

Variability and Diversity in Advanced Oat Lines under Temperate Condition

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ABSTRACT

The present study was conducted with 44 oats genotypes using RCBD with three replications at Dryland Agriculture Research Station, Budgam, Jammu & Kashmir and were grown during Kharif, 2017 to assess the variability and diversity analysis using thirteen different yield and yield contributing characters viz., days to 50% flowering, plant height (cm), number of tillers meter per row, inflorescence length (cm), flag leaf length (cm), culm diameter (mm), seeds per panicle (g), thousand seed weight (g), spikelet's per panicle, green fodder yield quintal per hectare, grain yield quintal per hectare, seed yield per plant (g), number of leaves per plant. Analysis of variance revealed significant differences exists among the genotypes for all the characters studied. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for, grain yield quintal per hectare, culm diameter (mm), green fodder yield quintal per hectare, inflorescence length (cm), seeds per panicle (g), and seed yield per plant. High heritability coupled with high genetic advance were recorded for almost all the characters. D² analysis was performed and clustering was done using Tocher's Method. All the genotypes were grouped into 8 clusters. Cluster number I contained highest number (12) of genotypes and cluster II, VI, VII and VIII contained lowest number (1) of genotypes. Cluster V, IV, III and I showed maximum distance between them suggesting higher probability of heterotic hybrids if selection of parents is done from these pairs of groups. Green fodder yield, dry fodder yield, plant height and days to maturity showed highest contribution to total divergence. This study gave an insight into the variability pattern of the advanced oat lines which will be helpful in their further utilisation.

Key words: Oat, Advanced lines, Diversity, Variability, Cluster analysis.

INTRODUCTION

Oats (*Avena sativa* L.) originated from Mediterranean region, is an important dual (grain and fodder) purpose annual crop of rabi season. Oat is a winter forage crop which is

grown worldwide. It belongs to family poaceae and ranks sixth in production among all cereal crops next to wheat, maize, rice, barley and sorghum in the world scenario¹.

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Oats taxonomic patterns are similar to that of wheat and consists of a polyploid series with seven basic ($x=7$) chromosomes number, i.e. diploid, tetraploid and hexaploid. The genomic constitution of common cultivated oat (*A. sativa*) is AACCCDD. Among the oats genomes, white oats (*Avena sativa* L.) and red oats (*Avena byzantiana*) are cultivated. All over the world, oats was cultivated over 10.29 million hectares with a production of 20.49 million tonnes. Oat is a constituent of breakfast cereal in most developed countries. The importance of oats in the biochemical and cosmetic industry is also on the rise². Grain yield needs improved to increase the area under oats as an alternative crop especially during winter cultivation. Oats production has continuously decreased, whereas the demand for oats as a human food has increased because of its dietary benefits of the whole grain and β -glucan content³. Since oats acreage is much lower than that of most other cereals, commercial efforts in oats breeding is also lower. It can able to tolerate biotic and abiotic stresses to a greater extent and is an alternative choice among the basket of crops for many regions to mitigate the current regime of climate change. Recently, with the advancement of enlarged dairy industries in India, the oats have enchanted the breeder's attention for its modernization due to its quality fodder with high nutritional quality and grains yield with more net energy gains⁴. In recent years, oat grain was mainly used as a livestock feed⁵. Oats production has continuously decreased, whereas the demand for oats as a human food has increased because of its dietary benefits of the whole grain and β -glucan content³. Oats is good source of antioxidants like avenanthramides, alphanatocopherol, alpha-tocotrienol and also total dietary fiber including beta-glucans⁶. Latest research have analyzed the oat consumption effects on health and benefits on health are beyond reducing cardio vascular risk like diabetes, controls blood-pressure levels, lowers blood cholesterol concentrations, controls and maintains weight and gastro-intestinal health. Assessment of the

genetic variability can be achieved using morphological measurements and phenotypic characterization. Pundhir et al.⁷, studied the genotypic and phenotypic coefficients of variation, heritability, expected genetic advance and correlation and path-analyses in 36 genotypes of oats (*Avena sativa* L.) over four environments which revealed moderate to high estimates of heritability coupled with high genetic advance for most of the traits. Bahadur et al.⁸, studied oats genotypes to determine the extent of variability for various fodder yield and quality traits under normal and late sown conditions where they found considerable variability existed for all the characters. Present study was undertaken to estimate the variability parameters and genetic diversity analysis between grain yield and its components characters in advanced oat lines under temperate conditions.

