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RESEARCH ARTICLE

GENETIC DIVERGENCE ANALYSIS IN DURUM WHEAT (*TRITICUM DURUM* L. DESF.)

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ABSTRACT

Genetic divergence study on durum wheat *Triticum durum* L. Desf. consisted 150 genotypes of diverse sources. The experiment was conducted at Indian Agricultural Research Institute, Regional Wheat Research Station, Indore in Rabi 2006-07 in Randomized Complete Block design replicated twice. Standard package and practices was given to raise healthy crop. Results of analysis revealed their association into sixteen clusters. Approximate configurations of the clusters based on the D² values. According to Mahalanobis' D² statistic it can be concluded that grain yield per plant, days to maturity, plant height, day to flowering hectolitre weight and 1000-grain weight contributed the most towards genetic diversity. Genotypes ID-1124 and GW-1 can be used as donors for more number of grains per spike while, few genotypes from cluster VIII and X can be utilized to improve the grain yield as a whole. The clustering pattern-indicated no parallelism between the geographical distribution and genetic diversity. Genotypes selected from the two major divergent groups *i.e.* MACS 3125, HI-8591, HI-8651, HI-8620, WHD937, IWP-5004-1, HI-8381, GW-1139, GW-1225, HI-8639 (from group-I) and IWP -5013, D-061, D-062, IWP-5007, P-6046 (from group -II), may be used as parents for hybridization after determining their combining abilities so as to obtained considerably better and promising segregats and recombinants.

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INTRODUCTION

Wheat is one of the major staple food crops, which provides 20% of the total food calories of human requirement (Bhawsar, 1993). Both in terms of area and production, India is the second largest wheat growing country in the world. Hard wheat is the second most important wheat species grown in the country. Approximately, 10 per cent of the total wheat area in the country is under *durum* wheat. Basically, in India, limited efforts have been made to improve *durum* wheat. Indian *durum* has very narrow genetic base for agronomic characters and disease resistance (Agrawal and Pandey 1978). To diversify the genetic base of Indian *durums*, work is in progress at various centers of ICAR and SAUs. Grain yield in wheat, as in other crops, is a complex character and is dependent on its main components, *viz.*, spike number per plant and grain weight per spike. These components, in turn, are also complex and their expression is again dependent on several morphological and developmental traits, which are interrelated with each other. Thus for the improvement of grain yield, knowledge of genetic variability for characters of economic importance and cause and effect relationship of yield and yield

components for the available genotypes are of utmost importance which help in planning of the future breeding programme. Besides these, the degree of divergence and relative contribution of different components to total divergence using Mahalanobis D² technique helps in the identification of selection parameters to be used as criteria for the improvement of yield in wheat.

Improvement in yield and quality of a crop is normally achieved by selection of a genotype with desired combination of characteristics existing in nature or by artificial methods like hybridization or mutation. The selection after hybridization is favoured by the genetic variations in the natural populations. The importance of genetic diversity within the overall limits of fitness for realizing heterotic response in the F₁ and broad spectrum of variability in segregating generation has been emphasized by Joshi and Dhawan (1996) Murty and Arunachalam (1966) and Bhatt (1970). In order to assess the degree of diversity, D²- statistic based on multivariate analysis developed by Mahalanobis (1936), has been adopted by Jain *et al.* (1979), in hexaploid wheats and by Lee and Kaltsikes (1973). It appears that relatively very little information is available on tetraploid wheats, hence an attempt has been made to study the genetic diversity in 150 *durum* genotypes.

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MATERIAL AND METHODS

Keeping in view the importance of genetic diversity in breeding for high yielding varieties studies on genetic divergence of 150 genotypes of *Triticum durum* were carried out at Regional Wheat Research Station, IARI, Indore Madhya Pradesh during Rabi season of 2006-2007. The 150 wheat accessions of indigenous and exotic origin were collected from Gujarat, Maharashtra, Karnataka and Andhra Pradesh. The experiment was laid in complete randomized block design replicated twice. Each genotype was accommodated in a double row plot of 2 m length with row to row and plant to plant spacing of 23 and 5 cm respectively. The sowing was done on 28th November 2006 by dibbling the seeds in rows. The experiment was conducted under irrigated and high fertility conditions. Proper care was taken to keep only one plant at each spot. Five plants were selected randomly from each plot and observation were recorded for the following characters

- (A) **Pre- harvest observations:-** (1) days to glowering (2) days to maturity
 (B) **Post- harvest observation:-** (1) Plant height(cm) (2) spikes per plant
 (3) spike length (cm) (4) number of grains per spike (5) grain weight per spike (g) (6) grain weight per plant (g) (7) 1000 grain weight (g) (8) hectolitre weight (g) (9) plot yield (g) were recorded as per recommended protocols.

