight (g); Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

5.3.2.3 Main and interaction effects on nutrient content, uptake and use efficiency

The three-way interaction ($V \times F \times Y$) effect for straw and grain nutrient concentrations and nutrient harvest index showed significant variation as indicated in [Table 5.20](#). The result showed that the highest SPC (0.08%) was observed from the interaction effect of Sorataf variety by 75% (30.8 kg N + 15 kg P/ha) fertilizer rate in the 2021 cropping season while the least (0.03%) was recorded from the interaction effect of SRCPX80Ab2291 variety by unfertilized treatment in the 2020 cropping season. Similarly, the highest SNC (0.71%) was observed from the interaction effect of SRCPX80Ab2291 variety by 175% (71.8 kg N + 35 kg P/ha) fertilizer rate in the 2021 cropping season while the interaction effect of Sorataf variety by unfertilized treatment in the 2020 cropping season had the least SNC (0.21%). The grain nutrient concentration also indicated that the highest GPC (0.33%) was observed by the interaction effect of the Sorataf variety by 150% (61.5 kg N + 30 kg P/ha) fertilizer rate in the 2020 cropping season while the interaction effect of SRCPX80Ab2291 variety by unfertilized treatment in the 2020 cropping season had the least (0.19%). Moreover, the interaction effect of Sorataf variety by 75% fertilizer rate in the 2021 cropping season produced the highest GNC (2.09%) while the interaction effect of CI-8251 variety by unfertilized treatment in the 2020 cropping season produced the least GNC (1.44%). Furthermore, the highest NHI (84.1%) was exhibited from the interaction effect of Sorataf variety by 100% (41.0 kg N + 20 kg P/ha) fertilizer rate in the 2020 cropping season while the interaction effect of CI-8251 variety by 125% (51.3 kg N + 25 kg P/ha) fertilizer rate in the 2021 cropping season produced the least NHI (58.4%).

The SNU and TNU were significantly influenced by the interaction effect of variety by fertilizer ([Table 5.21](#)). The results revealed that the highest (66.5 kg/ha) and lowest (12.4 kg/ha) SNU were observed from the interaction effect of CI-8251 variety by 150% (61.5 kg N + 30 kg P/ha) fertilizer rate and Sorataf variety by unfertilized treatment, respectively. Similarly, the highest TNU (204.9 kg/ha) was recorded from the interaction effect of SRCPX80Ab2291 variety by 175% (71.8 kg N + 35 kg P/ha) fertilizer rate while the lowest (58.0 kg/ha) was recorded from the interaction effect of CI-8251 variety by unfertilized treatment. Furthermore, the SNU and TNU were influenced significantly by cropping season ([Figure 5.10](#) left). The result revealed that the 2021 cropping season produced higher SNU (49.2 kg/ha) and TNU (168.1 kg/ha) compared to the 2020 cropping season.

Table 5.20 Interaction effect of variety by fertilizer by year for straw phosphorus and nitrogen concentrations, grain phosphorus and nitrogen concentrations, and nutrient harvest index performance of oat at Holetta

Parameter	Percent of fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
SPC	0%	0.04 ^{i-m}	0.03 ^m	0.04 ^{d-m}	0.03 ^{lm}	0.03 ^{j-m}	0.03 ^{k-m}
	25%	0.04 ^{d-k}	0.06 ^{b-e}	0.04 ^{d-l}	0.04 ^{d-l}	0.05 ^{c-f}	0.04 ^{e-m}
	50%	0.05 ^{c-i}	0.04 ^{h-m}	0.05 ^{d-i}	0.04 ^{d-l}	0.05 ^{c-i}	0.05 ^{d-j}
	75%	0.05 ^{d-j}	0.06 ^{b-d}	0.04 ^{d-l}	0.04 ^{h-m}	0.05 ^{c-i}	0.08 ^a
	100%	0.04 ^{d-k}	0.05 ^{c-g}	0.05 ^{c-h}	0.06 ^{b-d}	0.06 ^{b-d}	0.04 ^{h-m}
	125%	0.05 ^{d-i}	0.04 ^{d-k}	0.05 ^{d-i}	0.07 ^{ab}	0.05 ^{c-i}	0.04 ^{f-m}
	150%	0.05 ^{c-g}	0.04 ^{d-l}	0.05 ^{c-i}	0.05 ^{c-g}	0.05 ^{d-j}	0.06 ^{bc}
	175%	0.05 ^{c-i}	0.05 ^{c-i}	0.04 ^{e-m}	0.05 ^{d-i}	0.05 ^{c-g}	0.04 ^{g-m}
SNC	0%	0.22 st	0.23 ^{r-t}	0.21 ^t	0.36 ^{g-r}	0.31 ^{l-t}	0.38 ^{e-q}
	25%	0.30 ^{m-t}	0.33 ^{j-t}	0.27 ^{p-t}	0.37 ^{f-q}	0.45 ^{b-j}	0.48 ^{b-g}
	50%	0.33 ^{j-t}	0.26 ^{p-t}	0.34 ^{i-s}	0.45 ^{c-k}	0.36 ^{g-r}	0.50 ^{b-e}
	75%	0.25 ^{q-t}	0.35 ^{h-s}	0.30 ^{m-t}	0.45 ^{c-k}	0.53 ^{b-d}	0.57 ^b
	100%	0.38 ^{e-p}	0.35 ^{h-r}	0.28 ^{o-t}	0.42 ^{c-m}	0.52 ^{b-d}	0.47 ^{b-i}
	125%	0.31 ^{l-t}	0.37 ^{e-q}	0.29 ^{n-t}	0.54 ^{bc}	0.49 ^{b-f}	0.43 ^{c-l}
	150%	0.42 ^{c-n}	0.31 ^{l-t}	0.33 ^{j-t}	0.44 ^{c-l}	0.44 ^{c-l}	0.51 ^{b-d}
	175%	0.33 ^{j-t}	0.32 ^{k-t}	0.40 ^{d-o}	0.44 ^{c-l}	0.71 ^a	0.47 ^{b-h}
GPC	0%	0.21 ^{qr}	0.19 ^r	0.21 ^{p-r}	0.22 ^{o-r}	0.23 ^{n-q}	0.23 ^{n-q}
	25%	0.26 ^{g-n}	0.24 ^{j-p}	0.28 ^{e-k}	0.28 ^{d-k}	0.25 ^{i-o}	0.29 ^{c-h}
	50%	0.26 ^{g-o}	0.24 ^{l-q}	0.26 ^{f-n}	0.32 ^{a-c}	0.31 ^{a-e}	0.30 ^{a-f}
	75%	0.28 ^{d-i}	0.24 ^{k-q}	0.27 ^{e-l}	0.25 ^{h-o}	0.28 ^{d-k}	0.28 ^{d-i}
	100%	0.24 ^{j-p}	0.24 ^{m-q}	0.25 ^{i-o}	0.29 ^{c-g}	0.28 ^{d-i}	0.28 ^{c-i}
	125%	0.24 ^{m-q}	0.23 ^{m-q}	0.29 ^{c-i}	0.26 ^{g-n}	0.26 ^{f-n}	0.29 ^{c-i}
	150%	0.27 ^{f-m}	0.24 ^{k-q}	0.33 ^a	0.26 ^{g-o}	0.28 ^{c-i}	0.30 ^{a-f}
	175%	0.24 ^{j-p}	0.28 ^{d-j}	0.29 ^{b-g}	0.31 ^{a-d}	0.29 ^{c-h}	0.32 ^{ab}
GNC	0%	1.44 ^l	1.56 ^{i-l}	1.44 ^l	1.51 ^{kl}	1.54 ^{j-l}	1.54 ^{j-l}
	25%	1.87 ^{b-h}	1.83 ^{b-h}	1.77 ^{e-h}	1.72 ^{g-j}	1.83 ^{c-h}	2.04 ^{ab}
	50%	1.75 ^{f-i}	1.83 ^{c-h}	1.78 ^{d-h}	1.95 ^{a-f}	1.68 ^{h-k}	1.86 ^{b-h}
	75%	1.69 ^{g-k}	1.83 ^{b-h}	1.93 ^{a-f}	1.71 ^{g-k}	1.96 ^{a-e}	2.09 ^a
	100%	1.95 ^{a-f}	1.88 ^{a-h}	1.85 ^{b-h}	1.83 ^{b-h}	1.74 ^{f-i}	1.90 ^{a-g}
	125%	1.72 ^{g-j}	1.89 ^{a-g}	1.89 ^{a-g}	1.80 ^{c-h}	1.89 ^{a-g}	2.04 ^{ab}
	150%	1.95 ^{a-f}	1.99 ^{a-c}	1.86 ^{b-h}	1.98 ^{a-d}	1.82 ^{c-h}	1.85 ^{b-h}
	175%	1.82 ^{c-h}	1.83 ^{b-h}	1.97 ^{a-e}	1.89 ^{a-h}	1.94 ^{a-f}	1.85 ^{b-h}
NHI	0%	71.4 ^{g-n}	77.6 ^{a-i}	81.3 ^{a-d}	72.0 ^{e-n}	79.2 ^{a-g}	78.3 ^{a-h}
	25%	71.4 ^{g-n}	74.3 ^{d-m}	83.1 ^{ab}	70.0 ^{i-o}	72.5 ^{e-m}	77.1 ^{a-j}
	50%	72.0 ^{e-n}	77.0 ^{a-j}	77.5 ^{a-i}	64.1 ^{n-p}	74.7 ^{c-m}	76.2 ^{b-k}
	75%	74.4 ^{d-m}	72.5 ^{e-m}	82.9 ^{ab}	69.4 ^{j-o}	68.3 ^{k-o}	70.9 ^{h-o}
	100%	66.8 ^{m-o}	73.6 ^{d-m}	84.1 ^a	67.1 ^{l-o}	70.4 ^{h-o}	75.0 ^{c-l}
	125%	71.4 ^{g-n}	74.6 ^{d-m}	82.5 ^{a-c}	58.4 ^p	71.4 ^{g-n}	79.2 ^{a-g}
	150%	67.5 ^{l-o}	79.8 ^{a-e}	81.2 ^{a-d}	67.1 ^{l-o}	76.1 ^{b-k}	71.5 ^{f-n}
	175%	67.3 ^{l-o}	77.6 ^{a-i}	79.5 ^{a-f}	66.9 ^{m-o}	63.5 ^{op}	74.6 ^{d-m}

SPC = straw phosphorus concentration (%); SNC = straw nitrogen concentration (%); GPC = grain phosphorus concentration (%); GNC = grain nitrogen concentration (%); NHI = nutrient harvest index (%); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$.

Table 5.21 Interaction effect of fertilizer by variety for straw and total nutrient uptakes, partial nutrient balance, internal utilization efficiency, and agro-physiological efficiency of oat at Holetta

Parameter	Percent of fertilizer level	Variety		
		CI-8251	SRCPX80Ab2291	Sorataf
SNU	0%	16.3 ^{h-j}	14.7 ^{ij}	12.4 ^j
	25%	40.4 ^{d-g}	40.0 ^{e-g}	32.3 ^{f-i}
	50%	61.4 ^{a-c}	29.1 ^{g-j}	35.9 ^{fg}
	75%	42.1 ^{c-g}	45.8 ^{b-g}	38.7 ^{e-g}
	100%	56.6 ^{a-e}	41.7 ^{d-g}	34.1 ^{f-h}
	125%	57.4 ^{a-e}	50.7 ^{a-f}	34.3 ^{f-h}
	150%	66.5 ^a	38.5 ^{e-g}	45.4 ^{b-g}
	175%	59.9 ^{a-d}	62.0 ^{ab}	44.5 ^{b-g}
TNU	0%	58.0 ^g	68.1 ^g	60.8 ^g
	25%	138.4 ^{ef}	150.1 ^{c-f}	159.6 ^{b-f}
	50%	185.2 ^{a-d}	120.7 ^f	152.9 ^{b-f}
	75%	147.2 ^{d-f}	155.6 ^{b-f}	161.3 ^{a-f}
	100%	168.1 ^{a-e}	148.9 ^{d-f}	165.4 ^{a-e}
	125%	156.8 ^{b-f}	187.4 ^{a-d}	179.3 ^{a-e}
	150%	204.4 ^a	176.9 ^{a-e}	194.2 ^{a-c}
	175%	180.9 ^{a-e}	204.9 ^a	195.2 ^{ab}
PNBGY	25%	6.4 ^b	7.2 ^b	8.3 ^a
	50%	4.1 ^c	3.0 ^{de}	3.8 ^{cd}
	75%	2.3 ^{e-h}	2.4 ^{e-g}	2.7 ^{ef}
	100%	1.8 ^{f-h}	1.9 ^{f-j}	2.2 ^{e-i}
	125%	1.3 ^{ij}	1.8 ^{f-j}	1.9 ^{f-j}
	150%	1.5 ^{g-j}	1.5 ^{g-j}	1.6 ^{g-j}
	175%	1.1 ^j	1.3 ^{h-j}	1.4 ^{h-j}
IUEGY	25%	48.7 ^{a-d}	48.2 ^{a-e}	46.1 ^{c-f}
	50%	47.1 ^{b-f}	49.6 ^{a-c}	47.9 ^{a-e}
	75%	51.0 ^a	46.6 ^{b-f}	43.9 ^f
	100%	46.4 ^{b-f}	48.4 ^{a-e}	46.8 ^{b-f}
	125%	50.1 ^{ab}	46.7 ^{b-f}	44.7 ^{ef}
	150%	45.1 ^{d-f}	46.3 ^{b-f}	46.3 ^{b-f}
	175%	47.0 ^{b-f}	46.3 ^{b-f}	45.2 ^{d-f}
APEGY	25%	28.3 ^{a-c}	27.5 ^{a-c}	30.1 ^{ab}
	50%	27.2 ^{a-c}	28.2 ^{a-c}	30.0 ^{ab}
	75%	32.7 ^a	22.7 ^c	25.5 ^{a-c}
	100%	24.4 ^{bc}	25.9 ^{a-c}	31.6 ^{ab}
	125%	26.1 ^{a-c}	28.1 ^{a-c}	30.7 ^{ab}
	150%	24.6 ^{bc}	30.5 ^{ab}	29.9 ^{ab}
	175%	25.9 ^{a-c}	27.0 ^{a-c}	29.1 ^{a-c}

SNU = straw nutrient uptake (kg/ha); TNU = total nutrient uptake (kg/ha); PNBGY = partial nutrient balance of grain yield (kg/kg); IUEGY = internal utilization efficiency of grain yield (kg/ha); APEGY = agro-physiological efficiency of grain yield (kg/ha); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$.

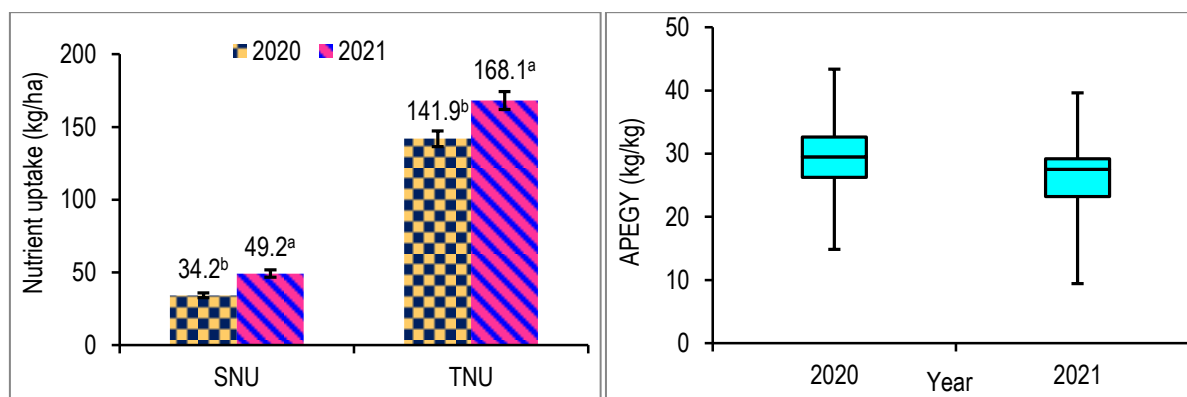
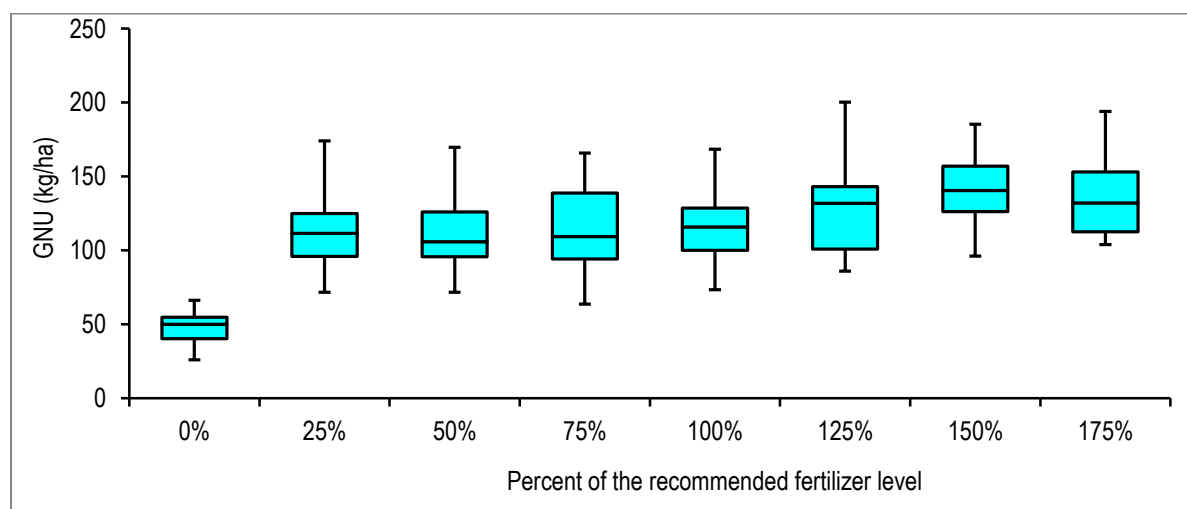


Figure 5.10 Effect of year on straw nutrient uptake (SNU) and total nutrient uptake (TNU) (left) and box and whisker plot of agro-physiological efficiency (APEGY) as influenced by year (right) at Holetta

The GNU varied significantly by the effects of fertilizer level, variety, and year (Figure 5.11 top). The result showed that the highest GNU (141.7 kg/ha) was recorded from application of the blanket recommended fertilizer of 150% (61.5 kg N+30 kg P/ha) followed by 175% (71.8 kg N + 35 kg P/ha), 125% (51.3 kg N + 25 kg P/ ha), and 100% (41.0 kg N + 20 kg P/ha) which produced 138.2, 127.1, and 116.7 kg/ha, respectively. However, unfertilized treatment had the least GNU (47.8 kg/ha). The box and whisker plot also showed the variability of GNU for oat varieties. Accordingly, the highest variability was recorded for the application of 125% fertilizer rate while the least was recorded for unfertilized treatment. Among the varieties, Sorataf (129.3 kg/ha) had the highest GNU followed by SRCPX80Ab2291 (111.3 kg/ha) while CI-8251 (104.8 kg/ha) had the least (Figure 5.11 bottom left). Moreover, the 2021 cropping season had a higher GNU (118.9 kg/ha) compared to the 2020 (107.7 kg/ha) cropping season (Figure 5.11 bottom right).



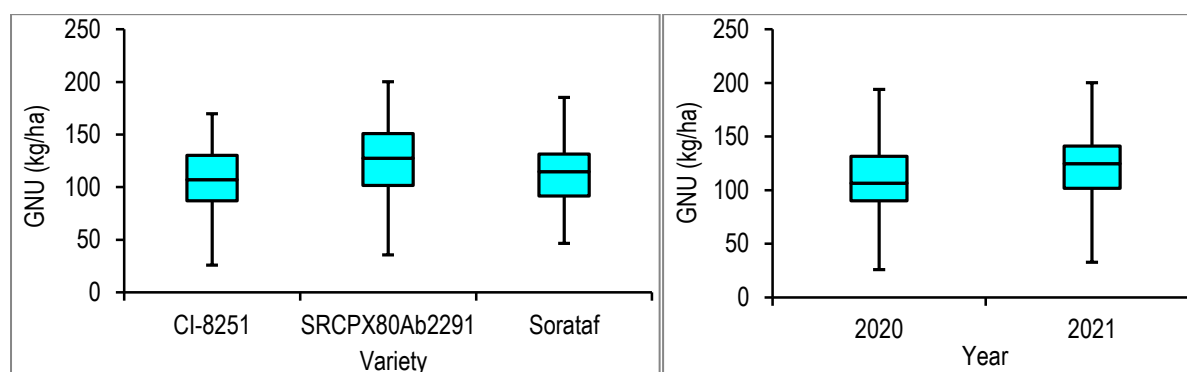


Figure 5.11 Box and whisker plot for grain nutrient uptake (GNU) as influenced by effects of fertilizer, variety and year at Holetta

The PNB, IUE, and APE of grain yield showed significant variation for the interaction effect of variety by fertilizer (Table 5.21). The result showed that the highest PNB (8.3 kg/kg) was observed by the interaction effect of Sorataf variety by 25% (10.3 kg N+5 kg P/ha) fertilizer rate while the interaction effect of CI-8251 variety by 175% (71.8 kg N +35 kg P/ha) fertilizer rate had the least PNB (1.1 kg/kg). Moreover, the highest IUE (51.0 kg/ kg) and APE (32.7 kg/kg) of grain yield was observed by the interaction effect of CI-8251 variety by 75% (30.8 kg N+15 kg P/ha) fertilizer rate. Furthermore, the effect of year on APE of grain yield was significant (Figure 5.10 right). The result showed that the 2020 cropping season had a higher APE (31.7 kg/kg) compared to the 2021 (24.6 kg/kg) cropping season. The interaction effect of fertilizer level by cropping season also showed significant variation for PNB (Figure 5.12). The result showed that the interaction effect of 25% fertilizer rate by the 2021 cropping season had the highest PNB (8.0 kg/kg) while 175% fertilizer rate by the 2021 cropping season had the lowest PNB (1.3 kg/kg).

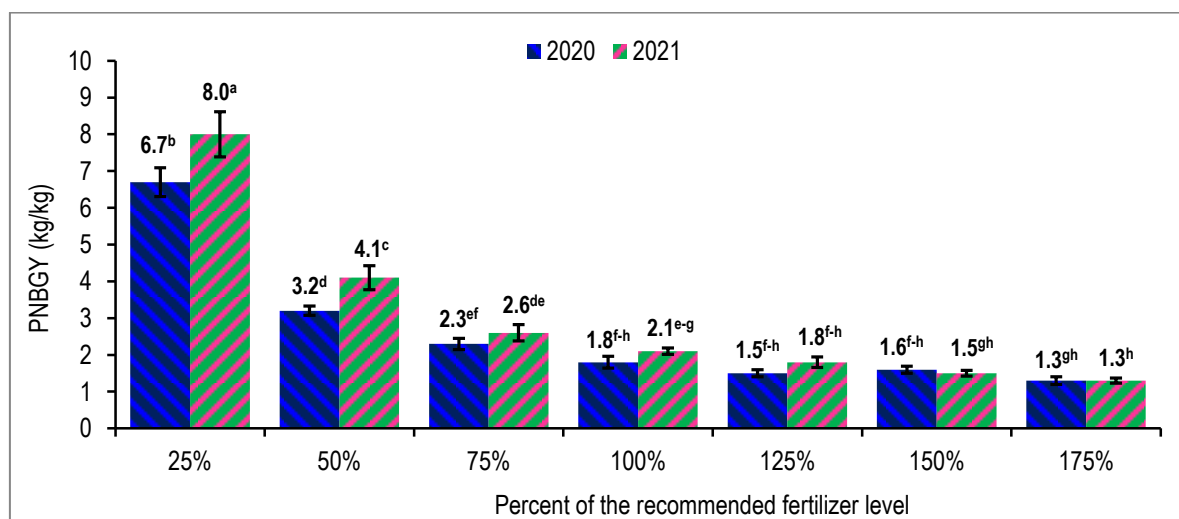


Figure 5.12 Interaction effect of recommended fertilizer level by year on partial nutrient balance of grain yield (PNBGY) at Holetta

The PFP and AE of grain yield showed significant variation for the effects of fertilizer level, variety, and year (Table 5.22). The results revealed that the application of 25% (10.3 kg N + 5 kg P/ha) fertilizer rate had the highest PFP (346.6 kg/kg) and AE (164.8 kg/kg) while the least PFP (59.4 kg/kg) and AE (33.4 kg/kg) was observed for 175% (71.8 kg N + 35 kg P/ha) fertilizer rate. Among the varieties, Sorataf variety had the highest PFP (143.3 kg/kg) and AE (74.9 kg/kg) while CI-8251 and SRCPX80Ab2291 varieties produced the lowest PFP (126.7 kg/kg) and AE (56.3 kg/kg), respectively. The second year of production (2021) produced the highest PFP (141.0 kg/kg) and AE (71.2 kg/kg) compared to the 2020 cropping season. Moreover, the PE of biological yield showed significant variation for oat varieties (Table 5.22). The result revealed that CI-8251 variety had the highest PE (91.0 kg/kg) followed by SRCPX80Ab2291 (76.6 kg/kg) while the lowest PE (70.5 kg/kg) was observed from Sorataf variety.

Table 5.22 Effects of fertilizer, variety and year on the performance of nutrient use efficiency (PFPGY, AEGY, and PEBY) in oat at Holetta

Parameter	Parameter		
	PFPGY	AEGY	PEBY
Percent of the recommended fertilizer rate			
25%	346.6 ^a	164.8 ^a	81.0
50%	173.1 ^b	82.3 ^b	86.3
75%	114.8 ^c	54.3 ^c	78.1
100%	92.0 ^d	45.5 ^c	76.6
125%	77.5 ^{de}	41.1 ^c	77.7
150%	70.7 ^e	40.4 ^c	76.0
175%	59.4 ^e	33.4 ^c	79.7
<i>P-value</i>	<.0001	<.0001	0.4194
Variety			
CI-8251	126.7 ^b	66.8 ^{ab}	91.0 ^a
SRCPX80Ab2291	130.4 ^b	56.3 ^b	76.6 ^b
Sorataf	143.3 ^a	74.9 ^a	70.5 ^b
<i>P-value</i>	0.0207	0.0156	<.0001
Year			
2020	125.9 ^b	60.7 ^b	78.4
2021	141.0 ^a	71.2 ^a	80.2
<i>P-value</i>	0.0034	0.0457	0.4898

PFPGY = partial factor productivity of grain yield (kg/kg); AEGY = agronomic efficiency of grain yield (kg/kg); and PEBY = physiological efficiency of biological yield (kg/kg); Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

5.3.2.4 Correlation analysis

The correlation coefficient of measured parameters with levels of fertilizer and grain yield is indicated in Table 5.23. The results revealed that the GY ($r = 0.84^{**}$), DSH ($r = 0.76^{*}$),

FLLGH ($r = 0.73^*$), PHGH ($r = 0.87^{**}$), GFP ($r = 0.88^{**}$), BYPR ($r = 0.82^*$), GSFR ($r = 0.84^{**}$), SY ($r = 0.82^*$), and TBY ($r = 0.83^*$) were significantly and positively correlated with fertilizer levels. Moreover, the SNC ($r = 0.87^{**}$), GNC ($r = 0.71^*$), GNU ($r = 0.84^{**}$), SNU ($r = 0.87^{**}$), and TNU ($r = 0.85^{**}$) had significant positive associations with fertilizer levels. On the other hand, NHI, PFP, PNB, IUE, and AE had significant inverse relationships with the levels of fertilizer.

Furthermore, the association of GY with DSH ($r = 0.75^*$), FLLGH ($r = 0.81^*$), PHGH ($r = 0.94^{***}$), GFP ($r = 0.80^*$), NSLPP ($r = 0.81^*$), BYPR ($r = 0.99^{***}$), GSFR ($r = 0.99^{***}$), SY ($r = 0.99^{***}$), TBY ($r = 0.99^{***}$), SPC ($r = 0.87^{**}$ and GPC ($r = 0.91^{**}$), SNC ($r = 0.93^{***}$), GNC ($r = 0.96^{***}$), GNU ($r = 0.99^{***}$), SNU ($r = 0.98^{***}$), and TNU ($r = 0.99^{***}$) were significant and positive. However, GY had significant inverse associations with TSW, NHI, and IUE. The relationship between selected plant parameters is also indicated in Figure 5.13. The results showed that HI had inverse associations with SY and TSW. The association of GSFR with GFP was positive while it had an inverse association with DSH. The GNC and SNC had positive associations with their respective phosphorus concentration. The NHI had a positive association with GNU while it had an inverse association with SNU. The correlations of PFP with PNB and IUE; and also AE with PE and APE were positive.

Table 5.23 Relationships of measured parameters with fertilizer levels and grain yield of oat varieties grown at Holetta

Parameter	With RFL	With GY	Parameter	With RFL	With GY
GY	0.84 ^{**}	—	SPC	0.62 ^{NS}	0.87 ^{**}
DSH	0.76 [*]	0.75 [*]	SNC	0.87 ^{**}	0.93 ^{***}
FLLGH	0.73 [*]	0.81 [*]	GPC	0.69 ^{NS}	0.91 ^{**}
PHGH	0.87 ^{**}	0.94 ^{***}	GNC	0.71 [*]	0.96 ^{***}
PLGH	0.53 ^{NS}	0.69 ^{NS}	GNU	0.84 ^{**}	0.99 ^{***}
GFP	0.88 ^{**}	0.80 [*]	SNU	0.87 ^{**}	0.98 ^{***}
NSPP	0.51 ^{NS}	0.62 ^{NS}	TNU	0.85 ^{**}	0.99 ^{***}
NSLPP	0.70 ^{NS}	0.81 [*]	NHI	-0.81 [*]	-0.83 [*]
BYPR	0.82 [*]	0.99 ^{***}	PFP	-0.84 [*]	-0.62 ^{NS}
GSFR	0.84 ^{**}	0.99 ^{***}	PNBGY	-0.84 [*]	-0.62 ^{NS}
TSW	-0.59 ^{NS}	-0.72 [*]	IUEGY	-0.88 ^{**}	-0.90 ^{**}
HI	-0.18 ^{NS}	-0.36 ^{NS}	AEGY	-0.82 [*]	-0.59 ^{NS}
SY	0.82 [*]	0.99 ^{***}	PEBY	-0.55 ^{NS}	-0.47 ^{NS}
TBY	0.83 [*]	0.99 ^{***}	APEGY	-0.31 ^{NS}	0.02 ^{NS}

GY = grain yield (t/ha); DSH = days to seed harvest (days); FLLGH = flag leaf length at grain harvest (cm); PHGH = plant height at grain harvest (cm); PLGH = panicle length at grain harvest (cm); GFP = grain filling period (days); NSPP = number of spikes per panicle (number); NSLPP = number of spikelets per panicle (number); BYPR = biological yield production rate (kg/ha/day); GSFR = grain sink filling rate (kg/ha/day); TSW = thousand-grain weight (g); HI = harvest index (%); SY = straw yield (t/ha); TBY = total biological yield (t/ha); SPC = straw phosphorus concentration (%); SNC = straw nitrogen concentration (%); GPC = grain phosphorus concentration (%); GNC = grain nitrogen concentration (%); GNU = grain nutrient uptake (kg/ha); SNU = straw nutrient uptake (kg/ha); TNU = total nutrient uptake (kg/ha); NHI = nutrient harvest index (%); PFP = partial factor productivity of grain yield (kg/kg); PNBGY = partial nutrient balance of grain yield (kg/kg); IUEGY = internal utilization efficiency of grain yield (kg/ha); AEGY = agronomic efficiency of grain yield (kg/kg); PEBY = physiological efficiency of grain yield (kg/kg); APEGY = agro-physiological efficiency of grain yield (kg/ha); RFL = recommended fertilizer level; NS = non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively.

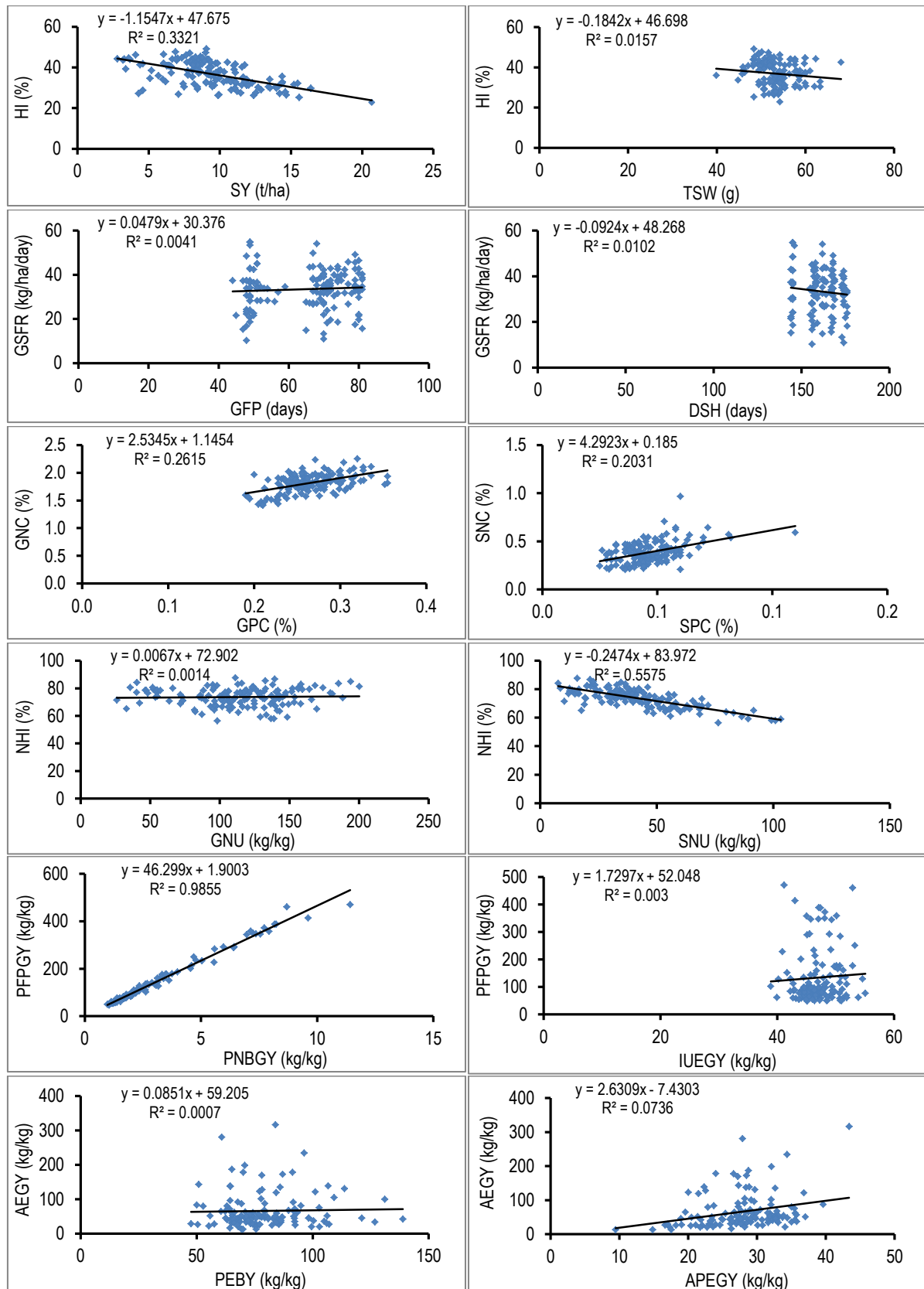


Figure 5.13 Relationships between selected plant parameters, nutrient uptake and use efficiency of three oat varieties sown with eight fertilizer levels at Holetta.

Note: HI = harvest index; SY = straw yield; TSW = thousand-grain weight; GSFR = grain sink filling rate; GFP = grain filling period; DSH = days to seed harvest; GPC = grain phosphorus concentration; GNC = grain nitrogen concentration; SPC = straw phosphorus concentration; SNC = straw nitrogen concentration; NHI = nutrient harvest index; GNU = grain nutrient uptake; SNU = straw nutrient uptake; PFPGY = partial factor productivity of grain yield; PNBGY = partial nutrient balance of grain yield; IUEGY = internal utilization efficiency of grain yield; AEGY = agronomic efficiency of grain yield; PEBY = physiological efficiency of grain yield; APEGY = agro-physiological efficiency of grain yield.

5.3.2.5 Economic analysis

The partial budget analysis for each oat variety and combined oat varieties over years is indicated in [Table 5.24](#). The results revealed that CI-8251 variety produced the highest net benefit (162,996.9 ETB/ha) for the application of 150% (61.5 kg N + 30 kg P/ha) of the blanket recommended fertilizer rate. The maximum net benefit of 158,322.0 ETB/ha was obtained from SRCPX80Ab2291 variety using application of 175% (71.8 kg N + 35 kg P/ha) of the blanket recommended fertilizer rate. The highest net benefit (157,593.5 ETB/ ha) was recorded for Sorataf variety using application of 150% of the blanket recommended fertilizer rate. Furthermore, the combined analysis of oat varieties indicated that application of 150% of the blanket recommended fertilizer rate produced the highest net benefit (156,207.2 ETB/ha).

Table 5.24 Partial budget analysis on the effect of fertilizer application in oat at Holetta

RFL	Adj. GY	Adj. SY	GYR	SYR	GB	TC	NB	MNB	MTC	NBCR	MRR%
CI-8251											
0%	2.2	4.8	60,500.0	24,000.0	84,500.0	34,789.2	49,710.8	–	–	1.4	–
25%	4.3	9.6	118,250.0	48,000.0	166,250.0	43,962.9	122,287.1	72,576.3	9,173.7	2.8	791.1
125%	4.4	10.3	121,000.0	51,500.0	172,500.0	46,375.3	126,124.7	3,837.6	2,412.4	2.7	159.1
100%	4.6	11.1	126,500.0	55,500.0	182,000.0	47,682.4	134,317.6	8,192.9	1,307.1	2.8	626.8
75%	4.8	9.6	132,000.0	48,000.0	180,000.0	47,867.9	132,132.1	-2,185.5	185.5	2.8	D
50%	5.2	12.3	143,000.0	61,500.0	204,500.0	49,000.0	155,500.0	23,367.9	1,132.1	3.2	2064.1
175%	5.1	12.4	140,250.0	62,000.0	202,250.0	51,296.0	150,954.0	-4,546.0	2,296.0	2.9	D
150%	5.6	12.5	154,000.0	62,500.0	216,500.0	53,503.1	162,996.9	12,042.9	2,207.1	3.0	545.6
SRCPX80Ab2291											
0%	2.7	4.5	74,250.0	22,500.0	96,750.0	34,884.0	61,866.0	–	–	1.8	–
50%	4.1	7.5	112,750.0	37,500.0	150,250.0	42,364.7	107,885.3	46,019.3	7,480.7	2.5	615.2
25%	4.8	8.1	132,000.0	40,500.0	172,500.0	44,163.5	128,336.5	20,451.2	1,798.8	2.9	1136.9
75%	4.6	8.5	126,500.0	42,500.0	169,000.0	44,722.3	124,277.7	-4,058.8	558.8	2.8	D
100%	4.7	7.7	129,250.0	38,500.0	167,750.0	44,919.6	122,830.4	-1,447.3	197.3	2.7	D
125%	5.8	9.6	159,500.0	48,000.0	207,500.0	50,064.7	157,435.3	34,604.9	5,145.1	3.1	672.6
150%	5.7	8.4	156,750.0	42,000.0	198,750.0	50,718.9	148,031.1	-9,404.2	654.2	2.9	D
175%	5.9	10.0	162,250.0	50,000.0	212,250.0	53,928.0	158,322.0	10,290.9	3,209.1	2.9	320.7
Sorataf											
0%	2.5	3.4	68,750.0	17,000.0	85,750.0	34,594.7	51,155.3	–	–	1.5	–
75%	4.8	6.8	132,000.0	34,000.0	166,000.0	45,698.0	120,302.0	69,146.7	11,103.3	2.6	622.8
50%	5.0	6.9	137,500.0	34,500.0	172,000.0	46,035.9	125,964.1	5,662.1	337.9	2.7	1675.7
25%	5.2	6.9	143,000.0	34,500.0	177,500.0	46,109.4	131,390.6	5,426.5	73.5	2.8	7383.0
100%	5.5	7.1	151,250.0	35,500.0	186,750.0	49,261.3	137,488.7	6,098.1	3,151.9	2.8	193.5
125%	5.8	7.7	159,500.0	38,500.0	198,000.0	50,731.0	147,269.0	9,780.3	1,469.7	2.9	665.5
175%	6.1	8.3	167,750.0	41,500.0	209,250.0	52,955.0	156,295.0	9,026.0	2,224.0	3.0	405.8
150%	6.1	8.6	167,750.0	43,000.0	210,750.0	53,156.5	157,593.5	1,298.5	201.5	3.0	644.4
Combined oat varieties											
0%	2.5	4.2	67,833.3	21,166.7	89,000.0	34,756.0	54,244.0	–	–	1.6	–
25%	4.8	8.2	131,083.3	41,000.0	172,083.3	44,745.2	127,338.1	73,094.1	9,989.3	2.8	731.7
50%	4.8	8.9	131,083.3	44,500.0	175,583.3	45,800.2	129,783.1	2,445.0	1,055.0	2.8	231.8
75%	4.7	8.3	130,166.7	41,500.0	171,666.7	46,096.1	125,570.6	-4,212.6	295.9	2.7	D
100%	4.9	8.6	135,666.7	43,166.7	178,833.3	47,287.8	131,545.6	5,975.0	1,191.7	2.8	501.4
125%	5.3	9.2	146,666.7	46,000.0	192,666.7	49,057.0	143,609.7	12,064.1	1,769.3	2.9	681.9
150%	5.8	9.8	159,500.0	49,166.7	208,666.7	52,459.5	156,207.2	12,597.5	3,402.5	3.0	370.2
175%	5.7	10.2	156,750.0	51,166.7	207,916.7	52,726.4	155,190.3	-1,016.9	266.9	2.9	D

RFL = recommended fertilizer level; Adj. GY = adjusted grain yield; Adj. SY = adjusted straw yield; GYR = grain yield revenue; SYR = straw yield revenue; GB = gross benefit; TC = total cost; NB = net benefit; MNB = marginal net benefit; MTC = marginal total cost; NBCR = net benefit to cost ratio; MRR = marginal rate of return; D = dominated suggesting treatment has a lower NB with higher TC compared to the preceding treatment NB and TC; 1kg DAP = 13.5 ETB in May, 2020 and 15.5 ETB in May, 2021 with a mean of 14.5 ETB; 1kg Urea = 16.2 ETB in May, 2020 and 18.6 ETB in May, 2021 with a mean of 17.4 ETB; 1kg grain = 25 ETB in January 01, 2021 and 30.0 ETB in January 01, 2022 with a mean of 27.5 ETB; 1kg straw = 4.5 ETB in January 01, 2021 and 5.5 ETB in January 01, 2022 with mean of 5.5 ETB; ETB = Ethiopian birr; Except fertilizer and threshing costs, land preparation (4000.0 ETB), planting (1822.9 ETB), weeding (8854.2 ETB), Keeping the field from birds and others from grain filling to maturity (2700.0 ETB), harvesting (3472.2 ETB), and Seed (2750.0 ETB) costs are the same for all treatments per hectare; The sum of the total cost except fertilizer and threshing costs is 23,599.3 ETB for all treatments; January 01, 2021 exchange rate (\$ 1 USD = 39.55 ETB) and January 01, 2022 exchange rate (\$ 1 USD = 49.15 ETB) and mean of two years exchange rate (\$ 1 USD = 44.35 ETB).

5.3.3 Fodder nutritional quality

5.3.3.1 Analysis of variance

The combined analysis of variance for the studied parameters is indicated in Table 5.25. The result showed that all the measured parameters were significant for varietal effect except ash and cellulose contents. However, the rates of fertilizer had a significant effect on all

measured parameters. On the other hand, all the measured parameters were influenced significantly by the year effect except ash, cellulose, and IVDMD. The interaction effect of variety by fertilizer had a significant effect on all measured parameters except CPY, IVDMD, DY, and TDNY. Moreover, the interaction of variety by year had a significant effect on ash, NDF, ADL, HC, C, DMI, RFV, and RFQ. Similarly, the interaction of fertilizer by year had a significant effect on all measured parameters except ash, CPY, DY, and TDNY. Furthermore, the interaction effect of variety by fertilizer by year was significant for all measured parameters except ash, DY, and TDNY.

Table 5.25 Combined analysis of variance for nutritive values of three oat varieties sown with eight fertilizer levels in 2020/21 and 2021/22 cropping seasons at Holetta

Parameter	Mean squares									Mean
	R	V	F	Y	V x F	V x Y	F x Y	V x F x Y	Error	
Ash	264.99 ^{NS}	210.70 ^{NS}	503.15 ^{**}	285.10 ^{NS}	325.57 ^{**}	1070.47 ^{***}	204.90 ^{NS}	128.74 ^{NS}	133.56	93.00
NDF	937.00 [*]	1000.76 [*]	1332.61 ^{***}	19927.79 ^{***}	685.00 ^{**}	3274.20 ^{***}	2249.726 ^{***}	653.45 ^{**}	263.53	708.52
ADF	312.89 [*]	1371.81 ^{***}	326.49 ^{***}	2740.44 ^{***}	312.03 ^{***}	73.78 ^{NS}	502.82 ^{***}	253.44 ^{***}	79.49	259.34
ADL	313.52 [*]	417.59 ^{**}	247.51 ^{**}	1395.83 ^{***}	262.30 ^{***}	251.79 [*]	181.61 [*]	160.50 [*]	75.92	48.09
HC	167.067 ^{NS}	1298.37 ^{**}	1140.96 ^{***}	7888.10 ^{***}	559.11 [*]	2375.67 ^{***}	1248.55 ^{***}	655.07 ^{**}	258.29	449.17
C	1252.77 ^{***}	276.31 ^{NS}	513.37 ^{***}	224.95 ^{NS}	347.32 ^{***}	532.28 ^{**}	346.29 ^{**}	281.20 ^{**}	101.64	211.25
CP	17.16 ^{NS}	3119.57 ^{***}	420.40 ^{***}	2394.14 ^{***}	232.90 ^{***}	75.64 ^{NS}	171.25 [*]	352.60 ^{***}	75.77	66.59
CPY	0.007 ^{NS}	0.12 [*]	0.83 ^{***}	0.83 ^{***}	0.07 ^{NS}	0.01 ^{NS}	0.04 ^{NS}	0.09 ^{**}	0.04	0.90
DCP	14.84 ^{NS}	2691.85 ^{***}	362.83 ^{***}	2066.46 ^{***}	201.01 ^{***}	65.26 ^{NS}	147.89 [*]	304.35 ^{***}	65.40	26.66
IVDMD	1268.14 ^{NS}	7664.74 ^{***}	3085.14 ^{**}	3575.34 ^{NS}	1590.46 ^{NS}	2589.53 ^{NS}	2336.17 [*]	3161.92 ^{***}	923.68	628.10
TDN	195.27 [*]	856.25 ^{***}	203.76 ^{***}	1710.93 ^{***}	194.77 ^{***}	46.07 ^{NS}	313.84 ^{***}	158.14 ^{***}	49.60	684.12
DDM	189.81 [*]	832.48 ^{***}	198.14 ^{***}	1663.28 ^{***}	189.39 ^{***}	44.83 ^{NS}	305.07 ^{***}	153.75 ^{***}	48.24	686.97
DY	0.01 ^{NS}	12.14 ^{**}	46.65 ^{***}	12.88 ^{**}	0.46 ^{NS}	2.66 ^{NS}	0.97 ^{NS}	2.07 ^{NS}	1.82	8.40
TDNY	0.04 ^{NS}	19.44 ^{***}	54.62 ^{***}	12.34 [*]	0.73 ^{NS}	1.21 ^{NS}	0.74 ^{NS}	1.84 ^{NS}	1.81	9.15
DMI	0.01 [*]	0.01 [*]	0.01 ^{***}	0.12 ^{***}	0.004 ^{**}	0.02 ^{***}	0.01 ^{***}	0.004 [*]	0.002	1.70
RFV	33.62 ^{**}	50.76 ^{**}	35.62 ^{***}	555.11 ^{***}	20.70 ^{***}	72.01 ^{***}	67.75 ^{***}	16.68 ^{**}	6.87	90.35
RFQ	37.08 ^{**}	56.26 ^{**}	39.19 ^{***}	610.71 ^{***}	22.83 ^{***}	78.75 ^{***}	74.54 ^{***}	18.35 ^{**}	7.55	94.36
DE	0.07 [*]	0.29 ^{***}	0.07 ^{***}	0.59 ^{***}	0.07 ^{***}	0.02 ^{NS}	0.11 ^{***}	0.05 ^{***}	0.02	12.62
ME	0.04 [*]	0.20 ^{***}	0.05 ^{***}	0.40 ^{***}	0.04 ^{***}	0.01 ^{NS}	0.07 ^{***}	0.04 ^{***}	0.01	10.35
NEI	0.02 [*]	0.09 ^{***}	0.02 ^{***}	0.19 ^{***}	0.02 ^{***}	0.004 ^{NS}	0.03 ^{***}	0.02 ^{***}	0.01	6.53
NE _m	0.03 [*]	0.13 ^{***}	0.03 ^{***}	0.25 ^{***}	0.03 ^{***}	0.01 ^{NS}	0.05 ^{***}	0.02 ^{***}	0.01	7.10
NE _g	0.03 [*]	0.13 ^{***}	0.03 ^{***}	0.25 ^{***}	0.03 ^{***}	0.01 ^{NS}	0.05 ^{***}	0.02 ^{***}	0.01	4.08

Ash = ash (g/kg DM); NDF = neutral detergent fiber (g/kg DM); ADF = acid detergent fiber (g/kg DM); ADL = acid detergent lignin (g/kg DM); HC = hemicellulose (g/kg DM); C = cellulose (g/kg DM); CP = crude protein (g/kg DM); CPY = crude protein yield (t/ha); DCP = digestible crude protein (g/kg DM); IVDMD = in-vitro dry matter digestibility (g/kg DM); TDN = total digestible nutrients (g/kg DM); DDM = digestible dry matter (g/kg DM); DY = digestible yield (t/ha); TDNY = total digestible nutrients yield (t/ha); DMI = dry matter intake (% body weight); RFV = relative feed value; RFQ = relative feed quality; DE = digestible energy (MJ/kg DM); ME = metabolizable energy (MJ/kg DM); NEI = net energy lactation (MJ/kg DM); NE_m = net energy maintenance (MJ/kg DM); NE_g = net energy gain (MJ/kg DM); R = replication; V = variety; F = fertilizer level; Y = year; V x F = variety by fertilizer level interaction; V x Y = variety by year interaction; F x Y = fertilizer level by year interaction; V x F x Y = variety by fertilizer level by year interaction; NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively.

5.3.3.2 Nutritive value of forage

5.3.3.2.1 Ash content

The interaction effects of variety by fertilizer and variety by year were significant for ash content (Table 5.26). The result showed that the interaction effect of Sorataf with the

application of 125% (51.3 kg N + 25 kg P/ha) of the recommended fertilizer rate gave the highest ash content (118.0 g/kg DM) while the interaction effect of CI-8251 with 25% (10.3 kg N + 5 kg P/ha) of the recommended fertilizer rate produced the lowest ash content (82.9 g/kg DM). Moreover, the interaction effect of Sorataf with the second year of production gave the highest ash content (102.0 g/kg DM) while the interaction effect of this variety with the first year of production produced the lowest ash content (88.9 g/kg DM).

Table 5.26 Interaction effects of variety by fertilizer rate and variety by year on ash contents (g/kg DM) of oat grown at Holetta

Factor	Variety		
	CI-8251	SRCPX80Ab2291	Sorataf
Percent of the recommended fertilizer rate			
0%	95.9 ^{bc}	88.0 ^c	92.5 ^c
25%	82.9 ^c	93.7 ^c	90.7 ^c
50%	111.2 ^{ab}	97.2 ^{bc}	95.4 ^c
75%	87.0 ^c	93.3 ^c	96.7 ^{bc}
100%	85.9 ^c	93.4 ^c	91.7 ^c
125%	92.4 ^c	93.4 ^c	118.0 ^a
150%	90.4 ^c	90.4 ^c	84.0 ^c
175%	90.0 ^c	83.6 ^c	94.3 ^c
Year			
2020	94.7 ^{ab}	91.2 ^b	88.9 ^b
2021	89.2 ^b	92.0 ^b	102.0 ^a

5.3.3.2.2 Fiber contents

The interaction effects of variety by fertilizer by year were significant for all measured fiber contents (Table 5.27). The result showed that the highest NDF (744.1 g/kg DM) was recorded for the Sorataf variety sown with the application of 100% (41.0 kg N + 20 kg P/ha) fertilizer rate in the 2020 cropping season. Similarly, the lowest NDF (664.9 g/kg DM) was recorded for the CI-8251 variety sown with the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate in the 2021 cropping season. Moreover, the highest ADF (280.2 g/kg DM) was obtained from the SRCPX80Ab2291 variety sown with the application of 100% fertilizer rate in 2020 cropping season while the lowest ADF (233.4 g/kg DM) was recorded for the Sorataf variety sown with 100% fertilizer rate in 2021 cropping season. Similarly, the highest ADL (80.4 g/kg DM) was obtained from the SRCPX80Ab291 variety sown with 75% (30.8 kg N + 15 kg P/ha) fertilizer rate in the 2020 cropping season. However, the lowest ADL (34.0 g/kg DM) was obtained from the SRCPX80Ab2291 variety sown with 175% (71.8 kg N + 35 kg P/ha) fertilizer rate in the 2021 cropping season. The highest HC

(483.1 g/kg DM) and C (229.2 g/kg DM) contents were obtained from the interaction effects of Sorataf variety sown with 100% fertilizer rate in 2020 and the same variety sown without fertilizer application in 2020 cropping season, respectively. However, the lowest HC (408.6 g/kg DM) content was obtained from the SRCPX80Ab2291 variety sown with 125% (51.3 kg N + 25 kg P/ha) fertilizer rate in the 2020 cropping season. Similarly, the interaction effect of the Sorataf variety sown with 125% fertilizer rate in the 2020 cropping season produced the lowest C (175.8 g/kg DM) content.

5.3.3.2.3 Crude protein contents and its yield and digestibility

The interaction effects of variety by fertilizer by year were significant for crude protein (CP), crude protein yield (CPY), and digestible crude protein (DCP) contents ([Table 5.28](#)). The results showed that the Sorataf variety sown with 175% (71.8 kg N + 35 kg P/ha) fertilizer rate in the 2020 cropping season produced the highest (111.3 g/kg DM) CP content while the CI-8251 variety sown with 75% (30.8 kg N + 15 kg P/ha) fertilizer rate in 2020 cropping season gave the lowest (46.2 g/kg DM) CP content. The highest CPY (1.66 t/ha) and DCP (68.2 g/kg DM) were recorded from the Sorataf variety sown with 175% fertilizer rate in 2020 cropping season. However, the lowest CPY (0.40 t/ha) was obtained from the Sorataf variety sown without fertilizer application in the 2020 cropping season. Similarly, the interaction effect of the CI-8251 variety sown with 75% fertilizer rate in the 2020 cropping season gave the lowest (7.7 g/kg DM) DCP content.

5.3.3.2.4 Feed digestibility

The interaction effects of variety by fertilizer by year were significant for IVDMD, TDN, and DDM contents ([Table 5.29](#)). The result revealed that the Sorataf variety sown with 50% (20.5 kg N + 10 kg P/ha) fertilizer rate in the 2021 cropping season produced the highest IVDMD (697.2 g/kg DM) while the Sorataf variety sown with 25% (10.3 kg N + 5 kg P/ha) fertilizer rate in 2021 cropping season gave the lowest IVDMD (545.8 g/kg DM). Similarly, the interaction effect of the Sorataf variety sown with the application of 100% (41.0 kg N + 20 kg P/ha) fertilizer rate in 2021 cropping season gave the highest TDN (704.6 g/kg DM) and DDM (707.2 g/kg DM). However, the lowest TDN (667.6 g/kg DM) and DDM (670.7 g/kg DM) were recorded for the interaction effect of SRCPX80Ab2291 variety sown with 100% fertilizer rate in the 2020 cropping season.

