

Genetic diversity analysis in durum wheat (*Triticum durum* Desf.)

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ABSTRACT

The genetic distance for 28 genotypes of durum wheat was estimated using Mahalanobis D^2 statistic. The results showed adequate genetic diversity for all the traits among all possible pairs of genotypes with values ranging from 9.33 to 583.88. The results revealed that 28 genotypes were grouped into seven clusters. Cluster II was the largest cluster comprised 13 genotypes followed by cluster I with seven genotypes, while cluster III and V contained two and three genotypes, respectively. Cluster IV, VI and VII were solitary clusters. The maximum inter cluster distance appeared between clusters I and VI ($D=21.0$) followed by clusters I and IV ($D=20.5$) and clusters III and VII ($D=20.2$) which may serve as potential parents for hybridization programme. The genetic divergence had little to do with the geographic factor as noticed by the random distribution of genotypes into various clusters. Thousand grain weight, plant height and grain yield per plant were the major attributes governing the total genetic divergence (86%) in durum wheat.

Keywords: D^2 statistic, genetic divergence, multivariate analysis, durum wheat

The knowledge on genetic distance is successfully utilized in wheat by several workers (Singh and Singh, 1994; Suri and Sharma, 1999; Bergale *et al.*, 2001; Dobariya *et al.*, 2006; Yadav *et al.*, 2006; Gashaw *et al.*, 2007 and Marker and Tripathi, 2008) for parents to be used in hybridization programme to obtain desirable segregants. Mahalanobis D^2 technique is a unique tool for identifying degree of divergence in a biological population at genetic level. Therefore, an effort has been made to assess the genetic diversity using ten traits recorded in 28 genotypes of durum wheat.

MATERIALS AND METHODS

The experimental material comprised of 28 diverse genotypes of durum wheat (*Triticum durum* Desf.) collected from germplasm maintained at Wheat Research Station, Junagadh Agril. University,

Junagadh, Gujarat. The field experiment was laid out in a randomized block design with three replications at Wheat Research Station, Junagadh Agril. University, Junagadh during *rabi* 2009-10. Each entry was sown in a single row of 2 m length with inter and intra row spacing of 22.5 cm and 10 cm, respectively. The recommended agronomic practices and plant protection measures were followed timely for the successful raising of the crop. Five random plants were selected from each plot for recording the observations on seed yield/plant and its component traits. The data were subjected to the statistical analysis as suggested by standard method of Mahalanobis (1936). The criteria used by Torcher as described by Rao (1952) were followed for making group constellations.

RESULTS AND DISCUSSION

The Mahalanobis D^2 statistic showed adequate genetic diversity between genotypes with D^2 values

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Table 1 Composition of clusters based on D^2 values in durum wheat

Cluster No.	No. of genotypes		Genotypes included in cluster	Source
I	07	04	HI 8498, HD 4702, HI 8680, HI 8682	IARI, New Delhi
		03	JD-07-02, JD-07-33, JD-07-04,	JAU, Junagadh
II	13	02	HI 8681, HD	IARI, New Delhi
		05	JD-07-08, JD-07-45, JD-07-17, GW 1258, GW 1250	JAU, Junagadh
		01	MPO 951	JNKVV
		01	UPD 32	GBPUT, Pantnagar
		01	MACS 2846	ARI, Pune
		01	AKDW 4021	PDKV, Akola
		01	GW 1151	SDAU, Vijapur
		01	RAJ 1555	RAU, Rajasthan
III	02	02	JD-07-46, JU 110	JAU, Junagadh
IV	01	01	WHD 931	HAU, Hisar
V	03	01	PDW 292	PAU, Ludhiana
		01	DWR 1001	UAS, Dharwad
		01	GW 1139	SDAU, Vijapur
VI	01	01	PDW 276	PAU, Ludhiana
VII	01	01	RAJ 6564	RAU, Rajasthan

between all possible pairs ranged from 9.33 between HI 8498 and HI 8682 to 583.88 between HI 8680 and DWR 1001. Based on D^2 statistics, 28 genotypes were grouped into seven clusters. The distribution of 28 genotypes in different clusters is given in Table 1. The D^2 values have been used for grouping of genotypes in the clusters in such a way that the genotypes in the cluster had smaller D^2 values than between clusters. Cluster I comprised of seven genotypes (four from IARI, New Delhi and three from JAU, Junagadh). Cluster II was the largest among all clusters which included 13 genotypes such as IARI, New Delhi (2), JAU, Junagadh (5) and one each from different parts of India as shown in Table 1. Cluster III and V contained two and three genotypes, respectively. The cluster IV, VI and VII were solitary cluster which comprised of one genotype from HAU, Hisar; PAU, Ludhiana and RAU, Rajasthan, respectively.

The genotypes belonging to same state or origin were grouped into different clusters and the genotypes belonging to different origin were grouped into a same cluster. Thus, the grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical

distribution of the genotypes. Murty and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater genetic diversity than geographic distance. Further, the free exchange of seed materials among the different regions consequently causes character constellations because of human interference and material may lose its individuality. Bergale *et al.* (2001); Gartan and Mittal (2003); Dwivedi *et al.* (2002) and Dobariya *et al.* (2006) also reported that genetic diversity was independent of geographic regions.

