Genetic Variability and Divergence Analysis in Oat (*Avena sativa*) under Rainfed Environment of Intermediate Himalayan Hills

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On the basis of D^2 analysis 70 oat genotypes were grouped into seven clusters and two ungrouped clusters. Cluster I was the largest and contained 16 genotypes. The genotype belonging to ungrouped cluster IX, namely, SJO-47 showed promise for green fodder yield, dry matter yield, green fodder productivity/day, tillers/plant and dry matter (%). The highest intra-cluster distance was observed in cluster VIII containing five genotypes. The most distant clusters were cluster II and cluster VIII followed by cluster II and VII and Cluster II and IX. The genotypes SJO-14, SJO-16, SJO-17, SJO-13, SJO-15, SJO-12, SJO-11 were distantly related with JO-55, SJO-56, SJO-54, SJO-52, SJO-53. The maximum (%) contribution towards genetic divergence was contributed by crop duration, followed by green fodder yield and plant height. High phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance as (%) of mean were reported for green fodder productivity, plant height, tillers/plant, dry matter yield and green fodder yield.

Key Words: *Avena sativa,* **Clusters, Divergence, Green fodder, Oat, Variability**

Introduction

Oat is one of the most nutritious non-leguminous fodder crops and is mainly grown during *rabi* season under irrigated as well as rainfed conditions in India. It provides green fodder during scarcity period in winter season of Himalayan regions. Oat green fodder contains 20% dry matter, 10% crude protein, 91% organic matter (DM basis) (Gupta *et al.*, 2004). In addition to green fodder, oat grains are also used for cattle feeding and preparation of nutritious instant foods for humans. Assessment of variability for the yield and its components becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement. The role of plant genetic resources in the improvement of cultivated plants has been well recognized. Characterization and evaluation of both exotic and indigenous collections to get information on useful traits forms the basic step for crop improvement programmes. Like any other crop species the first step in oat improvement is full assessment of the local materials, including collection, evaluation and molecular characterization of germplasm lines. Often, local varieties of crops are of excellent quality and flavour, have a good level of resistance to pests and diseases and may be superior to exotic materials (Abbas *et al.*, 2008). Study of genetic divergence among a set of genotypes will, therefore, enable a plant breeder to choose suitable parents and plan appropriate hybridization programme. Diederichsen (2008) characterized 10,105 accessions of hexaploid cultivated oat (*Avena sativa* L. sensu lato) from 85 countries. Eight environmentally stable morphological characters differentiated into 18 character states, were used to define genetically distinct morphological groups. The greatest richness of diversity was found in oat from countries with temperate climates and intensive oat breeding programmes. Achleitner *et al.* (2008) studied genetic diversity among 114 oat (*Avena sativa* L.) varieties of worldwide origin based on 77 molecular polymorphisms produced by eight selective AFLP primer combinations used for cluster analysis and principal component analysis. Their study demonstrated that diversity could be significantly enhanced using a global collection, and provides evidence for marker-trait associations that can be validated in segregating populations and exploited through marker-assisted selection. D^2 statistics has proved to be a powerful tool in discerning genetic divergence among groups based upon multiple growth characters, assessing relative characters and relative contribution of different components of total divergence. In fodder crops such informations are limited.

The present study was conducted to determine the magnitude of variability for green fodder yield and genetic divergence among the oat genotypes. Parameters such as genotypic and phenotypic coefficient of variability

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are useful in detecting the amount of variability present in the germplasm. Heritability and genetic advance help in determining the influence of environment on the expression of the genotype and the reliability of characters. Like grain yield in cereals, green fodder yield in oat is also not a unitary character but depends on a number of plant characters. Being highly influenced by environmental changes direct selection for green fodder yield is often not effective. The estimation of correlation coefficient among yield and its components has been useful to the breeders in selecting suitable plant type. Thus, in the present study efforts were made to explore the extent of genetic variability for the nine characters, to obtain information on genetic diversity present among the genotypes and to classify them into clusters.

