Range Management and Agroforestry 45 (2) : 230-238, 2024
ISSN 0971-2070 (Print); 2249-5231 (Online)
https://doi.org/10.59515/rma.2024.v45.i2.07

Research article

Genetic diversity and response to selection for yield and component traits in selected F_4 and F_5 progenies of oat

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Received: 12th February, 2024 Accepted: 28th October, 2024

Abstract

The present study was planned to record the response to selection and extent of genetic diversity in selected F_4 and F_5 generation progenies, which were derived from seven crosses of oats. The F_4 and F_5 progenies were evaluated in randomized block design over three replications during *Rabi*, 2019-20 and *Rabi*, 2020-21, respectively at the Experimental Farm of Fodder Section, CSKHPKV, Palampur. The utmost response to selection was depicted by grain yield per plant, fresh fodder yield per plant, biological yield per plant, harvest index, leaves per plant and plant height in most of the crosses. Hence, improvement through selection could be based on these traits. PCA studies revealed that the first five components accounted for more than 80% of the total variance among the progenies. Four PC in F_4 and five PC in F_5 generation possess eigen values > 1. The first principal component, *i.e.*, PC1 accounted for the maximum proportion of total variability in the set of all variables, *i.e.*, 36.97% and 30.29% in both F_4 and F_5 generations, respectively. The dendrogram showed that 34 genotypes of oat were grouped into three clusters in F_4 generation and 33 genotypes from F_5 into eight clusters. On the basis of divergence and cluster mean studies, it was suggested that maximum heterosis and good recombinants could be obtained in crosses between progenies of clusters II and III from F_4 generation and clusters I, V, VII from F_5 generation.

Keywords: Cluster, Oat, Principal component analysis, Quality, Selection response

Introduction

Oat (*Avena sativa* L.) is the most popular cereal fodder crop grown in the *Rabi* season under irrigated and rainfed conditions. Indeed, it is the most valuable multipurpose annual cereal crop cultivated globally for food and feed purposes (Priyanka *et al.*, 2022). It is known locally as 'jai' and grown on the foothills of the Himalayas. When fodder is scarce in winter, it gives animals green food, which is also turned into silage or hay for usage when there is a fodder shortage (Kumari *et al.*, 2024). Additionally, oats provide a cost-effective source of nutritional energy and succulent fodder for up to three cuttings (Bharti *et al.*, 2024). It has many benefits, including the ability to produce fodder early, high yield potential, nutritious fodder, fast regeneration, and greater dry matter content (Rana *et al.*, 2022). The nation currently has a net deficit of 44% concentrate feeds, 10.95% dry crop leftovers, and 35.6% green fodder. Due to the cattle population's steady growth at a rate of 1.23%, the shortfall may increase even more (Kumar *et al.*, 2023). Therefore, increasing fodder quantity and quality is essential to raising cattle productivity. Oats provide excellent cattle feed in the form of oatmeal and high-quality grain. Oat is palatable fodder with 10.0 to 11.5% crude protein, 55 to 63% NDF, 30 to 32% ADF, 22.0 to 23.5% cellulose and 17 to 20% hemicellulose (Anonymous, 2011; 2012). Oat grain has long been an important livestock feed, but it is now also being used for human consumption in the form of oat cookies, baby food, and breakfast cereal. However, the narrow genetic base in oat cultivars leads to the breakdown of disease resistance through the emergence of various new races of pathogens, which ultimately reduce the yield. To address this challenging scenario over the long term basis, it is necessary to expand the genetic base of oat cultivars with a variety of resistance sources by exploring untapped plant genetic resources (Singh *et al.*, 2011; Bari *et al.*, 2014). Thus, it is crucial to create and utilize genetic diversity for a real and effective breeding program for the generation of superior recombinants for increased productivity, wider adaption, and pest and disease resistance (Singh *et al.,* 2018; Wani *et al.,* 2018). Keeping the above in view, the present study was planned to record the response to selection and extent of genetic diversity in selected F_4 and F_5 generation progenies, which were derived from seven crosses of oat.

