Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.)

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Abstract : Fifty genotypes of bread wheat (*Triticum aestivum*) including Indian and exotic collections were evaluated for yield and other related characters. Five characters i.e., spikes /plant, grain yield/plant, plant height, flag leaf area and 1000 grain weight exhibited high variability. The remaining traits showed moderate to low variability. Following the Mahalanobis' D^2 analysis, all the 50 genotypes were grouped into eleven clusters. Genotypes of different areas often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes. This also suggested a lack of relationship between the genetic diversity and place of collection of genotypes. On the basis of the data on genetic divergence and mean performance of yield and other traits, diverse and superior genotypes, namely, NP 890, CPAN 3030, PBW 175, NI 5439, K 65, K 68, HI 1136, K 7410, Narmada –112, Sujata, CPAN 4018, PBW 321, HI 1418, Lok-1, HI 1077, WH 147, CPAN 3031, HUW 234, GW 173 and Sonalika were selected to involve in multiple crossing programme to recover transgressive segregants. Further, on the basis of cluster means, cluster III has been identified for selecting parents for incorporating early maturity, dwarfness, high flag leaf area and good harvest index; cluster IV for more grains per spike, Cluster x for number of spikes per plant; cluster XI for spike length and bold seed and cluster VI for grain yield per plant. Further, on the basis of character associations, it is argued that selection of plants with more spikes/plant, grains per spike, coupled with optimum harvest index should result in progenies with high grain yield potential in wheat. (*Key words: Wheat, Cluster analysis, Genetic divergence, Morpho-physiological traits, Variability*).

The germplasm, the reservoir of genetic diversity, is often exploited to most of the changing needs for developing improved crop varieties. It is also important that variability for economic traits must exist in the working germplasm for profitable exploitation following recombination breeding and selection. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop such as wheat to recover transgressive segregants has also been repeatedly emphasized (Murthy and Anand, 1966; Jatasara and Paroda, 1983). However, the genetic diversity of selected parents is not always based on factors such as geographic diversity/place of release or ploidy level. Hence, characterisation of genotypes should be based on sound statistical procedures such as D^2 statistic and on-hierarchial Euclidean cluster analysis. These procedures characterize genetic divergence using the criterion of similarity or dissimiliarity based on the aggregate effect of a number of agronomically important characters.

In view of these facts, fifty wheat genotypes were evaluated in this study: 1) to determine the magnitude of variability among the germplasm collection for yield and morpho-physiological traits; 2) to determine the grouping pattern of genotypes in different clusters and 3) to identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme aimed at improving grain yield potential of wheat.

Materials and Methods

Fifty genotypes collected from different centres of India (New Delhi, Indore, Wellington, Pantnagar, Powarkheda, Vijapur, Junagarh, Hissar, Ludhiana, Varanasi, Kanpur, Sanosara, Pune, Niphad and Kota) and from CIMMYT, Mexico were evaluated in a randomized complete block design with three replications at the IARI-Indore during rabi 1999-00. Each genotype was evaluated in a single row plot of 2 m length with plot to plot and plant to plant distances of 22 cm and 10 cm respectively. Recommended agronomic practices were followed to raise a good crop. The data on ten quantitative characters (Table 1) were recorded on five competitive plants in each plot.

S.Bergale, Billore Mridulla, A.S.Holkar, K.N.Ruwali and S.V.Sai Prasad

Table 1. Estimates of mean, range, co-efficient of variation (PCV and GCV) for ten characters and correlation co-efficients of grain yield with nine other characters.

Characters	Mean	Range		PCV	GCV	Correlation with grain yield
		Minimum	Maximum			
Days to Flowering	78	64	100	10.43	10.41	0.18*
Days to Maturity	128	115	139	4.00	3.97	0.34*
Plant height(cm)	94	68	130	18.20	18.17	0.39*
Flag leaf area (cm²)	21.7	16.0	30.5	16.4	15.7	-0.13*
Spike length (cm)	10.6	8.1	13.7	11.61	11.15	0.09
Spikes per plant	5.6	3.1	10.2	28.55	27.19	0.83*
Grains per spike	48.8	28.5	67.6	18.6	18.4	0.44*
1000 grain weight (g)	41.8	30.7	57.32	15.6	15.36	0.02
Grain yield/ plant (g)	9.07	4.92	17.0	27.47	26.20	
Harvest index (%)	36.6	29.4	40.2	8.59	8.45	0.39*

* Significant at 5 % level of significance.

