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GENETIC DIVERGENCE IN OAT (*AVENA SATIVA* L.) GERMPLASM

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ABSTRACT

Genetic diversity in 2576 oat germplasm lines using multivariate technique of principal component analysis followed by Euclidean cluster analysis indicated considerable diversity in the material. Study revealed the importance of 100-groat weight, 100-grain weight and seed width towards genetic divergence.

Key words: Oat, genetic divergence, principal component analysis.

A logical way to start any breeding programme is to survey the variation present in the germplasm. Precise information on the nature and degree of genetic divergence helps the plant breeder in choosing the diverse parents for purposeful hybridization [1–3]. In a breeding programme progenies derived from diverse crosses are expected to show a broad spectrum of genetic variability, providing a greater scope for isolating transgressive segregates in the advance generations [4–6].

MATERIALS AND METHODS

A set of 2576 diverse genotypes of oat were evaluated in an augmented design. Each entry had single row of 1 m length, placed 40 cm apart. Data were recorded on eleven quantitative traits.

Nonhierarchical Euclidean clustering method [7, 8] based on the principal component was followed for grouping of the genotypes.

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RESULTS AND DISCUSSION

The 2576 germplasm lines were grouped into 12 nonoverlapping clusters. Appropriateness of these clusters was tested by sequential F test which revealed that the 12-cluster arrangement was most appropriate for this set of materials. The cluster strength varied from 151 in cluster XI to 279 in cluster IX. The pattern of distribution of these germplasm lines into 12 clusters clearly showed diversity among the materials studied.

Estimates of cluster means, standard deviation, standard error and coefficient of variation for each trait (Table 1) showed that genotypes with medium heading duration, longer leaf, medium stature, high seed length, 100-grain and groat weight were grouped in cluster XI. The genotypes of cluster IV had taller plant and longer panicle, while genotypes with short stature and more grains per panicle were grouped in cluster V and cluster VIII, respectively. Early genotypes were included in cluster IX.

Coefficient of variation within and over the clusters was maximum for grains per panicle, followed by 100-grain and groat weight, leaf length and width, panicle length, seed width and plant height. Days to heading and maturity had less coefficient of variation.

The intracluster distances varied from 1.98 (cluster IX) to 2.90 (cluster VIII). Almost similar intracluster values suggested that the cluster compositions were fairly homogeneous. The maximum intercluster distance (9.95) was observed between clusters IV and VIII and minimum between clusters VII and X (Table 2).

The 12 cluster can be divided into three major groups (I, II, III). Group I consists of 10 clusters (I, II, III, V, VI, VII, IX, X, XI, XII) with the intercluster distance ranging from 2.04 (between cluster VII and X) to 3.84 (between I and VI). Groups II and III had one cluster each, i.e. IV and VIII, respectively. The distance between groups I and II was maximum, i.e. 7.18 (between clusters III and IV) while these two groups were separated from each other by a minimum distance of 3.58 (between clusters IX and IV). Group III separated from group II by a maximum distance of 9.95. Maximum distance was observed between groups I and III was 9.51 (between clusters I and VIII), and minimum between clusters VI and VIII (3.80).

Genotypes grouped in the same cluster are expected to have little genetic divergence in respect of aggregate of the 11 characters studied and crossing between members of the same cluster is not likely to produce desirable recombinants. The parental genotypes should be chosen on the basis of intercluster distance (Table 2) which represents the index of genetic diversity among clusters. For simplicity, mean statistical distance was computed and it was considered as truncation. The mean statistical distance (3.80) may be considered as a guide, and parents belonging to different clusters should be selected in such a way that distance

Table 1. Cluster means, standard deviation, standard error and coefficient of variation for eleven characters in oat germplasm

