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Principal Component and Diversity Metrics on Biochemical, Yield and its Attributing Traits of Oat Genotypes

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ABSTRACT

The present study was conducted during *rabi* November–February, 2022 at Forage Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, Haryana, India to to assess the genetic diversity and variability among different oat genotypes. Fifty (50) elite Oat genotypes was grown were grown with three replications in a randomised block design (RBD). The 16 morpho-physiological and biochemical observations were recorded in five randomly selected plants of each genotype across all three replications and the data were analysed. The diverse genotypes were clustered into six groups. Higher inter-cluster distances as compared to intra-cluster distances indicated greater homogeneity within clusters and cluster I exhibited the highest intra-cluster distance. Maximum inter-cluster distances were observed between clusters I and II, whereas the smallest distance was between clusters II and IV. Crosses among genotypes from Clusters I and II likely to produce novel recombinants due to the high degree of divergence. Six principal components (PCs) had eigenvalues greater than one, contributing to 72.61% of the variability. From the PCA and cluster analysis it was inferred that the genotypes RO 19, HFO 1123, PLP-27, HFO 806, HFO 1222 and HFO 1003 could be used for green fodder yield, whereas UPO-20-3, HFO-1003, HFO 806 for seed yield plant^{-1}.

KEYWORDS: Principal components, cluster analysis, genetic variability, genetic divergence

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1. INTRODUCTION

Oat (*Avena sativa* L.) is an important cereal cum forage crop of the temperate, sub-temperate and tropical climates of the world. It serves as food, feed, and fodder. The green fodder is primarily fed directly, while the surplus is preserved as silage or hay for use during periods of fodder scarcity. (Sutti et al., 2004). It is a *rabi* (November-March, 2022) season self-pollinated allohexaploid crop (2n=2x=42) bearing three different genomes viz., A, C and D (Peng et al., 2022). Oat like rye, are typically classified as a secondary crop, meaning they are developed from a weed of the principal cereal, wheat and barley (Zhou et al., 1999; Kumar et al., 2024). The global area and production of oat is approximately 27 million hectares and 40 metric tonnes respectively. The top five countries for oat production are Russia, Canada, Poland, Finland and Australia (Anonymous, 2023). In India, around 5.0 lakh hectares area is under oat cultivation. Uttar Pradesh has the largest area (34%), followed by Punjab (20%), Bihar (16%) Haryana (9%) and Madhya Pradesh (6%) under oat cultivation. Spring oat (*Avena sativa* L.) is a widely cultivated cereal recognized for its heart-health benefits and gluten-free nature, serving as an important resource for food, feed, and cosmetic applications worldwide (Rehman et al., 2025). One hectare of oat may produce between 35 and 40 tons of green fodder on average, making it a high yielding winter Rabi fodder crop. Under favourable temperature, the crop is an excellent source of hay, can be used for grazing and provides quality silage (Bichewar et al., 2023; Ruwali et al., 2013). Oat contain antioxidants such as α-tocotrienol, α-tocopherol and avenanthramides, and total dietary fibre, including soluble β-glucan (Kujur et al., 2017; Kumar et al., 2023). It has been increasingly popular for human consumption due to their dietary benefits and nutritional worth (Ahmad et al., 2016). Oat grain contains a high proportion of fructo-oligosaccharides (FOS), which are soluble nonstructural carbohydrates composed of short chains of fructose. FOS are known as "prebiotics" because to their ability to specifically encourage the growth and activity of beneficial gut bacteria. They also play important roles in eukaryotic biology and illness (Ibrahim et al., 2020; Ihsan et al., 2022).

Pearson (Pearson, 1901) first proposed the idea of PCA and Hotelling (Hotelling, 1933) later refined it. Now Principal Component Analysis (PCA) is widely used in contemporary data analysis due to its simplicity and non-parametric nature making it effective for extracting meaningful insights from intricate data sets (Jolliffe, 1990; Rezai and Frey, 1990; Giordani, 2018; Sachin et al., 2025). Several workers have emphasized the need of parental diversity in optimum magnitude to obtain superior genotypes in the segregating generations. (Kumari and Jindal, 2019). By requiring minimal input PCA offers a clear method for simplifying complex data unveiling potentially obscured patterns (Uarrota et al., 2017). Crop development success relies on the availability of heterogeneity in germplasm for key economic characteristics (Nikoloudakis et al., 2016; Oo et al., 2022). Hence, D^2 test is employed to evaluate genetic diversity, aiding breeders in selecting suitable parent pairs for breeding programs. Additionally, cluster analysis is a common tool utilized to group accessions based on genetic similarities assisting breeders and geneticists in identifying genotypes with potential for targeted breeding or genetic endeavours (Sachin et al., 2023). By evaluating the degree of diversification, it also calculates the proportionate contribution of each component character to the overall divergence. Hence, parents should be chosen based on a range of quantitatively distinct attributes to maximize yield, a criterion that Mahalanobis's D^2 statistic (1936) can fulfil. In order to check for genetic diversity, the current investigation was conducted with 50 oat genotypes.

