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The trade-off between qualitative and quantitative trait in forage oat (*Avena sativa* L.) genotypes

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Abstract

Oat forage represents a critical feed source in agricultural systems, where the relationship between quantitative traits and nutritional value plays a fundamental role in crop optimization and livestock nutrition. This study explores the genetic diversity and examines the relationship between quantitative and qualitative traits among thirteen oat genotypes, in two cropping seasons (2021–2023) at the Seed and Plant Improvement Institute in Karaj, Iran. A randomized block design was employed to assess quantitative and Qualitative traits. Significant genotypic variation was identified, with genotype 9 demonstrating superior forage yield and genotype 1 excelling in protein content. Genotype-by-year interactions notably influenced traits like flowering time and plant height, reflecting environmental effects. Correlation and principal component analyses revealed key trade-offs, such as a negative correlation between dry forage yield and protein content, and positive associations between flag leaf length and forage quality traits. Cluster analysis grouped genotypes by performance, highlighting promising candidates for breeding initiatives. Path analysis revealed that plant height ($C = 0.54$) and days to flowering ($C = 0.43$) are the strongest direct determinants of fresh forage yield, while flag leaf traits and panicle length exert weak or negligible effects. These results underscore the potential of oat genetic resources to simultaneously improve forage yield and nutritional quality, thereby advancing sustainable agriculture and enhancing food security.

Keywords

Oats, diversity, production, quantity, quality.

1 Introduction

Since the advent of agriculture, cereals such as barley and oats have played a central role as staple foods and key sources of animal feed (Barcchiya et al. 2017). Oats (*Avena sativa* L.) are cultivated across a wide range of agro-

climatic regions and rank sixth among global cereal crops, following wheat, maize, rice, barley, and sorghum (Ahmad et al. 2014). Traditionally, oats were primarily utilized for livestock feed, with limited incorporation into human diets (Ahmad et al. 2010). However, recent studies have underscored the nutritional potential of oats, highlighting their rich phytochemical composition and genotype-dependent variation in primary metabolites (Ibrahim et al. 2020).

Oat grains are a valuable source of starch-based carbohydrates, balanced proteins, and lipids. They are also rich in B vitamins—particularly thiamine, folate, biotin, and pantothenic acid (Gu et al. 2021)—and provide a well-balanced profile of essential amino acids, including methionine, cysteine, threonine, and others (Biel et al. 2020). Although oats contain lower levels of protein, fatty acids, and minerals compared to cereals such as wheat and maize, they remain a versatile winter crop with applications in food, medicine, and forage production.

In response to shifting agricultural practices and increasing water scarcity, the development of resilient, multipurpose crops has become a priority. Oats offer considerable promise for forage cultivation, particularly when breeding programs focus on genetic diversity and the selection of germplasms with superior quantitative traits (e.g., yield, biomass) and qualitative traits (e.g., protein content, digestibility). While germplasm exchange is common among breeders, it often occurs within narrow climatic compatibility zones, potentially limiting access to broader genetic variation.

Genetic diversity in oats has been investigated through various approaches, including pedigree analysis (Rodgers et al. 1983; Souza and Sorrells 1989), morphological characterization (Souza and Sorrells 1991), and molecular markers (Donoughue et al. 1994; Li et al. 2000; Baohong et al. 2003). In Iran, the National Plant Genetic Bank has conducted comprehensive evaluations, revealing significant variation in key traits that can be leveraged for breeding purposes (Shahmoradi et al. 2019).

Given the increasing challenges in meeting forage demands—an essential pillar of global food security—it is vital to assess genetic diversity and identify superior oat genotypes capable of producing high-quality, high-yield forage in early spring. Understanding the correlation between qualitative and quantitative traits is fundamental to breeding programs aimed at developing oat varieties that optimize both forage yield and nutritional value. This relationship is particularly important as producers aim to balance agronomic performance with the nutritional requirements of livestock, underscoring the need to understand trait–nutrition interactions for sustainable forage production systems. In this study, oat genotypes were evaluated to investigate genetic variation and identify potential correlations between traits affecting forage quantity and quality. The goal was to provide a comprehensive assessment of both agronomic and nutritional performance.

2 Materials and Methods

Experimental conditions

The experiment was conducted in the research field of the Seed and Plant Improvement Institute (SPII) Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran, over two cropping seasons (2021–2023). The experimental site was located at latitude 35°47'40" North and longitude 50°55'13" East. The elevation was 1,255

meters above mean sea level. The trial area represents an arid agroecological zone, receiving an average annual precipitation of 264 mm. The soil is characterized as clay loam with a pH of approximately 8.5 (Table1). Climatic variations—including temperature, precipitation, and evapotranspiration—over the course of the study are illustrated in Figure 1.

Table 1 Soil analysis results from the research field of the Seed and Plant Improvement Institute in Karaj

Soil depth (cm)	EC (dS.m ⁻¹)	pH	OC(%)	P(mg.kg ⁻¹)	K(mg.kg ⁻¹)	Texture	K ⁺ Na ⁺ Mg ⁺⁺ Ca ⁺⁺ SO ₄ ⁻ Cl ⁻ HCO ₃ ⁻ SAR							
							(meq.l ⁻¹)							
0-30	1.26	8.5	0.47	5.29	228	C.L	0.03	3.4	3.3	6.3	3.6	5.3	3.7	1.55

