A-6206
[1-9]

RESEARCH ARTICLE Indian Journal of Agricultural Research, Volume Issue : ()

Comprehensive Assessment of Genetic Variability and Selection Strategies in Oat Germplasm for Improved Fodder and Seed Yield in N-W Himalayan Mid-hill Environments

Rajni Devi[1], V.K. Sood[1], Anuradha[2], Amit Rana[1], Ajeta Katoch[1],
Shilpa Kamal[3], Abhishek Kumar[1]

10.18805/IJARe.A-6206

ABSTRACT

Background: Oat is an important dual purpose annual cereal crop with high adaptability and enhanced nutritional value. Expanding population and squeezing arable land has led to competition for utilization of land for food grains and fodder which necessitates intensified efforts toward more efficient forage production. Hence studying genetic variability in oats becomes crucial for selection of resilient genotypes with traits tailored for resilience and high yield by ensuring crop productivity in varying environmental conditions.

Methods: A total of 121 oat germplasm lines were evaluated for sixteen traits using simple lattice design for three years to study genetic variability, trait inter-relationships and conduct principal component and cluster analyses.

Result: Substantial genetic variability was observed for fodder yield and component traits. High coefficients of variation for flag leaf area alongwith its high heritability and genetic advance, underscore its suitability for selection while, moderate GA for tillers per plant and 1000-seed weight, suggested hybridization coupled with selection. Fodder yield displayed significant and positive correlations with multiple traits suggesting effective selection. Path coefficient and principal component analysis identified days to 50% flowering, plant height, leaves per plant, biological and seed yield, dry matter and crude protein yield as optimal selection indices for enhancing fodder yield. Cross-breeding among diverse genotypes from specific clusters within the evaluated panel offers promising avenues for future oat breeding and yield improvement programmes.

Key words: Avena sativa, Genetic diversity, Germplasm, Heritability, Principal component analysis.

INTRODUCTION

Oat (*Avena sativa* L.), a major cereal grain in the Gramineae family, is commonly recognized as spring or white oat. It is a hexaploid characterized by the genetic composition AACCDD, encompassing 42 chromosomes. Globally, it is cultivated with an annual production of approximately 25 million tons in 2019, with Russia and Canada contributing significantly, each representing 20% to the world output (FAO, 2021). Oats are consumed both as human food and fodder for cattle, providing nutritional value with high levels of essential dietary minerals, unsaturated fatty acids, unique galacto-lipids and the highest globular protein levels among cereals. They also have high levels of beneficial mixed $(1\rightarrow3)$, $(1\rightarrow4)$ β-D-glucans, aiding digestion and possessing cholesterol-lowering properties. The impact of oats on human health, including the stimulation of health-related microbial metabolites in the gut microbiome, has been studied, suggesting potential use as prebiotic substrates (Abbeele *et al.* 2018).

With the dairy industry rapidly growing in our country and recognizing the nutritional value of oats as a cereal grain for human consumption, the cultivation of oats as a feed and fodder crop presents substantial potential in Indian agriculture. However, challenges such as low production per hectare and the influence of biotic and abiotic factors, ultimately affect the yield. The productivity of a crop is shaped, either directly or indirectly, by numerous traits that contribute to yield. Consequently, plant breeders frequently prioritize the simultaneous selection of these traits. Each trait is assigned a specific economic weight based on its significance in influencing yield, forming a selection index. Understanding genetic variability, correlation and path coefficients is crucial for breeders to select superior genotypes and determine effective methodologies for crop

---

[1]Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062, Himachal Pradesh, India.

[2]Department of Vegetable Science and Floriculture, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062, Himachal Pradesh, India.

[3]Department of Floriculture and Landscape Architecture, University of Horticulture and Forestry, Nauni-173 230, Solan, Himachal Pradesh, India.

Corresponding Author: Rajni Devi, Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062, Himachal Pradesh, India.
Email: rajnidevi037@gmail.com

How to cite this article: Devi, R., Sood, V.K., Anuradha, Rana, A., Katoch, A., Kamal, S. and Kumar, A. (2024). Comprehensive Assessment of Genetic Variability and Selection Strategies in oat Germplasm for Improved Fodder and Seed Yield in N-W Himalayan Mid-hill Environments. Indian Journal of Agricultural Research. DOI: 10.18805/IJARe.A-6206.

Submitted: 12-01-2024 **Accepted:** 09-05-2024 **Online:** 18-07-2024

improvement. Forage and seed yield, being complex traits influenced by environmental fluctuations and polygenes (Piepho *et al.* 2008); necessitate the partitioning of observed variability into genotypic and phenotypic coefficients of variation. The study also considers heritability along with genetic advance for accurate prediction of genetic gain. Evaluating direct and indirect effects and its components provide a basis for successful breeding programs aimed at increasing yield. Mahalanobis's D^2 statistics, employed in various crops, serves as a powerful tool for identifying diverse parents for hybridization programs. The principal component score strategy, capturing maximum genetic diversity, has been successfully applied in germplasm evaluation for understanding relationships and correlations among variables studied. Hence, this investigation aims to study genetic variability, diversity and trait inter-relationships to facilitate yield improvement.

MATERIALS AND METHODS

Experimental site and germplasm source

In this study, 121 *Avena sativa* L. accessions from diverse origins, including indigenous and exotic collections were assessed for different qualitative and quantitative traits. The evaluations were conducted over a period of three consecutive years *i.e., rabi* 2015-16 to 2017-18 at Experimental Farm of the Fodder Section, CSK HPKV, Palampur. The farm is located at 32°6′ N latitude, 76°3′ E longitudeand an elevation of 1290.8 m (a.m.s.l), experienced timely sown irrigated conditions. Further details of the material are provided in Table 1.

