GENETIC VARIABILITY AND DIVERGENCE STUDIES IN OATS (*AVENA SATIVA* L.) FOR GREEN FODDER AND GRAIN YIELD

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SUMMARY

Genetic variability, heritability, genetic advance and genetic divergence for grain and fodder production in oats (*Avena sativa* L.) were studied for 30 genotypes of oats. Analysis of variance indicated that sufficient amount of genetic variability was present among the genotypes for all characters. High heritability along with high genetic advance was observed for tillers per metre row length and green fodder yield (q/ha). On the basis of multivariate analysis based on Mahalanobis D^2 statistic, 30 genotypes were grouped only into four clusters. Cluster I was the largest and consisted of 23 genotypes followed by II with five genotypes. Rest of the clusters III and IV had single genotype in each cluster. Inter cluster-distance was the highest between clusters II and IV and minimum inter-cluster distance was present between cluster I and cluster III. The clusters II and IV having maximum inter-cluster distance showed that their members were far apart from each other, while members of clusters I and III having minimum inter-cluster distance were quite close. The superior genotypes identified for dual purpose aspect were NDO-711, UPO-10-2, KENT and RO-19, which gave good green fodder yield and grain yield.

Key words : Genetic variability and divergence, oats

Oat (*Avena sativa* L.) is a cereal crop that is used worldwide for human food and animal feed. Compared to other cereal crops, oat is reputed to be better suited for production under marginal environments, including cool wet climates and soils with low fertility (Hoffmann, 1995). But its food grain use is now more focused on its benefits as a health food. Oat is a constituent of breakfast cereal in most developed countries.

The main objective in any plant breeding programme is to evolve promising and desirable varieties, possessing high yielding potential. Sufficient success has been achieved by genetic manipulation in the improvement of cereals and it is now possible to augment the grain yield potential of oat also. Success of plant breeding programme is largely dependent on the extent of genetic variability present in the population. The genetic facts are inferred from phenotypic observations. This observed variability may be grouped with the help of suitable parameters like phenotypic and genotypic coefficient of variation, heritability and genetic

advance to ascertain the basis for selection.

The extent of genetic variability and divergence for yield and other characters are useful in selecting desired plant types. The evaluation also helps in determining the comparative merit of different genotypes with respect to different characters which will provide basis for selecting appropriate parents for crosses. The selection of the genotypes can be done based on the information about various genetic parameters.

Variability refers to the presence of differences among the individuals of a plant population. Variability results due to the differences either in the genetic constitution of the individuals of a population or in the environment in which they are grown. The knowledge of the nature and magnitude of variation present in base material is of great importance for effective selection of superior genotypes from breeding material. Hence, it is essential that base population should possess a large amount of heritable variation. Therefore, the present study was undertaken to know genetic variability and genetic divergence study in 30 genotypes of oat crop.

MATERIALS AND METHODS

The present investigation was undertaken at Agricultural Research Station, Beechwal, Bikaner during rabi season of 2013-14. The climate of the region is typically hyper-arid which is characterized by extremes of temperature during summer and winter with aridity of atmosphere and salinity of rhizosphere. The average rainfall is about 260 mm, which is mostly received during July-September. The experimental material comprised of 30 genotypes of oats (*Avena sativa* L.) obtained from AICRP on Forage Crops and Utilization, ARS, Bikaner. The experimental material was laid out in a randomized block design (RBD) with three replications during **rabi** 2013-14. Each plot consisted of two rows each of 4.0 m length. The spacing between row to row was 25 cm. Normal and uniform cultural operations were followed during the crop season to raise a good crop. The experiment was sown on 20 November 2013 under irrigated conditions with the basal application of 40 kg N+40 kg P_2O_5/ha. While 40 kg N/ha was applied as top dressed 30 DAS. The observations were recorded on individual plant basis on five competitive randomly selected plants from each replication for plant height, leaf length, leaf width, panicle length and grains per panicle. While data were recorded on plot basis for days to 50 per cent panicle emergence, green fodder yield, dry matter yield, days to maturity, straw yield, seed index and grain yield.

The data were subjected to analysis of variance adopting standard statistical methods (Panse and Sukhatme, 1985; Singh and Choudhary, 1979). The coefficients of phenotypic and genotypic variations were calculated by using the formulae suggested by Burton (1952). Expected genetic advance was estimated as per the formula suggested by Johnson *et al*. (1955). Mahalanobis (1936) D^2 statistic as described by Rao (1952) was used following Tocher's method (Rao, 1952) for grouping the different genotypes into clusters.

