Estimation of Genetic Divergence among Durum Wheat (*Triticum durum* L.) Genotypes for Yield and Yield Contributing Traits

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Selection of genetically distant parents is an essential step in hybridization. Twenty indigenous germplasm lines were evaluated to assess the genetic diversity and variability. The significant mean sum of squares for all the ten characters indicated the presence of variability. All the 20 genotypes were grouped into five clusters according to Tocher's method. Cluster I and IV evolved as large clusters comprising six genotypes each. The maximum inter-cluster distance was exhibited by genotypes of cluster V, while it was minimum in the genotypes of clusters III, suggesting that crossing between the genotypes included in these two clusters is expected to generate heterotic combinations and thus facilitate the isolation of desirable genotypes.

Key Words: Genetic diversity, Inter-cluster, Durum wheat (*Triticum durum* L.)

Durum wheat is next only to bread wheat in respect of area (1.5 million hectares) as well as production of 1.2 million tones (Anonymous, 2007). In breeding programme, selection of parents for hybridization is largely based upon genetic diversity, wide adaptation and high yielding potential. Genetic diversity for selecting parents plays a key role in genetic variability in varietal improvement programme for any crop. The germplasm consisted of large number of varieties, lines, genotypes, landraces and wild relatives available to breeder, serve as a reservoir for providing variability in different traits under consideration for improvement but a very limited number can be used in hybridization programmes. Hence, involvement of genetically diverse parents /lines based on desirable character combinations collectively is essential to obtain more heterotic recombinants in segregating generations and thus offers a scope for maximum improvement. The present study was, therefore, planned to assess genetic diversity in 20 genotypes of durum wheat using Mahalanobis D^2 statistics (1936) to cluster the genotypes in different groups based on genetic divergence.

Materials and Methods

Twenty genotypes, *viz*, MPO 1153(MOJO/AIRON), RAJ 6566(RAJ 6496/POW215), NIDW 309(YAVA ROS-79), NIDW 295(BHOOMI R33/P1A1A), RD 1093(T. POLOnicum Lsp7/RD 75), AUKD 2(KYDRANASS A 30/SiLVER5), AUKD 3(MAGH72/RUFO//ALG86/RU/3/ALTAR 84/ALD/4), HI 8591(HI 8144/NI 8652), UAS 2021(THB/CEP7780//2MUSK-4), RD 1008(PBW 34/RD 20), DBPY 02-3(RAJ1555/DCB 93), RD 1009(PBW 34/RD 20), HD 4713(SCOT 29/TARA 1//AJAIA2), UAS 404, HI 8638(SEL.BUTTAH), HI 8645(HI8185/MESSAP 10//HI 8381/MESSAPI0), PDW 300(PDW 2421/PDW 233/PDW 232), MASA 499, NIDW 37(PARRON 1/MRB 5895//PARRON 1) and DBPY 04-5(DUKEM 12/2RASCON 21//POW 233) of durum wheat of different agroecological origins were evaluated in randomized block design with three replications at the Field Experimentation Centre of the Department of Genetics and Plant Breeding, College of Agriculture, Allahabad Agricultural Institute, Allahabad during *rabi* 2007-08 to assess genetic diversity using Mahalanobis D^2 statistics (1936). Paired row plot of 3m length of each genotype was grown in each replication with row-to-row and plant -to-plant spacing of 25 and 5cm, respectively. Recommended package of practices were followed to raise a healthy crop. Ten randomly selected plants from each plot per replications were scored for recording observations on the following traits, *viz.*, number of tillers per meter, number of tillers per plant, spike length (cm), number of seeds per spike, 1000 seed weight (g), biological yield per plant (g) and seed yield per plant (g). However, data on days to 50% heading, days to 50% flowering and days to maturity, were recorded on plot basis (the number of days taken from the date of sowing to 50 % head emergence/flowering/physiological maturity in each replication, respectively and were averaged). Mahalanobsis D^2 statistics was used to assess genetic diversity. Genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952).

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Results and Discussion

Analysis of variance (Table 1) revealed significant differences among genotypes for all the characters studied indicating sufficient genetic variation among the genotypes for all the traits in the present study.

The twenty durum wheat genotypes were grouped into 5 clusters on the basis of their relative magnitude of D^2 values, in such a way that of D^2 values within the cluster were much lower than those between clusters (Table 2). As regards the distribution pattern of genotypes in different clusters, the cluster I and IV were the largest with 6 genotypes each, followed by cluster III with four genotypes, cluster II with three genotypes and cluster V with only one genotype. The clustering pattern indicated that there was little association of genetic diversity with ecogeographical distribution of genotypes. Genotypes with different ecogeographical origins were grouped into same cluster, which, suggested that geographical diversity does not necessarily represent genetic diversity.

These results are in agreement with the findings of Khumkar *et al*. (2000), Bergale *et al*. (2001), Gupta *et al.* (2002), Dwivedi and Pawar (2004) and Goel *et al*. (2005). However, to some extent the genotypes related by their place of origin have sown tendency to group in the different clusters, which may be because of dependence upon the directional selection pressure that leads to evolve homeostatic mechanism that would favour consistency of the associated characters resulting in indiscriminate clustering as reasoned by Bergale *et al*. (2001) and Dwivedi and Pawar (2004). The clustering of genotypes from different ecogeographic locations into one cluster could be attributed to the frequent exchange of breeding material from one place to another and in further selection in different genotypic regions which could result in genetic drift as reasoned by Lad *et al.* (2002).