Table 2. Distribution pattern of fifty genotypes of wheat into eleven clusters based on D^2 statistics.

Cluster No	No. of genotypes in cluster	Cluster composition
I	11	HW 888, WH 147, HD 2278, HD 977, HI 1077, HI 1418, HD 2285, HUW 234, CPAN 3031, CPAN 4018, Lok –1.
II	9	CPAN 3030, NP 890, HW 2004, Narmada 112, Narmada 4, NP 4, K65, K 68, HI 1136.
III	7	HD 2009 (Arjun), GW 173, HD 2329, Sonalika, PBW 321, HD 2428, DL 788-2.
IV	6	WH 542, Kalyanasona, CPAN 3013, Veery "S", Bob white, CPAN 2099.
V	5	WL 711, J 24, CPAN 3050, Raj 1771, HI 1011
VI	4	PBW 175, K 7410, NI 5439, KW 741
VII	2	CPAN 2045, Raj 1777
VIII	2	CPAN 2051, MACS 2496
IX	2	Hyb 65, Hindi 62.
X	1	Sujata
XI	1	Mukta

Table 3. Estimates of average intra and inter-cluster distances for eleven clusters involving fifty genotypes of wheat.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	386										
II	2057	346									
III	654	3479	534								
IV	947	2426	1756	315							
V	876	1621	1687	692	576						
VI	850	977	1796	919	680	558					
VII	2609	2787	4017	1033	1235	1720	335				
VIII	2545	3547	3807	933	1336	1902	362	263			
IX	2680	1116	4254	1939	1360	1313	1176	1787	177		
X	3418	498	5231	3277	2290	1624	2857	3606	986	0.00	
XI	1244	571	2196	1975	1079	631	2827	3126	1078	1164	0.00

Table 4. Cluster means of 10 characters which contributed for genetic divergence

Cluster	Days to flowering	Days to maturity	Plant height	Flag leaf area	Spike length	Spikes /plant	Grains /spike	1000 grain weight	Grain Yield /plant	Harvest index
I	73	125	85	21.4	10.2	4.9	44.8	42.3	7.8	38.4
II	76	128	121	20.8	10.6	6.7	52.0	44.2	11.0	31.2
III	69	122	76	20.5	9.7	5.1	32.5	45.0	7.1	39.2
IV	83	129	81	22.1	10.8	5.4	59.8	35.9	9.9	38.9
V	82	129	91	22.1	11.8	4.6	49.7	46.1	8.2	37.2
VI	79	130	99	21.8	10.9	6.5	51.5	40.1	11.4	35.9
VII	96	137	88	24.2	10.5	5.9	53.2	32.6	8.5	38.1
VIII	97	139	81	24.9	10.1	6.2	57.8	38.0	9.8	38.2
IX	89	131	114	20.4	9.9	6.5	44.5	36.4	7.5	34.3
X	83	132	130	23.9	9.9	6.9	51.3	41.3	10.0	59.4
XI	76	131	111	24.9	13.0	6.3	45.9	52.6	10.7	35.2

The mean, range, genotypic and phenotypic co-efficient of variation (GCV and PCV respectively), correlation co-efficient and genetic distances were calculated as per the standard statistical procedures. Mahalanobis' D^2 statistic was conducted to estimate the intra and inter cluster distances and to group the genotypes into different clusters. The appropriate number of clusters to group fifty genotypes were determined following the sequential pseudo F-ratio tests (Beale, 1969).

Results and Discussion

The results of the present study showed moderate to high variability for all the ten characters under study. Considerable genetic divergence was also present among the genotypes. This suggested that adequate scope is available for selection of superior and diverse genotypes for use in a programme aimed at enhancing genetic yield potential of wheat.

The data presented in Table 1 showed wide range for all the 10 characters, but the estimates of PCV and GCV were high only for five traits like spikes/plant, grain yield/plant, plant height, flag leaf area and 1000 grain weight, whereas other characters showed relatively low variability. However, there is still ample scope for selection of superior genotypes for these traits.