Materials and Methods

Study site and design: The research material consists of 34 F_4 and 33 F_5 generation progenies along with five checks (RO-19, HJ-8, OS-6, Kent and PLP-1). The progenies were derived from seven different crosses *viz.,* PLP-1 × HJ-8, HJ-8 × JPO-46, HJ-8 × PLP-1, HJ-8 × EC528896, HJ-8 × *A. sterilis* cv. HFO-878, HJ-8 × KRR-AK-26 and PLP-1 × *A. byzantina* cv. HFO-60, which was performed in *Rabi*, 2016-17 at the Experimental Farm of Fodder Section, CSKHPKV, Palampur (HP). Among the parents used in these crosses, PLP-1, JPO-46, KRR-AK-26, EC528896 and *A. sterilis* were resistant to powdery mildew disease, whereas HJ-8 was highly susceptible. During *Rabi*, 2019-20, 34 F_4 progenies along with 5 checks were evaluated in RBD over three replications with three rows of 2 m each having row-to-row spacing of 25 and 10 cm for a plant to plant. About 28 F_5 generation progenies were selected based on yield and powdery mildew resistance and evaluated in *Rabi*, 2020-21, following the same procedure undertaken during the evaluation of F_4 generation. The observations were recorded on five randomly selected plants taken from each progeny of each replication for different fodder and its contributing traits *viz.,* days to 50% flowering, plant height (cm), number of tillers per plant, number of leaves per plant, leaf area (cm^2), fresh fodder yield per plant (g), dry matter percent, dry matter yield per plant (g), days to 75% maturity, grain yield per plant (g), harvest index (%) and 100-grain weight (g). At the biochemical aspect two traits *viz.,* crude protein content (%) and crude protein yield per plant (g) were taken into account.

Statistical analysis: Response to selection was calculated as the difference between the mean phenotypic values of the progeny of selected plants and the original population (Nyquist, 1991). PCA of recorded phenotypic data was performed using XLSTAT software. All the traits were measured on individual plants in both the generations and their parents. The clustering of D^2 values was formed by using Tocher's method as described by Rao (1952) using WINDOSTAT software.

Results and Discussion

The frequency distribution of different traits through histogram in F_4 and F_5 generations progenies showed continuous variation for all the yield-related traits (Figs 1-2),suggesting that they were under quantitative and polygenic control.

Response to selection: Response to selection values was higher for harvest index and biological yield per plant in cross PLP-1 × HJ-8, for harvest index, grain yield per plant, fresh fodder yield per plant, and plant height in cross HJ-8 × JPO-46 and grain yield per plant, number of leaves per plant and number of tillers per plant in cross HJ-8 × PLP-1 (Table 1). The highest response to selection was shown by cross HJ-8 × EC528896 for fresh fodder yield per plant followed by leaf area, total number of leaves per plant and plant height. Fresh fodder yield per plant and biological yield per plant showed a higher response in cross HJ-8 × *A. sterilis.* The maximum number of traits recorded the highest response to selection in cross HJ-8 × KRRRAK-26, which were fresh fodder yield per plant followed by total number of leaves per plant, leaf area, dry matter percent, dry matter yield per plant, biological yield per plant, harvest index, plant height and grain yield per plant. Cross PLP-1 × A. *byzantina* recorded a high selection response for only grain yield per plant. These results indicated an improvement in F_5 mean for all of these mentioned traits through selection in F_4 generation. Rani *et al.* (2021) also reported high response to selection values for the number of grains/ear, biological yield/plant and plant height in the progenies derived from cross WH 1105 × WH711, whereas for the number of grains/ear, harvest index, biological yield/ plant, grain yield/plant and number of spikelets/ear in the progenies of cross RAJ 3765 × WH 711 of wheat.

Principal component analysis: PCA was given initially by Pearson (1901) and later developed by Hotelling (1933). It is used for diversity studies because it is a function of primary variables and describes maximum variance within a data set. In the present study, PCA was used to recognize diagnostic characteristics of oats in F_4 and F_5 generation progenies, which contributed more to the diversity and hence are the important traits in differentiating the genotypes to be harnessed in future oat improvement programs. The principal component analysis aims to resolve the total variation of a set of traits into linear, independent composite traits, which successively maximize variability in the data (Johnson, 2012). Sample traits are generally inter-correlated to varying degrees and hence, not all principal components are needed to summarize the data adequately.