Cluster	No. of genotypes	Parameter	Days to heading	Leaf length (cm)	Leaf width (cm)	Plant height (cm)	Days to maturity	Panicle length (cm)	Grains per panicle	Seed length (cm)	Seed width (cm)	100-grain weight (g)	100-groat weight (g)
I	213	Mean	106.5	34.0	1.9	112.0	148.8	25.4	49.8	12.5	3.4	4.2	3.1
		S.D.	5.9	5.8	0.3	11.5	5.2	3.8	11.4	1.0	0.4	0.7	0.5
		S.E.	0.4	0.4	0.0	0.8	0.4	0.3	0.8	0.1	0.0	0.1	0.0
		C.V.%	5.0	17.1	14.4	10.3	3.5	15.1	22.9	7.8	11.7	16.0	16.6
II	264	Mean	102.6	33.6	1.7	128.2	146.1	26.1	51.2	12.7	2.6	3.2	2.3
		S.D.	5.7	5.2	0.2	12.4	5.4	4.1	11.7	0.8	0.3	0.5	0.4
		S.E.	0.3	0.3	0.0	0.8	0.3	0.2	0.7	0.1	0.0	0.0	0.0
		C.V.%	5.5	15.5	14.4	9.7	3.7	15.6	22.8	6.1	12.1	16.2	17.5
III	218	Mean	104.2	35.4	1.8	122.1	150.6	26.0	53.7	15.1	3.0	4.4	3.3
		S.D.	5.6	6.1	0.3	12.2	4.8	4.3	13.2	1.0	0.3	0.6	0.5
		S.E.	0.4	0.4	0.0	0.8	0.3	0.3	0.9	0.1	0.0	0.0	0.0
		C.V.%	5.3	17.1	15.2	10.0	3.2	16.4	24.9	6.4	15.5	12.6	14.1
IV	206	Mean	110.4	40.8	2.0	133.4	149.2	38.9	71.5	12.9	2.4	3.0	2.2
		S.D.	6.1	6.7	0.3	12.3	5.4	3.9	14.9	0.9	0.3	0.5	0.4
		S.E.	0.4	0.5	0.0	0.9	0.3	0.3	1.0	0.1	0.0	0.0	0.0
		C.V.%	5.5	16.4	17.5	9.2	3.6	10.1	20.9	6.8	12.2	16.8	17.7
V	204	Mean	114.6	36.8	1.8	95.4	151.3	24.1	46.7	13.1	2.7	3.4	2.5
		S.D.	6.4	5.6	0.3	10.1	5.3	3.7	11.1	0.9	0.3	0.1	0.4
		S.E.	0.4	0.4	0.0	0.7	0.4	0.3	0.8	0.1	0.0	0.0	0.0
		C.V.%	5.5	15.2	15.9	10.6	3.5	15.3	23.7	7.3	12.1	15.5	17.3
VI	197	Mean	120.1	35.0	2.0	119.1	156.2	29.1	66.4	12.6	2.4	2.8	2.1
		S.D.	5.6	5.8	0.3	13.5	3.6	4.3	13.4	0.9	0.3	0.5	0.4
		S.E.	0.3	0.4	0.0	1.0	0.3	0.3	1.0	0.1	0.0	0.0	0.0
		C.V.%	4.6	16.7	14.7	11.3	0.3	14.8	20.2	7.3	12.7	18.0	18.8

(Contd.)

Table 1 (contd.)