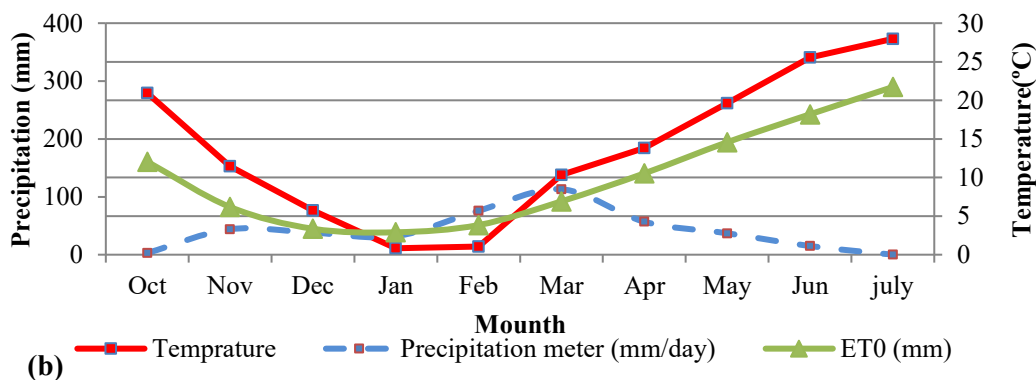
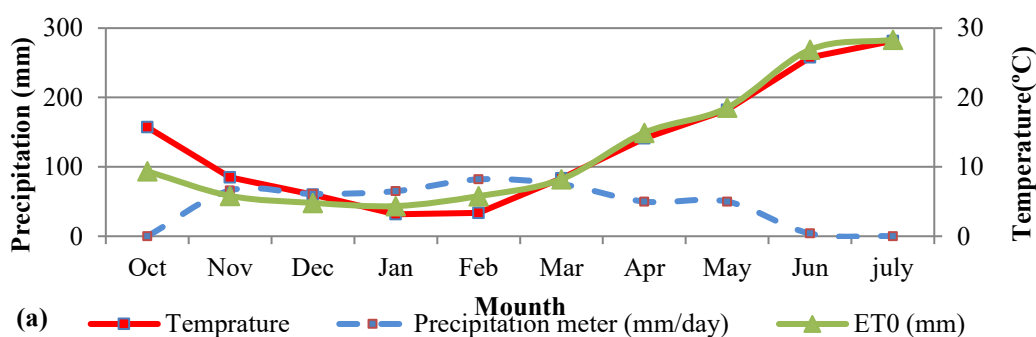


Fig. 1 Pattern of temperature and precipitation and evapotranspiration (ETo) change in 2021-2022(a) and 2022-2023(b) cropping seasons in Karaj

Plant materials and experimental design

Thirteen oat genotypes sourced from the National Plant Gene Bank of Iran, along with the introduced forage oat variety 'Euro' from South Australia, were assessed in this study (Table 2). The experiment was conducted using a complete randomized block design with three replications at the research farm of the Seed and Plant Improvement Institute in Karaj. Genotypes was planted in plots with four-meter rows and monitored throughout the growing period. Irrigation was managed via a drip system.

Table 2 Identification information and origin of the cultivated oat genotypes

Genotype	TN	KC*	Code	IC**	genus	species	Origin
1	499	61618	4	AVE 3077	<i>Avena</i>	<i>sativa</i>	ITA
2	500	61619	5	AVE 2840	<i>Avena</i>	<i>sativa</i>	CAN
3	501	61620	6	AVE 1731	<i>Avena</i>	<i>sativa</i>	SVK
4	502	61621	12	AVE 3428	<i>Avena</i>	<i>sativa</i>	USA
5	506	61625	16	AVE 3209	<i>Avena</i>	<i>sativa</i>	USA
6	511	61630	21	AVE 3418	<i>Avena</i>	<i>sativa</i>	USA
7	512	61631	22	AVE 3475	<i>Avena</i>	<i>sativa</i>	USA
8	516	61635	26	AVE 3288	<i>Avena</i>	<i>sativa</i>	USA
9	523	61642	33	AVE 4832	<i>Avena</i>	<i>sativa</i>	DEU
10	524	61643	34	AVE 3410	<i>Avena</i>	<i>sativa</i>	USA
11	531	61650	41	AVE 3461	<i>Avena</i>	<i>sativa</i>	USA
12	532	61651	42	AVE 4663	<i>Avena</i>	<i>sativa</i>	KEN
13	535	61654	45	AVE 5039	<i>Avena</i>	<i>sativa</i>	USA
14	Euro	-	-	-	<i>Avena</i>	<i>sativa</i>	AUS

*Identification code in National plant gene bank of Iran

**Identification code in IPK gene bank

Qualitative and quantitative traits

The traits measured included days to heading, flag leaf length and width (FLW), plant height (PH), panicle length (PL), and both fresh and dry forage yield (FFY, DFY). Forage yield was specifically assessed at the end of the milky stage.

To assess forage quality among oat genotypes, qualitative traits were measured during the second year of the experiment. These traits included Dry Matter Digestibility (DMD), Water Soluble Carbohydrates (WSC), Crude Protein (CP), Neutral Detergent Fiber (NDF), Acid Detergent Fiber (ADF), Crude Fiber, and Ash content. Measurements were conducted using Near Infrared Spectroscopy (NIR), based on the absorption and reflection of radiation within the 700–2500 nanometer wavelength range.

Statistical analysis

Prior to statistical analysis, the normality of the data and homogeneity of variances were confirmed using a variance uniformity test. To evaluate genotype responses across the two cropping seasons, combined analysis of variance (ANOVA) and mean comparisons were performed using SPSS software (version 27). For deeper insight and more accurate interpretation, correlation analysis, hierarchical clustering, and principal component analysis (PCA) were conducted using R software (version 4.3.3) and Statgraphics (version 19). Path analysis was performed to partition the phenotypic correlations between dry forage yield and its causal traits into direct and indirect effects. Analyses were conducted using standardized phenotypic data in R software (version 4.3.3).

3 Results

The results of the combined analysis of evaluated traits across oat genotypes over two cropping seasons are presented in Table 3. Analysis of the interaction between year and genotype revealed a statistically significant effect at the 5% probability level for the phenological trait of days to flowering. Additionally, this interaction was significant

for flag leaf width and plant height, indicating that genotypes responded differently across years in terms of these phenological and morphological traits.

Further examination of the genotype factor showed a significant influence on dry forage yield at the 5% probability level, and on days to flowering, plant height, panicle length, and fresh forage yield at the 1% probability level.