Table 5.27 Interaction effect of variety by fertilizer by year on neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), hemicellulose (HC), and cellulose (C) contents (g/kg DM) of oat grown at Holetta

Parameter	Percent of fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
NDF	0%	709.2 ^{b-k}	741.0 ^{ab}	722.9 ^{a-g}	715.9 ^{a-i}	721.7 ^{a-h}	724.6 ^{a-f}
	25%	693.7 ^{f-n}	712.6 ^{a-j}	701.7 ^{d-m}	679.7 ^{k-o}	717.5 ^{a-i}	719.5 ^{a-i}
	50%	741.7 ^{ab}	735.1 ^{a-c}	711.0 ^{b-k}	710.1 ^{b-k}	712.0 ^{a-j}	699.5 ^{e-m}
	75%	720.0 ^{a-h}	716.6 ^{a-i}	728.3 ^{a-e}	675.8 ^{l-o}	717.1 ^{a-i}	694.6 ^{f-n}
	100%	721.8 ^{a-h}	717.3 ^{a-i}	744.1 ^a	652.0 ^o	673.1 ^{l-o}	670.8 ^{m-o}
	125%	741.2 ^{ab}	671.3 ^{m-o}	711.6 ^{a-k}	686.9 ⁱ⁻ⁿ	712.4 ^{a-j}	689.4 ^{h-n}
	150%	733.3 ^{a-d}	715.3 ^{a-i}	739.9 ^{ab}	664.9 ^{no}	683.0 ⁱ⁻ⁿ	691.5 ^{g-n}
	175%	731.3 ^{a-e}	721.3 ^{a-h}	704.6 ^{c-l}	675.8 ^{l-o}	723.3 ^{a-g}	711.1 ^{b-k}
ADF	0%	257.6 ^{e-k}	268.9 ^{a-g}	277.5 ^{ab}	255.3 ^{f-l}	268.4 ^{a-g}	254.8 ^{f-l}
	25%	235.4 ^{mn}	276.9 ^{a-c}	259.0 ^{c-k}	247.2 ^{j-n}	258.8 ^{e-k}	245.0 ^{k-n}
	50%	264.3 ^{a-j}	263.8 ^{a-j}	254.5 ^{f-l}	263.4 ^{a-j}	259.8 ^{b-k}	252.3 ^{g-m}
	75%	263.4 ^{a-j}	266.8 ^{a-h}	261.2 ^{b-k}	237.9 ^{l-n}	259.6 ^{b-k}	249.4 ^{h-n}
	100%	263.4 ^{a-j}	280.2 ^a	261.0 ^{b-k}	234.3 ⁿ	254.1 ^{f-l}	233.4 ⁿ
	125%	276.6 ^{a-d}	262.6 ^{a-k}	239.4 ^{l-n}	271.3 ^{a-f}	273.9 ^{a-e}	260.1 ^{b-k}
	150%	274.3 ^{a-e}	267.0 ^{a-h}	270.4 ^{a-g}	255.1 ^{f-l}	267.9 ^{a-g}	248.6 ⁱ⁻ⁿ
	175%	271.3 ^{a-f}	263.9 ^{a-j}	249.4 ^{h-n}	249.6 ^{h-n}	253.1 ^{g-l}	266.1 ^{a-i}
ADL	0%	46.6 ^{b-h}	46.4 ^{b-h}	48.3 ^{b-h}	46.4 ^{b-h}	54.9 ^{b-e}	44.2 ^{c-h}
	25%	43.1 ^{d-h}	80.2 ^a	46.1 ^{b-h}	41.2 ^{d-h}	50.2 ^{b-h}	40.1 ^{d-h}
	50%	42.5 ^{d-h}	49.5 ^{b-h}	45.3 ^{c-h}	48.3 ^{b-h}	48.9 ^{b-h}	35.2 ^{gh}
	75%	49.5 ^{b-h}	80.4 ^a	47.4 ^{b-h}	38.9 ^{e-h}	47.1 ^{b-h}	44.2 ^{c-h}
	100%	51.7 ^{b-h}	54.4 ^{b-f}	48.0 ^{b-h}	44.2 ^{c-h}	39.6 ^{d-h}	35.8 ^{gh}
	125%	57.0 ^{b-d}	47.8 ^{b-h}	63.6 ^b	61.8 ^{bc}	46.9 ^{b-h}	52.4 ^{b-g}
	150%	51.5 ^{b-h}	49.5 ^{b-h}	46.3 ^{b-h}	36.6 ^{f-h}	44.0 ^{c-h}	46.7 ^{bh}
	175%	46.2 ^{b-h}	49.2 ^{b-h}	38.4 ^{e-h}	46.6 ^{b-h}	34.0 ^h	51.3 ^{b-h}
HC	0%	451.6 ^{a-i}	472.1 ^c	445.4 ^{b-m}	460.6 ^{a-h}	453.3 ^{a-i}	469.7 ^{a-e}
	25%	458.3 ^{a-i}	435.7 ^{f-n}	442.6 ^{c-m}	432.5 ^{h-n}	458.7 ^{a-i}	474.5 ^{a-c}
	50%	477.4 ^{ab}	471.3 ^{a-c}	456.4 ^{a-i}	446.7 ^{b-m}	452.2 ^{a-i}	447.2 ^{b-l}
	75%	456.6 ^{a-i}	449.9 ^{b-j}	467.1 ^{a-f}	437.9 ^{d-n}	457.5 ^{a-i}	445.2 ^{b-m}
	100%	458.5 ^{a-i}	437.1 ^{e-n}	483.1 ^a	417.7 ^{k-n}	419.0 ^{j-n}	437.3 ^{e-n}
	125%	464.6 ^{a-g}	408.6 ⁿ	472.3 ^{a-c}	415.6 ^{l-n}	438.5 ^{d-n}	429.3 ^{h-n}
	150%	459.0 ^{a-h}	448.3 ^{b-k}	469.4 ^{a-e}	409.8 ⁿ	415.1 ^{mn}	443.0 ^{c-m}
	175%	460.0 ^{a-h}	457.5 ^{a-i}	455.2 ^{a-i}	426.2 ⁱ⁻ⁿ	470.2 ^{a-d}	444.9 ^{c-m}
C	0%	211.0 ^{a-j}	222.5 ^{a-e}	229.2 ^a	209.0 ^{a-k}	213.5 ^{a-i}	210.6 ^{a-j}
	25%	192.3 ^{j-m}	196.8 ^{i-l}	212.9 ^{a-i}	205.9 ^{c-k}	208.6 ^{a-k}	204.9 ^{d-l}
	50%	221.8 ^{a-f}	214.3 ^{a-i}	209.2 ^{a-k}	215.2 ^{a-i}	210.9 ^{a-j}	217.1 ^{a-i}
	75%	213.9 ^{a-i}	186.4 ^{lm}	213.9 ^{a-i}	199.0 ^{h-l}	212.6 ^{a-i}	205.2 ^{c-l}
	100%	211.7 ^{a-j}	225.9 ^{ab}	213.0 ^{a-i}	190.0 ^{k-l}	214.5 ^{a-i}	197.6 ^{h-l}
	125%	219.6 ^{a-g}	214.8 ^{a-i}	175.8 ^m	209.5 ^{a-k}	227.1 ^{ab}	207.7 ^{b-k}
	150%	222.8 ^{a-e}	217.5 ^{a-h}	224.1 ^{a-d}	218.5 ^{a-g}	223.9 ^{a-d}	201.9 ^{f-l}
	175%	225.1 ^{a-d}	214.7 ^{a-i}	210.9 ^{a-j}	203.0 ^{e-l}	219.1 ^{a-g}	214.8 ^{a-i}

NDF = neutral detergent fiber (g/kg DM); **ADF** = acid detergent fiber (g/kg DM); **ADL** = acid detergent lignin (g/kg DM); **HC** = hemicellulose (g/kg DM); **C** = cellulose (g/kg DM); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$. Note variety 2291= SRCPX80Ab2291.

Table 5.28 Interaction effect of variety by fertilizer by year on crude protein (CP), crude protein yield (CPY), and digestible crude protein (DCP) contents (g/kg DM) of oat at Holetta

Parameter	Percent of fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
CP	0%	47.2 ^{no}	57.9 ^{i-o}	57.8 ^{i-o}	56.8 ^{i-o}	73.3 ^{b-i}	64.2 ^{e-n}
	25%	49.8 ^{m-o}	52.8 ^{k-o}	62.5 ^{g-o}	55.6 ^{j-o}	66.6 ^{c-m}	81.7 ^{b-d}
	50%	55.4 ^{i-o}	66.7 ^{c-m}	68.3 ^{c-l}	71.0 ^{c-j}	60.1 ^{h-o}	89.6 ^b
	75%	46.2 ^o	61.5 ^{h-o}	70.7 ^{c-j}	63.4 ^{f-o}	74.1 ^{b-i}	72.1 ^{c-j}
	100%	81.1 ^{b-e}	71.5 ^{c-j}	64.9 ^{d-m}	58.4 ^{i-o}	68.3 ^{c-l}	82.9 ^{bc}
	125%	57.5 ^{i-o}	57.9 ^{i-o}	67.5 ^{c-l}	57.6 ^{i-o}	79.7 ^{b-g}	82.9 ^{bc}
	150%	60.6 ^{h-o}	61.3 ^{h-o}	57.5 ^{i-o}	63.7 ^{e-n}	69.3 ^{c-k}	82.7 ^{bc}
	175%	51.0 ^{l-o}	61.5 ^{h-o}	111.3 ^a	64.1 ^{e-n}	76.9 ^{b-h}	80.6 ^{b-f}
CPY	0%	0.42 ^p	0.53 ^{m-p}	0.40 ^p	0.57 ^{l-p}	0.67 ^{j-p}	0.44 ^{op}
	25%	0.50 ^{n-p}	0.67 ^{j-p}	0.65 ^{j-p}	0.78 ^{g-p}	0.74 ^{i-p}	0.92 ^{c-m}
	50%	0.78 ^{f-p}	0.70 ^{i-p}	0.82 ^{e-o}	0.93 ^{b-l}	0.84 ^{d-n}	1.16 ^{b-g}
	75%	0.62 ^{k-p}	0.83 ^{e-n}	0.87 ^{c-n}	0.83 ^{e-o}	1.04 ^{b-j}	0.85 ^{c-n}
	100%	1.19 ^{b-e}	0.99 ^{b-k}	0.75 ^{h-p}	0.90 ^{c-m}	0.98 ^{b-k}	1.18 ^{b-f}
	125%	0.94 ^{b-l}	0.89 ^{c-n}	0.91 ^{c-m}	0.99 ^{b-k}	1.24 ^{bc}	1.32 ^b
	150%	1.02 ^{b-k}	1.01 ^{b-k}	0.76 ^{h-p}	1.09 ^{b-i}	1.15 ^{b-h}	1.23 ^{b-d}
	175%	0.81 ^{e-o}	1.02 ^{b-j}	1.66 ^a	1.16 ^{b-g}	1.16 ^{b-g}	1.20 ^{b-e}
DCP	0%	8.7 ^{no}	18.6 ^{i-o}	18.5 ^{i-o}	17.6 ^{i-o}	32.9 ^{b-i}	24.4 ^{e-m}
	25%	11.1 ^{m-o}	13.9 ^{k-o}	22.9 ^{g-o}	16.5 ^{j-o}	26.7 ^{c-m}	40.7 ^{b-d}
	50%	16.2 ^{k-o}	26.7 ^{c-m}	28.3 ^{c-l}	30.8 ^{c-j}	20.7 ^{h-o}	48.0 ^b
	75%	7.7 ^o	21.9 ^{h-o}	30.5 ^{c-j}	23.7 ^{h-o}	33.7 ^{b-i}	31.8 ^{c-j}
	100%	40.1 ^{b-e}	31.2 ^{c-j}	25.1 ^{d-m}	19.1 ^{i-o}	28.2 ^{c-l}	41.8 ^{bc}
	125%	18.2 ^{i-o}	18.6 ^{i-o}	27.5 ^{c-l}	18.3 ^{i-o}	38.8 ^{b-g}	41.9 ^{bc}
	150%	21.1 ^{h-o}	21.7 ^{h-o}	18.2 ^{i-o}	24.0 ^{e-m}	29.2 ^{c-k}	41.7 ^{bc}
	175%	12.2 ^{l-o}	22.0 ^{h-o}	68.2 ^a	24.4 ^{e-m}	36.3 ^{b-h}	39.7 ^{b-f}

CP = crude protein (g/kg DM); CPY = crude protein yield (t/ha); DCP = digestible crude protein (g/kg DM); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$. Note variety 2291= SRCPX80Ab2291.

The DY varied significantly among fertilizer levels (Figure 5.14 top). The result showed that the DY was increased with increasing levels of fertilizer application. Accordingly, application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rate gave the highest DY (10.2 t/ha) while oat sown without fertilizer produced the lowest DY (5.3 t/ha). Moreover, the DY varied significantly among oat varieties (Figure 5.14 bottom right) and year of production (Figure 5.14 bottom left). Among oat varieties, SRCPX80Ab2291 gave the highest DY (8.4 t/ha) while Sorataf gave the lowest DY (7.9 t/ha). A higher DY was also recorded for the second year of production (8.7 t/ha) than the first year (8.1 t/ha).

The TDNY varied significantly among fertilizer levels (Figure 5.15 top). The result showed that application of 75 (30.8 kg N + 15 kg P/ha), 100 (41.0 kg N + 20 kg P/ha), 125 (51.3 kg N + 25 kg P/ha), 150 (61.5 kg N + 30 kg P/ha), and 175% (71.8 kg N + 35 kg P/ha) of the blanket recommended fertilizer rates gave 8.9, 9.6, 10.6, 10.7, and 10.9 t/ha TDNY, respectively. On the other hand, oat sown without fertilizer application produced the lowest

TDNY (8.7 t/ha). The TDNY also varied significantly among oat varieties (Figure 5.15 bottom left) and year of production (Figure 5.15 bottom right). Among oat varieties, CI-8251 gave the highest TDNY (9.7 t/ha) followed by SRCPX80Ab2291 (9.2 t/ha) while Sorataf gave the lowest (8.5 t/ha). Moreover, the TDNY was higher in 2021 (9.4 t/ha) than in 2020 (8.9 t/ha) cropping season.

Table 5.29 Interaction effect of variety by fertilizer by year on in-vitro dry matter digestibility (IVDMD), total digestible nutrients (TDN), and digestible dry matter (DDM) contents (g/kg DM) of oat grown at Holetta

Parameter	Percent of fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
IVDMD	0%	627.0 ^{b-f}	619.2 ^{c-f}	630.9 ^{b-f}	616.4 ^{c-f}	609.3 ^{c-f}	648.3 ^{a-e}
	25%	637.3 ^{a-f}	590.8 ^{e-h}	662.4 ^{a-d}	640.4 ^{a-f}	603.7 ^{d-g}	545.8 ^h
	50%	639.7 ^{a-f}	647.2 ^{a-e}	606.8 ^{d-g}	637.7 ^{a-f}	609.6 ^{c-f}	697.2 ^a
	75%	621.7 ^{c-f}	612.0 ^{c-f}	629.7 ^{b-f}	666.1 ^{a-d}	617.2 ^{c-f}	683.7 ^{ab}
	100%	612.8 ^{c-f}	642.2 ^{a-f}	614.6 ^{c-f}	669.2 ^{a-c}	655.1 ^{a-d}	664.8 ^{a-d}
	125%	590.7 ^{e-h}	632.0 ^{b-f}	613.7 ^{c-f}	628.8 ^{b-f}	581.5 ^{f-h}	650.2 ^{a-e}
	150%	613.5 ^{c-f}	551.0 ^{gh}	649.8 ^{a-e}	590.9 ^{e-g}	605.3 ^{d-g}	658.2 ^{a-d}
	175%	618.8 ^{c-f}	657.3 ^{a-d}	633.8 ^{b-f}	632.2 ^{b-f}	617.5 ^{c-f}	665.2 ^{a-d}
TDN	0%	685.5 ^{d-j}	676.5 ^{h-n}	669.8 ^{mn}	687.3 ^{c-i}	677.0 ^{h-n}	687.7 ^{c-i}
	25%	703.1 ^{ab}	670.2 ^{l-n}	684.4 ^{d-l}	693.7 ^{a-e}	684.6 ^{d-k}	695.4 ^{a-d}
	50%	680.2 ^{e-n}	680.6 ^{e-n}	687.9 ^{d-i}	680.9 ^{e-n}	683.7 ^{d-m}	689.7 ^{b-h}
	75%	680.9 ^{e-n}	678.3 ^{g-n}	682.6 ^{d-m}	701.1 ^{a-c}	683.9 ^{d-m}	692.0 ^{a-g}
	100%	681.0 ^{e-n}	667.6 ⁿ	682.8 ^{d-m}	703.9 ^a	688.3 ^{c-i}	704.6 ^a
	125%	670.5 ^{k-n}	681.5 ^{d-n}	699.9 ^{a-c}	674.7 ⁱ⁻ⁿ	672.6 ^{j-n}	683.6 ^{d-m}
	150%	672.3 ^{j-n}	678.1 ^{g-n}	675.4 ^{h-n}	687.5 ^{c-i}	677.4 ^{h-n}	692.6 ^{a-f}
	175%	674.7 ⁱ⁻ⁿ	680.6 ^{e-n}	692.0 ^{a-g}	691.8 ^{a-g}	689.0 ^{c-h}	678.8 ^{f-n}
DDM	0%	688.3 ^{d-j}	679.5 ^{h-n}	672.8 ^{mn}	690.1 ^{c-i}	680.0 ^{h-n}	690.5 ^{c-i}
	25%	705.6 ^{ab}	673.3 ^{l-n}	687.2 ^{d-l}	696.5 ^{a-e}	687.4 ^{d-k}	698.1 ^{a-d}
	50%	683.1 ^{e-n}	683.5 ^{e-n}	690.7 ^{c-i}	683.8 ^{e-n}	686.6 ^{d-m}	692.5 ^{b-h}
	75%	683.8 ^{e-n}	681.2 ^{g-n}	685.5 ^{d-m}	703.7 ^{a-c}	686.8 ^{d-m}	694.7 ^{a-g}
	100%	683.8 ^{e-n}	670.7 ⁿ	685.7 ^{d-m}	706.5 ^a	691.1 ^{c-i}	707.2 ^a
	125%	673.5 ^{k-n}	684.4 ^{d-n}	702.5 ^{a-c}	677.7 ⁱ⁻ⁿ	675.6 ^{j-n}	686.4 ^{d-m}
	150%	675.3 ^{j-n}	681.0 ^{g-n}	678.3 ^{h-n}	690.3 ^{c-i}	680.3 ^{h-n}	695.4 ^{a-f}
	175%	677.6 ⁱ⁻ⁿ	683.5 ^{e-n}	694.8 ^{a-g}	694.6 ^{a-g}	691.8 ^{c-h}	681.7 ^{f-n}

IVDMD = in-vitro dry matter yield (t/ha); TDN = digestible nutrients (g/kg DM); DDM = digestible dry matter (g/kg DM); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$. Note variety 2291= SRCPX80Ab2291.

5.3.3.2.5 Feed intake and its relative value and quality

The interaction effects of variety by fertilizer by year were significant for DMI, RFV, and RFQ (Table 5.30). The result showed that the CI-8251 variety sown with the application of 100% (41.0 kg N + 20 kg P/ha) fertilizer rate in the 2021 cropping season had the highest DMI (1.85 % body weight) while the interaction effect of the Sorataf variety sown with 100% fertilizer rate in 2020 cropping season had the lowest DMI (1.61 % body weight). Similarly, the interaction effect of the CI-8251 variety sown with 100% fertilizer rate in the

2021 cropping season gave the highest RFV (101.1) and RFQ (105.7). On the other hand, the interaction effect of the CI-8251 variety sown with 125% (51.3 kg N + 25 kg P/ha) fertilizer rate in the 2020 cropping season gave the lowest RFV (84.5) and RFQ (88.3).

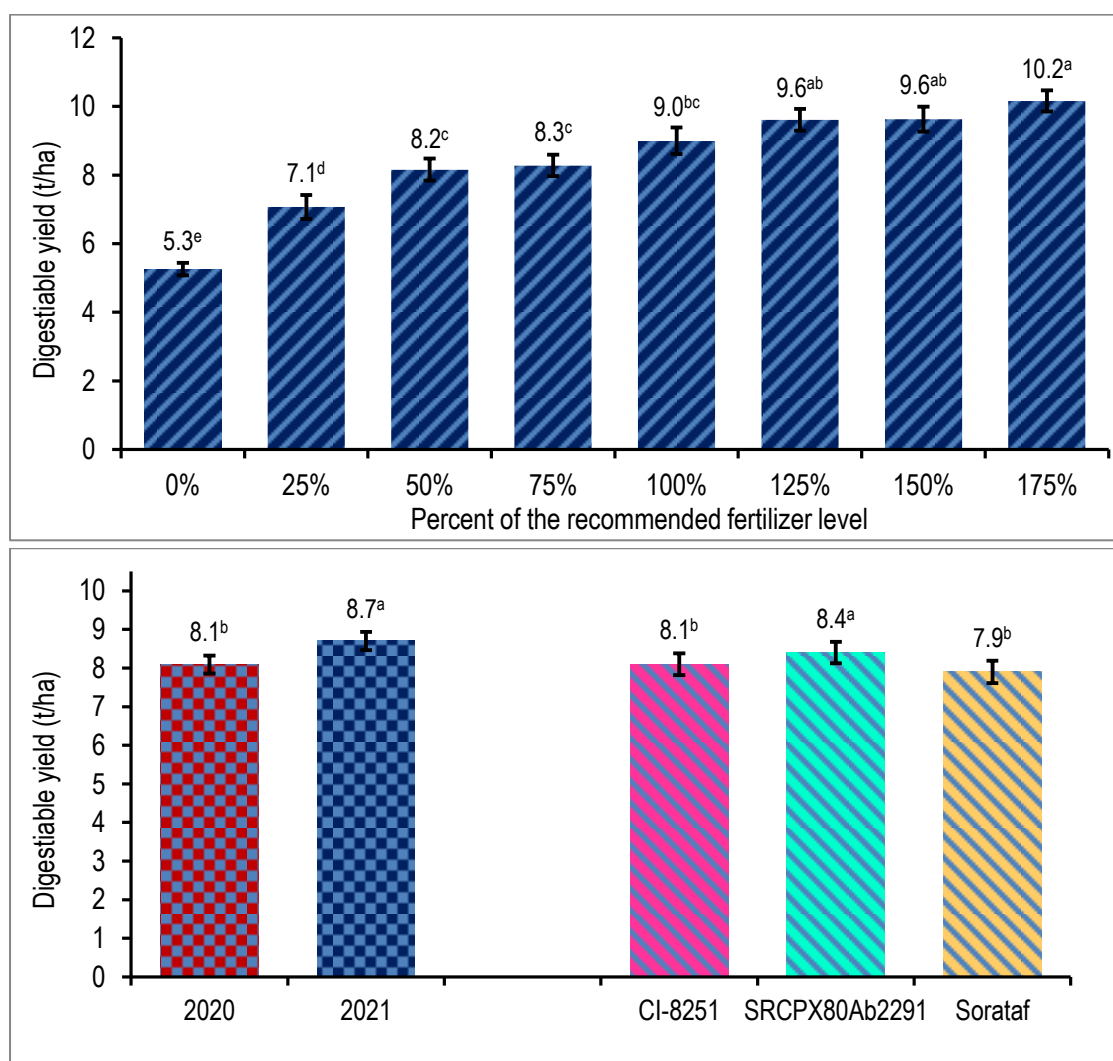


Figure 5.14 Digestible yield (t/ha) as influenced by fertilizer levels (top), year of production (bottom left), and variety (bottom right) of oat grown at Holetta

5.3.3.2.6 Feed energy

The interaction effects of variety by fertilizer by year were significant for DE, ME, NEI, NEm, and NEg (Table 5.31). The result showed that the CI-8251 variety sown with 100% (41.0 kg N + 20 kg P/ha) fertilizer rate in 2021, the Sorataf variety sown with 100% fertilizer rate in 2021, and the CI-8251 variety sown with 25% (10.3 kg N + 5 kg P/ha) fertilizer rate in 2020 cropping season gave the highest DE (13.0 MJ/kg DM). On the other hand, the SRCPX80Ab2291 variety sown with 100% fertilizer rate in the 2020 cropping season produced the lowest DE (12.3 MJ/kg DM). The ME was the highest (10.7 MJ/kg DM) for

the interaction effect of the CI-8251 and Sorataf varieties sown with 100% fertilizer rate in 2021 while the SRCPX80Ab2291 variety sown with 100% fertilizer rate in the 2020 cropping season gave the lowest ME (10.1 MJ/kg DM). The NEI was the highest (6.7 MJ/kg DM) for the CI-8251 and Sorataf varieties sown with 100% fertilizer rate in 2021 and the CI-8251 variety sown with 25% fertilizer rate in 2020 cropping season. However, the lowest NEI (6.4 MJ/kg DM) was recorded for the interaction effect of the Sorataf variety sown without fertilizer in the 2020 cropping season. The highest NEm (7.4 MJ/kg DM) was recorded for the Sorataf variety sown with 100% fertilizer rate in 2021 while the interaction effect of SRCPX80Ab2291 sown with 100% fertilizer rate in the 2020 cropping season gave the lowest NEm (6.9 MJ/kg DM). Similarly, the highest NEg (4.3 MJ/kg DM) was observed for the interaction effect of the CI-8251 and Sorataf varieties sown with 100% fertilizer rate in 2021 while the lowest NEg (3.9 MJ/kg DM) was recorded for the interaction effect of the SRCPX80Ab2291 variety sown with 100% fertilizer rate in 2020 cropping season.

Table 5.30 Interaction effect of variety by fertilizer by year on dry matter intake (DMI) (% body weight), relative feed value (RFV), and relative feed quality (RFQ) of oat at Holetta

Parameter	Percent of fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
DMI	0%	1.69 ^{f-o}	1.62 ^{no}	1.66 ^{i-o}	1.68 ^{g-o}	1.66 ^{i-o}	1.66 ^{j-o}
	25%	1.73 ^{b-j}	1.68 ^{g-o}	1.71 ^{d-m}	1.77 ^{b-f}	1.67 ^{h-o}	1.67 ^{h-o}
	50%	1.62 ^{no}	1.63 ^{m-o}	1.69 ^{f-o}	1.69 ^{g-n}	1.69 ^{f-o}	1.72 ^{c-l}
	75%	1.67 ^{h-o}	1.67 ^{h-o}	1.65 ^{k-o}	1.78 ^{a-e}	1.67 ^{h-o}	1.73 ^{b-k}
	100%	1.66 ^{i-o}	1.67 ^{h-o}	1.61 ^o	1.85 ^a	1.78 ^{a-d}	1.79 ^{a-c}
	125%	1.62 ^{no}	1.79 ^{a-c}	1.69 ^{f-o}	1.75 ^{b-h}	1.68 ^{g-o}	1.74 ^{b-i}
	150%	1.64 ^{m-o}	1.68 ^{g-o}	1.62 ^{no}	1.80 ^{ab}	1.76 ^{b-g}	1.74 ^{b-i}
	175%	1.64 ^{l-o}	1.66 ^{i-o}	1.70 ^{e-m}	1.78 ^{a-e}	1.66 ^{i-o}	1.69 ^{f-o}
RFV	0%	90.3 ^{e-m}	85.3 ^{mn}	86.6 ^{j-n}	89.7 ^{f-n}	87.6 ^{h-n}	88.7 ^{f-n}
	25%	95.0 ^{b-d}	87.9 ^{g-n}	91.1 ^{d-l}	95.3 ^{b-e}	89.1 ^{f-n}	90.3 ^{e-m}
	50%	85.7 ^{mn}	86.5 ^{k-n}	90.4 ^{e-m}	89.6 ^{f-n}	89.8 ^{f-n}	92.1 ^{c-i}
	75%	88.4 ^{g-n}	88.4 ^{f-n}	87.7 ^{h-n}	96.9 ^{a-c}	89.1 ^{f-n}	93.0 ^{c-g}
	100%	88.2 ^{g-n}	87.1 ⁱ⁻ⁿ	85.7 ^{mn}	101.1 ^a	95.6 ^{b-d}	98.1 ^{ab}
	125%	84.5 ⁿ	95.0 ^{b-e}	91.8 ^{c-j}	91.8 ^{c-k}	88.2 ^{h-n}	92.6 ^{c-h}
	150%	85.7 ^{mn}	88.6 ^{f-n}	85.3 ^{mn}	96.6 ^{a-c}	92.7 ^{c-h}	93.7 ^{b-f}
	175%	86.2 ^{l-n}	88.1 ^{g-n}	91.7 ^{c-k}	95.6 ^{b-d}	89.0 ^{f-n}	89.2 ^{f-n}
RFQ	0%	94.3 ^{e-l}	89.1 ^{lm}	90.4 ^{j-m}	93.7 ^{f-m}	91.5 ^{h-m}	92.6 ^{f-m}
	25%	99.3 ^{b-e}	91.8 ^{g-m}	95.2 ^{d-k}	99.6 ^{b-e}	93.1 ^{f-m}	94.3 ^{e-l}
	50%	89.5 ^{lm}	90.3 ^{j-m}	94.4 ^{e-l}	93.6 ^{f-m}	93.8 ^{f-m}	96.2 ^{c-i}
	75%	92.3 ^{g-m}	92.3 ^{f-m}	91.6 ^{h-m}	101.2 ^{a-c}	93.1 ^{f-m}	97.2 ^{c-g}
	100%	92.1 ^{g-m}	90.9 ^{j-m}	89.5 ^{lm}	105.7 ^a	99.8 ^{b-d}	102.5 ^{ab}
	125%	88.3 ^m	99.2 ^{b-e}	96.0 ^{c-i}	95.9 ^{c-j}	92.1 ^{g-m}	96.8 ^{c-h}
	150%	89.5 ^{lm}	92.5 ^{f-m}	89.1 ^{lm}	100.9 ^{a-c}	96.8 ^{e-h}	97.9 ^{b-f}
	175%	90.0 ^{k-m}	92.1 ^{g-m}	95.8 ^{c-j}	99.9 ^{b-d}	93.0 ^{f-m}	93.2 ^{f-m}

DMI = dry matter intake (% body weight); **RFV** = relative feed value; **RFQ** = relative feed quality; Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$. Note variety 2291= SRCPX80Ab2291.

Table 5.31 Interaction effect of variety by fertilizer by year on digestible energy (DE), metabolizable energy (ME), net energy for lactation (NEl), net energy for maintenance (NEm), and net energy for gain (NEg) (MJ/kg DM) of oat grown at Holetta

Parameter	Percent of fertilizer level	2020			2021		
		8251	2291	Sorataf	8251	2291	Sorataf
DE	0%	12.6 ^{c-g}	12.5 ^{g-m}	12.4 ^{lm}	12.7 ^{b-h}	12.5 ^{g-m}	12.7 ^{b-h}
	25%	13.0 ^a	12.4 ^{k-m}	12.6 ^{c-k}	12.8 ^{a-d}	12.6 ^{c-j}	12.8 ^{a-c}
	50%	12.6 ^{d-m}	12.6 ^{d-m}	12.7 ^{b-h}	12.6 ^{d-m}	12.6 ^{c-l}	12.7 ^{b-g}
	75%	12.6 ^{d-m}	12.5 ^{f-m}	12.6 ^{c-l}	12.9 ^{ab}	12.6 ^{c-k}	12.8 ^{a-f}
	100%	12.6 ^{d-m}	12.3 ^m	12.6 ^{c-l}	13.0 ^a	12.7 ^{b-h}	13.0 ^a
	125%	12.4 ^{j-m}	12.6 ^{c-m}	12.9 ^{ab}	12.5 ^{h-m}	12.4 ^{i-m}	12.6 ^{c-l}
	150%	12.4 ^{i-m}	12.5 ^{f-m}	12.5 ^{g-m}	12.7 ^{b-h}	12.5 ^{g-m}	12.8 ^{a-e}
	175%	12.5 ^{h-m}	12.6 ^{d-m}	12.8 ^{a-f}	12.8 ^{a-f}	12.7 ^{b-h}	12.5 ^{f-m}
ME	0%	10.4 ^{d-k}	10.2 ^{i-o}	10.1 ^{no}	10.4 ^{c-j}	10.2 ^{i-o}	10.4 ^{c-j}
	25%	10.6 ^{ab}	10.1 ^{m-o}	10.4 ^{d-m}	10.5 ^{a-e}	10.4 ^{d-l}	10.5 ^{a-d}
	50%	10.3 ^{e-o}	10.3 ^{e-o}	10.4 ^{c-j}	10.3 ^{e-o}	10.3 ^{d-n}	10.4 ^{b-i}
	75%	10.3 ^{e-o}	10.3 ^{g-o}	10.3 ^{d-m}	10.6 ^{a-c}	10.4 ^{d-m}	10.5 ^{a-g}
	100%	10.3 ^{e-o}	10.1 ^o	10.3 ^{d-n}	10.7 ^a	10.4 ^{c-j}	10.7 ^a
	125%	10.1 ^{l-o}	10.3 ^{d-o}	10.6 ^{a-c}	10.2 ^{j-o}	10.2 ^{k-o}	10.3 ^{d-n}
	150%	10.2 ^{k-o}	10.3 ^{g-o}	10.2 ^{j-o}	10.4 ^{c-j}	10.3 ^{h-o}	10.5 ^{a-f}
	175%	10.2 ^{j-o}	10.3 ^{e-o}	10.5 ^{a-g}	10.5 ^{a-h}	10.4 ^{c-j}	10.3 ^{f-o}
NEl	0%	6.6 ^{d-j}	6.5 ^{h-m}	6.4 ^{mn}	6.6 ^{c-i}	6.5 ^{h-m}	6.6 ^{b-i}
	25%	6.7 ^a	6.4 ^{l-n}	6.5 ^{d-k}	6.6 ^{a-e}	6.5 ^{d-j}	6.7 ^{a-d}
	50%	6.5 ^{e-n}	6.5 ^{e-n}	6.6 ^{b-i}	6.5 ^{e-n}	6.5 ^{d-l}	6.6 ^{b-h}
	75%	6.5 ^{e-n}	6.5 ^{f-n}	6.5 ^{d-m}	6.7 ^{ab}	6.5 ^{d-l}	6.6 ^{a-f}
	100%	6.5 ^{e-n}	6.4 ⁿ	6.5 ^{d-m}	6.7 ^a	6.6 ^{b-i}	6.7 ^a
	125%	6.4 ^{k-n}	6.5 ^{d-m}	6.7 ^{a-c}	6.4 ⁱ⁻ⁿ	6.4 ^{j-n}	6.5 ^{d-l}
	150%	6.4 ^{j-n}	6.5 ^{f-n}	6.4 ^{h-m}	6.6 ^{b-i}	6.5 ^{h-n}	6.6 ^{a-f}
	175%	6.4 ⁱ⁻ⁿ	6.5 ^{e-n}	6.6 ^{a-g}	6.6 ^{a-g}	6.6 ^{b-h}	6.5 ^{g-n}
NEm	0%	7.1 ^{d-k}	7.0 ⁱ⁻ⁿ	6.9 ^{mn}	7.1 ^{c-j}	7.0 ⁱ⁻ⁿ	7.1 ^{c-j}
	25%	7.3 ^{ab}	6.9 ^{l-n}	7.1 ^{d-l}	7.2 ^{a-e}	7.1 ^{d-k}	7.2 ^{a-d}
	50%	7.1 ^{e-n}	7.1 ^{e-n}	7.2 ^{c-j}	7.1 ^{f-n}	7.1 ^{d-m}	7.2 ^{b-i}
	75%	7.1 ^{e-n}	7.0 ^{g-n}	7.1 ^{d-m}	7.3 ^{a-c}	7.1 ^{d-m}	7.2 ^{a-h}
	100%	7.1 ^{e-n}	6.9 ⁿ	7.1 ^{d-m}	7.3 ^a	7.2 ^{c-j}	7.4 ^a
	125%	6.9 ^{l-n}	7.1 ^{d-n}	7.3 ^{a-c}	7.0 ^{j-n}	7.0 ^{k-n}	7.1 ^{d-m}
	150%	7.0 ^{k-n}	7.0 ^{f-n}	7.0 ^{j-n}	7.1 ^{c-j}	7.0 ^{j-j}	7.2 ^{a-f}
	175%	7.0 ^{j-n}	7.1 ^{e-n}	7.2 ^{a-g}	7.2 ^{a-h}	7.2 ^{c-j}	7.0 ^{f-n}
NEg	0%	4.1 ^{d-j}	4.0 ^{h-m}	3.9 ^{lm}	4.1 ^{c-i}	4.0 ^{h-m}	4.1 ^{c-i}
	25%	4.3 ^{ab}	3.9 ^{lm}	4.1 ^{d-k}	4.2 ^{a-e}	4.1 ^{d-k}	4.2 ^{a-d}
	50%	4.0 ^{e-m}	4.0 ^{e-m}	4.1 ^{c-i}	4.0 ^{e-m}	4.1 ^{d-l}	4.2 ^{b-h}
	75%	4.0 ^{e-m}	4.0 ^{f-m}	4.1 ^{d-l}	4.3 ^{a-c}	4.1 ^{d-l}	4.2 ^{a-g}
	100%	4.0 ^{e-m}	3.9 ^m	4.1 ^{d-l}	4.3 ^a	4.1 ^{c-i}	4.3 ^a
	125%	3.9 ^{k-m}	4.1 ^{d-m}	4.3 ^{a-c}	4.0 ^{i-m}	3.9 ^{k-m}	4.1 ^{d-l}
	150%	3.9 ^{j-m}	4.0 ^{g-m}	4.0 ^{h-m}	4.1 ^{c-i}	4.0 ^{h-m}	4.2 ^{a-f}
	175%	4.0 ^{i-m}	4.0 ^{e-m}	4.2 ^{a-g}	4.2 ^{a-g}	4.1 ^{c-i}	4.0 ^{f-m}

DE = digestible energy (MJ/kg DM); ME = metabolizable energy (MJ/kg DM); NEl = net energy for lactation (MJ/kg DM); NEm = net energy for maintenance (MJ/kg DM); NEg = net energy for gain (MJ/kg DM); Means followed by a common superscript letter within a column and row for each trait are not significantly different from each other at $P < 0.05$. Note variety 2291= SRCPX80Ab2291.

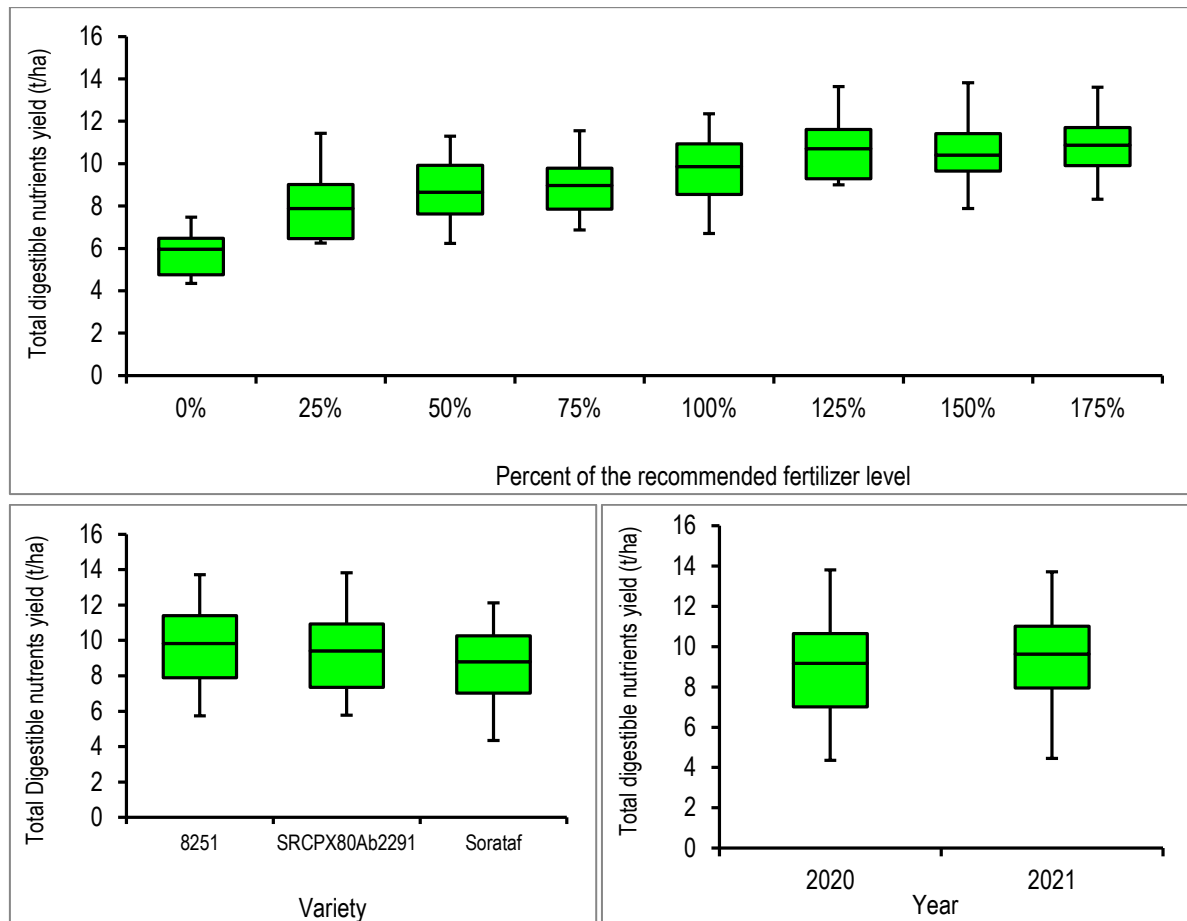


Figure 5.15 Box and Whisker plot of total digestible nutrients yield (t/ha) as influenced by fertilizer levels (top), variety (bottom left), and year of production (bottom right) of oat grown at Holetta

5.3.3.3 Relationships among measured parameters

The Pearson correlation analysis for measured parameters is displayed in [Table 5.32](#). The result showed that the rate of fertilizer had significant positive associations with yield parameters (FDMY and TDNY: $r = 0.73^{***}$), DY ($r = 0.71^{***}$), CPY ($r = 0.63^{***}$), crude protein and digestible crude protein (CP and DCP: $r = 0.25^{**}$). Similarly, the FDMY had significant positive associations with TDNY ($r = 1.00^{***}$), DY ($r = 0.97^{***}$), CPY ($r = 0.77^{***}$), DMI ($r = 0.20^{*}$), crude protein and digestible crude protein (CP and DCP: $r = 0.18^{*}$). The ash content had significant positive associations with ADL ($r = 0.18^{*}$) and IVDMD ($r = 0.17^{*}$). Moreover, the CP had significant positive associations with DCP ($r = 1.00^{***}$), CPY ($r = 0.76^{***}$), DY ($r = 0.22^{**}$), TDNY ($r = 0.19^{*}$), and IVDMD ($r = 0.18^{*}$). The NDF also had significant positive associations with HC ($r = 0.85^{***}$), ADF ($r = 0.51^{***}$), and C ($r = 0.39^{***}$). The ADF had significant positive associations with C ($r = 0.65^{***}$) and ADL ($r = 0.39^{***}$). The IVDMD had significant positive associations with relative feed parameters (RFV and RFQ: $r = 0.30^{***}$), DMI ($r = 0.29^{***}$), different

digestible parameters (DY, TDN, and DDM: $r = 0.22^{**}$), different energy parameters (DE, ME, NEL, NEm, and NEg: $r = 0.22^{**}$), and DCP ($r = 0.18^*$).

The CPY had significant positive associations with DY ($r = 0.78^{***}$), TDNY ($r = 0.77^{***}$), DCP ($r = 0.76^{***}$), and DMI ($r = 0.18^*$). The DY had significant positive associations with TDNY ($r = 0.97^{***}$), DMI ($r = 0.27^{***}$), DCP ($r = 0.22^{**}$), and relative feed parameters (RFV and RFQ: $r = 0.21^*$). The TDN had significant positive associations with DDM ($r = 1.00^{***}$) and both TDN and DDM had the same coefficients with relative feed parameters (RFV and RFQ: $r = 0.73^{***}$), DMI ($r = 0.52^{***}$), and perfect positive coefficients with DE, ME, NEL, NEm, and NEg. The DMI had significant positive associations with relative feed parameters (RFV and RFQ: $r = 0.96^{***}$), TDNY ($r = 0.24^{**}$), NEg ($r = 0.51^{***}$), and it had the same coefficients ($r = 0.52^{***}$) with DE, ME, NEL, and NEm. The RFV had significant positive associations with RFQ ($r = 1.00^{***}$) and both RFV and RFQ had the same coefficients with TDNY ($r = 0.18^*$) and perfect positive coefficients ($r = 1.00^{***}$) with DE, ME, NEL, NEm, and NEg. Moreover, the associations between all energy parameters were perfectly positive.

The rate of fertilizer had significant inverse associations with HC ($r = -0.20^*$) and also the FDMY had significant inverse associations with HC ($r = -0.29^{***}$) and NDF ($r = -0.20^*$). The NDF had had significant inverse associations with relative feed parameters (RFV and RFQ: $r = -0.96^{***}$), digestible parameters (TDN and DDM: $r = -0.51^{***}$), different energy parameters (DE, ME, NEL, NEm: $r = -0.51^{***}$), and NEg ($r = -0.50^{***}$), IVDMD ($r = -0.28^{***}$), DY ($r = -0.27^{***}$), TDNY ($r = -0.24^{**}$), and CPY ($r = -0.18^*$). The ADF also had significant inverse associations with different energy parameters (DE, ME, NEL, NEm, and NEg: $r = -1.00^{***}$), digestible parameters (TDN and DDM: $r = -1.00^{***}$), relative feed parameters (RFV and RFQ: $r = -0.73^{***}$), DMI ($r = -0.52^{***}$), and IVDMD ($r = -0.22^{**}$). Moreover, the ADL had significant inverse associations with C ($r = -0.44^{***}$), digestible parameters (TDN and DDM: $r = -0.39^{***}$), different energy parameters (DE, ME, NEL, NEm, and NEg: $r = -0.39^{***}$), and relative feed parameters (RFV and RFQ: $r = -0.23^{**}$). The HC had significant inverse associations with DMI ($r = -0.84^{***}$), relative feed parameters (RFV and RFQ: $r = -0.66^{***}$), DY ($r = -0.33^{***}$), TDNY ($r = -0.29^{***}$), CPY ($r = -0.21^*$), and IVDMD ($r = -0.19^*$). The C content also had significant inverse associations with NEg ($r = -0.66^{***}$), digestible parameters (TDN and DDM: $r = -0.65^{***}$), different energy parameters (DE, ME, NEL, NEm: $r = -0.65^{***}$), RFQ ($r = -0.53^{***}$), RFV ($r = -0.52^{***}$), and DMI ($r = -0.39^{***}$).

Table 5.32 Pearson correlation coefficients for the studied parameters of oat varieties sown with different fertilizer rates at Holetta

Parameter	RFL	FDMY	Ash	CP	NDF	ADF	ADL	HC	C	IVDMD	CPY	DY	DCP	TDN	DDM	DMI	RFV	RFQ	TDNY	DE	ME	NEI	NEm
FDMY	0.73***																						
Ash	-0.05 ^{NS}	0.02 ^{NS}																					
CP	0.25**	0.18*	0.12 ^{NS}																				
NDF	-0.14 ^{NS}	-0.20*	0.04 ^{NS}	-0.06 ^{NS}																			
ADF	0.05 ^{NS}	0.09 ^{NS}	0.04 ^{NS}	-0.10 ^{NS}	0.51***																		
ADL	-0.05 ^{NS}	-0.01 ^{NS}	0.18*	-0.16 ^{NS}	0.13 ^{NS}	0.39***																	
HC	-0.20*	-0.29***	0.02 ^{NS}	-0.01 ^{NS}	0.85***	-0.02 ^{NS}	-0.09 ^{NS}																
C	0.10 ^{NS}	0.10 ^{NS}	-0.11 ^{NS}	0.03 ^{NS}	0.39***	0.65***	-0.44***	0.05 ^{NS}															
IVDMD	0.01 ^{NS}	-0.03 ^{NS}	0.17*	0.18*	-0.28***	-0.22**	-0.12 ^{NS}	-0.19*	-0.11 ^{NS}														
CPY	0.63***	0.77***	0.09 ^{NS}	0.76***	-0.18*	-0.01 ^{NS}	-0.11 ^{NS}	-0.21*	0.08 ^{NS}	0.10 ^{NS}													
DY	0.71***	0.97***	0.06 ^{NS}	0.22**	-0.27***	0.03 ^{NS}	-0.04 ^{NS}	-0.33***	0.06 ^{NS}	0.22**	0.78***												
DCP	0.25**	0.18*	0.12 ^{NS}	1.00***	-0.06 ^{NS}	-0.10 ^{NS}	-0.16 ^{NS}	-0.01 ^{NS}	0.03 ^{NS}	0.18*	0.76***	0.22**											
TDN	-0.05 ^{NS}	-0.09 ^{NS}	-0.04 ^{NS}	0.10 ^{NS}	-0.51***	-1.00***	-0.39***	0.02 ^{NS}	-0.65***	0.22**	0.01 ^{NS}	-0.03 ^{NS}	0.10 ^{NS}										
DDM	-0.05 ^{NS}	-0.09 ^{NS}	-0.04 ^{NS}	0.10 ^{NS}	-0.51***	-1.00***	-0.39***	0.02 ^{NS}	-0.65***	0.22**	0.01 ^{NS}	-0.03 ^{NS}	0.10 ^{NS}	1.00***									
DMI	0.14 ^{NS}	0.20*	-0.04 ^{NS}	0.05 ^{NS}	-1.00***	-0.52***	-0.13 ^{NS}	-0.84***	-0.39***	0.29***	0.18*	0.27***	0.05 ^{NS}	0.52***	0.52***								
RFV	0.10 ^{NS}	0.13 ^{NS}	-0.05 ^{NS}	0.07 ^{NS}	-0.96***	-0.73***	-0.23**	-0.66***	-0.52***	0.30***	0.14 ^{NS}	0.21*	0.07 ^{NS}	0.73***	0.73***	0.96***							
RFQ	0.10 ^{NS}	0.13 ^{NS}	-0.05 ^{NS}	0.07 ^{NS}	-0.96***	-0.73***	-0.23**	-0.66***	-0.53***	0.30***	0.14 ^{NS}	0.21*	0.07 ^{NS}	0.73***	0.73***	0.96***	1.00***						
TDNY	0.73***	1.00***	0.02 ^{NS}	0.19*	-0.24**	0.02 ^{NS}	-0.04 ^{NS}	-0.29***	0.06 ^{NS}	-0.02 ^{NS}	0.77***	0.97***	0.19*	-0.02 ^{NS}	-0.02 ^{NS}	0.24**	0.18*	0.18*					
DE	-0.06 ^{NS}	-0.09 ^{NS}	-0.04 ^{NS}	0.10 ^{NS}	-0.51***	-1.00***	-0.39***	0.02 ^{NS}	-0.65***	0.22**	0.01 ^{NS}	-0.03 ^{NS}	0.10 ^{NS}	1.00***	1.00***	0.52***	0.73***	0.73***	-0.02 ^{NS}				
ME	-0.05 ^{NS}	-0.09 ^{NS}	-0.04 ^{NS}	0.11 ^{NS}	-0.51***	-1.00***	-0.39***	0.02 ^{NS}	-0.65***	0.22**	0.01 ^{NS}	-0.02 ^{NS}	0.11 ^{NS}	1.00***	1.00***	0.52***	0.73***	0.73***	-0.02 ^{NS}	1.00***			
NEI	-0.05 ^{NS}	-0.09 ^{NS}	-0.04 ^{NS}	0.10 ^{NS}	-0.51***	-1.00***	-0.39***	0.02 ^{NS}	-0.65***	0.22**	0.01 ^{NS}	-0.03 ^{NS}	0.10 ^{NS}	1.00***	1.00***	0.52***	0.73***	0.73***	-0.02 ^{NS}	1.00***	1.00***		
NEm	-0.05 ^{NS}	-0.09 ^{NS}	-0.04 ^{NS}	0.10 ^{NS}	-0.51***	-1.00***	-0.39***	0.02 ^{NS}	-0.65***	0.22**	0.01 ^{NS}	-0.03 ^{NS}	0.10 ^{NS}	1.00***	1.00***	0.52***	0.73***	0.73***	-0.02 ^{NS}	1.00***	1.00***	1.00***	
NEg	-0.05 ^{NS}	-0.09 ^{NS}	-0.04 ^{NS}	0.11 ^{NS}	-0.50***	-1.00***	-0.39***	0.03 ^{NS}	-0.66***	0.22**	0.01 ^{NS}	-0.03 ^{NS}	0.11 ^{NS}	1.00***	1.00***	0.51***	0.73***	0.73***	-0.02 ^{NS}	1.00***	1.00***	1.00***	1.00***

RFL = recommended fertilizer level; FDMY = forage dry matter yield; CP = crude protein; NDF = neutral detergent fiber; ADF = acid detergent fiber; ADL = acid detergent lignin; HC = hemicellulose; C = cellulose; IVDMD = in-vitro dry matter digestibility; CPY = crude protein yield; DY = digestible yield; DCP = digestible crude protein; TDN = total digestible nutrients; DDM = digestible dry matter; DMI = dry matter intake; RFV = relative feed value; RFQ = relative feed quality; TDNY = total digestible nutrient yield; DE = digestible energy; ME = metabolizable energy; NEI = net energy for lactation; NEm = net energy for maintenance; NEg = net energy for gain; p<0.05, **p<0.01, ***p<0.001, NS = non-significant at 5% probability level.

Note: The green and yellow colors indicate the strength of correlation; deep green color indicates perfect positive correlation; green to light green color indicate strong to weak positive correlation; deep yellow color indicates perfect negative correlation; yellow to light yellow color indicate strong to weak negative correlation.

5.4 Discussion

5.4.1 Fodder yield and yield related traits

5.4.1.1 Analysis of variance

The combined analysis of variance indicated that all measured parameters in oat varieties varied significantly except TDW, PDMY, and PNB. This indicated that the studied oat varieties had considerable inherent genetic variations for the studied parameters. Variations among oat varieties for measured parameters were also reported by different scholars (Singh, 1998; Byamungu and Jo, 2018; Ratan *et al.*, 2018; Gezahagn *et al.*, 2023a; Gezahagn *et al.*, 2023b). Moreover, the application of fertilizer influenced all measured parameters significantly except DFH, LSR, and PNB in oat. This indicated that the application of fertilizer on oat had a substantial effect on the studied parameters. The influence of fertilizer on various parameters of oat was also reported (Mahale *et al.*, 2003; Aklilu, 2005; Uma *et al.*, 2010; Ali *et al.*, 2017). The interaction effect of variety by fertilizer was significant for TDW, LSR, FPC, and FNC. Accordingly, the interaction effect of FPC and FNC was due to both the differential response of oat varieties and the differential influence of fertilizer on these parameters. However, the interaction effect of TDW and LSR was due to the differential influence of fertilizer on TDW and the differential response of varieties on LSR.

The cropping seasons also had significant effect on all measured parameters except TDW, NLFH, LLFH, LDMY, PFP, and AE due to variations in precipitation and temperatures. The studies also indicated that the year had a significant effect on various parameters of oat (Maral *et al.*, 2013; Gezahagn *et al.*, 2016; Kai *et al.*, 2019; Gezahagn *et al.*, 2021). The interaction effect of variety by year was significant for DFH and FPC due to both the differential response of varieties and differential influence of year on these parameters while TDW, NLFH, LDMY, and PDMY varied significantly due to either differential response of varieties or differential influence of year on these parameters. Moreover, the interaction effect of fertilizer by year also varied significantly for FPC, FNC, FPU, and APE due to both differential influences of fertilizer and year on these parameters while LLFH and LSR were influenced either by differential influence of fertilizer or year on these parameters. Furthermore, the interaction effect of variety by fertilizer by year was significant for NLFH, FPC, FNC, FNU, FTNU, and all measured nutrient use efficiency parameters except PNB.