2. MATERIALS AND METHODS

The study was conducted at the Forage Research area (29.144874' latitude and 75.685261' E longitude), Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, Haryana during Rabi 2022-23. A total of 50 Oat genotypes were sown using a randomised block design (RBD) with three replications.

The 16 observations namely, plant height (cm), days to 50% flowering, days to maturity, no. of tillers plant^{-1}, leaf weight plant^{-1} (g), stem weight (g), leaf stem ratio, flag leaf length (cm), flag leaf width (cm), internode length (cm), panicle length (cm), 100 seed weight (g), seed yield plant^{-1} (g), green fodder yield plant^{-1} (g), dry matter yield plant^{-1} (g) and crude protein content (%) were recorded in five randomly selected plants of each oat genotype in all three replications and analyzed using appropriate statistical methods.

The statistical analysis was performed using OPSTAT (Sheoran et al., 1998) software and R STUDIO (Anonymous, 2023). Methods of analysis originally developed by Mahalanobis (1936), with its application in genetic diversity assessment suggested by Rao, (1952). The genotypes were grouped based on minimum generalized distance using Tocher's/Ward method.

3. RESULTS AND DISCUSSION

3.1. Divergence analysis

Mahalanobis's D^2 statistic is a powerful tool for assessing genetic diversity in breeding materials. This study employing Mahalanobis's D^2 analysis, grouped 50 oat genotypes into six major clusters based on 16 morphological and biochemical

traits. Among the clusters, Cluster IV contained the most genotypes (14), followed by Cluster I (12), cluster III (7), cluster V (6), cluster VI (6) and cluster II (5) (Table 1). The distinct clustering pattern in dendrogram highlights divergence in the experimental material (Figure 1).

Higher inter-cluster distances as compared to intra-cluster distances indicated greater homogeneity within clusters and narrower genetic variability (Table 2). Cluster I exhibited the highest intra-cluster distance, followed by cluster V (68.10) cluster III (45.72), Cluster VI (45.68), Cluster IV (40.59) and cluster II (40.30). Maximum inter-cluster distances were observed between Cluster I and II followed by Clusters I and III and Clusters I and IV, whereas the smallest distance was between Clusters II and IV. Larger inter-cluster distances indicate the presence of wide variation for from one cluster to another and also suggest the potential for producing wide variability in segregating populations, enabling effective selection (Govindaraj et al., 2011, Kumari and Jindal (2019)).

Table 1: Distribution pattern of 50 Oat genotypes into 6 clusters

Cluster no.	No. of genotypes	Genotypes
Cluster I	14	BAUO-101, HFO 1013, HFO 1113, HFO 1207, HFO 1208, HFO 1217, HFO 707, OL-1942, OL-1949, OS 403, OS 6, PLP-27, RO 11-1 and RO 19
Cluster II	7	HFO 1014, HFO 1121, HFO 915, HFO 917, HFO-1016, OL-1960 and OL-1974
Cluster III	12	HFO 1108, HFO 1119, HFO 114, HFO 529, HFO 806, HFO-1003, HFO-1009, JHO 822 JO-08-37, Kent, SKO-244 and UPO-20-3
Cluster IV	5	HFO 1123, HFO 1209, HFO 904, JO-07-28 and OL-1977
Cluster V	6	HFO 1204, HFO 122, HFO 906, OL-1882, OS 377 and UPO-20-2
Cluster VI	6	HFO 1222, HFO 611, HJ 8, JH 851, OL-1944 and UPO 212