Experimental design and recorded observations

The experiment setup utilized a simple lattice design, with two rows of each genotype, measuring 1 m in length and a spacing of 25×5 cm^2. The individual plot size was maintained at 1.0×0.5 m^2. The data collection involved recording observations on sixteen agro-morphological traits from five randomly selected competitive plants in each replication. The traits included days to 50% flowering (DF 50%), plant height (PH), leaves per plant (LPP), tillers per plant (TPP), flag leaf area (FLA), leaf stem ratio (L/S), green fodder yield per plant (GFY), dry matter percent (DM %), dry matter yield per plant (DMY), crude protein content (CPC %), crude protein yield per plant (CPY), days to 75% maturity (DM 75%), biological yield per plant (BY), seed yield per plant (SY), harvest index (HI) and 1000- seed weight (1000 wt).

Statistical analysis of the recorded data

The mean data, computed for each trait, underwent analysis of variance using standard methods based on the simple lattice design model proposed by Federer (1963). Coefficients of variation and heritability were determined following the approach outlined by Burton and DeVane (1953). Coefficients of correlation were calculated using the procedures outlined by Al- Jibouri *et al.* (1958) and path analysis by Dewey and Lu (1959). Principal component analysis (PCA) and principal component scores were derived using XLSTAT software to unveil the best relationships among traits. Additionally, D^2 analysis was performed using software WINDOSTAT version 9.3 from indostat services.

RESULTS AND DISCUSSION

Mean performance and variation in morphological traits

Extensive variation was observed phenotypically among the genotypes for green fodder and seed yield related traits during all the three seasons. The range of the mean performance for each trait clearly depicted the wide

Table 1: List of indigenous and exotic genotypes of *Avena sativa* taken for study.

Source	Name of genotypes
PAU, Ludhiana	Kent (C), OL-125, OL-161, OL-822, OL-9
CCS HAU, Hisar	OS-6 (C), OS-10, OS-121, OS-9, OS-92, HJ-8, HFO-102, HFO-114, HFO-163, HFO-52
IGFRI, Jhansi	IG-03-203, IG-03-205, IG-03-208, IG-03-211, IG-03-213, IG-03-214, IG-03-216, IG-03-246, IG-03-247, IG-03-250, IG-03-251, IG-03-254, IG-03-48, IGO-14, JH0-862, JHO-813, JHO-822, JHO-99-2
Exotic collection	EC-523890, EC-528865, EC-528883, EC-528889, EC-528890, EC-528894, EC-528895, EC-528896, EC-528897, EC-528898, EC-528903, EC-528905, EC-528913, EC-558905, EC-605831, EC-605832, EC-605834, EC-605837, EC-605838, EC-605839
JNKVV, Jabalpur	JPO-3, JPO-4, JPO-5, JPO-8, JPO-10, JPO-13, JPO-14, JPO-17, JPO-18, JPO-19, JPO-20, JPO-21, JPO-22, JPO-24, JPO-25, JPO-28, JPO-29, JPO-30, JPO-31, JPO-35, JPO-36, JPO-38, JPO-40, JPO-41, JPO-44, JPO-45, JPO-46, JPO-50, JPO-55, JPO-73
Introduction	KRR-AK-06, KRR-AK-15, KRR-AK-26, KRR-AK-36, KRR-AK-42
Selections	Oat-102, Oat-17, Oat-79, Oat-80, Oat-8655, Oat-902
SKAUST, Sri Nagar	SK-217, SK-150, SK-199, SKO-28, Sabzaar
GBPUA & T, Pantnagar	UPO-102, UPO-102 -1649, UPO-119, UPO-130, UPO-30, UPO-212 (C)
MPKV, Rahuri	RO-19(C)
CSK HPKV, Palampur	PLP-1(C)
CSK HPKV, Palampur (maintained)	SNTM-90, TRS-106, K-353, KUE, No. 77, OG-77, H-B-8, Fragrati, ADG-214, ADG-96, AVE-3018, 99-1, Chorripatli, PO-1

spectrum of diversity (Table 2). The studies conducted by Ihsan *et al.* (2021 and 2022), as well as Kumar *et al.* 2023, also observed the substantial range of mean performance over different years, illustrating wide spectrum of heterogeneity.

Focusing on the major traits, ten genotypes *viz.,* EC-528865 followed by PO-1, AVE-3018, EC-528894, EC-528895, UPO-30, JPO-10, JPO-29, JPO-36 and JPO-50 showed superior GFY as compared to the best check PLP-1 while for SY it was EC-528865 followed by JPO-10, Oat-17, Oat-102, Oat-8655, JHO-99-2, KRR-AK-15, OL-9, JPO-24 and JPO-50 as compared to the best check Kent. These genotypes were also observed superior for other component traits as shown in Table 3. Zeki *et al.* (2016) in oats and Shekhawat *et al.* (2023) in fenugreek also reported similar outcomes from their respective analyses.