Based on Mahalanobis' D^2 analysis, fifty genotypes were grouped into 11 clusters with variable number of genotypes (Table 12) suggesting considerable amount of genetic diversity in the material. Genotypes were collected from various places (i.e., IARI-New Delhi, IARI-Indore, CIMMYT-Mexico, IARI-Wellington, GBPUAT-Pantnagar, DNP – Powarkheda, PAU-Ludhiana and CSSRI-Kanpur) and it was found that genotypes collected from the same place were scattered in different clusters, thus, each cluster had genotypes of different areas. This suggested that the genotypes within a cluster might have some degree of ancestral relationship.

The data of inter cluster distances (Table 3) and the mean performance of the cluster (Table 4) were used to select genetically diverse and agronomically superior genotypes from among the fifty genotypes studied. The maximum of eleven genotypes were grouped in cluster I, indicating overall genetic similarity among them. The members of clusters III & X exhibited the maximum divergence followed in descending order by the members of clusters III & IX, III & VII, III & VIII and VIII & X, respectively. The average

intra-cluster distance between the members of cluster V was the maximum followed in descending order by clusters VI, III and so on, suggesting that genotypes in cluster V were relatively more diverse than the genotypes in the above selected clusters. Two single variety clusters were formed possessing varieties like Sujata and Mukta. respectively.

Cluster means suggested that contribution of plant height was the maximum towards genetic divergence followed by days to flowering, grains per spike, 1000 grain weight and days to maturity. These results were in complete agreement with that of Singh (1992) for 1000 grain weight, Bhawsar (1993) for plant height and 1000 grain weight and Sharma et al. (1998) for grains per spike.

As the D^2 values represents the index of genetic diversity among the clusters, it would be most appropriate to make crosses between genotypes belonging to the cluster separated by high estimates of statistical distances. In view of this, the most divergent cluster i.e., cluster III and X separated by a D^2 value of 5231 have been chosen along with other clusters nearer to these two, to group them into two broad categories as below:

Group	Highly diverse clusters	Nearer clusters	Total number of genotypes
I	III	I	18
II	X	II, VI and IX	16

On the basis of yield performance and some specialized characters, ten genotypes from each of the two groups have been selected as being the most diverse and high yielding genotypes. The probability of getting better segregants and promising recombinants will be more, if crosses are attempted between genotypes belonging to these two groups. The composition of genotypes of the two groups were as follows:

Group I : CPAN 4018, PBW 321, HI 1418, Lok-1, HI 1077, WH 147, CPAN 3031, HUW 234, GW 173 and Sonalika.

Group II: NP 890, CPAN 3030, PBW 175, NI 5439, K 65, K 68, HI 1136, K 7410, Narmada –112 and Sujata

Based on cluster means, the clusters have been identified for selecting parents for future hybridization programme and accordingly, cluster III has been identified for selecting parents for incorporating early maturity, dwarfness, flag leaf area and harvest index; cluster IV for grains per spike, Cluster X for number of spikes per plant; cluster XI for spike length and bold seededness and cluster VI for grain yield per plant. The genotypes superior in the above clusters may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential.

It is observed that days to maturity, plant height, spikes per plant, grains per spike and harvest index is showing positive significant relationship with grain yield, so it is further suggested that spikes/ plant, grain yield and grain boldness may be used as a criteria for single plant selection in the early segregating generation derived from the multiple crosses among the selected genotypes. So, hybridization between genotypes of divergent clusters will lead to accumulation of favorable genes in a single variety and also it is suggested to create variability for developing the varieties involving a large number of divergent lines instead of closely related ones.

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Variability, heritability and genetic advance studies in napier grass (*Pennisetum purpureum.* K. Schum.)

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Abstract : Genetic variability and heritability studies involving 53 genotypes of napier grass germplasm indicated that there were highly significant differences between the genotypes for green fodder yield and eight other characters. The genotypic and phenotypic coefficients of variation did not differ widely indicating the lesser influence of environment on the characters. High genotypic co-efficient of variation was observed for panicle length, number of tillers per plant, leaf width, stem thickness and leaf length. Heritability estimates in general were high for most of the characters studied. High heritability coupled with high genetic advance as per cent of mean was observed for panicle length, number of tillers per plant and leaf width. Hence these three characters need be given more importance in selection as these are expected to be controlled by additive genes. *(Key words : Napier grass, Variability, Genetic Advance)*