MATERIAL AND METHODS

- a) **Experimental material and location:** Forty four advanced oat lines (*Avena sativa* L.) were grown using RCBD design with three replications at Dryland Agriculture Station, Budgam, Jammu & Kashmir in Kharif 2017. The experimental plot consisted of 7 rows each of 10 m length maintained with a row to row spacing of 5 cm. Recommended package of practices were followed for raising a good crop. Data were recorded on yield and different yield contributing traits viz, days to 50% flowering, plant height (cm), number of tillers meter per row, inflorescence length (cm), flag leaf length (cm), culm diameter (mm), seeds per panicle (g), thousand seed weight (g), spikelet's per panicle, green fodder yield quintal per hectare, grain yield quintal per hectare, seed yield per plant (g), number of leaves per plant.
- b) **Data analysis:** The analysis was carried out by applying standard statistical techniques for analysis of variance to establish significance level among the

advanced oat lines. Data were subjected to principal component and Mahalanobis D² statistical analysis extended by Rao. Intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary. Statistical software's viz. Window stat 9.1 and R (version 3.2.2) were used for analysis.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences exists among the genotypes for all the characters studied. The mean, range and estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h² (BS)) and genetic advance as per cent of mean (GA) are presented in Table 1.

Table 1: Genetic parameters for different characters in oats genotypes

Characters	Mean	Range	GCV (%)	PCV (%)	H ² (%)	GA (%) of mean
Days to 50% flowering	178.14	167.33 - 184.66	2.2385	2.2410	0.998	4.606
Plant height (cm)	118.04	97.60 – 146.12	9.3611	9.3808	0.996	19.243
No. of tillers meter row ⁻¹	140.47	123.76 - 169.39	8.3363	8.3517	0.994	17.141
No. of leaves plant ⁻¹	5.78	3.81 – 6.32	9.1502	9.1595	0.999	18.830
Flag leaf length (cm)	32.08	23.35 – 36.13	11.8750	11.9182	0.992	24.374
Culm diameter (mm)	5.05	3.36 – 6.25	15.3752	15.3883	0.997	31.646
Inflorescence length (cm)	33.86	27.73 – 45.50	13.5615	13.5818	0.990	27.895
Grain yield ha ⁻¹ (q)	20.23	14.27 – 26.78	16.7747	16.8003	0.991	34.504
Seeds panicle ⁻¹ (g)	50.90	39.22 – 67.34	12.4368	12.4670	0.989	25.558
1000 seed weight (g)	31.59	26.03 – 36.78	10.6997	10.7107	0.985	22.019
Spikelet's panicle ⁻¹	26.34	22.26 – 32.85	10.2566	10.2648	0.987	21.112
Green fodder yield ha ⁻¹ (q)	396.42	329.63 – 522.25	14.253	14.288	0.974	29.291
Seed yield plant ⁻¹ (g)	10.32	7.35 – 12.36	12.1198	12.1390	0.972	24.927

Days to 50% flowering showed a range of 167.33 to 184.66 with a mean of 178.14. The accession, SGO-19 was found to be very early. Estimates of phenotypic and genotypic coefficients of variation for this character were 2.24 and 2.23 per cent respectively. Plant height exhibited a range of 97.60 to 146.12 cm with a mean of 118.04 cm. Among all the accessions studied, SGO-3 had the shortest stature. Muhammad et al.¹², and Bibi et al.¹¹, reported significant difference for plant height in oats genotypes which agreed with the present findings. This character recorded phenotypic and genotypic coefficients of variation of 9.38 and 9.36 per cent respectively. Total number of tillers per plant varied from 123.76 to 169.39 with a mean of 140.47 among the accessions. The accession, JPO-42 had the lowest and SGO-21 had the highest total number of tillers per plant. Estimates of phenotypic and genotypic coefficients of variation for this character were 8.35 and 8.33 per cent respectively. Total

