

# Effect of environment on clustering pattern in bread wheat (*Triticum aestivum* L.)

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## SUMMARY

Genetic divergence was studied in 40 genotypes of bread wheat to assess the nature and extent of diversity over four diverse environments. Analysis of variance (ANOVA) revealed significant genotypic differences for all the environments studied. The genotypes were grouped in eight clusters each in E-I and E-II and six clusters each in E-III and E-IV. The only genotype MP-4010 in E-III was observed most divergent among all. The maximum contribution to the divergence was made for harvest index followed by grain yield. Three genotypes (HD-2643, NIAW-34 and RAJ-3077) were screened most desirable and stable for early heading and early maturing character. Four genotypes (GW-366, HD-2733, PBW-533 and SUJATA) were found most stable for high mean grain yield.

## Key words :

Genetic divergence, Bread wheat, Inter-and intra-cluster distances, Grain yield

The germplasm, the reservoir of genetic diversity, is often exploited to most of the changing needs for developing improved crop varieties. The importance of genetic diversity for selecting parents for recombination breeding in wheat to recover transgressive segregants has been emphasized (Jatasara and Paroda, 1983). Use of diverse parents in hybridization programme can serve the purpose of combining diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain recombination. Parents be selected on the basis of multivariate  $D^2$  analysis (Mahlanobis, 1936). This technique measures the forces of differentiation at intra-and inter-cluster levels. The present study is an attempt to classify 40 genotypes of bread wheat into different groups in four diverse environments and to quantify the magnitude of genetic divergence for their further use in recombination breeding with expectation of getting potential transgressive segregants.

## MATERIALS AND METHODS

Forty genotypes of bread wheat were evaluated in randomized block design with three replications under four diverse micro-environments for two successive crop seasons (2007-08 and 2008-09) at Agricultural Research Farm, C.C.R. P.G. College, Muzaffarnagar (U.P.), India. In each replication, the genotypes were evaluated in single row plot of 3m length

with a distance of 0.3m and 0.1m between rows and plants, respectively at two different dates of sowing (25th November and 20th December) in both the years. All the standard cultural practices and irrigation schedule were followed to raise the good crop. Five competitive plants/genotypes/replications were tagged and observations on 10 yield related characters were recorded in all the environments. Per cent contributions for these characters towards divergence in all four environments were computed using the formula :

$$\text{Per cent contribution of pth character} = \frac{pN}{n(n-1)/2} \times 100\%$$

where, N is the number of possible genotypic combinations and  $n(n-1)/2$  is the number of total possible genotypic combinations among n number of genotypes. The genetic divergence analysis was conducted on data collected on individual environments and inter-and intra-cluster distances were also analysed in each environment.

## RESULTS AND DISCUSSION

The ANOVA suggested adequate genetic variability for yield and other yield related traits *Triticum aestivum* using multivariate analysis (Table 1). A perusal of this table revealed that

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**Table 1 : Per cent contribution of different characters towards divergence in different environments**

Sr. No.	Characters	Environments				Mean over environments
		E-I	E-II	E-III	E-IV	
1.	Days to 75% heading	12.13	7.55	12.88	9.00	10.39
2.	Days to maturity	13.89	8.39	12.75	9.91	11.23
3.	Plant height (cm)	10.04	10.10	5.23	8.06	8.35
4.	Tiller number	10.91	11.54	11.79	10.88	11.28
5.	Spikelets per spike	11.14	11.30	9.97	8.69	10.27
6.	Grains per spike	4.75	8.90	5.56	9.30	7.12
7.	100-grain weight (g)	7.27	10.85	9.68	7.13	8.73
8.	Grain yield (g)	12.40	8.01	11.71	14.23	11.58
9.	Biological yield (g)	7.02	10.90	8.56	10.61	9.27
10.	Harvest index (%)	10.39	12.40	11.83	12.15	11.69

the maximum contribution to the divergence was made for harvest index and minimum for grains per spike. Grain yield, tiller number and days to maturity also showed significant contribution towards divergence.

The forty genotypes of bread wheat were classified in eight clusters each in E-I and E-II (Table 2) and six clusters each in E-III and E-IV (Table 3). It was evident from these tables that the pairs of genotypes like DBW-16 and DBW-17; DL-803-3 and HW-1085; HD-2864 and RAJ-4037; MACS-2496 and PBW-502 grouped together in more than one environments, indicating that these pairs of genotypes were not divergent from each other but these were divergent from the remaining genotypes. Group of three genotypes (GW-173, NW-2036 and RAJ-4077) was found divergent from other

genotypes studied but these three were not divergent from each other. Interestingly, the relative composition of different clusters varied markedly during two crop years (2007-08 and 2008-09). Sharma and Pawar, 2007 and Yadav *et al.*, 2006 predictions were almost similar to the present one.