Table 3 Combined analysis of variance for quantitative traits of oat genotypes in two cropping seasons 2021-2023

S.O.V	df	Days to Flowering	Flag Leaf Width	Flag Leaf Length	Plant Height	Panicle Length	Fresh Forage Yield	Dry Forage Yield
Year	1	22.01	2213.49**	8899.20 ^{ns}	629.76 ^{ns}	1152.92 ^{ns}	51.84 *	0.78 ^{ns}
Year * Block	4	2.012	11.21**	0.297 ^{ns}	764.29**	1.95 ^{ns}	5.03 **	0.35 **
Genotype	13	96.75**	4.34 ^{ns}	5.60 ^{ns}	765.16**	69.51**	2.83**	0.28*
Gen*Year	13	13.27**	3.30*	5.85 ^{ns}	92.68**	4.58 ^{ns}	0.45 ^{ns}	0.095 ^{ns}
Error	52	1.71	1.44	4.82	28.48	6.04	0.496	0.07

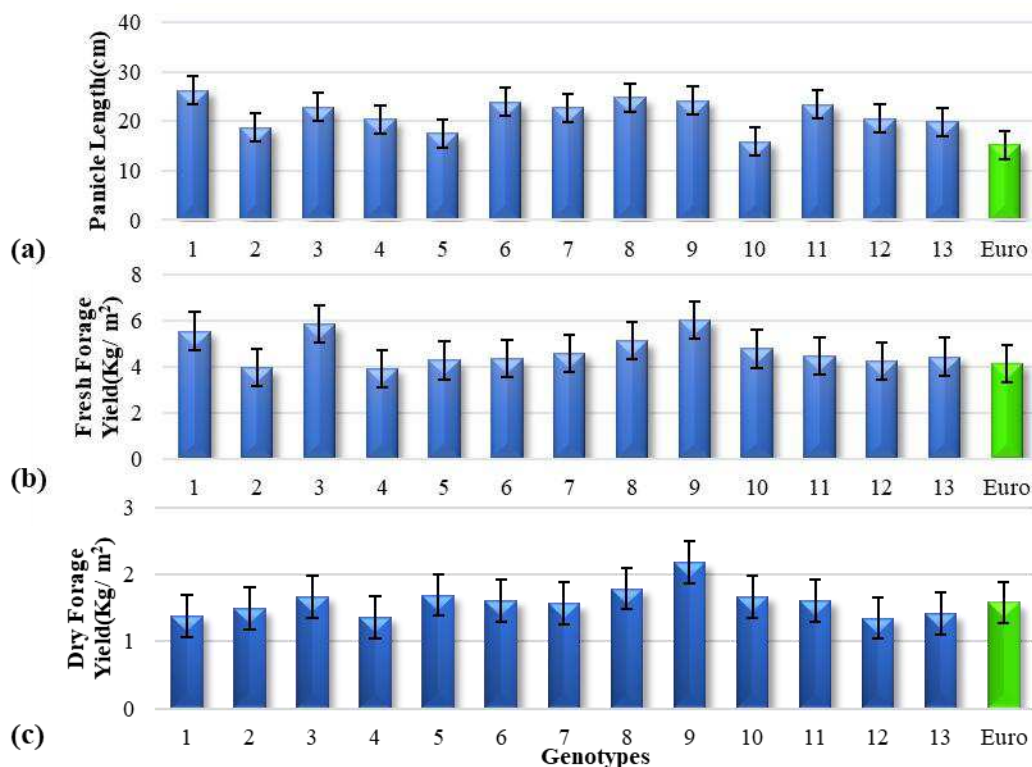


Fig. 2 Mean comparison of genotype effects on panicle length (a), fresh forage yield (b), and dry forage yield (c) in oat genotypes.

The comparison of mean panicle length among the evaluated oat genotypes (Figure 2-a) revealed that genotype 1 exhibited the highest average panicle length, approximately 25 centimeters, while the Euro variety recorded the lowest

mean of 15 centimeters. This difference was statistically significant, indicating a clear distinction between genotype 1 and the Euro variety.

In the analysis of mean values for fresh and dry forage yield (Figures 2-b and 2-c), genotype 9 demonstrated the highest performance in both traits. This genotype showed a significant difference compared to genotypes 2, 4, and 12, which had the lowest mean values for both fresh and dry forage yield.

Table 4 Mean comparison of genotype-by-year interaction effects on agronomic traits of oat genotypes across two cropping seasons (2021–2023).

Genotypes	Days to Flowering			Flag Leaf Width			Plant Height		
	Year 1	Year 2	Mean	Year 1	Year 2	Mean	Year 1	Year 2	Mean
1	192	187	190	2.1	1.7	1.9	90.3	94	92
2	177	176	176	1.67	1.5	1.58	80.3	84	82
3	181	180	181	2	1.86	1.93	105.0	114	110
4	177	179	178	1.73	1.16	1.45	87.3	107	97
5	175	176	176	1.63	1.36	1.5	78.3	94	86
6	181	180	181	1.7	1.26	1.48	106.7	112	109
7	180	180	180	1.7	1.26	1.48	79.0	102	90
8	182	181	182	1.63	1.3	1.47	88.3	109	99
9	178	183	180	2.03	1.3	1.67	103.3	111	107
10	176	179	178	1.46	1.3	1.38	84.3	104	94
11	176	179	177	1.6	1.4	1.5	88.7	111	100
12	179	177	178	2.36	2	2.18	91.0	108	99
13	173	175	174	2.13	1.3	1.71	92.7	114	104
Euro	178	181	179	1.7	1.23	1.46	51.7	78	65
LSD	1.44			1.39			3.21		

Table 4 presents the comparison of mean values for evaluated traits in oat genotypes relative to the Euro variety across two cropping seasons. Regarding days to flowering, genotype 13 exhibited the earliest maturity with an average of 174 days, followed by genotypes 2 and 5 (176 days). In contrast, genotype 1 had the latest maturity, with an average of 190 days. For plant height, genotypes 3, 6, and 9 recorded the tallest growth, whereas the Euro variety was the shortest, with an average height of approximately 65 centimeters.