Estimates of heritability and parameters of variability

The PCV, GCV, heritability and genetic advance as per cent of mean were calculated for all the traits (Table 2). The phenotypic based selection could be effective for yield improvement when the traits exhibit high heritability due to presence of additive gene action on expression of these traits (Shariatipour *et al.,* 2022). The heritability was observed to be high (>70%) for most of the traits except low for DM % and moderate for CPY, SY and HI in pooled data. High PCV and GCV (>20%) was observed for FLA, while it was low for DF 50%, DM % and DM 75%. The results showed minimum difference between PCV and GCV for highly heritable traits suggesting that selection of the genotypes can be done having high trait values. Similar observations were made by Chakraborty *et al.* (2014) and Yadav *et al.* (2017), suggesting ample opportunities for selection in

Table 2: Mean values and range for fodder yield, its component and quality traits in oat.

Traits	Mean± S.E. (m)	Range	PCV (%)	GCV (%)	Heritability h^2bs (%)	GA as (%) of mean	Superior genotypes pooled over years
DF (50%)	144.00±1.48	131.00-157.00	4.91	4.69	91.22	9.23	21
PH (cm)	113.28±3.72	64.67-139.58	11.95	11.01	84.92	20.91	9
LPP	37.64±2.88	22.29-53.75	15.78	13.25	70.51	22.92	67
TPP	8.37±0.45	4.54-12.17	16.81	14.97	79.34	27.48	20
FLA (cm^2)	32.09±1.61	11.75-60.00	31.39	30.58	94.88	61.36	25
L/S ratio	0.37±0.02	0.26-0.48	13.85	12.30	78.78	22.48	29
GFY (g)	115.45±5.11	78.75-150.83	12.77	11.13	75.99	19.99	10
DM (%)	20.15±0.70	17.33-23.31	6.75	4.60	46.59	6.47	1
DMY (g)	23.21±1.29	15.75-31.21	14.72	12.46	71.62	21.72	14
CPC (%)	9.57±0.37	7.44-11.09	10.06	8.43	70.16	14.55	-
CPY (g)	2.22±0.16	1.23-3.06	17.01	13.65	64.38	22.55	6
DM 75%	175.00±1.50	167.00-184.00	2.37	2.04	73.80	3.61	18
BY (g)	100.86±4.31	72.00-130.21	11.95	10.31	74.38	18.31	4
SY (g)	23.06±1.51	14.63-32.75	15.06	11.85	61.97	19.22	10
HI (%)	23.19±1.29	15.72-31.96	13.19	10.60	64.62	17.56	-
1000 wt (g)	32.94±1.89	21.53-44.52	17.09	15.04	77.45	27.26	20

Table 3: Most superior genotypes identified on the basis of pooled data for fresh fodder and seed yield per plant along with their superiority for component traits in oat.

Genotypes	Fresh fodder yield per plant (g)	Superiority for other yield attributes	Genotypes	Seed yield per plant (g)	Superiority for other yield attributes
EC-528865	150.83	DMY, BY, SY and LPP	EC-528865	32.75	DMY, BY, GFY and LPP
PO-1	148.75	DMY, CPY and 1000 wt	JPO-10	31.08	BY, GFY and LPP
AVE-3018	143.88	DMY and CPY	Oat-17	29.36	DF (50%) and LPP
EC-528894	141.79	DMY, BY, CPY and LPP	Oat-102	28.39	DF (50%), 1000 wt and LPP
EC-528895	139.79	FLA, L/S, DMY and BY	Oat-8655	28.15	FLA
UPO-30	138.71	PH, FLA, L/S, DMY and LPP	JHO-99-2	28.11	DF (50%)
JPO-10	138.29	BY, SY and LPP	KRR-AK-15	27.97	LPP
JPO-29	135.75	TPP, LPP and DMY	OL-9	27.89	TPP and LPP
JPO-36	135.08	CPY, DMY and LPP	JPO-24	27.75	DF (50%), LPP, FLA and L/S
JPO-50	134.42	FLA and SY	JPO-50	27.72	FLA and GFY

fodder and seed yield related traits. Genetic advance expressed as percentage of mean was observed high (>50%) for FLA and moderate (25-50%) for TPP and 1000-wt. High genetic advance coupled with high heritability estimates offers optimal conditions for selection. Selecting top 5% of high-yielding genotypes as parents, based on genetic advance as per cent of mean, is anticipated to enhance the average performance of resulting offspring. Our results indicated that traits such as FLA, TPP and 1000-wt exhibited high to moderate genetic advance, suggesting involvement of the additive gene action and potential effectiveness of selection based on phenotypic performance for improvement. This aligns with the findings from Jaipal and Shekhawat (2016a), Subbulakshmi *et al.* (2019) and Kebede *et al.* (2023a).

Correlation and path coefficient analysis

Understanding the associations between yield and related traits, discerning their nature and causation, is imperative for identifying superior genotypes and improving selection efficiency. Breeders can choose breeding methods based on these estimates to exploit valuable associations. Correlation studies (Fig 1) revealed that GFY had significant and positive association with DF 50%, LPP, FLA, DMY, DM 75%, BY, SY, PH and CPY illustrating that enhancing these traits through selection would ultimately lead to increased fodder yield and can be used as a marker traits for yield improvement in oat while, this character showed negative and significant correlation with HI. However, SY showed significant and positive correlation with PH, GFY, DMY and BY, HI and 1000-wt while negative with DF 50%, DM 75%, DM % and CPC. The traits with low (DMY) and moderate (CPY, SY and HI) heritability were significantly correlated with different high heritable traits like PH, FLA, DM 75% and DF 50%. Therefore, selecting genotypes with taller height, more days to flowering and maturity along with increased flag leaf area, would indirectly improve the low heritable traits. Sakhale *et al.* (2014) observed a positive and significant correlation of green fodder yield with dry matter yield, crude protein yield and leaf area, highlighting the importance of these characters for fodder yield improvement in *Avena*.

