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Short communication

Cluster analysis for heterosis in wheat [*Triticum aestivum* (L.) em. Thell.]

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Twenty-five wheat genotypes were selected from the wheat germplasm maintained at Banaras Hindu University, Varanasi and planted in Randomized Block Design in three replications in 1996-97 crop season. The plot size was double row of 3m length with inter and intra-row spacings of 25cm and 10cm, respectively. From these parents, 83 random crosses were made during *Rabi* 1996-97. The F_1 seeds were grown in 1997-98 crop season along with parents in RBD with 3 replications and double row of check parent HUW234 was planted after each 10th plot. The plot size in F_1 generation was also double row of 3m length with inter and intra-row spacing of 25cm and 10cm, respectively. Same crosses were also attempted in 1997-98 season and planted in 1998-99 crop season in above manner. The data were recorded from twenty randomly selected plants for days to 50% flowering, days to maturity, plant height (cm), productive tillers/plant, spike length (cm), spikelets/spike, grains/spike, grain weight/spike (g) and 100-seed weight (g) in parental as well as F_1 generation in two crop seasons. The double row plot was harvested and seeds were threshed for recording data on yield/plot (g) and harvest index (%). Data were pooled and correlation [1], path [2] and D^2-analysis [3] were done in parental population. Simultaneously, correlation and path analysis was done for F_1 generation along with estimation of standard heterosis over HUW234 for various metric traits. The analysis of variance for all the traits showed highly significant differences between genotypes in parental and crosses in F_1 generation.

Cluster analysis: The computed D^2 values for 300 combinations ranged from 203.61 to 12768.35 showing high divergence among the different genotypes. These 25 genotypes were grouped into six clusters (Table 1). Cluster I was the largest one with 13 genotypes. Cluster II, III and IV accommodated 5, 3 and 2 genotypes, respectively. Clusters V and VI containing one genotype each were most divergent. Clustering pattern revealed that there was no parallelism between genetic diversity and geographic diversity. Intra-cluster distances (D^2) ranged from 0.00 to 1458.54 whereas intercluster distance was ranged from 1719.02 to 11008.41 (Table 2). The minimum distance was occurred between clusters V and VI indicating a close relationship while the distance was highest between cluster IV and V indicating wide diversity between these two clusters. These maximum distances pointed out that the selection of the parents for hybridization programme should be made from these genetically diverse clusters. The % contribution of various traits to the genetic diversity worked out from their rank wise totals showed that days to 50% flowering had maximum contribution (13.12%) followed by productive tillers / plant (11.87%) and days to maturity (10.76%). Other traits had almost 9% contribution each except harvest index, which showed minimum contribution of 4.94%.

Table 1. Distribution of wheat genotypes in different clusters

S. No.	Cluster	Number	Genotypes
1.	I	13	BW1052, CPAN1990, CPAN3013, HD2160, HD2662, HP1761, HUW251, HUW452, HUW453, K9006, K9107, K9305, Sangi-4
2.	II	5	BW362, CPAN4007, CPAN4008, HP1731, HUW206
3.	III	3	CPAN2063, CPAN3067, HUW234
4.	IV	2	HP1633, HW2005
5.	V	1	CPAN3048
6.	VI	1	CPAN4003

Standard heterosis over HUW234: Heterosis or the superiority of F_1 hybrids over check variety for economic traits is crucial for any hybrid development programme. In the present investigations 83 crosses were evaluated for heterotic response with respect to yield traits for two consecutive crop seasons. Non-significant differences for year × genotype interactions were observed from the pooled analysis of variance and therefore, the data of both the years was pooled to work out the heterosis over check variety HUW234. In general, considerable heterosis over check

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Table 2. Intra and inter cluster distances (D^2) in wheat genotypes

Cluster	I	II	III	IV	V	VI
I	**1058.96** (32.54)	1791.84 (42.33)	1789.12 (42.31)	2797.20 (52.89)	5488.78 (74.09)	3669.28 (60.57)
II		**1458.54** (38.19)	2454.95 (49.55)	5786.21 (76.07)	4417.35 (66.46)	2263.49 (47.58)
III			**950.86** (30.84)	3834.40 (61.92)	2644.39 (51.42)	1930.84 (43.94)
IV				**1162.46** (34.09)	11008.41 (104.92)	8265.24 (90.91)
V					**00.00**	1719.02 (41.46)
VI						**00.00**