RESULTS AND DISCUSSION

The mean, range, coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean are presented in Table 1. The mean values of the genotypes showed a wide range for all the characters. The estimates of genotypic coefficient of variation (GCV) were high (›20%) for leaf : stem ratio, dry matter yield (q/ha), seed index, green fodder yield (q/ha) and grain yield (q/ha). Whereas it was moderate (10-20%) for plant height (cm), tillers per metre row length, panicle length (cm), grains per panicle and straw yield (q/ha). Phenotypic coefficient of variance (PCV) was high (›20%) for leaf : stem ratio, dry matter yield (q/ha), seed index, green fodder yield (q/ha) and grain yield (q/ha). Whereas it was moderate (10-20%) for plant height (cm), tillers per metre row length, leaf length (cm), leaf width (cm), panicle length (cm), grains per

TABLE 1

Estimates of range, genotypic and phenotypic coefficients of variation, heritability (broad sense %) and genetic advance of different characters of oat genotypes

S. No.	Characters	Mean	Range	G. C. V. (%)	P. C. V. (%)	Heritability (%)	GA as % of mean
1.	Days to 50% flowering	113.13	107.66-123.33	3.097	4.25	52.90	4.64
2.	Days to maturity	149.68	147.0-154.66	1.09	1.63	44.40	1.49
3.	Plant height (cm)	85.82	68.80-109.76	10.42	11.35	84.20	19.7
4.	Tillers/meter row length	99.40	74.00-148.66	15.60	17.32	81.20	28.97
5.	Leaf : stem ratio	1.24	0.60-2.60	35.49	40.01	78.70	64.88
6.	Leaf length (cm)	31.83	23.50-36.10	7.9	12.41	40.50	10.36
7.	Leaf width (cm)	1.37	1.0-1.83	9.49	19.61	23.40	9.46
8.	Panicle length (cm)	22.10	18.9-27.26	10.43	12.08	74.60	18.57
9.	Grains/panicle	48.85	38.0-60.33	11.63	14.4	65.20	19.34
10.	Dry matter (%)	15.99	12.92-17.95	6.15	8.74	49.80	8.99
11.	Dry matter yield (q/ha)	20.33	5.63-38.55	38.17	40.29	89.60	74.35
12.	Seed index	3.49	2.26-5.26	21.01	23.45	80.20	38.77
13.	Straw yield (q/ha)	46.14	31.36-62.66	17.82	19.48	83.60	33.57
14.	Green fodder yield (q/ha)	126.59	34.73-227.90	35.92	38.08	89.00	69.81
15.	Grain yield (q/ha)	13.4	8.36-21.40	21.07	23.61	79.70	38.76

panicle and straw yield (q/ha). Heritability estimates were moderate (50>75%) for days to 50 per cent flowering, panicle length (cm) and grains per panicle. While it was low (<50%) for days to maturity, leaf length (cm), leaf width (cm) and dry matter (%). Expected genetic advance as per cent over mean was high (›20%) for the characters, namely, tillers per metre row length, leaf : stem ratio, dry matter yield (q/ha), seed index, straw yield (q/ha), green fodder yield (q/ha) and grain yield (q/ha). Whereas genetic advance as per cent of mean was medium (10-20%) for plant height, leaf length panicle length, and grains per panicle. Low genetic advance as per cent over mean(<10%) was observed for days to 50 per cent flowering, days to maturity, leaf width (cm) and dry matter (%).

Average intra-and inter-cluster D^2 values among 30 genotypes (Table 2) revealed that clusters III and IV had only one genotype showing that both the genotypes were highly divergent from each other. The intra-cluster distance was maximum (18.23) in cluster II followed by cluster I (13.12). Average inter-cluster D^2 values were also calculated. The maximum (111.77) inter-cluster distance was observed between clusters II and IV and minimum (33.47) inter-cluster distance was present between clusters I and III. The clusters II and IV having maximum inter-cluster distance showed that their members were far apart from each other, while members of clusters I and III having minimum inter-cluster distance were quite close. Other inter-cluster distances

were categorized as low (<50), medium (50-100) and high (>100). The clusters I and II and clusters III and IV had medium inter-cluster distances, while clusters I and III, I and IV, II and III had low inter-cluster distance.

The distribution pattern of all the genotypes in four different clusters is presented in Table 3. Maximum numbers of genotypes 23 were present in cluster I followed by cluster II with five genotypes. Rest of the clusters, namely, III and IV had single genotype in each cluster. Based upon the cluster mean performance (Table 4), the cluster III had low mean values for days to 50 per cent flowering and days to maturity. It also had high mean value for leaf length (cm), panicle length and grains per panicle. While cluster IV had high mean value for plant height, tillers per metre row length, leaf width, dry matter (%), dry matter yield, seed index, straw yield, green fodder yield and grain yield. Cluster II had high mean value for leaf : stem ratio (cm).

Analysis of variance indicated existence of significant variability among the genotypes for all the 15 characters. The significant variation for these yield and yield related traits observed in the base population could be utilized to improve this crop by using simple breeding methods. The range of phenotypic variability was high for all the characters. The phenotypic variation is not a precise criterion for judging the amount of genotypic variation present in population. Therefore, the genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance were worked out in the present study because these provide a better estimate and amount of genetic variability present for each trait in the experimental material.