Table 5 summarizes the analysis of variance for forage quality traits among the oat genotypes and the Euro variety. Significant differences were observed at the 1% probability level for digestible dry matter (DMD) and water-soluble carbohydrates (WSC). Additionally, crude protein (CP), acid detergent fiber (ADF), and ash content showed significant variation among genotypes, while neutral detergent fiber (NDF) did not exhibit statistically significant differences.

Table 6 compares the mean values of forage quality traits. The Euro variety had the highest average DMD (58.9), whereas genotypes 5 and 11 recorded the lowest values (51.46 and 51.48, respectively). For WSC, genotypes 2 and 10, along with the Euro variety, showed the highest averages. DMD and WSC are key indicators of forage quality. Crude protein (CP), a vital component of forage nutritional value, was highest in genotype 1 (9.36), followed by

genotypes 4 and 12. Moreover, genotype 1, along with genotypes 3 and 12, exhibited the highest ash content among the evaluated genotypes.

Table 5 Analysis of variance for qualitative traits in forage of oat genotypes (Dry Matter Digestibility (DMD), Water Soluble Carbohydrates (WSC), Crude Protein (CP), Neutral Detergent Fiber (NDF), Acid Detergent Fiber (ADF), Crude Fiber, and Ash content)

S.O.V	df	DMD	WSC	CP	FBR	ADF	NDF	ASH
Genotype	13	10.46**	5.57 **	2.315**	3.73*	19.78 **	10.97	1.87 **
Repeat	2	3.08	0.46	1.65*	6.06 *	7.82	0.41	0.03
Error	26	2.11	0.78	0.45	1.66	3.86	6.57	0.21

**and * significant at $P \leq 0.01$ and $P \leq 0.05$, respectively

Table 6 Mean comparison for qualitative traits in forage of different oat genotypes (Dry Matter Digestibility (DMD), Water Soluble Carbohydrates (WSC), Crude Protein (CP), Neutral Detergent Fiber (NDF), Acid Detergent Fiber (ADF), Crude Fiber, and Ash content)

Gen	DMD	WSC	CP	FBR	NDF	ADF	ASH
1	55.16 bc	9.72 bcde	9.36 a	29.30 bc	70.88 bc	45.74 a	10.07 a
2	56.04 b	11.25 ab	6.94 def	31.38 ab	69.80 bc	40.33 cd	8.05 de
3	54.07 bcd	10.95 abc	7.75 bcde	28.72 c	70.85 bc	44.42 ab	9.98 a
4	53.69 bcd	8.60 ef	8.90 ab	29.60 bc	74.11 ab	45.36 ab	9.81 ab
5	51.46 d	8.72 def	7.76 bcde	30.80 abc	75.88 a	45.28 ab	8.63 cd
6	54.76 bc	10.32 abcd	8.05 bcd	29.72 bc	72.90 abc	42.86 abc	9.08 bc
7	55.17 bc	8.65 ef	8.00 bcde	30.56 bc	73.44 abc	41.82 bc	8.41 cde
8	53.71 bcd	9.68 bcde	6.41 f	30.32 bc	68.70 c	42.89 abc	9.56 ab
9	54.75 bc	8.47 ef	6.79 def	33.07 a	70.41 bc	42.20 abc	8.52 cd
10	54.25 bc	11.78 a	6.72 ef	31.37 ab	71.59 abc	40.39 cd	8.26 cde
11	51.48 d	7.62 f	7.54 cdef	30.91 abc	73.14 abc	45.05 ab	9.02 bc
12	52.71 cd	8.26 ef	8.60 abc	29.44 bc	72.97 abc	45.84 a	9.98 a
13	54.29 bc	9.55 cde	7.91 bcde	30.12 bc	72.00 abc	42.29 abc	9.02 bc
Euro	58.90 a	11.76 a	7.70 bcde	31.15 abc	70.61 bc	36.94 f	7.64 e

An important determinant of forage quality is the proportion of cell wall components, which include both digestible and indigestible fractions. Research has shown that lower cell wall content enhances nutrient intake and digestibility in livestock (Juskiw et al. 2000). Consequently, reducing the concentrations of acid detergent fiber (ADF) and neutral detergent fiber (NDF) can improve forage palatability and digestibility. A comparison of ADF percentages among the oat genotypes revealed that genotypes 1 and 12 had the highest averages (45.74 and 45.84, respectively), while the Euro variety exhibited the lowest average (Table 6).

Figure 3 presents a correlation matrix illustrating relationships among forage yield and quality traits in oat genotypes. The phenological trait of days to flowering showed a strong positive correlation (at the 1% probability level) with panicle length (PL) and fresh forage yield (FFY), and a positive correlation (at the 5% level) with plant

height (PH). These results suggest that late-flowering genotypes tend to produce longer panicles, taller plants, and higher fresh forage yields. A significant positive correlation between plant height and fresh forage yield was also observed at the 1% level.

Regarding forage quality traits, digestible dry matter (DMD) exhibited a significant positive correlation with water-soluble carbohydrates (WSC). Both DMD and WSC were significantly negatively correlated with ADF and NDF at the 1% probability level, indicating that higher fiber content reduces digestibility and carbohydrate availability. Ash content showed a significant negative correlation with fiber content (FBR) and a positive correlation with ADF (Figure 3).

Further analysis revealed that fresh forage yield (FFY) was positively correlated with both ADF and ash content (at the 5% and 1% levels, respectively), while dry forage yield (DFY) was positively correlated with fiber percentage (FBR). In contrast, DFY showed a significant negative correlation with crude protein (CP) at the 1% level, suggesting that increased dry matter yield may be associated with reduced protein content (Figure 3).

Additionally, plant height demonstrated a significant negative correlation with key forage quality traits such as DMD and WSC.