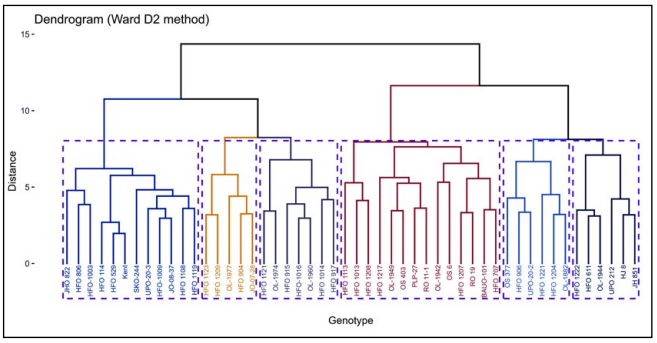

Figure 1: Dendrogram representing genetic relationship among Oat genotypes based on Euclidean distance

Clusters with higher intra-cluster distances may have greater heterogeneity and varying pedigrees, making them ideal for selecting desirable traits. Clusters containing a larger number of lines exhibited lower genetic diversity, indicating that the lines within them were more closely related (Kumar et al., 2016; Reddy et al., 2024). For example, genotypes from Clusters I, V and III can be used for further breeding programmes.

Based on cluster mean values (Table 3), the data indicated significant differences among the clusters for most of the characters under study. The maximum mean value leaf weight plant^{-1} (66.21), leaf stem ratio (0.85), flag leaf length (28.08), flag leaf width (1.59) and green fodder yield plant^{-1} (128.55) was observed in the genotypes of cluster I. Green fodder yield plant^{-1} was included in cluster I hence cluster I may be considered as best cluster among all six clusters. Cluster II has the maximum mean value for the stem weight plant^{-1} (82.78), 100 seed weight (4.15) and crude protein content % (9.60). Likewise, for Cluster III had maximum mean values for the traits for days to 50% flowering (104.14), days to maturity (128.28) panicle length (43.08), 100 seed weight (4.15) and seed yield plant^{-1} (54.10). Cluster IV had the maximum mean value for internode length only that was 26.28. The maximum mean value for plant height was observed in cluster V (116.59) Cluster VI had the maximum mean value for the number of tillers plant^{-1} (10.46) and dry matter yield plant^{-1} (32.67). The genotypes exhibited

Table 2: Inter and Intra-cluster distance among different clusters of oat

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	70.94	81.03	75.38	74.04	72.78	75.05
Cluster II		40.30	51.48	44.20	70.13	66.06
Cluster III			45.72	58.18	59.62	55.84
Cluster IV				40.59	60.61	64.69
Cluster V					68.10	67.29
Cluster VI						45.68

Table 3: Cluster means for different characters in oat

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
PH	105.37	88.14	104.86	82.52	116.59	113.15
DFF	104.14	101.14	104.36	98.87	99.44	94.39
DM	127.17	120.67	128.28	119.33	122.11	114.11
TPP	9.24	7.55	8.12	6.94	7.53	10.46
LW	66.21	48.47	54.08	56.01	51.46	59.15
SW	79.12	82.78	77.28	73.67	78.18	78.05
L:S	0.85	0.60	0.71	0.76	0.66	0.76
FLL	28.08	23.86	19.87	20.36	24.72	23.50
FLW	1.59	1.33	1.39	1.37	1.33	1.57
IL	21.85	23.65	21.77	26.28	26.06	22.72
PL	37.14	41.64	43.08	32.50	36.75	40.08
100 SW	4.15	4.15	4.15	3.71	3.83	3.96
DMYPP	25.32	20.12	26.26	17.83	30.97	32.67
CPC %	9.54	9.60	9.28	8.98	9.32	8.75
SYPP	41.38	48.08	54.10	40.80	34.77	41.70
GFYPP	128.55	103.55	110.61	108.21	110.70	123.55

PH: Plant height; DFF: Days to 50% flowering; DM: Days to maturity; TPP: No. of tillers plant^{-1}; LW: Leaf weight plant^{-1}; SW: Stem weight plant^{-1}; L:S: Leaf stem ratio; FLL: Flag leaf length; FLW: Flag leaf width; IL: Internode length; PL: Panicle length; 100 SW: 100 Seed weight; DMYPP: Dry matter yield plant^{-1}; CPC%: Crude protein content %; SYPP: Seed yield plant^{-1}; GFYPP: Green fodder yield plant^{-1}

significant differences across all characters, indicating potential for further genetic studies.