In this study, the first five principal components represented a sizeable amount of diversity among the genotypes investigated. This implied that several traits were involved in explaining the variation among the genotypes. PCA studies revealed that the first five components, accounting for more than 80% of total variance among the progenies, are important in both

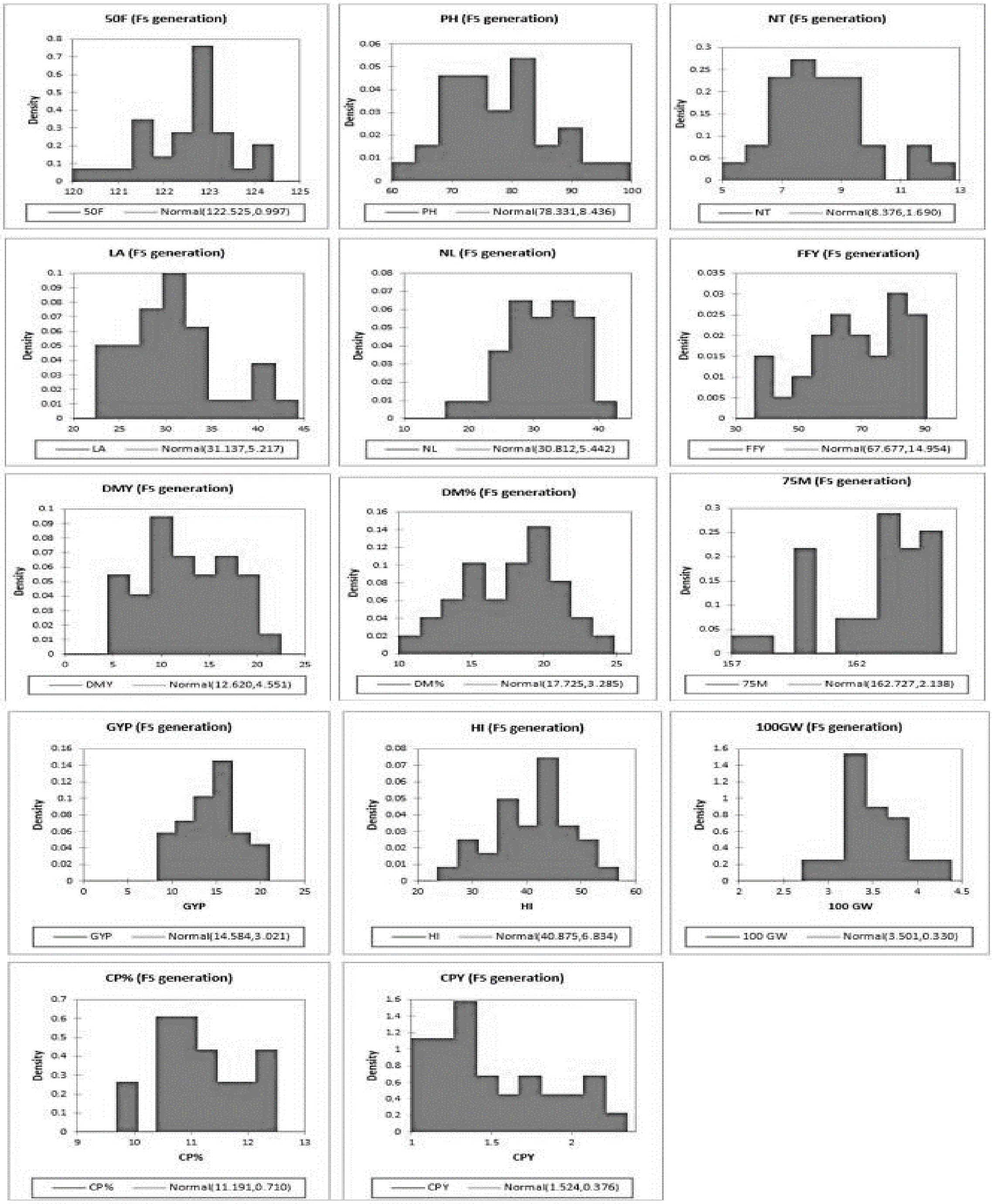
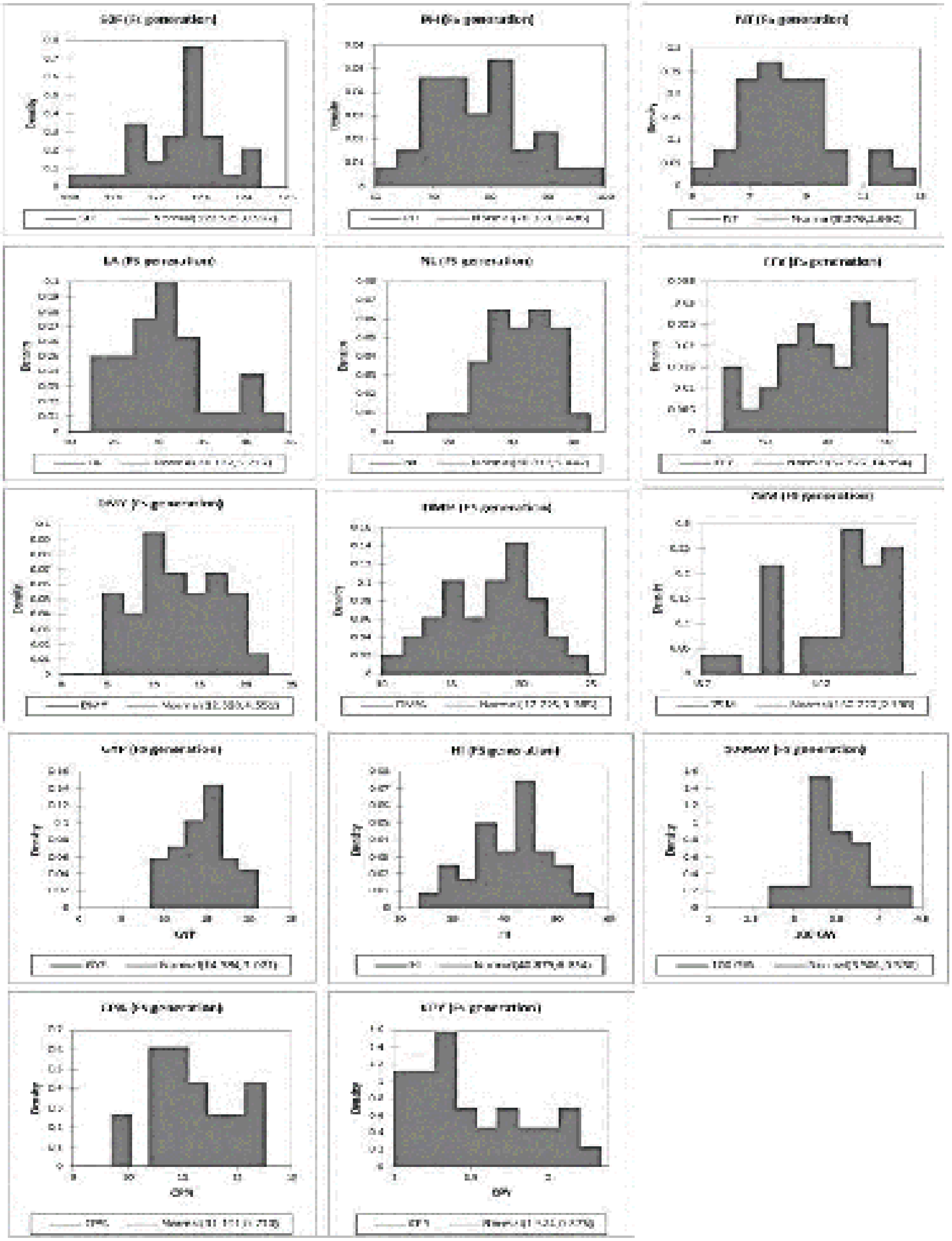