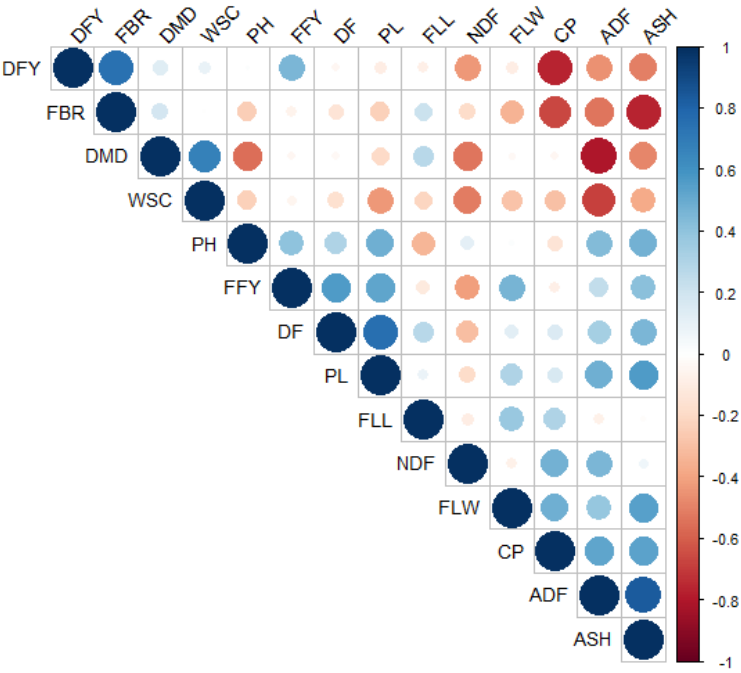


Fig. 3 Correlation coefficients of the forage yield quality and quantity traits in oat genotypes based on Pearson's method (DF: Days to Flowering, PH: Plant height, PL: Panicle Length, FFY: Fresh Forage Yield, DFY: Dry Forage Yield, FLL: Flag Leaf Length, FLW: Flag Leaf Width, WSC: water soluble carbohydrates, CP: crude protein, FBR: fiber, ADF: acid detergent fiber, DMD: dry matter digestibility, NDF: neutral detergent fiber)

Figure 4 presents a heat map illustrating the clustered correlation matrix between oat genotypes and various forage yield and quality traits. The accompanying dendrograms display the relationship distances among oat genotypes (left dendrogram) and forage traits (top dendrogram). In the heat map, darker shades represent higher trait values.

Cluster analysis grouped the oat genotypes into four distinct clusters, with the average trait values for each group summarized in Table 7. The first cluster comprised only the Euro cultivar, which exhibited the highest dry matter digestibility (DMD) and the lowest values for ash (ASH) and acid detergent fiber (ADF). However, the Euro cultivar also showed lower averages for plant height and panicle length compared to other genotypes (Figure 4).

The second cluster included genotypes 2, 8, 9, and 10, which recorded the highest averages for dry forage yield (DFR) and fiber content (FBR). The third cluster, also consisting of four genotypes, displayed relatively low averages for DFR, DMD, and water-soluble carbohydrates (WSC). The fourth cluster comprised genotypes 1, 3, 6, 7, and 13, which had the highest averages for days to flowering, flag leaf width, panicle length, and plant height.

Overall, the second cluster—genotypes 2, 8, 9, and 10—was the most agronomically desirable, as it combined high forage yield and fiber content with favorable values for most forage quality traits, excluding crude protein (Figure 4).

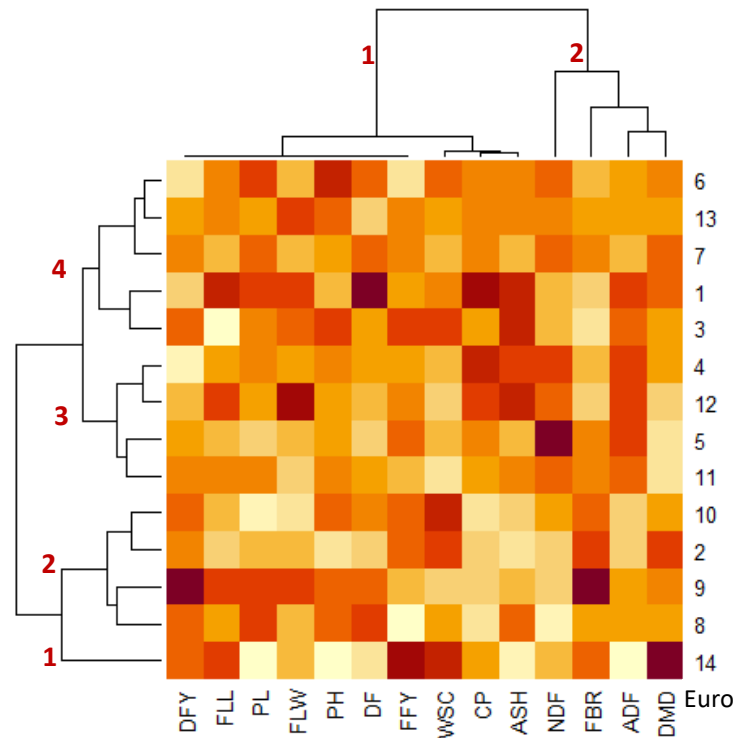


Fig. 4 Heat map of clustered correlation matrix of oat genotypes based on agronomic and forage qualitative traits (DF: Days to flowering, PH: Plant height, PL: Panicle Length, FFY: Fresh Forage Yield, DFY: Dry Forage Yield, FLL: Flag Leaf Length, FLW: Flag Leaf Width, WSC: water soluble carbohydrates, CP: crude protein, FBR: fiber, ADF: acid detergent fiber, DMD: dry matter digestibility, NDF: neutral detergent fiber)

Table 7 Means for agronomic and forage qualitative traits of oat genotypes in groups resulting from cluster analysis

Cluster

Traits		1	2	3	4
Days to Flowering	DF	175.67	180.00	177.92	180.60
Flag Leaf Width	FLW	1.70	1.70	1.83	1.93
Flag Leaf length	FLL	24.50	21.72	22.07	21.71
Panicle Length	PL	18.33	24.83	23.83	27.00
Plant Height	PH	71.00	93.83	93.08	97.00
Fresh Forage Yield(kg/m ²)	FFY	4.55	5.74	4.98	5.88
Dry Forage Yield (Kg/m ²)	DRY	1.58	1.67	1.39	1.43
Dry matter digestibility	DMD	58.90	54.69	52.34	54.69
Water soluble carbohydrates	WSC	11.76	10.29	8.30	9.84
Crude protein	CP	7.70	6.71	8.20	8.21
Fiber	FBR	31.15	31.54	30.19	29.68
Acid detergent fiber	ADF	36.94	41.45	45.38	43.43
Neutral detergent fiber	NDF	70.61	70.13	74.02	72.02
Ash	ASH	7.64	8.60	9.36	9.31
Cluster Members		1	4	4	5

To gain deeper insight into the relationships between traits and genotypes, principal component analysis (PCA) was performed on both quantitative and qualitative traits. The analysis identified five principal components contributing to the coefficient matrix, collectively explaining 89.9% of the total trait variance (table not shown). The first two components alone accounted for 59.8% of the observed variation, providing a robust basis for visual interpretation.

