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GENETIC DIVERSITY IN A LARGE COLLECTION OF WHEATS (*TRITICUM* SPP.)

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ABSTRACT

Three hundred genotypes of bread and durum wheats including Indian and exotic collections were evaluated for 10 yield and other related characters. Five characters (grain and biological yields, tiller number, grain weight/ear and grains/ear) exhibited high variability. Of the remaining five traits, flag leaf area and 100-grain weight showed moderate variability while plant height, peduncle length and harvest index showed relatively low variability. Following the non-hierarchical euclidean cluster analysis, all the 300 genotypes were grouped into 16 clusters with variable number of genotypes. Genotypes of heterogeneous origin/ place of release, and of different ploidy levels (bread and durum wheats) 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 the ploidy level of genotypes. On the basis of the data on genetic divergence and mean performance of yield and other traits, five diverse and superior genotypes, namely MUW 109, CPAN 3064, CPAN 1556, MUW 104, and CPAN 1998 were selected. Each of these genotypes was exceptionally good for one or more characters and was reasonable for other characters relatives to those of the best check varieties. Therefore, these genotypes may be involved in multiple crossing programme to recover transgressive segregates. Further, on the basis of character associations, it is argued that selection of plants with high biological yield coupled with optimum harvest index (50%) should result in progenies with high grain yield potential in wheat.

Key words : Wheats, morphophysiological traits, cluster analysis, genetic divergence.

The germplasm is the reservoir of genetic diversity which is often exploited to meet the changing needs for developing improved varieties of a crop. It is also important that considerable variability for economic traits must exist in the germplasm for profitable exploitation following recombination breeding or selection. The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop such as wheat to recover transgressive segregates has also been repeatedly emphasized [1-3]. However, the genetic diversity of selected parents is not always based on factors such as geographic diversity/place of release [4-7] or ploidy level [7, 8]. Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as D^2 statistic and non-hierarchical Euclidean cluster analysis [9-11]. These procedures characterize genetic divergence using the criterion of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters. In view of these facts, 300 wheat genotypes were evaluated in this study : (i) to determine the magnitude of variability among the germplasm collection for yield and morpho-physiological traits, (ii) to determine the grouping pattern of genotypes in different clusters, and (iii) 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

Three hundred wheat genotypes (297 test genotypes + 3 checks) maintained at the Department of Agricultural Botony, Ch. Charan Singh University, Meerut, constituted the material for the present study. Of these, 273 genotypes were of bread wheat *(Triticum aestivum* L.), with 240 indigenous (including three check varieties, namely HD 2329, WL 711 and Sonalika--these varieties were used as checks in All India Coordinated Trials in the year 1991-92 when this experiment was conducted) and 33 exotic collections. The remaining 27 genotypes were of durum wheat *(Triticum durum* L.), including 25 indigenous and two exotic collections. All the exotic genotypes (i.e., MUW series) were obtained from CIMMYT, Mexico.

The material was evaluated in an augmented block design with twenty blocks at the Department of Agricultural Botony Research Farm, Ch. Charan Sigh University, Meerut, with each block containing 15 different test genotypes plus three checks. The last block, however, contained only 12 remaining test genotypes and the three checks. In the blocks each genotypes was evaluated in a single row plot of 1.5 m length, with plot to plot and plant to plant distances of 23 cm and 10 cm, respectively. Recommended agronomic practices were followed to raise a good crop. The data on 10 quantitative characters (Table 1) were recorded on five competitive plants in each plot. Adjusted mean values for all the characters of 297 test genotypes and the estimates of error mean squares were obtained following Federer [12] and used for subsequent statistical analyses.

The mean, range, phenotypic coefficient of variation (P.CV) and correlation coefficient were calculated as per the standard statistical procedures. The non-hierarchical Euclidean cluster analysis [10, 11] 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 300 genotypes was determined following the 'sequential pseudo F-ratio tests' [10, 11].

RESULTS AND DISCUSSION

The results of the present study showed moderate to high variability for all the 10 characters under study. Considerable genetic divergence was also present among the genotypes. This suggested adequate scope for selection of superior and diverse genotypes for use in a programme aimed at enhancing genetic yield potential of wheat.