In pooled over environments, nine traits showed significant and positive correlation with fresh fodder yield but when direct and indirect contribution of the correlation was estimated at phenotypic level (Table 4), the direct effect were found to be positive and high for DMY (1.064) followed by SY (0.046), CPY (0.035) and LPP (0.026), whereas direct effect of rest of the traits were observed to be negligible. On the other hand, negative direct effects on fodder yield were recorded by DM % (-0.4926) followed by HI (-0.0385) and TPP (-0.0134). Although DM % had the highest negative direct effect on yield, its indirect effect *via* DMY (0.5019) followed by CPY (0.0121) and HI (0.0059) were positive. Likewise, indirect effects of HI *via* DM%, SY and DF 50% were positive and in case of TPP, it was positive through DMY and LPP. Based on this analysis, DMY, SY, CPY and LPP were found to have direct as well as indirect positive effects along with DM% and DF 50% on GFY, suggesting that direct selection for these traits would be effective. Krishna *et al.* (2014) evaluated 50 genotypes of fodder oat and observed that leaf: stem ratio and dry matter had the maximum positive direct effect on green fodder yield. The same results were also documented by Jaipal and

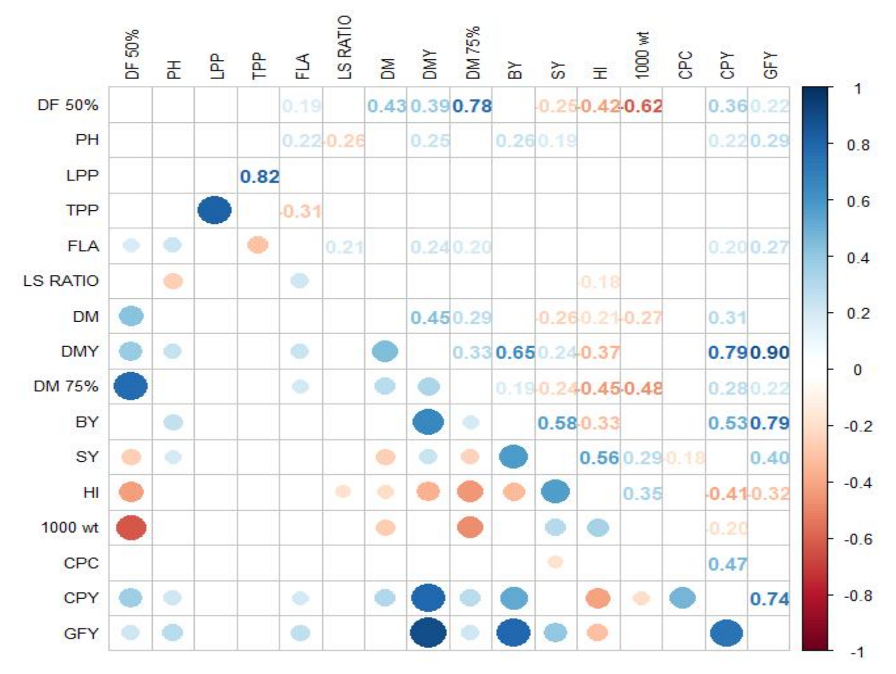

Fig 1: Correlations for 16 agro morphological traits in all genotypes for pooled over years.

Table 4: Phenotypic path coefficient showing direct and indirect effects of various traits on green fodder yield per plant in oat pooled over years.