A two-dimensional PCA biplot was generated to illustrate the distribution and relationships among genotypes and traits (Figure 5). In this plot, vectors representing qualitative traits are shown in green, while those representing quantitative traits are depicted in blue, allowing for clear differentiation and interpretation of trait contributions and genotype clustering.

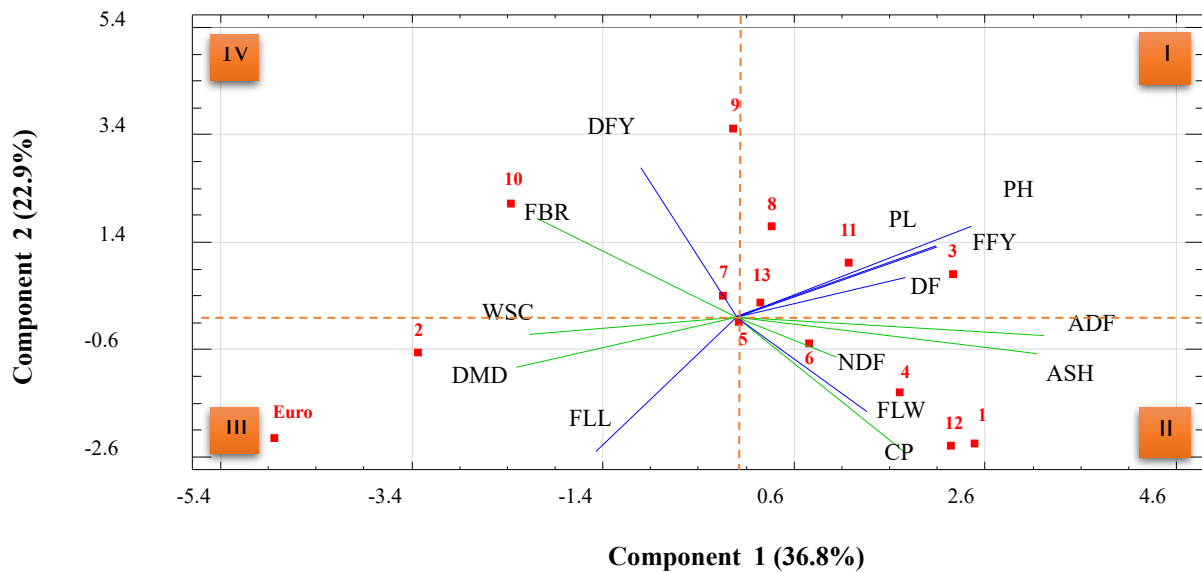


Fig. 5 Bi-plot of first two principal components for qualitative (blue line) and quantitative (green line) characters in oat genotypes (DF: Days to Flowering, PH: Plant height, PL: Panicle Length, FFY: Fresh Forage Yield, DFY: Dry Forage Yield, FLL: Flag Leaf Length, FLW: Flag Leaf Width, WSC: water soluble carbohydrates, CP: crude protein, FBR: fiber, ADF: acid detergent fiber, DMD: dry matter digestibility, NDF: neutral detergent fiber)

The sharp angles observed between vectors for panicle length (PL), plant height (PH), fresh forage yield (FFY), and days to flowering (DF) in the PCA biplot (Figure 5) indicate a strong positive association among these traits, consistent with the correlation matrix presented in Figure 3. A notable relationship was also identified between flag leaf width (FLW) and crude protein (CP), with genotypes 1 and 12—positioned near these vectors—exhibiting elevated values for both traits.

Genotypes 1 and 10, located close to the dry forage yield (DFY) vector, demonstrated superior performance in this trait. The DFY vector's opposition to the CP vector suggests an inverse relationship between dry forage yield and crude protein content. Additionally, the proximity of the fiber content (FBR) vector to DFY implies that higher dry forage yields are associated with increased fiber content in oat forage (Figure 5).

Flag leaf length (FLL) showed a strong positive correlation with dry matter digestibility (DMD) and water-soluble carbohydrates (WSC), reinforcing its importance as a morphological trait linked to forage quality. Based on these associations, genotype 2 and the Euro cultivar emerged as superior in terms of digestibility and carbohydrate content.

Path coefficient analysis was performed to partition the correlations between dry forage yield and its causal traits into direct and indirect effects (Fig 6). The path diagram presents a structural model explaining variation in fresh forage yield (FFY) and dry forage yield (DFY) through a combination of phenological, morphological, and leaf traits.