The average intra and inter cluster distance (D) between two populations (Table 2) varied from 5.4 (cluster III) to 9.6 (Cluster V) and 8.5 (Between cluster IV and VI) to 21.0 (between cluster I and VI), respectively. The three clusters *viz.*, IV, VI and VII had only single genotype indicating solitary clusters so their intra cluster distances were zero. The maximum inter cluster distance appeared between clusters I and VI ($D=21.0$) followed by clusters I and IV ($D=20.5$) and clusters III and VII ($D=20.2$). It has been well established that more genetically diverse parents used in hybridization programme, the greater will be the chance of obtaining high heterotic

Table 2 Average Inter and Intra (Diagonal and bold) cluster distance (D) values in durum wheat

Cluster	I	II	III	IV	V	VI	VII
I	7.1	15.4	11.1	20.5	18.7	21.0	18.8
II		9.3	13.8	11.7	13.2	11.4	13.0
III			5.4	19.8	18.7	17.6	20.2
IV				0.0	13.9	8.5	10.1
V					9.6	16.2	15.7
VI						0.0	15.7
VII							0.0

hybrids and broad spectrum of genetic variability (Arunachalam, 1981). Therefore, in the present study, the genotypes belonging to these clusters separated by high statistical distance could be used in hybridization programme. In this context, based on high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from clusters VII and IV with the genotypes of cluster I, which may lead to the generation of broad spectrum of favourable genetic variability for grain yield improvement in durum wheat.

The cluster means for ten characters are presented in Table 3 with their per cent contribution toward the

total genetic divergence. The perusal of Table 3 revealed that 1000 grain weight contributed maximum (52.91%) as a first ranker towards the total divergence with its average ranging from 39.66 g in cluster IV to 53.60 g in cluster I. The next major contribution came from plant height with 17.20 % and grain yield per plant with 16.670 % contribution towards divergence. The plant height ranged from 62.20 cm (cluster III) to 78.91 cm (cluster V), while grain yield per plant ranged from 8.14 g (cluster III) to 18.32 g (cluster VII). On the other hand, rest of the traits had lower contribution (below 5 %) towards the total genetic divergence. A considerable diversity of 86.78 % was observed due to these three characters. Hence, selection for divergent parents

Table 3 Cluster means of genotypes for different characters in durum wheat

Cluster	Ear head emergence	Grain filling period	Maturity period	Plant height (cm)	No. of effective tillers per plant	Spike length (cm)	No. of spikelets per spike	Peduncle length (cm)	1000 grain weight (g)	Grain yield per plant (g)
I	63.43	41.90	118.33	63.36	6.91	5.64	14.90	30.96	53.60	15.07
II	64.15	38.13	119.54	64.44	7.28	6.11	15.17	31.54	44.75	11.38
III	59.83	38.00	116.50	62.20	5.57	5.95	14.43	27.40	49.47	8.14
IV	70.33	43.67	120.00	66.90	7.00	6.63	16.23	30.03	39.66	13.10
V	67.78	37.67	117.67	78.91	7.18	6.61	14.81	33.32	44.28	12.29
VI	71.00	41.67	112.67	60.63	6.47	6.27	15.00	30.93	40.30	7.36
VII	68.00	38.00	118.33	63.90	8.93	6.10	15.60	26.37	42.56	18.32
Mean	64.65	39.33	118.90	65.49	7.07	6.05	15.05	31.02	46.83	12.33
S.Em±	0.91	0.75	1.10	1.00	0.51	0.30	0.57	0.76	0.70	0.50
C.V.%	2.50	3.39	1.62	2.71	12.79	8.87	6.78	4.32	2.66	7.15
% Contribution	4.50	3.17	0.79	17.20	0.00	1.06	0.26	3.44	52.91	16.67
towards divergence	(17)	(12)	(03)	(65)	(00)	(04)	(01)	(13)	(200)	(63)

Value in parenthesis indicates the number of times the characters achieved first rank in contribution towards the total genetic divergence.

based on these characters would be useful for heterosis breeding in durum wheat.

The cluster means for different traits were reflections of genetic differences with each other for one or more traits prevalent among the clusters. The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. Cluster III was early for ear head emergence, while cluster V was good for grain filling period. The cluster VI was good for days to maturity and dwarf plant height, while cluster VII was good for more number of effective tillers per plant and maximum grain yield per plant. Cluster IV had higher mean length of main spike and number of spikelets per spike. Cluster I was good for peduncle length and maximum grain weight. Therefore, intercrossing of genotypes involved in these clusters would be useful for inducing variability in respective characters and their rationale improvement for increasing the grain yield in wheat. The genotypes with high mean values of character in any cluster as well as high D^2 values between clusters can be used either for direct adoption or for hybridization programme in order to breed for better genotypes of durum wheat.

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