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

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SUMMARY

Genetic diversity among 50 genotypes was carried out using Mahalanobis D^2 statistics for 16 characters. Based on the D^2 values, all genotypes were grouped into seven clusters depending upon the similarity in the expression of their genetic divergence. Maximum number of genotypes were grouped in cluster VI (12) followed by cluster IV (11), I (9), II (8), III (4) and clusters V and VII had three genotypes each. The highest intra cluster D^2 value was observed for cluster V (5.304) followed by cluster I (5.174), cluster III (5.054), cluster VI (4.771), cluster II (4.470), cluster VII (4.501) and cluster IV (4.104).The average inter cluster distance was found to be highest between cluster V and VII (8.558), cluster III and V (7.165), cluster III and VI (5.919) whereas the lower inter-cluster distance was observed between clusters II and IV (5.075), followed by clusters IV and VI (5.328). Out of 16 characters, contribution of seedling dry weight was maximum (39.76%), followed by seed yield/plant (13.71%), seed vigour index II (10.94%), axis length (8.41%) and germination% (7.43%), whereas the remaining characters like 100-seed weight (4.33%), seed vigour index I (2.78%), seedling length (2.61%), days to maturity (2.37%), days to 50% flowering (2.29%), number of tillers/plant (1.80%), flag leaf length (1.47%), inetrnode length (1.22%), number of spikelets/ panicle (0.16%), peduncle length (0.65%) and plant height (0.08%) contributed very little for divergence.

Key words : Genetic divergence, oat, yield traits, genotypes

Oat (*Avena sativa* L.) a constituent of family Poaceae ranks sixth in the world cereal production. It is cultivated for use as food, feed and fodder. The crop has been adopted well by the farmers because of its multi-cut nature and high yield of nutritious palatable fodder. The loss of genetic diversity has become an important problem both in natural plant populations and in important crop species. This loss led to calls for the genetic conservation of crop germplasm (Frankel and Bennett, 1970).The pre-requisite of any breeding programme is the evaluation of existing genetic stock. The success of a systematic breeding programme depends mainly on judicious selection of promising parents from the gene pool. In order to initiate any effective breeding programme to create more variability for further advancement in seed yield and for effective crossing programme, it is pre-requisite to have a thorough understanding about the mutual relationship among the yield and its component traits. It is also essential to classify the available germplasm into clusters for getting more useful transgressive segregants.

MATERIALS AND METHODS

The field experiment was conducted on 50 genotypes of oat at Forage Research Area and Seed Science & Technology Laboratory of the Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar during rabi 2014-15. All the genotypes were grown in randomized block design (RBD) with three replications, each genotype having single row of three metre length with 15 cm plant to plant and 45 cm row to row spacing. All the recommended package of practices were adopted to raise a good crop. The observations were recorded for plant height (cm), flag leaf length (cm), peduncle length (cm), internode length (cm), axis length (cm), number of spikelets/panicle, number of tillers/plant, days to 50 per cent flowering, days to maturity, 100-seed weight (g), germination (%), seedling length (cm), seedling dry weight (g), seed vigour index I, seed vigour index II and seed yield/plant (g). Seed quality parameters viz., standard germination test (%), shoot length (cm), root length (cm), seedling length (cm) and seedling dry weight (g) were estimated as per

ISTA (2009), while seed vigour indices were calculated according to the method suggested by Baki and Anderson (1970).

The mean values of these 16 characters were subjected to Mahalanobis (1936) D^2-statistics to measure genetic divergence and clusters were formed by Tocher's method as suggested by Rao (1952).

RESULTS AND DISCUSSION

The mean sums of squares due to genotypes for all the traits studied were highly significant thereby revealing sufficient amount of genetic variation among the genotypes for all the 16 characters studied.

To quantify genetic divergence between any two genotypes or group of genotypes, Mahalanobis' D^2 statistics (1936) as described by Rao (1952) was used and the genotypes were grouped into different clusters on the basis of Ward's minimum variance method (Fig. 1)

All the 50 oat genotypes were grouped into seven clusters based on the relative magnitude of their D^2 values in such a way that genotypes in each cluster had smaller D^2 value than between the clusters. Table 1 reveals the distribution pattern of genotypes in different clusters. Cluster pattern revealed that clusters VI and IV were the largest ones with 12 and 11 genotypes, respectively, followed by cluster I with nine genotypes, cluster II with eight genotypes, cluster III with four genotypes, and clusters V and VII each with three genotypes.

The intra-and inter-cluster D^2 values among genotypes are given in Table 2. The results showed that inter-cluster distances were more than intra-cluster distances which indicated the presence of narrow genetic variation within a cluster. The highest intra cluster D^2 value was observed for cluster V (5.304) followed by cluster I (5.174), cluster III (5.054), cluster VI (4.771), cluster II (4.470), cluster VII (4.501) and cluster IV (4.104).