Analysis of variance of plot means for different characters were calculated as per standard procedures. To study the genetic diversity in the above characters the data were processed further by using Mahalanobis D^2 statistics describe by Rao (1952). The simultaneous test of differences between mean values of the character studies was done by using Wilks criterion (Rao 1952). Treating D^2 as the square of generalized distance, all genotype were grouped into a number of clusters, according to the method described by Tocher (Rao 1952). The average intra-cluster and inter cluster distances were calculated following the method described by Singh and Choudhri (1970).

RESULTS AND DISCUSSION

The present study was undertaken to evaluate the performance of *durum* wheat genotypes for various yield and its attributes.

Multivariate analysis of divergence

The quantitative assessment of genetic divergence was carried out for all the 11 characters, using Mahalanobis' D^2 statistic. To estimate the D values, correlated means of characters were transformed to standard uncorrelated characters, using pivotal condensation method. The statistical distance between pairs of treatments was obtained as the sum of squares of the differences between the pair of corresponding uncorrelated values of any two treatments considered at a time.

Grouping of lines into various clusters

All the genotypes were grouped into sixteen clusters to study the genetic variability existing among the lines. Tocher's

procedure (Singh and Chaudhary, 1977) was adopted for grouping. The distribution of line into clusters and their mean values have been presented in Table 4.6 and 4.7, respectively.

Intra and Inter cluster divergence D^2 Values

The average D^2 values within (intra) and between (inter) clusters were calculated as per the procedure given by Singh and Chaudhary (1977) and have been presented in Table- 4.8.

The average intra-cluster divergence (diagonal D^2 values in the table) varied from 2.3 to 5.2. The maximum intra cluster divergence was found within the cluster V (5.2) followed by cluster I (4.9), XI (4.9) and the minimum was found within the cluster XII (2.3). Cluster VIII contained the maximum number of genotypes (23) followed by cluster II (16 genotypes), X (15 genotypes) while clusters VI, XV, and XVI contained 2 genotypes each. The maximum inter cluster distance was reported between X and XV (80.6); followed by between clusters VIII and XV (74.6) and between clusters XIV and XV (73.1), while minimum between cluster VI and IX (9.1). The cluster mean values for various characters (Table 4.7) ranged from 61.3 to 87.8 for days to flowering, 110.0 to 128.5 for days to maturity, 46.90 to 113.0 cm for plant height, 3.73 to 6.68 for productive tillers, 6.58 to 8.88 cm for spike length, 29.0 to 51.3 for grains per spike, 1.07 to 2.77 g for grain weight per spike, 34.3 to 56.5 for 1000-grain weight, 3.20 to 13.21 g for grain yield per plant, 75.3 to 82.7 g for hectolitre weight and 249 to 935 g grain yield per plot.

The present investigation on genetic divergence was carried out using Mahalanobis' D^2 statistics. The study revealed a wide diversity among the genotypes studied. As the genotypes were grouped into XVI clusters. Cluster VIII had the maximum number of genotypes (23) followed by cluster II (16 genotypes), cluster X, (15 genotypes), cluster IV (14 genotypes), V (13 genotypes), IX (12 genotypes), VII and XIV (10 genotypes each), XII (9 genotypes), III (8 genotypes), I (6 genotypes), XIII (5 genotypes), XI (3 genotypes), VI, XV and XVI (2 genotypes each).

The inter cluster D^2 value was maximum (80.6) between cluster X and cluster XV and thus genotypes included in these clusters were genetically most divergent. Cluster means for various characters in present study indicated that grain yield per plant followed by days to maturity, plant height, days to flowering, hectolitre weight and 1000- grain weight contributed the most towards divergence among genotypes.

Earliest maturity genotypes were observed in cluster V, whereas, genotypes having higher spike length and more number of grains per spike in cluster VI. In cluster VIII, genotypes with high grain weight per spike and high 1000-grain weight were grouped and in cluster X, genotypes grouped with high grain yield per plant and with high hectolitre weight. It was observed that genotypes ID-1124 and GW-1 can be used as donors for more number of grains per spike while, few genotypes from cluster VIII and X can be utilized to improve the grain yield as a whole. The present investigation was an attempt to determine various parameters of genetic divergence among 150 genotypes of *durum* wheat. The method used to assess genetic divergence was Mahalanobis' D^2 statistic