Table 1. Estimates of mean, range and phenotypic coefficient of variation (PCV) for 10 characters and the correlation coefficients of grain yield with nine other characters

S.No.	Character (with abbreviation)	Mean	Range	PCV (%)	Correlation with GY/P
1.	Grain yield/plant (GY/P)	16.57	5.44 - 40.57	32.83	-
2.	Plant height (PH)	92.42	38.80-125.10	12.84	0.30**
3.	Flag leaf area (FLA)	32.57	16.49 - 58.15	19.25	0.22**
4.	Peduncle length (PDL)	37.02	17.90 - 55.90	13.64	0.23**
5.	Tillers/plant (TL/P)	9.22	3.40 - 21.80	28.42	0.69**
6.	Grains/ear (G/E)	60.36	28.10-101.50	21.85	0.07
7.	Grain weight/ear (GW/E)	2.13	0.91 - 3.69	23.47	0.24**
8.	100-grain weight (GW)	3.60	2.30 - 5.76	17.50	0.26**
9.	Biological yield/plant (BY/P)	39.13	12.02-104.80	30.16	0.93**
10.	Harvest index (HI)	42.35	25.88 - 52.44	11.69	0.43**

**Significant at 1% level.

The data presented in Table 1 show wide ranges for all the 10 characters, but the estimates of PCV were high only for following five traits : grain and biological yields, tiller number, grain weight/ear and grains/ear. Among the remaining five characters, which also showed wide ranges, flag leaf area and 100-grain weight showed moderate variability while plant height, peduncle length and harvest index showed relatively low variability. However, there is still ample scope for selection of superior genotypes for these traits.

Based on non-hierarchical Euclidean cluster analysis, the 300 genotypes were grouped into 16 clusters with variable number of genotypes (Table 2), suggesting considerable amount of genetic diversity in the material. Genotypes collected/originated from the same place (e.g., MUW series collected from CIMMYT,

Table 2. Distribution pattern of 300 genotypes of wheats into 16 clusters

Cluster No.	No. of genotypes	Name of genotypes
I	15	CPAN 6097, CPAN 1556, HD 1502, WH 385, HS 172, HD 2564, HD 4541*, MUW 108, HD 2462, CPAN 6140, CPAN 2051, HDR 77, K 8384, Lerma rojo, MUW 112
II	17	WH 536, MUW 99, Raj 3651, HW 203, CPAN 1990, VW 120, BHW 341, VL 640, Swati HI 784, PBW 181, Eagle, HW 480, CPAN 3040, MUW 221*, Shekshark 7410, K 7053, CPAN 1842
III	29	CPAN 3023, VL 631, MUW 121, VL 691, VL 490, WH 538, CPAN 3080, CPAN 3081, VL 401, CPAN 3031, CPAN 1909, CPAN 2009, MUW 116, MUW 117, NI 1144, CPAN 1962, WH 574, BAU 2177, Raj 3653, K 8815, CC 464, VL 635, VL 634, CPAN 6125*, Raj 3654, K 8817, BAU 2196, WH 537, HB 507
IV	17	MUW 53, MUW 258, BR 2104, VL 687, HD 1925, PBW 308, MUW 104, WRF 2385, CPAN 3073, HS 207, Raj 3687, CPAN 3074, HDR 17, CPAN 1998, CPAN 3005, MUW 98, MUW 70
V	44	VL 692, 1221, WH 416, HD 2582, Raj 3684, 6WA 740, Pawan 5, VL 682, HI 1144, WH 539, Raj 1442, K 8020, Raj 3655, HUW 319, Raj 3717, HI 1011, HD 789, CPAN 2061, MUW 102, VL 639, VL 694, K 8352, NI 8063, WH 542, K 8565*, H 744, IPW 1013, PBW 305, Raj 3689, MUW 91, MP 845, CPAN 6066, HI 1076, CPAN 6098*, PBW 301, HD 2278, CPAN 2088, CPAN 3057, BAU 2185, APS 2, IPW 1020, UP 2321, HB 1303, K 2148
VI	5	HI 68, MUW 109, MUW 114, CPAN 3064, HD 2504
VII	14	WH 558, MUW 100, DWL 5023*, MUW 57, Janak 6w 189, 48-A-1, HW 4530, PBW 216*, M 975-8-7*, MUW 103, CPAN 2094, PBW 287, MUW 10
VIII	23	HUW 234, MUW 64, N 54, PBW 65, I 348, NI 866, CPAN 6132*, MUW 44, CPAN 1927, DW 148, HW 4552, HW 559, H 747-19, HUW 262, M 76, MACS 2496, VL 689, MUW 115, DWR 59, HI 1116, MACS-9*, DL 802-2, HI 8177
IX	13	MUW 21, Sr 12Mg, HI 8270, Compare, HW 706, HW 971, HI 8296*, VL 921, VL 641, SI 27, HW 741, Raj 3668, HW 1045
X	6	HI 1136, HI 8629, I 617, HI 1270, CPAN 6083*, Janak
XI	11	PBW 218*, WH 503, CPAN 6137*, VL 637, MUW 27, HD 2307, HD 1286, PBW 306, CPAN 3072, WR 2061, PBW 215*