When diversity was studied among the clusters based on the inter-cluster D^2 values, it showed a range of 8.558 to 5.328. The average inter-cluster distance was found to be highest between cluster V and VII (8.558), clusters III and V (7.165), clusters V and VI (6.931) whereas the lower inter clusters distance was observed between cluster II and IV (5.075), followed by clusters IV and VI (5.328). The higher inter-cluster distance

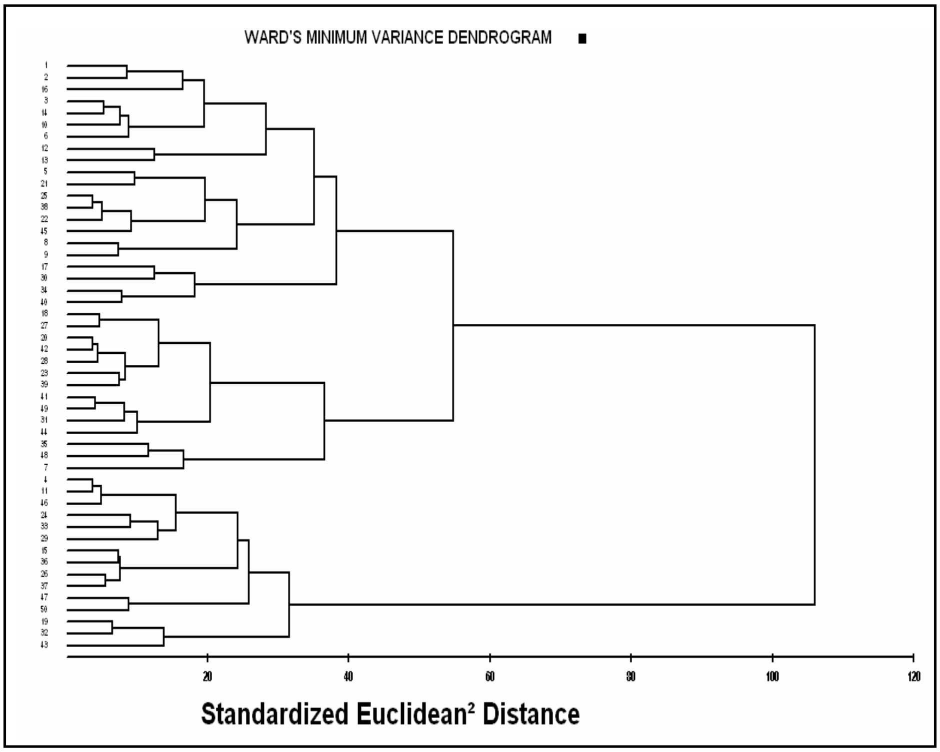

Fig. 1. Clustering by Ward's minimum variance method.

TABLE 1

Clustering of fifty genotypes of oat on the basis of D^2 statistics

Cluster	No. of genotypes	Name of genotypes
I	9	HFO-24, HFO-28, HFO-298,, HFO-30, HFO-243, HFO-118, HFO-79, HFO-221 and HFO-222
II	8	HFO-75, HFO-446, HFO-455, HFO-851, HFO-447, JHO 2000-4, HFO-87 and HFO-112
III	4	HFO-302, HFO-698, HFO-833, Dunav
IV	11	HFO-314, HFO-613, HFO-439, HJ-8, HFO-687, HFO-452, OS-377, HFO-114, JHO-822, HFO-709 and NDO-I
V	3	HFO-834, Kent, HFO-82
VI	12	HFO-52, HFO-192, RO-19, HFO-453, HFO-784, HFO-688, HFO-244, HFO-842, HFO-467, HFO-843, Kalojan and JHO 2006-2
VII	3	HFO-413, HFO-715 and SKO-90

TABLE 2

Average intra (diagonal) and inter (above diagonal) cluster D^2 values in fifty genotypes of oat

Cluster	I	II	III	IV	V	VI	VII
I	5.174	5.478	5.846	5.481	6.453	6.106	6.879
II		4.470	5.883	5.075	6.075	5.514	6.579
III			5.054	5.515	7.165	5.919	6.448
IV				4.104	5.703	5.328	6.589
V					5.304	6.931	8.558
VI						4.771	5.508
VII							4.501

indicated the presence of more diversity among the genotypes included in these clusters.

Out of 16 characters, contribution of seedling dry weight was maximum (39.76%) for divergence, followed by seed yield/plant (13.71%), seed vigour index II (10.94%), axis length (8.41%) and germination% (7.43%), whereas the remaining characters like 100-seed weight (4.33%), seed vigour index I (2.78%), seedling length (2.61%), days to maturity (2.37%), days to 50% flowering (2.29%), number of tillers/plant (1.80%), flag leaf length (1.47%), internode length (1.22%), peduncle length (0.65%), number of spikelets/panicle (0.16%) and plant height (0.08%) contributed very little for divergence (Table 3). Similar results were reported by Achleitner *et al.* (2008), Ahmed *et al.* (2011) and Krishna *et al.* (2014) in oat.