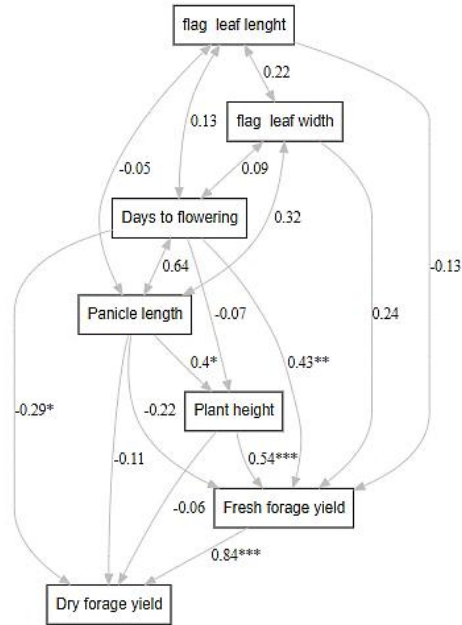


Fig. 6 Path diagram representing direct and indirect effects of traits on fresh forage yield and dry forage yield in oat genotypes. One-way vectors (→) show standardized coefficients with significant level and two-way vectors (↔) are covariances among exogenous traits

The path analysis diagram (figure 6) elucidates the causal relationships among phenological, morphological, and yield traits in oat forage. Fresh forage yield is directly influenced by five explanatory variables, with plant height exhibiting the strongest positive direct effect ($C = 0.54$, $p < 0.001$). Reflecting the important role of plant height in determining forage yield. The second important factor for fresh forage yield is phenological trait of days to flowering, this trait directly affected the trait ($C = 0.43$, $p < 0.01$). Flag leaf width, flag leaf length and panicle length exert weak to moderate negative or negligible direct effects, while panicle length indirectly showed a significant positive effect on fresh forage yield through plant height ($C = 0.4$, $p < 0.01$). Dry forage yield is predominantly determined by fresh forage yield itself ($C = 0.84$, $p < 0.001$), indicating that variation in dry matter is largely mediated through total biomass accumulation. Days to flowering, despite its substantial beneficial effect on fresh yield, shows a significant negative direct effect on dry forage yield ($C = -0.29$, $p < 0.01$), while plant height and panicle length had no direct influence.

Discussion

The experiment revealed significant differences among oat genotypes across most evaluated traits, underscoring the genetic diversity and agronomic potential within the studied population. While some genotypes excelled in forage yield, others demonstrated superior nutritional quality.

Genotypic variation and genotype by environment interactions

The analysis revealed substantial genetic variability among the evaluated oat genotypes for both quantitative and qualitative traits, which aligns with previous research documenting extensive genetic diversity within oat germplasm (Singh et al. 2024; Devi et al. 2024; Zhao et al. 2025). The significant genotype effects observed for morphological traits such as plant height and panicle length, as well as yield components including fresh and dry forage yield,

demonstrate the presence of valuable genetic diversity for breeding programs aimed at improving forage production (Uhlarik et al. 2022; Singh et al. 2024).

The detection of significant genotype $\times$ year interactions for days to flowering, flag leaf width, and plant height indicates that genotypes responded differently across cropping seasons, revealing differential environmental sensitivity among the evaluated materials (Kim et al. 2006; Uhlarik et al. 2022; Singh et al. 2024; Devi et al. 2024; Alexander et al. 2025; Zhao et al. 2025). Climatic fluctuations, particularly in temperature and precipitation, affect plant physiological processes and contribute to year-to-year variation in trait expression (Shahmoradi, 2022; Shavrukove et al. 2017). These findings emphasize that environmental conditions play an important role in trait expression, highlighting the need for evaluations across multiple environments to obtain more reliable genotype recommendations. The environmental sensitivity observed is expected in field crops and has important implications for breeding programs and variety recommendations across different growing regions.

The magnitude of genetic variation provides opportunities for both direct selection of superior genotypes and strategic hybridization programs targeting specific trait combinations (Devi et al. 2024). The identification of genotypes with contrasting performance profiles, such as genotype 9's superiority for forage yield versus genotype 1's excellence in panicle length and protein content, demonstrates the complementary nature of available genetic resources (Uhlarik et al. 2022; Singh et al. 2024; Devi et al. 2024). This diversity suggests that cross-breeding among genotypes from specific performance clusters offers promising avenues for future oat breeding and yield improvement programs.

The consistent detection of genotype-by-environment interactions across multiple traits reinforces the importance of multi-environment testing for accurate genotype evaluation and selection (Goncalves et al. 2025; Zhao et al. 2025). Future research should integrate molecular marker technology with multi-environmental, multi-year evaluations to provide more robust scientific foundations for oat genetic improvement while enhancing selection efficiency.

Forage quality analysis and trade offs

The forage quality evaluation demonstrated substantial genetic variation among oat genotypes for key nutritional parameters, with significant differences observed for digestible dry matter (DMD), water-soluble carbohydrates (WSC), crude protein (CP), acid detergent fiber (ADF), and ash content (Webster and Wood 2011; Uhlarik et al. 2022; Singh et al. 2024). The Euro variety achieved the highest DMD content at 58.9%, while genotypes 5 and 11 recorded the lowest values, demonstrating the range of digestibility potential within the evaluated germplasm.

Critical trade-offs emerged between quantitative and qualitative traits, particularly the inverse relationship between plant height and key forage quality indicators such as DMD and WSC (Uhlarik et al. 2022; Singh et al. 2024; Devi et al. 2024). This negative correlation suggests that taller, higher-yielding genotypes may compromise forage quality, with late-maturing and taller genotypes tending to produce higher hay yields but lower hay quality (Uhlarik et al. 2022). Additionally, the significant negative correlation between dry forage yield and crude protein content indicates that increased biomass production may be associated with reduced nutritional quality (Uhlarik et al. 2022; Zhao et al. 2025).

The fiber content analysis revealed important relationships affecting forage palatability and digestibility. Both DMD and WSC showed significant negative correlations with ADF and NDF, indicating that higher fiber content reduces digestibility and carbohydrate availability (Uhlarik et al. 2022). Research has demonstrated that moderately significant

negative correlations between biomass traits and anti-quality components such as NDF and ADF indicate that increased biomass can decrease fiber concentrations, which is favorable for forage quality (Ahmed et al. 2023; Bakhtavar et al. 2020).

Despite these trade-offs, the cluster analysis identified genotypes that successfully balanced yield and quality characteristics. The second cluster, comprising genotypes 2, 8, 9, and 10, emerged as most agronomically desirable by combining high forage yield and fiber content with favorable values for most forage quality traits, excluding crude protein. This finding demonstrates that strategic breeding can identify genotypes that optimize both yield and quality parameters, providing valuable breeding materials for future improvement programs.