number of leaves per plant varied from 3.81 to 6.32 with a mean of 5.78. The accession, SGO-20 had the highest total number of leaves per plant. This character recorded phenotypic and genotypic coefficients of variation of 9.152 and 9.150 per cent respectively. Flag leaf length (cm) varied from 23.35 to 36.13 with a mean of 32.08. The accession, SGO-10 had the lowest and SGO-7 had the highest flag leaf length (cm). Estimates of phenotypic and genotypic coefficients of variation were 11.91 and 11.87 per cent respectively. Culm diameter (mm) varied from 3.36 to 6.25 with a mean of 5.05 among the accessions. The accession, SKO-31 had the lowest and SGO-24 had the highest culm diameter (mm) respectively. Phenotypic and genotypic coefficients of variation for this character were 15.38 and 15.37 per cent respectively. Inflorescence length (cm) ranged from 27.73 to 45.50 with a mean of 33.86. The accessions, SGO-12 and SGO-20 had recorded the lowest and highest inflorescence length (cm)

respectively. This character recorded phenotypic and genotypic coefficients of variation of 13.58 and 13.56 per cent respectively. Grain yield quintal per hectare showed a range of 14.27 to 26.78 with a mean of 20.23 among the accessions. The accessions, JPO-42 and SKO-96 recorded the lowest and highest grain yield quintal per hectare respectively. Phenotypic and genotypic coefficients of variation estimates for this character were 16.80 and 16.77 per cent respectively. Seeds per panicle (g) ranged from 39.22 to 67.34g with a mean of 50.90 g. The accessions, SGO-8 and SGO-17 recorded the lowest and highest Seeds per panicle (g) respectively. Phenotypic and genotypic coefficients of variation estimates for this character were 12.46 and 12.43 per cent respectively. Thousand seed weight (g) showed a range of 26.03g to 36.78g with a mean of 31.59g. The accessions, SGO-24 and SGO-20 respectively recorded the lowest and highest thousand seed weight (g). Phenotypic and genotypic coefficients of variation estimates were 10.71 and 10.69 respectively. Spikelet's per panicle varied from 22.26 to 32.85 with a mean of 26.34 among the accessions. The accessions, SKO-170 and SGO-21 recorded the lowest and highest Spikelet's per panicle respectively. Estimates of phenotypic and genotypic coefficients of variation were 10.26 and 10.25 per cent

respectively. Green fodder yield quintal per hectare showed a range of 329.63 to 522.25 with a mean of 396.42. The accessions, SKO-160 and SGO-23 recorded the lowest and highest green fodder yield quintal per hectare. Estimates of phenotypic and genotypic coefficients of variation were 14.28 and 14.25 per cent respectively. Seed yield per plant (g) varied between 7.35 to 12.36g with a mean of 10.32. The accessions, JPO-42 and SKO-96 recorded the lowest and highest. Seed yield per plant (g). Estimates of phenotypic and genotypic coefficients of variation were 12.13 and 12.11 per cent respectively.

Cluster analysis is a multivariate technique which aims to classify a sample on basis of a set of measured variables into a number of different groups such that similar subjects are placed in same group. It provides a way for scientists to discover potential relationships and assists to construct systematic structures in large number of variables and observations. The dendrogram representing the genetic diversity among 44 genotypes is presented in Fig. 1. It reflects potential relationship among the genotypes studied. Forty-four advanced oat lines were grouped into 8 different clusters by using clustering techniques given by Tocher and explained by Rao. Distribution of oat lines into various clusters is presented in Table 2.