Fig 1. Frequency distribution histograms for various yield and related traits in F_4 generation of oat

generations. Four PC in F_4 and five PC in F_5 generation possess Eigen values > 1. The Eigenvalues, contribution rate to variability, and cumulative contribution rate were recorded (Table 2). The first principal component, *i.e.*, PC1, accounted for the maximum proportion of total variability in the set of all variables, *i.e.*, 36.97 and 30.29% in F_4 and F_5 generations, respectively. PC2, PC3, PC4 and PC5 accounted for 18.12, 17.12, 13.79, 13.95, 7.40, 10.24, 6.20, and 8.47% for the biochemical, fodder and yield-related traits in F_4 and F_5 generations, respectively. The five components, therefore, were considered for further analysis. PC1 for dry matter percent, crude protein yield per plant, dry matter yield per plant, and fresh fodder yield per plant, and PC2 for grain yield per plant, number of tillers per plant, and number of leaves per plant showed high factor loading in both F_4 and F_5 generations. PC3 had a high loading score for days to 50% flowering in both generations and for days to 75% maturity and crude protein content (%) in F_5 generation. PC_4 showed high loading for harvest index in F_4 and for



Note: 50F: Date to 50% flowering; PH: Plant height (cm); NL: No. of leaves per plant; NT: Number of tillers per plant; LA: Leaf area; FFY: Fresh fodder yield; DM%: Dry matter percent; DMY: Dry matter yield per plant; HI: Harvest index; GYP: Grain yield per plant; 100 GW: 100-Grain weight; CP%: Crude protein percent; CPY: Crude protein yield

Fig 2. Frequency distribution histograms for various yield and related traits in F5 generation of oat

Table 1. Response to selection for various traits in seven different crosses of oat