Materials and Methods

The present investigation was carried out at the Regional Agricultural Research Station, (SKUAST-J), Rajouri. The experimental material for the present study consisted of 70 diverse genotypes of oat (*Avena sativa* L). All the genotypes were evaluated in randomized block design with three replications during *rabi*-2007-08 and 2008-09 under rainfed environment. Each plot consisted of five rows of 4 m length, spaced 25 cm apart and maintaining an inter-plant distance of 10 cm within rows. All the recommended agronomic practices were followed to raise the good crop. The crop experienced moisture stress during early development in November-December in both the years. However, the crop recovered well following sufficient rains from the month of January onwards. Observations were recorded on nine characters. Observations on plant height, tillers/plant and leaf stem ratio were recorded on randomly selected five plants in each plot and in each replication, whereas observations on days to flowering, crop duration (days), dry matter (%), green fodder productivity, green fodder yield and dry matter yield were recorded on plot basis. Standard statistical procedures were followed for estimating genetic constants *i.e.* phenotypic and genotypic coefficients of variation (Burton, 1952), heritability in broad sense (Hanson *et al.*, 1956) and expected genetic advance (Johnson *et al.*, 1955). Pooled analysis of variance (ANOVA) was used to quantify the genetic differences among the genotypes. The multivariate analysis was performed through Window State Software (Indostat Service, India) using Mahalanobis's D² statistics (Mahalanobis,

1936). Treating D² as a generalized statistical distance, the criteria used by Toucher (Rao, 1952) was applied for determining the group constellation and clustering was done accordingly (Fig. 1). The character-wise rank totals were used to calculate the % contribution of each character to the total divergence. Average inter- and intra-cluster distances were estimated as per the method recommended by Singh and Chaudhary (1985).

Results and Discussion

A wide range of phenotypic variability was observed for all the characters studied. The mean squares (ANOVA) for nine characters indicated highly significant differences between genotypes for all the characters (Table 1). The estimates of both phenotypic (PCV) and genotypic coefficients of variation (GCV) for the nine characters were studied and are presented in Table 2. The variability estimates, in general, revealed that the estimates of PCV were greater than the estimates of GCV for all the traits. This suggested the role of environment in the expression of the characters (Singh and Singh, 2009). PCV/GCV ratio was highest for leaf stem ratio and was lowest for plant height. Highest GCV was obtained for dry matter yield (35.82%) followed by green fodder yield productivity (30.14%), green fodder yield (29.86%) plant height (24.34%) and tillers/plant (21.98). Moderate estimates of GCV were obtained for dry matter percent, for all other characters GCV was low. The green fodder yield showed the estimate of PCV (38.28%) in comparison to GCV of 35.82% suggesting environmental influence on this character, which was confirmed by its heritability. The least difference between PCV and GCV for plant height suggested that this character is least affected by environment. In such a situation, selection can be effective on the basis of phenotype alone with equal probability of success.