The results show significant potential for improving germplasm through selection and heterosis breeding. The study found significant heterogeneity across oat genotypes in terms of green fodder yield and grain yield. Kumar et al. (2023), Pankaj et al. (2022), Arora et al. (2021), Yarvaan and Zongwen (2020), Poonia et al. (2020) and Poonia et al. (2017) found significant variation in oat germplasm, which can be used to improve traits through selection.

3.2. Principal component analysis

Principal component analysis (PCA) is a powerful method for reducing variability in multiple traits by transforming them into principal components, with the first principal component capturing the maximum variability. Correlation-based PCA was employed to study the interrelationships among various traits. This approach is particularly effective as it does not rely on the assumption of normal population distribution (Sharma et al., 2020). Principal components with larger eigenvalues, along with variables showing strong factor loadings and high PC scores, were considered the most effective representatives of the system attributes (wagh et al., 2019).

In this study, PCA was conducted to analyse yield and other attributes in oat genotypes. Out of the 16 Principal components (PCs), six had more than one Eigen value and accounted for 72.61% of the total included variability (Table 4). Specifically, PC1 explained 18.40% of the total variability, followed by PC2 (16.07%), PC3 (13.65%), PC4 (9.45%), PC5 (8.71%) and PC6 (6.33%) respectively. Similar results were reported by Kumari and Jindal (2019), Bichewar et al. (2023), Chawla et al. (2024), Poonia et al. (2021) and Zahid et al. (2023) in Oat, whereas Kavithamani et al. (2019) reported similar findings in sorghum. The results indicated that the majority of variability was captured within the first six principal components, with PC1 contributing the most.

The strong influence of yield traits on PC1 highlights the crucial role of GFY, DMY, TPL and SY in driving the overall variability within the population. This aligns with the well-established notion that yield traits are critical

Table 4: Total variance explained by different principal components in oat genotypes

	PC1	PC2	PC3	PC4	PC5	PC6
Eigen values	2.94	2.57	2.18	1.51	1.39	1.01
Proportion	18.40	16.07	13.65	9.45	8.71	6.33
Cumulative proportion (%)	18.40	34.48	48.13	57.58	66.28	72.61

determinants of a crop's economic and agronomic value (Poonia et al., 2021). The observed relationship between PC1 and yield traits suggests that genetic factors governing these traits were closely linked to the variability captured by PC1. This insight underscores the possibility that specific genes related to yield traits are major contributors to the variation, offering significant potential for targeted breeding initiatives.

Table 5 shows the factor loading for 16 examined characters with varimax rotation. The data in table clearly showed that PC-1 was loaded on leaf weight plant^{-1} (0.482), leaf stem ratio (0.422), green fodder yield plant^{-1} (0.416), flag leaf length (0.387) and flag leaf width (0.238). Similarly, PC-2 showed a strong and positive factor with the traits like plant height (0.408), panicle length (0.388), dry matter yield plant^{-1} (0.329), 100 seed weight (0.325), days to maturity (0.316) and number of tillers plant^{-1} (0.274). The PC-3 was loaded with the diverse traits like days to 50% flowering (0.416), days to maturity (0.379), 100 seed weight (0.307), Leaf stem ratio (0.277), seed yield plant^{-1} (0.238) and leaf weight plant^{-1} (0.229).

PC-4 exhibited a strong and positive factor loading with the traits stem weight plant^{-1} (0.665), crude protein content (0.501), days to 50% flowering (0.227), flag leaf length (0.175) and green fodder yield plant^{-1} (0.157). PC-5 exerted a strong and positive factor loading with plant height (0.250), days to 50% flowering (0.334), days to maturity (0.420), internode length (0.302), dry matter yield plant^{-1} (0.220) while PC-6 had crude protein content (0.546). These results closely correspond to the findings of Tanoli et al. (2016), Ihshan et al. (2021)who identified plant height, number of tillers plant^{-1}, days to maturity and seed yield plant^{-1} as key contributors to principal component variation.

Traits with high positive or negative factor loadings made the greatest contributions to diversity, with the sign indicating the nature of the relationship between the trait and the principal component. For instance, PC1 exhibited a negative factor loading for panicle length (-0.204), highlighting a negative correlation with this trait.