5.4.1.2 Main and interaction effects on agro-morphological traits

The NTPP is generally influenced by variety, biotic and abiotic factors, management conditions, and their interaction effects. However, under optimum growing and management conditions, the NTPP is varied due to differences in the tillering performance of oat varieties. Application of fertilizer at 125% (51.3 kg N + 25 kg P/ha) increased the NTPP by 30.8% compared to unfertilized treatment. The increase in NTPP due to the application of fertilizer was also reported in oat (Singh *et al.*, 2002; Malik *et al.*, 2015; Ratan *et al.*, 2018; Kumar *et al.*, 2023). Among oat varieties, the grain type oat variety (Sorataf) increased the NTPP by 14.3% over the forage type oat variety (CI-8251), and variation in NTPP was also reported among oat varieties (Ali *et al.*, 2017; Bibi *et al.*, 2021; Gezahagn *et al.*, 2023a). The NTPP was 22.2% higher in the 2021 cropping season compared to 2020 due to better-growing conditions in the former year of production in terms of amount and distribution of precipitation and maximum and minimum temperatures. The TDW is an important trait that indicates the growing ability of the plant at the early growth stage. The TDW, which showed the vigorous growth of the plant at the tillering stage, varied significantly for the interaction effect of variety by fertilizer. The result showed that the TDW for grain type oat which was sown with 125% fertilizer rate was higher by 25.9% compared to the forage type oat which was sown with 25% (10.3 kg N + 5 kg P/ha) fertilizer rate. Moreover, the TDW for forage type oat which was sown in 2020 had a 10.6 % advantage over the grain type oat which was sown in the same cropping season. Gezahagn *et al.* (2023a) also reported that oat varieties varied in TDW at the early growth stage due to inherent genetic differences in growing performance.

The NLFH has a significant contribution to higher fodder yield and fodder quality. The NLFH usually depends on plant height, number of nodes per plant, and internode length and it is generally influenced by variety, edaphic factors, climatic conditions, management factors, and the effects of their interactions. The influences of fertilizer application (Bhilare and Joshi, 2007; Ayub *et al.*, 2010; Waheed *et al.*, 2012) and varieties (Tessema and Getinet, 2020; Gezahagn *et al.*, 2023a) on NLFH were also reported in oat. The increase in the number of leaves per plant might be due to fertilizer application stimulating the vegetative growth of the crop which increases plant height, the number of nodes, and inter-node thus resulting in a higher number of leaves per plant and this result is in close conformity with that of Ali *et al.* (2017). Forage type oat variety (CI-8251) which was sown with 125% (51.3 kg N + 25 kg P/ha) fertilizer rate in

2020 was 56.8% higher in NLFH compared to the dual type oat variety (SRCPX80Ab2291) which was sown with 150% (61.5 kg N + 30 kg P/ha) fertilizer rate in 2021 cropping season. Moreover, the LLFH varied among oat varieties and a variety with higher LLFH has better fodder yield-producing performance due to efficient utilization of solar energy for photosynthesis. The forage type oat produced 35.0% higher LLFH compared to the dual type oat variety. This result is also in close conformity with the findings of Tanvi (2016), Atman (2017), and Gezahagn *et al.* (2023a), who reported that LLFH varied among oat varieties. Moreover, the interaction effect of fertilizer by year also varied significantly for LLFH. Application of 125% fertilizer rate in the 2020 cropping season produced 32.0% higher LLFH compared to the application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rate in the 2021 cropping season.

The PHFH is one of the most important traits that can influence the fodder yield significantly in forage crops. Application of 125% fertilizer rate in this study increased the PHFH by 8.7% compared to unfertilized treatment. The higher PHFH with a higher fertilizer rate might be due to better absorption of nutrients, improved vegetative growth (increase in cell division and elongation), increased assimilation rate, and better metabolic activities in plants (Massey and Gaur, 2006; Mathukia *et al.*, 2014; Satpal *et al.*, 2020; Kumar *et al.*, 2021a). Singh *et al.* (2002) also reported that the application of 50 kg N/ha and 40 kg P₂O₅/ha gave the highest plant height over the lower doses. Bereket *et al.* (2014) also reported that the application of nitrogen and phosphorous fertilizers can increase plant height with increasing doses. Among oat varieties, the forage type oat (CI-8251) variety and dual type oat (SRCPX80Ab2291) variety produced 40.2 and 17.2% higher PHFH compared to the grain type oat (Sorataf) variety, respectively. Lynch and Frey (1993) and Tao *et al.* (2021) also reported that high-grain yield-producing genotypes generally have shorter plant height compared to low-grain (or high biomass) yield-producing genotypes. Variation in PHFH was also reported in oat varieties (Ashenafi, 2018). The observed PHFH in the 2021 cropping season was higher by 3.0% over the 2020 cropping season. The variation in PHFH between the two production seasons could be due to variations in rainfall and temperature and this result is in agreement with the findings of Maral *et al.* (2013) and Gezahagn *et al.* (2021).

Yields of morphological fractions indicate the relative proportions of the leaf, stem, and panicle. Application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rate gave 93.9% higher SDMY

compared to unfertilized treatment. The increase in SDMY with the application of fertilizer was also reported in oat (Amanullah and Stewart, 2013). Among oat varieties, the forage type oat (CI-8251) variety and dual type oat (SRCPX80Ab2291) variety produced 23.4 and 14.9% higher SDMY over the grain type oat (Sorataf) variety, respectively. The SDMY is highly influenced by the stem length in oat varieties. Thus, a lower SDMY in grain-type oat than in forage and dual-type oat varieties was due to its shorter stem length which resulted in a lower accumulation of SDMY. Variation in SDMY was also reported among oat varieties (Fekede, 2004; Gezahagn *et al.*, 2023a). The SDMY recorded in the 2021 cropping season was higher by 23.9% compared to the 2020 cropping season. The observed higher SDMY in the first year of production might be due to the efficient utilization of growth resources. The LDMY increased with increasing levels of fertilizer up to 125 % (51.3 kg N + 25 kg P/ha). Thus, application of 125% fertilizer rate in this study increased the LDMY by 82.1% over unfertilized treatment. The effect of fertilizer application on the LDMY of oat was also reported (Amanullah and Stewart, 2013). Moreover, the interaction effect of variety by year was significant for LDMY and PDMY. The forage-type oat which was sown in the 2021 cropping season produced 29.7% higher LDMY than the grain-type oat which was sown in the 2020 cropping season. Similarly, the forage type oat sown in 2020 and the dual type oat sown in 2021 gave 23.5% higher PDMY over the forage type oat sown in the 2021 cropping season. The effect of variety on LDMY and PDMY in oat was also reported (Fekede, 2004; Gezahagn *et al.*, 2023a).

The LSR is one of the most agro-morphological traits that used to estimate the quality of fodder and it decreases as the crop maturity increases. With increasing maturity, the proportion of leaves decreases while the stems proportion increases which results in decreased quality of feed. Variation in LSR among oat varieties was also reported by different scholars (Fekede, 2004; Choudhary and Prabhu, 2016; Gezahagn *et al.*, 2021). The forage type oat sown with 25% (10.3 kg N + 5 kg P/ha) fertilizer rate gave 52.9% higher LSR over the dual type oat sown with the same fertilizer level. Application of 25% fertilizer rate in 2020 increased the LSR by 59.4% compared to the application of 150% (61.5 kg N + 30 kg P/ha) and 175% fertilizer rates in 2021 cropping season. The LSR was also influenced by the application of fertilizer in oat varieties (Ali *et al.*, 2017). The growing environment, management conditions, and variety generally have a higher effect on DFH. Under optimum growing and management conditions, the late maturing varieties usually can produce higher yields due to efficient utilization of growth

resources. However, early maturing varieties produce better yields under sub-optimal growing and management conditions when compared to the late maturing varieties. A significant effect of inorganic fertilizers on DFH in oat has also been reported (Waheed *et al.*, 2012). Forage type oat variety which was sown in the 2021 cropping season required 16.2% more DFH compared to the dual type oat variety which was sown in the same cropping season. Significant variety-by-year interaction effect for DFH was also reported in oat varieties (Ashenafi, 2018).

The FYPR and FDMY varied significantly for fertilizer, variety, and year effects. The FYPR increased with increasing levels of fertilizer and application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rate increased the FYPR by 90.6% over unfertilized treatment. Among oat varieties, the dual type and fodder type oat varieties gave 11.2 and 3.7% higher FYPR over the grain type oat variety, respectively. Variation in FYPR among oat varieties was also reported (Gezahagn *et al.*, 2023a; Gezahagn *et al.*, 2023b). The FYPR was higher by 8.7% in the 2021 cropping season over the 2020 cropping season. The FDMY increased with increasing levels of fertilizer up to 175%. Application of 75% (30.8 kg N + 15 kg P/ha), 100% (41.0 kg N + 20 kg P/ha), 125% (51.3 kg N + 25 kg P/ha), 150% (61.5 kg N + 30 kg P/ha), and 175% fertilizer rates increased the FDMY by 54.8, 66.7, 85.7, 88.1, and 89.3% over unfertilized treatment, respectively. Application of optimum nutrients usually improves leaf production and expansion rate that are used to intercept more photosynthetically active radiation which leads to higher fodder yield accumulation (Kumar *et al.*, 2017; Ihtisham *et al.*, 2018). The research findings also indicated that the combined application of 50 kg N/ha and 40 kg P₂O₅/ha in oat crops is beneficial to get higher fodder yield (Patel and Rajagopal, 1998). Singh *et al.* (2002) also observed that the highest forage dry matter yield was obtained with the application of 80 kg N/ha and 40 kg P₂O₅/ha. The study also indicated that the application of 90 kg N/ha and 30 kg P₂O₅/ha in a combined way gave higher dry matter yield (Tripathi, 1993). Sood and Kumar (1994) also observed that dry matter yield in oat increases up to 75 kg N/ha and 75 kg P₂O₅/ha. Among oat varieties, the forage and dual-type oat varieties produced 15.4 and 10.6% higher FDMY over the grain-type oat variety, respectively. The second year of production gave 5.4% higher FDMY over the 2020 cropping season. The increase in the fodder yield could be attributed to increased growth parameters viz., plant height and number of tillers and this result is in line with that of Getnet and Ledin (2001) and Jehangir *et al.* (2013b).

5.4.1.3 Main and interaction effects on nutrient content, uptake, and use efficiency

The FPC was significant for the interaction of variety by fertilizer by year. The result showed that the grain type oat (Sorataf) variety sown with the application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rate in the 2020 cropping season had 220.0% higher FPC compared to the forage type oat (CI-8251) variety sown without fertilizer in the 2021 cropping season. Similarly, application of 175% fertilizer for grain-type oat in the 2020 cropping season gave 169.7% higher FNC compared to the forage-type oat sown without application of fertilizer in the same cropping season. The existence of higher nitrogen and phosphorus concentrations in oat fodder under higher nutrient application might be associated with increased absorption of nutrients and this result is in line with the findings of Jehangir *et al.* (2012). The concentrations of nitrogen and phosphorus in oat fodder were higher in low fodder-producing oat variety (Sorataf) compared to high fodder-producing oat variety (CI-8251). The lower nutrient concentration in a higher fodder-producing variety could be associated with higher nutrient dilution effects in fodder yield. This result is in close conformity with Greenwood *et al.* (1990), who reported that the nutrient concentration decreased with increasing fodder yield due to high nutrient dilution effects. The results also indicated that the level of nitrogen application affects its concentration in oat (Sood and Kumar, 1994; Devi *et al.*, 2010; Kherawat *et al.*, 2012). According to Sharma *et al.* (2002a), the nitrogen content in oat fodder increased significantly with the application of 100 kg N/ha.

The FPU varied significantly among oat varieties. The results showed that the dual-type oat (SRCPX80Ab2291) variety was 15.0% higher in FPU compared to the forage-type oat (CI-8251) variety. Moreover, application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rate in the 2020 cropping season had 332.0% higher FPU compared to oat sown without fertilizer application in the 2021 cropping season. Shikha and Singh (2018) also reported that the amount of phosphorus uptake varied among oat varieties. Similarly, the grain type oat (Sorataf) variety which was sown with the application of 175% fertilizer in the 2020 cropping season had 409.2 and 407.9% higher FNU and FTNU, respectively, compared to the same variety which was sown without fertilizer application in the same cropping season. Stood and Kumar (1994) and Kherawat *et al.* (2012) also pointed out that the uptake of nitrogen is influenced substantially by the levels of nitrogen applied in oat. Singh *et al.* (1995a) also reported that the application of 80

kg N/ha showed the highest nitrogen uptake in oat fodder. The study also indicated that the nutrient uptake increased with increasing levels of fertilizer up to 75 kg N + 60 kg P₂O₅/ha in oat (Patel and Rajgopal, 2002). The application of fertilizer significantly increased nitrogen and phosphorus uptake and the highest uptake of these nutrients was registered under 125% of the recommended dose of fertilizer (Choudhary and Prabhu, 2016). The increase in nutrient uptake with fertilizer levels might be due to higher nutrient content and fodder yield (Rawat and Agrawal, 2010; Jehangir *et al.*, 2012; Jat *et al.*, 2013).

The nutrient use efficiency is a function of the ability of plants to take nutrients from the soil and the capacity of the soil to supply sufficient nutrients to the plant for growth, development, and yield formation. The nutrient use efficiency is generally higher under lower rates of fertilizer application compared to the application of higher levels of fertilizer unless the sown variety is efficient in nutrient use efficiency or the loss of nutrients from the root zone is reduced through various management practices. The studies also indicated that nutrient use efficiency decreased with increasing levels of fertilizer (Sharma *et al.*, 1999; Gunri *et al.*, 2004; Shekara *et al.*, 2009; Shekara *et al.*, 2019). The PNB varied significantly for fertilizer and year effects. The result showed that the PNB decreased with increasing levels of fertilizer application up to 175% (71.8 kg N + 35 kg P/ha) fertilizer. Accordingly, the application of 25% (10.3 kg N + 5 kg P/ha) fertilizer rate gave 328.6% higher PNB compared to the application of 175% fertilizer rate. The lower PNB with application of higher fertilizer levels was also reported (Dressa *et al.*, 2012). The PNB in the 2021 cropping season was higher by 10.5% compared to the 2020 cropping season.

The interaction effect of variety by fertilizer by year was significant for PFP, IUE, AE, and APE. The forage type oat (CI-8251) variety which was sown with 25% fertilizer in the 2021 cropping season was 562.0% higher in PFP compared to the grain type oat (Sorataf) variety which was sown with 175% fertilizer rate in the 2021 cropping season and this result is in harmony with the findings of Desire *et al.* (2020). Moreover, the forage type oat variety which was sown with 75% (30.8 kg N + 15 kg P/ha) fertilizer rate in the 2020 cropping season had 95.8% higher IUE compared to the grain type oat variety which was sown with 175% fertilizer rate in the same cropping season. However, the grain type oat variety which was sown with 25% fertilizer rate in the 2021 cropping season had 505.9% higher AE compared to the dual type oat

(SRCPX80Ab2291) variety which was sown with 50% (20.5 kg N + 10 kg P/ha) fertilizer rate in the 2020 cropping season. The lower AE with increasing fertilizer levels was also reported (Adjewor, 2015; Anowarul and Adjewor, 2019; Shekara *et al.*, 2021; Nanda and Nilanjaya, 2022). The forage-type oat variety which was sown with 75% fertilizer rate in the 2020 cropping season had 358.2% higher APE compared to the dual-type oat variety which was sown with 50% fertilizer rate in the same cropping season. Generally, the forage type oat had higher PFP, IUE, and APE while the grain type oat had higher AE under lower levels of fertilizer in fodder yield of oat.

5.4.1.4 Correlation analysis

The Pearson correlation analysis was done on agro-morphological traits and parameters of fodder nutrient concentration and its nutrient uptake and use efficiency of oat varieties with fertilizer levels and fodder yield. The results revealed that the NTPP, LDMY, SDMY, PDMY, FYPR, and FDMY were significantly and positively correlated with fertilizer levels. This showed that the performance of the above-mentioned traits increased remarkably with increasing levels of fertilizer application. The associations of NTPP, LDMY, SDMY, PDMY, FYPR, and PHFH were also significant and positive with FDMY. This showed that selection of oat varieties based on these traits would be effective for fodder yield improvement. The associations of LDMY and SDMY with FDMY were also positive in oat (Sahu *et al.*, 2023). Gezahagn *et al.* (2023c) also reported that FDMY had significant and positive associations with PHFH and FYPR. The positive association of PHFH with FDMY was also reported by different scholars (Bahadur and Choubey, 2008; Atman, 2017; Wagh *et al.*, 2018). On the other hand, TDW, LLFH, and PHFH had non-significant positive associations with fertilizer levels. Moreover, TDW and LLFH had non-significant positive associations with FDMY. The non-significant positive association between TDW and FDMY was also reported in oat varieties (Gezahagn *et al.*, 2023c). However, non-significant inverse associations were observed for the NLFH, DFH, and LSR with fertilizer levels and FDMY. This indicated that selection of oat varieties using NLFH, DFH, and LSR would not be effective for improving fodder yield. The inverse associations of NLFH and LSR with FDMY might be due to the leafy varieties having shorter plant height with higher number of nodes or shorter internode lengths compared to the less leafy varieties. Moreover, the inverse association between FDMY and DFH might be due to

late-maturing varieties being less efficient in utilizing the growth resources compared to early-maturing varieties.

The FNC, FPU, FNU, and FTNU were significant and positive with fertilizer levels. Studies also indicated that the contents of nutrients and uptake of nutrients increased with increasing levels of fertilizer in different crops (Ardeshna *et al.*, 1993; Shalini *et al.*, 2021). Moreover, the FPC, FNC, FPU, FNU, and FTNU had significant positive associations with FDMY indicating that higher nutrient concentration and uptake had a remarkable contribution to increase FDMY. The nutrient use efficiency indicated that the PFP, PNB, and AE had significant inverse associations with fertilizer levels. The inverse associations of the above parameters with fertilizer levels might be related to loss of nitrogen from the root zone due to leaching (Cameron *et al.*, 2013), volatilization (Sommer *et al.*, 2004), denitrification (Freney *et al.*, 1990), and high phosphorus fixation under acidic soil conditions. Moreover, the IUE, PFP, PNB, and AE also had significant inverse associations with FDMY. The inverse association of FDMY with IUE, PFP, PNB, and AE might be related to the loss of nutrients from the soil (Duan *et al.*, 2014; Huang *et al.*, 2016; Ke *et al.*, 2017) and higher plant N loss after uptake and accumulation due to photorespiration (Xu *et al.*, 2012). However, the APE had a significant positive association with fertilizer level and FDMY, indicating higher fertilizer level increases the APE which leads to higher FDMY.

The Pearson correlation analysis was also performed among measured parameters. The results showed that the NTPP and NLFH had positive associations with TDW. A significant positive association between NTPP and TDW in oat was also reported (Gezahagn *et al.*, 2023c). The PHFH had a positive association with FYPR while DFH had an inverse association with FYPR. Gezahagn *et al.* (2023c) also reported that PHFH had a significant positive association with FYPR in oat. Similarly, the SDMY and PDMY had positive associations with LDMY. Sahu *et al.* (2023) also reported that LDMY had a positive association with SDMY. The FPU had also a positive association with FNU and FTNU. Dobariya *et al.* (1985) also reported that the nitrogen uptake by fodder increased with increasing phosphorus uptake. Moreover, the association between FNC and FPC was positive indicating both have synergistic effects. Similarly, the AE with APE and also PFP with PNB and IUE were positive.

5.4.1.5 Economic analysis

The partial budget analysis indicated that the application of fertilizer substantially increased the net benefit of fodder yield in oat. Different scholars also indicated that application of fertilizer gave higher net benefit compared to unfertilized treatment in different crops (Pradhan and Mishra, 1994; Sharma *et al.*, 2002b; Edwin *et al.*, 2015; Ali *et al.*, 2017; Subrahmanya *et al.*, 2019; Shekara *et al.*, 2021). The net benefits obtained from unfertilized treatments of forage type oat (CI-8251), dual type oat (SRCPX80Ab2291), and grain type oat (Sorataf) varieties were 43,621, 40,789, and 24,637 ETB/ha, respectively. With increasing fertilizer rates, the corresponding maximum net benefits of 90,697, 89,101, and 77,875 ETB/ha were obtained from oat varieties using the application of 175% (71.8 kg N + 35 kg P/ha), 150% (61.5 kg N + 30 kg P/ha), and 125% (51.3 kg N + 25 kg P/ha) of the blanket recommended fertilizer rates, respectively. This indicated that forage-type oat variety required the highest fertilizer rate followed by dual and grain-type oat varieties to produce a higher net benefit. The highest net benefit obtained by forage type oat compared to other oat varieties might be due to its higher fodder yield performance which is associated with better growth, higher plant height, and better response for applied fertilizer. Moreover, cultivation of forage-type oat variety without fertilizer application gave relatively better net benefit compared to dual and grain-type oat varieties indicating that the forage-type oat variety had better nutrient mining ability from the soil to produce higher fodder yield which resulted in higher profit. Different studies also indicated that the net benefit varied among oat varieties (Ali *et al.*, 2017; Dabhi *et al.*, 2017; Singh *et al.*, 2018; Kumar *et al.*, 2021b). The combined partial budget analysis indicated that oat varieties gave the lowest net benefit (36,349 ETB/ha) under unfertilized conditions and a higher net benefit of 83,440 ETB/ha was obtained with the application of 125% fertilizer. The higher net benefit at the application of 125% fertilizer rate in oat varieties might be due to the overall better fodder productivity that results in higher net benefit.

The MRR for the highest net benefit produced fertilizer level was highly variable among the studied oat varieties. The forage type oat (CI-8251), dual type oat (SRCPX80Ab2291), and grain type oat (Sorataf) varieties with the corresponding fertilizer rates of 175% (71.8 kg N + 35 kg P/ha), 150% (61.5 kg N + 30 kg P/ha), and 125% (51.3 kg N + 25 kg P/ha) gave the MRR of 210, 1,815, and 14,786%, respectively. This indicated that forage type oat, dual type oat, and grain type oat varieties earn 2.10, 18.15, and 147.86 ETB, respectively, per unit of Ethiopian

birr investment for fodder production in the study area. Similarly, the combined analysis for oat varieties also indicated that the highest net benefit produced fertilizer level gave the MRR of 12,636% using the application of 125% fertilizer rate. This indicated that the farmers can earn 126.36 ETB per unit of Ethiopian birr investment for fodder production from oat varieties. Thus, the cultivation of oat varieties using the application of 125% fertilizer rate could produce a higher net benefit and the highest MRR. Hence, the production of fodder from oat varieties using application of 125% fertilizer rate is found to be the most profitable in the study area. Accordingly, the lowest acceptable MRR (100%) coupled with the highest net benefit would give better profit and it should be recommended for smallholder farmers to produce fodder from oat. CIMMYT (1988) stated that a treatment that has the highest net benefit coupled with the minimum acceptable MRR (100%) is the most economical to recommend for farmers. CIMMYT (1988) also stated that farmers would be willing to change from one treatment to another if the MRR of that change is greater than the minimum acceptable rate of return (100%).

All the fertilizer rates applied for forage type oat (CI-8251) were dominant except unfertilized treatment and application of 75% (30.8 kg N + 15 kg P/ha) fertilizer which were dominated. Moreover, all the dominant fertilizer levels applied for forage-type oat were above the minimum acceptable MRR (100%). Similarly, the dual type oat variety (SRCPX80Ab2291) was also dominant for all fertilizer levels except unfertilized treatment, 50% (20.5 kg N + 10 kg P/ha) fertilizer, and 100% (41.0 kg N + 20 kg P/ha) fertilizer. Accordingly, all the dominant fertilizer levels in the dual-type oat variety gave above the lowest value of MRR. On the other hand, the grain type oat (Sorataf) had dominant MRR only for application of 100%, 125% (51.3 kg N + 25 kg P/ha), and 175% (71.8 kg N + 35 kg P/ha) fertilizer, and these dominant fertilizer rates were above the minimum MRR values. The combined analysis for oat varieties showed that the dominant fertilizer levels of 50, 100, and 125% had MRR above the minimum acceptable level while unfertilized and 175% fertilizers were dominated. In the combined analysis of oat varieties, the dominant fertilizer rates of 75 and 150% were below the minimum acceptable MRR which leads to lower profit. Generally, all the dominant fertilizer levels in each oat variety and application of 50, 100, and 125% fertilizer in the combined analysis of oat varieties showed above the minimum acceptable MRR, indicating that these dominant fertilizer rates are more profitable. However, all the dominated fertilizer levels are less profitable than the dominant fertilizer levels. Thus, the dominated fertilizer rates should not be considered for economic

analysis. The net benefit-to-cost ratio for dominant fertilized treatments indicated that per unit of Ethiopian birr investment, the net benefit ranged from 3.3 to 3.5 ETB for forage type oat; from 3.1 to 3.7 ETB for dual-type oat; from 2.9 to 3.4 ETB for grain type oat; and from 2.8 to 3.5 ETB for combined analysis of oat varieties. This showed that all the net benefit-to-cost ratio values were above two indicating that the application of fertilizer gave better profit for smallholder farmers. However, the net benefit-to-cost ratio of unfertilized treatments for forage type oat, dual type oat, grain type oat, and combined analysis of oat varieties were 2.1, 1.9, 1.1, and 1.7 ETB, respectively, indicating their low profitability.

The fertilizer and labor costs will be expected to increase in the future. So, sensitivity analysis was performed to determine the economic feasibility of oat fodder production in the coming five years in the study area. The results of sensitivity analysis indicated that the MRR for CI-8251, SRCPX80Ab2291, and Sorataf oat varieties using application of 175% (71.8 kg N + 35 kg P/ha), 150% (61.5 kg N + 30 kg P/ha), and 125% (51.3 kg N + 25 kg P/ha) fertilizer and combined oat varieties which received 125% fertilizer will be expected to be 55.14, 857.55, 7342.89, and 6267.82%, respectively. This indicated that except the forage type oat (CI-8251), dual type oat (SRCPX80Ab2291), grain type oat (Sorataf), and combined oat varieties had MRR above 100%. This revealed that the recommended fertilizer levels for dual-type oat, grain-type oat, and combined oat varieties are profitable when the costs of fertilizer and labor increase to 100% (20% per year) for the coming five years. If the fertilizer and labor costs increase by 100% in the coming five years, the farmers who cultivate forage-type oat using 175% fertilizer; dual type oat using 150% fertilizer; grain-type oat using 125% fertilizer; and combined oat varieties using 125% fertilizer can earn 0.55, 8.58, 73.43, and 62.88 ETB per unit of Ethiopian birr investment, respectively.

5.4.2 Grain yield and yield related traits

5.4.2.1 Analysis of variance

The pooled analysis of variance revealed that oat varieties had significant variations for all measured parameters except SPC, SNC, and TNU. The variation among oat varieties revealed the existence of substantial inherent variability for the studied parameters. The presence of considerable variations in oat varieties was also reported (Getnet *et al.*, 2004; Ashenafi, 2018;

Shikha and Singh, 2018; Gezahagn *et al.*, 2021). The levels of fertilizer also influenced all the measured parameters significantly except DSH, HI, IUE, PE, and APE. Different scholars also reported that fertilizer application had a significant influence on various traits in oat (Sajjad *et al.*, 2014; Shikha and Singh, 2018; Uma *et al.*, 2019). The two cropping seasons in this study also significantly influenced about 64% of the measured parameters. The variations between the two cropping seasons on some of the measured parameters might be associated with differences in the amount and distribution of precipitation and temperatures. The influence of cropping seasons on different parameters of oat were also reported by different scholars (Malhi *et al.*, 2006; Arenhardt *et al.*, 2017; Byamungu and Jo, 2018; Khan *et al.*, 2019). From the significant variety by fertilizer interaction effect, about 58% of the interaction effects were due to both the differential response of varieties for fertilizer levels and the fertilizer levels influencing the varieties differently. Similarly, about 78% of the significant variety-by-year interaction effects were due to both differential responses of varieties for cropping seasons and the cropping seasons influenced the varieties differently. Moreover, about 75% of the significant fertilizer-by-year interaction effects were due to both the fertilizer levels influenced by the cropping seasons and the response of cropping seasons varied with fertilizer levels on measured parameters. Furthermore, about 40% of the significant variety by fertilizer by year interaction effects was due to the simultaneous effects of variety, fertilizer, and year on measured parameters.

5.4.2.2 Main and interaction effects on agro-morphological traits

The interaction effect of variety by year varied for DSH. The longer DSH was recorded for the interaction effect of forage type oat (CI-8251) with the 2021 cropping season compared to the interaction effect of dual type oat (SRCPX80Ab2291) with the 2020 cropping season. The inherent genetic variation among oat varieties coupled with the differential influence of cropping season on oat varieties was the major reason for variation in DSH. Similarly, the interaction effect of variety by year also varied for GFP. The GFP was 63% higher for the grain type oat (Sorataf) in the 2021 cropping season compared to the interaction effect of dual type oat sown in the 2020 cropping season. This indicated that the grain-type oat exploit more growth resources due to better-growing conditions in 2021 than the 2020 cropping season. Moreover, the interaction effect of fertilizer by year differed for GFP. The longer GFP was

recorded for the application of 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate in the 2021 cropping season which was 52% higher compared to unfertilized treatment in 2020. Research findings indicated that the rate and duration of grain filling have a substantial effect on productivity (Yang and Zhang, 2006). Under less favorable growing conditions, the crops usually shorten their grain filling period and enhance the assimilate remobilization rate from the sources to sink to maximize yield (Halilou *et al.*, 2020). On the other hand, the results also indicated that the NSPP and NSLPP varied for fertilizer levels and the interaction effect of variety by year. Accordingly, the NSPP and NSLPP increased linearly with increasing levels of fertilizer rates up to 125% (51.3 kg N + 25 kg P/ha). The interaction effect of grain type oat with the 2020 cropping season and the forage type oat with the same cropping season had the highest NSPP and NSLPP, respectively. This indicated that a higher grain yield performance in oat is more associated with NSPP compared to NSLPP.

The PHGH varied for the interaction effects of variety by year and variety by fertilizer. The results showed that the forage-type oat in the 2020 cropping season was 54% higher in PHGH compared to the grain-type oat in the same cropping season. The inherent genetic variation among oat varieties was the major reason for the difference in PHGH. Moreover, the interaction effect of variety by fertilizer showed that the forage type oat which received 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate increased its PHGH by 74% over the grain type oat which was sown without fertilizer. Kinfe *et al.* (2020) also reported that the combined application of nitrogen and phosphorus fertilizer increases the plant height substantially. The observed shorter plant height in oat varieties which was sown without fertilizer might be associated with a lower availability of essential nutrients for plant growth (Detebo *et al.*, 2021). However, the application of balanced fertilizer can increase plant height due to better vegetative growth through optimum cell division and cell elongation (Souri *et al.*, 2019; Kinfe *et al.*, 2020). Another study also indicated that the increase in plant height with fertilizer application is because fertilizer promotes plant growth, and increases the number and length of internodes which results in higher plant height (Gasim, 2001). The PLGH also varied for the effect of variety and the interaction effect of fertilizer by year. Similar to PHGH, the forage type oat was 76% higher in PLGH compared to the grain type oat indicating that the panicle length had less contribution to grain yield. The variation in PLGH indicates the presence of substantial inherent variability among oat varieties (Gezahagn *et al.*, 2023a). Moreover, the interaction effect of

fertilizer by year showed that application of 125% (51.3 kg N + 25 kg P/ha) of the recommended fertilizer rate in the 2020 cropping season was 40% higher in PLGH compared to unfertilized treatment in the 2021 cropping season. Similarly, the FLLGH varied for fertilizer levels and the interaction effect of variety by year. The FLLGH increased linearly with increasing levels of fertilizer up to 125% and it was increased by 38% using the application of 125% fertilizer rate compared to unfertilized treatment. The interaction effect of variety by year also revealed that the forage-type oat in the 2020 cropping season was 33% higher in FLLGH than the grain-type oat in the 2021 cropping season.

The BYPR and GSFR varied for fertilizer rates. The application of fertilizer at the rate of 175% (71.8 kg N + 35 kg P/ha) and 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer increased the BYPR and GSFR by 133 and 131% over unfertilized treatment, respectively. This indicated that fertilizer application had a substantial contribution to increasing BYPR and GSFR in oat varieties. Moreover, BYPR, GSFR, and TSW varied among oat varieties, and similar results were also reported in oat genotypes (Gezahagn *et al.*, [2023a](#)). The BYPR for forage-type oat was increased by 22% over the grain-type oat. However, the GSFR for grain and dual-type oat varieties was increased by 15% over the forage-type oat. The dual type oat had 8% higher in TSW compared to the grain type oat indicating that the grain type oat had relatively lower grain size than the dual type oat. This result is in line with the findings of Shah *et al.* ([2002](#)), Inan *et al.* ([2005](#)), and Gezahagn *et al.* ([2023d](#)) who reported that TSW varied among oat varieties. The TSW also varied between the two cropping seasons due to variations in the amount and distribution of precipitation and temperatures. Accordingly, a 6% higher TSW was recorded in 2021 than 2020 cropping season. The HI differed for the interaction effects of variety by year and fertilizer by year. Thus, the grain-type oat in the 2020 cropping season produced 43% higher HI compared to the forage-type oat in the same cropping season. The higher HI in grain type oat variety compared to the forage type might be associated with the performance of higher GY and/ or lower SY or both in the former oat variety compared to the latter. The unfertilized treatment in the 2021 cropping season produced 20% higher HI compared to the unfertilized treatment in the 2020 cropping season. The higher HI from unfertilized treatment in the 2021 cropping season could be attributed to lower SY performance and higher translocation of assimilates from vegetative organs to grain.

The SY and TBY showed variation in the interaction effect of variety by fertilizer. The interaction effect of fodder type oat with 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate increased the SY and TBY by 266 and 205% over the grain type oat which was sown without fertilizer, respectively. This indicated that the application of fertilizer had a remarkable contribution to increasing SY and TBY in oat varieties. The GY varied for fertilizer level, variety, and year effects. The results showed that application of 100% (41.0 kg N + 20 kg P/ha), 125% (51.3 kg N + 25 kg P/ha), 150% (61.5 kg N + 30 kg P/ha), and 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rates were increased the GY by 96, 111, 132, and 125% over unfertilized treatment, respectively. Increasing the rate of fertilizer above 150% decreased the GY indicating that the optimum yield was already attained at the rate of 150% fertilizer application. Research results also indicated that the GY increased with increasing nitrogen levels in oat (Muurinen *et al.*, 2007). Yadav *et al.* (2000) also revealed that increasing the dose of fertilizers usually increased the grain and straw yields. Yang and Zhang (2006) reported that a decrease in GY for higher fertilizer doses caused due to higher vegetative growth, lower number of grains per plant, longer vegetative period, shorter grain filling period, and delayed maturity. The combined application of fertilizer increased the GY and the highest GY was obtained with 60 kg N + 45 kg P₂O₅/ha as reported by Kubresh and Bezsilko (1990). Among oat varieties, the GY for grain type oat and dual type oat varieties were increased by 14 and 6% over the forage type oat, respectively. The existence of substantial variations in GY was also reported among oat genotypes (Fekede, 2004; Ashenafi, 2018; Gezahagn *et al.*, 2021). Moreover, the GY in the 2021 cropping season was increased by 6% over the 2020 cropping season due to better growing conditions which enhances the uptake of nutrients to maximize yield.

5.4.2.3 Main and interaction effects on nutrient content, uptake, and use efficiency

The SPC and GPC varied for the interaction effect of variety by fertilizer by year. The result showed that the SPC of grain type oat which received 75% (30.8 kg N + 15 kg P/ha) of the recommended fertilizer rate in the 2021 cropping season was increased by 167% over the dual type oat which sown without fertilizer in the 2020 cropping season. Similarly, the grain type oat which received 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate in the 2020 cropping season was 74% higher in GPC over the dual type oat which sown without fertilizer in

the same cropping season. Moreover, the SNC and GNC varied for the interaction effect of variety by fertilizer by year. The result revealed that the SNC of the dual type oat which was sown with 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate in the 2021 cropping season was increased by 238% over the grain type oat which was sown without fertilizer in the 2020 cropping season. However, the GNC of the grain-type oat which received 75% of the recommended fertilizer in the 2021 cropping season was increased by 45% over the forage and dual-type oat varieties sown without fertilizer in the 2020 cropping season. The application of nitrogen fertilizer increased the nitrogen content of oat grain and straw up to 100 kg N/ha (Sharma *et al.*, 2001). According to Sood and Kumar (1994), the application of optimum phosphorus fertilizers increased its concentration and uptake which resulted in higher yield. The lower concentration of nutrients in this study might be associated with dilution effects due to the production of higher biomass yield. According to Greenwood *et al.* (1990), the nutrient concentration decreased as biomass dry matter accumulation increased due to dilution effects. The concentration of nutrients (nitrogen and phosphorus) is higher in grain than shoot at harvest, indicating a higher rate of essential growth nutrient translocation from shoot to grain in cereals as well as in legumes. During the grain filling period, nitrogen and phosphorus contents of non-grain tissue generally decrease while grain nitrogen and phosphorus contents increase due to remobilization of assimilates from shoot to grain (Wilhelm *et al.*, 2002). However, shoot dry weight increased with age advancement up to the flowering growth stage and then decreased (Fageria and Baligar, 2003). The decrease in shoot dry weight at harvest is related to the translocation of assimilates from the shoot to grain during flowering to maturity growth stages. Higher concentration of P in seeds has a remarkable effect on growth performance and seed yield potential of various forage crops. Higher concentration of P in seeds of various crops had been found to increase yield of seedlings and crop grown from seeds of high P irrespective of soil P (Jagadish *et al.*, 2019).

The interaction of variety by year effect showed variation for SNU and TNU. The interaction effect of forage-type oat sown with 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate was 436% higher in SNU over the grain-type oat which was sown without fertilizer. Similarly, the TNU for dual-type oat which received 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate was increased by 253% over the forage type oat sown without fertilizer. On the other hand, the SNU and TNU varied between the two cropping

seasons due to variations in growing conditions. Accordingly, the SNU and TNU in the 2021 cropping season were increased by 44 and 18% over the 2020 cropping season, respectively. The lower nutrient uptake in 2020 than in 2021 is associated with lower yield performance and nutrient concentration. The GNU also differed for fertilizer level, variety, and year effects. The results indicated that application of 100% (41.0 kg N + 20 kg P/ha), 125% (51.3 kg N + 25 kg P/ha), 150%, and 175% of the recommended fertilizer rates had increased the GNU by 144, 166, 196, and 189% over unfertilized treatment, respectively. The GNU of unfertilized treatment was 47.8 kg/ha indicating that oat varieties mine this amount of nutrients from the soil for their growth and yield formation. High removal of nutrients from the soil without replacing it can deplete the soil fertility. According, to Massey *et al.* (2020), the uptake of nutrients from unfertilized plots indicates the ability of a crop to use nutrients from other sources besides anthropogenic inputs. Among oat varieties, the grain type and dual type oat varieties had 23 and 6% GNU advantages over the forage type oat, respectively. In line with this result, variation in nutrient uptake in oat varieties has been also reported by Shikha and Singh (2018). The GNU in the 2021 cropping season was increased by 10% over the 2020 cropping season. The GNU often comes from remobilization of photoassimilates from the vegetative organs during grain-filling period and from soil uptake. Bakhshandeh *et al.* (2014) reported that 57% of grain nitrogen is related to nitrogen remobilization from vegetative organs in pre-anthesis and 11% is provided from direct soil nitrogen uptake and nitrogen remobilization after anthesis. The linear response of nutrient uptake up to 75 kg N + 60 kg P₂O₅/ha was also reported in oat (Patel and Rajgopal, 2002).

The NHI varied for the interaction effect of variety by fertilizer by year. The NHI of grain type oat sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate in the 2020 cropping season was increased by 44% over the forage-type oat sown with 125% (51.3 kg N + 25 kg P/ha) of the recommended fertilizer rate in the 2021 cropping season. According to Kinfel *et al.* (2020), NHI decreased with increasing levels of the combined nitrogen and phosphorus application. The PNB also varied for the interaction effects of variety by fertilizer and fertilizer by year. The grain type oat which received 25% (10.3 kg N + 5 kg P/ha) of the recommended fertilizer rate was 655% higher in PNB over the forage type oat which received 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate. Similarly, the interaction effect of 25% fertilizer rate in the 2020 cropping season and 25% fertilize rate in the 2021 cropping season

were 415 and 515% higher in PNB over the application of 175% fertilizer rate in the respective cropping season, respectively. This indicated that the PNB decreased linearly with increasing levels of fertilizer. Dressa *et al.* (2012) also reported a decreasing trend in PNB with increasing fertilizer rates. Moreover, the IUE and APE varied for the interaction effect of variety by fertilizer. The IUE and APE of forage type oat sown with 75% (30.8 kg N + 15 kg P/ha) of the recommended fertilizer rate were increased by 16 and 44% over the grain type oat and dual type oat which was sown with 75% fertilizer rate, respectively. The APE is also influenced by cropping seasons due to variations in growing conditions. Accordingly, the APE in the 2020 cropping season was increased by 29% over the 2021 cropping season.

The PFP and AE varied for fertilizer level, variety, and year effects. The results showed that the application of 25% (10.3 kg N + 5 kg P/ha) of the recommended fertilizer rate 484 and 393% higher in PFP and AE over the application of 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer rate, respectively. This indicated that the PFP and AE decreased linearly with increasing fertilizer rates. Desire *et al.* (2020) also reported that PFP decreased with increasing rates of fertilizer application. The finding of this study is also in line with the result of Dressa *et al.* (2012) who reported that AE is decreasing with increasing fertilizer rates. Among oat varieties, the PFP for grain-type oat was increased by 13% over the forage-type oat. Similarly, the AE for grain-type oat was increased by 33% over the dual-type oat. The inherent genetic variation among oat varieties is the major reason for differences in PFP and AE. The cropping season indicated that the 2021 cropping season had 12 and 17% advantages in PFP and AE over the 2020 cropping season, respectively. This is due to better growing conditions in the 2021 cropping season to utilize the applied nutrient efficiently. The PE also varied among oat varieties. Accordingly, the PE of forage-type oat was increased by 29% over grain-type oat. The higher PE in forage-type oat compared to grain type might be associated with better biomass production performance in forage types than grain-type oat.

5.4.2.4 Correlation analysis

The Pearson correlation analysis was done on agro-morphological traits and parameters of grain and straw nutrient concentrations, nutrient uptake, and nutrient use efficiency of oat varieties with fertilizer levels and grain yield. The results showed that the GY, DSH, FLLGH, PHGH, GFP, BYPR, GSFR, SY, and TBY were significantly and positively associated with levels of

fertilizer application. The above-mentioned agro-morphological traits and the NSLPP also had significant positive associations with GY. This indicates that selection based on these traits would be effective for the improvement of grain yield in oat varieties. Gezahagn *et al.* (2023c) also reported that GY had a significant positive association with GSFR and NSLPP in oat genotypes. According to Anne (2014), Melesse (2017), Byamungu and Jo (2018), and Kassu *et al.* (2021), the GY had positive associations with fertilizer rates in different crops. Getinet (2015) also reported that DSH, PHGH, GY, SY, and TBY had significant positive associations with nitrogen fertilizer levels while HI had a significant inverse association with fertilizer levels. The inverse association of HI with fertilizer levels might be associated with lower biomass partitioning to grain production when fertilizer was increased rather than encouraging vegetative growth. The GY had a positive association with DSH, PHGH (Getinet, 2015), SY (Getinet, 2015; Temesgen *et al.*, 2021), and TBY (Getinet, 2015; Temesgen *et al.*, 2021) while it had an inverse association with HI (Getinet, 2015) in different crops.

The SNC, GNC, GNU, SNU, and TNU were increased with increasing levels of fertilizer application. These plant parameters also had significant positive associations with GY. Moreover, the SPC and GPC had significant positive associations with GY. According to Shawl *et al.* (2021), GY had a significant positive association with GNC, SNC, and TNU. Getinet (2015) also reported that GNC, SNC, GNU, SNU, and TNU had a significant positive association with fertilizer rates while SPC and GPC had a non-significant positive association with fertilizer levels. However, the NHI, PFP, PNB, IUE, and AE had significant inverse associations with fertilizer levels. This might be associated with loss of nitrogen from the root zone due to leaching, runoff, volatilization, denitrification, and unavailability of phosphorus (high P-fixation) due to its reaction with iron and aluminum in acidic soil conditions. This result is in line with the findings of Meharie and Kindie (2019), who reported that NHI, PFP, and IUE had an inverse association with fertilizer rates. The GY in this study also had an inverse association with NHI, PFP, PNB, IUE, AE, and PE. This might be associated with loss of nutrients and low remobilization of photoassimilates from the sources to sink during the GFP.

The Pearson correlation analysis was also performed among selected measured parameters. The HI had inverse associations with TSW and SY. The GSFR had positive association with GFP while it had an inverse association with DSH. Moreover, the NHI had positive association with

GNU while it had an inverse association with SNU. The longer GFP contributed to higher accumulation of photoassimilates which resulted in higher GY that leads to maximum GSFR. The GNC and SNC had positive associations with their respective phosphorus concentration. Moreover, PFP with PNB and IUE; AE with PE, and APE had positive associations. This result is in agreement with the findings of Muurinen and Peltonen-Sainio (2006) and Etesami *et al.* (2018), who reported that PFP had a positive association with PNB and IUE.

5.4.2.5 Economic analysis

The partial budget analysis revealed that the application of fertilizer gave a higher net benefit over unfertilized treatment. Different studies also indicated that the application of fertilizers had a better net benefit compared to unfertilized plots in different crops (Singh *et al.*, 1995b; Khanday *et al.*, 2009; Beyenesh *et al.*, 2017; Kassu *et al.*, 2021; Shawl *et al.*, 2021; Temesgen *et al.*, 2021). The highest net benefit of 162,996.9, 158,322.0, and 157,593.5 ETB/ha were recorded for the corresponding forage type (CI-8251), dual type (SRCPX80Ab2291), and grain type oat (Sorataf) at the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate for forage type and grain type oat varieties while 175% (71.8 kg N + 35 kg P/ha) fertilizer rate for grain type oat. The highest net benefit obtained from forage type oat followed by dual type oat and grain type oat might be associated with high straw yield performance coupled with comparable grain production ability of forage type oat compared to the grain and dual type oat varieties. Moreover, the economic feasibility for combined analysis of oat varieties showed that the highest net benefit (156,207.2 ETB/ha) was obtained from a treatment that received 150% fertilizer while the lowest net benefit (54,244.0 ETB/ha) was obtained from unfertilized treatment. The dual type oat produced the maximum net benefit (158,322.0 ETB/ha) from the application of 175% fertilizer rate while forage type oat and grain type oat produced maximum net benefits of 162,996.9 and 157,593.5 ETB/ha using the application of 150% fertilizer rate, respectively. This indicated that the nutrient requirements of dual-type oat varieties were higher compared to forage and grain-type oat varieties to get better net benefits. The relative profitability varied among oat varieties due to differences in straw and grain yield productivity. This result is in line with the findings of Islam and Adjewi (2019) who reported that the differences in revenue among cultivars are due to differences in yield accumulation among cultivars.

The highest net benefit-producing fertilizer levels for each variety had marginal rates of return (MRR) of 545.6, 320.7, and 644.4% for forage, dual, and grain-type oat varieties, respectively. This indicated that per unit of Ethiopian birr investment to produce the above respective variety, it was possible to earn 5.46, 3.21, and 6.44 ETB, respectively. Moreover, the highest net benefit produced fertilizer level in the combined analysis had 370.2% MRR indicating that the farmers obtained an additional income of 3.70 ETB per unit of ETB investment. Thus, the combined analysis which received 150% (61.5 kg N + 30 kg P/ha) fertilizer rate had the highest net benefit and acceptable MRR, thus it is found to be an economically feasible fertilizer rate for grain yield production in the study area. In the economic analysis, it is assumed that farmers require a minimum MRR of 100%, demonstrating an increase in a net return of at least one Ethiopian birr per unit of Ethiopian birr investment. The highest net benefit coupled with a minimum acceptable MRR (100%) would be the best economically profitable treatment to recommend for farmers. According to CIMMYT (1988), the highest MRR is not necessarily an indication of the best treatment for recommendation but the highest net benefit together with an acceptable MRR treatment would be the best to recommend for farmers.

All the non-dominated treatments had MRR greater than 100% indicating that these non-dominated treatments are economically feasible compared to the dominated treatments. The dominated treatment is economically less profitable than the non-dominated treatment and thus, it should be excluded from the economic analysis. The dominance analysis indicated that fertilizer application at the rate of 75% (30.8 kg N + 15 kg P/ha) and 175% (71.8 kg N + 35 kg P/ha) for forage type oat, 75%, 100% (41.0 kg N + 20 kg P/ ha), and 150% (61.5 kg N + 30 kg P/ha) for dual purpose oat and 75% and 175% for combined analysis of oat varieties were dominated suggesting that these treatments were less profitable than the respective preceding treatment. On the other hand, the grain-type oat did not show dominated treatment indicating that all the fertilizer levels had relatively better profitability. On the other hand, the net benefit to cost ratio for combined analysis of oat varieties indicated that per unit of Ethiopian birr investment, the net benefit ranged from 1.6 ETB for unfertilized treatment to 3.0 ETB for application of 150% fertilizer for the dominant treatments. All the net benefit-to-cost ratio values obtained from the application of various fertilizer rates were above two indicating that the entire applied fertilizer rates had a reasonable threshold for covering the risk associated with fertilizer application among financially constrained smallholder farmers. However, the net

benefit-to-cost ratio for the unfertilized treatment of CI-8251, SRCPX80Ab2291, Sorataf, and combined analysis of oat varieties were 1.4, 1.8, 1.5, and 1.6, respectively, indicating their low profitability.

The total cost (fertilizer and labor costs) will be expected to rise in the future as a result sensitivity analysis was performed to estimate the economic profitability of oat grain production. The result of sensitivity analysis revealed that the MRR for forage type, grain type, and combined oat varieties at the rate of 150% (61.5 kg N + 30 kg P/ha) fertilizer application as well as the dual type oat which received 175% (71.8 kg N + 35 kg P/ha) fertilizer will be expected to be 222.8, 272.2, 135.1, and 110.3%, respectively. This indicated that the MRR values are still above 100% indicating that the recommended fertilizer levels for each oat variety and combined analysis of oat varieties will be profitable when the total cost increases to 100% (20% per annum) for the coming five years. If the TC increases by 100% in the next five years, farmers who cultivate oat using the application of fertilizer at the rate of 150% for forage type, grain type, and combined analysis of oat varieties as well as 175% fertilizer application for the dual type oat can earn 2.2, 2.7, 1.4, and 1.1 ETB for every unit of Ethiopian birr investment, respectively.

5.4.3 Fodder nutritional quality

5.4.3.1 Analysis of variance

The pooled analysis of variance indicated that all nutritive values except ash and cellulose contents varied significantly among oat varieties. This indicated that the studied oat varieties had substantial inherent genetic variations for measured parameters. The variations in nutritive value among oat varieties were also reported by different scholars (Fekede *et al.*, 2008; Chaturvedi *et al.*, 2020; Gezahagn *et al.*, 2021; Chawla *et al.*, 2022; Gezahagn *et al.*, 2023b). Moreover, all the measured nutritive parameters were influenced significantly by fertilizer application. Different scholars also reported that the application of fertilizer had substantial effects on nutritive value of oat varieties (Ratan *et al.*, 2018; Kumar *et al.*, 2023). The cropping seasons also had significant effect on all measured nutritive parameters except ash, cellulose, and IVDMD. The existence of variations between the two cropping seasons might be associated with differences in the amount and distribution of precipitation and variations in minimum and maximum temperatures. The effect of production year on nutritive value of oat varieties were

also reported (Mut *et al.*, 2015; Gezahagn *et al.*, 2021). The interaction effect of variety by fertilizer was significant for about 81.8% of the studied parameters. This is due to the differential response of varieties on fertilizer application and/or the differential influence of fertilizer on the performance of oat varieties. Moreover, the interaction effect of variety by year was significant for 36.4% of the studied parameters due to the differential response of varieties for year variability and/or the production year influences the varieties differently. The three-way interaction was also significant for 86.4% of the studied parameters due to either the differential influence of at least one factor on these measured parameters or the combined influence of all factors (variety, fertilizer, and year) on these measured parameters.

5.4.3.2 Herbage Nutritional values

5.4.3.2.1 Ash contents

Ash is the inorganic residue that is left after removing the organic materials from the dried plant samples using high temperatures. It defines the amount of essential mineral concentration that is present in the feed and indicates the extent of nutritional value of fodder. Its concentration in the feed can be affected by factors of genetics, morphological fractions, harvesting stages, and weather, soil, and management conditions. The ash content in this study indicated that the Sorataf variety sown with 125% fertilizer rate had 42.3% higher ash content compared to the CI-8251 variety sown with 25% fertilizer rate. Similarly, the Sorataf variety sown in 2021 gave 14.7% higher ash content than the same variety sown in 2020 cropping season. The studies also indicated that the ash content increased with increasing nitrogen fertilization which improves the level of nutrients in plants (Ruso, 2006; Kumari *et al.*, 2014). The variation of ash content in different forage crops was also reported (Fekede, 2004; Ayub *et al.*, 2011; Khan *et al.*, 2014; Samal *et al.*, 2023). The variation in ash content among forage crops might be due to differences in nutrient absorption from soil and efficient utilization of nutrients for growth and development. Like protein, carbohydrates, fat, and vitamins, minerals are the major nutrients and play an important role in animal nutrition, production, health, and reproduction (Sharma *et al.*, 2007; Bindari *et al.*, 2013; Katoch *et al.*, 2018). Deficiencies of one or more essential minerals may lead to poor performance of animals because lack of minerals in the feed generally depressed the feed intake and its utilization in different categories of livestock (Underwood, 1981). Thus, animals require an optimum level of minerals for their better

production and health. However, most forage crops are deficient in various essential minerals and the deficient minerals should be supplemented to enhance livestock production (McDowell and Conrad, 1990). Moreover, the rumen microorganisms require different essential minerals for their growth and metabolism, and deficiencies of one or more minerals could depress the fiber digestion and protein synthesis ability of the rumen microorganisms (Spears, 1994). Therefore, the selection of high ash-producing varieties is very important to improve livestock production and productivity.

5.4.3.2.2 Fiber contents

Forage contains a substantial portion of plant cell-wall (40-80%) and the amount and type of plant cell-wall greatly influences its utilization by animals. The insoluble portion of the forage (NDF) contains cellulose, hemicellulose, lignin, and silica. A young plant cell has a single outer layer (primary cell wall) and a thicker secondary cell wall is developed inside the cell with advancing plant maturity. The higher NDF content with advancing plant maturity generally limits the dry matter intake. In this study, the Sorataf variety sown with 100% fertilizer rate in 2020 had 11.9% higher NDF content over the CI-8251 variety sown with 150% fertilizer rate in 2021 cropping season. Studies also indicated that the application of nitrogen fertilizer generally decreases the NDF polysaccharides contents (cellulose, hemicellulose, and lignin) in the feed and these cell wall polysaccharides are usually degradable if non-lignified (Kumar, 2001; Bhilare and Joshi, 2007; Patel *et al.*, 2007; Balabanli *et al.*, 2010). At the early growth stages, the hemicellulose and lignin contents are very low due to a higher leaf-to-stem ratio and lower lignification of the tissue that resulted in lower NDF content which is desirable for animals. According to Van Soest (1982), grasses are classified as poor quality when the NDF content is above 600 g/kg DM and it could be classified as moderate quality when the NDF content ranges from 500-600 g/kg DM. According to the recommendation of NRC (2001), the minimum NDF contents are 250-290 g/kg DM during early lactation and 320-340 g/kg DM during mid to late lactation.

