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*Short Communication*

# Heterosis and combining ability studies for yield components and grain protein content in bread wheat *Triticum aestivum* (L.)

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Wheat is the second most important food crop of the country and contributes nearly one third of the total food grain production [1]. The annual production of wheat in India during 2010-11 was 85.93 m t [2] which was a tremendous improvement over the production level four decades back (12.57 m t in 1964) due to the rapid growth in irrigated areas and popularization of high yielding varieties. Rajasthan comprises NWPZ (North Western Plain Zone) and Central Zone of wheat sharing about 10 per cent both in terms of area and production at the national level. After the incorporation of dwarfing gene 'Norin 10' production was tremendously capitalized, which brought food self-sufficiency and promoted the build-up of buffer stocks in the country. However, to meet the wheat production targeted at 100 mt by the year 2030, sustained research efforts are needed to keep the upward trend in wheat production well above the population growth.

Wheat being a highly self-pollinated crop, scope for exploitation of hybrid vigour depends on the direction and magnitude of heterosis, biological feasibility of crop and nature of gene action. It is realized that high yielding lines may not necessarily be able to transmit their superiority to their hybrids [3]. Hence, an estimate of GCA and SCA effects may be more reliable test rather than their *per se* performance [4, 5]. The idea of the high inbreeding coefficient make breeder enable to eliminate segregating progenies at early stages to save limited resources, time and space. The present study was therefore conducted to ascertain the extent of heterosis, inbreeding depression and estimation of combining ability effects in $F_1$ and $F_2$ generations in a 10 x 10 diallel set of elite wheat varieties.

The present investigation was conducted at Instructional Farm of Rajasthan College of Agriculture, Udaipur, Rajasthan. Ten diverse wheat genotypes namely Raj 1482, PBW 502, PBW 343, PBW 373, DBW 16, DBW 17, HD 2687, UP 2338, Raj 4083 and Raj 4037 were selected as parents on the basis of their origin, adaptability, diversity and yield potential. Crosses were attempted during *rabi*, 2007-08 in diallel fashion excluding reciprocals (method 2 and Model I Griffing, 1956) [6]. Further 45$F_1$s were multiplied during off-season so as to obtain $F_2$ generation. Final experimental trial comprising 10 parents along with 45 $F_1$s and 45 $F_2$s was evaluated during *rabi,* 2008-09 in randomized block design with two replications. Parents, $F_1$s were grown in single row while $F_2$s in three rows at a distance of 10 cm within the rows of 2 m length with row to row spacing of 25 cm. The observations on seven traits *viz*., days to maturity, spike area, peduncle area [7], spikelets per spike, grains per spike, harvest index and grain protein content [8] were recorded on ten randomly selected competitive plants in parents and $F_1$s, while 30 in $F_2$s per treatment per replication. Heterosis, heterobeltiosis [9] and inbreeding depression were calculated as per standard procedures. The combining ability analysis was carried out according to method 2 Model-I (fixed effects) of [6].

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The analysis of variance revealed significant differences for all the characters indicating presence of adequate genetic variation among the genotypes. Further partitioning of mean squares due to $F_1$s and $F_2$s were significant for all the characters, except harvest index in both the generations and for days to maturity in $F_2$ generation. Mean squares due to parent Vs hybrid component were also significant for all the characters which depicted presence of heterosis for all the characters. The mean heterosis, heterobeltiosis and inbreeding depression for days to maturity were exhibited as 4.16, 3.43 and 2.80, respectively. Estimates of heterosis for days to maturity were significant in twenty-five crosses and ranged from -8.91 (PBW 343 x HD 2687) to 0.60 (Raj 1482 x PBW 373) (Table 1). Significant heterobeltiosis for days to maturity was depicted in fifteen crosses, which ranged from -8.00 (PBW 343 x HD 2687) to –0.40 (Raj 1482 x PBW 343). Significant inbreeding depression for days to maturity was noticed in eight crosses, and ranged from -8.70 (PBW 343 x HD 2687) to 4.53 (HD 2687 x Raj 4083). None of the parent exhibited negative significant GCA effect for days to maturity in both $F_1$ and $F_2$ generations (Table 2). Only one cross Raj 1482 x PBW 502 exhibited negative SCA effects in both $F_1$ and $F_2$ generations.