Table 1. Composition of the clusters of durum wheat genotypes

Cluster	No. of genotypes	Composition of the genotypes
I	6	Karnataka local, P 6046, IWP 5013, HD 4709, D 061 and D 062
II	16	NIDW 9, AKDW 3347, MACS 2846, HI 7747, HI 8664, HI 8666, CDW 04, UAS 412, Raj 6069, NIDW 70, WHO 913, VD 2001-14, MACS 2694, NI 5749, NIDW 295 and PDW 231
III	8	Yuk, B 206, HI 8652, HI 8653, CPAN 6139, PDSN 689, PDSN 694 and A 624
IV	14	HD 4703, HI 8620, Altar 84, AKDW 4240, HI 8663, AKDW 4155, Raj 6516, MPO 1106, DWL 5023, DWR 185, WH 912, PDW 34, PDW 274 and DBP 01-09
V	13	N 59, Meghdoot, Bijaga Yellow, Local yellow, Local red, A 28, DWR 137, GW -2, MACS 9, Jay, Vijay, Amrut and NP -4
VI	2	ID 1124 and GW -1
VII	10	Sarangpur local, Dahod local, Mandsaur local, Bansi local, Trinakaria, Kathia 25, Guji 'S', Line 1172, PDSN 1085 and Baxi 228-18
VIII	23	B 146, MPO 215, WH 896, PDW 233, PDW 245, PDW 274, HD 4672, HD 4692, HD 4693, HD 4696, HI 8381, HI 8591, HI 8620, HI 8627, HI 8629, HI 8651, AKDW 4151, WHD 938, PDW 304, WHD 937, CPAN 6038, MPO 321 and Raj 911
IX	12	JU 12, Bijaga Red, Jairaj, IWP 5019, Raj 6566, IWP 5061, HI 8656, HI 8668, MACS 3493, HI 8657, HD 4502 and HD 4530
X	15	MACS 3125, Raj 1555, PDW 215, GW 1139, HD 4695, HI 8498, HI 8634, HI 8639, B 4446-WA, B 4447-WA, HI 8662, UAS 404, PWD 306, UAS 410 and PDW 303
XI	3	B 662, B 414 and IWP 5007
XII	9	A 739, Raj 6562, HD 4694, HI 8550, HI 8661, MACS 3313, CPAN 6236, DWR 1006 and DBP 01-11
XIII	5	Malvi local, Motia, NP 404, A 206 and A 9-30-1
XIV	10	NIDW 15, ID 2644, HG 110, MACS 1967, IWP 5004-1, IWP 5070, HI 8645, GW 1225 and HD 4685
XV	2	Sawer local and ED 2398 - A
XVI	2	ID 1221 and CIMB 1538

Table 2. Average intra and inters cluster D² value between the clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	4.9															
II	10.0	2.8														
III	11.1	10.0	4.2													
IV	16.6	9.7	9.3	2.4												
V	9.7	13.5	20.6	20.8	5.2											
VI	21.7	25.9	13.2	20.8	19.9	4.5										
VII	13.1	9.2	10.3	15.6	12.0	20.5	4.5									
VIII	27.4	9.5	14.8	10.4	29.4	19.5	20.5	2.6								
IX	14.4	12.1	16.5	9.1	15.2	21.7	14.1	16.2	3.6							
X	29.5	15.4	15.8	12.1	24.0	24.2	24.6	9.7	15.0	2.6						
XI	13.2	23.9	18.7	24.6	36.8	40.4	28.4	38.2	28.3	40.3	4.9					
XII	17.0	10.8	10.4	14.6	16.4	18.4	10.6	10.7	13.0	14.7	32.8	2.3				
XIII	16.2	17.1	19.4	26.4	14.1	24.8	10.5	29.3	11.0	23.3	32.6	21.3	3.9			
XIV	27.0	11.0	15.0	11.4	16.8	15.4	15.9	13.1	9.9	11.2	51.8	13.0	17.9	3.8		
XV	28.7	53.7	40.3	61.3	50.7	55.2	29.6	74.6	51.0	80.6	29.3	53.7	32.8	73.1	3.8	
XVI	37.7	41.1	14.8	35.9	56.1	25.5	27.6	28.3	46.2	42.9	37.5	34.3	33.1	37.6	36.0	3.2

Table 3. Mean values of the characters of the clusters

Clusters / Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
Days to flowering	70.2	70.0	76.0	70.5	61.3	69.0	73.9	73.5	66.6	68.0	73.7	72.2	74.7	68.6	87.5	87.8
Day to maturity	114.8	114.4	119.2	114.7	110.0	116.0	117.4	117.1	113.0	114.9	121.3	114.6	116.8	114.5	123.8	128.5
Plant height	81.8	81.1	83.2	81.2	105.3	99.9	113.0	83.9	91.6	81.7	46.9	101.6	105.5	109.3	107.9	100.4
Productive tillers	3.77	4.66	4.42	4.16	5.22	4.65	4.18	4.90	5.89	5.99	3.73	4.52	6.68	5.84	4.00	4.70
Spike length	7.36	6.49	8.46	6.86	7.64	8.88	6.95	7.63	6.58	6.92	7.32	6.79	6.87	7.36	7.28	8.80
Grains per spike	33.3	37.1	41.4	48.6	33.9	51.3	34.5	48.2	40.3	47.8	38.9	44.9	34.1	44.2	29.0	48.6
Grain weight / spike	1.67	2.10	2.24	2.52	1.66	2.45	1.91	2.77	1.93	2.54	1.69	2.32	1.71	2.50	1.07	2.45
1000 grain weight	49.4	54.6	52.6	50.4	49.2	48.1	54.2	56.5	44.9	52.6	39.6	49.6	48.8	55.9	34.3	49.8
Grain yield / plant	5.53	8.93	8.43	9.42	7.66	10.26	7.16	11.86	9.85	13.21	5.28	9.13	10.22	12.81	3.20	9.13
Hectolitre weight	78.4	81.8	80.7	82.6	78.7	75.3	79.0	82.5	80.8	82.7	80.8	81.7	78.0	80.2	76.8	78.5
Grain yield / plot	437	722	649	760	558	716	525	897	711	835	311	935	313	884	249	525