The ADF is the least digestible fiber portion of forage and this highly indigestible part of forage includes cellulose, lignin, silica, and insoluble forms of nitrogen. The forage becomes less digestible when the ADF increases with advancing maturity. The lower lignin content in the feed produces lower ADF content which is desirable for better animal production. In this study,

the SRCPX80Ab2291 variety sown with 100% fertilizer rate in 2020 had 20.1% higher ADF content than the Sorataf variety sown with the same fertilizer level in 2021 cropping season. The studies also indicated that the ADF content decreased with increasing levels of nitrogen fertilization in different fodder crops (Kering *et al.*, 2011; Sharma *et al.*, 2012; Kumari *et al.*, 2014; Paul *et al.*, 2014). The NDF content lies within the range of 55 to 76% and the ADF falls between 33 to 59% reported for high-quality roughages (Nsahlai *et al.*, 1996). High fiber content (NDF and ADF) reduces the voluntary intake and amount of digestible energy from feedstuff. Njidda (2014) also reported that moderate levels of NDF and ADF at early growth stages may be responsible for high digestibility in fodder crops.

The main structural components of cell walls are complex carbohydrates, cellulose, and hemicellulose. With advancing maturity, the plant's primary and secondary cell walls develop a non-carbohydrates complex compound (lignin) which gives the plant additional tensile strength and rigidity. Lignin is a non-digestible cell-wall material and its presence limits the fermentation of the cellulose and hemicellulose portion of the forage using rumen microorganisms. In this study, the SRCPX80Ab2291 variety sown with 75% fertilizer rate in 2020 had 136.5% higher ADL content than the same variety sown with 175% fertilizer rate in the 2021 cropping season. Similarly, the Sorataf variety sown with 100% fertilizer rate in 2020 had 18.2% higher HC content than the SRCPX80Ab2291 variety sown with 125% fertilizer rate in the 2020 cropping season. Moreover, the Sorataf variety sown without fertilizer in 2020 had 30.4% higher C content than the same variety sown with 125% fertilizer rate in the same cropping season. Studies also indicated that fertilizer application enhances plant growth, leaf number, and tiller number resulting in fiber reduction in the feed which leads to higher feed intake and digestibility (Chanthakhoun *et al.*, 2012; Mupenzi *et al.*, 2017).

The digestibility of forage is highly affected by lignin concentration when compared to other chemical components (Van Soest and Robertson, 1979; Van Soest, 1982; Jung and Allen, 1995; Katoch *et al.*, 2018). The ADL content substantially influences the digestibility of feed when the content exceeds 60 g/kg DM (Van Soest, 1982). The digestibility of cell wall carbohydrates is highly limited when a small amount of lignin is present in the feed because the digestibility of the feed is inversely associated with lignin concentration (Ford *et al.*, 1979; Van Soest, 1994; Mustafa *et al.*, 2000). Van Kuijk *et al.* (2015) also stated that the digestion of cellulose and

hemicellulose contents by rumen microorganisms is highly limited by one of the main constituents of plant cell wall (ADL content). Wolf *et al.* (1993) and Lundvall *et al.* (1994) also stated that the presence of higher hemicellulose content in the feed substantially depressed the intake and digestibility of forage by animals. The ruminants have bacteria and microbes in their digestive tract and due to the existence of symbiotic relationships between animals and microbes in the rumen digestive system, the animals can ferment the cell-wall compounds (cellulose and hemicellulose) into useable nutrients. Moore and Hatfield (1994) and Cardinal *et al.* (2003) reported that the digestion of cell walls was significantly influenced by cellulose content in the feed.

5.4.3.2.3 Crude protein content and its yield and digestibility

The CP content of the forage is one of the most important criteria for determining the nutritional quality of livestock feeds (Caballero *et al.*, 1995; Bali *et al.*, 1998; Abdalla *et al.*, 2007; Edwin *et al.*, 2012). The feed intake, rumen microbial growth, and nutrient assimilation efficiency of animals increased with increasing levels of CP in the feed (McDonald *et al.*, 2010; Katoch *et al.*, 2018). The CP content of feeds generally varies with species, stage of maturity, morphological fractions, weather, soil fertility, and management conditions. In this study, the interaction effect of variety by fertilizer by year was significant for CP, CPY, and DCP. Accordingly, the Sorataf variety sown with 175% fertilizer rate in 2020 had 140.9% higher CP over the CI-8251 variety sown with 75% fertilizer rate in the same cropping season. Similarly, the Sorataf variety sown with 175% fertilizer in 2020 had 315.0% higher CPY than the same variety sown without fertilizer in the same cropping season. Moreover, the Sorataf variety sown with 175% fertilizer rate in 2020 had 785.7% higher DCP than the CI-8251 variety sown with 75% fertilizer rate in the same cropping season. The variation in CP content among oat varieties was also reported (Fekede, 2004; Dabhi *et al.*, 2017; Gezahagn *et al.*, 2021; Gezahagn *et al.*, 2023e; Samal *et al.*, 2023). The increase in CP content with increasing nitrogen fertilizer is reported in different forage crops (Rostamza *et al.*, 2011; Tajul *et al.*, 2013; Kumari *et al.*, 2014; Abraha *et al.*, 2015; Ratan *et al.*, 2016; Shekara *et al.*, 2021).

The optimum CPY was attributed to higher forage dry matter yield (FDMY) and CP content with increasing levels of fertilizer application. Application of fertilizer generally enhances the CPY in forage because fertilizer improves the accumulation of photosynthates which leads to

higher FDMY production and also fertilizer increases nitrogen accumulation and its conversion to protein in different forage crops (Joshi *et al.*, 2012; Choudhary and Prabhu, 2014; Ratan *et al.*, 2018; Shekara *et al.*, 2019; Prajapati *et al.*, 2020). Moreover, the application of optimum phosphorus, which is an essential component of DNA and RNA, enhances protein synthesis which leads to higher CP and CPY. The roughages were classified as high, medium, and low when the CP content ranged from 10–15, 7–9, and 3–6, respectively (Nsahla *et al.*, 1996). The ruminants required the CP content of 60–70 g/kg DM for maintenance (Smith, 1993); 80–130 g/kg DM for moderate milk production (10–15 kg/cow/day) by dairy cows (Humphreys, 1991); and about 150 g/kg DM for high milk production (> 15 kg/cow/day) of dairy cows (ARC, 1984). However, the voluntary feed intake is significantly declined when the CP content of the feed is below 60–70 g/kg DM (Minson, 1990).

5.4.3.2.4 Feed digestibility

Feeds with higher protein and lower fiber contents usually have better digestibility potential by different categories of animals. The digestibility of feed is influenced by species, harvesting stage, soil fertility, and management conditions. In this study, the interaction effect of variety by fertilizer by year was significant for IVDMD, TDN, and DDM. The Sorataf variety sown with 50% fertilizer rate in 2021 had 27.7% higher IVDMD over the same variety sown with 25% fertilizer in the same cropping season. Similarly, the Sorataf variety sown with 100% fertilizer rate in 2021 had 5.5% higher TDN and DDM over the SRCPX80Ab2291 variety sown with 100% fertilizer in 2020 cropping season. The TDN includes the digestible crude protein, crude fiber, starch, sugars, and fats. Thus, the digestibility of the TDN depends on the relative proportion of its components. The variation in IVDMD was also reported in different forage crops (Fekede, 2004; Gezahagn *et al.*, 2021; Kaur *et al.*, 2021; Gezahagn *et al.*, 2023f). The increase in IVDMD with increasing nitrogen fertilizer was also reported in different forage crops (Pathan *et al.*, 2012; Kaur *et al.*, 2021). The increase in IVDMD with increasing fertilizer might be associated with a decrease in fiber and cell wall contents of the feed (Yalchi and Hajieghrari, 2010). The IVDMD is highly depends on the contents of cellulose and hemicellulose which in turn affected by the extent of lignification and fiber concentration (Luthra *et al.*, 1988; Van-Soest and Jones, 1968). The ruminants required about 550 g/kg DM IVDMD for maintenance (Smith, 1993); 600–700 g/kg DM for moderate milk production (10–

15 kg/cow/day) by dairy cows (ARC, 1984); and above 700 g/kg DM for high milk production (>15 kg/cow/day) by dairy cows (ARC, 1984).

The DY is influenced significantly by the application of fertilizer, variety, and year of production. The DY increased with increasing levels of fertilizer. Application of 175% fertilizer rate gave 92.5% higher DY over unfertilized treatment. Among oat varieties, SRCPX80Ab2291 gave 6.3% higher DY over Sorataf variety. The second year of production had a 7.4% higher DY over the first year. The variation in DY among oat varieties was also reported (Gezahagn *et al.*, 2021; Gezahagn *et al.*, 2023f). The TDNY also varied significantly for fertilizer, variety, and year effects. The TDNY generally increased with increasing levels of fertilizer application. Application of 175% fertilizer rate had 25.3% higher TDNY over unfertilized treatment. Among oat varieties, CI-8251 gave 141% higher TDNY over the Sorataf variety. The second year of production produced 5.6% higher TDNY than the first year of production.

5.4.3.2.5 Feed intake and its relative value and quality

The quality of feed is usually determined using physical, chemical, and biological values of the feed. Higher quality feeds generally have higher voluntary DMI with lower refusal of feeds which resulted in efficient conversion of feed for higher production. The RFV is an index used to measure the quality of alfalfa and other forages using the values of NDF and ADF. The NDF is used as an indicator of forage intake and ADF is used as an indicator of digestibility. Thus, this index is used to measure the quality of feed based on the potential feed intake (NDF) and digestibility (ADF) of fiber (Undersander and Moore, 2002). At full boom of alfalfa, the RFV is taken as 100 and the quality of feed decreases when the RFV is lower than 100 while the quality of feed increases with increasing level of RFV. Dunham (1998) reported that the quality of feed decreased when the RFV decreased below 100 and its quality increased when the value increased above this threshold level. Dunham (1998) also stated that feed with RFV greater than 100 is considered to be of better quality than full-bloom alfalfa hay and the values lower than this threshold have lower feed quality for higher productive animals. The CP content decreased when the NDF and ADF contents increased which resulted in decreased RFV of the feed. Forage with NDF value of 53% and ADF value of 41% has RFV of 100 (full bloom alfalfa). If forage has RFV lower than 100, it has lower feed quality compared with the forage containing

53% NDF and 41% ADF. The forage with RFV 100 would not be considered excellent forage because high milk-producing cows usually require RFV of 150 or higher.

The RFQ is an improved version of RFV used to measure the quality of feed using the same numbers and scale as with RFV. However, the value of RFQ is higher than RFV and it accurately reflects the forage's true value because it accounts for true TDN instead of DDM (Moore and Undersander, 2002). This makes RFQ a better predictor of feed quality than RFV. In this study, the interaction effect of variety by fertilizer by year was significant for DMI, RFV, and RFQ. The CI-8251 variety sown with 100% fertilizer rate in 2021 had 14.9% higher DMI over the Sorataf variety sown with the same fertilizer rate in 2020 cropping season. Moreover, the CI-8251 variety sown with 100% fertilizer rate in 2021 had 19.6% and 19.7% higher RFV and RFQ, respectively, over the same oat variety sown with 125% fertilizer rate in 2020 cropping season. The variations in RFV were also reported in different forage crops (Habtamu *et al.*, 2013; Diriba *et al.*, 2014; Mekuanint *et al.*, 2015; Mut *et al.*, 2015; Akim *et al.*, 2019). According to Horrocks and Vallentine (1999) classification, the forage is considered prime, premium, good, fair, poor, and reject when its RFV is above 151, between 150–125, 124–103, 102–87, 86–75, and lower than 75, respectively. Based on this classification, the RFV of this study (85–101) falls in the fair and poor groups. Similarly, the value of RFQ (88–106) in this study falls in the good and fair groups. Thus, in an oat-based feeding system, high milk-producing cows should be supplemented with other high-quality feed.

5.4.3.2.6 Feed energy

The energy value of feeds is highly affected by the concentration of ADF which in turn is influenced by the stage of harvest. Highly digestible feeds usually provide high DE, ME, and NE for animals. The DE indicates the actual amount of energy obtained from the feed that can be available for use by animals. It is estimated by subtracting energy lost in feces from the gross intake energy. The ME can be used for the maintenance and production of animals. The ME can be partitioned into growth, or milk production, or reproduction, or used for draught power when the ME exceeds the maintenance needs. According to Nehring and Haenlein (1973), the energy value of feed can be determined using gross energy (GE), DE, ME, and NE. The energy value of forage is highly dependent on its quality which in turn is affected by species, maturity status, soil fertility, cropping season, and management conditions. In this study, the interaction effect of

variety by fertilizer by year was significant for DE, and ME. The CI-8251 and Sorataf varieties sown with 100% fertilizer rate in 2021 and the CI-8251 variety sown with 25% fertilizer rate in 2020 had 5.7% higher DE over the SRCPX8Ab2291 variety sown with 100% fertilizer rate in 2020 cropping season. The CI-8251 and Sorataf varieties sown with 100% fertilizer rate in 2021 had 5.9% higher ME over the SRCPX8Ab2291 variety sown with the same fertilizer rate in 2020 cropping season.

The NE is the portion of ME remaining after the energy used for body heat is removed. The NE is further partitioned into the net energy for maintenance (NEm—no gain or loss of body weight), net energy for gain (NEg—growth in body weight), and net energy for lactation (NEl—production of milk). The quality of feeds depends on the concentration of nutrients and energy value as well as the presence of anti-nutritional factors (Hanafey and Abdelnaser, 2013). The NE (NEl, NEm, and NEg) of the feed varied in different forage crops (Akim *et al.*, 2019). The application of fertilizer increased the NE value of the feed by increasing its feed quality. In this study, the interaction effect of variety by fertilizer by year was significant for NEl, NEm, and NEg. The CI-8251 and Sorataf varieties sown with 100% fertilizer rate in 2021 and the CI-8251 variety sown with 25% fertilizer rate in 2020 had 4.7% higher NEl over the Sorataf variety sown without fertilizer in the 2020 cropping season. Similarly, the Sorataf variety sown with 100% fertilizer rate in 2021 had 7.2% higher NEm over the SRCPX8Ab2291 variety sown with the same fertilizer rate in 2020 cropping season. Moreover, the CI-8251 and Sorataf varieties sown with 100% fertilizer in 2021 had 10.3% higher NEg over the SRCPX8Ab2291 variety sown with the same fertilizer rate in the 2020 cropping season.

5.4.3.3 Relationships among measured parameters

The Pearson correlation analysis indicated that fertilizer application had significant and positive association with FDMY, CP, CPY, DY, DCP, and TDNY indicating that fertilizer application for higher FDMY would also improve these nutritive values. Similarly, the FDMY had significant and positive association with CP, CPY, DY, DCP, TDNY, and DMI suggesting that indirect selection through these nutritional quality parameters would be effective for FDMY improvement in oat varieties. However, it had significant but inverse association with NDF and HC contents demonstrating that selection through these parameters would not be effective for FDMY improvement in oat varieties. Significant and positive associations between FDMY and

CPY in oat (Gupta and Mehta, 2019) and between FDMY and CP in lablab (Melkam *et al.*, 2023) were also reported. The ash content had significant and positive association with ADL and IVDMD. Moreover, the association of CP with IVDMD, CPY, DY, and DCP were significant and positive. Different scholars also reported that the CP associated significantly and positively with IVDMD in vetch (Gezahagn, 2011) and DCP in different forage crops (Yisehak and Janssens, 2013).

The NDF had significant and positive association with HC, ADF, and C contents while it had significant but inverse association with IVDMD, CPY, and DY. This indicated that oat varieties with higher NDF, ADF, HC, and C contents would have lower IVDMD, CPY, and DY. The NDF was also significantly and negatively associated with CPY in vetch (Gezahagn, 2011) and IVDMD in oat (Fekede, 2004) while it had significantly and positively correlated with ADF in oat (Mut *et al.*, 2015) and C in oat (Fekede, 2004). The ADF had significant and positive association with ADL and C while it had significant but inverse association with IVDMD. The ADF is also associated significantly and positively with ADL in vetch (Gezahagn, 2011) and also ADL and C contents in oat (Fekede, 2004). The ADL had significant but inverse association with C content. The HC content had significant but inverse association with IVDMD, CPY, DY, DMI, TDNY, RFV, and RFQ. The HC content is also associated significantly and negatively with CPY in vetch (Gezahagn, 2011). The fiber contents (NDF, ADF, ADL, and C) had significant but inverse associations with DMI, RFV, RFQ, TDNY, TDN, DDM, DE, ME, NEL, NEm, and NEg indicating that selection based on the above fiber contents would not be effective to improve these nutritional parameters in oat varieties. The NDF also had significant but inverse association with DMI and TDN in buffel grass (Alemayehu *et al.*, 2024). The study also indicated that the NDF and ADF contents were significantly and negatively correlated with RFV and TDN (Mut *et al.*, 2015). The NDF and ADF are also associated significantly and negatively with DDM, DMI, TDN, RFV, and NEL (Prajapati *et al.*, 2019). Moreover, the NDF and ADF were significantly and negatively associated with DE and ME (Yisehak and Janssens, 2013; Jung and Beob, 2021).

The IVDMD had significant and positive association with DY, DCP, TDN, DDM, DMI, RFV, RFQ, DE, ME, NEL, NEm, and NEg. This indicated that selection based on IVDMD would improve the aforementioned nutritional parameters in oat varieties. Similarly, the CPY had

significant and positive association with DY, DCP, DMI, and TDNY. Moreover, the DY had significant and positive association with DCP, DMI, RFV, RFQ, and TDNY. Furthermore, the association between DCP and TDNY was significant and positive. The association of TDN with DDM, DMI, RFV, and RFQ were significant and positive. The result is in close conformity with the findings of Prajapati *et al.* (2019) who reported that TDN had significant and positive association with DDM, DMI, and RFV. The DDM also had significant and positive association with DMI, RFV, and RFQ. Prajapati *et al.* (2019) also reported that DDM had significant and positive association with DMI and RFV. Moreover, the DMI had significant and positive association with RFV, RFQ, and TDNY. A significant and positive association between DMI and RFV is also reported (Prajapati *et al.*, 2019). The RFV also had significant and positive association with RFQ and TDNY. The association between RFQ and TDNY was significant and positive. Similarly, the associations of TDN, DDM, DMI, RFV, and RFQ with DE, ME, NEI, NEm, and NEg were significant and positive. Moreover, the associations between DE, ME, NEI, NEm, and NEg were significant and positive. The association between DE and ME was also significant and positive (Jung and Beob, 2021). The study also indicated that TDN, DDM, DMI, and RFV had significant and positive association with NEI (Prajapati *et al.*, 2019).

5.5 Conclusion

The study indicated that the application of NP fertilizer significantly improved fodder yield, yield components, nutrient concentration, nutrient uptake, and use efficiency in oat varieties. Application of 125% (51.3 kg N + 25 kg P/ha) fertilizer gave better growth and fodder yield which resulted in higher farm profit in the study area. Similarly, the application of NP fertilizer significantly increased the agro-morphological traits, nutrient concentration, nutrient uptake, nutrient use efficiency, and economic profitability of grain yield compared to unfertilized treatment. Based on this result, the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer could improve the grain yield productivity of oat varieties and farm profitability in the study area. Moreover, the nutritive value of oat varieties improved with the application of fertilizer. Therefore, the application of 125% fertilizer for fodder yield and nutritional quality and 150% for grain yield were recommended to improve the productivity of oat and nutritive value in the study area. However, these recommended rates should be verified by doing similar research under wider areas of oat-growing environments.

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Chapter VI

Experiment 4: Yield, nutrient uptake, nutrient and land-use efficiency and nutritional value of oat (*Avena sativa* L.) grown in oat/vetch mixed cropping system under different fertilizer levels



Yield, nutrient uptake, nutrient and land-use efficiency and nutritional value of oat (*Avena sativa* L.) grown in oat/vetch mixed cropping system under different fertilizer levels

Abstract

The study aimed to investigate the effect of fertilizer rates on agro-morphological traits, nutrient uptake and use efficiency, competitive ability, and economic feasibility of oat under oat/vetch mixed cropping and mixtures nutritive value at Holetta during the 2020/2021 and 2021/2022 cropping seasons. The oat/vetch mixture was sown with eight fertilizer rates (0, 25, 50, 75, 100, 125, 150, and 175%), and also sole oat and vetch were sown with their recommended fertilizer rates (100%) using a randomized complete block design with three replications. The results showed that fertilizer and year significantly affected all measured agro-morphological traits, nutrient concentration, and nutrient uptake and use efficiency of oat. Accordingly, all the measured agro-morphological traits of oat increased with increasing levels of fertilizer up to 150% (61.5 kg N + 30 kg P/ha), and the highest performance of oat was observed in the second year. Thus, applying 150% fertilizer gave a 107.4% fodder yield advantage over oat sown without fertilizer. The nutrient concentration of oat increased with increasing rates of fertilizer up to 175% (71.8 kg N + 35 kg P/ha). Similarly, the total fodder nutrient uptake of oat increased with increasing levels of fertilizer up to 150%. However, the nutrient use efficiency decreased with increasing levels of fertilizer and the highest efficiency was recorded from the application of 25% (10.3 kg N + 5 kg P/ha) fertilizer. Moreover, the Pearson correlation analysis indicated that the fodder yield of oat was associated significantly and positively with all measured agro-morphological traits, nutrient concentration, and uptake while it had significant and inverse associations with nutrient use efficiencies. The partial budget analysis also indicated that the application of 150% fertilizer rate produced the highest net benefit (97,854 birr/ha) and marginal rate of return (2287.7%). The productivity of oat under the oat/vetch mixed cropping system was also assessed using different indices. The results of biological efficiency showed that the over-yielding oat (OYO), land equivalent coefficient (LEC), area time equivalent ratio (ATER), and land equivalent ratio (LER) were higher in the first year while oat equivalent yield (OEY) and system productivity index (SPI) were recorded in the second year. All the values of measured biological efficiency increased with increasing fertilizer rates and the highest values were recorded from the application of 150% fertilizer. A higher crowding coefficient of oat (KO), actual yield loss of oat (AYLO), intercropping advantages of oat (IAO), and competitive ratio of oat (CRO) were higher in the first year. All the values of competitive indices except aggressivity of oat (AO) increased with increasing fertilizer rates up to 150%. The economic efficiency of oat/vetch mixtures showed that the higher values of monetary advantage index (MAI), relative value total (RVT), replacement value of intercropping (RVI), and relative net return index (RNRI) were recorded for the first year. Moreover, all the values of economic efficiency (MAI, RVT, RVI, and RNRI) increased with increasing fertilizer rates, and the highest values were recorded for the application of 150% fertilizer rate. All the nutritional value of oat/vetch mixtures varied significantly for fertilizer application. Moreover, the year had a significant effect on all measured nutritive values except ash and hemicellulose (HC) contents. All the nutritive values except fiber contents (NDF-neutral detergent fiber, ADF-acid detergent fiber, ADL-acid detergent lignin, HC, and C-cellulose) were higher in the second year. Among oat/vetch mixtures, the highest ash, crude protein yield (CPY), digestible dry matter (DDM), dry matter intake (DMI), in-vitro dry matter digestibility (IVDMD), digestible yield (DY), total digestible nutrients (TDN), total digestible nutrient yield (TDNY), relative feed value (RFV), and relative feed quality (RFQ) were recorded for application of 150% fertilizer rate. On the other hand, the NDF, ADF, ADL, and C contents decreased with increasing fertilizer rates and oat/vetch mixtures sown without fertilizer gave higher fiber contents. Application of 175% fertilizer rate on oat/vetch mixtures gave the highest crude protein (CP) and digestible crude protein (DCP) while mixtures sown without fertilizer gave the lowest values. Moreover, all the measured energy parameters increased with increasing fertilizer rates up to 150%. The Pearson correlation analysis also indicated that fertilizer application had significant and inverse associations with NDF, ADF, ADL, and C contents while it had significant and positive associations with the remaining measured parameters. Therefore, the application of 150% fertilizer rate would increase the fodder yield, competitive ability, and economic profitability of oat under oat/vetch mixture and nutritive value of mixtures.

Keywords: correlation, forage yield, indices, mixed cropping, nutrient uptake, nutrient use, nutritive value, partial budget

6.1 Introduction

Intercropping/mixed cropping is the simultaneous growing of two or more crops in the same field to intensify crop production in temporal and spatial dimensions (Mousavi and Eskandari, 2011; Rana *et al.*, 2013; Ashenafi, 2016; Walelign *et al.*, 2020). Among the types of intercropping, mixed cropping refers to the growing of two or more crop species together in the field without using any spatial and/or temporal configuration while strip intercropping refers to the growing of two or more crop species in separate, but adjacent, rows using spatial and/or temporal configuration (Bybee-Finley and Ryan, 2018). Different studies indicated that grass/legume mixed cropping has significant benefits that affect crop yield and has been considered an important practice in low-input crop production because the mixture crop species provide complementarities in the utilization of resources and sustains productivity (Watson *et al.*, 2002; Hauggaard-Nielsen *et al.*, 2003; Knudsen *et al.*, 2004; Vasilakoglou *et al.*, 2005; Ramos *et al.*, 2011). Mixtures of legumes with cereals are expected to have advantages over pure stands in terms of yield advantages (Getachew *et al.*, 2006; Dhima *et al.*, 2007), resources use efficiency (Jahanzad *et al.*, 2011; Walelign, 2020), yield stability (Dapaah *et al.*, 2003; Tsubo *et al.*, 2005), weed control (Banik *et al.*, 2006; Ashenafi, 2016), insect pest and disease control (Smith and McSorley, 2000), and return per unit area of land (Chu *et al.*, 2004).

Among different forage crops, oat (*Avena sativa* L.) is the most appropriate annual forage grass grown with vetch in mixed cropping systems (Thomson *et al.*, 1992; Getnet, 1999; Johnston *et al.*, 1999; Undersander, 2003; Ross *et al.*, 2004). Mixtures of oat and vetch have great potential for forage production and higher yields have been documented for intercropping of oat and vetch (Lithourgidis *et al.*, 2006; Ansar *et al.*, 2010; Gezahagn *et al.*, 2024a). The mixtures of oat-vetch produced higher yield than sole culture and the highest forage yield was reported at the ratio of 75/25 in oat/vetch seeding rates, respectively (Ansar *et al.*, 2013). Canan and Orak (2007) also reported that mixtures of oat/vetch were more productive than sole vetch sowing and the highest herbage yield was obtained from a mixture of oat/vetch while the lowest herbage yield was from sole stands of vetch.

Forage legumes with effective biological nitrogen fixation (BNF) can be grown with less applied nitrogen (N) fertilizer. The benefits of intercropping can be increased by applying fertilizer in an appropriate manner and at the right time and amount (Undie *et al.*, 2012). Fodder

nutrient uptake and use must be as efficient as possible to lower production costs and increase profit, given the growing expense of chemical fertilizers. Therefore, it is especially crucial to intercrop grasses with forage legumes in nations where N fertilizer is expensive and/or scarce. Due to their high cost, inorganic fertilizers are rarely used (Rebka *et al.*, 2013) however; legumes with strong BNF can be planted with cereals that require less N fertilizer. Because of the transfer of rhizome-deposited nitrogen from the legume to the associated grass, grasses under mixed cropping with legumes have the capacity to absorb more nitrogen than those under single cropping (Xiao *et al.*, 2004; Rasmussen *et al.*, 2007). The death and decay of the legumes' roots and root nodules (Laidlaw *et al.*, 1996), direct exudation from the legume roots (Paynel *et al.*, 2001), and hyphal links created by arbuscular mycorrhizal fungi between the legume and grassroots (He *et al.*, 2009) are a few routes of nitrogen transfer from the legume to the grass. Among these pathways, Laidlaw *et al.* (1996) reported that the death and decay of roots and root nodules of the legumes could be considered the major source of transferable N in the grass-legume mixed cropping system (Laidlaw *et al.*, 1996). Intercrops showed lower nutrient utilization efficiency than cereal monocultures under a high fertilizer application rate, indicating that intercrops with legumes required a lower amount of N to produce the same amount of yield. Lithourgidis and Dordas (2010), and Dordas and Lithourgidis (2011) also reported that the nutrient utilization efficiency of mixtures was lower than the cereal monocrops. Intercropping also significantly reduced N fertilizer utilization by 15– 50% with the additional benefit of 16– 30% higher productivity of wheat under wheat-faba bean intercropping (Xiao *et al.*, 2018).

Most studies on the intercropping/mixed cropping system focus on the plant population density of both cereal/grass and legume crops. The nutrient requirement of mixed cropping is completely different from that of the respective monocultures. However, in most mixed cropping, the amount of fertilizer used in mixed cropping is equal to that of the main crops (cereal/grass) recommendation. Accordingly, the application of fertilizer in a mixed cropping system may not meet the nutrient requirements of the component crops in the intercropping/mixed cropping system (Ghosh *et al.*, 2009; Rostaei *et al.*, 2015). The competition for soil resources is much higher than the competition for light under intercropping/mixed cropping systems (Ghosh *et al.*, 2006) and the use of the blanket recommendation of fertilizer for sole culture may not fulfill the nutrient demand of the intercropping/mixed cropping system (Fonduge *et al.*, 2001; Agoume and Birang, 2009). However, the effect of fertilizer application

on fodder yield, nutrient uptake, use efficiency, and economic profitability of oat under oat/vetch mixed cropping system and nutritional quality of oat/vetch mixtures has not been well studied and properly documented in Ethiopia. Therefore, this study was designed to: (i) evaluate the effect of fertilizer application on agro-morphological traits, nutrient uptake and use efficiency of oat under oat/vetch mixed cropping; (ii) assess the effect of fertilizers on biological efficiency and competitive indices of oat under oat/vetch mixtures and economic efficiency of mixed cropping; (iii) examine the effect of fertilizer rates on the nutritional value of oat/vetch mixture; (iv) determine the correlation coefficients for measured parameters of oat under oat/vetch mixed cropping; and (v) estimate the effect of fertilizer application on the profitability of oat under oat/vetch mixed cropping in the central highlands of Ethiopia.

6.2 Materials and Methods

6.2.1 Description of the study site

The study was conducted during the main cropping seasons of 2020/2021 and 2021/2022 at Holetta Agricultural Research Center (HARC) (09°03'42"N, 38°29'59"E, and at an altitude of 2400 meters above sea level) in the central highlands of Ethiopia ([Figure 6.1](#)). The long term (50-year: 1970-2019) and cropping seasons (2020/2021 and 2021/2022) precipitation, minimum and maximum temperatures of the study area are indicated in [Table 6.1](#). The soil samples were collected from 0 to 20 cm of soil depth at both cropping seasons before planting. After manual homogenization of the soils, the samples were ground to pass a 2-mm sieve and analyzed at HARC following the standard soil analysis procedures. Accordingly, the soil physico-chemical properties of the study site are presented in [Table 6.2](#). The soil type of the area is acidic Eutric Nitosol and the study area is characterized by a mixed crop-livestock production system (Gezahagn *et al.*, [2023](#)).

6.2.2 Experimental treatments and design

The oat/vetch mixed cropping system was sown with 0, 25, 50, 75, 100, 125, 150, and 175% of the recommended fertilizer levels (100 kg/ha DAP at sowing and 50 kg/ha urea at tillering) for oat in Ethiopia ([Table 6.3](#)). Moreover, sole oat and sole vetch were sown using their recommended fertilizer rate of 20 kg P/ha + 41 kg N/ha and 20 kg P/ha + 18 kg N/ha, respectively. Among vetch species, wooly-pod vetch (*Vicia dasycarpa*) and hairy vetch (*Vicia*

villosa) seem to be the well-adapted species to the Ethiopian highlands (Astatke, 1984; Lulseged *et al.*, 1996). However, *Vicia villosa* was used for this study due to its better performance at Holetta conditions. At sowing, the recommended seeding rate of 100 kg/ha for sole oat (Astatke, 1979) and 25 kg/ha for sole *Vicia villosa* (Gezahagn, 2011) were used. Moreover, 75/25% of the sole recommended seeding rate (i.e. 75 kg/ha oat and 6.25 kg/ha *Vicia villosa*) were used for oat/vetch mixed cropping system (Astatke, 1979; Lulseged, 1981). The experiment was conducted using a randomized complete block design (RCBD) with three replications. The treatment randomization was performed using PROC PLAN seed procedures of the SAS general linear model version 9.4 (SAS, 2012). Each treatment was sown to a plot area of 4 m² consisting of 5 rows of 4 m length and 1 m width with 0.2 m row spacing. The spacing between plots and blocks was 0.5 m and 1.5 m, respectively. One outermost row at both sides and 0.10 m row length from both sides of row endings were left as guard rows to avoid the border effects on treatment. Thus, three rows with a net plot size of 3.8 m by 0.6 m (2.28 m²) were used for data collection. Seeds of both crops (oat and vetch) were rejuvenated during the main cropping season of 2019/2020 under the same management condition at HARC to avoid the initial variation due to differences in seed age and seed nitrogen (Liao *et al.*, 2008; Gemechu, 2012).

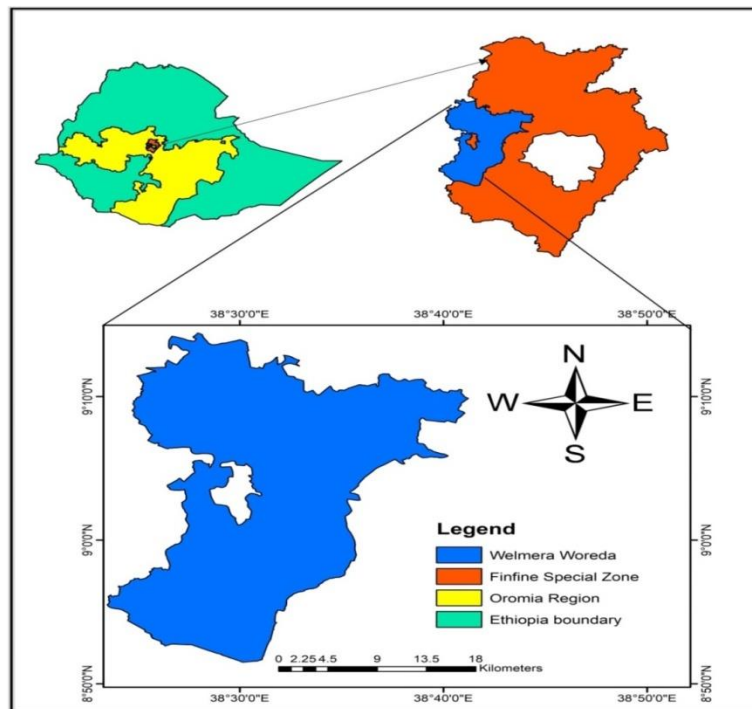


Figure 6.1 Map of the experimental site of Holetta (Welmera Woreda) in the central highlands of Ethiopia

Table 6.1 Monthly total rainfall and average minimum and maximum temperatures during the cropping seasons (2020/2021 and 2021/2022) and 50-year (1970–2019) at Holetta

Months	50 years (1970-2019)			2020/2021			2021/2022		
	Min. temp (°C)	Max. temp (°C)	Rainfall (mm)	Min. temp (°C)	Max. temp (°C)	Rainfall (mm)	Min. temp (°C)	Max. temp (°C)	Rainfall (mm)
January	3.6	23.3	17.0	5.3	24.4	0.0	3.0	23.6	3.6
February	5.1	24.0	31.0	6.5	24.4	0.0	6.8	24.6	84.8
March	6.8	24.5	53.5	8.1	25.6	73.2	6.4	25.5	16.2
April	8.2	23.8	74.5	9.0	25.2	92.4	7.4	25.4	53.4
May	9.0	24.4	66.1	9.2	24.6	100.6	8.5	24.7	87.6
June	7.8	22.6	118.8	9.0	23.2	126.1	8.2	24.6	127.8
July	9.2	20.2	238.9	9.8	21.4	263.4	8.3	22.3	304.1
August	9.1	19.7	252.7	9.7	20.6	334.2	8.8	21.8	287.6
September	7.7	20.4	130.5	8.6	21.2	216.2	9.1	21.9	250.9
October	4.9	22.0	21.4	5.7	22.8	31.6	7.5	23.0	73.6
November	2.4	22.5	10.0	2.8	23.6	8.0	4.4	24.8	0.0
December	1.8	22.9	5.3	2.0	23.1	3.2	2.4	24.7	0.0
Mean/annual	6.3	22.5	1019.6	7.1	23.4	1248.9	8.7	23.9	1289.6

Table 6.2 Description of the test location for physico-chemical properties of the soils

Parameter	Cropping season		References for methods of analysis
	2020/21	2021/22	
pH (1:2.5 H ₂ O)	5.40	5.20	McLean, 1982
OC (%)	1.91	1.75	Walkley and Black, 1934
P (ppm)	18.52	9.86	Bray and Kurtz, 1945
TN (%)	0.19	0.18	Nelson and Sommers, 1982
CEC (meq/100g)	21.07	20.97	Black, 1965
Sand (%)	15.00	11.50	Bouyoucos, 1996
Silt (%)	27.50	24.50	Bouyoucos, 1996
Clay (%)	57.50	64.00	Bouyoucos, 1996
Textural class	Clay	Clay	Rowell, 1994

pH = power of hydrogen; OC = organic carbon; TN = Total nitrogen; C/N = carbon to nitrogen ratio; AP = Available phosphorus; CEC = cation exchange capacity; ppm = parts per million; meq = milliequivalent.

Table 6.3 List of experimental treatments for the study

SN	Forage crops	Recommended fertilizer rate (%)	Tested fertilizer rate
1	SRCPX80Ab2806/ <i>Vicia villosa</i>	0	0/0 kg/ha DAP/Urea
2	SRCPX80Ab2806/ <i>Vicia villosa</i>	25	25/12.5 kg/ha DAP/Urea
3	SRCPX80Ab2806/ <i>Vicia villosa</i>	50	50/25 kg/ha DAP/Urea
4	SRCPX80Ab2806/ <i>Vicia villosa</i>	75	75/37.5 kg/ha DAP/Urea
5	SRCPX80Ab2806/ <i>Vicia villosa</i>	100	100/50 kg/ha DAP/Urea
6	SRCPX80Ab2806/ <i>Vicia villosa</i>	125	125/62.5 kg/ha DAP/Urea
7	SRCPX80Ab2806/ <i>Vicia villosa</i>	150	150/75 kg/ha DAP/Urea
8	SRCPX80Ab2806/ <i>Vicia villosa</i>	175	175/87.5 kg/ha DAP/Urea
9	Sole oat: SRCPX80Ab2806	100	100/50 kg/ha DAP/Urea
10	Sole vetch: <i>Vicia villosa</i>	100	100 kg/ha DAP

DAP = diammonium phosphate (100 kg DAP = 18/46 kg N/P₂O₅ or 18/20 N/P); 100 kg Urea = 46 kg N; 0% = 0/0 kg/ha DAP/Urea; 25% = 25/12.5 kg/ha DAP/Urea; 50% = 50/25 kg/ha DAP/Urea; 75% = 75/37.5 kg/ha DAP/Urea; 100% = 100/50 kg/ha DAP/Urea; 125% = 125/62.5 kg/ha DAP/Urea; 150% = 150/75 kg/ha DAP/Urea; 175% = 175/87.5 kg/ha DAP/Urea. SRCPX80Ab2806 = oat variety; *Vicia villosa* = vetch species

6.2.3 Data collection

6.2.3.1 Agro-morphological traits

Data were collected either on a plot basis or from five randomly selected oat plants per plot under oat/vetch mixed cropping system. Data collected on a plant basis were the number of tillers per plant (NTPP), tillers dry weight (TDW), number of leaves at forage harvest (NLFH), leaf length at forage harvest (LLFH), and plant height at forage harvest (PHFH). Similarly, the plot basis data were also collected on days to forage harvest (DFH), oat forage dry matter yield (OFDMY), vetch forage dry matter yield (VFDMY), total forage dry matter yield (TFDMY), oat forage yield production rate (OFYPR), and total forage yield production rate (TFYPR). These data were collected following the standard procedures (For detail see [Table 3.3](#); [Chapter 3](#)). The oat and vetch fodder yields were estimated at their recommended harvesting stages. Accordingly, the oat forage dry matter yield (OFDMY) and total forage dry matter yield (TFDMY) were determined at the soft dough stage of the oat while the vetch forage dry matter yield (VFDMY) was estimated at 50% flowering of vetch. The oat/vetch mixtures harvested at soft dough stage was used to determine the TFDMY. Moreover, the harvested herbage samples from oat/vetch mixtures were separated into oat and vetch. The oat and vetch samples were separately weighed using a spring balance and the weight was taken as total fresh weight for each crop. From weighed samples, about 500 g sample for oat and vetch was taken from each plot and submitted for yield determination. From the submitted 500 g samples, a 300 g sample was taken from oat and vetch using a sensitive table balance at the laboratory and then oven-dried for 24 hours at a temperature of 105 °C to estimate the oven-dry weight.

6.2.3.2 Nutrient uptake and use efficiency

The fodder yield was harvested at the recommended forage harvesting stage to determine the nutrient concentration, nutrient uptake, and use efficiency of oat under oat/vetch mixed cropping and sole cultures. About 500 g fodder samples were taken from each plot and oven-dried at 65 °C for 72 h and then ground to pass a 1 mm sieve to determine the concentration of nitrogen (N) using Kjeldahl digestion (Nelson and Sommers, [1982](#)) and phosphorus (P) using the Molybdenum blue method (Mills and Jones, [1996](#)). The fodder nutrient uptake was estimated by multiplying the fodder yield with the respective N and P concentrations and then dividing by 100. Total forage nutrient uptake (TFNU) is the sum of forage phosphorus uptake (FPU) and

forage nitrogen uptake (FNU). Moreover, the nutrient use efficiency for partial factor productivity (PFP), partial nutrient balance (PNB), internal utilization efficiency (IUE), agronomic efficiency (AE), and agro-physiological efficiency (APE) were estimated as reported by other scholars (Fageria and Barbosa, 2007; Getachew *et al.*, 2016; Niaz *et al.*, 2016). The nutrient use efficiency were determined using different equations (For detail see Table 5.3; Chapter 5).

6.2.3.3 Assessment on the performance of mixed cropping

6.2.3.3.1 Determination of biological efficiency

Different indices of biological efficiency were developed to measure the effect of intercropping and mixed cropping for different crops (Getachew *et al.*, 2006; Getachew *et al.*, 2008; Sadeghpour *et al.*, 2013a; Choudhary, 2014; Yaseen *et al.*, 2014; Yayeh *et al.*, 2014; Doubi *et al.*, 2016; Gitari *et al.*, 2020). The indices used in this study were land equivalent ratio (LER), land equivalent coefficient (LEC), area time equivalent ratio (ATER), land use efficiency (LUE), system productivity index (SPI), over yielding oat (OYO), and oat equivalent yield (OEY). The equation of these biological efficiency indices and their descriptions are indicated in Table 6.4. The average market price (two seasons) for one kg oat fodder was 7.65 Ethiopian birr (ETB) while for vetch, it was 8.10 ETB.

6.2.3.3.2 Estimation of competitive indices

Among the different indices developed, relative crowding coefficient (K), aggressivity (A), competitive ratio (CR), actual yield loss (AYL), and intercropping advantage (IA) were used in this study to measure the competitive indices of mixed cropping (Ghosh, 2004; Dhima *et al.*, 2007; Yang *et al.*, 2017; Machiani *et al.*, 2018; Ashenafi, 2020). The equations of these competitive indices with their descriptions are indicated in Table 6.5.

6.2.3.3.3 Assessment of economic efficiency

The economic efficiency of different crops under mixed cropping systems was evaluated using various indices (Ghosh, 2004; Darabad *et al.*, 2011; Gitari *et al.*, 2020). The indices of economic efficiency used in this study were the monetary advantage index (MAI), relative value total (RVT), replacement value of intercropping (RVI), and relative net return index (RNRI). The

equation used to estimate the economic efficiency of mixed cropping and their descriptions are indicated in [Table 6.6](#).

Table 6.4 Indices of biological efficiency and their descriptions used to assess the performance of oat and oat/vetch mixtures under mixed cropping system

Indices	Abbreviations	Formula/ equation	Descriptions	References
The land equivalent ratio of oat	LER _{ij}	$LER_{ij} = \frac{Y_{ij}}{Y_{ii}}$	The positive effect of intercropping when LER > 1. But, intercropping has negative effects when LER < 1. No intercropping effect when LER = 0.	Ofori and Stern, 1987; Yayeh <i>et al.</i> , 2014
The land equivalent ratio of the total	LER _T	$LER_T = \frac{Y_{ij}}{Y_{ii}} + \frac{Y_{ji}}{Y_{jj}}$		
Land equivalent coefficient	LEC	$LEC = \frac{Y_{ij}}{Y_{ii}} \times \frac{Y_{ji}}{Y_{jj}}$	For a two-crop mixture, the minimum expected productivity coefficient is 25%, that is, a yield advantage is obtained if LEC value > 0.25.	Adetiloye <i>et al.</i> , 1983; Choudhary, 2014
Area time equivalent ratio	ATER	$ATER = \frac{(LER_{ij} \times t_i) + (LER_{ji} \times t_j)}{T}$	If ATER > 1, productive advantage occurs; if ATER = 1 no productive advantage occurs; and if ATER < 1, a productive disadvantage occurs.	Mead and Willey, 1980; Doubi <i>et al.</i> , 2016
Land use efficiency	LUE	$LUE = \left(LER_T + \frac{ATER}{2} \right) \times 100$	The higher the LUE value indicates better intercropping advantages and vice versa.	Mead and Willey, 1980; Yaseen <i>et al.</i> , 2014
System productivity index	SPI	$SPI = Y_{ij} + \left(\frac{Y_{ii}}{Y_{jj}} \right) \times Y_{ji}$	The higher the SPI, the more productive the intercropping system and vice versa.	Odo, 1991; Getachew <i>et al.</i> , 2008
Over yielding oat	OYO	$OYO_{ij} = \left(\frac{Y_{ij} - Z_{ij} \times Y_{ii}}{Z_{ij} \times Y_{ii}} \right) \times 100$	Positive over-yielding indicates an advantage and a negative value denotes a yield disadvantage of the intercropping system.	Li <i>et al.</i> , 2011; Sadeghpour <i>et al.</i> , 2013b
Oat equivalent yield	OY	$EY_i = Y_i + \left(\frac{Y_j \times P_j}{P_i} \right)$	The highest value of OEY indicates the highest yield of the main crop (oat) under a mixed cropping system.	Prasad and Srivastava, 1991; Getachew <i>et al.</i> , 2006

LER_{ij} = land equivalent ratio of oat in the intercrop; LER_{ji} = land equivalent ratio of vetch in the intercrop; LER_T = land equivalent ratio of the total; Y_{ij} = yield of oat in the intercropping; Y_{ii} = yield of oat in the pure stand; Y_{ji} = yield of vetch in the intercropping; Y_{jj} = yield of vetch in the pure stand; t_i = growth period in days between planting and forage harvesting for oat; t_j = growth period in days between planting and forage harvesting for vetch; T = the duration of the component crop with the longest growing period; Z_{ij} = sown proportion of oat in the intercropping; P_i = market price of oat; P_j = market price of vetch; 1kg dry oat fodder = 7.30 ETB on January 01, 2021, and 8.00 ETB on January 01, 2022, with a mean of 7.65 ETB; 1 kg dry vetch fodder = 7.80 ETB on January 01, 2021 and 8.40 ETB in January 01, 2022 with a mean of 8.10 ETB; ETB = Ethiopian birr.

Table 6.5 Competitive indices and their descriptions used to assess the performance of oat and oat/vetch mixtures under a mixed cropping system

Indices	Abbreviations	Formula/ equation	Descriptions	References
Relative crowding coefficient of oat	K_{ij}	$K_{ij} = \frac{Y_{ij} \times Z_{ji}}{(Y_{ii} - Y_{ij}) \times Z_{ij}}$	If the product of the two coefficients is > 1, there is a yield advantage for intercropping whereas $K = 1$ indicates of no yield advantage. When $K < 1$, there is a yield disadvantage of the intercropping system compared with monoculture.	de Wit, 1960; Ghosh, 2004
Relative crowding coefficient of total	K_T	$K_T = \left(\frac{Y_{ij} \times Z_{ji}}{(Y_{ii} - Y_{ij}) \times Z_{ij}} \right) \times \left(\frac{Y_{ji} \times Z_{ij}}{(Y_{jj} - Y_{ji}) \times Z_{ji}} \right)$		
Aggressivity of oat	A_{ij}	$A_{ij} = \left(\frac{Y_{ij}}{Y_{ii} \times Z_{ij}} \right) - \left(\frac{Y_{ji}}{Y_{jj} \times Z_{ji}} \right)$	A positive A_{ij} indicates the dominance of oat over vetch when it is negative; it indicates that vetch is the dominating species. If $A_{ij} = 0$ both crops in the intercropping system are equally competitive.	McGilchrist, 1965; Machiani <i>et al.</i> , 2018
Competitive ratio of oat	CR_{ij}	$CR_{ij} = \left(\frac{LER_{ij}}{LER_{ji}} \right) \times \left(\frac{Z_{ji}}{Z_{ij}} \right)$	The $CR_{ij} < 1$ indicates positive benefits for intercropping and the species can be grown in a mixture.	Willey and Rao, 1980; Dhima <i>et al.</i> , 2007
Actual yield loss of oat	AYL_{ij}	$AYL_{ij} = \left(\frac{Y_{ij} \times Z_{ii}}{Z_{ij} \times Y_{ii}} \right) - 1$	The positive and negative values of the AYL indicate the advantages and disadvantages of the intercropping system, respectively.	Banik, 1996; Yang <i>et al.</i> , 2017
Actual yield loss of total	AYL_T	$AYL_T = \left(\frac{Y_{ij} \times Z_{ii}}{Z_{ij} \times Y_{ii}} \right) - 1 + \left(\frac{Y_{ji} \times Z_{jj}}{Z_{ji} \times Y_{jj}} \right) - 1$		
Intercropping advantage of oat	IA_{ij}	$IA_{ij} = \left[\left(\frac{Y_{ij} \times Z_{ii}}{Z_{ij} \times Y_{ii}} \right) - 1 \right] \times P_i$	The highest the IA value indicates the lowest yield loss in the intercropping system and vice versa.	Banik, 1996; Ashenafi, 2020
Intercropping advantage of total	IA_T	$IA_T = \left[\left(\frac{Y_{ij} \times Z_{ii}}{Z_{ij} \times Y_{ii}} \right) - 1 \times (P_i) \right] + \left[\left(\frac{Y_{ji} \times Z_{jj}}{Z_{ji} \times Y_{jj}} \right) - 1 \times (P_j) \right]$		

Y_{ij} = yield of oat in the intercrop; Z_{ji} = sown proportion of vetch in the intercrop; Y_{ii} = yield of oat in the pure stand; Z_{ij} = sown proportion of oat in the intercrop; Y_{ji} = yield of vetch in the intercrop; Y_{jj} = yield of vetch in the pure stand; LER_{ij} = land equivalent ratio of oat in the intercrop; LER_{ji} = land equivalent ratio of vetch in the intercrop; P_i = market price of oat; P_j = market price of vetch; 1kg dry oat fodder = 7.30 ETB on January 01, 2021 and 8.00 ETB in January 01, 2022 with a mean of 7.65 ETB; 1 kg dry vetch fodder = 7.80 ETB in January 01, 2021 and 8.40 ETB in January 01, 2022 with a mean of 8.10 ETB; ETB = Ethiopian birr.

Table 6.6 Indices of economic efficiency and their descriptions used to assess the performance of oat/vetch mixed cropping system

Indices	Abbreviations	Formula/ equation	Descriptions	References
Monetary advantage index	MAI	$MAI = \left(\frac{LER_T - 1}{LER_T} \right) \times [(Y_{ij} \times P_i) + (Y_{ji} \times P_j)]$	The higher the index value, the more profitable is the mixed cropping system.	Willey, 1979; Ghosh, 2004
Relative value total	RVT	$RVT = \frac{(Y_{ij} \times P_i) + (Y_{ji} \times P_j)}{Y_{ii} \times P_i}$	The RVT value > 1 indicates that mixed cropping gives higher returns compared to pure stand.	Alabi and Esobhawan, 2006; Darabad <i>et al.</i> , 2011
Replacement value of intercropping	RVI	$RVI = \frac{(Y_{ij} \times P_i) + (Y_{ji} \times P_j)}{Y_{ii} \times P_i - VC_{ii}}$	The RVI value > 1 indicates that mixed cropping gives higher returns compared to pure stand.	Moseley, 1994; Gitari <i>et al.</i> , 2020
Relative net return index	RNRI	$RNRI = \frac{[(Y_{ij} \times P_i) + (Y_{ji} \times P_j)] + (VC_{ij} - VC_{ii})}{Y_{ii} \times P_i}$	The RNRI value > 1 indicates that mixed cropping gives higher returns compared to pure stand.	Mead and Willey, 1980; Gitari <i>et al.</i> , 2020

LER_T = land equivalent ratio of total; Y_{ij} = yield of oat in the intercrop; P_i = market price of oat; Y_{ji} = yield of vetch in the intercrop; P_j = market price of vetch; VC_{ii} = the variable cost of oat (main crop) in a pure stand; VC_{ij} = the variable cost of oat/vetch intercropping; 1kg dry oat fodder = 7.30 ETB in January 01, 2021 and 8.00 ETB in January 01, 2022 with a mean of 7.65 ETB; 1 kg dry vetch fodder = 7.80 ETB in January 01, 2021 and 8.40 ETB in January 01, 2022 with a mean of 8.10 ETB; **ETB** = Ethiopian birr; 1kg DAP = 13.5 ETB in May, 2020 and 15.5 ETB in May, 2021 with a mean of 14.5 ETB; 1kg Urea = 16.2 ETB in May, 2020 and 18.6 ETB in May, 2021 with a mean of 17.4 ETB; Except fertilizer and seed cost, land preparation (4000.0 ETB/ha), planting (1914.1 ETB/ha), weeding (9296.9 ETB/ha), and harvesting (3645.8 ETB/ha) costs are the same for all treatments per hectare; 1 kg oat seed = 25 birr in 2020 and 30 birr in 2021; 1 kg vetch is 30 ETB in 2020 and 40 ETB in 2021; Average sole oat seed cost = 2750.0 ETB/ha; Mixed oat average seed cost = 2062.5 ETB/ha; Mixed vetch average seed cost = 218.8 ETB/ha; The sum of total cost except fertilizer and seed cost is 18,856.8 ETB for all treatments; January 01, 2021 exchange rate (\$ 1 USD = 39.55 ETB) and January 01, 2022 exchange rate (\$ 1 USD = 49.15 ETB) and mean of the two years exchange rate (\$ 1 USD = 44.35 ETB).

6.2.3.4 Determination of herbage nutritional quality

At the forage harvesting stage of the oat/vetch mixture, the herbage was clipped and a 500 g herbage sample was taken from each plot and then oven-dried for 72 hours at a temperature of 65 °C to estimate the nutritional quality of oat/vetch mixtures. The oven-dried oat and vetch herbage samples were then separately ground to pass a 1 mm sieve to be used for nutritional quality determination. Based on the forage dry matter yield proportion of oat and vetch under mixtures, the ground 3 g herbage mixtures samples were prepared from each experimental unit and submitted to the feeds and nutrition research program laboratory of HARC for nutritive value analysis. Following the standard laboratory procedures, the samples were analyzed for ash, crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), and in-vitro dry matter digestibility (IVDMD). Moreover, the crude protein yield (CPY), digestible yield (DY), digestible crude protein (DCP), hemicellulose (HC), cellulose (C), digestible dry matter (DDM), dry matter intake (DMI), total digestible nutrients (TDN), total digestible nutrient yield (TDNY), relative feed value (RFV), relative feed quality (RFQ), metabolizable energy (ME), digestible energy (DE), net energy for lactation (NEL), net

energy for maintenance (NEm), and net energy for gain (NEg) were also estimated using different equations (For detail see [Table 5.4](#); [Chapter 5](#)).