On the basis of GCV, it is possible to determine the amount of heritable variation. It can be found out with greater degree of accuracy when heritability in conjunction with genetic advance is studied. Hence, both heritability and genetic advance were determined to study the scope of improvement in various characters through selection. The heritability estimates ranged from 53.50% for leaf stem ratio to 97.50% for plant height. High estimates of heritability were also observed for green fodder productivity, days to flowering, crop duration and dry matter yield and moderate estimates for tillers/plant, dry matter (%), green fodder yield and
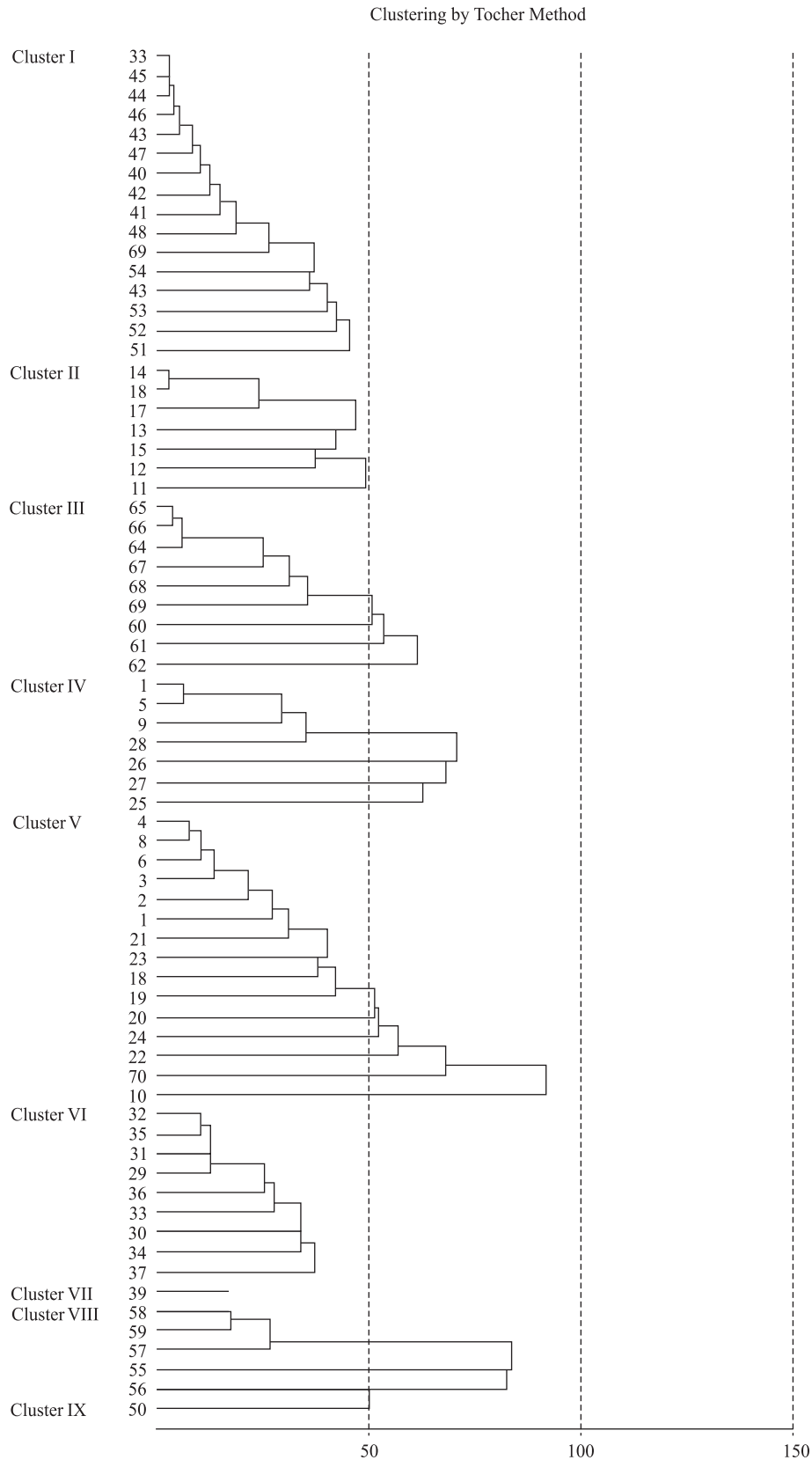
Fig. 1. Different clusters showing the position of genotypes (mentioned by serial numbers)

Table 1. Estimates of mean, range, mean square, genotypic coefficient of variation, (GCV), phenotypic coefficient of variation (PCV), genetic advance (GA) as percent of mean, heritability for eight characters in oat.

Character	Mean	Range		Mean square	GCV	PCV	GA as % of Mean	h² (broad sense)	r_g with green fodder yield
		Min.	Max.						
Days to flowering	139.05	121.33	165.33	296.02**	7.05	7.32	13.99	92.70	0.232**
Crop duration(days)	151.43	135.33	171.33	226.24**	5.64	5.91	11.10	91.20	0.290**
Plant height (cm)	119.15	57.33	172.73	2544.94**	24.34	24.65	49.50	97.50	0.101
Tillers / plant	22.42	14.55	31.52	79.81**	21.98	24.93	39.93	77.70	0.970**
Leaf/stem ratio	0.46	0.39	0.57	0.006**	8.40	11.47	12.65	53.50	0.134*
Dry matter (%)	21.12	17.20	30.63	24.21**	12.67	14.88	22.24	72.60	0.404**
Green Fodder Productivity (q/ h/ d)	2.07	1.16	3.70	1.17**	29.86	30.93	59.38	93.20	0.985**
Green Fodder Yield (q/ h)	313.86	169.48	553.48	30496.85**	30.14	35.77	52.31	71.00	–
Dry Matter Yield (q/ h)	69.45	33.45	170.54	1944.35**	35.82	38.28	69.05	87.60	0.933**

*,** = Significant at 5% and 1% level, respectively.

leaf/stem ratio. Moderate estimates of heritability for these characters indicated that environmental effects constitute a sufficient portion of the total phenotypic variation and hence, selection for these characters will be less effective. Expected genetic advance as % of mean for various characters (Table 1) revealed that dry matter yield, green fodder productivity, green fodder yield, tillers/plant and plant height exhibited the high genetic advance. These characters exhibited high GCV, heritability together with high genetic advance indicated the predominance of additive gene effects in controlling these characters. Therefore the characters like dry matter yield, green fodder productivity, green fodder yield and plant height possessing high GCV, heritability and genetic advance as % of mean could be effectively used in selection, as it has been suggested that characters with high heritability coupled with high GA as % of mean would respond to selection better than those with high heritability and low genetic advance.