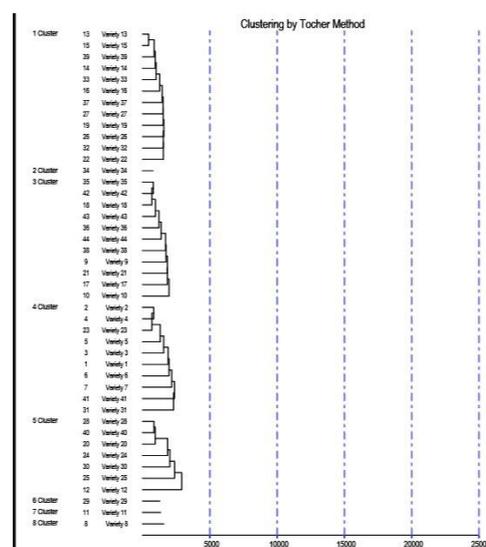


Fig. 1: Dendrogram for the 44 Genotypes using Tocher's method

Table 2: Distribution of 44 advanced oat lines in 8 different clusters

Cluster	No. of genotypes in the cluster	Name of the genotypes
I	12	SGO-10, SKO-20, SGO-5, SKO-108, SGO-11, SKO-31, P-2, SGO-16, SKO-186, SGO-3, SGO-2, SGO-14
II	1	SKO-170
III	11	SGO-25, SKO-207, SGO-8, SKO-233, SGO-1, SKO-160, SGO-18, SGO-15, JPO-67, SKO-204, SGO-7
IV	10	SGO-22, SGO-20, SGO-4, SGO-17, SGO-21, SGO-23, SKO-225, SGO-13, SKO-175, SGO-12
V	7	SGO-24, JPO-42, SGO-6, SKO-166, SGO-9, JPO-57, SGO-19
VI	1	JPO-40
VII	1	SKO-96
VIII	1	SKO-90

The maximum number of genotypes (12) were grouped in cluster I which was followed by cluster III (11), IV (10) and cluster V (7). The cluster II, VI, VII and VIII contained one lines and occupied least position. Large number of genotypes in a single cluster depicts that these genotypes are more closely related and had less genetic variation among them. It further implies that hybridization programme employing these genotypes inhabiting a

common cluster will be of little use and diverse clusters are beneficial for hybridization programme in oat improvement. D^2 analysis carried out involving 44 advanced oat lines for 13 characters revealed that altogether 8 clusters have been formed (Figure 1). Inter and intra-cluster distance ($D = \sqrt{D^2}$) values were worked out from divergence analysis and are listed in Table 3 and shown in Figure 2.

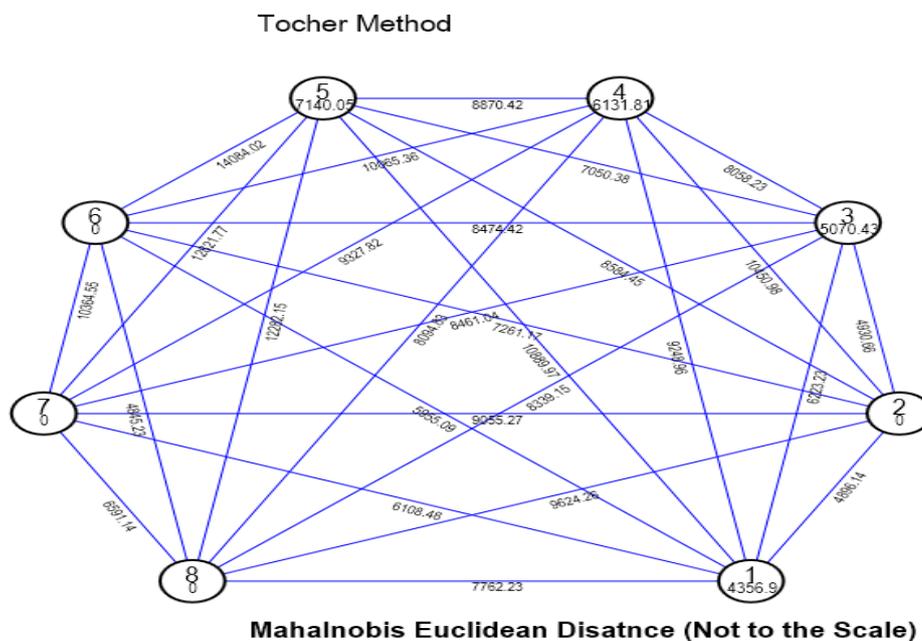


Fig. 2: Intra and Inter Cluster Distances

Table 3: Average intra- (bold) and inter-cluster distance (D²) for 44 advanced oat lines obtained on the basis of 13 morphological characters

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
1	4356.90	4896.14	6223.23	9248.96	10889.97	5955.09	6108.48	7762.23
2		0.00	4930.66	10450.98	8584.45	7261.17	9055.27	9624.26
3			5070.43	8058.23	7050.38	8474.42	8461.04	8339.15
4				6131.81	8870.42	10065.36	9327.82	8094.83
5					7140.05	14084.02	12821.77	12282.15
6						0.00	10364.55	4845.23
7							0.00	6591.14
8								0.00