6.2.4 Statistical analysis

The treatment means were compared using the analysis of variance (ANOVA) procedures of the SAS general linear model (SAS, [2012](#)). The validity of assumptions of ANOVA for each year and over years was computed using the Bartlett test and F-max method of Hartley, respectively (For detail see subsection [3.2.6.1](#); [Chapter 3](#)). After testing the homogeneity of error variance using the F-max method of Hartley, combined analyses of variance was performed using the PROC GLM procedure where fertilizer and year effects were fixed, therefore a linear fixed model was used for data analysis. Thus, the studied both factors were tested against the last mean square error (residuals). The F-test method was used to determine the statistical significance and Duncan's Multiple Range Test at a 5% probability level was used for mean comparisons following the procedures suggested by Gomez and Gomez ([1984](#)). The statistical model used for combined ANOVA is presented below.

$$Y_{ijk} = \mu + (B/Y)_{ik} + F_j + Y_k + (FY)_{jk} + \varepsilon_{ijk}$$

where Y_{ijk} = measured response of fertilizer j in block i (at year) k ; μ = grand mean; $(B/Y)_{ik}$ = the effect of block i (within year k); F_j = effect of fertilizer j ; Y_k = effect of year k ; $(FY)_{jk}$ = interaction effect between fertilizer j and year k ; and ε_{ijk} = residual or effect of random error. Moreover, the Pearson correlation analysis was performed following the SAS CORR procedure of version 9.4 (SAS, [2012](#)).

6.2.5 Economic analysis

The partial budget analysis was performed using the CIMMYT ([1988](#)) procedures to assess the effect of fertilizer application on the profitability of total forage dry matter yield (TFDMY) and oat forage dry matter yield (OFDMY) under the oat/vetch mixed cropping system. The total cost (TC), gross benefit (GB), net benefit (NB), net benefit to cost ratio (NBCR), and marginal rate of return (MRR) were estimated using the CIMMYT ([1988](#)) procedures (For detail see subsection [5.2.5](#); [Chapter 5](#)).

6.3 Results

6.3.1 Agro-morphological traits

6.3.1.1 Analysis of variance

The pooled analysis of variance indicated that all the studied parameters on oat varied significantly for the effects of fertilizer and year of production under the oat/vetch mixed cropping system (Table 6.7). The result showed that the application of fertilizer and year of production had a significant effect on NTPP, TDW, NLFH, LLFH, PHFH, DFH, OFDMY, VFDMY, TFDMY, OFYPR, and TFYPR. However, the interaction effect of fertilizer by year was non-significant for the aforementioned agro-morphological traits of oat under oat/vetch mixed cropping and sole cultures. Moreover, the nutrient concentration, nutrient uptake, and use efficiency of oat under oat/vetch mixed cropping system are also influenced by fertilizer application and year of production (Table 6.7). The results showed that fertilizer application and year of production had significant effects on FPC, FNC, FPU, FNU, TFNU, PFPFY, PNBFY, IURFY, AEFY, and APEFY.

Table 6.7 Combined ANOVA for different studied parameters of oat sown with eight fertilizer levels under oat/vetch mixed cropping system in 2020/21 and 2021/22 cropping seasons at Holetta

Parameters	Mean squares					CV	Mean
	R	F	Y	F x Y	Error		
NTPP	1.88**	3.33***	5.54***	0.21 ^{NS}	0.24	12.32	3.99
TDW	40.96***	102.43***	48.74**	6.14 ^{NS}	4.35	7.87	26.51
NLFH	0.40*	1.36***	13.20***	0.09 ^{NS}	0.11	6.98	4.80
LLFH	97.44***	80.21***	247.90***	5.64 ^{NS}	2.57	5.17	30.96
PHFH	120.98 ^{NS}	1313.93***	1235.54***	29.92 ^{NS}	49.14	5.23	133.96
DFH	76.35***	179.82***	90.74***	2.49 ^{NS}	3.25	1.68	107.63
OFDMY	2.90**	43.94***	21.41***	0.59 ^{NS}	0.34	4.48	13.00
VFDMY	0.06 ^{NS}	5.21***	0.12*	0.02 ^{NS}	0.03	10.02	1.64
TFDMY	3.39***	58.42***	23.73***	0.54 ^{NS}	0.36	4.21	14.22
OFYPR	530.23***	2507.97***	1003.63***	58.87 ^{NS}	32.63	4.76	120.13
TFYPR	616.57***	3461.79***	1082.73***	53.44 ^{NS}	36.54	4.60	131.38
FPC	0.00 ^{NS}	0.02***	0.01***	0.001***	0.00	3.74	0.21
FNC	0.00 ^{NS}	0.18***	0.34***	0.03***	0.00	2.42	1.18
FPU	21.75**	1034.62***	696.96***	37.74***	2.85	5.93	28.46
FNU	261.28*	15592.17***	20573.40***	998.00***	61.21	4.97	157.49
TFNU	432.93*	24340.21***	28824.18***	1324.88***	84.21	4.94	185.94
PFPFY	1815.44*	175985.42***	12150.79***	1286.77*	450.50	7.39	287.31
PNBFY	0.14 ^{NS}	17.59***	9.81***	0.10 ^{NS}	0.10	7.88	3.92
IUEFY	4.99 ^{NS}	437.76***	1226.14***	34.53***	4.59	3.02	70.92
AEFY	570.30*	2670.47***	4516.32***	613.52**	163.05	13.06	97.78
APEFY	42.52*	107.94***	1804.43***	30.87*	11.89	7.26	47.49

NTPP = number of tillers per plant (number); TDW = tillers dry weight (g); NLFH = number of leaves at forage harvest (number); LLFH = leaf length at forage harvest (cm); PHFH = plant height at forage harvest (cm); DFH = days to forage harvest (days); OFDMY = oat forage dry matter yield (t/ha); VFDMY = vetch forage dry matter yield (t/ha); TFDMY = total forage dry matter yield (t/ha); OFYPR = oat forage yield production rate (kg/ha/day); TFYPR = total forage yield production rate (kg/ha/day); FPC = fodder phosphorus concentration (%); FNC = fodder nitrogen concentration (%); FPU = fodder phosphorus uptake (kg/ha); FNU = fodder nitrogen uptake (kg/ha); TFNU = total fodder nutrient uptake (kg/ha); PFPFY = partial factor productivity of fodder yield (kg/kg); PNBFY = partial nutrient balance of fodder yield (kg/kg); IUEFY = internal utilization efficiency of fodder yield (kg/kg); AEFY = agronomic efficiency of fodder yield (kg/kg); APEFY = agro-physiological efficiency of fodder yield (kg/kg); R = replication; F = fertilizer level; Y = year; F x Y = fertilizer level by year interaction; NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively.

6.3.1.2 Effects of year and fertilizer levels on oat performance

The effects of production year and fertilizer application on measured agro-morphological traits of oat under oat/vetch mixed cropping and sole cultures are presented in Table 6.8. The results revealed that significantly higher NTPP, TDW, NLFH, LLFH, PHFH, DFH, TFDMY, OFYPR, and TFYPR were observed in the second year compared to the first year of production. Moreover, the above-mentioned agro-morphological traits of oat under oat/vetch mixed cropping system increased with increasing levels of fertilizer up to 150% (61.5 kg N + 30 kg P/ha) of the blanket recommended fertilizer for sole oat. However, DFH increased with increasing levels of fertilizer up to 175% (71.8 kg N + 35 kg P/ha) of the blanket recommended fertilizer for sole oat. Application of 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate for sole oat gave higher NTPP, TDW, NLFH, LLFH, PHFH, and DFH compared to its counterparts under oat/vetch mixed cropping system. Moreover, sole oat sown with 100% fertilizer produced lower TFDMY, OFYPR, and TFYPR compared to its counterparts under the oat/vetch mixed cropping system.

Table 6.8 Effects of year of production and fertilizer levels on performance of oat under oat/vetch mixed cropping system at Holetta

Factors	Parameters								
	NTPP	TDW	NLFH	LLFH	PHFH	DFH	TFDMY	OFYPR	TFYPR
Year									
2020	3.7 ^b	25.6 ^b	4.3 ^b	28.8 ^b	129.2 ^b	106.3 ^b	13.6 ^b	115.8 ^b	126.9 ^b
2021	4.3 ^a	27.5 ^a	5.3 ^a	33.1 ^a	138.7 ^a	108.9 ^a	14.9 ^a	124.4 ^a	135.9 ^a
<i>P</i> -value	<.0001	0.0020	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Percent of the recommended fertilizer level									
Mixed oat 0%	2.9 ^f	20.5 ^e	4.0 ^e	25.0 ^g	107.9 ^g	101.0 ^f	8.8 ^g	80.5 ^g	86.8 ^g
Mixed oat 25%	3.2 ^{ef}	22.2 ^e	4.4 ^d	27.0 ^f	119.1 ^f	102.0 ^{ef}	11.2 ^f	101.0 ^f	109.7 ^f
Mixed oat 50%	3.4 ^{d-f}	23.1 ^{de}	4.5 ^{cd}	28.6 ^{ef}	124.7 ^{ef}	103.5 ^{de}	12.5 ^e	109.8 ^e	120.8 ^e
Mixed oat 75%	3.7 ^{c-e}	25.4 ^{cd}	4.7 ^{b-d}	30.0 ^{de}	129.6 ^{de}	104.3 ^d	13.8 ^d	120.0 ^d	132.7 ^d
Mixed oat 100%	3.8 ^{c-e}	27.6 ^{bc}	4.9 ^{bc}	31.6 ^{cd}	136.2 ^{cd}	107.5 ^c	15.1 ^c	126.7 ^{cd}	140.2 ^c
Mixed oat 125%	4.2 ^c	28.9 ^b	5.0 ^b	33.0 ^{bc}	142.6 ^{bc}	108.5 ^c	16.5 ^b	137.0 ^b	152.2 ^b
Mixed oat 150%	5.6 ^a	33.8 ^a	5.6 ^a	36.2 ^a	153.3 ^a	112.7 ^b	18.8 ^a	148.8 ^a	167.1 ^a
Mixed oat 175%	4.9 ^b	28.9 ^b	5.1 ^b	34.7 ^{ab}	146.0 ^{ab}	117.2 ^a	17.2 ^b	131.0 ^{bc}	146.6 ^{bc}
Sole oat 100%	4.0 ^{cd}	28.3 ^b	5.1 ^b	32.7 ^{bc}	146.2 ^{ab}	112.0 ^b	14.2 ^d	126.4 ^{cd}	126.4 ^{de}
<i>P</i> -value	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001

NTPP = number of tillers per plant (number); TDW = tillers dry weight (g); NLFH = number of leaves at forage harvest (number); LLFH = leaf length at forage harvest (cm); PHFH = plant height at forage harvest (cm); DFH = days to forage harvest (days); TFDMY = total forage dry matter yield (t/ha); OFYPR = oat forage yield production rate (kg/ha/day); TFYPR = total forage yield production rate (kg/ha/day); Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

The OFDMY varied significantly for the year of production and application of fertilizer under the oat/vetch mixed cropping system (Figure 6.2). The result showed that the second year of production gave significantly higher OFDMY compared to the first year of production. Moreover, the application of fertilizer increased the OFDMY up to 150% (61.5 kg N + 30 kg P/ha) fertilizer for sole oat. The OFDMY obtained from sole oat which was sown with 100% (41.0 kg N + 20 kg P/ha) fertilizer rate was compared to its counterparts under oat/vetch mixed cropping system. The OFDMY ranged from 8.1 to 16.8 t/ha with a mean of 13.0 t/ha under oat/vetch mixed cropping and sole cultures using different fertilizer rates. Similarly, the VFDMY is also significantly influenced by the year of production and fertilizer application under oat/vetch mixed cropping and sole vetch cultures (Figure 6.3). The result revealed that the second year of production gave significantly higher VFDMY compared to the first year. Moreover, the application of fertilizer increased the VFDMY with an increasing level of fertilizer up to 150% fertilizer under the oat/vetch mixed cropping system. However, sole vetch sown with 100% (20 kg P/ha + 18 kg N/ha) of its recommended fertilizer rate gave the highest VFDMY compared to vetch sown under a mixed cropping system.

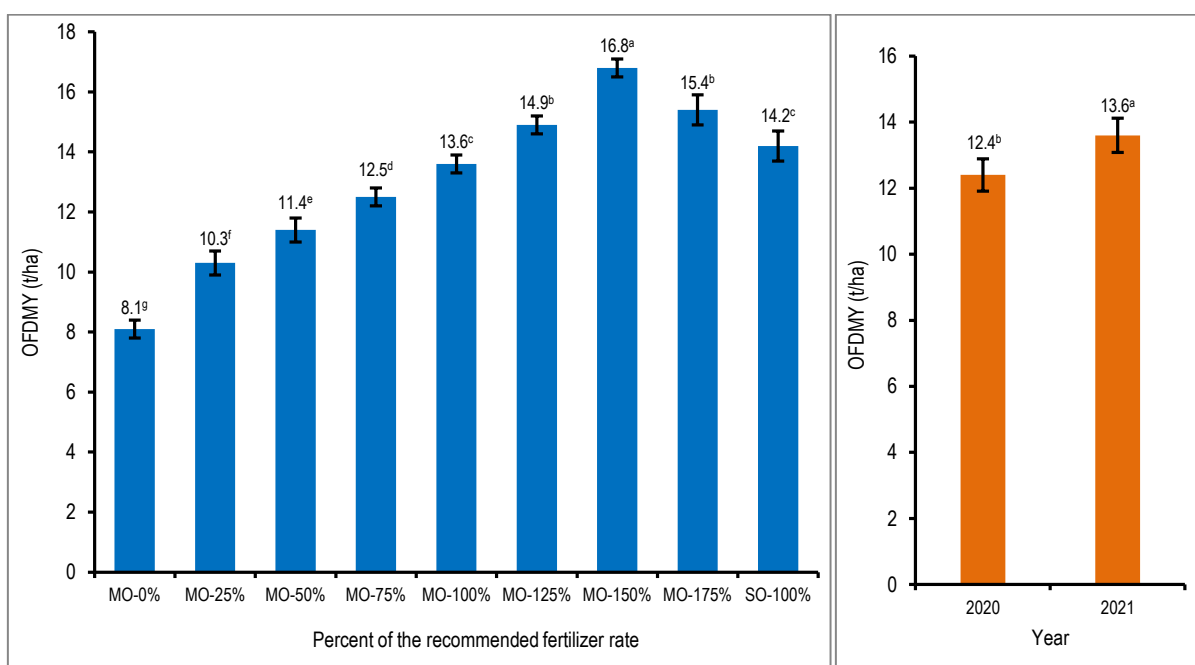


Figure 6.2 Effect of fertilizer levels and year of production on oat forage dry matter yield (OFDMY) under oat/vetch mixed cropping system at Holetta. **Note:** MO = mixed oat; SO = sole oat.

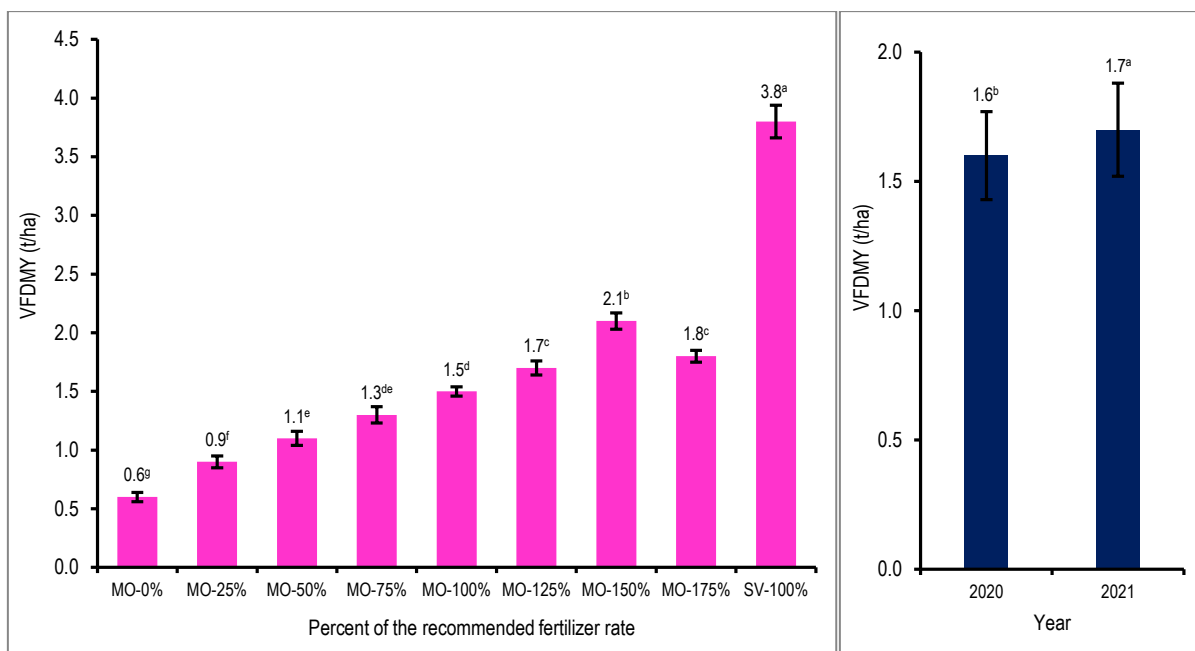


Figure 6.3 Effect of fertilizer levels and year of production on vetch forage dry matter yield (VFDMY) under oat/vetch mixed cropping system at Holetta. **Note:** MO = mixed oat; SV = sole vetch.

6.3.1.3 Effects of year and fertilizer levels on nutrient uptake and use efficiency

The nutrient concentration, nutrient uptake, and use efficiency of oat under the oat/vetch mixed cropping system were significantly influenced by the effect of production year (Table 6.9). The results revealed that the FPC, FNC, FPU, FNU, PFPFY, PNBFY, and AEFY were significantly higher in the second year compared to the first year of production. However, significantly higher IUEFY and APEFY were observed in the first year compared to the second year of production. The nutrient concentration, nutrient uptake, and use efficiency of oat were also influenced significantly by fertilizer rates under the oat/vetch mixed cropping system (Table 6.9). The results showed that the FPC and FNC increased significantly with increasing levels of fertilizer up to 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer for sole oat. Moreover, the FPU increased with increasing levels of fertilizer up to 175% while the FNU increased with increasing levels of fertilizer up to 150% (61.5 kg N + 30 kg P/ha) fertilizer. Furthermore, the measured nutrient use efficiencies (PFPFY, PNBFY, IUEFY, AEFY, and APEFY) were decreased with increasing levels of fertilizer by up to 150%. The higher nutrient use efficiency was observed for sole oat sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate compared to its counterparts of oat under the oat/vetch mixed

cropping system. However, the nutrient concentrations (FPC and FNC) and FNU were higher in oat which was sown with 100% fertilizer rate under oat/vetch mixed cropping compared to its counterparts of sole oat.

Table 6.9 Effects of cropping season and fertilizer levels on nutrient uptake and use efficiency of oat under oat/vetch mixed cropping system at Holetta

Factors	Parameters								
	FPC	FNC	FPU	FNU	PPFPY	PNBFY	IUEFY	AEFY	APEFY
Year									
2020	0.19 ^b	1.10 ^b	28.9 ^b	138.0 ^b	271.4 ^b	3.5 ^b	76.0 ^a	88.1 ^b	53.6 ^a
2021	0.22 ^a	1.26 ^a	32.1 ^a	177.0 ^a	303.2 ^a	4.4 ^a	65.9 ^b	107.5 ^a	41.4 ^b
<i>P-value</i>	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Percent of the recommended fertilizer level									
Mixed oat 0%	0.131 ^g	0.826 ^f	10.7 ^f	66.9 ^h	-	-	-	-	-
Mixed oat 25%	0.152 ^f	0.999 ^e	15.8 ^e	102.8 ^g	675.4 ^a	7.8 ^a	87.2 ^a	142.1 ^a	54.9 ^a
Mixed oat 50%	0.146 ^f	1.159 ^d	16.5 ^e	132.0 ^f	372.7 ^b	4.9 ^b	76.8 ^b	106.0 ^b	46.2 ^{bc}
Mixed oat 75%	0.175 ^e	1.213 ^c	21.9 ^d	152.1 ^e	273.6 ^c	3.8 ^c	72.3 ^c	95.8 ^{bc}	46.4 ^{bc}
Mixed oat 100%	0.222 ^d	1.226 ^c	30.3 ^c	167.2 ^d	223.2 ^d	3.3 ^d	69.5 ^d	89.9 ^{bc}	46.9 ^b
Mixed oat 125%	0.256 ^c	1.311 ^b	38.2 ^b	195.2 ^c	194.8 ^e	3.1 ^d	64.6 ^e	88.1 ^c	44.8 ^{bc}
Mixed oat 150%	0.273 ^b	1.345 ^a	45.9 ^a	226.1 ^a	183.1 ^e	3.0 ^d	62.5 ^{ef}	94.2 ^{bc}	45.8 ^{bc}
Mixed oat 175%	0.299 ^a	1.350 ^a	46.1 ^a	208.5 ^b	143.8 ^f	2.4 ^e	61.3 ^f	67.6 ^d	42.1 ^c
Sole oat 100%	0.216 ^d	1.166 ^d	30.9 ^c	166.6 ^d	232.0 ^d	3.3 ^d	73.2 ^c	98.6 ^{bc}	52.9 ^a
<i>P-value</i>	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001

FPC = fodder phosphorus concentration (%); FNC = fodder nitrogen concentration (%); FPU = fodder phosphorus uptake (kg/ha); FNU = fodder nitrogen uptake (kg/ha); PPFPY = partial factor productivity of fodder yield (kg/kg); PNBFY = partial nutrient balance of fodder yield (kg/kg); IUEFY = internal utilization efficiency of fodder yield (kg/kg); AEFY = agronomic efficiency of fodder yield (kg/kg); APEFY = agro-physiological efficiency of fodder yield (kg/kg); Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

The box and whisker plot also showed that the TFNU varied significantly between the two production years (Figure 6.4 right). Accordingly, a higher TFNU was observed in the second year of production (209.0 kg/ha) compared to the first year (162.8 kg/ha) of production. The effect of fertilizer application on oat TFNU under oat/vetch mixed cropping system is presented using a box and whisker plot (Figure 6.4 left). The results showed that the TFNU by oat increased with increasing levels of fertilizer up to 150% (61.5 kg N + 30 kg P/ha) under the oat/vetch mixed cropping system. The TFNU for 0% (0 kg N + 0 kg P/ha), 25% (10.3 kg N + 5 kg P/ha), 50% (20.5 kg N + 10 kg P/ha), 75% (30.8 kg N + 15 kg P/ha), 100% (41.0 kg N + 20 kg P/ha), 125% (51.3 kg N + 25 kg P/ha), 150% (61.5 kg N + 30 kg P/ha), and 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer for sole oat under oat/vetch mixed cropping system were 77.6, 118.5, 148.5, 174.0, 197.5, 233.4, 271.9, and 254.7 kg/ha, respectively. Moreover,

the TFNU of oat under sole culture using 100% (41.0 kg N + 20 kg P/ha) fertilizer rate was 197.5 kg/ha.

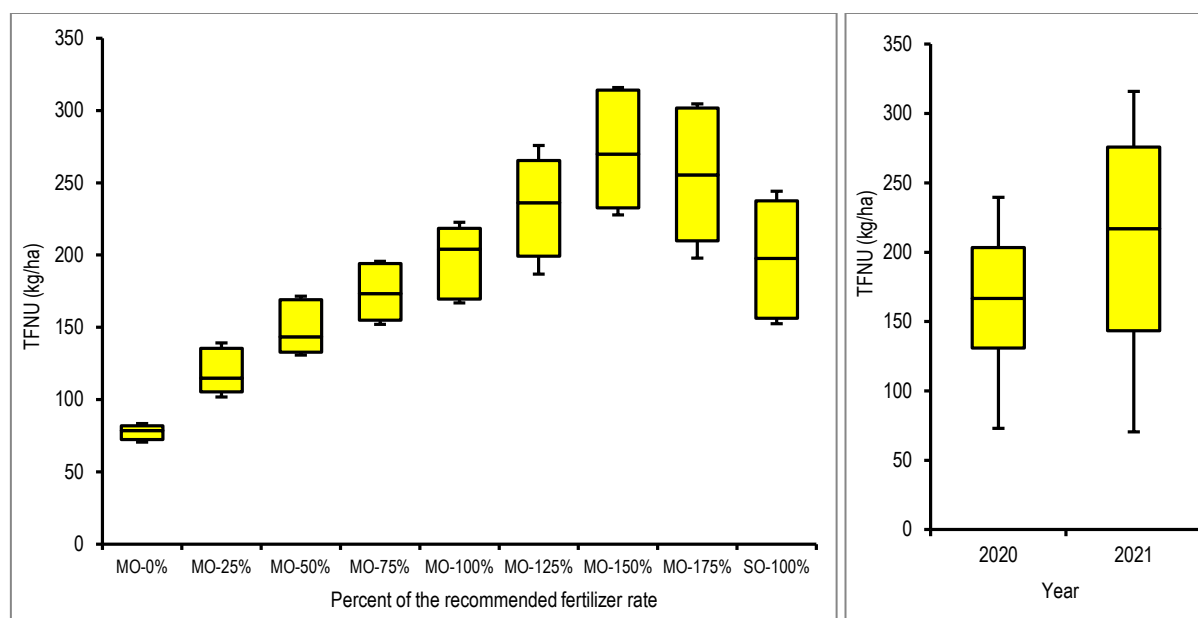


Figure 6.4 Box and whisker plot for total forage nutrient uptake (TFNU) in oat as influenced by fertilizer level and year of production under oat/vetch mixed cropping system at Holetta. **Note:** MO = mixed oat; SV = sole vetch.

6.3.1.4 Relationships among measured parameters

The relationships of fertilizer rates with agro-morphological traits are presented in [Figure 6.5](#). The results showed that fertilizer rates had significant and positive associations with OFDMY ($r = 0.92^{***}$), DFH ($r = 0.86^{***}$), OFYPR ($r = 0.86^{***}$), PHFH ($r = 0.83^{***}$), TDW ($r = 0.80^{***}$), NTPP ($r = 0.78^{***}$), LLFH ($r = 0.72^{***}$), and NLFH ($r = 0.56^{***}$). The correlation analysis of fertilizer rates with nutrient concentration (FPC and FNC), nutrient uptake (FPU and FNU), and nutrient use efficiencies (PFPFY, PNBFY, AEFY, and APEFY) of oat under oat/vetch mixed cropping system is displayed in [Figure 6.6](#). The result showed that the nutrient concentration (FPC: $r = 0.92^{***}$; FNC: $r = 0.80^{***}$) and nutrient uptake (FPU: $r = 0.93^{***}$; TFNU: $r = 0.90^{***}$; FNU: $r = 0.89^{***}$) of oat had significant and positive associations with fertilizer levels under oat/vetch mixed cropping system. However, the nutrient use efficiencies (IUEFY: $r = -0.86^{***}$; PPFY: $r = -0.85^{***}$; PNBFY: $r = -0.83^{***}$; AEFY: $r = -0.67^{***}$; and APEFY: $r = -0.39^{*}$) of oat were significantly but inversely associated with fertilizer rates under oat/vetch mixed cropping system.

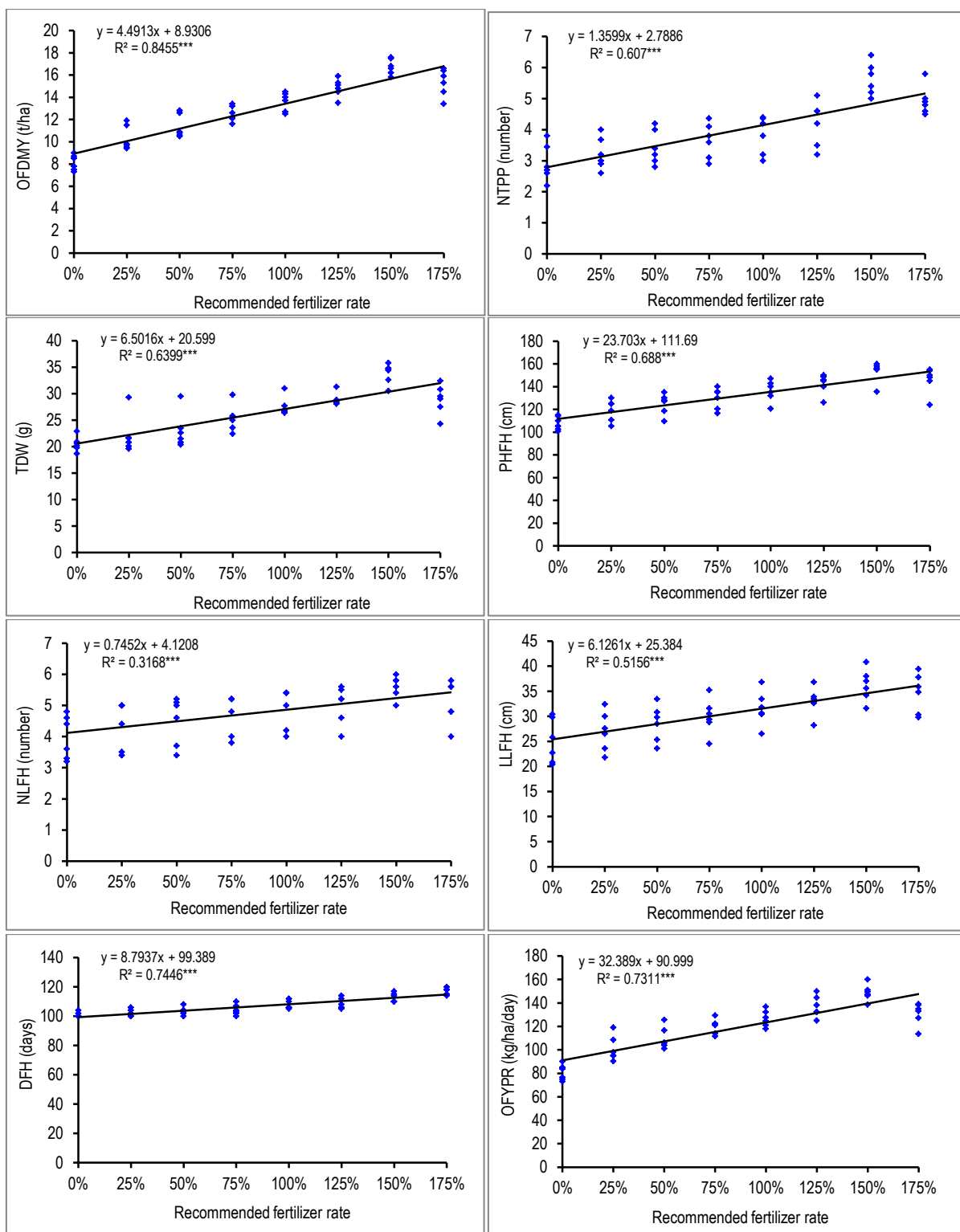


Figure 6.5 Relationships between agro-morphological traits of oat sown with different levels of fertilizer under oat/vetch mixed cropping system at Holetta

Note: OFDMY = oat forage dry matter yield (t/ha); NTPP = number of tillers per plant (number); TDW = tillers dry weight (g); PHFH = plant height at forage harvest (cm); NLFH = number of leaves at forage harvest (number); LLFH = leaf length at forage harvest (cm); DFH = days to forage harvest (days); OFYPR = oat forage yield production rate (kg/ha/day).

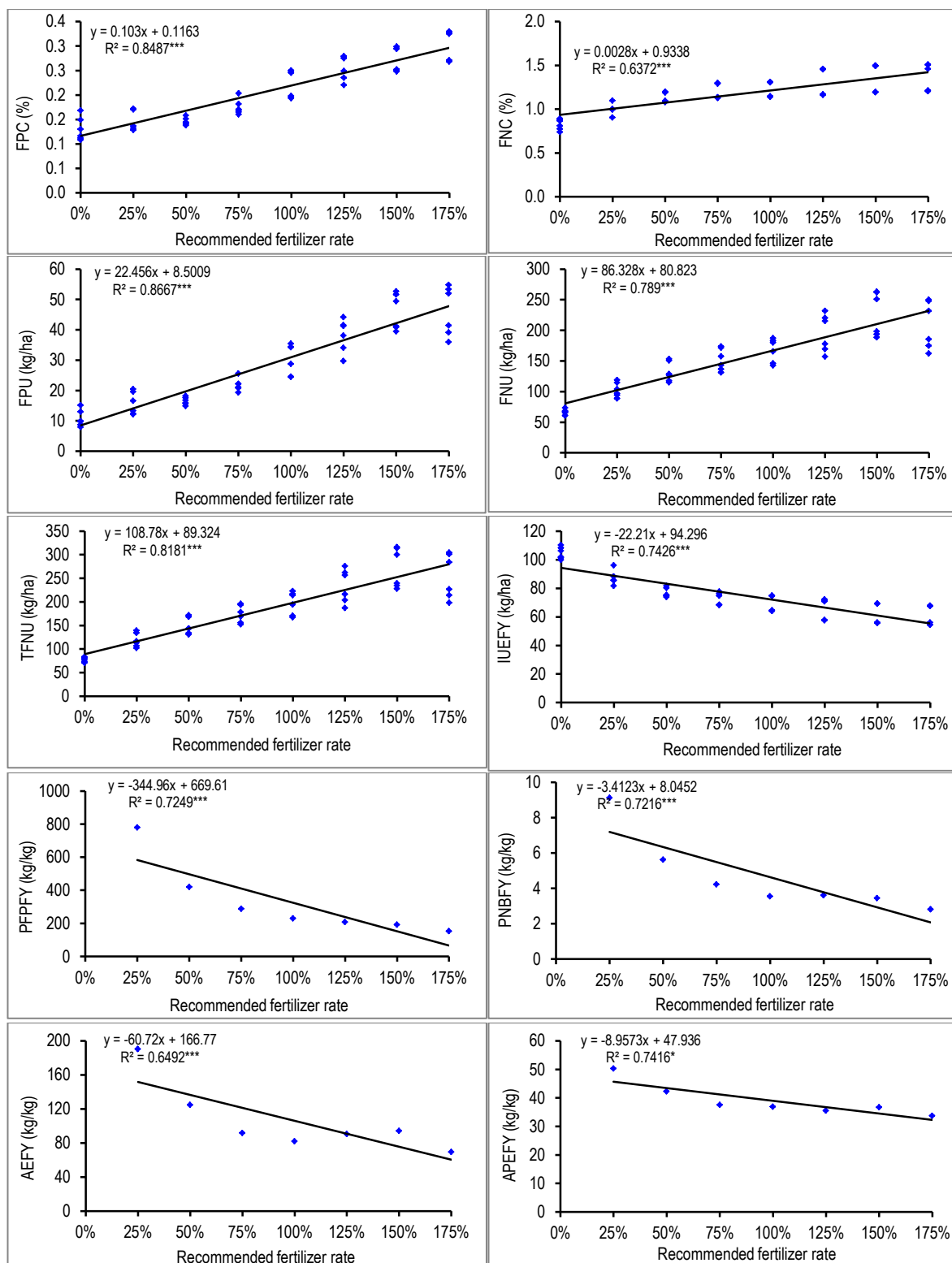


Figure 6.6 Relationships between nutrient concentration, nutrient uptake and use efficiency of oat sown with different levels of fertilizer under oat/vetch mixed cropping system at Holetta

Note: FPC = forage phosphorus concentration (%); FNC = forage nitrogen concentration (%); FPU = forage phosphorus uptake (kg/ha); FNU = forage nutrient uptake (kg/ha); PPFY = partial factor productivity of forage yield (kg forage/kg nutrient applied); PNBFY = partial nutrient balance of forage yield (kg nutrient uptake by forage/kg nutrient applied); AEFY = agronomic efficiency of forage yield (kg forage/kg nutrient applied); APEFY = agro-physiological efficiency of forage yield (kg forage/kg nutrient uptake by biological yield).

The Pearson correlation analysis for measured parameters is indicated in Table 6.10. The result showed that the OFDMY had significant and positive associations with NTPP ($r = 0.80^{***}$), TDW ($r = 0.89^{***}$), PHFH ($r = 0.94^{***}$), NLFH ($r = 0.76^{***}$), LLFH ($r = 0.75^{***}$), DFH ($r = 0.78^{***}$), OFYPR ($r = 0.98^{***}$), FPC ($r = 0.90^{***}$), FNC ($r = 0.86^{***}$), FPU ($r = 0.94^{***}$), FNU ($r = 0.97^{***}$), and TFNU ($r = 0.97^{***}$) while it had significant but inverse associations with PFPFY ($r = -0.73^{***}$), PNBFY ($r = -0.66^{***}$), IUEFY ($r = -0.90^{***}$), AEFY ($r = -0.40^{**}$), and APEFY ($r = -0.50^{***}$). All the pairwise associations between agro-morphological traits were significant and positive. Moreover, the nutrient concentrations and nutrient uptake also had significant and positive associations with all measured agro-morphological traits. However, all the nutrient use efficiencies (PFPFY, PNBFY, IUEFY, AEFY, and APEFY) had inverse associations with all measured agro-morphological traits (NTPP, TDW, PHFH, NLFH, LLFH, DFH, and OFYPR), nutrient concentrations (FPC and FNC), and nutrient uptake (FPU, FNU, and TFNU). Moreover, all the pairwise associations between nutrient use efficiencies (PFPFY, PNBFY, IUEFY, AEFY, and APEFY) were positive.

Table 6.10 Pearson correlation analysis for measured parameters of oat sown with different fertilizer rates under oat/vetch mixed cropping system at Holetta

Parameter	NTPP	TDW	PHFH	NLFH	LLFH	DFH	OFYPR	FPC	FNC	FPU	FNU	TFNU	PFPFY	PNBFY	IUEFY	AEFY	APEFY
OFDMY	0.80***	0.89***	0.94***	0.76***	0.75***	0.78***	0.98***	0.90***	0.86***	0.94***	0.97***	0.97***	-0.73***	-0.66***	-0.90***	-0.40**	-0.50***
NTPP	1.00	0.79***	0.79***	0.72***	0.81***	0.66***	0.76***	0.80***	0.69***	0.83***	0.79***	0.81***	-0.55***	-0.49***	-0.70***	-0.28NS	-0.40**
TDW		1.00	0.79***	0.65***	0.73***	0.59***	0.90***	0.79***	0.72***	0.85***	0.85***	0.86***	-0.60***	-0.55***	-0.75***	-0.33*	-0.38*
PHFH			1.00	0.87***	0.75***	0.75***	0.91***	0.85***	0.80***	0.89***	0.91***	0.91***	-0.60***	-0.52***	-0.83***	-0.27NS	-0.49***
NLFH				1.00	0.71***	0.60***	0.74***	0.69***	0.67***	0.72***	0.76***	0.76***	-0.32*	-0.21NS	-0.65***	-0.01NS	-0.60***
LLFH					1.00	0.65***	0.71***	0.77***	0.75***	0.77***	0.78***	0.79***	-0.55***	-0.46**	-0.74***	-0.17NS	-0.53***
DFH						1.00	0.64***	0.87***	0.74***	0.86***	0.81***	0.82***	-0.64***	-0.59***	-0.75***	-0.49***	-0.51***
OFYPR							1.00	0.82***	0.82***	0.88***	0.92***	0.92***	-0.68***	-0.61***	-0.87***	-0.32*	-0.43**
FPC								1.00	0.80***	0.99***	0.90***	0.93***	-0.70***	-0.64***	-0.82***	-0.49***	-0.53***
FNC									1.00	0.84***	0.95***	0.94***	-0.66***	-0.53***	-0.98***	-0.39*	-0.85***
FPU										1.00	0.95***	0.97***	-0.70***	-0.63***	-0.85***	-0.46**	-0.54***
FNU											1.00	1.00***	-0.71***	-0.60***	-0.95***	-0.41**	-0.70***
TFNU												1.00	-0.71***	-0.62***	-0.94***	-0.42**	-0.67***
PFPFY													1.00	0.98***	0.78***	0.81***	0.38*
PNBFY														1.00	0.66***	0.86***	0.23NS
IUEFY															1.00	0.47**	0.80***
AEFY																1.00	0.16NS
APEFY																	1.00

NTPP = number of tillers per plant (number); TDW = tillers dry weight (g); PHFH = plant height at forage harvest (cm); NLFH = number of leaves at forage harvest (number); LLFH = leaf length at forage harvest (cm); DFH = days to forage harvest (days); OFDMY = oat forage dry matter yield (t/ha); OFYPR = oat forage yield production rate (kg/ha/day); FPC = fodder phosphorus concentration (%); FNC = fodder nitrogen concentration (%); FPU = fodder phosphorus uptake (kg/ha); FNU = fodder nitrogen uptake (kg/ha); TFNU = total fodder nutrient uptake (kg/ha); PFPFY = partial factor productivity of fodder yield (kg/kg); PNBFY = partial nutrient balance of fodder yield (kg/kg); IUEFY = internal utilization efficiency of fodder yield (kg/kg); AEFY = agronomic efficiency of fodder yield (kg/kg); APEFY = agro-physiological efficiency of fodder yield (kg/kg); NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively.

Note: The green, orange, and yellow colors indicate the strength of correlation; green color is positively correlated; green to light green color indicate strong to weak positive correlation; orange color is negatively correlated; orange to light orange color indicate strong to weak negative correlation; and yellow color is positively and negatively correlated; yellow to light yellow color indicate very weak to no correlation.

6.3.1.5 Partial budget analysis

The partial budget analysis for oat fodder yield under oat/vetch mixed cropping system using different fertilizer levels is indicated in Table 6.11. The results showed that the highest gross benefit of 122,472 birr/ha was obtained from oat sown with the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate under oat/vetch mixed cropping followed by the application of 125% (51.3 kg N + 25 kg P/ha) fertilizer rate which gave the gross benefit of 108,621 birr/ha. However, oat sown without fertilizer application gave the lowest gross benefit of 59,049 birr/ha under the oat/vetch mixed cropping system. Similarly, the application of 150% fertilizer rate gave the highest net benefit of 97,854 birr/ha and a net benefit-to-cost ratio of 4.0 followed by the application of 125% fertilizer which gave a net benefit of 84,583 birr/ha and net benefit-to-cost ratio of 3.5 while oat sown without fertilizer gave the lowest net benefit to cost ratio of 1.8 under oat/vetch mixed cropping.

Table 6.11 Partial budget analysis of oat fodder yield as influenced by fertilizer application under oat/vetch mixed cropping system at Holetta

RFR	Adj. yield	GB	TC	NB	MNB	MTC	NBCR	MRR%
OFDMY								
MO-0%	7.3	59049	21138	37911	-	-	1.8	-
MO-25%	9.3	75087	21718	53369	15458	580	2.5	2665.6
MO-50%	10.3	83106	22298	60808	7439	580	2.7	1282.3
MO-75%	11.3	91125	22878	68247	7439	580	3.0	1282.8
MO-100%	12.2	99144	23458	75686	7439	580	3.2	1282.8
SO-100%	12.8	97767	23927	73840	-1846	469	3.1	D
MO-125%	13.4	108621	24038	84583	10743	111	3.5	9660.8
MO-150%	15.1	122472	24618	97854	13271	580	4.0	2287.7
MO-175%	13.0	104976	25198	79778	-18076	580	3.2	D
TFDMY								
MO-0%	7.9	64152	21138	43014	-	-	2.0	-
MO-25%	10.1	81648	21718	59930	16916	580	2.8	2917.1
MO-50%	11.3	91125	22298	68827	8897	580	3.1	1533.7
MO-75%	12.4	100602	22878	77724	8897	580	3.4	1534.2
MO-100%	13.6	110079	23458	86621	8897	580	3.7	1534.2
SO-100%	12.8	97767	23927	73840	-12781	469	3.1	D
MO-125%	14.9	120285	24038	96247	22407	111	4.0	20150.0
MO-150%	16.9	137052	24618	112434	16187	580	4.6	2790.4
MO-175%	15.5	125388	25198	100190	-12244	580	4.0	D

RFR = recommended fertilizer rate; Adj. yield = adjusted fodder yield; GB = gross benefit; TC = total cost; NB = net benefit; MNB = marginal net benefit; MTC = marginal total cost; NBCR = net benefit to cost ratio; MRR = marginal rate of return; D = dominated suggesting treatment has a lower NB with higher TC compared to the preceding treatment NB and TC; 1kg DAP = 13.5 ETB in May, 2020 and 15.5 ETB in May, 2021 with a mean of 14.5 ETB; 1kg Urea = 16.2 ETB in May, 2020 and 18.6 ETB in May, 2021 with a mean of 17.4 ETB; 1kg natural pasture hay = 7.30 ETB in January 01, 2021 and 8.00 ETB in January 01, 2022 with a mean of 7.65 ETB; 1 kg Oat/vetch mixtures = 7.80 ETB in January 01, 2021 and 8.40 ETB in January 01, 2022 with a mean of 8.10 ETB; ETB = Ethiopian birr; Except fertilizer and seed cost, land preparation (4000.0 ETB/ha), planting (1914.1 ETB/ha), weeding (9296.9 ETB/ha), and harvesting (3645.8 ETB/ha) costs are the same for all treatments per hectare; 1 kg oat seed = 25 birr in 2020 and 30 birr in 2021; 1 kg vetch is 30 ETB in 2020 and 40 ETB in 2021; Average sole oat seed cost = 2750.0 ETB/ha; Mixed oat average seed cost = 2062.5 ETB/ha; Mixed vetch average seed cost = 218.8 ETB/ha; The sum of total cost except fertilizer and seed cost is 18,856.8 ETB for all treatments; January 01, 2021 exchange rate (\$ 1 USD = 39.55 ETB) and January 01, 2022 exchange rate (\$ 1 USD = 49.15 ETB) and mean of the two years exchange rate (\$ 1 USD = 44.35 ETB).

The partial budget analysis for the total forage dry matter yield of oat/vetch mixed cropping system under different fertilizer levels is also indicated in [Table 6.11](#). The results showed that application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate gave the highest gross benefit (137,052 birr/ha), net benefit (112,434 birr/ha), and net benefit to cost ratio (4.6) followed by application of 125% (51.3 kg N + 25 kg P/ha) fertilizer rate which gave the gross benefit of 125,388 birr/ha, net benefit of 100,190 birr/ha, and net benefit to cost ratio of 4.0. On the other hand, oat/vetch mixed cropping sown without fertilizer gave the lowest gross benefit (64,152 birr/ha), net benefit (43,014 birr/ha), and net benefit to cost ratio (2.0) compared to other treatments.

6.3.2 Efficiency and competitive ability of mixed cropping

6.3.2.1 Biological efficiency of mixed cropping

The biological efficiency of oat and oat/vetch mixtures under a mixed cropping system is indicated in [Table 6.12](#). The results showed that the year of production had a significant effect on OYO, OEY, LEC, LUE, SPI, and ATER. Among these biological efficiency indices, OYO, LEC, LUE, and ATER were significantly higher in the 2020 cropping season. However, significantly higher OEY and SPI were recorded in 2021 than 2020 cropping season. The fertilizer levels also had a significant effect on OYO, OEY, LEC, LUE, SPI, and ATER of the oat/vetch mixed cropping system ([Table 6.12](#)). The results showed that the indices of OYO, OEY, LEC, LUE, SPI, and ATER increased with increasing rates of fertilizer up to 150% (61.5 kg N + 30 kg P/ha). The oat/vetch mixed cropping system sown without fertilizer application gave the lowest indices of biological efficiency. All the biological efficiency indices were non-significant for the interaction effect of the year by fertilizer.

The effect of cropping seasons on LER is displayed in [Figure 6.7](#). The results showed that the production year had a significant effect on LERO. However, the LERT was non-significant between the two cropping seasons. The LERO and LERT were higher in 2020 than the 2021 cropping season. The effect of fertilizer application on the LERO and LERT under oat/vetch mixed cropping system is presented in [Figure 6.8](#). The result showed that fertilizer application had a significant effect on LERO and LERT. The LERO and LERT increased with increasing levels of fertilizer application under mixed cropping. The highest LERO and LERT were

recorded for the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate followed by 175% (71.8 kg N + 35 kg P/ha) fertilizer application and 125% (51.3 kg N + 25 kg P/ha) fertilizer while mixed cropping sown without fertilizer application produced the least LERO and LERT.

Table 6.12 Fodder yield and biological efficiency of oat under oat/vetch mixed cropping system as influenced by year of production and fertilizer rates at Holetta, in the central highlands of Ethiopia

Parameters	OYO	OEY	LEC	LUE	SPI	ATER
Year						
2020	27.3 ^a	13733 ^b	0.37 ^a	197.5 ^a	16970 ^b	1.32 ^a
2021	16.2 ^b	14891 ^a	0.33 ^b	184.4 ^b	18943 ^a	1.23 ^b
<i>P-value</i>	<.0001	<.0001	0.0035	<.0001	<.0001	<.0001
Percent of the recommended fertilizer level						
Mixed oat 0%	-22.9 ^g	8804 ^g	0.10 ^h	111.8 ^h	10480 ^h	0.75 ^h
Mixed oat 25%	-2.8 ^f	11236 ^f	0.17 ^g	144.3 ^g	13580 ^g	0.96 ^g
Mixed oat 50%	7.4 ^e	12567 ^e	0.24 ^f	165.5 ^f	15570 ^f	1.10 ^f
Mixed oat 75%	18.6 ^d	13910 ^d	0.31 ^e	185.0 ^e	17421 ^e	1.23 ^e
Mixed oat 100%	29.1 ^c	15152 ^c	0.37 ^d	202.5 ^d	19009 ^d	1.35 ^d
Mixed oat 125%	40.7 ^b	16597 ^b	0.46 ^c	223.3 ^c	21001 ^c	1.49 ^c
Mixed oat 150%	58.7 ^a	18939 ^a	0.65 ^a	260.3 ^a	24418 ^a	1.74 ^a
Mixed oat 175%	45.0 ^b	17292 ^b	0.53 ^b	235.3 ^b	22170 ^b	1.57 ^b
Sole oat 100%	-	-	-	-	-	-
Sole vetch 100%	-	-	-	-	-	-
Mean	21.7	14312	0.35	191.0	17956	1.27
<i>P-value</i>	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Y x F	NS	NS	NS	NS	NS	NS

OFDMY = oat forage dry matter yield (kg/ha); **VFDMY** = vetch forage dry matter yield (kg/ha); **OYO** = over-yielding oat; **OEY** = oat equivalent yield (kg/ha); **LEC** = land equivalent coefficient; **LUE** = land use efficiency; **SPI** = system productivity index (kg/ha); **ATER** = area-time equivalent ratio; Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

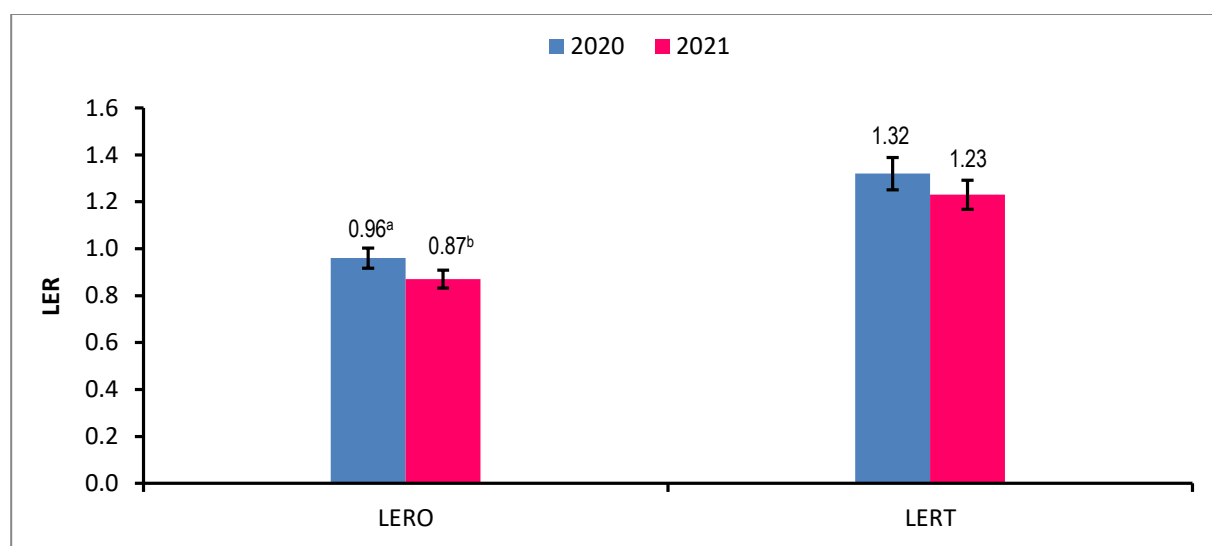


Figure 6.7 Land equivalent ratio of oat and total under oat/vetch mixed cropping system as influenced by year of production at Holetta, Ethiopia. **Note:** LERO = land equivalent ratio of oat; LERT = land equivalent ratio of total.

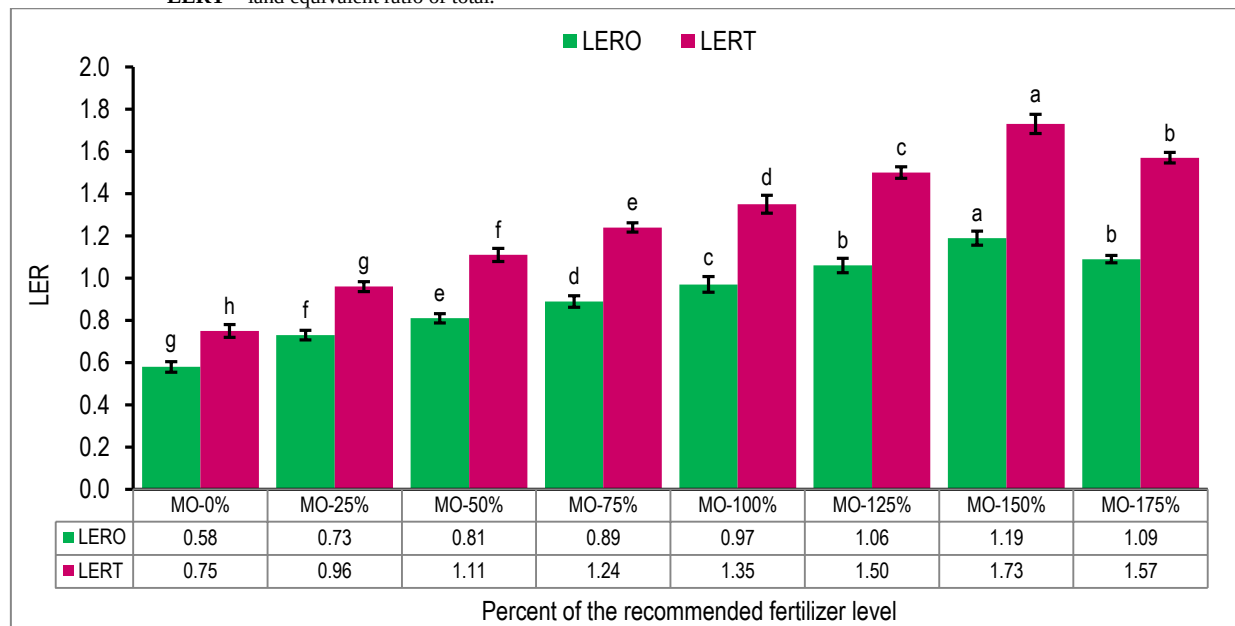


Figure 6.8 Land equivalent ratio of oat and total under oat/vetch mixed cropping system as influenced by fertilizer rates at Holetta, Ethiopia. **Note:** LERO = land equivalent ratio of oat; LERT = land equivalent ratio of total; MO = mixed oat.

6.3.2.2 Competitive ability of oat under mixed cropping

The competitive indices of oat and total under oat/vetch mixed cropping are indicated in [Table 6.13](#). The results showed that cropping seasons had a significant effect on KO, K, AYLO, AYLT, IAO, and IAT. The highest competitive indices (KO, K, AYLO, AYLT, IAO, and IAT) were recorded in the first year of production. Moreover, the year-by-fertilizer interactions were significant for KO and K while non-significant interactions were observed for AYLO, AYLT, IAO, and IAT. Application of fertilizer had a significant effect on KO, K, AYLO, AYLT, IAO, and IAT of oat and total under oat/vetch mixed cropping system ([Table 6.13](#)). All the competitive indices measured in this study increased with increasing rates of fertilizer up to 150% (61.5 kg N + 30 kg P/ha). On the contrary, oat/vetch mixed cropping sown without fertilizer application showed the least competitive indices (KO, K, AYLO, AYLT, IAO, and IAT).