Statistical distances between the clusters (inter-cluster distance) represent the extent of diversity amongst the genotypes which were accommodated into different clusters. A perusal of the distance matrix (Table 4 and 5) indicated that the inter cluster distance was maximum 6.272 between clusters I and VII (in E-I), 6.709 between clusters III and VI (in E-II), 6.597 between clusters II and III (in E-III) and 6.822 between clusters I and III (in E-IV). The intra-cluster distance was the lowest 1.577

**Table 2 : Distribution of 40 genotypes of bread wheat in different clusters for environments (E-I and E-II)**

Cluster	E-I		E-II	
	Number of genotypes	Name of genotypes	Number of genotypes	Name of genotypes
I	6	DBW-14, DBW-16, DBW-17, DL-803-3, HW-1085, PBW-533	6	HD-2643, HW-2045, NIAW-34, NW-2036, RAJ-4083, UP-2620
II	5	DWR-162, GW-190, MACS-2496, MW-1012, NIAW-917	7	DBW-17, DWR-162, HD-2824, HD-1731, HUW-478, MACS-2496, PBW-502
III	6	DL-788-2, GW-173, HD-2833, MP-4010, NIAW-34, RAJ-3077	4	DL-788-2, GW-173, MP-4010, RAJ-3077
IV	5	HD-2824, HD-2733, PBW-343, PBW-502, PBW-550	11	DBW-16, DL-803-3, GW-190, GW-322, GW-366, HD-2733, HI-977, HW-1085, PBW-343, PBW-533, PBW-550
V	7	HD-2643, HD-1731, HUW-468, HW-2045, NW-1014, NW-2036, RAJ-4083	4	HD-2833, HD-2864, MW-1012, NIAW-917
VI	5	GW-322, GW-366, K-0307, K-9107, UP-2620	2	DBW-14, GW-273
VII	2	HD-2864, RAJ-4037	3	K-0307, NW-1014, RAJ-4037
VIII	4	C-306, GW-273, HI-977, SUJATA	3	C-306, K-9107, SUJATA

**Table 3 : Distribution of 40 genotypes of bread wheat in different clusters for environments (E-III and E-IV)**

Cluster	E-III		E-IV	
	Number of genotypes	Name of genotypes	Number of genotypes	Name of genotypes
I	12	GW-173, HD-2824, HD-2833, HD-2864, HD-1731, HW-468, NW-1014, NW-2036, PBW-533, PBW-550, RAJ-3077, RAJ-4083	4	GW-173, HUW-468, NIAW-917, NW-2036
II	7	DWR-162, GW-190, MACS-2496, MW-1012, NIAW-917, PBW-343, PBW-502	4	DBW-16, DBW-17, GW-190, HD-1731
III	1	MP-4010	4	C-306, HI-977, K-9107, SUJATA
IV	4	DBW-14, DBW-16, DBW-17, HW-1085	7	DL-803-3, DWR-162, HD-2824, HW-1085, MACS-2496, PBW-343, PBW-502
V	5	DL-788-2, HD-2643, HW-2045, NIAW-34, RAJ-4037	9	DBW-14, DL-788-2, HD-2643, HD-2833, MP-4010, NIAW-34, RAJ-3077, RAJ-4083, UP-2620
VI	11	C-306, DL-803-3, GW-273, GW-322, GW-366, HD-2733, HI-977, K-0307, K-9107, SUJATA, UP-2620	12	GW-273, GW-322, GW-366, HD-2864, HD-2733, HW-2045, K-0307, MW-1012, NW-1014, PBW-533, PBW-550, RAJ-4037

**Table 4 : Average inter-and intra-cluster (bold values) distances involving 40 genotypes of bread wheat in E-I and E-II**

Cluster	I	II	III	IV	V	VI	VII	VII
I	2.088 (1.869)							
II	4.055 (3.175)	1.771 (1.917)						
III	4.250 (2.654)	3.046 (3.374)	2.400 (1.809)					
IV	3.252 (3.300)	2.366 (2.359)	3.320 (3.913)	1.577 (2.047)				
V	3.909 (3.055)	2.314 (3.097)	2.788 (3.829)	2.718 (3.138)	1.802 (1.708)			
VI	2.688 (5.346)	3.308 (6.138)	3.876 (6.709)	3.907 (4.505)	3.456 (4.547)	1.919 (1.584)		
VII	6.272 (3.980)	4.638 (4.728)	3.081 (4.530)	4.704 (2.689)	4.398 (4.560)	5.660 (4.345)	2.476 (1.693)	
VIII	3.316 (5.210)	4.156 (5.334)	4.271 (6.545)	3.424 (3.951)	4.273 (4.866)	2.999 (5.345)	5.608 (3.832)	2.101 (1.615)

Values in parenthesis are for E-II

for cluster IV (in E-I), 1.584 for cluster VI (in E-II), 2.096 for cluster II (in E-III) and 1.494 for cluster II (in E-IV). This indicated that these clusters were the most compact than others. The genotypes included in clusters having more intra-cluster distance are more heterogenous that is, diverse among themselves.

Further, it is of interest to note that the genotypes released from different places were grouped together in more than one environments and some of the genotypes

released from the same place appeared to be scattered in different clusters. Thus, geographical distribution is an inferential criterion which may not always be effective in quantifying the genetic diversity between biological populations as also concluded by Dixit, 1980; Murthy and Anand, 1986 and Kumar, 2006.

**Table 5 : Average inter-and intra-cluster (bold values) distances involving 40 genotypes of bread wheat in E-III and -IV**

Cluster	I	II	III	IV	V	VI
I	2.143 (2.273)					
II	2.341 (3.434)	2.096 (1.494)				
III	5.592 (6.822)	6.597 (4.749)	0.000 (2.098)			
IV	3.770 (3.717)	4.413 (2.567)	6.198 (4.503)	2.464 (2.073)		
V	2.546 (3.051)	3.679 (2.412)	5.610 (5.039)	5.513 (3.993)	2.265 (1.800)	
VI	3.002 (4.078)	3.410 (2.885)	6.413 (3.436)	2.981 (3.029)	4.199 (3.495)	2.197 (2.263)

Values in parenthesis are for E-IV

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