The heterosis, heterobeltiosis and inbreeding depression for spike area ranged from -8.98 to 70.35, 0.36 to 61.42 and –68.70 to 46.91, respectively. The highest inbreeding depression was depicted in cross DBW 16 x Raj 4083. GCA effects computed for spike area revealed that parents PBW 502 and PBW 343 depicted significant positive effects in both $F_1$ and $F_2$ generations. Whereas, significant positive SCA effects were depicted in two crosses *viz.*, DBW 16 x UP 2338 and Raj 4083 x Raj 4037 in both $F_1$ and $F_2$ generations. Significant heterobeltiosis for peduncle area was exhibited in seventeen crosses, and ranged from 5.49 (Raj 1482 x UP 2338) to 131.49 (DBW 17 x Raj 4083). Significant inbreeding depression for peduncle area was noticed in twenty two crosses, which ranged from –43.75 (PBW 373 x UP 2338) to 66.58 (DBW 17 x Raj 4083). For peduncle area none of the parent recorded significant positive GCA effects in both $F_1$ and $F_2$ generations. However, parents HD 2687 and Raj 4083 exhibited significant positive GCA effects in $F_1$s, whereas, parents PBW 373 and Raj 4037 showed positive significant GCA effects in $F_2$ generations. Only cross Raj 1482 x HD 2687 depicted significant positive SCA effects in both $F_1$ and $F_2$ generations for the trait.

The heterosis for spikelets per spike ranged from –13.48 (PBW 502 x Raj 4037) to 61.41(HD 2687 x Raj 4037). The highest estimates of positive heterobeltiosis was depicted by the cross HD 2687 x Raj 4037 (56.71). Raj 1482 and PBW 502 exhibited significant positive GCA effects for spikelets per spike in both the generations thus could be regarded as good general combiners for this trait. SCA effects revealed that the crosses UP 2338 x HD 2687, HD 2687 x Raj 4037 and Raj 4083 x Raj 4037 were positively significant in both $F_1$ and $F_2$ generation. The mean heterosis, heterobeltiosis and inbreeding depression for grains per spike were depicted as 24.36, 13.72 and 18.89, respectively (Table 1). Heterosis in grains per spike is an important quantitative trait to determine the final yield of an entry and to select the segregating genotypes with high yield attributes [10]. Significant heterobeltiosis for grains per spike was noticed in fifteen crosses, and ranged from 0.69 (PBW 343 x DBW 16) to 38.40 (PBW 502 x Raj 4083). Significant inbreeding depression for grains per spike was depicted in twenty-five crosses.

**Table 1.** Mean (%) and range of heterosis, heterobeltiosis and inbreeding depression for seven characters in bread wheat

| Characters | MP* | | BP* | | ID* | |
|---|---|---|---|---|---|---|
| | Mean | Range | Mean | Range | Mean | Range |
| Days to maturity | 4.16 | –8.91-0.60 | 3.43 | –8.00-(-)0.40 | 2.80 | –8.70-4.53 |
| Spike area | 27.01 | –8.98-70.35 | 18.96 | 0.36-61.42 | 18.75 | –68.70-46.91 |
| Peduncle area | 33.44 | –21.64-163.42 | 29.09 | 5.49-131.49 | 28.83 | –43.75-66.58 |
| Number of spikelets/spike | 16.48 | –13.48-61.41 | 10.16 | 0.34-56.71 | 13.18 | –14.94-36.90 |
| Number of grains/spike | 24.36 | –31.78-49.54 | 13.72 | 0.69-38.40 | 18.89 | –32.79-45.83 |
| Harvest index | 8.39 | 1.24-15.79 | 6.88 | 0.06-14.78 | 4.23 | –5.89-15.01 |
| Grain protein content | 17.10 | –20.43-36.65 | 10.77 | 1.34-36.50 | 6.89 | –27.11-27.72 |

*MP : Mid-parent; *BP : Best-parent; ID : Inbreeding Depression

**Table 2.** Estimation of GCA effects for days to maturity, spike area, peduncle area, number of spikelets/spike, number of grains/spike, harvest index and grain protein content in bread wheat