Antiqued values are intra-cluster distances; D^2 values are in parenthesis

variety was observed for all the traits except days to 50% flowering and grain weight/spike. Several crosses were found superior for yield traits but only 23 crosses showed significantly positive heterosis over standard variety, HUW234 for yield/plot in which 11 crosses out yielded check variety by a margin of 10% or more. Three crosses, i.e., CPAN2063/HUW251, CPAN4007/HUW251, CPAN1990 /HUW453 showed standard heterosis of more than 20% - the minimum level for exploitation at commercial level. CPAN4008/ HUW251, CPAN3013/HUW234, BW1052/HP1633 and Sangi-4/K9006 were other promising cross combinations for yield/plot. Some cross combinations namely, CPAN 3013/K9107, CPAN4003/ HUW251, CPAN4003/ K9107, CPAN1990/HUW206, CPAN2063/HUW206, CPAN1990/HUW453 and CPAN3048/ K9107 showed significantly high heterosis over HUW234 for several traits.

Clustering pattern and heterosis: From the results, it was observed that CPAN entries contributed significantly for heterosis. This may be due to wide variability existing in these genotypes. It was found that most of the cross combinations showing standard heterosis were belonging to those clusters which were neither too distant nor too close. Crosses between parents from cluster I and II, I and III and I and IV were heterotic for most of the traits. On the other hand, out of 45 significant crosses for yield, harvest index, highest grains/spike and productive tillers/plant, 13 crosses are such that involved parents from the same cluster. Among these crosses, CPAN3013/K9107, CPAN1990/HUW453, BW1052/K9107, CPAN 1990/K9006 and Sangi-4/K9006 were promising for yield and component traits. The results indicated that most divergent parents always did not produce heterotic crosses. However, optimum diversity between parents either from same cluster or near related cluster is required for obtaining most heterotic crosses.

Character association: Parents vs. F_1 hybrids: In general the values of genotypic correlations were higher than the corresponding phenotypic correlations. Yield/plot had high and significant association with plant height, spike length, grain weight/spike and 100-seed weight in both the generation. In F_1 generation, yield/plot was also significantly associated with productive tillers/plant, spikelets/spike and grains/spike. This trend of correlation supports the plant type of higher yield according to which plant should be medium dwarf with more number of productive tillers, long spiked, having more seeds/spike of bold size. Apart from associations with yield, spike length had highly significant associations with days to 50% flowering, plant height, spikelets/spike, grains/spike and grain weight/spike in positive direction. Ear characters i.e. spikelets/spike, grains/spike and grain weight/spike were also associated with each other. Almost similar trend was observed for character association in both the generations except for plant height. Increased height showed although non-significant but negative impact for other traits. This is in accordance to the concept of reduced plant height for high yielding genotypes that can withstand lodging.

Path analysis: Parents vs. F_1 hybrids: Although number of grains/spike is one of the major yield components, it had highest direct effect on yield in negative direction in parental population. This negative effect resulted in non-significant association of grains/spike with yield. In parental populations, spikelets/spike had maximum effect on yield in positive direction followed by grain weight/spike and productive tillers/plant. On the other hand, productive tillers/plant had shown highest positive effect on yield followed by grain weight / spike and 100-seed weight in F_1 generation. 100-seed weight had maximum correlation coefficient with yield in parental as well as F_1 generation probably due to high indirect effect of grain weight/spike. In parental generation, grain weight / spike had high association with yield due to its high direct effect. Similarly, productive tillers / plant in F_1 generation had high association with yield due to its high direct effect on yield. The results on path analysis indicated the importance of 100-seed weight, i.e., test weight in parental as well as in F_1 generation and particularly grain weight/spike in parental and productive tillers/plant in F_1 generation for maximizing yield potential.

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