The aggressivity (A) of oat under oat/vetch mixed cropping system is indicated in [Figure 6.9](#). The result showed that the aggressivity of oat sown without fertilizer and at 25% fertilizer application under oat/vetch mixed cropping was positive while the aggressivity of oat at higher

fertilizer rates was negative. The aggressivity of oat generally decreased with increasing rates of fertilizer up to 150% (61.5 kg N + 30 kg P/ha). The interaction effect of year by fertilizer for aggressivity of oat under oat/vetch mixed cropping was non-significant. The CR of oat under oat/vetch mixed cropping was non-significant for cropping seasons (Figure 6.10 right). The result showed that numerically a higher CR for oat was observed in 2020 than 2021 cropping season. However, the CR of oat under oat/vetch mixed cropping was influenced significantly by the application of fertilizer (Figure 6.10 left). The results showed that the CR of oat under oat/vetch mixed cropping decreased with increasing levels of fertilizer application by up to 175%.

Table 6.13 Competitive indices of oat and total under oat/vetch mixed cropping system as influenced by year of production and fertilizer rates at Holetta, in the central highlands of Ethiopia

Parameters	KO	K	AYLO	AYLT	IAO	IAT
Year						
2020	1.79 ^a	0.72 ^a	0.27 ^a	0.72 ^a	2.00 ^a	5.49 ^a
2021	0.82 ^b	0.29 ^b	0.16 ^b	0.60 ^b	1.17 ^b	4.57 ^b
<i>P-value</i>	0.0052	0.0040	<.0001	0.0123	<.0001	0.0177
Percent of the recommended fertilizer level						
Mixed oat 0%	0.26 ^b	0.04 ^b	-0.23 ^g	-0.57 ^h	-1.68 ^g	-4.28 ^h
Mixed oat 25%	0.41 ^b	0.07 ^b	-0.03 ^f	-0.10 ^g	-0.20 ^f	-0.73 ^g
Mixed oat 50%	0.52 ^b	0.13 ^b	0.08 ^e	0.26 ^f	0.55 ^e	2.03 ^f
Mixed oat 75%	0.69 ^b	0.19 ^b	0.19 ^d	0.57 ^e	1.36 ^d	4.33 ^e
Mixed oat 100%	0.98 ^b	0.31 ^b	0.29 ^c	0.82 ^d	2.11 ^c	6.21 ^d
Mixed oat 125%	1.44 ^b	0.51 ^b	0.41 ^b	1.14 ^c	2.96 ^b	8.69 ^c
Mixed oat 150%	4.59 ^a	2.19 ^a	0.59 ^a	1.76 ^a	4.28 ^a	13.45 ^a
Mixed oat 175%	1.53 ^b	0.62 ^b	0.45 ^b	1.38 ^b	3.28 ^b	10.57 ^b
Mean	1.30	0.51	0.22	0.66	1.58	5.03
<i>P-value</i>	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Y x F	**	***	NS	NS	NS	NS

KO = crowding coefficient of oat; K = crowding coefficient; AYLO = actual yield loss of oat; AYLT = actual yield loss of total; IAO = intercropping advantage of oat; IAT = intercropping advantage of total; Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

6.3.2.3 Economic efficiency of oat/vetch mixed cropping

The economic efficiency of the oat/vetch mixed cropping system is indicated in Table 6.14. The results showed that the MAI between the two cropping seasons was non-significant. However, the two cropping seasons varied significantly for RVT, RVI, and RNRI. Accordingly, higher MAI, RVT, RVI, and RNRI were recorded in 2020 than 2021 cropping season. The interaction effect of year by fertilizer was significant for MAI and RNRI while it was non-significant for RVT and RVI. The oat/vetch mixed cropping system sown with different fertilizer rates had a

significant effect on MAI, RVT, RVI, and RNRI (Table 6.14). The results showed that the MAI, RVT, RVI, and RNRI increased with increasing levels of fertilizers up to 150% (61.5 kg N + 30 kg P/ha). Moreover, the application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rate on oat/vetch mixed cropping system gave significantly higher MAI, RVT, RVI, and RNRI than all other fertilizer rates except the application of 150% fertilizer rate.

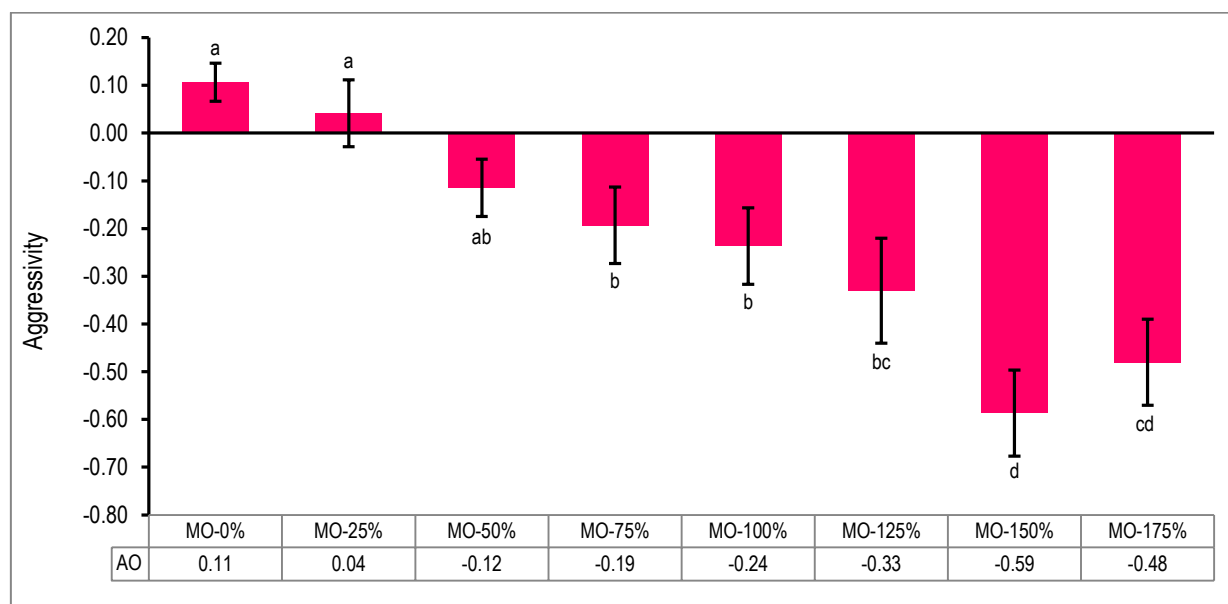


Figure 6.9 Aggressivity of oat under oat/vetch mixed cropping system as influenced by fertilizer rates at Holetta, Ethiopia. **Note:** AO = aggressivity of oat; MO = mixed oat.

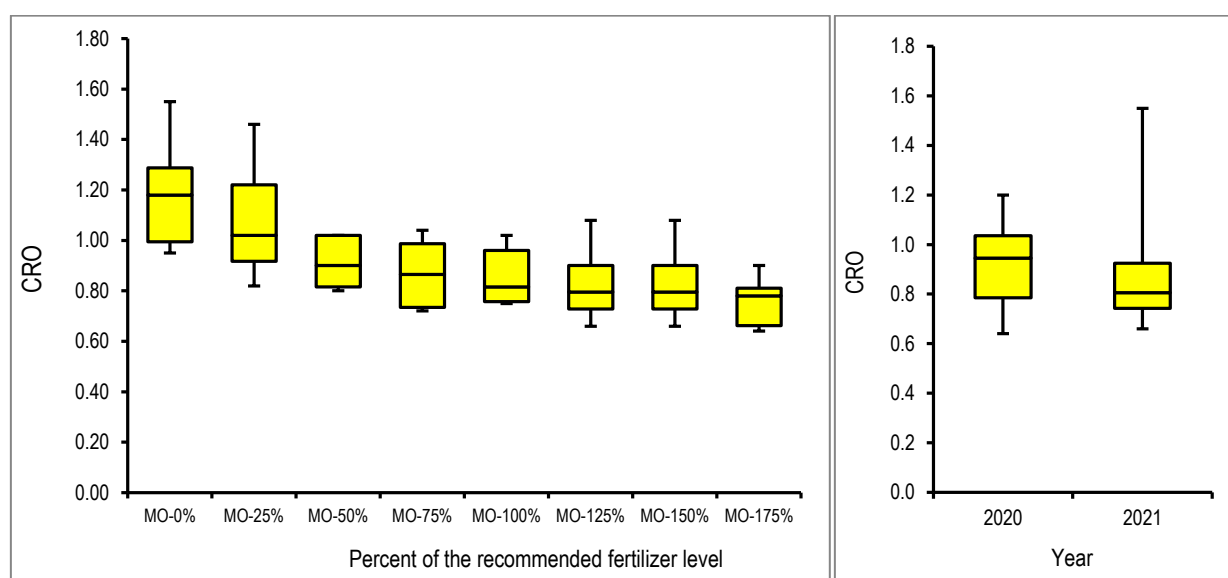


Figure 6.10 Competitive ratio of oat under oat/vetch mixed cropping system as influenced by fertilizer rates and year of production at Holetta, Ethiopia. **Note:** CRO = competitive ratio of oat; MO = mixed oat.

Table 6.14 Economic efficiency of oat/vetch mixed cropping system as influenced by year of production and fertilizer rates at Holetta, in the central highlands of Ethiopia

Factor	MAI	RVT	RVI	RNRI
Year				
2020	23564	1.07 ^a	1.38 ^a	1.06 ^a
2021	21548	0.97 ^b	1.23 ^b	0.96 ^b
<i>P-value</i>	0.0810	<.0001	<.0001	<.0001
Percent of the recommended fertilizer level				
Mixed oat 0%	-23890 ^h	0.63 ^h	0.81 ^h	0.60 ^h
Mixed oat 25%	-3762 ^g	0.80 ^g	1.02 ^g	0.78 ^g
Mixed oat 50%	8734 ^f	0.89 ^f	1.15 ^f	0.88 ^f
Mixed oat 75%	19907 ^e	0.99 ^e	1.27 ^e	0.98 ^e
Mixed oat 100%	29531 ^d	1.08 ^d	1.39 ^d	1.07 ^d
Mixed oat 125%	41299 ^c	1.18 ^c	1.52 ^c	1.18 ^c
Mixed oat 150%	60878 ^a	1.35 ^a	1.73 ^a	1.35 ^a
Mixed oat 175%	47754 ^b	1.23 ^b	1.58 ^b	1.24 ^b
Mean	22556	1.02	1.31	1.01
<i>P-value</i>	<.0001	<.0001	<.0001	<.0001
Y x F	*	NS	NS	*

MAI = monetary advantage index (ETB/ha); RVT = relative value total; RVI = replacement value of intercropping; RNRI = relative net return index; Y x F = year by fertilizer interaction; Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

6.3.3 Fodder nutritional quality

6.3.3.1 Analysis of variance

The combined analysis of variance for nutritional quality of oat/vetch mixtures are indicated in [Table 6.15](#). The result showed that all the measured nutritional qualities were significant ($P < 0.001$) for fertilizer rates. Moreover, all the nutritional qualities of oat/vetch mixtures varied significantly with year except ash and hemicellulose contents. The interaction effects of fertilizer by year were significant for crude protein (CP), crude protein yield (CPY), and digestible crude protein (DCP) parameters of oat/vetch mixtures.

6.3.3.2 Nutritive values of fodder

6.3.3.2.1 Ash concentration

The ash content of oat/vetch mixtures was influenced significantly by various fertilizer rates ([Figure 6.11](#) left). The result revealed that the lowest ash content (82.5 g/kg DM) was recorded for oat/vetch mixtures sown without fertilizer application. On the other hand, the highest ash content (97.7 g/kg DM) was obtained from the application of 150% (61.5 kg N + 30 kg P/ha) of

the recommended fertilizer rate compared to other mixtures. The sole oat sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate gave higher ash content compared to oat/vetch mixtures sown without fertilizer and 25% (10.3 kg N + 5 kg P/ha) of the recommended fertilizer rate. However, the sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate gave the highest ash content (102.6 g/kg DM) compared to the oat/vetch mixtures and sole oat. Generally, the ash content of oat/vetch mixtures increased with increasing fertilizer rates. The ash content was not statistically different between the two production years (Figure 6.11 right). However, the second year of production gave higher ash content (92.0 g/kg DM) compared to the first year of production (90.2 g/kg DM).

Table 6.15 Combined analysis of variance for fodder yield and nutritive value of oat/vetch mixed cropping under different fertilizer levels in 2020/21 and 2021/22 cropping seasons at Holetta

Parameter	Mean squares					CV (%)	R ²	Mean
	R	F	Y	F x Y	Error			
Ash	98.6*	219.4***	48.2 ^{NS}	2.6 ^{NS}	20.7	4.99	0.74	91.14
NDF	734.2 ^{NS}	7751.2***	2114.6*	153.0 ^{NS}	304.0	2.70	0.87	646.77
ADF	153.7 ^{NS}	12462.0***	1440.6**	63.2 ^{NS}	163.2	4.20	0.95	304.20
ADL	7.6 ^{NS}	1420.3***	112.6***	6.1 ^{NS}	5.7	3.77	0.98	63.40
HC	423.9 ^{NS}	2775.3***	64.5 ^{NS}	168.1 ^{NS}	360.0	5.50	0.67	342.57
C	206.1 ^{NS}	5639.9***	747.7*	70.6 ^{NS}	169.4	5.40	0.89	240.80
CP	6.5 ^{NS}	9875.6***	1812.8***	125.9***	2.9	1.98	0.99	85.99
CPY	0.01**	0.8***	0.9***	0.04***	0.003	4.92	0.99	1.05
DCP	5.7 ^{NS}	8523.2***	1566.7***	108.7***	2.5	3.51	0.99	44.68
IVDMD	236.2 ^{NS}	11394.5***	1979.2*	66.1 ^{NS}	411.0	3.38	0.87	599.54
TDN	96.2 ^{NS}	7778.0***	897.8**	39.6 ^{NS}	101.9	1.56	0.95	648.69
DDM	93.4 ^{NS}	7563.6***	873.3**	38.6 ^{NS}	99.0	1.53	0.95	652.03
DY	1.0**	49.1***	11.0***	0.3 ^{NS}	0.2	5.43	0.98	7.91
TDNY	1.7***	58.3***	11.4***	0.3 ^{NS}	0.2	4.85	0.99	8.59
DMI	0.0 ^{NS}	0.1***	0.02*	0.002 ^{NS}	0.003	2.74	0.87	1.86
RFV	28.3 ^{NS}	640.1***	122.1**	6.7 ^{NS}	10.5	3.44	0.94	94.36
RFQ	31.7 ^{NS}	710.8***	133.2**	7.3 ^{NS}	11.5	3.45	0.94	98.46
DE	0.03 ^{NS}	2.7***	0.3**	0.01 ^{NS}	0.03	1.56	0.95	11.97
ME	0.02 ^{NS}	1.8***	0.2**	0.01 ^{NS}	0.02	1.56	0.95	9.8
NEI	0.01 ^{NS}	0.8***	0.1**	0.004 ^{NS}	0.01	1.68	0.95	6.17
NEm	0.01 ^{NS}	1.1***	0.1**	0.01 ^{NS}	0.02	1.84	0.95	6.67
NEg	0.01 ^{NS}	1.1***	0.1**	0.01 ^{NS}	0.02	3.36	0.95	3.65

Ash = ash (g/kg DM); NDF = neutral detergent fiber (g/kg DM); ADF = acid detergent fiber (g/kg DM); ADL = acid detergent lignin (g/kg DM); HC = hemicellulose (g/kg DM); C = cellulose (g/kg DM); CP = crude protein (g/kg DM); CPY = crude protein yield (t/ha); DCP = digestible crude protein (g/kg DM); IVDMD = in-vitro dry matter digestibility (g/kg DM); TDN = total digestible nutrients (g/kg DM); DDM = digestible dry matter (g/kg DM); DY = digestible yield (t/ha); TDNY = total digestible nutrients yield (t/ha); DMI = dry matter intake (% body weight); RFV = relative feed value; RFQ = relative feed quality; DE = digestible energy (MJ/kg DM); ME = metabolizable energy (MJ/kg DM); NEI = net energy lactation (MJ/kg DM); NEm = net energy maintenance (MJ/kg DM); NEg = net energy gain (MJ/kg DM); R = replication; F = fertilizer level; Y = year; F x Y = fertilizer level by year interaction; NS = Non-significant; *, **, and *** = significantly different at 5, 1, and 0.1%, respectively.

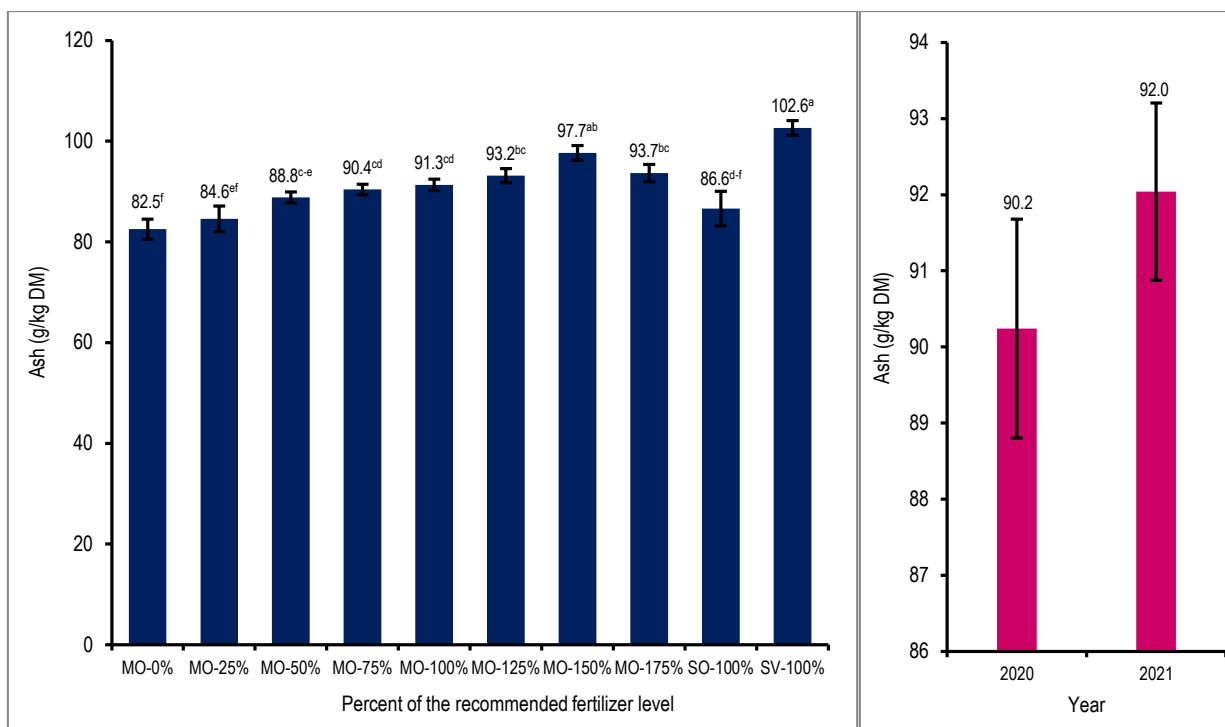


Figure 6.11 The mean ash content of oat/vetch mixed cropping under different fertilizer levels (left) and year of production (right) at Holetta. **Note:** MO = mixed oat; SO = sole oat; SV = sole vetch.

6.3.3.2.2 Cell wall concentrations

The effect of production year on the fiber contents of oat/vetch mixtures is indicated in [Table 6.16](#). The result showed that the neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), and cellulose (C) contents of oat/vetch mixtures were significantly influenced by year of production. The higher NDF, ADF, ADL, C, and hemicellulose (HC) contents were recorded in 2020 compared to the 2021 cropping season. Similarly, fertilizer application had a significant effect on all fiber contents of oat/vetch mixtures ([Table 6.16](#)). The result revealed that fertilizer application generally decreases the NDF, ADF, ADL, and C contents of oat/vetch mixtures. The oat/vetch mixtures sown without fertilizer had the highest NDF (703.2 g/kg DM), ADF (366.0 g/kg DM), ADL (83.5 g/kg DM), and C (282.5 g/kg DM) contents. Among oat/vetch mixtures, the lowest NDF (619.8 g/kg DM), ADF (248.7 g/kg DM), ADL (42.3 g/kg DM), and C (206.3 g/kg DM) contents were recorded from the application of 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate. However, the lowest (315.6 g/kg DM) and highest (378.6 g/kg DM) contents of HC were recorded from the application of 50% (20.5 kg N + 10 kg P/ha) and 175% (71.8 kg N + 35 kg P/ha) of the recommended

fertilizer rates, respectively. Similarly, sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate gave the lowest NDF, ADF, ADL, HC, and C contents compared to sole oat and all mixtures. Moreover, application of 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate on oat/vetch mixtures gave the lowest NDF (638.9 g/kg DM), ADF (289.7 g/kg DM), ADL (62.2 g/kg DM), and C (227.5 g/kg DM) contents compared to sole oat sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate.

Table 6.16 Mean fodder neutral detergent fiber, acid detergent fiber, acid detergent lignin, hemicellulose, and cellulose contents of oat/vetch mixed cropping under different fertilizer levels and year of production at Holetta

Factor	g/kg DM				
	NDF	ADF	ADL	HC	C
Year					
2020	652.7 ^a	309.1 ^a	64.8 ^a	343.6	244.3 ^a
2021	640.8 ^b	299.3 ^b	62.0 ^b	341.5	237.3 ^b
<i>P</i> -value	0.0120	0.0051	<.0001	0.6745	0.0423
Percent of the recommended fertilizer level					
Mixed oat 0%	703.2 ^a	366.0 ^a	83.5 ^a	337.2 ^{cd}	282.5 ^a
Mixed oat 25%	683.0 ^{ab}	352.2 ^{ab}	82.3 ^a	330.8 ^{cd}	269.8 ^{ab}
Mixed oat 50%	658.3 ^{cd}	342.7 ^{bc}	75.3 ^b	315.6 ^d	267.3 ^{ab}
Mixed oat 75%	649.0 ^{c-e}	329.2 ^c	73.0 ^b	319.8 ^d	256.2 ^b
Mixed oat 100%	638.9 ^{d-f}	289.7 ^d	62.2 ^d	349.2 ^{bc}	227.5 ^c
Mixed oat 125%	632.5 ^{ef}	271.7 ^e	55.3 ^e	360.8 ^{ab}	216.3 ^{cd}
Mixed oat 150%	619.8 ^f	248.7 ^f	42.3 ^g	371.2 ^{ab}	206.3 ^d
Mixed oat 175%	646.3 ^{c-e}	267.7 ^e	52.5 ^f	378.6 ^a	215.2 ^{cd}
Sole oat 100%	665.3 ^{bc}	333.0 ^c	66.3 ^c	332.3 ^{cd}	266.7 ^{ab}
Sole vetch 100%	571.6 ^g	241.3 ^f	41.2 ^g	330.2 ^{cd}	200.2 ^d
<i>P</i> -value	<.0001	<.0001	<.0001	<.0001	<.0001

NDF = neutral detergent fiber (g/kg DM); **ADF** = acid detergent fiber (g/kg DM); **ADL** = acid detergent lignin (g/kg DM); **HC** = hemicellulose (g/kg DM); **C** = cellulose (g/kg DM); Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

6.3.3.2.3 Crude protein and dry matter intake

The effect of year was significant for crude protein (CP), crude protein yield (CPY), digestible crude protein (DCP), digestible dry matter (DDM), and dry matter intake (DMI) of oat/vetch mixtures (Table 6.17). Significantly higher contents of CP (91.5 g/kg DM), CPY (1.17 t/ha), DCP (49.8 g/kg DM), DDM (655.8 g/kg DM), and DMI (1.88 % body weight) were recorded in 2021 compared to 2020 cropping season. Similarly, the application of fertilizer had a significant effect on CP, CPY, DCP, DDM, and DMI parameters of oat/vetch mixtures (Table 6.17). The result showed that the oat/vetch mixtures sown without fertilizer application produced the lowest CP (51.6 g/kg DM), CPY (0.45 t/ha), DCP (12.7 g/kg DM), DDM (603.9 g/kg DM), and

DMI (1.71 % body weight). On the other hand, application of fertilizer at the rate of 150% (61.5 kg N + 30 kg P/ha) on oat/vetch mixtures gave the highest CPY (1.59 t/ha), DDM (695.3 g/kg DM), and DMI (1.94 % body weight). However, the highest CP (84.4 g/kg DM) and DCP (43.2 g/kg DM) contents of oat/vetch mixtures were recorded from the application of 175% (71.8 kg N + 35 kg P/ha) of the recommended fertilizer. The sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer gave the highest CP (197.8 g/kg DM), DCP (148.6 g/kg DM), DDM (701.0 g/kg DM), and DMI (2.11 % body weight) compared to sole oat and all mixtures. The oat/vetch mixtures sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate produced higher CP (76.6 g/kg DM), CPY (1.16 t/ha), DCP (36.0 g/kg DM), DDM (663.3 g/kg DM), and DMI (1.88 % body weight) contents compared to sole oat sown with the same fertilizer rate (100% of the recommended fertilizer).

Table 6.17 Mean fodder crude protein, crude protein yield, digestible crude protein, digestible dry matter, and dry matter intake of oat/vetch mixed cropping under different fertilizer levels and year of production at Holetta

Factor	CP	CPY	DCP	DDM	DMI
Year					
2020	80.5 ^b	0.92 ^b	39.6 ^b	648.2 ^b	1.85 ^b
2021	91.5 ^a	1.17 ^a	49.8 ^a	655.8 ^a	1.88 ^a
<i>P-value</i>	<.0001	<.0001	<.0001	0.0051	0.0138
Percent of the recommended fertilizer level					
Mixed oat 0%	51.6 ^g	0.45 ^h	12.7 ^g	603.9 ^f	1.71 ^g
Mixed oat 25%	62.4 ^f	0.70 ^g	22.8 ^f	614.6 ^{ef}	1.76 ^{fg}
Mixed oat 50%	72.4 ^e	0.91 ^f	32.1 ^e	622.1 ^{de}	1.83 ^{de}
Mixed oat 75%	75.8 ^d	1.05 ^e	35.2 ^d	632.6 ^d	1.85 ^{c-e}
Mixed oat 100%	76.6 ^d	1.16 ^d	36.0 ^d	663.3 ^c	1.88 ^{b-d}
Mixed oat 125%	81.9 ^c	1.36 ^c	40.9 ^c	677.4 ^b	1.90 ^{bc}
Mixed oat 150%	84.1 ^b	1.59 ^a	42.9 ^b	695.3 ^a	1.94 ^b
Mixed oat 175%	84.4 ^b	1.46 ^b	43.2 ^b	680.5 ^b	1.86 ^{c-e}
Sole oat 100%	72.9 ^e	1.04 ^e	32.5 ^e	629.6 ^d	1.81 ^{ef}
Sole vetch 100%	197.8 ^a	0.76 ^g	148.6 ^a	701.0 ^a	2.11 ^a
<i>P-value</i>	<.0001	<.0001	<.0001	<.0001	<.0001

CP = crude protein (g/kg DM); CPY = crude protein yield (t/ha); DCP = digestible crude protein (g/kg DM); DDM = digestible dry matter (g/kg DM); DMI = dry matter intake (% body weight); Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

6.3.3.2.4 Forage digestibility and its yield

The in-vitro dry matter digestibility (IVDMD) of oat/vetch mixtures varied significantly with fertilizer application (Figure 6.12 left). The result showed that the IVDMD of oat/vetch mixtures increased with increasing fertilizer rates. The oat/vetch mixtures sown without fertilizer application gave the lowest IVDMD (532.7 g/kg DM) while application of 150% (61.5 kg N +

30 kg P/ha) of the recommended fertilizer rate on oat/vetch mixtures produced the highest IVDMD (638.0 g/kg DM) compared to sole oat and other mixtures. On the other hand, the oat/vetch mixtures sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate gave higher IVDMD (598.5 g/kg DM) compared to sole oat sown with the same recommended fertilizer rate. However, sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate gave the highest IVDMD (681.0 g/kg DM) compared to sole oat and all mixtures. The IVDMD of oat/vetch mixtures was also significantly influenced by the year of production (Figure 6.12 right). The results showed that the highest IVDMD (605.3 g/kg DM) was recorded in 2021 compared to 2020 (593.8 g/kg DM) cropping season.

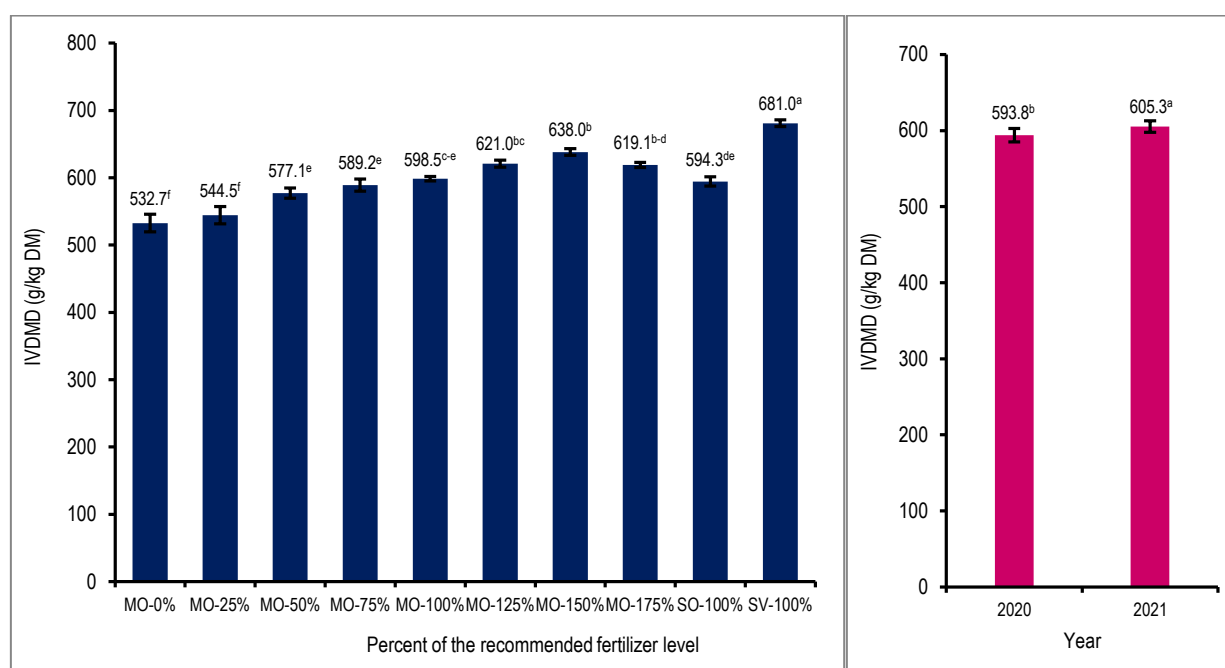


Figure 6.12 Mean in-vitro dry matter digestibility of oat/vetch mixed cropping under different fertilizer levels (left) and year of production (right) at Holetta. **Note:** IVDMD = in-vitro dry matter digestibility; **MO** = mixed oat; **SO** = sole oat; **SV** = sole vetch.

The digestible yield (DY) of oat/etch mixtures varied significantly with the application of fertilizer (Figure 6.13 left). The result showed that the DY increased with increasing fertilizer rates. Accordingly, the oat/vetch mixtures sown without fertilizer application produced the lowest DY (4.7 t/ha) while the oat/vetch mixtures sown with 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate gave the highest DY (12.0 t/ha). On the other hand, the oat/vetch mixtures sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate gave higher DY (9.0 t/ha) compared to sole oat sown with the same fertilizer rate. The sole

vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate generally produced the lowest DY (2.6 t/ha) compared to sole oat and all mixtures. The DY also varied significantly with cropping seasons (Figure 6.13 right). The result showed that oat/vetch mixtures sown in the 2021 cropping season had higher DY (8.3 t/ha) compared to the 2020 (7.5 t/ha) cropping season.

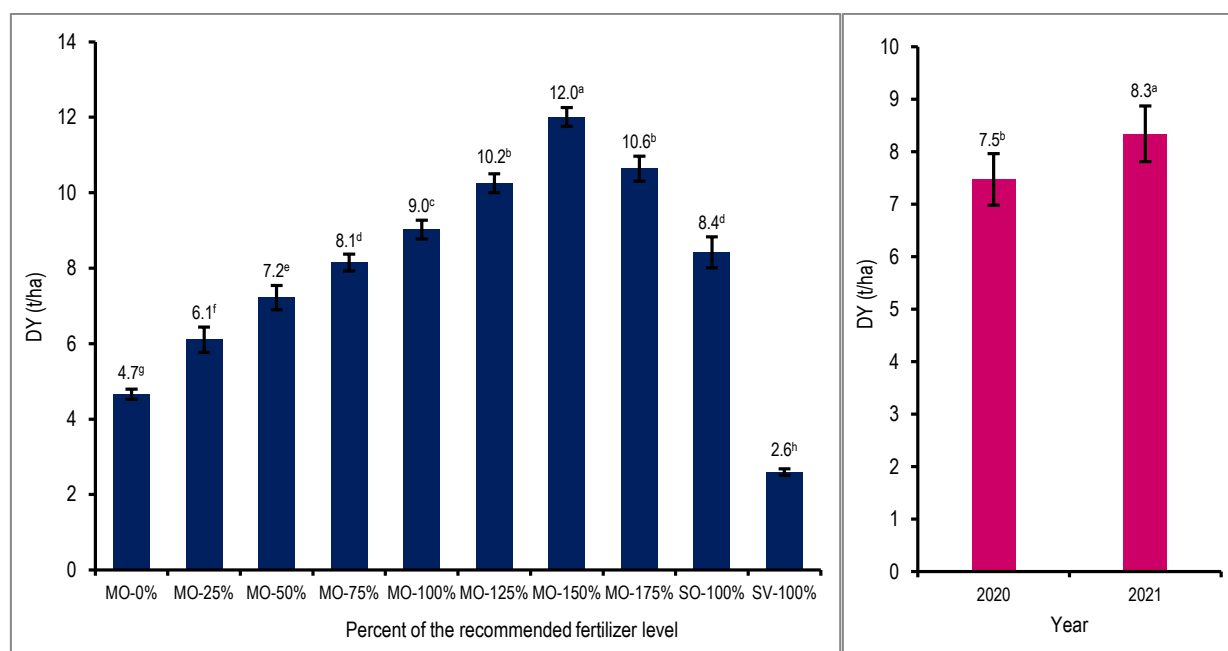


Figure 6.13 The mean digestible yield of oat/vetch mixed cropping under different fertilizer levels (left) and year of production (right) at Holetta. **Note:** DY = digestible yield; MO = mixed oat; SO = sole oat; SV = sole vetch.

6.3.3.2.5 Digestible nutrients and their yield

The total digestible nutrients (TDN) of oat/vetch mixtures varied significantly with fertilizer application (Figure 6.14 left). The TDN of oat/vetch mixtures increased with increasing fertilizer rates. Accordingly, the lowest TDN (599.9 g/kg DM) was observed for oat/vetch mixtures sown without fertilizer application. On the other hand, the highest TDN (692.6 g/kg DM) was recorded for oat/vetch mixtures sown with 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate compared to sole oat and other mixtures. The oat/vetch mixtures sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate gave higher TDN (66.2 g/kg DM) compared to sole oat sown with the same fertilizer rate. However, sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate produced the highest TDN (698.3 g/kg DM) compared to sole oat and all mixtures. The TDN of oat/vetch mixtures

also varied significantly with cropping seasons (Figure 6.14 right). The result showed a higher TDN (652.6 g/kg DM) was recorded in 2021 compared to 2020 (644.8 g/kg DM) cropping season.

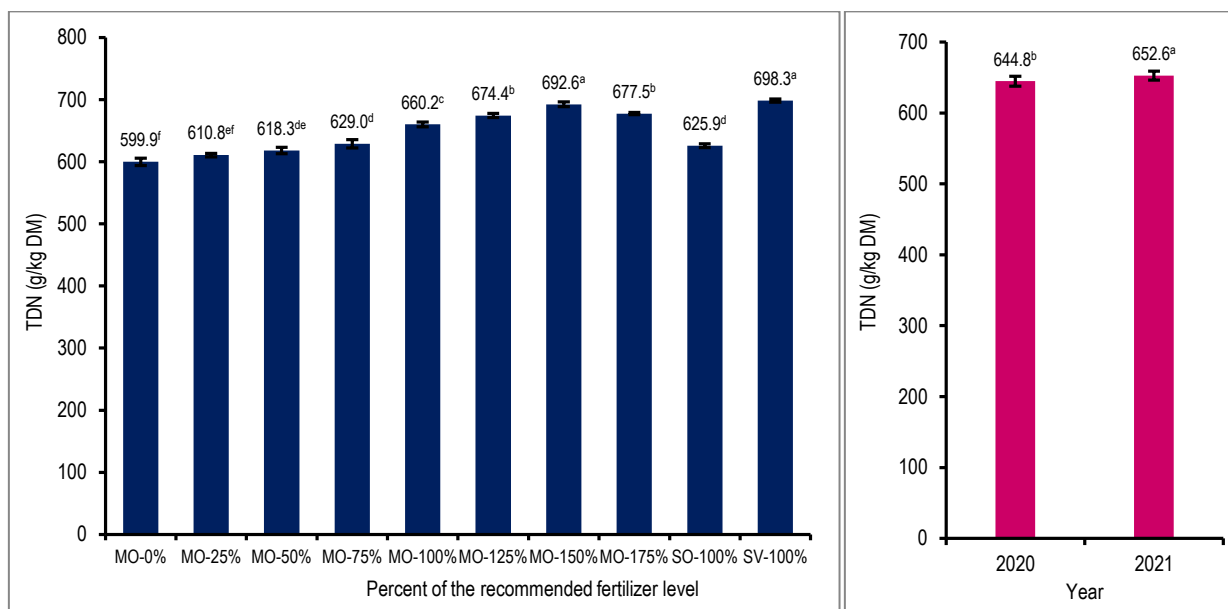


Figure 6.14 Mean total digestible nutrient of oat/vetch mixed cropping under different fertilizer levels (left) and year of production (right) at Holetta. **Note:** TDN = total digestible nutrient; MO = mixed oat; SO = sole oat; SV = sole vetch.

The total digestible nutrient yield (TDNY) of oat/vetch mixtures varied significantly with fertilizer application (Figure 6.15 left). The result showed that the oat/vetch mixtures sown without fertilizer application had the lowest TDNY (5.3 t/ha) while oat/vetch mixtures sown with 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate gave the highest TDNY (13.0 t/ha). The oat/vetch mixtures sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate had higher TDNY (10.0 t/ha) compared to sole oat sown with the same fertilizer rate. Moreover, the sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate had the lowest TDNY (2.7 t/ha) compared to sole oat and all mixtures. The TDNY of oat/vetch mixtures varied significantly with cropping season (Figure 6.15 right). The result showed that the TDNY was higher (9.0 t/ha) in 2021 than 2020 cropping season.

6.3.3.2.6 Relative feed value and quality

The relative feed value (RFV) of oat/vetch mixtures varied significantly with fertilizer application (Figure 6.16 left). The RFV of oat/vetch mixtures increased with increasing fertilizer

rates. Accordingly, the oat/vetch mixtures sown without fertilizer had the lowest RFV (79.9) while application of 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate on oat/vetch mixtures gave the highest RFV (104.4) compared to sole oat and other mixtures. The oat/vetch mixtures sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate had higher RFV (96.6) compared to sole oat sown with the same fertilizer rate. The sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate had the highest RFV (114.3) compared to oat/vetch mixtures and sole oat. Similarly, the production year had a significant effect on the RFV of oat/vetch mixtures (Figure 6.16 right). The result showed that a higher RFV (95.8) was observed in 2021 compared to 2020 (92.9) cropping season.

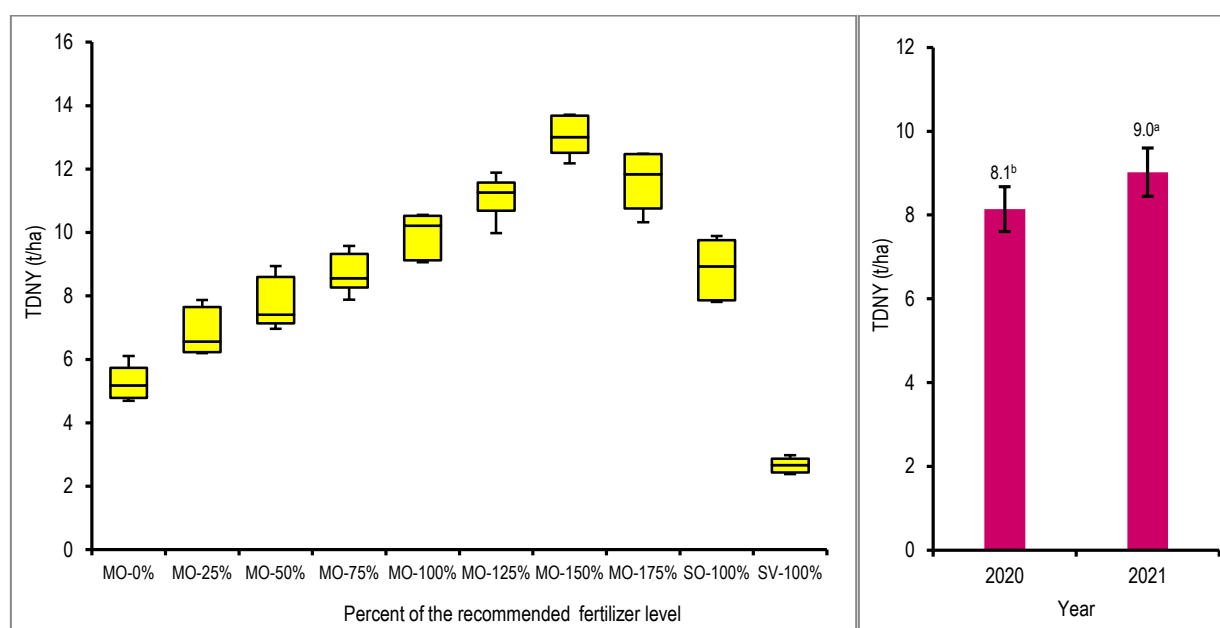


Figure 6.15 The mean total digestible nutrient yield of oat/vetch mixed cropping under different fertilizer levels (left) and year of production (right) at Holetta. **Note:** TDNY = total digestible nutrient yield; MO = mixed oat; SO = sole oat; SV = sole vetch.

The relative feed quality (RFQ) of oat/vetch mixtures varied significantly with fertilizer application (Figure 6.17 left). The result showed that the highest RFQ (109.0) was recorded for oat/vetch mixtures sown with 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate compared to sole oat and other mixtures while the lowest RFQ (83.3) was recorded for oat/vetch mixtures sown without fertilizer application. The sole oat sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate gave a lower RFQ (91.9) while oat/vetch mixtures sown with the same fertilizer rate gave a higher RFQ (96.6). The sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate gave the highest RFQ (119.5)

compared to oat/vetch mixtures and sole oat. The RFQ of oat/vetch mixtures also varied significantly with production years (Figure 6.17 right). The highest RFQ (100.0) was recorded in 2021 than in 2020 (97.0).

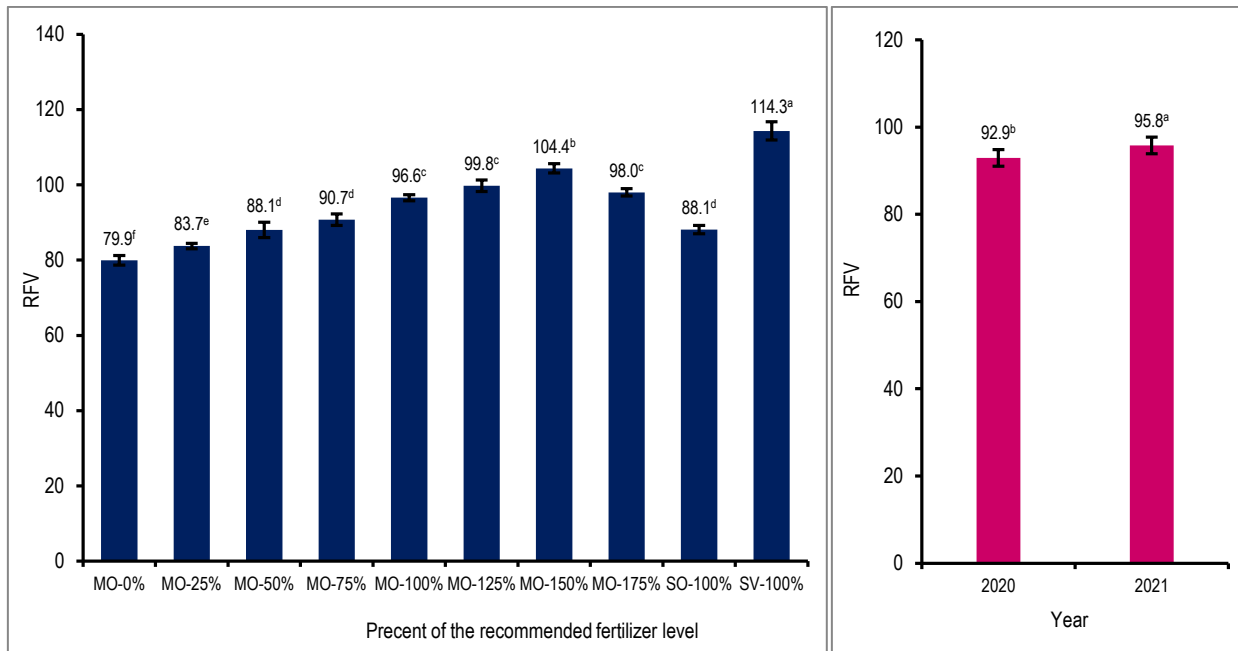


Figure 6.16 Mean relative feed value of oat/vetch mixed cropping under different fertilizer levels (left) and year of production (right) at Holetta. **Note:** RFV = relative feed value; MO = mixed oat; SO = sole oat; SV = sole vetch.

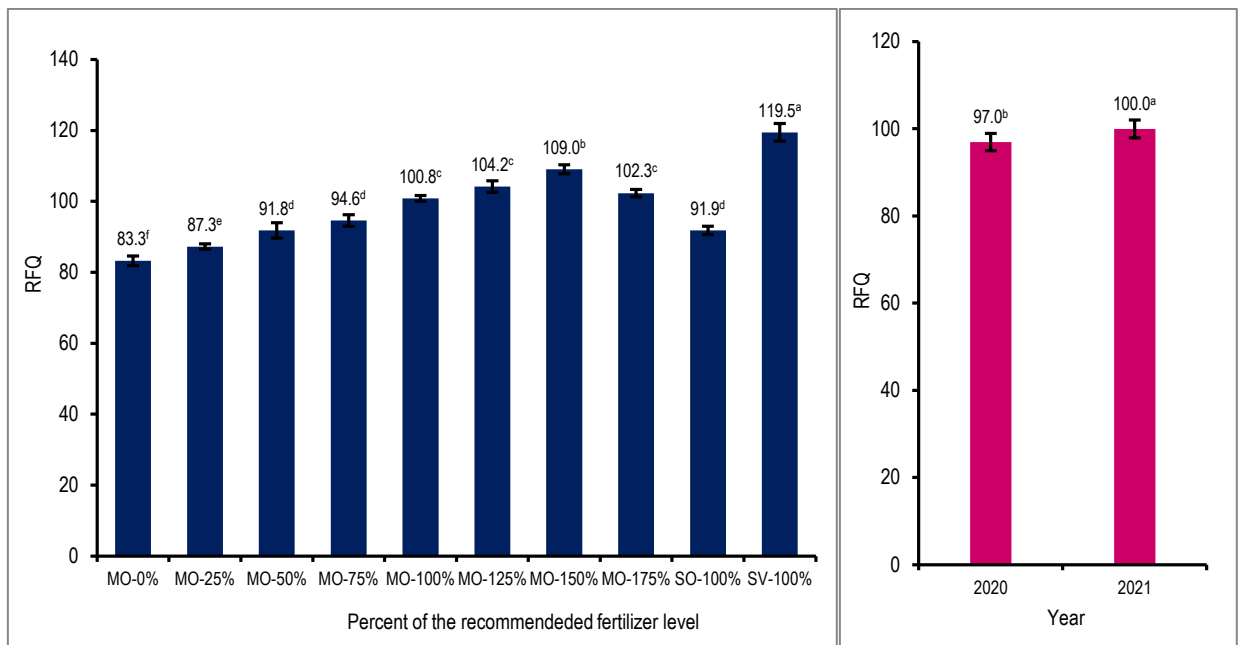


Figure 6.17 Mean relative feed quality of oat/vetch mixed cropping under different fertilizer levels (left) and year of production (right) at Holetta. **Note:** RFQ = relative feed quality; MO = mixed oat; SO = sole oat; SV = sole vetch.

6.3.3.2.7 Energy fractions of the feed

The digestible energy (DE), metabolizable energy (ME), net energy for lactation (NEL), net energy for maintenance (NEm), and net energy for gain (NEg) of oat/vetch mixtures varied significantly for cropping seasons (Table 6.18). The result showed that oat/vetch mixtures had higher DE (12.0 MJ/kg DM), ME (9.8 MJ/kg DM), NEL (6.2 MJ/kg DM), NEm (6.7 MJ/kg DM), and NEg (3.7 MJ/kg DM) in 2021 than 2020 cropping season. The oat/vetch mixtures sown with different fertilizer rates had a significant effect on DE, ME, NEL, NEm, and NEg (Table 6.18). The result showed that the DE, ME, NEL, NEm, and NEg generally increased with increasing fertilizer rates. Accordingly, the oat/vetch mixtures sown without fertilizer application gave the lowest DE (11.1 MJ/kg DM), ME (9.1 MJ/kg DM), NEL (5.7 MJ/kg DM), NEm (6.1 MJ/kg DM), and NEg (3.1 MJ/kg DM). On the other hand, application of 150% (61.5 kg N + 30 kg P/ha) of the recommended fertilizer rate on oat/vetch mixtures gave the highest DE (12.8 MJ/kg DM), ME (10.5 MJ/kg DM), NEL (6.6 MJ/kg DM), NEm (7.2 MJ/kg DM), and NEg (4.2 MJ/kg DM) compared to sole oat and other mixtures.

Table 6.18 Mean fodder digestible energy, metabolizable energy, net energy for lactation, net energy for maintenance, and net energy for gain of oat/vetch mixed cropping under different fertilizer levels and year of production at Holetta

Factor	MJ/kg DM				
	DE	ME	NEL	NEm	NEg
Year					
2020	11.9 ^b	9.8 ^b	6.1 ^b	6.6 ^b	3.6 ^b
2021	12.0 ^a	9.9 ^a	6.2 ^a	6.7 ^a	3.7 ^a
<i>P-value</i>	0.0052	0.0059	0.0053	0.0050	0.0051
Percent of the recommended fertilizer level					
Mixed oat 0%	11.1 ^f	9.1 ^f	5.7 ^f	6.1 ^f	3.1 ^f
Mixed oat 25%	11.3 ^{ef}	9.2 ^{ef}	5.8 ^{ef}	6.2 ^{ef}	3.2 ^{ef}
Mixed oat 50%	11.4 ^{de}	9.4 ^{de}	5.9 ^{de}	6.3 ^{de}	3.3 ^{de}
Mixed oat 75%	11.6 ^d	9.5 ^d	6.0 ^d	6.4 ^d	3.4 ^d
Mixed oat 100%	12.2 ^c	10.0 ^c	6.3 ^c	6.8 ^c	3.8 ^c
Mixed oat 125%	12.4 ^b	10.2 ^b	6.4 ^b	7.0 ^b	4.0 ^b
Mixed oat 150%	12.8 ^a	10.5 ^a	6.6 ^a	7.2 ^a	4.2 ^a
Mixed oat 175%	12.5 ^b	10.2 ^b	6.5 ^b	7.0 ^b	4.0 ^b
Sole oat 100%	11.5 ^d	9.5 ^d	5.9 ^d	6.4 ^d	3.4 ^d
Sole vetch 100%	12.9 ^a	10.6 ^a	6.7 ^a	7.3 ^a	4.3 ^a
<i>P-value</i>	<.0001	<.0001	<.0001	<.0001	<.0001

DE = digestible energy (MJ/kg DM); ME = metabolizable energy (MJ/kg DM); NEL = net energy for lactation (MJ/kg DM); NEm = net energy for maintenance (MJ/kg DM); NEg = net energy for gain; Means followed by a common superscript letter within a column for each factor are not significantly different from each other at $P < 0.05$.

The oat/vetch mixtures sown with 100% (41.0 kg N + 20 kg P/ha) of the recommended fertilizer rate had higher DE (12.2 MJ/kg DM), ME (10.0 MJ/kg DM), NEI (6.3 MJ/kg DM), NEm (6.8 MJ/kg DM), and NEg (3.8 MJ/kg DM) compared to sole oat sown with the same fertilizer rate. The sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate gave the highest DE (12.9 MJ/kg DM), ME (10.6 MJ/kg DM), NEI (6.7 MJ/kg DM), NEm (7.3 MJ/kg DM), and NEg (4.3 MJ/kg DM) compared to oat/vetch mixtures and sole oat.

6.3.3.3 Associations among measured parameters

The associations between fertilizer rates and measured parameters of oat/vetch mixtures are indicated in Table 6.19. The result showed that all the measured parameters of oat/vetch mixtures had significant ($P < .0001$) associations with rates of fertilizer application. Among the measured parameters, the NDF ($r = -0.74^{***}$), ADF ($r = -0.92^{***}$), ADL ($r = -0.93^{***}$), and C ($r = -0.87^{***}$) contents of oat/vetch mixtures were significantly and inversely associated with fertilizer rates. On the other hand, the remaining measured parameters were significantly and positively associated with rates of fertilizer application.

Table 6.19 Interrelationships between fertilizer rates and measured parameters of oat/vetch mixed cropping at Holetta

Parameter	Coefficient with RFR	P-value	Significance level	Parameters	Coefficient with RFR	P-value	Significance level
RFR	1.00	-	-	TDN	0.92	<.0001	***
Ash	0.73	<.0001	***	DDM	0.92	<.0001	***
NDF	-0.74	<.0001	***	DY	0.93	<.0001	***
ADF	-0.92	<.0001	***	TDNY	0.94	<.0001	***
ADL	-0.93	<.0001	***	DMI	0.74	<.0001	***
IVDMD	0.84	<.0001	***	RFV	0.87	<.0001	***
CP	0.80	<.0001	***	RFQ	0.88	<.0001	***
TFDMY	0.93	<.0001	***	DE	0.92	<.0001	***
CPY	0.89	<.0001	***	ME	0.92	<.0001	***
HC	0.68	<.0001	***	NEI	0.92	<.0001	***
C	-0.87	<.0001	***	NEm	0.92	<.0001	***
DCP	0.80	<.0001	***	NEg	0.92	<.0001	***

RFR = Recommended fertilizer rates; Ash = ash (g/kg DM); NDF = neutral detergent fiber (g/kg DM); ADF = acid detergent fiber (g/kg DM); ADL = acid detergent lignin (g/kg DM); IVDMD = in-vitro dry matter digestibility (g/kg DM); CP = crude protein (g/kg DM); TFDMY = total forage dry matter yield (t/ha); CPY = crude protein yield (t/ha); HC = hemicellulose (g/kg DM); C = cellulose (g/kg DM); DCP = digestible crude protein (g/kg DM); TDN = total digestible nutrients (g/kg DM); DDM = digestible dry matter (g/kg DM); DY = digestible yield (t/ha); TDNY = total digestible nutrients yield (t/ha); DMI = dry matter intake (% body weight); RFV = relative feed value; RFQ = relative feed quality; DE = digestible energy (MJ/kg DM); ME = metabolizable energy (MJ/kg DM); NEI = net energy for lactation (MJ/kg DM); NEm = net energy for maintenance (MJ/kg DM); NEg = net energy for gain (MJ/kg DM); *** = significantly different at 0.1%.