The maximum intra- cluster distance (D = 7140.05) was observed in cluster V followed by cluster IV (D = 6131.81), III (D =5070.43) and cluster I (4356.90). The highest inter-cluster distance (D = 14084.02) was observed between clusters VI and VII followed by clusters VII and VIII (D = 12821.77), suggesting more divergence in genetic makeup of the oat lines included in these cluster pairs. From the table, it was revealed that the inter-cluster distances were larger than the intra-cluster distances indicating wide diversity

among the oat lines of different clusters. Therefore, combinations with high heterotic response and superior recombinants may be obtained through hybridizations between genotypes across the clusters¹³. Low levels of intra-cluster distances were pinpointing of narrow genetic variation within a cluster. The genetic differences between clusters were reflected in their cluster means. Cluster mean values for 13 yield related characters are presented in Table 4.

Table 4: Cluster means for morphological and quality component traits in different clusters of advanced oat genotypes

Characters	I	II	III	IV	V	VI	VII	VIII
Days to 50% flowering	176.94	176.94	176.94	176.94	176.94	176.94	176.94	176.94
Plant height (cm)	116.39	116.39	116.39	116.39	116.39	116.39	116.39	116.39
No. of tillers meter row ⁻¹	136.84	136.84	136.84	136.84	136.84	136.84	136.84	136.84
No. of leaves plant ⁻¹	5.68	5.68	5.68	5.68	5.68	5.68	5.68	5.68
Flag leaf length (cm)	28.18	28.18	28.18	28.18	28.18	28.18	28.18	28.18
Culm diameter (mm)	4.67	4.67	4.67	4.67	4.67	4.67	4.67	4.67
Inflorescence length (cm)	32.24	32.24	32.24	32.24	32.24	32.24	32.24	32.24
Grain yield ha ⁻¹ (q)	19.16	19.16	19.16	19.16	19.16	19.16	19.16	19.16
Seeds panicle ⁻¹ (g)	48.68	48.68	48.68	48.68	48.68	48.68	48.68	48.68
1000 seed weight (g)	31.39	31.39	31.39	31.39	31.39	31.39	31.39	31.39
Spikelet's panicle ⁻¹	25.04	25.04	25.04	25.04	25.04	25.04	25.04	25.04
Green fodder yield ha ⁻¹ (q)	373.14	373.14	373.14	373.14	373.14	373.14	373.14	373.14

The highest mean values for days to flowering, spikelets per panicle, green fodder yield quintal per hectare and inflorescence length (cm) were observed in the cluster VIII. Number of leaves per plant, seeds per panicle (g), grain yield quintal per hectare and seed yield per plant (g) were found maximum in cluster VII. Culm diameter (mm) was found

maximum in cluster VI. Flag leaf length was found maximum in cluster V. Whereas, plant height (cm) and number of tiller meter per row were found maximum in cluster IV. Thousand seed weight (g) was found to be maximum in cluster II. Required minimum days to flowering were observed in cluster IV indicating the early lines in this group. Cluster

III showed minimum plant height indicating that this cluster includes the shorter lines. The highest yield was produced by the lines of cluster VII followed by cluster VIII. Considering all the characters it appears that the lines in the cluster VII and cluster VIII performed better. The lines in this cluster had highest seed yield per plant (g), green fodder yield quintal per hectare and grain yield quintal per hectare compared to all other clusters. Hence, for the improvement of different characters viz. Days to flowering, 1000 seed weight (g), grain yield (q/ha) and seed yield per plant (g) under the present study, inbred lines should be selected from clusters IV, II and VII.

CONCLUSION

Genetically diverse parents are expected to produce higher heterosis¹⁴, Mian, M.A.K¹⁵, and Moll, R.H¹⁶. Endang et al.¹⁷, stated parents from diverse clusters could be selected for crossing which are likely to generate the higher heterosis and good amount of variability for effective selection of various economic traits. Keeping this in view, the findings from the present study indicated that the cluster VI and V, VII and V, IV and II showed higher distance between them. The selection of parents for further breeding programme from these clusters would exert high heterosis in hybrids and wide variability in genetic architecture of subsequent generations. From this study it is evident that the clusters VI and VII were highly divergent and the lines belonging to these clusters could be used effectively in hybridization program.

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