In the biplot (Figure 2) the direction of the arrows indicates the direction of maximum variance and their length reflects the magnitude of change. An acute angle (<90°) between traits or principal component axes indicates a positive association, an obtuse angle (>90°) indicates a negative association and a right angle (=90°) signifies no correlation between the traits. Tillers per plant, plant height, leaf weight per plant, flag leaf length had acute angle with green fodder yield plant^{-1} signifies that there is positive correlation between the traits. Similar results have been reported by other researchers (Gupta and Mehta, 2020; Chawla et al.,

Table 5: Factor loading scores of different characters with respect to different principal factor (Varimax rotation) of oat

Traits	PC-1	PC-2	PC-3	PC-4	PC-5	PC-6
PH	0.121	0.408	-0.375	-0.085	0.250	0.052
DFF	0.035	0.232	0.416	0.227	0.334	-0.337
DM	0.078	0.316	0.379	-0.035	0.420	-0.056
TPP	0.199	0.274	-0.253	0.029	-0.404	0.023
LW	0.482	-0.082	0.229	0.046	-0.134	0.088
SW	0.056	-0.090	-0.090	0.665	-0.097	-0.274
L:S	0.422	-0.013	0.277	-0.341	-0.054	0.261
FLL	0.387	-0.092	-0.054	0.175	0.006	0.128
FLW	0.238	0.006	0.042	0.067	-0.204	-0.555
IL	-0.034	-0.378	-0.014	-0.014	0.302	0.089
PL	-0.204	0.388	-0.024	0.176	0.002	0.195
100 SW	-0.116	0.325	0.307	-0.144	-0.220	-0.050
DMYPP	0.171	0.329	-0.424	-0.071	0.220	-0.088
CPC%	-0.017	0.024	0.074	0.501	0.155	0.546
SYPP	-0.246	0.237	0.238	0.105	-0.450	0.179
GFYPP	0.416	0.130	0.007	0.157	-0.039	0.135

PH: Plant height; DFF: Days to 50% flowering; DM: Days to maturity; TPP: No. of tillers plant^{-1}; LW: Leaf weight plant^{-1}; SW: Stem weight plant^{-1}; L:S: Leaf stem ratio; FLL: Flag leaf length; FLW: Flag leaf width; IL: Internode length; PL: Panicle length; 100 SW: 100 Seed weight; DMYPP: Dry matter yield plant^{-1}; CPC%: Crude protein content %; SYPP: Seed yield plant^{-1}; GFYPP: Green fodder yield plant^{-1}

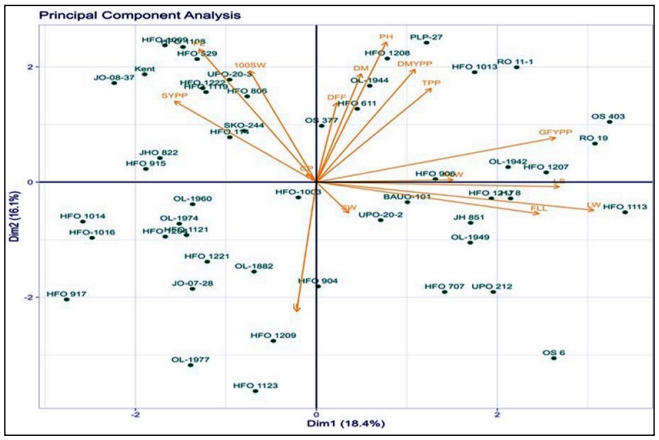

Figure 2: Distribution of oat genotypes based on principle factor 1 and 2

2022). Panicle length, 100 seed weight, internode length and seed yield plant^{-1} had obtuse angle with green fodder yield plant^{-1} means these traits are negatively correlated with green fodder yield plant^{-1}.

The genotypes RO 19, HFO 1207, OS 403 and OL-1942 clustered on the positive side of the first principal component, indicating their superiority in terms of green fodder yield plant^{-1}. Meanwhile, the genotypes HFO 1013, HFO 1208, RO 11-1, PLP-27 and OL-1944 clustered on the positive side of the second principal component, suggesting that they had more number of tillers plant^{-1}, late days of flowering and maturity. Hence, the genotypes PLP-27, HFO 1013 and RO 19 were positioned positively on both components, making them the best for green fodder yield plant^{-1}.