The cluster means for seed yield /plant and its component characters are presented in Table 4. The data revealed considerable differences among all the clusters for most of the characters studied. It was evident that plant height was lowest in cluster IV (111.624 cm) and the highest in cluster III (125.408 cm). Cluster V recorded the highest flag leaf length (25.667 cm), while cluster II recorded the lowest (20.542 cm). Peduncle length was recorded minimum for cluster III (29.008 cm) and maximum for cluster V (37.200 cm). Cluster V revealed the highest mean value, for internode length (13.444), whereas cluster VII had the lowest mean value (11.178). For axis length, cluster V (33.700) had the highest mean value while cluster VII had the lowest mean value (23.922). Cluster III showed the maximum mean value (54.283) for number of spikelets/panicle and cluster VII showed the lowest mean value (47.822). For number of tillers/plant, the highest mean value was possessed by cluster III (12.600) and the lowest value was possessed by cluster VII (9.289). Days to 50 per cent flowering was the highest in cluster VII (86.44) and the lowest in cluster IV (82.303). Cluster VII recorded the highest mean value of days to maturity (114.667) and the lowest in cluster IV (107.212). 100-seed weight was recorded maximum for cluster V (3.327) and the minimum for cluster I (2.237).

Cluster I revealed the highest mean value for germination% (84.407), whereas cluster VII had the

TABLE 3

Contribution of different characters towards divergence

S. No.	Source	Times ranked 1st	Contribution towards divergence (%)
1.	Plant height (cm)	1	0.08
2.	Flag leaf length (cm)	18	1.47
3.	Peduncle length (cm)	8	0.65
4.	Internode length (cm)	15	1.22
5.	Axis length (cm)	103	8.41
6.	No. of spikelets/panicle	2	0.16
7.	No. of tillers/plant	22	1.80
8.	Days to 50% flowering	28	2.29
9.	Days to maturity	29	2.37
10.	100-Seed weight (g)	53	4.33
11.	Germination (%)	91	7.43
12.	Seedling length (cm)	32	2.61
13.	Seedling dry weight (g)	487	39.76
14.	Seed vigour index I	34	2.78
15.	Seed vigour index II	134	10.94
16.	Seed yield/plant (g)	168	13.71

TABLE 4

Cluster mean for sixteen characters in 50 oat genotypes

Characters Clusters	Plant height (cm)	Flag leaf length (cm)	Peduncle length (cm)	Internode length (cm)	Axis length (cm)	No. of spikelets/ panicle	No. of of tillers/ plant	Days to 50% flowering	Days to maturity	100-Seed weight (g)
I.	120.496	25.126	31.100	12.207	31.256	49.044	11.126	84.593	111.556	2.237
II.	115.750	20.542	32.246	13.004	30.512	49.746	10.675	85.708	110.000	2.574
III.	125.408	22.458	29.008	11.667	25.017	54.283	12.600	84.417	108.333	2.258
IV.	111.624	22.576	33.870	13.158	27.715	51.688	10.333	82.303	107.212	2.419
V.	118.222	25.667	37.200	13.444	33.700	53.844	11.667	83.333	110.444	3.327
VI.	112.767	23.653	33.061	12.236	28.683	48.769	10.646	84.194	108.556	2.268
VII.	111.956	22.578	29.444	11.178	23.922	47.822	9.289	86.444	114.667	2.286
GM	115.674	23.144	32.463	12.520	28.948	10.804	10.804	84.193	104.493	2.409

contd.

Table 4 contd.

Characters Clusters	Germination (%)	Seedling length	Seedling dry weight	Seed vigour index I	Seed vigour index II	Seed yield/ plant (g)
I.	84.407	37.785	0.086	3202.666	7.247	9.416
II.	84.000	36.750	0.087	2952.863	7.649	7.434
III.	80.667	35.900	0.086	3119.617	7.023	9.019
IV.	80.788	38.686	0.089	3035.542	7.069	8.897
V.	82.444	38.056	0.096	3042.289	7.143	8.648
VI.	78.944	35.108	0.078	2784.661	6.767	7.550
VII.	77.556	35.856	0.073	2887.689	5.820	6.759
GM	81.407	36.914	0.085	2990.444	7.047	8.300

lowest mean value (77.556). Cluster IV showed the maximum mean value (38.636) for seedling length and cluster VI showed the minimum mean value (35.108). For seedling dry weight, the highest mean value was possessed by cluster V (0.096) and the lowest value was possessed by cluster VII (0.073). Seed vigour index I was the highest in cluster I (3202.666) and the lowest in cluster VI (2784.661). Seed vigour index II was recorded minimum for cluster VII (5.820) and maximum for cluster II (7.649). For seed yield/plant, cluster I (9.416) had the highest mean value, while cluster VII had the lowest mean value (6.759). Similar results were reported by, Achleitner *et al.* (2008), Ahmed *et al.* (2011), Bibi *et al.* (2012), Vaisi *et al*. (2013), Krishna *et al.* (2014) and Jaipal and Shekhawat (2016) in oat. They reported diversity among the genotypes measured by inter-cluster distance was adequate for improvement of forage oat by hybridization and selection. Tiller number, number of leaves and flag leaf length were the main traits for selection of high yielding types.

This comparison indicates that clusters I, III and V had better cluster means for most of the characters. Therefore, clusters I, III and V might be considered better for selecting genotypes which may be used as promising parents for hybridization to obtain high heterotic response and thus better segregants for seed yield in forage oat.

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