The 70 genotypes were grouped into seven grouped clusters and two ungrouped clusters (Fig. 1) using Tocher's method with variable number of entries (Table 2), suggesting adequate scope for selecting superior and diverse parents to be exploited for any breeding programme. Cluster I had the maximum number of genotypes (16) with intra-cluster distance 5.50, indicating diversity within the cluster but not to the extent so that they can form separate clusters as there existed genetic similarities among themselves on the basis of multiple characters causing them to belong into a single character. Cluster V consisted of 15 genotypes while cluster III and VI contained 9 genotypes each representing different eco-geographical regions. Cluster II and IV also had equal number of genotypes (7 each). Further, cluster VIII had 5 genotypes while rests of two clusters were solitary entry clusters. The intra- and inter-

cluster distances (D^2 values) are presented in Table 3. Cluster VIII recorded maximum intra-cluster distance (9.21) followed by cluster IV (8.30) and cluster V (7.54), indicating existence of considerable genetic divergence among constituent genotypes. Hence, parents within the cluster can also be chosen for hybridization programme. The relative distance of each cluster from other clusters (inter-cluster distances) indicated greatest divergence between cluster II and cluster VIII (D=24.28) followed by cluster II and VII (D=23.7), II and IX (D=21.66), V and VIII (D=20.02), indicating greater diversity between genotypes belonging to respective pairs of clusters The genotypes of the most distant cluster *i.e.* cluster II and VIII were quite contrasting in performance with respect to plant height, tiller/plant, days to flowering and crop duration. The genotypes of cluster II showed promise with regard to plant height. Ungrouped genotype in cluster IX (SJO-47) seem to be quite promise for many of the green fodder yield attributing traits as it had the highest mean performance for green fodder yield, dry matter yield, green fodder productivity/day, tillers/plant and dry matter (%). This genotype also had contrasting traits with cluster II with respect to plant height, tillers/plant, dry matter (%), and green fodder yield. The contrasting genotypes of these clusters are expected to yield desirable segregants upon hybridization following single plant selection in later generations, suitable for rain-fed conditions with early maturing and high green fodder yield. The clusters I and VII had the lowest inter cluster genetic distance (D = 8.35), suggesting that the cluster VII which have solitary genotype represents more similarity with cluster I, which differed mainly for characters plant height and dry matter (%). The small inter-cluster distance indicates less diversity between the genotypes contained in the clusters. However, these genotypes can be undertaken for hybridization in order to exploit variability for the

specific characters for which the genotype of the two clusters showed marked difference.

In the present study, hybridization between genotypes having higher D-distance are expected to generate exploitable variability for the improvement in the fodder yield and yield related traits as well as are likely to throw desirable transgressive segregants in later generations of hybridization. In the present study, D^2 analysis revealed the presence of considerable diversity among the genotypes and was observed to be distributed into nine different clusters. Since, the genotype present in the same cluster indicate their close relationship as compared to others (Table 3), it could be expected that all the 16 genotypes present in cluster I were some how genetically related among themselves and were diverse from the genotypes belonging to other classes.

The cluster means of genotypes (Table 4) revealed considerable genetic differences between the groups. The cluster IX registered the highest mean value for green fodder yield (553.48q/h) dry matter yield (170.54q/h), green fodder productivity/day (3.70q/h), tillers/plant (31.52) and dry matter (30.63%). The highest average cluster mean for plant height was reported in cluster II (162.94) followed by cluster V (148.47), whereas, highest cluster mean value for crop duration was observed in cluster IV. The lowest mean value of character days to flowering, which is desirable, was reported in cluster VIII (125.13). The clusters contributing maximum to D^2 values are to be given greater emphasis for deciding the clusters for the purpose of further selection and hybridization. The maximum percent contributing towards genetic divergence was showed by the characters crop duration