Dumlupinar et al. (2012) reported that biplot analysis facilitates the identification of genotypes exhibiting superior trait combinations, thereby enhancing their utility in breeding programs. On the biplot, genotypes positioned closer to one another are more similar, while those farther apart are more divergent (Sharma et al., 2020). The distance between two genotypes on the score plot is inversely proportional to their similarity.

Genotypes located near the origin contribute less to variability, whereas those positioned farther from the origin are extremes. These extreme genotypes are often favourable for breeding programs due to their potential for introducing variability (Kiprotich et al., 2015). The selected top oat accessions were ranked based on their PC scores (values more than one) in descending order (Table 6).

PCA clusters germplasms according to their principal component scores and identifies the smallest number of factors that account for the maximum variation (Wang et al., 2019). In the present study, genotypes were identified based on principal component (PC) scores. The top ten genotypes with the highest PC1 scores, in descending order, were HFO 1123, PLP-27, HFO 806, HFO 1222, HFO-1003, OL-1960, RO 19, HFO 917, JO-08-37 and HFO-1009. These genotypes exhibited the highest mean values for traits positively associated with PC1, which included yield and yield-contributing traits, characterized by high factor loadings. In contrast, traits seed yield plant^{-1} and days to 50% flowering were associated with PC3. The top PC3 scoring genotypes were HFO-1003, JH 851, HFO 806, UPO-20-3, OS 6, HFO 611, HFO 1208 and OS 403. These findings were consistent with the biplot analysis.

Both Mahalanobis' D^2 statistics and PCA showed that there

Table 6: List selected top genotypes based on their PC scores (values more than one)

Principal components	No. of genotypes	Genotypes
PC I	10	HFO 1123 (1.989), PLP-27 (1.889), HFO 806 (1.795), HFO 1222 (1.530), HFO-1003 (1.481), OL-1960 (1.290), RO 19 (1.251), HFO 917 (1.235), JHO-08-37 (1.139) and HFO-1009 (1.127)
PC II	10	HFO 1013 (1.510), HFO 1217 (1.481), OL-1974 (1.463), Kent (1.339), SKO-244 (1.332), OL-1960 (1.244), UPO 212 (1.190), JO-07-28 (1.168), JH 851 (1.109) and HFO 904 (1.073)
PC III	8	HFO-1003 (1.928), JH 851 (1.857), HFO 806 (1.673), UPO-20-3 (1.597), OS 6 (1.484), HFO 611 (1.472), HFO 1208 (1.174) and OS 403 (1.165)
PC IV	7	HFO 1121(2.520), HFO 1113 (2.310), HFO 915 (2.130), PLP-27(1.621), HFO-1009 (1.305), HFO 1204 (1.019) and HFO 1222 (1.014)
PC V	9	OS 377 (2.377), HFO 707 (2.025), RO 11-1 (1.932), OL-1942 (1.313), BAUO-101(1.245), HFO-1016 (1.110), UPO 212 (1.103), HFO-1009 (1.069) and HFO 1108 (1.031)
PC VI	10	HFO 1123 (2.417), HFO 1209 (1.588), HFO 904 (1.524), HFO 1119 (1.414), HFO 1222 (1.204), OL-1949 (1.081), OL-1942 (1.070), OL-1960 (1.057), UPO 212 (1.040) and HFO 1208 (1.032)

was significant divergence present among 50 genotypes. The genotype RO 19, HFO 1123, BAUO-101 suitable for green fodder yield whereas UPO-20-3, HFO-1003, HFO 806 for seed yield plant^{-1}. These findings indicate strong potential for selecting these traits among the studied genotypes, offering opportunities to exploit heterosis in hybrids and achieve a broad spectrum of variation in segregating material for yield-related traits.

Chawla et al. (2024), Kebede (2023), Devi et al. (2024), Poonia et al. (2021) and Krishna et al. (2014) conducted principal component analysis on oat and found that transfer of several correlated factors into a few independent principal components explained much of the variability. Hemavathy's (2020) principal component analysis study on sweet corn yielded similar findings.

4. CONCLUSION

The study used Mahalanobis's D^2 and PCA approaches to identify significant genetic difference across 50 oat genotypes. For green fodder yield traits, Cluster I was found to be superior among six different clusters that showed differing levels of intra- and inter-cluster variability. PCA showed that yield-related traits drove the most variation, with the first six components accounting for more than 72% of the overall variability. RO 19, PLP-27, and HFO 1123 were the promising genotypes for grain and fodder production.

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