Traits	DF	PH	LPP	TPP	FLA	L/S ratio	DM	DMY	DM 75%	BY	SY	HI	1000-wt	CPC	CPY	Direct effects	Total Indirect effects	Total correlation to GFY(g)
DF (50%)		0.0000	0.0000	0.0022	0.001	-0.0006	-0.178	0.3563	-0.0006	-0.0003	-0.0108	0.0143	-0.0026	-0.0003	0.011	-0.0124	0.1916	0.1792*
PH (cm)	-0.0003		0.0018	0.001	0.0012	0.001	0.009	0.2300	0.0000	-0.0005	0.0075	0.0012	-0.0005	0.0000	0.007	0.0020	0.2584	0.2605*
LPP	0.0000	0.0001		-0.0103	-0.0008	0.0002	-0.0252	0.1696	0.0000	-0.0004	0.0023	0.0042	-0.0006	-0.0007	0.0056	0.0260	0.1440	0.1702*
TPP	0.0020	-0.0002	0.0200		-0.0015	0.0004	-0.0114	0.0461	0.0001	0.0000	-0.0013	0.0023	-0.0001	-0.0005	0.0018	-0.0134	0.0577	0.0442
FLA (cm²)	-0.0022	0.0004	-0.004	0.0037		-0.0008	0.0012	0.2352	-0.0002	-0.0004	0.0045	0.0005	-0.0002	0.0003	0.0067	0.0053	0.2447	0.2503*
L/S ratio	-0.0019	-0.0005	-0.0013	0.0015	0.0011		-0.0233	0.0976	-0.0001	-0.0001	-0.0043	0.0055	0.0000	-0.0011	0.0041	-0.0040	0.0772	0.0732
DM (%)	-0.0045	0.0000	0.0013	-0.0003	0.0000	-0.0002		0.5019	-0.0002	0.0001	-0.0084	0.0059	-0.0009	0.0013	0.0121	-0.4926	0.5081	0.0155
DMY (g)	-0.0041	0.0004	0.0041	-0.0006	0.0012	-0.0004	-0.2323		-0.0002	-0.0015	0.0121	0.0120	-0.0005	0.0014	0.0283	1.0644	-0.1801	0.8843*
DM 75%	-0.0089	0.0000	-0.0004	0.0022	0.0009	-0.0003	-0.112	0.2938		-0.0004	-0.0091	0.0142	-0.0018	0.0004	0.0079	-0.0009	0.1865	0.1857*
BY (g)	-0.0014	0.0005	0.0041	-0.0002	0.0008	-0.0001	0.0297	0.6842	-0.0001		0.0267	0.0115	-0.0002	0.0008	0.0183	-0.0023	0.7746	0.7723*
SY (g)	0.0029	0.0003	0.0013	0.0004	0.0005	0.0004	0.0902	0.2800	0.0002	-0.0013		-0.0226	0.001	0.0017	0.005	0.0459	0.3600	0.4060*
HI (%)	0.0046	-0.0001	-0.0028	0.0008	-0.0001	0.0006	0.0759	-0.3303	0.0003	0.0007	0.027		0.0013	0.0014	-0.0119	-0.0385	-0.2326	-0.2712*
1000 wt (g)	0.0071	-0.0002	-0.0036	0.0004	-0.0003	0.0000	0.0971	-0.1243	0.0004	0.0001	0.0105	-0.011		0.0015	-0.0064	0.0046	-0.0287	-0.0242
CPC (%)	-0.0003	0.0000	0.0014	-0.0006	-0.0002	-0.0004	0.0548	-0.1246	0.0000	0.0002	-0.0066	0.0045	-0.0006		0.0176	-0.0120	-0.0548	-0.0666
CPY (g)	-0.0038	0.0004	0.0041	-0.0007	0.001	-0.0005	-0.1677	0.8496	-0.0002	-0.0012	0.0065	0.0129	-0.0008	-0.0059		0.0355	0.6937	0.7292*

* Significant at P= 0.05.

Shekhawat (2016b), Gogoi *et al.* (2024) and Kebede *et al.* (2023b).

Principal component analysis

The PCA is employed to identify the key traits contributing to the total variation. On the basis of this, out of sixteen principal components, only five components have eigen values ≥1 and explained total of 73.16 per cent of the analysed characters variability, whereas remaining eleven contributed just 26.84 per cent variability. Similar findings were reported by Chahal and Gosal (2002), emphasizing that initial PCs generally have greater impact on total variation. Traits with eigenvectors above 0.3 made significant contribution towards total variation in specific PC, while those below 0.3 were considered less influencial, as reported by Kebede *et al.* (2023). On the basis of factor loadings (Table 5), it was observed that the first principal component (PC1) explained 26.83 per cent of total variance which was contributed mainly by DMY (0.427), CPY (0.399), GFY (0.388) and BY (0.327). PC2 explained 17.08 per cent of total variance contributed by SY, BY and 1000-wt; PC3 explained 12.85 per cent through LPP and TPP; PC4 explained 8.70 per cent mainly through traits like L/S and CPC and PC5 explained 7.71 per cent through PH and CPC. Considering the eigen vectors relative to the first and second components on pooled basis, it can be inferred that characters, that is DMY, CPY, GFY, BY, SY together with 1000-wt are the major sources of diversity among these oat germplasm lines.

To assess the contribution of vectors, a biplot was generated using first two PCs (Fig 2). The length of trait vector from the origin displayed its importance in total variation, with closer vectors playing a lesser role. Traits such as CPY, DMY and GFY had long vector and closer towards X-axis indicating their high contribution towards PC1 compared to SY, which contributed more to PC2. The angle between the trait vectors reflects the relationship between them (<90° for positive, = 90° for zero and >90° for negative correlation). The PCA biplot clustered trait vectors into four groups on the basis of their closeness towards origin, axis and length forming acute angle, hence depicting positive correlation among them and between some of traits of different groups. Major traits, such as seed and fodder yield, showed a positive relation with each other and with other respective traits like BY, DMY, CPY, PH, FLA and TPP, confirming the correlation results. Additionally, genotypes were distributed along both axes with minimum overlap, indicating their distinctiveness. Direct selection of the genotypes plotted closer to the trait vectors can be performed due to their high trait values. Comparable results were documented by Kujur *et al.* (2017), Poonia *et al.* (2021) and Kebede *et al.* (2023c).

Diversity analysis

A heatmap based on Euclidean distance and morphological traits grouped the genotypes into 12 clusters (Fig 3). Both indigenous and exotic collections fall under different clusters indicating huge genetic diversity in the population. Similarly, Kebede et al. (2023c) in their study, observed 4 clusters for 120 oat genotypes, suggesting genotypes of same origin could be grouped into different clusters. The colour variation in the heatmap depicted the lowest trait value (dark red) and maximum trait value (dark green) for the respective traits among different genotypes.

Table 5: Eigenvectors for the first five components of different traits in 121 genotypes of oat in pooled over environments.