Table 2. Grouping of 70 genotypes into nine clusters

Cluster	No. of genotypes	Genotypes
I	16	SJO-35, SJO-42, SJO-41, SJO-43, SJO40, SJO-44, SJO-37, SJO-39, SJO-38, SJO-45, SJO-66, SJO51, SJO-46, SJO-50, SJO-49, SJO-484
II	7	SJO-14, SJO-16, SJO-17, SJO-13, SJO-15, SJO-12, SJO-11
III	9	SJO-62, SJO-63, SJO-61, SJO-64, SJO-65, SJO-60, SJO-57, SJO-58, SJO-59
IV	7	SJO-1, SJO-5, SJO-9, SJO-25, SJO-23, SJO-24, Palampur-1
V	15	SJO-4, SJO-8, SJO-6, SJO-3, SJO-2, SJO-7, OS-6, SJO-21, Kent, SJO-18, SJO-19, SJO-22, SJO-20, Sabzar, SJO-10
VI	9	SJO-29, SJO-32, SJO-28, SJO-26, SJO-33, SJO-30, SJO-27, SJO-31, SJO-34
VII	1	SJO-36
VIII	5	SJO-55, SJO-56, SJO-54, SJO-52, SJO-53
IX	1	SJO-47

Table 3. Average intra-cluster (diagonal bold) and inter-cluster distances (D values) among the nine clusters in oat

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**5.60**	18.47	12.14	11.79	13.83	15.40	8.35	13.12	11.27
II		**7.07**	18.58	15.03	11.60	17.98	23.79	24.28	21.66
III			**7.16**	15.51	14.30	12.78	13.30	10.86	17.86
IV				**8.30**	12.71	16.76	15.86	19.68	17.45
V					**7.54**	18.76	19.55	20.02	19.83
VI						**5.89**	15.05	14.63	17.09
VII							**0.00**	10.47	12.16
VIII								**9.21**	16.47
IX									**0.00**

Table 4. Cluster means and (%) contribution of characters towards divergence in oat

Clusters	Days to flowering	Crop duration (days)	Plant height (cm)	Tillers/plant	Leaf/stem ratio	Dry matter (%)	Green fodder productivity (q/ h/d)	Green fodder yield (q/h)	Dry matter yield (q/h)
I	138.13	152.13	110.81	27.96	0.46	22.09	2.85	434.01	95.72
II	145.00	153.57	162.94	21.22	0.46	19.05	1.86	286.25	65.51
III	130.89	144.89	98.93	15.89	0.43	21.58	1.35	195.69	42.36
IV	157.48	167.81	132.18	26.35	0.46	22.83	2.14	358.60	82.15
V	135.60	146.89	148.47	21.94	0.48	21.36	1.99	292.83	62.69
VI	143.74	156.74	92.30	17.29	0.47	17.96	1.41	222.15	47.86
VII	139.67	153.67	78.67	28.15	0.49	19.81	2.87	442.00	87.66
VIII	125.13	139.13	72.60	20.28	0.42	21.06	1.95	272.77	57.24
IX	135.33	149.33	111.67	31.52	0.48	30.63	3.70	553.48	170.54
Contribution (%)	2.17	35.88	14.87	10.83	0.15	14.12	1.04	19.46	1.49

(35.88) followed by green fodder yield (19.46), plant height (14.87) and dry matter (14.12%) tiller/plant (10.83). More than 80% contribution towards total genetic divergence was mainly because of these five characters. Hence, these traits may be considered to be the more important traits for higher green fodder yield. It is observed that the genotypes desirable for different traits belonged to different clusters. On the basis of inter-cluster distances genotypes in cluster II (SJO-14, SJO-16, SJO-17, SJO-13, SJO-15, SJO-12, SJO-11) and in cluster VIII (SJO-55, SJO-56, SJO-54, SJO-52, SJO-53) were found suitable for hybridization programme. The selection of diverse genotypes with desirable traits and in turn utilizing them for multiple crossing programmes amongst themselves is expected to be effective in accumulation of favourable genes for bringing together different desirable traits in to the common genetic background. On the other hand genotype included in the same cluster with a high order of divergence will be expected to provide the best breeding material for achieving the maximum genetic gain for yield *per se*, provided other factors do not operate to limit the realization of the potential. It is encouraging that the divergence revealed in the present genotypes studied due to these characters will offer a good scope of improving green fodder yield in oat. Thus, a crossing programme involving parents selected on the basis of divergences for yield traits may likely to produce an improved genotype of oat suitable for rainfed ecosystem of intermediate Himalayan hills.

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