Characters	PLP-1 × HJ-8	HJ-8 × JPO-46	HJ-8 × PLP-1	HJ-8 × EC528896	HJ-8 × *A. sterilis*	HJ-8 × KRRRAK-26	PLP-1 × *A. byzantina*
Days to 50% flowering	0.27	-0.25	-1.42	0.00	-0.73	-0.33	-0.78
Plant height (cm)	-1.37	1.09	-2.10	2.00	-0.15	1.49	-0.09
No. of tillers per plant	0.20	-0.44	1.77	0.93	0.56	0.01	-0.24
No. of leaves per plant	0.22	0.68	2.47	1.42	-0.75	3.54	0.17
Leaf area (cm^2)	-0.29	0.43	0.87	2.24	0.60	3.11	0.31
Fresh fodder yield per plant (g)	-0.02	1.71	0.02	2.37	3.80	4.24	-0.70
Dry matter per cent	-0.37	0.51	0.21	-0.27	0.22	3.02	0.72
Dry matter yield per plant (g)	0.05	0.08	0.55	0.40	0.71	2.58	0.29
Days to 75% maturity	0.27	-0.25	-1.42	0.00	-0.73	-0.33	-0.78
Grain yield per plant (g)	0.57	2.13	2.68	0.13	-0.96	1.23	1.30
Biological yield per plant (g)	1.62	-0.09	0.92	-0.19	1.38	2.34	-0.77
Harvest index (%)	2.81	2.56	0.60	-0.15	0.02	2.13	0.73
100 grain weight (g)	0.18	0.40	0.86	0.86	0.21	0.53	0.12
Crude protein content (%)	0.38	0.07	0.29	0.80	-0.24	0.73	-0.68
Crude protein yield per plant (g)	-0.71	-0.82	-0.27	-0.03	-0.14	0.30	-0.41

Table 2. Eigenvalues and cumulative variability with factor loading for biochemical and yield-related traits in first five components in F_4 and F_5 progenies of oat

Component	PC1		PC2		PC3		PC4		PC5	
	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5
50F	-0.492	-0.281	0.470	0.063	**0.564**	**0.770**	-0.066	0.269	0.168	-0.144
PH	**0.714**	0.200	-0.356	-0.625	-0.302	-0.427	0.030	0.295	-0.273	0.231
NT	0.381	0.462	**0.595**	**0.734**	-0.449	-0.116	-0.409	-0.140	0.043	0.297
NL	0.529	0.596	**0.608**	**0.561**	-0.357	-0.279	-0.334	-0.172	-0.146	0.196
LA	0.502	0.373	-0.192	-0.541	0.370	-0.270	0.072	0.554	-0.234	-0.237
FFY	**0.868**	**0.888**	0.095	-0.143	0.371	0.208	-0.027	-0.061	0.238	-0.106
DMY	**0.894**	**0.964**	0.154	-0.132	0.337	0.162	-0.045	-0.072	0.169	-0.092
DM%	0.929	0.930	-0.049	-0.089	0.234	0.071	0.032	-0.008	-0.097	-0.012
75M	-0.567	0.114	**0.593**	0.228	0.228	**0.633**	-0.177	0.470	0.103	-0.016
GYP	0.213	0.015	**0.620**	**0.626**	-0.542	-0.389	**0.318**	**0.575**	0.131	-0.049
HI	0.253	0.206	0.464	**0.510**	-0.144	-0.306	**0.767**	0.360	0.041	-0.502
100 GW	0.099	0.137	-0.514	-0.267	-0.302	-0.245	-0.030	0.264	**0.736**	**0.514**
CP%	0.198	0.064	-0.413	0.141	-0.477	**0.409**	-0.133	**0.384**	0.014	**0.620**
CPY	**0.924**	**0.867**	0.084	-0.121	0.252	0.253	-0.061	-0.104	0.144	-0.071
Eigenvalue	5.18	4.24	2.54	2.40	1.93	1.95	1.04	1.43	0.87	1.19
Variability (%)	36.97	30.29	18.12	17.12	13.79	13.95	7.40	10.24	6.20	8.47
Cumulative %	36.97	30.29	55.09	47.40	68.89	61.35	76.29	71.59	82.49	80.06