Variable	PC1	PC2	PC3	PC4	PC5
Eigenvalue	4.292	2.733	2.055	1.392	1.233
Variation (%)	26.828	17.079	12.845	8.697	7.707
Cumulative (%)	26.828	43.907	56.752	65.450	73.157
DF (50%)	0.316	-0.328	-0.118	-0.162	0.028
PH (cm)	0.138	0.187	-0.013	-0.224	0.566
LPP	0.081	0.023	0.607	-0.089	-0.017
TPP	-0.018	0.020	0.643	-0.072	-0.120
FLA (cm^2)	0.157	0.080	-0.343	0.060	0.081
L/S ratio	0.083	-0.085	-0.130	0.440	-0.496
DM (%)	0.188	-0.242	0.014	-0.278	-0.258
DMY (g)	0.427	0.165	0.016	-0.081	-0.193
CPC (%)	0.029	-0.113	0.132	0.643	0.442
CPY (g)	0.399	0.076	0.083	0.315	0.117
DM 75%	0.291	-0.292	-0.135	-0.182	0.039
BY (g)	0.327	0.336	0.019	0.020	-0.037
SY (g)	0.030	0.517	-0.079	-0.129	0.006
HI (%)	-0.286	0.257	-0.126	-0.184	0.047
1000 wt (g)	-0.203	0.334	-0.051	0.177	-0.293
GFY (g)	0.388	0.308	0.023	0.047	-0.085

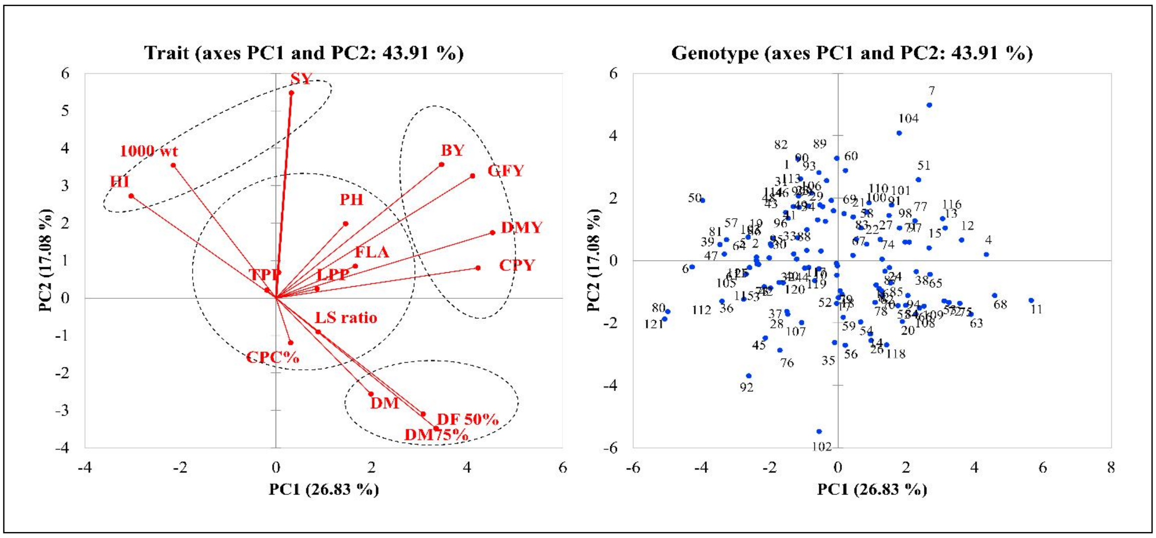

Fig 2: Plots based on principal component analysis depicting variables (a) and genotypes (b) pooled over environments.

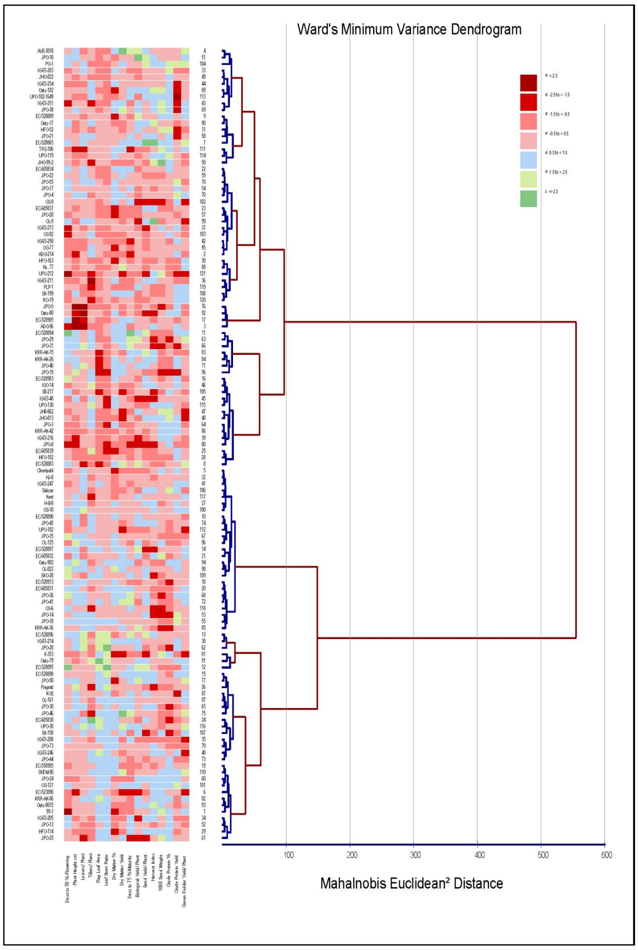

Fig 3: Heatmap and dendrogram clustering 121 genotypes into 12 clusters.