The Pearson correlation coefficients for measured parameters of oat/vetch mixtures are indicated in [Table 6.20](#). The result showed that all the pairwise correlation coefficients were significant except the correlation coefficients of NDF with HC and HC with DMI. The ash content was significantly and positively correlated with all measured parameters except fiber contents (NDF, ADF, ADL, and C) which had inverse associations with ash content. The NDF had significant positive associations with ADF ($r = 0.81^{***}$), ADL ($r = 0.77^{***}$), and C ($r = 0.79^{***}$) contents. Moreover, the ADF had significant positive associations with ADL ($r = 0.94^{***}$) and C ($r = 0.99^{***}$). However, the fiber contents (NDF, ADF, and ADL) had significant inverse associations with IVDMD, CP, TFDMY, CPY, DCP, TDN, DDM, DY, TDNY, DMI, RFV, RFQ, DE, ME, NEL, NEm, and NEg. The IVDMD had significant positive associations with CP, TFDMY, CPY, and HC. The CP had significant positive associations with TFDMY, CPY, and HC. The TFDMY had also significant positive associations with CPY and HC. Moreover, the IVDMD, CP, TFDMY, and CPY had significant inverse associations with C content while these parameters had significant positive associations with DCP, TDN, DDM, DY, TDNY, DMI, RFV, RFQ, and energy parameters. The DCP, TDN, and DDM had significant positive associations with DY, TDNY, DMI, RFV, RFQ, and energy parameters. Similarly, the DY, TDNY, and DMI had significant positive associations with RFV, RFQ, DE, ME, NEL, NEm, and NEg. The RFV and RFQ had significant positive associations with DE, ME, NEL, NEm, and NEg. Moreover, all the pairwise correlations of feed energy parameters (DE, ME, NEL, NEm, and NEg) were significant and positive.

Table 6.20 Pearson correlation coefficients for total fodder yield and nutritive value of oat/vetch mixed cropping at Holetta

Parameter	Ash	NDF	ADF	ADL	IVDMD	CP	TFDMY	CPY	HC	C	DCP	TDN	DDM	DY	TDNY	DMI	RFV	RFQ	DE	ME	NEI	NE _m
NDF	-0.64***																					
ADF	-0.70***	0.81***																				
ADL	-0.76***	0.77***	0.94***																			
IVDMD	0.76***	-0.72***	-0.82***	-0.85***																		
CP	0.70***	-0.72***	-0.74***	-0.78***	0.74***																	
TFDMY	0.75***	-0.81***	-0.93***	-0.94***	0.86***	0.86***																
CPY	0.74***	-0.78***	-0.88***	-0.91***	0.83***	0.95***	0.97***															
HC	0.44**	-0.20 ^{NS}	-0.74***	-0.68***	0.53***	0.41**	0.63***	0.58***														
C	-0.64***	0.79***	0.99***	0.87***	-0.77***	-0.69***	-0.89***	-0.83***	-0.74***													
DCP	0.70***	-0.72***	-0.74***	-0.78***	0.74***	1.00***	0.86***	0.95***	0.41**	-0.69***												
TDN	0.70***	-0.81***	-1.00***	-0.94***	0.82***	0.74***	0.93***	0.88***	0.74***	-0.99***	0.74***											
DDM	0.70***	-0.81***	-1.00***	-0.94***	0.82***	0.74***	0.93***	0.88***	0.74***	-0.99***	0.74***	1.00***										
DY	0.77***	-0.80***	-0.93***	-0.95***	0.90***	0.85***	0.99***	0.96***	0.64***	-0.88***	0.85***	0.93***	0.93***									
TDNY	0.74***	-0.81***	-0.96***	-0.96***	0.86***	0.84***	1.00***	0.96***	0.67***	-0.92***	0.84***	0.96***	0.96***	0.99***								
DMI	0.64***	-1.00***	-0.81***	-0.77***	0.72***	0.72***	0.81***	0.78***	0.21 ^{NS}	-0.79***	0.72***	0.81***	0.81***	0.80***	0.81***							
RFV	0.70***	-0.94***	-0.96***	-0.91***	0.81***	0.77***	0.92***	0.87***	0.52***	-0.94***	0.77***	0.96***	0.96***	0.91***	0.93***	0.94***						
RFQ	0.70***	-0.94***	-0.96***	-0.91***	0.81***	0.77***	0.92***	0.87***	0.53***	-0.94***	0.77***	0.96***	0.96***	0.91***	0.93***	0.94***	1.00***					
DE	0.70***	-0.81***	-1.00***	-0.94***	0.82***	0.74***	0.93***	0.88***	0.74***	-0.99***	0.74***	1.00***	1.00***	0.93***	0.96***	0.81***	0.96***	0.96***				
ME	0.70***	-0.80***	-1.00***	-0.94***	0.82***	0.74***	0.93***	0.88***	0.74***	-0.99***	0.74***	1.00***	1.00***	0.93***	0.96***	0.81***	0.96***	0.96***	1.00***			
NEI	0.70***	-0.81***	-1.00***	-0.94***	0.82***	0.74***	0.93***	0.88***	0.74***	-0.99***	0.74***	1.00***	1.00***	0.93***	0.96***	0.81***	0.96***	0.96***	1.00***	1.00***		
NE _m	0.70***	-0.80***	-1.00***	-0.94***	0.82***	0.74***	0.93***	0.88***	0.74***	-0.99***	0.74***	1.00***	1.00***	0.93***	0.96***	0.81***	0.96***	0.96***	1.00***	1.00***	1.00***	
NE _g	0.70***	-0.81***	-1.00***	-0.94***	0.81***	0.74***	0.93***	0.88***	0.74***	-0.99***	0.74***	1.00***	1.00***	0.93***	0.96***	0.81***	0.96***	0.96***	1.00***	1.00***	1.00***	1.00***

Ash = ash (g/kg DM); **NDF** = neutral detergent fiber (g/kg DM); **ADF** = acid detergent fiber (g/kg DM); **ADL** = acid detergent lignin (g/kg DM); **IVDMD** = in-vitro dry matter digestibility (g/kg DM); **CP** = crude protein (g/kg DM); **TFDMY** = total forage dry matter yield (t/ha); **CPY** = crude protein yield (t/ha); **HC** = hemicellulose (g/kg DM); **C** = cellulose (g/kg DM); **DCP** = digestible crude protein (g/kg DM); **TDN** = total digestible nutrients (g/kg DM); **DDM** = digestible dry matter (g/kg DM); **DY** = digestible yield (t/ha); **TDNY** = total digestible nutrients yield (t/ha); **DMI** = dry matter intake (% body weight); **RFV** = relative feed value; **RFQ** = relative feed quality; **DE** = digestible energy (MJ/kg DM); **ME** = metabolizable energy (MJ/kg DM); **NEI** = net energy for lactation (MJ/kg DM); **NE_m** = net energy for maintenance (MJ/kg DM); **NE_g** = net energy for gain (MJ/kg DM); **NS** = Non-significant; ** and *** = significantly different at 1 and 0.1%, respectively.

Note: The green, orange, and yellow colors indicate the strength of correlation; green color is positively correlated; green to light green color indicates strong to weak positive correlation; orange color is negatively correlated; orange to light orange color indicates strong to weak negative correlation; and yellow color is positively and negatively correlated; yellow to light yellow color indicates very weak to no correlation.

6.4 Discussion

6.4.1 Agro-morphological traits

6.4.1.1 Analysis of variance

The pooled analysis of variance indicated that fertilizer application had a significant effect on all measured agro-morphological traits of oat under oat/vetch mixed cropping system. This indicated that the application of fertilizer had a remarkable effect on NTPP, TDW, NLFH, LLFH, PHFH, DFH, OFDMY, and OFYPR in oat under oat/vetch mixed cropping. Different scholars also reported that fertilizer application on cereal/grass-legume intercropping/mixed cropping was significant for yield and yield components in different crops (Berhane *et al.*, 2015; Almaz, 2016; Ansarul *et al.*, 2018; Salah *et al.*, 2019; Dian *et al.*, 2020). Moreover, the nutrient concentration, nutrient uptake, and use efficiency of oat under oat/vetch mixed cropping were significant for fertilizer application. This indicated that fertilizer application had a substantial contribution to nutrient concentration (nitrogen and phosphorus), nutrient uptake (nitrogen, phosphorus, and total), and nutrient use efficiency (PFP, PNB, IUE, AE, and APE) of oat under oat/vetch mixed cropping system.

In this study, all the studied agro-morphological traits of oat under the oat/vetch mixed cropping system were also influenced by the year of production. This indicated that the two cropping seasons varied significantly in the amount and distribution of rainfall and minimum and maximum air temperatures. The influences of year on various agro-morphological traits of mixture crops were also reported (Tuna and Orak, 2007; Talukder *et al.*, 2015; Verónica *et al.*, 2017; Poloko *et al.*, 2018; Katarzyna *et al.*, 2021). Moreover, the year of production had a significant effect on nutrient concentration, nutrient uptake, and use efficiency of oat under oat/vetch mixed cropping. The interaction effects of fertilizer by year were significant for all measured parameters of nutrient concentration, nutrient uptake, and use efficiency except PNB due to both differential influences of fertilizer and year on these parameters. However, the interaction effects of fertilizer by year were non-significant for all measured agro-morphological traits, indicating that fertilizer application had a stable performance on agro-morphological traits of oat under oat/vetch mixed cropping in both production years.

6.4.1.2 Effects of year and fertilizer levels on oat performance

The effect of cropping season had a significant effect on the agro-morphological traits of oat under the oat/vetch mixed cropping system. The NTPP, TDW, NLFH, LLFH, and DFH were

higher in 2021 than 2020 cropping season. This indicated that the second year of production was more favorable for the growth of oat under the oat/vetch mixed cropping system. The weather data also indicated that the second year of production had a better amount and distribution of precipitation and relatively higher maximum and minimum temperatures which could stimulate the growth and development of oat under oat/vetch mixed cropping system. The study also indicated that cropping seasons influence the agro-morphological traits of oat under oat/vetch mixed cropping system (Puzynska *et al.*, 2021). Moreover, the agro-morphological traits of different crops were influenced by the year of production under the intercropping/mixed cropping system (Saleem *et al.*, 2011; Hamd *et al.*, 2014; Mukesh *et al.*, 2018).

The yield performance of main and component crops generally varies with population density, fertilizer application, climatic factors, and soil conditions under intercropping/mixed cropping systems. All crops generally require optimum growing conditions to express their maximum genetic potential. The yield of a crop is usually the function of genetics, environment, and management conditions. In this study, the forage yield and its production rate were significantly influenced by the year of production. The OFDMY, VFDMY, TFDMY, OFYPR, and TFYPR in the 2021 cropping season were higher by 9.7, 6.3, 9.6, 7.4, and 7.1% compared to the 2020 cropping season, respectively. The higher forage yield and forage yield production rate in the second year of production might be associated with better-growing conditions and higher performances of NTPP, TDW, NLFH, LLFH, PHFH, and DFH which resulted in higher growth and development, better resource use, and higher accumulation of dry matter yield. Different scholars also reported that the fodder dry matter yield of oat/vetch is significantly influenced by cropping seasons under various intercropping/mixed cropping systems (Saleem *et al.*, 2011; Mukesh *et al.*, 2018; Puzynska *et al.*, 2021; Wang *et al.*, 2021). The effect of cropping season on total forage yield under a mixed cropping system was also reported due to variations in environmental conditions like rainfall and temperature (Iqbal *et al.*, 2006a; Tuna and Orak, 2007; Labuschagne *et al.*, 2020). The nitrogen-fixing ability of vetch roots and transfer of fixed nitrogen by vetch to oat, extensive root system for absorption of water and nutrients, and less competition but higher facilitative effects of vetch on oat resulted in a higher yield of oat under oat/vetch mixed cropping system. Previous studies also indicated that the amount of nitrogen fixed by legume under the cereal/legume intercropping system was higher compared to the monocropping legume (Schipanski and Drinkwater, 2011). According to Duchene *et al.* (2017), this resource facilitation could be direct, where the

rhizosphere acts as an interface for the transfer of nutrients from legume to cereal/grass, or indirect, where a beneficial change in the rhizosphere improves the nutrient availability for the component crop.

Application of fertilizer on oat under oat/vetch mixed cropping system also had a significant effect on measured agro-morphological traits. The NTPP, TDW, NLFH, LLFH, and PHFH increased with increasing levels of fertilizer up to 150% (61.5 kg N + 30 kg P/ha) while DFH increased up to the application of 175% (71.8 kg N + 35 kg P/ha) fertilizer rates. The values of NTPP, TDW, NLFH, LLFH, and PHFH obtained from the application of 150% fertilizer rate on oat under oat/vetch mixed cropping system were higher by 93.1, 64.9, 40.0, 44.8, and 42.1% over oat sown without fertilizer under oat/vetch mixed cropping system. This indicated that the application of fertilizer had a remarkable contribution to the growth performances of oat under the oat/vetch mixed cropping system. The effect of fertilizer application on agro-morphological traits of different crops under intercropping/mixed cropping system is also reported by different scholars (Saleem *et al.*, 2011; de Motta *et al.*, 2020; Jardim *et al.*, 2020). Studies also indicated that increasing fertilizer rates could reduce interspecific competition in an intercropping system which resulted in better performance of agro-morphological traits (Shah *et al.*, 2010; Li *et al.*, 2011). Application of 175% fertilizer in this study delayed the forage harvesting date of oat by 16.0% compared to oat sown without fertilizer application under oat/vetch mixed cropping system. This indicated that the application of fertilizer kept vegetative growth active which resulted in delayed maturity. Studies also indicated that the application of nitrogen and phosphorus fertilizers significantly delayed days to maturity (Zelalem *et al.*, 2009; Israel *et al.*, 2012; Melkamu and Minwyet, 2018).

The yield of intercrops is higher and more stable due to the complementarity effects of the system via efficient partitioning and facilitation of growth resources and decreasing the intraspecific and interspecific competitions of mixture crops. The higher intercropping or mixed cropping yield advantage over sole cropping might be attributed to lower interspecific competition of the associated crops for growth resources compared to intraspecific competition of the crops of sole cultures. The interspecific competition between cereals and legumes at their optimum plant density makes cereals obtain high soil nitrogen which forces the legumes to fix more nitrogen and thus improves the resource use efficiency of the system (Li *et al.*, 2013). The higher yield of oat/vetch mixed cropping system might be associated

with better interception of solar radiation, higher utilization of symbiotically fixed nitrogen by associated grass, increased water and nutrient uptake, enhanced suppression of weeds, creation of suitable micro-environment for growth, and improve soil conservation. This complementarity effect enhances the growth parameters like plant height, number of tillers, number of leaves, root characteristics, leaf-to-stem ratio, and dry matter accumulation which resulted in higher forage yield and this result is also in accordance with other findings (Nasri *et al.*, 2014; Patil *et al.*, 2018; Singh and Verma, 2018). The studies also showed that mixed cropping produced higher yield compared to sole culture due to the complementarity effect of the system (Thompson *et al.*, 1992; Umunna *et al.*, 1995; Anil *et al.*, 1998; Sengul, 2003; Lauk and Lauk, 2009; Hindoriya *et al.*, 2019).

A higher intercropping advantage was also reported due to the higher biological response of crops to growing conditions and the competing ability of crops for growth resources such as water, light, and nutrients (Sadeghpour *et al.*, 2013b). According to Malay *et al.* (2014), the higher yield advantage of intercropping over sole culture was due to differences in nutrient requirements, root systems, plant height, growth duration, and photosynthetic systems of the associated crops. Getachew *et al.* (2008) also reported that the cooperation of nitrogen from nodulation of legume may exist under cereal-legume intercropping system which resulted in higher yield but the yield usually decreased due to competition when the associated crops have similarities in their needs for growth resources. Fertilizer application improves the fodder dry matter yield of oat and vetch under a mixed cropping system. This is due to fertilizer enhances the growth and development of crops and compatible crops generally utilize the available growth resources more efficiently for yield formation under a mixed cropping system compared to sole culture. The higher yield in the intercropping/mixed cropping system could be associated with minimal competition for the same niche areas and thereby tend to utilize the growth resources in a complementary way (Bacchi *et al.*, 2021).

In this study, the OFDMY, VFDMY, TFDMY, OFYPR, and TFYPR were influenced significantly by the application of fertilizer under the oat/vetch mixed cropping system. Accordingly, the OFDMY, VFDMY, TFDMY, OFYPR, and TFYPR increased with increasing levels of fertilizer up to 150% (61.5 kg N + 30 kg P/ha). Application of 150, 125, 100, 75, 50, and 25% fertilizer rates on oat under oat/vetch mixed cropping system increased the OFDMY by 107.4, 84.0, 67.9, 54.3, 40.7, and 27.2% over oat sown without fertilizer application. Similarly, application of 150, 125, 100, 75, 50, and 25% fertilizer rates increased the TFDMY by 113.6, 87.5, 71.6, 56.8, 42.0, and 27.3% over oat/vetch mixed

cropping sown without fertilizer application, respectively. The fodder dry matter yield of oat was higher than that of the respective vetch fodder yield with different fertilize rates. This is due to either genetic differences between oat and vetch or a stronger interspecific competitive ability of oat over vetch for growth resources during the growing period. This result is also confirmed by Li *et al.* (2014); Feng *et al.* (2015); and Wang *et al.* (2021), who reported that oat intercepted more light due to higher plant height compared to vetch which resulted in higher fodder yield of oat. Similarly, the forage dry matter yield of oat/vetch mixtures was generally higher compared to the sole culture of vetch (Tuna and Orak, 2007; Erol *et al.*, 2009; Ansar *et al.*, 2010; Ullah *et al.*, 2015; Barsila, 2018; Kedija, 2022). The TFDMY of oat/vetch mixtures observed in this study was different compared to other scholars (Fantahun, 2016; Kedija, 2022). This yield variation might be due to differences in factors of genetic, climatic, soil, management, and their interactions. Gezahagn *et al.* (2024a) also reported that the FDMY accumulation of oat/vetch mixtures differed due to differences in varieties, moisture availability, temperature, soil conditions, crop management, and their interactions.

The nutrient utilization efficiency and productivity of different crops are higher under intercropping/mixed cropping compared to monocropping due to better partitioning of resources that are used to utilize the available resources completely by crops that are intercropped/mixed cropped (Zhang and Li, 2003; Dhima *et al.*, 2007; Getachew *et al.*, 2008; Walelign, 2008; Mucheru-Muna *et al.*, 2010). The mixed cropping of vetch with oat considerably increased the dry matter yield in associated oat (Tuna and Orak, 2007; Erol *et al.*, 2009; Tarui *et al.*, 2013a; Tarui *et al.*, 2013b; Ullah *et al.*, 2015). The crops selected for intercropping/mixed cropping should have different rooting depth, phenology, and plant architecture to minimize competition and increase resource partitioning (Tsubo *et al.*, 2001; Litrico and Violle, 2015; Bybee-Finley and Ryan, 2018). Studies also indicated that the application of fertilizer increases the yield of main crops under mixtures in different crops (Abebe *et al.*, 2013; Jat *et al.*, 2014). The highest fodder yield of oat/vetch mixtures might be due to the result of grass being able to give support for the climbing vetch thus increasing the interception of solar radiation and vetch in turn might provide the atmospheric N₂-fixation with the grass counterpart and resulting in higher yield. Application of 150% fertilizer rate increased the OFYPR and TFYPR by 84.8 and 92.5% over the oat/vetch mixtures sown without fertilizer application, respectively. The VFDMY under oat/vetch mixed cropping was lower compared to sole vetch which was sown with its recommended fertilizer rate.

6.4.1.3 Effects of year and fertilizer levels on nutrient uptake and use efficiency

The nutrient content and uptake of oat under oat/vetch mixed cropping system were different for each production year due to variations in rainfall and temperature. Accordingly, the FPC, FNC, FPU, FNU, and TFNU of oat under oat/vetch mixed cropping system varied significantly between the two cropping seasons. The higher FPC, FNC, FPU, FNU, and TFNU were recorded in the second year compared to the first year of production. The presence of suitable growing conditions in the second year favors the concentration and uptake of nutrients by oat under oat/vetch mixed cropping system. The studies also indicated that nitrogen and phosphorus concentrations and their uptake are influenced by variations in growing seasons under the intercropping system (Latati *et al.*, 2019; Gecaite *et al.*, 2021). The higher nitrogen concentration and also the uptake of nitrogen and phosphorus were also reported for intercropping when compared to monocropping (Naudin *et al.*, 2010; Wang *et al.*, 2014; Latati *et al.*, 2019). The availability of soil moisture generally influences root growth, transpiration, and mobility of nutrients in the soil which results in lower concentration of nutrients and their uptake (Fageria *et al.*, 2002; Gunes *et al.*, 2006).

The variation in the availability of moisture and temperature influences the efficiency of nutrient utilization for better growth and productivity of crops. In this study, the cropping season also significantly influenced the PFP, PNB, IUE, AE, and APE of oat under the oat/vetch mixed cropping system. Among the nutrient use efficiency, significantly higher PFP, PNB, and AE were observed in the second year of production while IUE and APE were higher in the first year of production. This indicated that nutrient use efficiency is generally influenced by variations in growing seasons which is very essential for efficient utilization of the available growth nutrients for the growth and development of plants. The effect of nutrient use efficiency under mixed cropping systems in different crops was also reported (Molaaldoila *et al.*, 2017; Gezahagn *et al.*, 2024b; Gezahagn *et al.*, 2024c).

The nutrient concentration and nutrient uptake of oat under oat/vetch mixed cropping system are influenced significantly by the application of fertilizer. The FPC and FNC generally increased with increasing fertilizer rates up to 175% (71.8 kg N + 35 kg P/ha). Application of 175% fertilizer rate gave 128.2% higher FPC compared to oat sown without fertilizer application under oat/vetch mixed cropping system. Similarly, the FNC increased by 63.4% when oat sown with 175% fertilizer rate compared to oat sown without fertilizer under oat/vetch mixed cropping system. The micronutrient concentration and uptake of oat were

increased with increasing levels of nitrogen fertilizer under the oat/pea mixed cropping system (Reinhard and Hans-Peter, 2016). The nitrogen and phosphorus concentrations of oat under oat/vetch mixed cropping system were higher compared to sole oat culture (Arata *et al.*, 2013). Another study also indicated that intercropping/mixed cropping had greater nitrogen concentration compared to the respective sole crops (Chu *et al.*, 2004). The nitrogen uptake of cereal/grass crops mainly depends on the N₂-fixation capacity of legumes under a mixed cropping system. Moreover, the availability of phosphorus increased the N₂-fixation of legumes (Li *et al.*, 2008; Isaac *et al.*, 2011). The mixed cropping of vetch with oat considerably increased the nitrogen uptake in the associated oat (Tarui *et al.*, 2013a; Tarui *et al.*, 2013b). In this study, the nitrogen uptake in oat increased under mixed cropping with vetch due to nitrogen transfer from the associated vetch. The fixed nitrogen that accumulated in the root nodules of vetch during the vegetative growth stage could be transferred to the associated oat. Studies also indicated that intercropping of cereal-legume provides a higher yield of cereal components due to weak interspecific competition and the legume-mediated enhancement of nitrogen and phosphorus uptake by intercropped cereal (Grisley, 1997; Li *et al.*, 1999; Zhang and Li, 2003). The FPU increased with increasing levels of fertilizer up to 175% while the FNU and TFNU increased with increasing levels of fertilizer up to 150% (61.5 kg N + 30 kg P/ha). Similarly, the application of 175% fertilizer rate on oat increased the FPU by 330.8% over oat sown without fertilizer application under oat/vetch mixed cropping system. Moreover, the application of 150% fertilizer rate on oat increased the FNU and TFNU by 238.0 and 250.4% over oat sown without fertilizer application under oat/vetch mixed cropping system.

The nutrient use efficiency is significantly influenced by the application of fertilizer. The nutrient use efficiency was higher for lower fertilizer rate. Application of 25% (10.3 kg N + 5 kg P/ha) fertilizer rate on oat under oat/vetch mixed cropping system had 369.7, 225.0, 42.3, 110.2, and 30.4% higher in PFP, PNB, IUE, AE, and APE of oat compared to oat sown with 175% (71.8 kg N + 35 kg P/ha) fertilizer rate under oat/vetch mixed cropping system, respectively. Similar to these results, Jiang *et al.* (2000); Zemenchik and Albrecht (2002); Comakli *et al.* (2005) also reported that the application of the least nitrogen provides the highest efficiency of nitrogen compared to the application of the highest fertilizer doses. The study also indicated that there is a severe reduction in soil nitrogen retention efficiency under higher application of nitrogen which resulted in decreased nitrogen use efficiency (Huggins and Pan, 2003). The study also indicated that AE decreased with increasing rate of nitrogen

application (Ayneband *et al.*, 2012). The lowest fertilizer application also gave the highest APE in the mixed cropping system (Jankowski *et al.*, 2014). The nutrient demand of plants at the early growth stage is very low but the application of the highest rate of nitrogen at this stage may lead to high losses of nitrogen from the soil via leaching, denitrification, volatilization, and immobilization from the time of application to nitrogen uptake.

6.4.1.4 Relationships among measured parameters

The Pearson correlation analysis indicated that the application of fertilizer had a significant effect on agro-morphological traits, nutrient concentration, nutrient uptake, and use efficiency of oat under oat/vetch mixed cropping system. Accordingly, the application of fertilizer had significant and positive associations on OFDMY, NTPP, TDW, PHFH, NLFH, LLFH, DFH, and OFYPR of oat under oat/vetch mixed cropping system. This indicated that fertilizer application improves the yield components of oat which resulted in higher fodder dry matter yield. Thus, selection based on NTPP, TDW, PHFH, NLFH, LLFH, DFH, and OFYPR would be effective for fodder yield improvement in oat. This result is also in close conformity with the findings of Gezahagn *et al.* (2024b) who reported that NTPP, FDMY, and FYPR of oat had significant and positive associations with fertilizer applications. The OFDMY had significant and positive associations with NTPP, TDW, NLFH, LLFH, PHFH, DFH, and OFYPR of oat under the oat/vetch mixed cropping system. Gezahagn *et al.* (2023) also reported that FDMY had significant and positive associations with NLFH, LLFH, PHFH, and FYPR in oat. A significant and positive association of FDMY with NTPP, PHFH, and FYPR was also reported in oat (Gezahagn *et al.*, 2024b). Moreover, a significant and positive association of FDMY with PHFH was also reported by different scholars (Fekede, 2004; Wagh *et al.*, 2018).

The effects of fertilizer application had significant and positive associations with FPC, FNC, FPU, FNU, and TFNU of oat under oat/vetch mixed cropping system. This indicated that the nutrient concentrations and uptake of oat fodder increased with increasing levels of fertilizer application. Studies also indicated that the nutrient concentrations and uptake of oat had significant and positive associations with fertilizer levels (Shalini *et al.*, 2021; Gezahagn *et al.*, 2024b). However, the application of fertilizer had significant but inverse associations with PFP, PNB, IUE, AE, and APE of oat forage yield under oat/vetch mixed cropping system. This result is also in close conformity with the finding of Zorica *et al.* (2016) who reported that fertilizer application has significant but inverse associations with nitrogen use efficiency

(NUE), AE, and APE in mixture crops due to loss of nutrients from the root zone (Freney *et al.*, 1990; Sommer *et al.*, 2004; Cameron *et al.*, 2013). The inverse association of nutrient use efficiency with fertilizer levels is also reported in oat (Gezahagn *et al.*, 2024b). Moreover, the associations of OFDMY with FPC, FNC, FPU, FNU, and TFNU were significant and positive. Similarly, a significant and positive association of fodder yield with nutrient concentration and uptake was also reported in oat (Gezahagn *et al.*, 2024b). Significant and positive associations of yield with FPC and FNC were also reported in different crops under the intercropping/mixed cropping system (Ahmed *et al.*, 2020). However, the OFDMY had significant but inverse associations with PFP, PNB, IUE, AE, and APE of oat forage yield under the oat/vetch mixed cropping system. This study is also in line with the findings of Gezahagn *et al.* (2024b) who reported that nutrient use efficiency had an inverse association with the fodder yield of oat due to loss of nutrients from the soil.

All the pairwise associations on agro-morphological traits of NTPP, TDW, PHFH, NLFH, LLFH, DFH, and OFYPR of oat were significant and positive under oat/vetch mixed cropping. This indicated that selection based on one of the above traits may improve the performance of other traits in oat. Significant and positive associations of PHFH with NLFH, LLFH, and FYPR were also reported in oat varieties (Gezahagn *et al.*, 2023). All the pairwise associations of agro-morphological traits (NTPP, TDW, PHFH, NLFH, LLFH, DFH, and OFYPR) with nutrient concentration and uptake parameters of FPC, FNC, FPU, FNU, and TFNU were significant and positive indicating that a higher concentration and uptake of nutrients improves the performance of agro-morphological traits in oat. Moreover, all the pairwise associations of FPC, FNC, FPU, FNU, and TFNU were significant and positive indicating that nutrient concentration and uptake in oat fodder had a synergistic effect. A positive association of nutrient concentration with nutrient uptake was also reported in oat (Gezahagn *et al.*, 2024b). All the pairwise associations for nutrient use efficiency of PFP, PNB, IUE, AE, and APE in oat were significant and positive except the associations of APE with PNB and AE under oat/vetch mixed cropping system. A positive association of PFP with PNB and IUE was also reported in oat fodder (Gezahagn *et al.*, 2024b). The nutrient use efficiency of PFP, PNB, IUE, AE, and APE had significant but inverse associations with the agro-morphological traits of NTPP, TDW, PHFH, NLFH, LLFH, DFH, and OFYPR and nutrient concentration and uptake parameters of FPC, FNC, FPU, FNU, and TFNU. Moreover, the association of AE with NTPP, PHFH, NLFH, and LLFH and also PNB with NLFH were non-significant inverse associations.

6.4.1.5 Partial budget analysis

The partial budget analysis indicated that the net benefit of oat fodder increased substantially with the application of fertilizer under the oat/vetch mixed cropping system. Accordingly, the net benefit of oat fodder increased with increasing level of fertilizer up to 150% (61.5 kg N + 30 kg P/ha), indicating that fertilizer application had a significant contribution to fodder yield improvement which is associated with increasing plant vigor, number of tillers per plant, number of leaves per plant, plant height, and days to maturity. The net benefit of oat fodder obtained from the application of 150% fertilizer rate was 97,854 birr/ha which is 158.1% higher than the net benefit obtained from oat which was sown without the application of fertilizer under oat/vetch mixed cropping. Studies also indicated that the net benefit of intercropping/mixed cropping increased with increasing levels of fertilizer application in different crops (Khaliq *et al.*, 2006; Srivastava *et al.*, 2007; Hauggaard-Nielsen *et al.*, 2009; Saleem *et al.*, 2011; Moghadam and Mirshekari, 2014). Similarly, the total forage dry matter yield (oat + vetch) increased with increasing levels of fertilizer application up to 150% under oat/vetch mixed cropping. The total forage dry matter yield under the application of 150% fertilizer gave the net benefit of 112,434 birr/ha which is 161.4% higher than the oat/vetch mixture that was sown without fertilizer application. Moreover, the net benefit obtained from total forage dry matter yield using the application of 150% fertilizer was increased by 14.9% compared to the same rate of fertilizer application on oat fodder dry matter yield under oat/vetch mixed cropping. The higher net benefit for total forage dry matter yield over oat forage dry matter yield under oat/vetch mixed cropping system might be associated with higher productivity, better response to fertilizer application, and increased nutrient use efficiency. This result is in close conformity with the findings of Ghosh *et al.* (2006); Jat and Ahlawat (2010); Kumar *et al.* (2013); and Yang *et al.* (2018) who reported that fertilizer application increased the net benefit of total yield under intercropping/mixed cropping system. Other studies also indicated that intercropping gives higher economic return compared to monocropping due to its better use of growth resources and lower interspecific and intraspecific competition of component crops (Getachew *et al.*, 2006; Ngwira *et al.*, 2012; Rusinamhodzi *et al.*, 2012; Walelign, 2014; Parvez *et al.*, 2017; Kumar *et al.*, 2018).

Application of different fertilizer rates generally affects the marginal rate of return (MRR %) of oat forage dry matter yield and total forage dry matter yield (oat + vetch) under the oat/vetch mixed cropping system. Accordingly, the MRR for oat forage dry matter yield and total forage dry matter yield using the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer

were 2287.7 and 2790.4%, respectively. This indicated that the application of 150% fertilizer rate can earn 22.88 and 27.90 Ethiopian birr (ETB) per unit of ETB investment for the production of oat forage dry matter yield and total forage dry matter yield under oat/vetch mixed cropping system, respectively. Mutegi et al. (2012); and Liza et al. (2014) also reported that application of fertilizer generally improved productivity and reduced cost of production which resulted in higher profit and acceptable MRR. The MRR obtained from the production of total forage dry matter yield using the application of 150% fertilizer would be 22.0% higher compared to the MRR earned from the production of oat forage dry matter yield using the same fertilizer rate under oat/vetch mixed cropping system. The higher MRR earned from the production of total forage dry matter yield compared to oat forage dry matter yield could be associated with higher total forage dry matter yield due to better utilization of growth resources. Thus, the production of oat forage dry matter yield and total forage dry matter yield using the application of 150% fertilizer could produce higher net benefit and acceptable MRR under the oat/vetch mixed cropping system. Hence, the production of oat forage dry matter yield and total forage dry matter yield using the application of 150% fertilizer under the oat/vetch mixed cropping system was found to be the most profitable in the study area. According to CIMMYT (1988), treatment with the highest NB coupled with greater than the minimum acceptable MRR (100%) is the most economical to recommend for smallholder farmers.

The MRR obtained from the production of oat forage dry matter yield and total forage dry matter yield was non-dominated for all fertilizer rates except the application of 100% (41.0 kg N + 20 kg P/ha) fertilizer in sole oat and application of 175% (71.8 kg N + 35 kg P/ha) fertilizer in oat/vetch mixtures. This indicated that the dominated fertilizer rates were less profitable compared to the non-dominated fertilizer rates and it should be excluded from the analysis. All the MRRs for the non-dominated fertilizer rates were above the minimum acceptable MRR (100%) values for both production of oat forage dry matter yield and total forage dry matter yield, indicating that the use of these fertilizer rates gave better farm profit in the study area. Application of 125% (51.3 kg N + 25 kg P/ha) fertilizer rate produced the highest MRR for oat forage dry matter yield (9660.8%) and total forage dry matter yield (20150.0%) under oat/vetch mixed cropping system. This indicated that the application of 125% fertilizer can earn 96.61 and 201.50 ETB per unit of ETB investment for the production of oat forage dry matter yield and total forage dry matter yield under the oat/vetch mixed cropping system, respectively. Moreover, the net benefit-to-cost ratio of the non-dominated

fertilizer rates increased with increasing rates of fertilizer for the production of oat forage dry matter yield and total forage dry matter yield under the oat/vetch mixed cropping system. Accordingly, all the values of the net benefit-to-cost ratio were above two, indicating that the farmers can earn better profit in the study area when fertilizer is applied to produce oat forage dry matter yield and total forage dry matter yield under oat/vetch mixed cropping system. The benefit-to-cost ratio of intercropping/mixed cropping is higher compared to monocropping due to the efficient use of growth resources (Verma *et al.*, 1997; Khatun *et al.*, 2001; Munir *et al.*, 2004; Adeniyi, 2011).

The costs of labor and fertilizer will be expected to rise shortly due to the dynamic nature of the farmers' socio-economic conditions in the study area. Thus, the economic profitability of oat forage dry matter yield and total forage dry matter yield in the study area for the coming five years was performed using sensitivity analysis. The results of sensitivity analysis revealed that the use of this recommended fertilizer rate (150%: 61.5 kg N + 30 kg P/ha) for the production of oat forage dry matter yield and total forage dry matter yield will be expected to give the MRR of 1094.05 and 1345.43% under oat/vetch mixed cropping system in the study area, respectively. This indicated that the application of 150% fertilizer will give MRR above the minimum acceptable value (100%). Thus, the application of 150% fertilizer for the production of oat forage dry matter yield and total forage dry matter yield is profitable when the costs (labor and fertilizer) of production increase by 100% (20% per annum) for the coming five years in the study area. If the production cost (labor and fertilizer) increases by 100% in the coming five years in the study area, the farmers who produce oat forage dry matter yield and total forage dry matter yield using application of 150% fertilizer under oat/vetch mixed cropping system can earn 10.94 and 13.45 ETB per unit of ETB investment, respectively.

6.4.2 Efficiency and competitive ability of mixed cropping

6.4.2.1 Biological efficiency of oat under oat/vetch mixed cropping

The cropping seasons also significantly affect the biological efficiency of OYO, OEY, LEC, LUE, SPI, ATER, and LER under the oat/vetch mixed cropping system. The cropping season of 2020 was less favorable for plant growth and development due to relatively lower moisture availability and cold weather conditions compared to the 2021 cropping season. The OYO, LUC, LUC, ATER, and LER were higher in 2020 which had unfavorable growing conditions while OEY and SPI were higher in 2021 which was relatively favorable

for growth and yield formation. The lower OYO, LEC, LUE, ATER, and LER in 2021 than in 2020 could be associated with the relative yield proportions of mixed to sole cultures under favorable growing conditions being lower compared to their counterparts under unfavorable growing conditions. This indicated that the relative yield increase of sole culture to mixtures was higher under unfavorable growing conditions than its counterparts under favorable growing conditions due to higher interspecific completion between oat and vetch in the former than in the latter for growth resources. Studies also indicated that the LER, LEC, ATER, A, and equivalent yield in finger millet (Pradhan *et al.*, 2014) and tall sorghum (Egbe, 2010) were affected by cropping seasons under the intercropping system. The influence of cropping seasons on LER of mixed cropping in different crops was also reported (Getachew *et al.*, 2008; Walelign, 2014; Talukder *et al.*, 2015). Though the OYO was higher in 2020 than in 2021, both cropping seasons had positive values indicating mixed cropping had higher yield advantages over monocropping. The values of LEC for both cropping seasons were greater than 0.25, indicating the existence of yield advantages under a mixed cropping system due to the efficient use of growth resources. Because the minimum expected productivity coefficient is 25% when a two-crop mixture is sown in the intercropping or mixed cropping system (Adetiloye *et al.*, 1983; Egbe *et al.*, 2010). The higher LUE in 2020 indicates a better yield advantage of mixed cropping compared to the 2021 cropping season. The two cropping seasons had ATER values greater than unity indicating that mixed cropping had productive advantages compared to monocropping.

The LER is one of the most important parameters used to evaluate the efficiency of crops for growth resources under sole cropping and intercropping systems and is defined as the relative land area required for sole crops to produce the same yields as the intercrops/ mixed crops (He *et al.*, 2013; Tang *et al.*, 2016). The two cropping seasons significantly influence the LER of oat but not the total LER. The LER was higher in 2020 than in 2021, indicating that the ratio of mixtures to sole cultures yield was lower compared to its counterparts. This could be due to differences in the relative yield proportion of sole culture and mixtures in both cropping seasons. Walelign (2014) also stated that a higher LER could be obtained from the higher yield of intercrops coupled with their lower yield of monocropping. The existence of lower moisture and temperature in 2020 decreased the yield advantages of mixed cropping by increasing the sole crop yield more than the respective mixed crops due to higher interspecific competition for growth resources. This result is in line with the findings of Tesfamichael and Reddy (1996); and Getachew *et al.* (2006), who reported that

monocropping has a higher yield advantage than mixed cropping under moisture stress conditions due to high competition for growth resources under mixed cropping than monocropping. However, other studies indicated that under lower moisture availability, intercropping/mixed cropping has a higher yield advantage over the sole culture of different crops due to the efficient use of growth resources (Getachew *et al.*, 2008; Walelign, 2014). The total LER was higher than unity in both cropping seasons, indicating mixed cropping had better yield advantages over sole culture. The OEY and SPI were significantly higher in 2021 compared to 2020 cropping season. This could be due to the existence of favorable growing conditions in 2021 which is suitable to produce higher yield. The higher OEY in the 2021 cropping seasons indicates a better yield of oat under mixed cropping. Similarly, the SPI was also higher in 2021, indicating that mixed cropping was more productive than sole culture due to the better complementary effect of one crop on the other to improve the overall system productivity.

The application of fertilizer also significantly influences the biological efficiency of the oat/vetch mixed cropping system. The biological efficiency such as OYO, OEY, LEC, LUE, SPI, ATER, and LER increased with increasing fertilizer rates. The OYO values were negative for mixed oat sown with 0 and 25% of the recommended fertilizer rates. This indicated that mixed cropping had a yield disadvantage under the lower rate of fertilizer application due to higher interspecific competition for growth resources. However, the OYO was positive with increasing fertilizer rates specifying a better advantage of mixed cropping compared to monocropping. The LEC exceeding 0.25 indicates the superiority of mixed cropping of two crops in relation to its sole cultures. The LEC in this study was lower than 0.25 at the application of 0, 25, and 50% fertilizer rates. This indicated that mixed cropping had a yield disadvantage under lower fertilizer applications due to high interspecific competition between oat and vetch crops. However, the LEC was exceeded 0.25 with increasing fertilizer rates, showing mixed cropping had a better yield advantage due to the efficient use of growth resources. Thus, oat can be grown in a mixture with vetch under optimum fertilizer rate without major adverse effects on system productivity (Joseph and Balan, 2008; Egbe *et al.*, 2010).

The LER overestimates the yield advantages of intercropping/mixed cropping because it doesn't consider the crop growth duration (planting to harvesting); therefore, ATER has been developed to overcome the limitation of LER (Hiebsch and McCollum, 1987; Walelign, 2014; Doubi *et al.*, 2016). The ATER values at the application of 0 and 25%

fertilizer were lower than unity demonstrating mixed cropping had a yield disadvantage compared to monocropping. However, the ATER values exceed unity with increasing fertilizer rates indicating better yield advantage of mixed cropping. Accordingly, the ATER at 150% fertilizer rate was 1.74, which indicated that the oat/vetch mixed cropping had a biological yield advantage of 74% in land use and in time. The higher values of OEY, LUE, and SPI with increasing fertilizer rates indicate the existence of higher yield advantages under a mixed cropping system. According to Getachew *et al.* (2008) and Oseni and Aliyu (2010), the index of SPI generally standardizes the yield of the secondary crop (vetch) in relation to the main crop (oat). The vetch fodder productivity was converted to the oat forage yield using the SPI and the oat/vetch mixed cropping sown with 150% fertilizer gave 24,418 kg/ha fodder dry matter yield, indicating its better yield advantage as its SPI was higher than that of the oat sole culture (14,152 kg/ha).

The LER of any crop is greater than one when the crops use the environmental resources more efficiently for growth and development while it is less than unity when the growth resources are used less efficiently. The LER of oat at 125, 150, and 175% fertilizer application was higher than unity. This indicated that the application of higher fertilizer rates under mixed cropping gave higher yield advantages. However, the vetch and oat in this study were sown with 25 and 75% of the recommended seeding rates under a mixed cropping system, respectively. Thus, the partial LER of vetch above 0.25 and oat above 0.75 had yield advantages under a mixed cropping system. Accordingly, the application of fertilizers above 25% had partial LER of oat above 0.75, indicating oat had yield advantages under the oat/vetch mixed cropping system. On the other hand, the total LER was lower than unity under lower fertilizer application rates of 0 and 25% while it increased with increasing fertilizer rates. This result is also in line with the findings of Birhanu *et al.* (2022), who reported that the LER increased with increasing NP fertilizer in wheat-sweet lupine intercropping. The total LER for oat/vetch mixed cropping sown without application of fertilizer was 0.75, implying that 75% of the yield on mixed crops is mono-crops. In other words, the farmers might be using only 75% of the land in mixed crops of oat/vetch to produce the same yield of oat and vetch if they are sown in pure stand. This might be associated with higher competition for growth resources between the two crops.

The partial LER of oat showed that the yield loss decreased with increasing fertilizer rates under oat/vetch mixed cropping. The fodder yield loss in oat is relatively lower than the respective yield loss in vetch at each fertilizer rate. This indicated that oat is more competent

for growth resources compared to vetch. Studies also indicated that cereals/grasses have high competing ability than legumes under intercropping or mixed cropping systems (Quainoo *et al.*, 2000; Ghosh, 2004; Banik *et al.*, 2006; Muoneke *et al.*, 2007; Wang *et al.*, 2021). The overall fodder yield of mixed cropping at 150% fertilizer rate was 74% ($LER_T = 1.74$), which indicates that mixed cropping had a 74% yield advantage over sole cropping and an additional 0.74 hectare of land required for sole cultures to produce the same amount of fodder yield of the respective mixed cropping. The importance of fertilizer application to increase the LER of mixed cropping has been also reported (Masoud, 2015). The higher LER value indicates that mixed cropping is more efficient in land use than a pure stand of its crops, and mixed cropping is biologically more sustainable than sole culture. Moreover, the yield advantages have been reported in different cereal-legume intercropping systems, including maize-common bean (Walelign, 2008), maize-mungbean (Saleem *et al.*, 2015), maize-peanut (Xia *et al.*, 2019), and oat-vetch (Erol *et al.*, 2009; Fantahun, 2016; Kedija, 2022). The efficient use of environmental resources such as water, light, and nutrients is the major reason for yield advantages in intercropping than the corresponding sole cropping system (Liu *et al.*, 2006).

6.4.2.2 Competitive ability of oat under oat/vetch mixed cropping

The competitive indices are very useful for measuring the efficiency of crops under a mixed cropping system. The competitive indices measured in this study varied significantly between the two cropping seasons. The higher competitive indices of KO, K, AYLO, AYLT, IAO, IAT, AO, and CRO were recorded in 2020 than 2021 cropping season. This could be associated with the lower yield performance of sole culture in 2020 compared to 2021 under the oat/vetch mixed cropping system. The effect of cropping seasons on the competitive indices of KO, K, AYLO, AYLT, IAO, IAT, AO, and CRO was also reported (Gitari *et al.*, 2020). The K value of oat in 2020 was higher than unity, indicating yield advantage under a mixed cropping system. The AYL is the proportionate yield loss or gain of mixed crops in comparison to the respective sole crop (Banik *et al.*, 2000; Dhima *et al.*, 2007). The AYL of oat and total were positive in both cropping seasons, indicating mixed cropping had a yield advantage. The positive AYL of maize when intercropped with cowpea was also reported in both cropping seasons (Hamd *et al.*, 2014). Vlachostergios *et al.* (2017) also reported that the positive value of AYL indicates the advantage of intercrops over monocrops. The higher IA of oat and total in 2020 showed that the yield loss due to mixed cropping was lower compared to sole culture. The A of oat in both cropping seasons was negative; indicating

that the associated vetch was the dominant crop over oat under the oat/vetch mixed cropping system. This result is also in close conformity with the findings of Egbe (2010), who reported that soybean, is the dominant crop when planted with sorghum under intercropping system. The CR of oat in both cropping seasons was lower than unity, indicating the positive benefits of a mixed cropping system.

Application of fertilizer increases the competitive indices of oat and oat/vetch under a mixed cropping system. The K of oat at 0, 25, 50, 75, and 100% fertilizer rates were less than unity, indicating mixed cropping of oat/vetch under lower fertilizer rate had a yield disadvantage. However, the K value of oat with the application of fertilizer at 125, 150, and 175% were higher than unity, indicating that oat had a yield advantage under the oat/vetch mixed cropping system. The partial K values for oat were higher than that of the respective vetch, which is indicative of a strong interspecific competition, so the vetch is dominated by oat in the mixed cropping system. However, the product of the partial values of oat and vetch at 150% fertilizer was higher than unity, which shows the existence of higher mixed cropping compatibility between these crops. The intercropping or mixed cropping has produced K values greater than, equal to, or less than unity when the associations give higher yield, the same yield, or less yield over sole culture, respectively (Willey, 1979; Getachew *et al.*, 2008; Ashenafi, 2020). The AYL of oat and total were negative at lower rates of fertilizer application, indicating the disadvantage of mixed cropping over sole culture. However, the AYL of oat and total with increasing fertilizer rates were positive under the oat/vetch mixed cropping system, indicating the advantage of intercropping. The positive coefficient of AYL indicates the advantages of intercropping over monocropping (Ashenafi, 2020). Similarly, the IA of oat and total were negative for lower rates of fertilizer application. On the other hand, the IA of oat and total were positive with increasing fertilizer rates, indicating that the loss of yield under mixed cropping was low compared to monocropping. The highest IA of oat and total were recorded at 150% fertilizer application. This indicated that the yield loss due to mixed cropping is the lowest under higher fertilizer rates compared to lower rates of fertilizers. Ashenafi (2020) also reported that the onion has negative IA indicating the onion loses its yield when intercropped with rosemary in 80% population density.

The A is one of the important indices to determine the competitive ability of a crop when grown in association with another crop. The A value of a crop is numerically the same but opposite sign with a companion crop. The dominant crop has positive signs while the dominated crop has negative signs. In this study, the A of oat at 0 and 25% fertilizer

application was positive, indicating the dominance of oat over vetch under lower rate of fertilizer application. On the other hand, vetch was the dominant crop over oat with increasing fertilizer levels under the oat/vetch mixed cropping system. Different studies also indicated that the dominant crop has positive aggressivity while the dominated crop has negative aggressivity value (Olubode *et al.*, 2009; Mallikarjuna *et al.*, 2011; Hamd *et al.*, 2014; Ashenafi, 2020). The CR of oat with lower rates of fertilizer was greater than unity. This indicated that mixed cropping had less yield benefit compared to sole culture under oat/vetch mixed cropping system. However, the CR of oat decreased with increasing fertilizer rates, and the lowest CR of oat was recorded at 150% fertilizer. This showed that the CR of oat was lower than unity which resulted in a higher benefit of mixed cropping system over sole culture. The CR of oat showed higher values than that of vetch at lower fertilizer rates (0 and 25%). Thus, oat had higher competitive ability than vetch at lower fertilizer rates under a mixed cropping system and this scenario was confirmed by the A of oat over vetch at lower fertilizer rates (0 and 25%), which were positive and indicates the dominance of oat in the mixed cropping system. The CR values less than unity showed positive benefits and the crop can grow in association while the values greater than unity indicated negative benefits (Egbe, 2010).

6.4.2.3 Economic efficiency of oat/vetch mixed cropping

The economic efficiency of MAI, RVT, RVI, and RNRI varied between the two cropping seasons. The higher MAI, RVT, RVI, and RNRI were recorded in 2020 than 2021 cropping season. The influence of cropping seasons on MAI, RVT, RVI, and RNRI was also reported in potato-legume intercropping systems (Gitari *et al.*, 2020). All the economic efficiency indices used in this study were higher under unfavorable growing conditions compared to favorable growing conditions. This could be due to the relatively lower yield performance of sole culture under lower moisture and cold temperature weather conditions compared to that of the yield obtained at higher moisture and relatively hot weather conditions. The MAI was higher in 2020, indicating that mixed cropping was more profitable than sole culture. The positive MAI values in both cropping seasons indicated the profitability of mixed cropping compared with the monocropping system (Sadeghpour *et al.*, 2013a; Gitari *et al.*, 2020). The RVT, RVI, and RNRI values were significantly higher in 2020 and the values were greater than one. This indicated that mixed cropping gave higher economic returns than sole culture. The effect of cropping seasons on RVT, RVI, and RNRI values of intercropping were also reported (Gitari *et al.*, 2020).

Application of fertilizer on oat/vetch mixed cropping system was significant for measured indices of economic efficiency. The MAI values at 0 and 25% fertilizer application were negative. This indicated that mixed cropping under lower rates of fertilizer application was not profitable compared to higher rates of fertilizer application. However, the MAI values increased with increasing fertilizer rates, and the highest value was recorded at 150% fertilizer application. This showed that the application of 150% fertilizer rate under the oat/vetch mixed cropping system gave the highest profit. The higher MAI in the mixed cropping system could be due to its higher yield formation with optimum fertilizer application. The higher LER is closely related to higher MAI values which emphasize the benefits of intercropping (Ghosh, 2004; Dhima *et al.*, 2007). The RVT and RNRI values were below unity at 0, 25, 50, and 75% fertilizer application. This revealed that mixed cropping of oat/vetch gave lower returns under lower rates of fertilizer application. However, the returns were increased with increasing fertilizer rates and the highest values of RVT and RNRI were recorded at 150% fertilizer application. The RVT values of 0.63, 0.80, 0.89, and 0.99 indicate the farmers that practiced mixed cropping of oat/vetch under 0, 25, 50, and 75% fertilizer rates could be making 63, 80, 89, and 99% of the income of the farmers who are involved in oat and vetch monocropping. This could be due to high competition between oat and vetch for growth resources under lower rates of fertilizer application in the oat/vetch mixed cropping system.

The LER does not account for the economic value of crops and to avoid the limitation of LER, the RVT index has been developed (Alabi and Esobhawan, 2006). However, the RVI index is superior to the RVT index because it accounts for the variable cost used for production (Singh *et al.*, 2015). The RVI value was less than unity at 0% fertilizer application which indicated that mixed cropping sown without fertilizer application gave the lowest return. However, the returns were increased with increasing fertilizer rates and the highest RVI was recorded at 150% fertilizer rate. This showed that the application of 150% fertilizer on oat/vetch mixed cropping system would give the highest return compared to sole culture. The RVI value of 1.73 at the application of 150% fertilizer indicated that the farmers who planted oat and vetch mixed cropping could be making a profit of 73% more than the farmers who are involved in monocropping of oat and vetch crops.

6.4.3 Fodder nutritional quality

6.4.3.1 Analysis of variance

The combined analysis of variance revealed that all the measured yield parameters (CPY, DY, and TDNY) and nutritive value (ash, NDF, ADF, ADL, HC, C, CP, DCP, IVDMD, TDN, DDM, DMI, RFV, RFQ, DE, ME, NEL, NEm, and NEg) of oat/vetch mixtures differed significantly with application of fertilizer rates. This indicated that fertilizer application had a remarkable contribution to improving the yield and nutritional quality of oat/vetch mixtures. The study also indicated that the fodder yield and nutritional quality of the legume-grass/cereal mixed cropping system improved due to fertilizer application (Chen *et al.*, 2004). Cropping seasons also had a significant effect on measured yield parameters (CPY, DY, and TDNY) and all nutritional quality parameters except ash and HC contents of feed obtained from oat/vetch mixtures. This showed that the two cropping seasons varied in the amount and distribution of precipitation and maximum and minimum temperatures. The effect of year on fodder yield and the nutritional quality of legume-grass/cereal mixtures were also reported by different scholars (Chen *et al.*, 2004; Pedraza *et al.*, 2017; Mosebi *et al.*, 2018). The fertilizer-by-year interaction was significant only for CP, CPY, and DCP contents of oat/vetch mixtures. This indicated that the performance of oat/vetch mixtures sown with different fertilizer rates was consistent for most measured yield and nutritive value parameters in both cropping seasons. Significant fertilizer-by-year interaction effect on CP, DCP, and CPY of oat/vetch mixtures might be associated with the differential influence of fertilizer application on oat/vetch mixtures and/or the differential influence of production year on these measured parameters of oat/vetch mixtures.

6.4.3.2 Ash concentration

The ash content is an indication of mineral concentration in the feed and this mineral concentration depends on plant, soil, climate, and management factors (McDonald *et al.*, 2002; McDowell, 2003; Katoch *et al.*, 2018; Gezahagn *et al.*, 2021). Like energy and protein, minerals are the major nutrients required to improve the performance of animals (Bindari *et al.*, 2013). The higher ash content of the feed indicates a higher mineral concentration and vice versa. The feed with higher ash content is preferable due to its higher voluntary intake, better digestibility, and higher energy values to improve the performance of animals. Minerals are highly required by rumen microorganisms and their deficiency significantly affects the growth of microorganisms which leads to lower fiber digestion and

protein synthesis by rumen microbes (Spears, 1994). The extent of minerals in the feed is substantially influenced by fertilizer application (Jukenvicius and Sabiene, 2007). Accordingly, the ash content of oat/vetch mixtures in this study was significantly improved with the application of fertilizer. The oat/vetch mixtures sown with the application of 150% of the recommended fertilizer rate had an advantage of 18.4% ash content over the oat/vetch mixtures sown without fertilizer application. Moreover, the oat/vetch mixtures sown with 100% of the recommended fertilizer increased their ash content by 5.4% compared to the sole oat sown with the same recommended fertilizer rate. Similarly, the sole vetch sown with 100% of the recommended fertilizer rate had 18.5 and 5.0% ash content advantages over the sole oat sown with 100% of the recommended fertilizer rate and oat/vetch mixtures sown with 150% of the recommended fertilizer, respectively. This indicated that the ash content is higher in legumes compared to cereal/grass under a mixed cropping system (Dahmardeh *et al.*, 2009; Pathak *et al.*, 2013; Asangla and Gohain, 2016). The ash content of oat/vetch mixtures was not statistically different between the two cropping seasons, indicating the effect of year on the performance of oat/vetch mixtures for ash content was generally low. However, a higher ash content of oat/vetch mixtures was observed in 2021 compared to 2020 cropping season.