Correlation analysis and trait relationships

The correlation analysis provided critical insights into trait relationships that can guide breeding strategies and selection programs (Greveniotis et al. 2022). The strong positive correlations observed between days to flowering, panicle length, plant height, and fresh forage yield demonstrate that late-flowering genotypes tend to produce longer panicles, taller plants, and higher fresh forage yields (Devi et al. 2024; Zhao et al. 2025).

These positive associations among morphological traits and yield parameters confirm established relationships in oat genetics, with most trait correlations reaching highly significant levels (Zhao et al. 2025). The relationship between plant height and fresh forage yield was particularly notable, providing opportunities for indirect selection where less stable traits can be improved through selection for more stable characteristics (Greveniotis et al. 2022).

However, important trade-offs emerged between quantitative and qualitative traits, particularly the significant negative correlations between plant height and key forage quality indicators such as digestible dry matter and water-soluble carbohydrates (Aydin et al. 2010; Singh et al. 2024; Devi et al. 2024). This inverse relationship indicates that taller, higher-yielding genotypes may compromise forage quality, reflecting a common challenge in forage crop breeding.

The mechanism underlying the biomass-quality trade-off in forage systems can be explained through nutrient dilution effects and shifts in plant tissue composition. As grass yield increases, forage nutritional value systematically decreases, with yield showing negative correlations with crude protein (CP) content. This occurs because higher biomass accumulation leads to the "dilution" of essential nutrient elements such as nitrogen and phosphorus, causing their concentrations to decline as total biomass increases (Li et al., 2022).

The analysis also revealed moderately significant negative correlations between biomass traits and fiber components (ADF and NDF), indicating that increased biomass can decrease fiber concentrations, which is favorable for forage quality (Ahmed et al. 2023; Bakhtavar et al. 2020). Additionally, the negative correlation between dry forage yield and crude protein content reflects a fundamental trade-off where increased biomass production may be associated with reduced nutritional quality (Zhao et al. 2025; Mut et al. 2015). Flag leaf length's association with DMD and WSC further emphasizes its role in forage quality. As the primary site for photo-assimilate accumulation in cereals, the flag leaf significantly influences productivity (Johnson et al. 1990; Ba et al. 2020; Du et al. 2022). Morphological traits such as flag leaf size and area have been positively linked to yield-related parameters (Fan et al. 2015; Zhang et al. 2014).

These correlation patterns provide a foundation for developing selection indices and identifying optimal trait combinations for genetic improvement (Devi et al. 2024). The relationships identified enable both direct selection of superior genotypes and strategic breeding approaches that balance yield and quality objectives through careful consideration of trait associations.

Breeding implications and future directions

The substantial genetic variability demonstrated among the evaluated oat genotypes provides excellent opportunities for genetic improvement through strategic crossing and selection programs (Singh et al. 2024; Devi et al. 2024; Zhao et al. 2025). The identification of complementary genotypes with contrasting trait profiles offers a foundation for developing mapping populations to investigate the genetic architecture underlying important agricultural traits (Singh et al. 2024). Cross-breeding among diverse genotypes from specific clusters within the evaluated panel offers promising avenues for future oat breeding and yield improvement programs.

The correlation patterns identified provide valuable guidance for indirect breeding strategies, where statistically significant correlations enable selection of traits with low stability through more stable traits that promote adaptation (Greveniotis et al. 2022). The positive associations among days to flowering, panicle length, plant height, and fresh forage yield suggest that selection for late-maturing, tall genotypes could simultaneously improve multiple yield-related traits (Singh et al. 2024; Devi et al. 2024). However, breeding programs must carefully balance yield and nutritional objectives due to the negative correlation between dry forage yield and crude protein content (Singh et al. 2024).

The trade-offs between quantitative and qualitative traits emphasize the need for balanced selection strategies that optimize both yield and quality parameters (Zhao et al. 2025). The second cluster genotypes (2, 8, 9, and 10) provide excellent breeding materials as they successfully combine high forage yield with favorable quality characteristics, demonstrating that strategic breeding can overcome traditional yield-quality trade-offs.

The results highlight a clear trade-off between fresh and dry forage yield components: traits that increase succulent biomass directly (panicle length) or indirectly (days to flowering) tend to reduce dry-matter concentration, reflecting the higher water content of reproductive structures. Consequently, selection for maximum fresh forage yield (e.g., for silage or green chop) should prioritize longer panicles and wider flag leaves, whereas breeding for dry-matter yield (e.g., hay production) requires balanced improvement of fresh biomass while avoiding excessive panicle elongation. The near-perfect transmission of effects from fresh to dry yield (0.84***) confirms that, in this population and environment, increasing total biomass remains the most effective primary strategy for enhancing dry forage yield, with secondary adjustments needed to optimize dry-matter partitioning.

These findings underscore the value of path analysis in dissecting direct and indirect contributions of agronomic traits and in guiding trait-based selection in dual-purpose forage breeding programs.

Future breeding programs should integrate molecular marker technology with multi-environmental, multi-year evaluations to provide more robust scientific foundations for oat genetic improvement while enhancing selection efficiency and accelerating breeding cycles. This integrated approach will address the environmental sensitivity observed in key traits and enable more accurate genotype evaluation across different growing regions. The comprehensive trait assessment framework established in this study demonstrates the potential for developing varieties

tailored to specific end-uses and provides practical selection indices for enhancing fodder yield in future breeding programs.

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Author Contributions

Shakiba Shahmoradi conceived and designed the experiments and also conceived the main body of the manuscript. Behzad Sorkhi and Vida Ghotbi helped with in field experimental studies and data analysis. Simin Taheri Ardestani helped with diseases evaluation and Hamid Reza Nikkhah provided the materials for the experiment. All authors read the publication and gave their final approval.

Declarations

The authors have no Declarations.

Competing interests

The authors have no competing interests to declare that are relevant to the content of this article.

Data availability

The data that support this study will be shared upon reasonable request to the corresponding author.

Conflicts of interest

The authors declare that they have no conflicts of interest.

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