applied to a set of 11 characters related to productivity. These 150 genotypes were chosen from a large stock of wheat genotypes available at the Indian Agriculture Research Institute, Regional Wheat Research Station, Indore. The results so obtained in the present investigation have been discussed hereunder:

Divergence of cultivars and derivatives

The importance of genetic diversity within the overall limits of fitness for realizing heterotic response in the F_1 and broad spectrum of variability in segregating generation has been emphasized by Joshi and Dhawan (1996) Murty and Arunachalam (1966) and Bhatt (1970). Generalized distance analysis have been used by many geneticists among cultivars, within a crop under the assumption that cultivar within the group are genetically related where as diverse cultivars are classified in to different clusters. In the present study, dispersion amongst variable for aggregate effect of the 11 characters as tested by Wilk's criterion was however, highly significant indicating the existence of considerable divergence in the material under study. The clustering pattern of genotypes also confirmed the same since all the 150 wheat genotypes were classified into as many as 16 clusters on the basis of Mahalanobis D^2 statistic.

At intra cluster level, cluster V was highly diverse and comprised 13 entries, of mostly old *durum* varieties. The maximum number of genotypes were included in cluster VIII (23 genotypes) followed by cluster II (16 genotypes) and cluster X (15 genotypes). The diversity in the material was further revealed by existence of appreciable genetic diversity among the genotypes as the statistical D^2 value represents the index of genetic diversity among the clusters. It would be appropriate to make crosses between genotypes belonging to the cluster separated by high estimates of statistical differences. In view of this, the most divergent clusters i.e., cluster X and cluster XV separated by a D^2 value of 80.6 have been chosen along with other clusters nearer to these two highly diverse clusters, to group them in two broad categories as below:

Group	Highly diverse cluster	Nearer cluster	Total number of genotypes
Group I	X	VIII, XIV	48
Group II	XV	I, XI	11

On the basis of yield performance and some specialized characters, ten genotypes from group I and five genotypes from group II have been selected as being the most diverse and high yielding genotypes. The probability of getting better segregate and promising recombinants will be more if crosses are attempted between genotypes belonging to these two groups.

The compositions of genotypes with good yield of these two groups have been given hereunder:

GROUP-I	MACS 3125, HI-8591, HI-8651, HI-8620, WHD 937, IWP-5004-1, HI-8381, GW-1139, GW-1225, HI-8639
GROUP-II	IWP-5013, D-061, D-062, IWP-5007, P-6046

Genetic differences between the clusters were reflected in cluster means also. The cluster differed from each other for one or more characters. Cluster-XV and Cluster-XVI comprising two genotypes each justified their separation into different clusters by having quite low or high mean values for one or more characters. The divergent position occupied by these clusters with respect to different characters at intracluster level is quite in agreement with that obtained by these clusters at intercluster level. The present investigation revealed that days to maturity, grains per spike, and days to flowering, 1000-grain weight and grain yield per plant were the main contributors for the diversity as reflected by their intracluster group means.

Earliest maturity genotypes were observed in cluster V, whereas, genotypes having higher spike length and more number of grains per spike in cluster VI. In cluster VIII, genotypes with high grain weight per spike and high 1000-grain weight were grouped and in cluster X, genotypes grouped with high grain yield per plant and with high hectolitre weight. It was observed that genotypes ID-1124 and GW-1 can be used as donors for more number of grains per spike while, few genotypes from cluster VIII and X can be utilized to improve the grain yield as a whole. These results were in accordance with the findings of Ahmed *et al.* (1980), Yadav and Murty (1981), Raut *et al.* (1985), Kuruwadi (1988), Sethi *et al.* (1992), Singh (1992), Bhawsar (1993) Mehta and Dhagat (1992), Shoran and Tondan (1995), Jain *et al.* (1979), Mel'nikova *et al.* (2009), Milotova *et al.* (2008), Laidò *et al.* (2013) and Terzi *et al.* (2007).

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