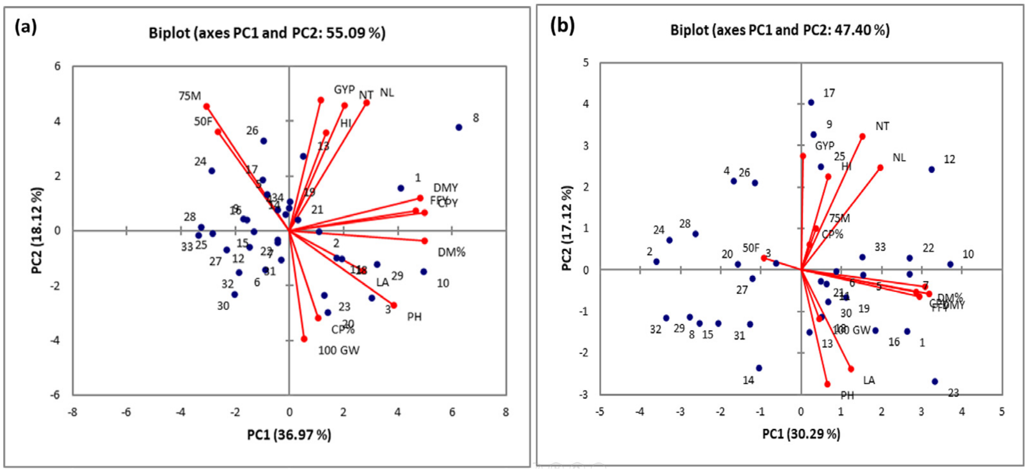


Fig 3. Biplots of F_4 (a) and F_5 (b) generations progenies for PC1 and PC2 of different traits in oat

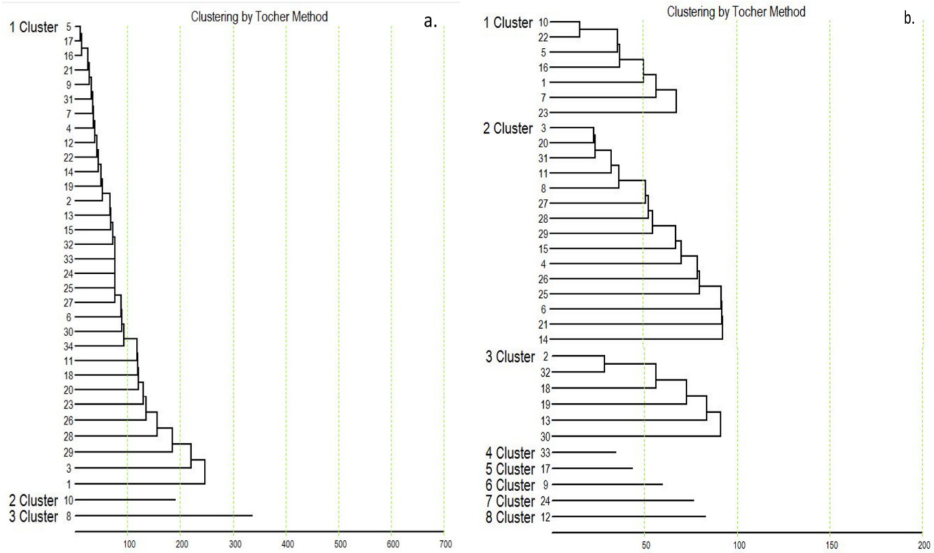


Fig 4. Dendogram of F_4 (a) and F_5 (b) generations progenies in oat

grain yield per plant in F_5 generation. 100 seed weight carried high loading in PC5 in both generations. So these PCs were regarded as grain and fodder yield factors and these traits contributing more to the diversity were considered as important in differentiating the genotypes. Biplots for F_4 and F_5 progenies were carried out (Fig 3). The lines in Figure 3 showed the contribution (direction and magnitude) of 14 yield and biochemical traits in principal components PC1 and PC2. Vaisi *et al.* (2013), Krishna *et al.* (2014), Kujur *et al.* (2017) and Kumari *et al.* (2019) conducted principal component analysis in oat and transferred many correlated variables into a few independent principal components explaining much of the variability of the original set.

Cluster analysis: Out of 14 characters studied, the character crude protein yield per plant contributed the highest towards genetic diversity with values 29.59 and 55.06%, followed by grain yield per plant (27.99 and 16.67%) and crude protein content (13.19 and 8.71%) in F_4 and F_5 generations, respectively (Table 3). Dendrogram using the Tocher method showed that 34 genotypes of oats were grouped into 3 clusters from F_4 generation (Fig 4a) and 33 genotypes from F_5 into 8 clusters (Fig 4b).