The genetic divergence is an outcome of several factors such as exchange of breeding material, genetic drift, natural variation and artificial selection other than ecological and geographical diversification. Therefore, selection of parents for hybridization should be based on genetic diversity rather than geographic diversity to get more heterotic recombinants and desired transgressive segregates. However, caution should be taken in selecting very divergent genotypes because such crosses may not yield proportionate heterotic response. Therefore, a hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high means for almost all component traits and further these divergent parents should have better combining ability to give results proportionate to heterotic response. Arunachalam (1981) also observed that more diverse the parents within its overall limits of fitness, the greater are the chances of heterotic expression of F^1's and a broad spectrum of variability in segregating generations.

The intra and inter-cluster average D^2 values given in Table 3. The magnitude of intra-cluster distances measures the extent of genetic diversity between the genotypes of the same cluster. Inter-cluster distance is a measure of genetic distance between two clusters. The intra-cluster distances ranged from 0.00 (cluster V) to 338.24 (cluster I) which indicated the presence of

Table 1. Mean sum of squares obtained from the analysis of variance for various traits in durum wheat

Characters	Sources of variation		
	Replications	Genotypes	Error
d.f	2	19	38
Days to 50% heading	4.46	45.29**	1.62
Days to 50% flowering	1.05	59.17**	1.78
Days to maturity	4.51	28.91**	2.32
Number of tillers per meter	0.74	701.66**	1.77
Effective tillers per plant	0.73	2.84*	0.11
Spike length	0.02	3.80*	0.03
Number of grains per spike	0.90	33.34**	1.01
1000-grain weight	0.49	92.73**	0.27
Biological yield per plant	81.12	252.97**	4.64
Seed yield per plant	5.85	21.10**	2.13

** Significance at 1% level of significance
* Significance at 5% level of significance

Table 2. Clustering of 20 genotypes of durum wheat based on D^2 statistics

Cluster	Number of genotypes	Genotypes
I	6	MPO 1153, AUKD 2, HI 8638, PDW 300, RD 008, RD 1009
II	3	NIDW 309, HI 8591, RAJ 6566
III	4	HI 8645, MASA 499, DBPY 04-5, DBPY 02-3
IV	6	NIDW 295, USA 404, HD 4713, NIDW 37, RD 1093, USA 2021
V	1	AUKD 3

sufficient amount of diversity among different clusters. The inter-cluster distances varied from 406.399 (between I and III) to 5744.840 (between III and V). The inter-cluster D^2 value was much higher than any intra-cluster average D^2 values. The maximum genetic diversity was observed between cluster III and V (5744.840) followed by that between cluster I and V (4719.071). Among these clusters, the cluster I, III and V performed outstanding on the basis of better cluster means for most of the characters. Out of three possible combinations from these selected clusters, most divergent cluster combinations were I and V as well as III and V. The involvement of genotypes belonging to cluster V with genotypes of clusters I and III in hybridization is advocated in order to achieve high transgressive segregates for grain yield, as these clusters showed maximum genetic diversity for grain yield and its components.

The mean values of different clusters for 10 characters are given in Table 4. The cluster means for different traits were reflections of genetic differences prevalent among the clusters. The clusters showed difference with each other for one or more traits. Cluster I took least time for days to 50% heading and days to 50% flowering. Cluster II took least time for days to maturity. Cluster III had highest mean values for number tillers per meter row and effective tillers per plant. The highest cluster mean for spike length was exhibited by cluster V, while number of grains per spike by cluster I. The cluster V exhibited the highest cluster mean value for 1000 seed weight, biological yield per plant and seed yield per plant. Thus cluster I, III and V performed outstanding on the basis of better cluster means for most of the characters. Hence, the genotypes included in these clusters were divergent as well as had higher mean values for important yield component traits. Therefore, hybridization involving genotypes of clusters I, III and V is advocated in order to achieve high yielding segregates by utilizing the crosses between cluster I and V and III and V. The genotypes, *viz.*, AUKD 3, PDW 300, RAJ 6566, HI 8638, DBPY 04-5 and MPO 1153 were found more divergent and having superior performance for most of the yield component traits can be utilized in crossing programme to generate useful genetic variability in segregating durum wheat populations.

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Table 3. Intra (diagonal) and inter-cluster D^2 (average) values among 20 durum wheat genotypes

Cluster number	I	II	III	IV	V
I	338.24	471.73	406.39	845.01	4719.07
II		266.28	422.86	427.24	3914.64
III			217.77	956.98	5744.84
IV				223.28	2573.89
V					0.0

Table 4. Mean values of different clusters for 10 characters in durum wheat

Cluster	Characters									
	Days to 50% heading	Days to 50% flowering	Days to maturity	Number tillers per meter	Effective tillers per plant	Spike length	Number of grains per spike	1000 grain weight	Biological yield per plant	Seed yield per plant
I	78.88	86.33	123.55	101.48	11.52	8.09	59.30	41.84	57.07	28.77
II	79.00	86.66	121.11	119.74	11.88	7.9	56.33	37.99	58.66	25.44
III	79.50	87.25	121.25	121.36	12.76	7.48	56.28	37.99	58.66	27.33
IV	81.83	89.88	124.61	111.29	11.87	8.18	57.19	36.41	57.90	27.05
V	80.00	87.33	123.33	101.69	11.27	8.55	57.87	48.61	65.67	33.67
GM	79.66	87.40	122.76	111.60	11.89	8.18	58.34	51.91	59.59	28.25
CV(%)	2.11	2.21	2.52	2.20	0.57	0.29	1.66	0.86	3.56	2.41

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