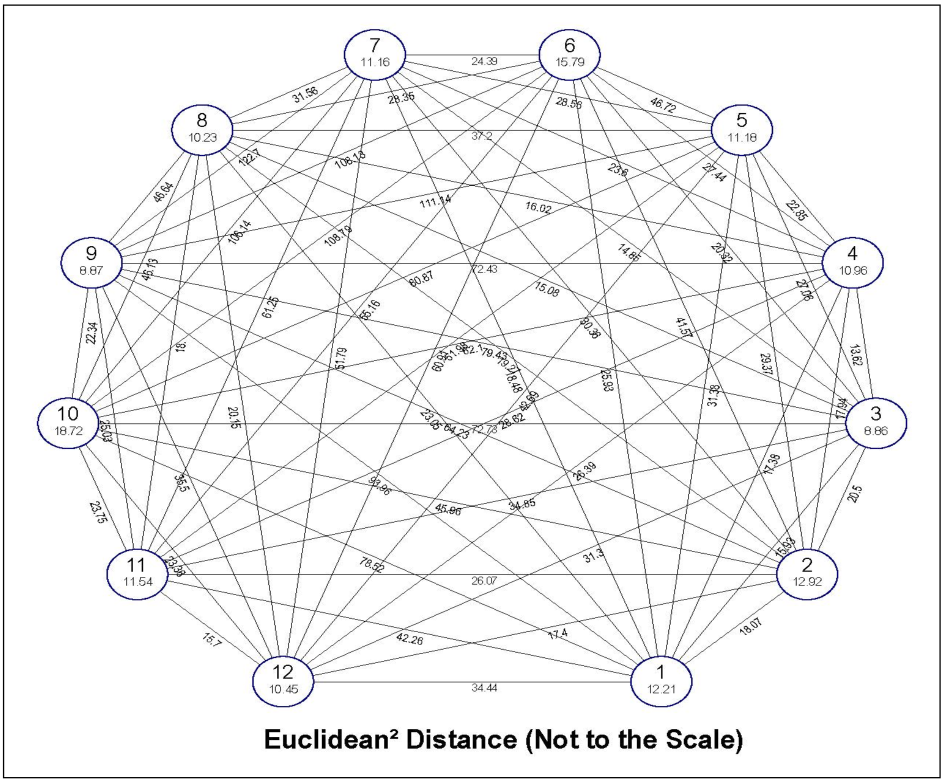

Fig 4: Inter and intra cluster distance based on D-value for oat genotypes.

Likewise, genotype EC-528865 showed maximum value for biological, seed and green fodder yield while; UPO-130, IG-03-254 and EC-605838 (also for leaves per plant) had highest value for tillers per plant and EC-528895 and JPO-28 for flag leaf area. Therefore, direct selection and hybridization based on the character and genotype association can be done based on this analysis.

The average intra and inter cluster distances are shown in Fig 4. The average inter cluster distance exceeded the intra cluster distance, indicating greater variability between different groups than within them. Intra cluster distance ranged from 54.89 (cluster IX) to 98.77 (cluster VIII). The inter cluster distance was maximum between cluster III and cluster V (560.18) signified extensive genetic diversity among the genotypes from distinct groups. On the other hand, it was minimum between cluster I and cluster II (87.62) indicated close relationship or similarities between the genotypes. Selection of parents from diverse clusters for hybridization programme to improve fresh fodder yield is recommended. Therefore, genotypes with higher inter and intra cluster distances can be used for intervarietal hybridization to exploit heterosis, as suggested by Singh and Gautam (1987). Cross-breeding genotypes of cluster III with V, V with IV and within cluster VIII (with high intra cluster distance) is expected to yield better genetic recombinants and segregation in their progenies. Similar findings were reported by Krishna *et al.* (2014) where fifty oat genotypes were grouped into ten clusters based on euclidean distance.

CONCLUSION

To get an improved variety, it is essential to explore the variations in morphological and quality parameters, as well as their interr-elationships and direct and indirect impacts on the dependent variable. The results identified genotypes EC-528865, JPO-10 and JPO-50 as the top performers for both fresh fodder and seed yield among the evaluated genotypes. These selected accessions hold promise as breeding materials for enhancing oat yields. The analyzed parameters exhibited significant associations and high heritability, indicating their potential utility in future breeding programs for selecting high performing candidate lines. Cluster analysis demonstrated a diverse range of genotypes suggesting their suitability in future crop improvement programs to generate transgressive segregants and identification of traits of economic value. Hence, this research provided valuable insights into utilization of these germplasm lines for oat genetic improvement.

ACKNOWLEDGEMENT

The authors gratefully acknowledge the Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, India for providing the research facilities for this research.

Conflict of interest

All author declare that they have no conflict of interest.

REFERENCES

Al-Jibouri, H.A., Miller, P.A., Robinson, H.F. (1958). Genotypic and environmental variance and covariance in an upland cotton cross of interspecific origin. Agronomy Journal. 50: 633-636.

Burton, G. and De Vane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 45: 478-481.

Chahal, G.S. and Gosal, S.S. (2002). Principles and procedures of plant breeding: Biotechnological and Conventional Approaches, vol. 21, Narosa Publishing House, New Delhi, pp. 64-89

Chakraborty, J., Arora, R.N., Joshi, U.N., Chhabra, A.K. (2014). Evaluation of *Avena* species for yield, quality attributes and disease reaction. Forage Research. 39: 179-184.

Dewey, D.R. and Lu, K.H. (1959). Correlation and path coefficient analysis of crested wheat grass seed production. Agronomy Journal. 51: 515-518.