The intra and inter-cluster distances among F_4 and F_5 generation oat progenies were also recorded (Tables 4 and 5). The results showed that inter-cluster distances were more than intra-cluster distances for all the clusters, which indicated the presence of narrow genetic variation within a cluster. In F_4 generation, the highest intra-cluster distance was observed for cluster I (10.94) followed by cluster II (0.00) and III (0.00), whereas in F_5, the highest intra-cluster distance was observed for cluster III (9.84) followed by cluster II (9.03), I (8.00), IV (0.00), V (0.00), VI (0.00), VII (0.00) and VIII (0.00). The narrow intra-cluster

Table 3. Percent contribution of various characters to diversity

Characters	Contribution in F_4 generation (%)	Contribution in F_5 generation (%)
Days to 50% flowering	0.71	0.00
Plant height (cm)	1.25	0.38
No. of tillers per plant	1.60	3.03
No. of leaves per plant	0.00	0.38
Leaf area (cm^2)	0.89	1.14
Fresh fodder yield per plant (g)	3.39	2.27
Dry matter percent	6.95	1.33
Dry matter yield per plant (g)	1.07	3.03
Days to 75% maturity	6.60	1.89
Harvest index (%)	0.36	0.95
100-grain weight (g)	6.42	4.17
Crude protein content (%)	13.19	8.71
Crude protein yield per plant (g)	29.59	56.06
Grain yield per plant (g)	27.99	16.67

Table 4. Intra and inter-cluster distances among F_4 generation oat progenies

	Cluster I	Cluster II	Cluster III
Cluster I	**10.94**	20.93	31.59
Cluster II	20.93	**0.00**	18.33
Cluster III	31.59	18.33	**0.00**

distance showed that genotypes were genetically related. When diversity was studied among the clusters based on inter-cluster distance, it showed a range of 18.33 to 31.59 in F_4 generation oat progenies and a range between 9.80 to 20.59 in F_5 generation oat progenies. In F_4 generation, the average inter-cluster distance was highest between clusters I and III (31.59), followed by clusters I and II (20.93) and clusters II and III (18.33). In F_5 generation, the highest inter-cluster distance was found between clusters I and V (20.59), followed by clusters IV and V (20.22), clusters IV and VII (19.88) and clusters I and VII (19.54), whereas the lowest inter-cluster distance was observed between cluster V and VI (9.80). The higher inter-cluster distance indicated the presence of more diversity among the genotypes included among these clusters. The cluster means for various biochemical, fodder and seed yield-related traits studied in F_4 and F_5 generation progenies of oat revealed considerable differences among the entire clusters. Cluster-wise mean and overall cluster mean for the characters in F_4 and F_5 generation oat progenies were recorded (Table 6). The cluster means for 14 quantitative traits studied in progenies of oat revealed considerable differences among all the clusters. In F_4 generation, cluster I, having 32 progenies, had the highest cluster mean value for 100 seed weight (3.14). Cluster II had only one progeny and was associated with characters like days to 50% flowering (120.00), plant height (130.28), leaf area (35.43), days to 75% maturity (155.33), and crude protein percent (11.80%). Cluster III also had only one progeny with the highest number of tillers per plant (10.24),

Table 5. Intra and inter-cluster distances among F_5 generation oat progenies

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**8.00**	16.73	13.14	9.81	**20.59**	16.81	**19.54**	10.13
Cluster II	16.73	**9.03**	12.01	15.88	11.42	10.78	13.22	17.60
Cluster III	13.14	12.01	**9.84**	11.43	16.27	13.19	15.96	15.31
Cluster IV	9.81	15.88	11.43	**0.00**	**20.22**	17.36	**19.88**	13.05
Cluster V	20.59	11.42	16.27	20.22	**0.00**	**9.80**	15.77	**18.09**
Cluster VI	16.81	10.78	13.19	17.36	9.80	**0.00**	14.75	15.80
Cluster VII	19.54	13.22	15.96	19.88	15.77	14.75	**0.00**	**18.90**
Cluster VIII	10.13	17.60	15.31	13.05	18.09	15.80	18.90	**0.00**

Table 6. Cluster means for various biochemical and yield-related traits in F_4 and F_5 generations oat progenies

F_4 generation

	50 F	**PH**	**NT**	**NL**	**LA**	**FFY**	**DM%**	**DMY**	**75 M**	**HI**	**100 GW**	**CP %**	**CPY**	**GY**
Cluster I	121.04	96.80	8.31	31.35	31.17	67.69	17.90	14.92	160.83	38.47	**3.14**	11.10	1.67	15.72
Cluster II	**120.00**	**130.28**	9.45	40.43	**35.43**	101.72	30.90	31.87	**155.33**	31.44	2.92	**11.80**	3.76	8.87
Cluster III	123.00	100.25	**10.24**	**40.70**	34.12	**145.98**	**37.45**	**47.55**	164.33	**44.74**	2.42	9.96	**4.73**	**18.42**
Mean	121.35	109.11	9.33	37.49	33.57	105.13	28.75	31.45	160.16	38.22	2.83	10.95	3.39	14.34