(*Table 2 contd.*)

XII	8	VL 616, HW 971, Narbada 112, HI 6260*, Hyb. 65, CPAN 2042, HD 2565, Men 7
XIII	27	HD 2567, PBW 285, MUW 106, CPAN 3006, APS 4, BW 152, VL 630, HW 1964, Raj 1972, VL 696, MUW 28, 6UA 737, B-Yellow*, J 8329, HUW 318, PR 5, HW 334, K 8267, HW 517, VL 695, 6WA 103, CPAN 3138*, HI 779, HD 2567, DL 203-7, VL 690, MUW 110
XIV	23	HW 103, HUW 326, HUW 23, VL 693, WH 291, MUW 68, PBW 226, HUW 329, MP 847, Raj 3657, DL 788-2, K 8915, HW 923, DW 36, N 8757*, Raj 2535, Raj 3077, Raj 3232, WH 554, WH 561, CPAN 3009, HUW 190, HUW 266
XV	22	MUW 95, Sarbati Sonora, CPAN 6095*, VL 700, PBW 238, PBW 34*, MUW 107, MP 843, H 744, PB 34, PBW 282, PBW 225, HI 9075, MUW 45*, DWL 5025, CPAN 1815, UP 2297, Raj 911*, MUW 296, MUW 119, WH 369*, HD 2329
XVI	26	MUW 74, HI 1172, MUW 105, WH 283, Raj 3686, MUW 47, HD 2134, UP 2323, Kundan-DL-153-2, HI 6035, HI 1177, HI 1127, VL 699, I 459, Raj 3688, Raj 3685, WH 562, Raj 3656, CPAN 6144*, HD 2307, CPAN 6116*, Raj 3658, MUW 118, MUW 56, WL 711, Sonalika

*Indicates durum wheat genotypes.

Mexico; HD series developed at New Delhi; UP series developed at Pantnagar, UP; HUW series developed at Varanasi, UP; WH series developed at Hisar, Haryana; and Raj series developed at Durgapura, Rajasthan) were scattered in different clusters each cluster having genotypes of different origins. This suggested that the genotypes within a cluster may have some degree of ancestral relationship.

The grouping pattern of different genotypes into different clusters (Table 2) also demonstrates that 27 durum wheat genotypes were scattered in all the clusters (except two clusters) and thus were grouped with bread wheat genotypes. This suggested that there is no significant bearing of ploidy level on genetic divergence of bread and durum wheats. The grouping of the bread and durum wheats in the same clusters may be attributed to their cytoplasms which were originally derived from a common source, probably the B genome donor of wheats [13-15].

The data on inter-cluster distances (Table 3) and the mean performance of the genotypes (data not given in Table) was used to select genetically diverse and agronomically superior genotypes from among the 300 genotypes studied. The members of clusters VI and VII exhibited maximum divergence followed in descending order by the members of clusters I and VI, VI and XI, III and VI, VI and XV, VII and XII, and IV and VI. The average intra-cluster distance between the members of cluster VI was maximum followed in descending order by clusters IX, I, VII, XII, III

Table 3. Estimates of average intra- and inter-cluster distances for 16 clusters involving 300 genotypes of wheat