Comparison of coefficient of variance indicated that the phenotypic coefficient of variance was higher than the genotypic coefficient of variance for all the characters which indicated effect of environment on the expression of characters. Among all the characters, both high GCV and PCV were observed for leaf : stem ratio,

TABLE 2
Average intra-and inter-cluster distance based on corresponding D^2 values

Clusters	I	II	III	IV
I	13.12	50.63	33.47	47.35
II		18.23	37.31	111.77
III			0.0	66.30
IV				0.00

TABLE 3
Clustering pattern of different genotypes in different clusters

Cluster	No. of genotypes	Genotypes
I	23	JO-09-504, NDO-1709, RSO-59, JHO-10-1, JO-03-97, JO-04-11, JHO-10-2, NDO-10, OS-6, OS-403, KENT, OL-1775, JHO-2012-5, OL-1709, JHO 822, JO-03-99, RO-19, JHO-2012-1, UPO-10-2, OL-125, UPO-212, SKO-188 and JHO-2012-4
II	5	UPO-10-1, UPO-05-1, UPO-06-1, SKO-167 and SKO-170
III	1	OS-387
IV	1	NDO-711

dry matter yield (q/ha), seed index, green fodder yield (q/ha) and grain yield (q/ha) in comparison to other characters indicating the presence of high amount of genetic variability for these characters. Selection for these characters would be effective because the response to selection is directly proportional to the variability present in the experimental material. Medium GCV and PCV were observed for plant height (cm), tillers per metre row length, panicle length (cm), grains per panicle and straw yield (q/ha).The significant variability for most of the traits was commonly reported in natural population of oats. Matiello *et al.* (1999) and Altaf *et al.* (2003) reported wide genetic variability. High and significant variability was reported by Kumar *et al.* (2005), Shekhawat *et al.* (2007), Nirmalkumari *et al.* (2013) and Roy *et al.* (2013) for morphological characters.

       Genetic coefficient of variance does not provide the clear indication of proportion of heritable components of variation. The heritability estimate of a quantitative character is very important as phenotypic expression of a genotype may be altered by environment at various stages of its development. Heritability indicates the effectiveness with which selection for genotypes can be done on the basis of its phenotypic variation. It expresses the extent to which individual phenotypes are determined by their genotypes. The heritability estimates serve as a useful guide to the breeder because selection would be fairly easy for the

characters with high heritability. Thus, there would be a close correspondence between the genotypes and phenotypes due to a relatively smaller contribution of the environment to phenotype. But for a character with low heritability, selection may not be as effective due to the masking effect of environment on genotypic effect. The response to selection depends upon the relative magnitude of heritable variation present in relation to the phenotypic variation. Therefore, it is desirable to partition observed variability into its heritable and non-heritable components. Burton (1952) suggested that GCV along with heritability would give a better idea about the efficiency of selection. Thus, a character with high GCV and high heritability will be more valuable in selection programme. In the present investigation, heritability estimates were moderate (50>75%) for days to 50 per cent flowering, panicle length (cm), grains per panicle and grain yield (q/ha). While it was low (<50%) for days to maturity, leaf length (cm), leaf width (cm) and dry matter (%). The heritability estimates alone do not provide reliable information about the gene governing the expression of a particular character and this does not provide the information of the amount of genetic gain that would result from the selection of best individuals. Johnson *et al.* (1955) had pointed about that the heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting the response to selection. In the present

TABLE 4

Mean values of oat genotypes present in different clusters for different characters

Cluster	Characters							
	Day to 50% flowering	Days to maturity	Plant height (cm)	Tillers/meter row length	Leaf : stem ratio	Leaf length (cm)	Leaf width (cm)	Panicle length (cm)
I	112.33	149.35	88.37	102.51	1.16	31.66	1.38	21.58
II	117.27	151.60	71.23	77.87	1.77	32.41	1,31	23.35
III	111.00	148.67	76.27	86.33	1.10	32.80	1.50	27.27
IV	112.00	149.00	109.77	148.67	0.67	31.87	1.57	22.73

Cluster	Characters						
	Grains/ panicle	Dry matter (%)	Dry matter yield (q/ha)	Seed index	Straw yield (q/ha)	Green fodder yield (q/ha)	Grain yield (q/ha)
I	47.55	16.08	22.84	3.68	48.60	141.93	14.07
II	52.13	16.00	7.05	2.45	33.15	44.34	9.33
III	59.67	12.92	10.82	2.70	38.00	83.77	10.53
IV	51.67	17.04	38.55	5.27	62.67	227.90	21.40

investigation, genetic advance was estimated for all the traits. Expected genetic advance as per cent over mean was high (›20%) for tillers per metre row length, leaf : stem ratio, dry matter yield (q/ha), seed index, straw yield (q/ha), green fodder yield (q/ha) and grain yield (q/ha). It was moderate (10-20%) for plant height (cm), leaf length, panicle length and grains per panicle. For the rest of the characters, it was low.

Heritability and genetic advance are two complementary concepts. Thus, heritability values may be used to estimate the genetic advance through selection for predicting the utility and value of selection. In the present investigation, high heritability along with high genetic advance was observed for tillers per metre row length and green fodder yield (q/ha) which indicated that these characters might be governed by additive genetic variance and hence simple selection procedure would be effective in the improvement of oat genotypes. It was low for days to maturity, leaf length (cm) and leaf width (cm). However, none of the characters showed medium heritability and medium to low genetic advance.

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