Cluster	No. of genotypes	Parameter	Days to heading	Leaf length (cm)	Leaf width (cm)	Plant height (cm)	Days to maturity	Panicle length (cm)	Grains per panicle	Seed length (cm)	Seed width (cm)	100-grain weight (g)	100-groat weight (g)
VII	212	Mean	108.5	47.5	1.8	127.8	152.3	27.8	59.0	13.8	2.9	4.0	2.9
		S.D.	5.1	5.8	0.2	10.3	4.4	3.8	11.8	1.0	0.4	0.7	0.5
		S.E.	0.3	0.4	0.0	0.7	0.3	0.3	0.8	0.1	0.0	0.1	0.0
		C.V.%	4.7	12.2	14.1	8.1	2.9	12.8	20.0	7.0	12.6	18.0	16.4
VIII	187	Mean	110.3	42.0	2.0	122.1	150.7	29.2	96.3	13.0	2.6	3.3	2.4
		S.D.	6.4	6.5	0.3	13.0	5.3	4.6	14.4	1.1	0.3	0.6	0.5
		S.E.	0.5	0.5	0.0	1.0	0.4	0.3	1.1	0.1	0.0	0.0	0.0
		C.V.%	5.8	15.6	15.3	10.6	3.5	15.6	15.0	8.1	12.3	19.0	20.0
IX	279	Mean	101.4	33.8	1.8	106.1	139.3	25.7	53.2	13.3	2.7	3.6	2.6
		S.D.	5.2	5.6	0.3	11.3	4.7	3.7	12.4	0.9	0.3	0.5	0.4
		S.E.	0.3	0.3	0.0	0.7	0.3	0.2	0.7	0.1	0.0	0.0	0.0
		C.V.%	5.2	15.4	15.0	10.7	3.3	14.3	23.4	6.7	11.1	14.9	15.8
X	230	Mean	109.5	47.4	2.2	124.1	147.0	25.8	56.1	13.0	2.6	3.2	2.4
		S.D.	5.5	5.8	0.3	11.6	5.3	3.9	12.4	1.0	0.3	0.5	0.4
		S.E.	0.4	0.4	0.0	0.8	0.4	0.3	0.3	0.1	0.0	0.0	0.0
		C.V.%	5.0	12.3	12.3	9.4	3.6	15.2	22.1	7.4	11.6	16.6	17.3
XI	151	Mean	109.5	48.6	2.3	118.5	151.2	31.2	64.2	14.9	3.3	4.8	3.5
		S.D.	5.2	6.0	0.3	13.1	5.3	4.6	13.9	0.9	0.4	0.7	0.5
		S.E.	0.4	0.5	0.0	1.1	0.4	0.4	1.1	0.1	0.0	0.1	0.0
		C.V.%	4.8	12.3	13.2	11.1	3.5	14.6	21.6	6.2	11.7	14.4	15.0
XII	215	Mean	110.8	40.2	2.6	124.2	149.6	30.0	54.8	12.6	2.7	3.3	2.5
		S.D.	6.0	6.1	0.2	13.1	5.4	4.3	13.6	0.9	0.3	0.5	0.4
		S.E.	0.4	0.4	0.0	0.9	0.4	0.3	0.9	0.1	0.0	0.0	0.0
		C.V.%	5.4	15.2	9.2	10.6	3.6	14.4	21.0	7.2	12.1	15.6	17.1

Table 2. Mean values of intracluster (in bold) and intercluster distances (D) in oat germplasm

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**2.13**											
II	2.43	**2.03**										
III	2.75	2.61	**2.15**									
IV	6.14	4.76	7.18	**2.82**								
V	2.53	2.84	3.16	4.41	**2.18**							
VI	3.84	2.96	3.69	3.98	3.52	**2.21**						
VII	2.90	2.33	2.97	3.99	2.51	2.82	**2.09**					
VIII	9.51	6.02	7.20	9.95	7.05	3.80	5.12	**2.90**				
IX	2.56	2.17	3.15	3.58	2.30	3.26	2.81	6.57	**1.98**			
X	3.10	2.30	2.89	6.13	2.89	2.77	2.05	4.87	2.90	**2.07**		
XI	2.81	2.50	2.38	6.21	2.81	3.30	2.47	6.85	3.00	2.72	**2.26**	
XII	2.61	2.58	2.40	5.19	2.72	2.88	3.00	7.05	2.75	2.89	2.66	**2.13**

between two clusters is at least 3.80, i.e. the mean statistical distance. Genotypes within the clusters should be selected on the basis of other considerations such as disease reaction, quality, lodging index etc. Thus, hybridization between genetically distant genotypes should result in promising breeding materials [9–13].

The principal components corresponding to the two largest eigen values supplied by the two best orthogonal vectors indicated that 100-groat weight (21.3%), 100-grain weight (21.1%) and seed width (16.8%) were the most important primary cause of divergence having recorded high linear functions in the first component (Table 3). Leaf length (19.5%) followed by panicle length (11.9%), leaf width (10.6%) and plant height (9.9%) were the secondary cause of divergence as they had highest linear function in the second component. Thus, it is clear that these are the basic attributes of plant architecture which needed greater attention.

Table 3. Contribution of different quantitative characters to the total diversity based on the first two principal components in oat germplasm

Variable	Principal component	
	Eigen vector 1	Eigen vector 2
Days to heading	7.6	2.1
Leaf length	1.2	19.5
Leaf width	2.7	10.6
Plant height	4.2	9.9
Days to maturity	2.2	8.7
Panicle length	7.3	11.9
Grains per panicle	7.6	9.2
Seed length	7.9	7.3
Seed width	16.8	4.3
100-grain weight	21.0	8.3
100-groat weight	21.2	8.2

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