6.4.3.3 Cell wall concentrations

The cell wall contents such as the neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), hemicellulose (HC), and cellulose (C) are important forage quality parameters and the higher values of these fiber concentrations in the feed usually decrease the quality of feed (Caballero *et al.*, 1995; Gezahegn *et al.*, 2024a). The fiber contents in fodder can be reduced through the optimum harvesting stage, fertilizer application, use of grass-legume mixed cropping system, and use of higher quality forage crops. The NDF content measures the voluntary intake of the forage and it has an inverse association with digestibility and feed energy (Sayar *et al.*, 2014). Moreover, the ADF is an important forage quality parameter that is used to predict the digestibility of forage (Caballero *et al.*, 1995; Corleto *et al.*, 2009). The digestibility of forage usually increases when the ADF content of forage decreases. In this study, the fiber contents (NDF, ADF, ADL, HC, and C) decreased with increasing fertilizer rates up to 150% of the recommended fertilizer rate. The lowest NDF, ADF, ADL, and C contents were observed for sole vetch sown with 100% of the recommended fertilizer rate followed by oat/vetch mixtures sown with 150% of the recommended fertilizer while the highest values were recorded for oat/vetch mixtures sown without fertilizer application.

The lower cell wall contents in sole vetch followed by oat grown with vetch using a higher fertilizer rate might be due to better nitrogen nutrition from applied fertilizer and N₂ fixation by legumes that improves the availability of nitrogen to crops which resulted in higher leaf-to-stem ratio and production of succulent plant parts. However, the observed higher cell wall contents in sole oat followed by oat/vetch mixtures sown without fertilizer might be attributed to higher storage of assimilates as cell wall contents during photosynthates partitioning and this result is also in line with others' findings (Rasool *et al.*, 2017; Islam *et al.*, 2018). The inclusion of legumes in mixtures generally reduced the NDF contents of feed compared to the sole culture of grass/cereal crops (Hauggaard-Nielsen *et al.*, 2001; Surve and Arvadia, 2011). Studies also indicated that the legume-grass/cereal mixed cropping system has lower ADF content than cereal/grass monoculture (Aasen *et al.*, 2004; Tuna and Orak, 2007; Strydhorst *et al.*, 2008). Oat sown in pure culture had higher fiber contents than sole vetch suggesting that oat had higher lignocellulosic material (Caballero *et al.*, 1995). Cropping seasons also had a significant effect on fiber contents (NDF, ADF, ADL, and C) of oat/vetch mixtures. Accordingly, the NDF, ADF, ADL, and C contents in 2020 were increased by 1.9, 3.3, 4.5, and 2.9% compared to 2021, respectively. This indicated that under the favorable growing season of 2021, the oat/vetch mixtures grew faster and had a higher leaf-to-stem ratio which resulted in lower fiber contents.

6.4.3.4 Crude protein and dry matter intake

The crude protein (CP) is one of the most important nutritional quality parameters used to measure the quality of feed (Caballero *et al.*, 1995; Collins and Fritz, 2003; Lithourgidis *et al.*, 2007; Eskandari *et al.*, 2009; Yolcu *et al.*, 2009) and the livestock farming system can be more profitable when the harvested forage gives higher protein per unit area (Sadeghpour *et al.*, 2014). The CP content of sole vetch sown with 100% of the recommended fertilizer rate was increased by 171.3 and 134.7% over the sole oat sown with 100% of the recommended fertilizer rate and oat/vetch mixtures sown with 150% of the recommended fertilizer rate, respectively. Moreover, the application of 150% of the recommended fertilizer rate on oat/vetch mixtures had 63.0 and 15.4% CP advantages compared to oat/vetch mixtures sown without fertilizer application and sole oat sown with 100% of the recommended fertilizer rate, respectively. This indicated that fertilizer application and mixed cropping had a remarkable contribution to improving the CP content of oat/vetch mixtures. The higher CP content has been reported for maize-cowpea intercropping under the application of 150:100:100 kg N:P₂O₅:K₂O/ha fertilizers while a lower value of CP attained in sole maize

sown without fertilizer application, indicating the CP content increased with fertilizer application (Iqbal *et al.*, 2006b). The higher CP content in vetch compared to sole oat and oat/vetch mixtures might be attributed to higher nitrogen content and succulent plant parts in vetch as compared to sole oat and this result is confirmed by Malik *et al.* (1992). Moreover, the higher CP content in sole legumes compared to the sole culture of cereal/grass and legume-cereal/grass mixtures was reported in different crops (Lithourgidis *et al.*, 2007; Dura *et al.*, 2012; Dhima *et al.*, 2013; Haq *et al.*, 2018; Kedija, 2022). On the other hand, different scholars also reported that legume-cereal/grass mixtures had higher CP content compared to sole culture of cereal/grass in different crops (Jannink *et al.*, 1996; Carr *et al.*, 2004; Liu *et al.*, 2006; Dawo *et al.*, 2007; Albayrak *et al.*, 2011; Haq *et al.*, 2018; Sani *et al.*, 2020). The higher CP content in oat/vetch mixtures compared to sole oat might be due to higher fixation of atmospheric nitrogen by vetch resulting in higher nitrogen uptake which leads to higher CP content in mixtures.

The crude protein yield (CPY) is an important measure of the CP content that can be harvested for better livestock feeding (Diriba and Vaars, 2000; Cazzato *et al.*, 2013; Eshetie *et al.*, 2018). Since CPY is a function of CP content and forage dry matter yield, higher values of these parameters increased the CPY under a mixed cropping system. Application of fertilizer on oat/vetch mixtures had substantial effects on the CPY of oat/vetch mixtures. Accordingly, application of 150% of the recommended fertilizer rate had 109.2, 52.9, and 253.3% CPY advantages over sole vetch sown with 100% fertilizer rate, sole oat sown with 100% fertilizer rate, and oat/vetch mixtures sown without fertilizer, respectively. Despite vetch having a higher CP content, the higher CPY was obtained from oat/vetch mixtures. This might be due to the lower fodder yield performance of vetch compared to oat/vetch mixtures which resulted in lower CPY in sole vetch. Studies also indicated that the legume-cereal/grass mixtures produce higher CPY as compared to the respective sole cultures of legume and cereal/grass crops (Jensen, 1996; Lauk and Lauk, 2005). The sole vetch sown with 100% of the recommended fertilizer gave the highest digestible crude protein (DCP), digestible dry matter (DDM), and dry matter intake (DMI) followed by oat/vetch mixtures sown with 150% of the recommended fertilizer while the lowest values were recorded for oat/vetch mixtures sown without fertilizer. This indicated that fertilizer application decreases the lignified structural carbohydrates in the feed which resulted in higher DCP, DDM, and DMI in oat/vetch mixtures. The higher DDM is a good indication of quality feed because the animals can digest the highest portion of the dry matter when the feed has a higher DDM

(Van Saun, 2015). The higher DDM content in vetch is mainly attributed to more CP and lower fiber contents which improve the digestion of feed by rumen microbes. On the other hand, the higher accumulation of cell wall contents in oat compared to vetch acts as a physical barrier to digest polysaccharides by rumen microbial enzymes which resulted in lower DDM, and this result is supported by the findings of other scholars (Karayilanli and Ayhan, 2016; Jagadeesh *et al.*, 2017; Prajapati *et al.*, 2020). The inclusion of legumes in mixtures usually increases the palatability and digestibility of feed by reducing the fiber contents which resulted in higher DMI in the feed and this result is in line with other reports (Karayilanli and Ayhan, 2016; Manoj *et al.*, 2020). The performance of oat/vetch mixtures varied significantly between the two cropping seasons for CP, CPY, DCP, DDM, and DMI. This could be due to variations in climatic conditions between the two cropping seasons. Accordingly, the CP, CPY, DCP, DDM, and DMI of oat/vetch mixtures were higher in 2021 by 13.7, 27.2, 25.8, 1.2, and 1.6% compared to 2020, respectively. The effect of cropping seasons on the CPY of mixed cropping systems was also reported (Atis *et al.*, 2012).

6.4.3.5 Forage digestibility and its yield

In-vitro dry matter digestibility (IVDMD) is one of the most important parameters to evaluate the quality of feed. The digestibility of feed depends on the extent of cell contents, CP contents, and lignified structural carbohydrates in the feed, and the feed with higher cell and CP contents accompanied by lower lignified cell wall constituents could be considered high-quality feed (Gezahagn *et al.*, 2016). In this study, the IVDMD of oat/vetch mixtures was significantly influenced by fertilizer application. Accordingly, the IVDMD of oat/vetch mixtures increased with increasing fertilizer rates up to 150% of the recommended fertilizer rate. In this study, the oat/vetch mixtures sown with 150% of the recommended fertilizer rate had IVDMD advantages of 7.4 and 19.8% over sole oat sown with 100% of the recommended fertilizer and oat/vetch mixtures sown without fertilizer, respectively. Similarly, the IVDMD of sole vetch sown with 100% of the recommended fertilizer rate was increased by 14.6 and 6.7% over sole oat sown with 100% of the recommended fertilizer rate and oat/vetch mixtures sown with 150% of the recommended fertilizer rate, respectively. The higher IVDMD with application of fertilizer on oat/vetch mixtures might be associated with decreased structural carbohydrates which lead to reduction in cell wall lignification and dilution of CP content. Studies also indicated that the intercropping of maize with different legumes increases the CP content and decreases the NDF and ADF contents compared to sole maize which resulted in higher digestibility (Javanmard *et al.*, 2009; Eskandari, 2012).

The IVDMD of the feed can be increased by reducing the NDF and ADF contents of fodder through the inclusion of high protein-rich crops in a mixed cropping system (Vranic *et al.*, 2009). The cropping seasons also had a significant effect on the IVDMD of oat/vetch mixtures. Accordingly, the IVDMD of oat/vetch mixtures sown in 2021 was higher by 1.9% compared to the 2020 cropping season. This indicated that the oat/vetch mixtures had higher CP content in 2021 which leads to higher feed intake and digestibility. Since digestible yield (DY) is a function of forage dry matter yield and IVDMD content, the higher values of forage dry matter yield and IVDMD content lead to the highest DY (Prajapati *et al.*, 2019). The DY of oat/vetch mixtures varied significantly with fertilizer application. This indicated that the fodder yield and CP content of oat/vetch mixtures increased with fertilizer application which leads to higher DY. In this study, the DY generally increased with increasing fertilizer rates. Consequently, the DY of oat/vetch mixtures sown with 150% of the recommended fertilizer rate increased by 361.5, 42.9, and 155.3% over the sole vetch sown with 100% of the recommended fertilizer, sole oat sown with 100% of the recommended fertilizer rate, and oat/vetch mixtures sown without fertilizer, respectively. Similarly, the DY of oat/vetch mixtures varied significantly between the two cropping seasons due to variations in climatic conditions. Hence, the DY of oat/vetch mixtures in 2021 was higher by 10.7% compared to the 2020 cropping season.

6.4.3.6 Digestible nutrients and their yield

The total digestible nutrients (TDN) measure the digestible nutrients of feeds that are available for animals and it is a function of NDF and ADF concentration in the feed. The TDN of oat/vetch mixtures in this study varied significantly with the application of fertilizer. The highest TDN (698.3 g/kg DM) was recorded for sole vetch sown with 100% of the recommended fertilizer followed by oat/vetch mixtures (692.6 g/kg DM) sown with 150% of the recommended fertilizer rate while the lowest (599.9 g/kg DM) was recorded for oat/vetch mixtures sown without fertilizer. Application of fertilizer improves the CP contents of oat/vetch mixtures by reducing the cell wall contents in the feed which leads to higher TDN content. Studies indicated that the TDN contents of the feed increased with the inclusion of legumes in the mixtures (Lithourgidis *et al.*, 2006; Karagic *et al.*, 2011). The lower ADF contents in mixtures resulted in higher nutrient availability which leads to higher palatability and digestibility of the feed. The lower ADF content in mixtures of the current study resulted in higher TDN contents in the feed and this result is also in line with other findings (Yadav *et al.*, 2019; Manoj, 2020). Moreover, the year of production had a significant effect on the

TDN of oat/vetch mixtures. A higher TDN (652.6 g/kg DM) was recorded in 2021 than 2020 (644.8 g/kg DM) cropping season. The total digestible nutrient yield (TDNY) is a function of forage dry matter yield and TDN content and the higher values of forage dry matter yield and TDN content lead to the highest TDNY. The TDNY of oat/vetch mixtures in the present study varied significantly with fertilizer application. Accordingly, the TDNY of oat/vetch mixtures sown with 150% of the recommended fertilizer rate increased by 381.5, 46.1, and 145.3% over sole vetch sown with 100% of the recommended fertilizer rate, sole oat sown with 100% of the recommended fertilizer rate, and oat/vetch mixtures sown without fertilizer, respectively. The lower TDNY in sole vetch could be attributed to its lower forage dry matter yield compared to oat/vetch mixtures and sole culture of oat. The cropping seasons also had a significant effect on the TDNY of oat/vetch mixtures, indicating the climatic conditions are so variable between the two growing seasons. Thus, the TDNY of oat/vetch mixtures was higher by 11.1% in 2021 compared to the 2020 cropping season.

6.4.3.7 Relative feed value and quality

The relative feed value (RFV) index, which is derived from DDM and DMI, is used to determine the intake and energy values of different forage crops. The RFV of forage can be affected by species, climatic factors, soil fertility, management conditions (stage of harvest, fertilizer application, cropping system, etc.), and their interactions. The RFV of oat/vetch mixtures in this study varied significantly with fertilizer application. The sole vetch sown with 100% of the recommended fertilizer had the RFV advantages of 29.7 and 9.5% over the sole oat sown with 100% of the recommended fertilizer and oat/vetch mixtures sown with 150% of the recommended fertilizer, respectively. This result is in close conformity with the findings of Yilmaz *et al.* (2015) who reported that the sole culture of vetch produced higher RFV compared to pure stand of grass/cereal and mixtures of grass/cereal-legume. The inclusion of legumes in a mixed cropping system resulted in higher CP content accompanied by lower fiber contents that led to higher RFV (Karayilanli and Ayhan, 2016; Manoj, 2020). Similarly, oat/vetch mixtures sown with 150% of the recommended fertilizer rate had 18.5 and 30.7% RFV advantages over the sole oat sown with 100% of the recommended fertilizer and oat/vetch mixtures sown without fertilizer, respectively. This indicated that cultivation of oat/vetch mixtures using optimum fertilizer gave better quality feed compared to sole oat and mixtures sown without fertilizer. According to Dunham (1998) and Yavuz (2005), the RFV below 100 generally indicates low-quality feed. On the other hand, the RFV above 150 would be considered high-quality feed and the feed should not be used for highly productive

animals when the RFV is below 75 (Horrocks and Vallentine, 1999). The RFV also varied significantly between the two cropping seasons due to variations in climatic conditions. Consequently, the RFV was higher by 3.1% in 2021 compared to 2020 cropping season.

Similarly, the relative feed quality (RFQ) as RFV measures the quality of feed and its values below 100 showed lower quality of feed and vice versa. The quality of feed is more predicted with RFQ compared to RFV because it uses TDN for determination of feed quality (Moore and Undersander, 2002). In this study, the RFQ of oat/vetch mixtures varied significantly with the application of fertilizer. The RFQ of oat/vetch mixtures increased with increasing fertilizer rates. The sole vetch sown with 100% of the recommended fertilizer rate produced the highest RFQ followed by oat/vetch mixtures sown with 150% of the recommended fertilizer while the lowest RFQ was recorded for oat/vetch mixtures sown without fertilizer. This indicated that fertilizer application improves the TDN content of sole vetch which resulted in higher RFQ. The RFQ also varied significantly between the two cropping seasons and a higher RFQ was recorded in 2021 compared to the 2020 cropping season due to differences in moisture availability and temperature.

6.4.3.8 Energy fractions of the feed

All animals usually require high energy providing feed to improve their production and productivity. The energy value of feed is highly dependent on the concentration of lignified structural constituents in the feed and a higher CP content of the feed accompanied with lower ADF contents is considered as high-quality feed and it provides better energy for animals. In the present study, the digestible energy (DE), metabolizable energy (ME), net energy for lactation (NEL), net energy for maintenance (NE_m), and net energy for gain (NE_g) of oat/vetch mixtures varied significantly with fertilizer application. The highest DE (12.9 MJ/kg DM), ME (10.6 MJ/kg DM), NEL (6.7 MJ/kg DM), NE_m (7.3 MJ/kg DM), and NE_g (4.3 MJ/kg DM) were recorded for the sole vetch sown with 100% of the recommended fertilizer followed by oat/vetch mixtures sown with 150% of the recommended fertilizer while the lowest values of these energy parameters were recorded from oat/vetch mixtures sown without fertilizer. This indicated that the sole vetch and oat/vetch mixtures sown with optimum fertilizer rates had higher CP and TDN contents along with lower cell wall constituents which resulted in better energy fractions in the feed. The higher NEL and ME in sole vetch sown with the recommended fertilizer rate and oat/vetch mixtures sown with 150% fertilizer is mainly attributed to lower ADF content in the feed and this result is in line

with the findings of Manoj *et al.* (2020) who reported that the fodder with lower ADF content provides higher NEL and ME for animals. The energy value of fodder can be improved through the inclusion of legume crops in different cropping systems (Vasilakoglou and Dhiam, 2008). The fodder obtained from cereal-legume intercropping has higher methionine and threonine amino acids which may lead to increased metabolization and release of energy (Pozdisek *et al.*, 2011; Prajapati *et al.*, 2018; Manoj *et al.*, 2020). The DE, ME, NEL, NEm, and NEg also significantly influenced with cropping seasons. Consequently, higher values of DE, ME, NEL, NEm, and NEg were recorded in 2021 compared to the 2020 cropping season due to the presence of favorable growing conditions in the former than in the latter growing season.

6.4.3.9 Associations among measured parameters

The Pearson correlation analysis indicated that the herbage yield and nutritional quality of oat/vetch mixtures were significantly associated with fertilize rates. This indicated that fertilizer application had a remarkable contribution to increasing the yield and nutritive value of oat/vetch mixtures. The ash content of oat/vetch mixtures had a significant positive association with fertilizer rates. This indicated that fertilizer application increases the uptake of nutrients from the soil which leads to higher mineral concentration in oat/vetch mixtures. All the fiber contents (NDF, ADF, ADL, and C) of oat/vetch mixtures except HC content had significant inverse associations with fertilizer rates. This demonstrates that the fiber contents of oat/vetch mixtures could be significantly reduced by increasing fertilizer rates. The inverse association of fiber contents with fertilizer application has been also reported (Mupenzi *et al.*, 2017; Beyadglin *et al.*, 2022). The relationships of fertilizer rate with TFDMY, CP, DCP, CPY, IVDMD, DY, TDN, and TDNY were significant and positive under the oat/vetch mixed cropping system. The DDM, DMI, RFV, and RFQ of oat/vetch mixtures were significantly and positively associated with fertilizer rates. All the measured energy parameters viz. DE, ME, NEL, NEm, and NEg had a significant positive association with fertilizer rates under the oat/vetch mixed cropping system.

The ash content of oat/vetch mixtures had significant inverse associations with NDF, ADF, ADL, and C contents. However, it had significant positive associations with IVDMD, CP, TFDMY, CPY, HC, DCP, TDN, DDM, DY, TDNY, DMI, RFV, RFQ, DE, ME, NEL, NEm, and NEg. A significant positive association of yield (TDNY, CPY, DY, and TDNY) with ash content of the feed suggested that accumulation of minerals in the feed generally

improves the forage dry matter yield which leads to higher TFDMY, CPY, DY, and TDNY and this result is concurred by Prajapati *et al.* (2019). The associations of NDF with ADF, ADL, and C; ADF with ADL and C; and ADL with C contents were significant and positive. On the other hand, NDF, ADF, ADL, and C contents of oat/vetch mixtures had significant inverse associations with IVDMD, CP, TFDMY, CPY, DCP, TDN, DDM, DY, TDNY, DMI, RFV, RFQ, DE, ME, NEL, NEm, and NEg. Significant inverse associations of NDF and ADF with CP, DDM, DMI, TDN, RFV, ash, and NEL were also reported (Prajapati *et al.*, 2019). The inverse association between ADF and TDN has been also reported (Nadeem *et al.*, 2010). The inverse associations of NEL and ME with the ADF content of fodder intercropping have been also noticed (Manoj *et al.*, 2020). The inverse association of CP with cell wall components was also reported by different scholars (Jancik *et al.*, 2008; Azo *et al.*, 2012). The inverse association of cell wall contents with DDM, DMI, and RFV might be due to the cell wall contents acting as a physical barrier for microbial enzymes to digest polysaccharides and this result is confirmed by others' findings (Sohail *et al.*, 2007; Prajapati *et al.*, 2017). The strong negative association between DDM and ADF indicates the DDM of the feed using rumen microbial enzymes decreased with increasing ADF contents in the feed and this result is supported by other findings (Caballero *et al.*, 1995; Horrocks and Vallentine, 1999; Muttappanavar and Shekara, 2023). Similarly, the associations of DMI with NDF and TDN with ADF were negative suggesting that the higher NDF and ADF contents of the feed generally reduce the intake and nutrient digestibility of feed and this result is concurred by Muttappanavar and Shekara (2023).

All the pairwise correlation coefficients of IVDMD, CP, TFDMY, CPY, DCP, TDN, DY, and TDNY were significant and positive in oat/vetch mixtures. Moreover, these parameters had significant positive associations with DDM, DMI, RFV, RFQ, DE, ME, NEL, NEm, and NEg. This indicated that selection based on these nutritional parameters would be effective in improving the TFDMY of oat/vetch mixtures under different fertilizer rates. The study also indicated that all the pairwise associations for CP, DMI, DDM, RFV, TDN, and NEL were significant and positive (Prajapati *et al.*, 2019). The CP content was also significantly and positively associated with forage yield and CPY under the intercropping system (Ram and Singh, 2003). A significant positive association of RFV with DDM and DMI has been reported since RFV is estimated from DDM and DMI (Prajapati *et al.*, 2019; Muttappanavar and Shekara, 2023). All the pairwise associations for energy parameters viz. DE, ME, NEL, NEm, and NEg were significant and positive. Moreover, these all energy parameters had

significant and positive associations with DDM, DMI, RFV, and RFQ. The study also showed that the net energy had a significant and positive association with DDM, DMI, and RFV (Prajapati *et al.*, 2019).

6.5 Conclusion

The study revealed that fertilizer application had a significant effect on all measured agromorphological traits, nutrient concentration, nutrient uptake, and use efficiency of oat under oat/vetch mixed cropping system. Moreover, the indices of economic efficiency, competitive ability, and economic efficiency of oat under oat/vetch mixtures were significantly influenced by fertilizer application. Similarly, the nutritive value of oat/vetch mixtures also varied significantly with the application of fertilizer. Therefore, the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate increases fodder yield, profitability, biological efficiency, and competitive ability of oat under the oat/vetch mixed cropping system and also economic efficiency and nutritive value of oat/vetch mixtures in the study area. However, to recommend this for different oat-growing areas and similar agro-ecologies, this experiment should be conducted again in diverse environments of Ethiopia.

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Chapter VII

Summary, Conclusions, and Recommendations

Summary, Conclusions, and Recommendations

7.1 Summary and Conclusions

Feed shortage both in terms of quantity and quality is a critical problem in Ethiopia. This shortage is even more in the central highlands of Ethiopia due to high population pressure which leads to a decrease in pasture lands due to urbanization, industrialization, and competition for lands for food and forage crops. The major livestock feed resources in Ethiopia are natural pasture and crop residues which are very low in nutritional quality. Moreover, the agro-industrial byproducts, which are nutritionally very good feed, are less available, inaccessible, and expensive for rural farmers. The livestock feed cost accounts for 60-80% of the total production cost and it is increasing alarmingly and severely hampering the livestock productivity in Ethiopia. However, cultivated forage crops have better nutritional quality and produce substantial forage per unit area to enhance the production and productivity of livestock in the country.

Among cultivated forage crops, oat is one of the most important annual forage crops grown mostly in the central highlands of Ethiopia. To boost livestock production and productivity in the study areas, evaluation and selection of high-yielding and stable oat genotypes across environments are very essential to reduce the feed shortage problem. The productivity of any crop can be increased through breeding and agronomic management like fertilizer application, intercropping/mixed cropping, population density, crop rotation, weeding, row planting, and others. Therefore, this study was designed to assess and properly exploit the agro-morphological variability of 120 oat genotypes for selection and future breeding activities of the oat improvement program. Of which, 24 oat genotypes were selected and their yield and stability performances were assessed under diverse environments (Holetta, Ada-Berga, Ginchi, Jeldu, D/Zeit, Kulumsa, Bekoji, Kuyu, and Debreworkos) of oat growing areas in 2020/2021 cropping season. Oat genotypes are generally grouped as forage type, grain type, and dual-type oat. From 24 oat genotypes studied, a total of 3 oat genotypes (forage, grain, and dual type oat) one from each group was selected and evaluated for their yield performance, nutrient uptake and use efficiency, nutritional quality, and profitability under different fertilizer levels at Holetta for two consecutive years (2020/2021 to 2021/2022). Similarly, one compatible oat genotype with vetch was also selected from 24 oat genotypes studied and assessed for yield performance, nutrient uptake and use efficiency,

productivity using different indices, nutritive value, and profitability using different fertilizer rates under oat/vetch mixed cropping system at Holetta for two consecutive years (2020/2021 to 2021/2022). From these four research studies, the major findings are summarized below:

Experiment I

The results of the first study demonstrated the existence of considerable variation among 120 oat genotypes evaluated based on agro-morphological traits at Holetta and Ada-Berga in the central highlands of Ethiopia. Estimates of very high to moderately high heritability accompanied by high to moderate genetic advance and variability were observed in FDMY, NLFH, SDMY, FYPR, GY, NSPP, PLGH, and HI, indicating these traits were controlled more by additive gene action. This indicates that phenotypic-based genetic selection on these traits could be reliable for improvement. Selection of genotypes based on high FDMY coupled with better NLFH, SDMY, and FYPR could be effective for fodder yield improvement in oat genotypes. On the other hand, grain yield improvement in oat genotypes could be effective through selections made on genotypes of high GY along with better HI, PLGH, and NSPP. For improvements on SY and TBY, the selection of genotypes having higher respective yields along with better BYPR would be effective. Accordingly, genotypes such as S-122, T-1926513, CI-1480, CI-1677, Bona-bas, and CI-1674, had high FDMY along with better NLFH, SDMY, and FYPR. Among high FDMY-producing genotypes, CI-1480, S-122, Bona-bas, and CI-1674 genotypes also produced better GY. On the other hand, genotypes SRCPX80Ab2806, SRCPX80Ab2267, CI-715, CI-1463, SRCPX80Ab2291, and A-505 produced high GY along with better HI, PLGH, and NSPP. Out of high GY-producing genotypes, CI-715, CI-1463, SRCPX80Ab2806, and A-505 genotypes also gave better fodder yield. Therefore, these genotypes could be selected for both direct production to enhance the current productivity of fodder and grain yields and for further evaluation under diverse environmental conditions for commercial release.

The phenotypic and genotypic correlations and path coefficients analyses revealed that FYPR was the most important trait for the indirect selection of FDMY as it showed a significant positive correlation with FDMY accompanied by a high positive direct effect on FDMY. Furthermore, all measured traits, except the NTPP, TDW, and TSW had high positive indirect effects on FDMY mainly via FYPR. So, this study demonstrated that the direct selection of FYPR and traits that showed considerable positive indirect effects via

FYPR should be considered simultaneously as indirect selection criteria for FDMY improvement in oat genotypes. The correlation and path coefficient analyses also revealed high direct effects of BYPR and HI on GY and significant positive correlations of both traits with GY at phenotypic and genotypic levels. The GSFR had a significant positive association with GY and exerted a high direct effect on GY at the genotypic level. The GSFR had also a high positive indirect effect on GY via mainly BYPR and HI, both at phenotypic and genotypic levels. This suggested that selection based on mainly BYPR, HI, and GSFR will ultimately improve the GY in oat genotypes. On the other hand, the breeding progress in FDMY and GY could be adversely affected by NTPP and TSW because these traits had negative direct effects on FDMY and GY at the genotypic level. Therefore, plant breeders should not necessarily give due attention to higher NTPP and TSW in the selection programs to improve FDMY and GY in oat genotypes.

The cluster analysis grouped the genotypes into four clusters based on the performances of measured traits. The second cluster had high forage yield-producing genotypes while the third cluster had high grain yield-producing genotypes. The genetic divergence also indicated the presence of variability among the clusters. The highest inter-cluster genetic distance was recorded between the third and fourth clusters followed by between the second and third clusters while the lowest was between the first and second clusters. Moreover, the studied traits had different contributions to the total variation in oat genotypes. The first two principal components had a high contribution to the total variation in oat genotypes. Among the studied traits, FYPR, BYPR, PLGH, FDMY, NSLPP, HI, GY, NLFH, and PHGH had a high contribution to the total variation in oat genotypes. Therefore, selection based on these traits could be effective for yield improvement in oat genotypes. Moreover, the occurrence of remarkable variation among oat genotypes for measured traits indicates the potential of oat genotypes in future breeding programs for improving the forage yield, grain yield, and yield-related traits.

Experiment II

Twenty-four oat genotypes were tested across nine environments in the central highlands of Ethiopia using a randomized complete block design using three replications. The genotype, environment, and GEI showed significant differences for measured agro-morphological traits and fodder nutritive values of oat genotypes. Most of the studied genotypes performed inconsistently across environments due to the presence of significant interaction effects.

Thus, conducting the stability analysis using the biplot of the first two AMMI interaction principal component axes is very important to select high-yielding and stable genotypes. Due to the significant GEI effect, simultaneous consideration of both superior genotypes and stability performance using the first two AMMI-IPCA is very important for fodder yield improvement in oat genotypes. Genotypes that produced fodder yield above the grand mean were G6, G10, G23, G7, G9, G18, G13, G1, G24, G15, G2, G3, G19, G4, and G11 but most of these genotypes perform inconsistently compared to some genotypes which produced fodder yield below the grand mean. The most stable genotypes based on the first two AMMI biplot analyses were G23, G22, G5, and G12 but all these genotypes except G23 had fodder yield below the grand mean. On the other hand, G9, G23, G11, G1, G10, G6, G3, G15, G7, G2, G4, and G19 were superior in fodder yield performance and relatively stable across environments. Among relatively stable and superior genotypes, G11, G3, G2, G4, and G19 have released varieties. However, G6, G2, and G23 were adapted to favorable and unfavorable environments. Similarly, G3, G7, and G10 were promising genotypes for cultivation under unfavorable environments while G9 performed better under favorable environments. Among these, G2 and G3 were the released varieties.

The stability analysis for fodder yield was also carried out using the GGE biplot to identify high-yielding with consistently performing genotypes across environments. The results showed that the environment's main effect had the highest influence on the fodder yield of oat genotypes followed by GEI and genotypic effects. Among the studied genotypes, G6, G10, G3, G2, G7, G4, G23, G24, G15, G19, G13, G9, G1, G11, and G18 exhibited mean fodder yield above the grand mean. The polygon view of the GGE biplot classified the testing environments into two mega-environments (MEs) with superior-performing genotypes at each ME. The winning genotypes in the first ME which contained E7, E1, E8, E3, E9, E2, and E4 environments were G6 and G2 while the winning genotype in the second ME (E5 and E6) was G13. The discriminating and representative environments were E7, E1, and E8. However, the most discriminating and representative environment was E7 which was closer to the center of the concentric circles and considered an ideal environment while E1 and E8 environments which were located closer to E7 were considered favorable environments. Among high fodder-yielding genotypes, G13 and G24 were the most unstable while G15, G19, G2, G7, and G4 were moderately stable genotypes. The least desirable genotypes which located far from the ideal genotype were G16, G5, G22, G17, and G20. However, among the top fodder yield-producing genotypes, G6, G10, G3, G23, and G9 had

consistent performance across environments. Moreover, G6 was considered the ideal genotype while G10, G3, G23, and G9 were desirable genotypes. Among these genotypes, G3 was the released variety in Ethiopia.

Different univariate stability parameters (SD , CV_i , b_i , S_{di}^2 , R^2 , σ_i^2 , B_i , D_{ji} , W_i , P_i , ASV , YSI , $S^{(1)}_i$, and $S^{(2)}_i$) were also employed and the result revealed that high fodder-yielding genotypes had better stability performance than low fodder-yielding genotypes when the genotypes assessed using the stability parameters of P_i , YSI , R^2 , and CV_i . This indicates that the selection of oat genotypes using these stability parameters would be efficient for fodder yield improvement in oat genotypes. The genotypes such as G1, G2, G3, G4, G6, G7, G9, G10, G11, G13, G15, G18, G19, G23, and G24 had fodder dry matter yield above the grand mean. These genotypes had a relatively stable performance at least in one of the stability parameters of P_i , YSI , R^2 , and CV_i . However, low fodder-yielding genotypes were performed consistently across environments when evaluated using σ_i^2 , W_i , D_{ji} , b_i , $S^{(1)}_i$, ASV , $S^{(2)}_i$, S_{di}^2 , B_i , and SD stability parameters, suggesting that selection of oat genotypes using these stability parameters would not be efficient for fodder yield improvement in oat genotypes. The Spearman's rank correlation coefficients also indicated that FDMY had significant positive associations with CV_i , R^2 , P_i , and YSI while the remaining stability parameters had non-significant negative associations with FDMY except the B_i stability parameter. The result revealed that fodder yield had the highest significant positive association with P_i ($r = 0.96$) followed by YSI ($r = 0.47$), R^2 ($r = 0.44$), and CV_i ($r = 0.43$). Moreover, the PCA indicated that FDMY with the stability parameters of R^2 , P_i , CV_i , SD , and YSI had dynamic/agronomic stability patterns, suggesting that the selection of oat genotypes using these stability parameters was more promising for fodder yield improvement than other stability parameters which had static/biological stability pattern. According to the stability parameters of P_i , CV_i , R^2 , and YSI , G6, G7, G9, G10, and G23 genotypes that produced better fodder yield had stable performance across environments.

Similar to fodder yield, the stability of oat genotypes was also assessed for grain yield using different statistical analysis models. The development of consistently high-yielding and widely adaptable varieties is a prerequisite to enhancing the production and productivity of oat grain in the country. The result of AMMI analysis of variance indicated that oat grain yield performances were significantly influenced by environments followed by genotypes and their interactions, indicating that the study environments were diverse due to biotic and abiotic factors. Moreover, the AMMI analysis of variance further partitioned the GEI

variance into interaction principal component axes to examine the stability performance of genotypes across environments. For effective selection and recommendation of superior oat genotypes, both grain yield and the first two AMMI interaction principal components should be taken into account simultaneously. Accordingly, high grain-yielding genotypes in this study were G8, G17, G12, G5, G19, G14, G11, G22, G16, and G4 but these genotypes changed their yield performance across environments compared to some of the low grain-yielding genotypes. Based on the first two AMMI analyses, the most stable genotypes were G23, G10, G15, G9, G4, and G22 but all these genotypes except G4 and G22 had mean grain-yield below the grand mean. Among superior genotypes, G4, G11, G12, and G22 had relatively stable performances across environments. Although the adaptability of top grain yield performing genotypes such as G17, G8, G5, and G19 was promising both at favorable and unfavorable environments, the yield performances of these genotypes fluctuated across environments though produced better yield at favorable environments. Among high grain yielding and relatively stable genotypes, G12, G19, G5, G4, and G11 were released varieties. The top grain-yielding genotypes such as G8 and G17 were selected for cultivation both in favorable and unfavorable environments while G22 was selected only for favorable environments.

The grain yield stability of oat genotypes was also assessed using the GGE biplot analysis. The presence of GEI indicates the differential response of genotypes across environments and the importance of stability analysis. The genotypes that had mean grain yield above the grand mean in this study were G8, G17, G5, G14, G19, G22, G12, G11, G4, and G16. The results revealed a better expression of the GEI by the GGE biplot analysis because it provides useful information in mega-environment analysis and genotype evaluation. The “which-won-where” or polygon view of the GGE biplot identified four mega-environments with winning genotypes. Thus, the winning genotypes at the first (E3), second (E7 and E8), and fourth (E6) mega-environments were G16; G12; and G8 and G17, respectively. However, the third mega-environment which included E1, E2, E4, E5, and E9 had no winning genotype. Among the environments, E2, E5, E1, and E4 were discriminating and representative of the other environments. The most discriminating and representative environment was E2 which was considered an ideal environment while E5, E1, and E4 environments were considered favorable environments because they are closer to the ideal environment. E3, E6, E7, E8, and E9 which were neither discriminating nor representative environments are unfavorable for grain yield production of oat genotypes. The GGE biplot

of the first two PC analyses indicated that the top grain-yielding genotypes such as G19, G14, G8, G11, G12, G17, and G22 had relatively consistent yield performances across environments. Among these high-yielder and stable genotypes, G19 was considered the ideal genotype while the remaining genotypes were desirable genotypes. Among these, G19, G14, G11, and G12 were released varieties while G8, G17, and G22 have not been yet released.

Different statistical tools have been developed to study the stability performance of various crops grown across environments. In this study, a stability analysis for grain yield was also performed using various univariate parametric and nonparametric stability statistics to select superior and widely adaptable genotypes simultaneously. Lower-yielding genotypes generally showed more stable yield across environments than higher-yielding genotypes, when assessed based on SD, S_{di}^2 , σ_i^2 , D_{ji} , W_i , ASV, and $S^{(2)}_i$ indicating that selection using these stability parameters would not be effective for grain yield improvement in oat genotypes. However, higher-yielding genotypes showed consistent performance using the stability parameters P_i , B_i , and YSI, indicating that the selection of oat genotypes using these stability parameters would be efficient for grain yield improvement. The stability parameters P_i , B_i , and YSI showed a significant and positive association with grain yield, and the grain yield showed a non-significant positive association with CV_i , b_i , R^2 , and $S^{(1)}_i$. By contrast, stability parameters of SD, S_{di}^2 , σ_i^2 , D_{ji} , W_i , ASV, and $S^{(2)}_i$ showed a negative association with grain yield. Based on Spearman's rank correlation and PC analysis, useful stability parameters, namely, P_i , B_i , and YSI were identified for selection and future breeding programs. Accordingly, G5, G8, G11, G12, G14, G16, G17, G19, and G22 representing genotypes with high yield performance and good stability were selected for grain yield improvement in oat genotypes.

Experiment III

Three oat genotypes (forage, grain, and dual-type oat) were evaluated for agro-morphological traits, nutrient uptake and use efficiency, and profitability under eight fertilizer levels at Holetta in the 2020/21 and 2021/22 cropping seasons. The study indicated that the application of NP fertilizer significantly improved fodder yield, yield components, nutrient concentration, nutrient uptake, and use efficiency in oat varieties. Accordingly, applications of 25, 50, 75, 100, 125, 150, and 175% of the recommended fertilizer rates of oat increased the fodder dry matter yield by 36.9, 52.4, 54.8, 66.7, 85.7, 88.1, and 89.3% over unfertilized treatment, respectively. The fodder type oat (CI-8251) and dual type oat

(SRCPX80Ab2291) varieties had 15.4 and 10.6% advantages of fodder yield over the grain type oat (Sorataf), respectively. Significantly higher fodder yield was obtained in 2021 than 2020 cropping season. Moreover, the interaction effect of variety by fertilizer by year was significant for nutrient concentration and uptake. Accordingly, the grain-type oat sown with the highest fertilizer dose (175%) in 2020 had the highest FPC (0.32%) and FNC (1.78%), FNU (264.8 kg/ha), and FTNU (313.4 kg/ha). The PNB decreased with increasing fertilizer rate up to 175%. Among the nutrient use efficiency, PFP, IUE, AE, and APE were significant for the interaction effect of variety by fertilizer by year. The fodder type oat sown with lower fertilizer rates in 2021 and 2020 had the highest PFP (915.6 kg FDMY/kg nutrient applied) and IUE (131.0 kg FDMY/kg nutrient uptake), respectively. Similarly, the grain-type oat sown with a lower fertilizer rate in 2021 produced the highest (289.6 kg FDMY/kg nutrient applied) AE.

The Pearson correlation analysis indicated that all measured agro-morphological traits had positive associations with fertilizer rates and fodder yield except the NLFH, DFH, and LSR. Similarly, except for agro-physiological efficiency, nutrient concentration, and nutrient uptake, all nutrient use efficiencies had inverse associations with fertilizer rate and fodder yield. The partial budget analysis for fodder yield revealed that application of 175, 150, and 125% of the blanket recommended fertilizer rates on forage type oat, dual type oat, and grain type oat gave the highest net benefit of 90,697, 89,101, and 77,875 ETB/ha along with the acceptable marginal rate of return of 2.10, 18.15, and 147.86 ETB/ha per unit of investment, respectively. Moreover, the combined analysis for oat varieties indicated that the application of 125% fertilizer produced a higher net benefit (83,440 ETB/ha) with the highest benefit-to-cost ratio (3.5) and marginal rate of return (126.36 ETB/ha) per unit of investment.

The grain yield performance of oat genotypes was also assessed under eight fertilizer levels. The results showed that the application of NP fertilizer significantly increased the agro-morphological traits, nutrient concentration, nutrient uptake, nutrient use efficiency, and economic profitability of oat compared to unfertilized treatment. All the measured parameters showed significant variation among oat varieties except SPC, SNC, and TNU. Similarly, all the measured parameters also varied significantly among fertilizer levels except DSH, TSW, HI, IUE, PE, and APE. Application of 100, 125, 150, and 175% of the blanket recommended fertilizer rates had 96, 111, 132, and 125% grain yield advantages over unfertilized treatment, respectively. The highest grain yield producing oat variety (Sorataf) had 14 and 8% grain yield advantages over forage type (CI-8251) and dual type

(SRCPX80Ab2291) of oat variety, respectively. The second cropping season (2021) had a 6% grain yield advantage compared to the first (2020) cropping season. Oat varieties had 144, 166, 196, and 189% grain nutrient uptake advantages over unfertilized treatment when receiving 100, 125, 150, and 175% fertilizer, respectively. The nutrient use efficiency generally decreased with increasing levels of fertilizer.

The Pearson correlation analysis also indicated that the agro-morphological traits except TSW and HI, nutrient concentration, and nutrient uptake had positive associations with fertilizer level and grain yield. However, the NHI and nutrient use efficiency had inverse associations with fertilizer level and grain yield. The combined partial budget analysis for oat varieties revealed that the highest net benefit (156,207.20 ETB/ha) with a cost-to-benefit ratio of 3.0 and marginal rate of return of 370.2% was obtained from the application of a blanket recommended fertilizer level of 150% (61.5 kg N + 30 kg P/ha).

The effect of fertilizer application, variety, and year on the nutritive value of oat genotypes was also assessed and the results indicated that most measured nutritional parameters varied significantly for the effects of variety, fertilizer, year, and their interaction effects. The highest DY (10.2 t/ha), and TDNY (10.9 t/ha) were obtained from the application of 175% (71.8 kg N + 35 kg P/ha) fertilizer while oat sown without fertilizer gave the lowest DY (5.3 t/ha) and TDNY (5.7 t/ha). Among oat varieties, CI-8251 gave the highest TDNY (9.7 t/ha) but the highest DY (8.4 t/ha) was recorded for SRCPX80Ab2291. However, the Sorataf variety gave the lowest DY (7.9 t/ha) and TDNY (8.5 t/ha). Moreover, the second year of production gave higher DY (8.7 t/ha) and TDNY (9.4 t/ha) compared to the first year of production. The interaction effect of variety by fertilizer by year varied significantly for CP, CPY, DCP, IVDMD, TDN, DDM, DMI, DE, ME, NEI, NEm, and NEg. Accordingly, the highest CP (113.9 g/kg DM), CPY (1.66 t/ha), and DCP (68.2 g/kg DM) were obtained from the interaction effect of Sorataf variety sown with 175% fertilizer in 2020 cropping season. Similarly, the highest IVDMD (697.2 g/kg DM) was recorded for the interaction effect of the Sorataf variety sown with 50% (20.5 kg N + 10 kg P/ha) fertilizer in the 2021 cropping season. Moreover, the highest TDN (704.6 g/kg DM) and DDM (707.2 g/kg DM) were recorded for the interaction effect of Sorataf variety sown with 100% (41.0 kg N + 20 kg P/ha) fertilizer in 2021 cropping season. The highest DMI (1.85% body weight) was obtained from the interaction effect of the CI-8251 variety sown with 100% fertilizer in the 2021 cropping season.

The highest feed energy parameters of DE (13.0 MJ/kg DM), ME (10.7 MJ/kg DM), NEI (6.7 MJ/kg DM), and NEg (4.3 MJ/kg DM) were obtained from the interaction effect of CI-8251 and Sorataf varieties sown with the application of 100% fertilizer in 2021 cropping season. Moreover, the highest NEm (7.4 MJ/kg DM) was obtained from the interaction effect of the Sorataf variety sown with 100% fertilizer rate in the 2021 cropping season. The Pearson correlation analysis also indicated that some of the measured nutritional parameters were significant and positive indicating that selection based on these parameters would improve other positively correlated parameters simultaneously.

Experiment IV

The effect of fertilizer rate and year on the fodder yield performance of oat under oat/vetch mixed cropping system was assessed and the results revealed that fertilizer application had a significant effect on all measured agro-morphological traits, nutrient concentration, nutrient uptake, and use efficiency of oat under oat/vetch mixed cropping system. The results showed that the measured agro-morphological traits increased with increasing fertilizer rates up to 150% (61.5 kg N + 30 kg P/ha). However, days to forage harvesting increased with increasing rates of fertilizer up to 175% (71.8 kg N + 35 kg P/ha). Accordingly, application of 25, 50, 75, 100, 125, 150, and 175% of the recommended fertilizer rates for sole oat increased the forage dry matter yield of oat under oat/vetch mixed cropping system by 27.2, 40.7, 54.3, 67.9, 84.0, 107.4, and 90.1% over unfertilized oat/vetch mixed cropping system, respectively. All the measured agro-morphological traits were significantly higher in 2021 than 2020 cropping season. The nutrient concentration and nutrient uptake generally increased with increasing fertilizer rates while nutrient use efficiency decreased with increasing fertilizer rates. Similarly, all the nutrient use efficiencies were higher in the second year of production except IUE and APE.

The Pearson correlation analysis also indicated that agro-morphological traits, nutrient concentration, and nutrient uptake had significant and positive associations with increasing rates of fertilizer. However, the associations between fertilizer rates and nutrient use efficiencies were significant and negative. The partial budget analysis for fodder yield also indicated that the highest net benefit of 97,854 birr/ha was recorded for oat sown with 150% fertilizer under the oat/vetch mixed cropping system. Similarly, the highest net benefit (112,434 birr/ha) for total forage dry matter yield of the oat/vetch mixed cropping system was recorded from the application of 150% fertilizer under the oat/vetch mixed cropping system.

The fodder productivity of oat under oat/vetch mixed cropping system was also assessed using different indices of biological efficiency, competitive ability, and economic efficiency. The results revealed that all the biological efficiencies measured in this study varied significantly between the two cropping seasons. Significantly higher values of OYO (27.3), LEC (0.37), LUE (197.5), ATER (1.32), and LER (1.19) were observed in 2020 whereas the values of OEY (14891) and SPI (18943) were higher in 2021. Moreover, the application of fertilizer also had a significant effect on all measured biological efficiency indices. Accordingly, all biological efficiencies measured in this study increased with increasing levels of fertilizers up to 150% (61.5 kg N + 30 kg P/ha). The values of OYO, OEY, LEC, LUE, SPI, ATER, and LER of oat sown with the application of 150% fertilizer under oat/vetch mixed cropping system were 58.7, 18939, 0.65, 260.3, 24418, 1.74, and 1.19, respectively.

The competitive ability of oat and mixtures under oat/vetch mixed cropping system was estimated using different indices. The results showed that cropping season and fertilizer application had significant effects on the competitive ability of oat and mixtures under oat/vetch mixed cropping. The results showed that except for AO and CRO, all measured competitive indices in this study varied significantly between the two cropping seasons. Accordingly, higher values of KO (1.79), K (0.72), AYLO (0.27), AYLT (0.72), IAO (2.00), and IAT (5.49) were recorded in the first year. The competitive indices of oat (KO, AYLO, and IAO) and total (K, AYLT, and IAT) increased with increasing fertilizer rates up to 150% whereas the AO and CRO decreased with increasing rates of fertilizer up to 150%. The economic efficiency of oat/vetch mixed cropping was also determined using different indices. The results showed that the measured economic efficiency in this study varied significantly with cropping season and fertilizer application. The economic efficiency of the MAI (23564), RVT (1.07), RVI (1.38), and RNRI (1.06) were higher in the first year. Similarly, all the economic efficiencies increased with increasing fertilizer rates up to 150%. Application of fertilizer at the rate of 150% gave the MAI, RVT, RVI, and RNRI values of 60878, 1.35, 1.73, and 1.35, respectively.

The nutritional value of oat/vetch mixtures under different fertilizer rates and over years was also assessed and the results showed that cropping season had a significant effect on all measured nutritive values except ash and HC contents. Higher fiber (NDF, ADF, ADL, and C) contents were recorded in 2020 whereas the CP, CPY, DCP, DDM, DMI, IVDMD, DY, TDN, TDNY, RFV, RFQ, and energy parameters (DE, ME, Nel, NEm, and NEg) were

higher in 2021. Moreover, the application of fertilizer had a significant effect on all measured nutritive values. Among oat/vetch mixed cropping, the NDF, ADF, ADL, and C contents decreased with increasing fertilizer rates up to 150% (61.5 kg N + 30 kg P/ha). Accordingly, the NDF, ADF, ADL, and C contents of oat/vetch mixtures sown without fertilizer application were higher by 13.5, 47.2, 97.4, and 36.9% compared to oat/vetch mixtures sown with 150% fertilizer rate. However, the ash, CPY, DDM, DMI, IVDMD, DY, TDN, TDNY, RFV, RFQ, DE, ME, NEL, NEm, and NEg increased with increasing fertilizer rates up to 150%. Thus, the application of 150% fertilizer rate improved the DDM, DMI, IVDMD, TDN, RFV, and RFQ by 15.1, 13.5, 19.8, 15.5, 30.7, and 30.9% compared to oat/vetch mixtures sown without fertilizer application. Similarly, the application of 150% fertilizer rate had 15.3, 15.4, 15.8, 18.0, and 35.5% advantages in DE, ME, NEL, NEm, and NEg, respectively, compared to oat/vetch mixtures sown without fertilizer application. Among oat/vetch mixtures sown with different fertilizer rates, application of 175% (71.8 kg N + 35 kg P/ha) fertilizer gave the highest CP (84.1 g/kg DM) whereas oat/vetch mixtures sown without fertilizer produced the lowest CP (51.6 g/kg DM).

Generally, sole vetch sown with 100% (18 kg N + 20 kg P/ha) of the recommended fertilizer rate had the highest ash, CP, DCP, DDM, DMI, IVDMD, TDN, RFV, RFQ, DE, ME, NEL, NEm, and NEg followed by oat/vetch mixtures and sole oat. On the other hand, the nutritional yields (CPY, DY, and TDNY) were the highest in mixtures followed by sole oat and sole vetch. Similarly, the fiber (NDF, ADF, ADL, and C) contents were the highest for sole oat followed by mixtures and sole vetch. The Pearson correlation analysis indicated that fertilizer application had significant associations with all measured nutritional parameters. Accordingly, the application of fertilizer had significant inverse associations with fiber (NDF, ADF, ADL, and C) contents but it had significant positive associations with the remaining measured nutritional parameters. Similarly, the fiber (NDF, ADF, and ADL) had significant inverse associations with IVDMD, CP, DCP, TDN, DDM, DMI, RFV, RFQ, yield parameters (TFDMY, CPY, DY, and TDNY), and energy parameters (DE, ME, NEL, NEm, and NEg).

7.2 Recommendations and Way Forward

- ❖ Out of high grain yield producing genotypes, CI-715, CI-1463, SRCPX80Ab2806, and A-505 oat genotypes also gave better fodder yield. Similarly, among high fodder-producing genotypes, CI-1480, S-122, Bona-bas, and CI-1674 genotypes also

produced better grain yield. Thus, these genotypes could be used as potential parents for improving the genetic gain in oat breeding programs.

- ❖ Based on the AMMI, GGE, and univariate stability statistics, G6, G9, G10, and G23 were recommended for fodder yield whereas G8, G17, and G22 were recommended for grain yield improvement. Therefore, these genotypes should be verified under diverse environmental conditions before registration/release of them as a variety(s) in Ethiopia.
- ❖ From sole oat study, the application of 125% (51.3 kg N + 25 kg P/ha) of the blanket recommended fertilizer rate gives better growth, fodder yield, and nutritive value for oat varieties which resulted in higher farm profit in the study area. However, to recommend this dose of NP fertilizer for wider areas of oat-growing environments, the study should be conducted in more representative environments of Ethiopia.
- ❖ Application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate on sole oat could improve the grain yield productivity of oat varieties and farm profitability in the study area. However, to recommend this fertilizer rate for similar agro-ecologies of Ethiopia, the result should be verified by doing similar research under wider areas of oat growing environments. Therefore, the results of this research can be used as a base for future research in the areas of oat grain improvement through the application of optimum fertilizer rate.
- ❖ From oat/vetch mixture study, the application of 150% (61.5 kg N + 30 kg P/ha) fertilizer rate increases fodder yield, nutritive value, and profitability of oat under the oat/vetch mixed cropping system in the study area. However, to recommend this for different oat-growing areas and similar agro-ecologies, this experiment should be conducted again in diverse environments of Ethiopia.

BIOGRAPHICAL SKETCH

The author, Gezahagn Kebede, was born in 1982 in Oromia Regional State, East Showa Zone, at Wonji/Showa, Ethiopia. He attended his elementary and junior secondary school at Wonji/Showa Tigil Le-idiget School. Then he followed his secondary education at Wonji Comprehensive Secondary School. After successfully passing the Ethiopian School Leaving Certificate Examination, he joined Mekelle University in September 1999 and graduated with a B.Sc. degree in Dryland Crop Science in July 2003. After graduation, he was recruited by the Ethiopian Institute of Agricultural Research (EIAR) as a junior researcher and assigned to work in the Forage and Pasture Crops Research Program at Holetta Agricultural Research Center (HARC) in December 2003. As a staff member, he has been actively engaged in the highland forage agronomy and breeding research activities.

In 2008/2009, he joined Hawassa University and obtained a Master of Science degree in agronomy in 2010/2011. After graduation, the author resumed his career in forage research at Holetta Agricultural Research Center and served the institute (EIAR) as the National Forage and Pasture Crops Research Program Coordinator position and also the center (HARC) as Feeds and Nutrition Research Process head position. After serving for seven years in the research positions of assistant researcher III to senior researcher, he again joined Hawassa University in 2018/2019 in the School of Plant and Horticultural Sciences for his PhD study in Agronomy.

During his research engagement in forage crops, the author contributed to the process of variety development and release of more than twenty forage crop varieties with their production packages. Among these, the author is a major contributor to the release/registration of thirteen forage crop varieties (5 oat; 3 Napier grass; 3 alfalfa; 1 tree lucerne; and 1 vetch) and also a co-contributor to the release/registration of seven forage crop varieties (3 desho grass; 3 oat; and 1 rye grass). The author also serve as a technical committee for forage crops variety release in the country. He advised three MSc. students (1 from Addis Ababa University and 2 from Hawassa University) during his PhD study period. The author published more than one hundred fifty articles in journals and proceedings. From his PhD study, the author also published twenty-three articles (11 journal articles and 12 papers in proceedings). Gezahagn is married and a father of three sons.