F_5 generation

	50F	PH	NT	NL	LA	FFY	DM%	DMY	75M	HI	100GW	CP %	CPY	GY
Cluster I	122.24	**82.53**	8.26	32.95	**37.47**	**84.49**	**21.52**	**18.36**	163.10	44.09	3.45	11.01	**2.02**	14.30
Cluster II	122.64	78.54	7.99	29.46	31.25	61.72	16.40	10.41	162.33	40.77	3.52	11.03	1.23	15.24
Cluster III	122.56	80.93	7.95	28.67	27.43	62.50	16.78	11.39	162.89	32.67	3.46	11.59	1.58	11.33
Cluster IV	124.33	66.29	9.55	28.75	27.81	87.34	20.12	17.62	161.33	47.05	3.40	11.32	1.99	9.48
Cluster V	122.33	69.30	**12.78**	39.15	25.40	56.40	18.37	10.50	164.33	46.38	3.55	**12.43**	1.30	**19.93**
Cluster VI	122.00	63.75	10.01	**41.67**	23.04	82.17	14.56	12.27	165.33	39.42	3.31	11.70	1.43	18.65
Cluster VII	**121.00**	68.38	6.79	26.39	28.05	36.26	12.09	4.58	**159.67**	**50.41**	**3.73**	9.91	1.24	17.24
Cluster VIII	123.00	75.80	11.91	36.18	27.57	78.98	**22.47**	**18.45**	165.33	49.42	**3.95**	11.90	**2.19**	19.23
Mean	122.51	73.19	9.41	32.90	28.50	68.73	17.79	12.95	163.04	43.78	3.55	11.36	1.62	15.68

number of leaves per plant (40.70), fresh fodder yield per plant (145.98), dry matter percent (37.45), dry matter yield per plant (47.55), harvest index (44.74), crude protein yield per plant (4.73) and grain yield per plant (18.42). Cluster I had six progenies and possessed the highest cluster mean value for plant height (82.53), leaf area (37.47), fresh fodder yield per plant (88.49), dry matter percent (21.52%), dry matter yield per plant (18.36) and crude protein yield per plant (2.02). Cluster II had fifteen progenies, cluster III had six, and cluster IV had only one progeny. Cluster V had one progeny with the highest mean values for a number of tillers per plant (12.78), crude protein content (12.43%) and grain yield per plant (19.93). Cluster VI had only one progeny and was associated with number of leaves per plant (41.67), whereas cluster VII also had one progeny, which was associated with characters like days to 50% flowering (121.00), days to 75% maturity (159.67), harvest index (50.41%) and 100 seed weight (3.73). Comparative evaluation of cluster means suggested that for improving specific character, the genotypes should be taken from the cluster having a high mean value for that character. This comparison indicated that clusters II and III from F_4 generation and clusters I, V, and VII from F_5 generation had better cluster means for most of the characters; therefore, these clusters might be considered better for selecting genotypes. The results of the present investigation were in agreement with previous studies carried out on oats by several workers (Singh and Singh, 2009; Krishna *et al.*, 2014; Bind *et al.*, 2016; Kumari *et al.*, 2019).

Conclusion

The present study revealed that the utmost response to selection was depicted by traits, namely, grain yield per plant, fresh fodder yield per plant, biological yield per plant, harvest index, number of leaves per plant and plant height in most of the crosses. Hence, improvement through selection could be based on these traits in these crosses. Significant diversity existed among oat progenies for all the traits studied. PC1, PC2, PC3, PC4, and PC5 were regarded as grain and fodder yield factors and the traits contributing more to the diversity were considered as important in differentiating the genotypes. The incorporation of more divergent parents in hybridization could enhance the chances of attaining potential varieties and provide a broad spectrum of genetic variability in segregating generations. Therefore, based on cluster analysis, crosses between progenies of clusters II and III from F_4 generation and clusters I, V, and VII from F_5 generation might help in achieving high yields. Efficient exploitation of this diversity might help to identify oat parental lines for a hybrid breeding program.

Acknowledgment

The author would like to thank the Department of Genetics & Plant Breeding, CSKHPKV Palampur, for providing the necessary facilities for the research.

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