FAO. (2021). World Food and Agriculture-Statistical Yearbook 2021.

Federer, W.T. (1963). Procedures and designs useful for screening material in selection and allocation with a bibliography. Biometrics. 19: 553-587.

Gogoi, L.R., Behera, P.P., Borah, N. and Sarma, R.N. (2024). Genetic Variability and Correlation Studies for Yield and Yield Attributing Traits in Mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research. doi: 10.18805/LR-5241.

Ihsan, M., Nazir, N., Ghafoor, A., Khalil, A.A.K., Zahoor, M., Nisar, M., Khames, A., Ullah, R., Shah, A.B. (2021). Genetic diversity in local and exotic *Avena sativa* L. (Oat) germplasm using multivariate analysis. Agronomy. 11(9):1713.

Ihsan, M., Nisar, M., Nazir, N., Zahoor, M., Khalil, A.A.K., Ghafoor, A., Khan, A., Mothana, R.A., Ullah, R., Nisar, A. (2022). Genetic diversity in nutritional composition of oat (*Avena sativa* L.) germplasm reported from Pakistan. Saudi Journal of Biological Sciences. 29(3): 1487-1500.

Jaipal and Shekhawat, S.S. (2016a). Genetic variability and divergence studies in oats (*Avena sativa* L.) for green fodder and grain yield. Forage Research. 42(1): 51-55.

Jaipal and Shekhawat, S.S. (2016b). Character association studies in oat (*Avena sativa* L.) for green fodder and grain yield. Forage Research. 42: 24-29.

Kebede, G., Worku, W., Feyissa, F., Jifar, H. (2023a). Agro-morphological traits-based genetic diversity assessment on oat (*Avena sativa* L.) genotypes in the central highlands of Ethiopia. All Life. 16:1.

Kebede, G., Worku, W., Feyissa, F., Jifar, H. (2023b). Correlation and path coefficient analysis for quantitative traits of oat (*Avena sativa* L.) genotypes in the central highlands of Ethiopia. Tropical Agriculture. 100: 68-88.

Kebede, G., Worku, W., Jifar, H., Feyissa, F. (2023c). Multivariate analysis for yield and yield-related traits of oat (*Avena sativa* L.) genotypes in Ethiopia. Ecological Genetics and Genomics. 28: 100184.

Krishna, A., Ahmed, S., Pandey, H.C., Kumar, V. (2014). Correlation, path and diversity analysis of oat (*Avena sativa* L.) genotypes for grain and fodder yield. Journal of Plant Science and Research. 1: 110

Kujur, M., Mehta, A., Bilaiya, S., Patil, P. (2017). Estimation of genetic diversity among genotypes of fodder oat based on principal component analysis. International Journal of Bio-resource and Stress Management. 8(6): 807-810.

Kumar, R., Varghese, S., Jayaswal, D., Jayaswall, K., Yadav, K., Mishra, G. (2023). Agro-morphological and genetic variability analysis in oat germplasms with special emphasis on food and feed. PLoS ONE. 18(2): e0280450.

Piepho, H.P., Mohring, J., Melchinger, A.E., Buchse, A. (2008). BLUP for phenotypic selection in plant breeding and variety testing. Euphytica. 161: 209-228.

Poonia, A., Phogat, D.S., Versha, Kumar, S. (2021). Principal component analysis in oat (*Avena sativa* L.) genotypes for green fodder yield and its attributing traits. Forage Research. 46 (4): 315-319.

Sakhale, S.A., Mehta, A.K., Sawarkar, S.S., Patil, H.V. (2014). Evaluation of morphological determinants of fodder yield as selection criterion in induced mutants of oat. International Journal of Tropical Agriculture. 32: 715-721.

Shariatipour, N., Heidari, B., Shams, Z., Richards, C. (2022). Assessing the potential of native ecotypes of *Poapratensis* L. for forage yield and phytochemical compositions under water deficit conditions. Scientific Reports. 12: 1121.

Shekhawat N., Meena Singh Vijay, Singh Kartar, Rani K., Gupta V. (2023). Studies on genetic variability, Heritability and genetic advance for morphological traits in fenugreek (*Trigonella foenum-graecum* L.) for arid climate of Rajasthan. Legume Research. 46(3): 312-315. doi: 10.18805/LR-5046

Singh, P.K. and Gautam, P.L. (1987). Genetic divergence in durum wheat germplasm. Narendra Deva Journal of Agricultural Research. 2: 45-49.

Subbulakshmi K., Ravikesavan R., Babu C., Iyanar K. (2019). Study of genetic variability in pearl millet [*Pennisetum glaucum* (L.) R. Br.] hybrids for grain yield and quality parameters. Agricultural Science Digest. 38(4): 289-292. doi:10. 18805/ag.D-4822

Van den Abbeele, P., Kamil, A., Fleige, L., Chung, Y., De Chavez, P., Marzorati, M. (2018). Different oat ingredients stimulate specific microbial metabolites in the gut microbiome of three human individuals in vitro. ACS Omega. 3(10):12446-12456.

Yadav, R., Rajpoot, P., Verma, O.P., Singh, P.K., Singh, P., Pathak, V. (2017). Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) for grain yield and its contributing attributes under sodic soil. Journal of Pharmacognosy and Phytochemistry. 6: 1294-1296.

Zeki, M., Ozge, D.E.K, Hasan, A. (2016). Grain yield and some quality traits of different oat (*Avena sativa* L.) genotypes. International Journal of Environmental and Agriculture Research. 2: 83-88.