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	**2.03**	4.15	2.20	3.87	2.80	7.96	2.58	4.79	4.17	6.67	2.60	6.12	3.21	4.59	3.15	4.10
II		**2.40**	3.57	4.34	2.79	5.13	5.68	3.00	3.43	4.36	4.43	3.17	4.15	3.47	4.89	3.91
III			**1.64**	2.66	2.22	7.27	3.07	3.61	3.45	5.21	2.68	4.93	2.68	3.53	2.39	3.09
IV				**2.07**	3.05	6.80	4.66	2.86	4.91	5.15	3.67	4.03	4.65	3.94	2.71	2.63
V					**1.77**	5.63	3.33	2.64	3.28	4.42	2.99	3.96	2.51	2.16	2.40	2.26
VI						**2.73**	8.37	4.31	7.01	5.48	7.51	4.15	6.73	4.39	7.11	5.35
VII							**2.03**	5.51	4.80	6.93	3.15	7.11	2.52	4.43	2.44	4.17
VIII								**1.97**	4.96	4.33	4.85	2.60	4.43	2.24	3.93	2.74
IX									**2.47**	3.60	3.12	4.66	3.39	4.36	4.18	3.85
X										**1.67**	5.37	2.95	5.29	4.19	5.22	3.87
XI											**1.73**	5.43	3.13	4.41	2.48	2.86
XII												**1.98**	5.74	3.87	5.28	3.54
XIII													**1.81**	2.87	2.87	3.37
XIV														**1.81**	3.32	2.45
XV															**1.62**	2.14
XVI																**1.77**

Diagonal (bold face) values are average intra-cluster distances, and underlined values are the highest (8.37) and the lowest (2.14) inter-cluster distances.

and XV (Table 3), suggesting that the genotypes in cluster VI were relatively more diverse than the genotypes in the above selected clusters. Furthermore, cluster VI contained minimum number of entries (5 genotypes) and had highest mean values for the characters flag leaf area, tiller number, biological yield, grain yield and 100-grain weight, while moderate mean values for peduncle length, grain weight/ear and harvest index. The moderate mean values for the last three characters were comparable to those of the best check. Therefore, this cluster was deemed "best" for selecting diverse and agronomically desirable genotypes. In this study, the genotypes which were exceptionally good in respect to one or more characters and atleast comparable in respect to other characters to the best check were deemed desirable. The desirable genotypes were also selected from other clusters which were widely separated from cluster VI as well as *inter alia,* and simultaneously had the desirable genotypes. On the basis of these criteria, five genetically diverse and superior (desirable) genotypes were selected mainly from cluster VI and two other clusters, viz., I and IV (Table 4). As these five divergent genotypes were often exceptionally superior to all the remaining genotypes (tested in this study) for one or more traits and concurrently were not poor for any trait, it is proposed that these genotypes may be involved in a multiple crossing programme to recover transgressive segregates with high genetic yield potential. Similar approach was also followed by several workers in the past, such as Johnson *et al.* in wheat [16], Barbacki *et al.* in barley [17] and Cox and Frey [18] in oat [18] who recovered transgressive segregates for protein content from crosses involving divergent parents. It is further suggested that biological yield may be used as a criterion for single plant selection in the early segregating generation(s) derived from the multiple crosses among the selected genotypes. The selection of the plants with high biological yield coupled with optimum harvest index (~50%) should result in progenies with high grain yield potential in wheat [19]. To circumvent the difficulties associated with recording of data on these two traits on large number of plants in segregating generations, it is suggested that the data on biological yield and grain yield of desirable plants may be recorded to obtain progenies with high grain yield potential in the later generation(s).

Table 4. List of diverse and superior genotypes selected from different clusters.

S.No.	Name of genotype	Cluster No.	Desirable characters$^+$
1.	MUW 109	VI	FLA, TL/P, BY/P, GY/P*, GW and HI
2.	CPAN 3064	VI	FLA*, PDL, TL/P, BY/P*, GY/P, GW* and HI
3.	CPAN 1556	I	PH, FLA, TL/P, BY/P
4.	MUW 104	IV	TL/P, BY/P, G/E, GW/E, GW and HI
5.	CPAN 1998	IV	FLA, PDL, G/E, GW/E, GW and HI

$^+$The means were either comparable to or higher than the best check mean.

*Characterized with the highest mean among atleast the genotypes of selected clusters.

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