| Genotype | Days to maturity | | Spike area | | Peduncle area | | Number of spikelets/spike | | Number of grains/spike | | Harvest index | | Grain protein content | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ |
| Raj 1482 | 0.87 | 0.01 | –1.86* | 1.01 | –0.17 | 0.11 | 0.95** | 1.18** | 0.24 | 2.37** | –0.69 | –0.04 | 0.78** | 0.37 |
| PBW 502 | 0.49 | 0.30 | 2.70** | 1.72** | –0.13 | –0.21 | 1.03** | 0.67* | –0.42 | –1.38* | –0.57 | –0.67 | –0.03 | 0.07 |
| PBW 343 | –0.84 | 0.26 | 1.72* | 1.41* | 0.20 | 0.20 | –0.20 | 0.15 | 0.08 | –0.05 | 0.20 | –0.67 | –0.00 | 0.81** |
| PBW 373 | –1.09 | -0.28 | 0.58 | –1.08 | –0.24 | 0.83** | 0.40 | 0.13 | 0.79 | 1.53* | 0.68 | 0.55 | –0.56* | –0.30 |
| DBW 16 | 1.28* | 0.72 | 0.53 | –2.32** | 0.16 | –0.31 | 0.47 | -1.08** | 3.73** | 0.70 | 0.02 | 0.57 | –0.09 | –0.36 |
| DBW 17 | –0.72 | 0.13 | –0.59 | 0.14 | –0.42 | –0.73* | 0.02 | 0.15 | –1.01 | 1.11 | 0.50 | 0.90 | –0.05 | –0.64** |
| HD 2687 | –0.59 | –0.83 | 1.33 | 2.69** | 1.03** | –0.13 | –0.34 | 0.46 | 0.21 | 0.57 | 0.26 | –0.07 | –0.27 | –0.23 |
| UP 2338 | 0.20 | 1.34* | 0.69 | –1.57** | –0.57 | –0.37 | 0.50 | 0.61 | 1.85** | 0.80 | –0.06 | –0.49 | –0.49* | –0.50* |
| Raj 4083 | –0.17 | –1.08 | –2.17** | –2.18** | 0.94** | –0.11 | –1.15** | –0.95** | –1.68** | –2.38** | –0.21 | –0.23 | 0.23 | 0.06 |
| Raj 4037 | 0.58 | –0.58 | –2.91** | 0.18 | –0.79* | 0.71* | –1.67** | –1.33** | –3.79** | –3.26** | –0.12 | 0.15 | 0.48* | 0.72** |
| (SE) $g_i$ | 0.69 | 0.23 | 0.57 | 0.30 | 0.38 | 0.22 | 0.60 | 0.54 | 0.63 | 0.19 | 0.51 | 0.25 | 0.46 | 0.20 |

*,**Significant at 5 and 1 per cent levels, respectively.

None of the parent revealed significant positive GCA effects for grains per spike in both the generations. However, DBW 16 and UP 2338 in $F_1$, and Raj 1482 and PBW 373 exhibited significant positive GCA effect in $F_2$ generation. Estimates of SCA effects revealed that nine crosses in $F_1$ and $F_2$ exhibited positive significant SCA effects. The average heterosis for harvest index ranged from 1.24 (Raj 1482 x PBW 502) to 15.79 (UP 2338 x Raj 4037). The highest estimates of positive heterobeltiosis was exhibited by the hybrid UP 2338 x Raj 4037 followed by PBW 343 x Raj 4037 and DBW 17 x UP 2338. Biomass is strongly and positively correlated with grain yield. Hence, it is contemplate to deploy the biomass and dissipate the yield plateau [11, 12]. Inbreeding depression for harvest index ranged from -5.89 (Raj 4083 x Raj 4037) to 15.01 (PBW 502 x PBW 343). None of the parent exhibited significant positive GCA effects in both the generations for harvest index. Estimation of SCA effects revealed that crosses *viz.*, UP 2338 x Raj 4037 followed by PBW 502 x DBW 17 and PBW 502 x Raj 4083 displayed significant positive SCA effects in $F_1$ generations while only one cross DBW 17 x Raj 4083 (3.40) depicted significant positive SCA effects in $F_2$.

The mean heterosis, heterobeltiosis and inbreeding depression for grain protein content were registered as 17.10, 10.77 and 6.89 per cent, respectively. The estimates of heterosis for grain protein content ranged from –20.43 (PBW 373 x HD 2687) to 36.65 (Raj 1482 x HD 2687). The highest estimates of positive heterobeltiosis was displayed by hybrid Raj 1482 x HD 2687 (36.50) followed by PBW 502 x PBW 343 (32.52) and Raj 1482 x DBW 16 (32.20). Significant inbreeding depression for grain protein content was estimated in six crosses which, ranged from –27.11 (PBW 343 x HD 2687) to 27.72 (DBW 16 x DBW 17) revealing epistatic effects involving additive effects in $F_2$ generation. General and specific combining ability effects computed for grain protein content revealed that Raj 4037 as a good combiner in both the generations, while three crosses *viz.*, PBW 343 x DBW 17, PBW 343 x Raj 4083 and HD 2687 x Raj 4037 depicted significant positive SCA effects in both $F_1$ and $F_2$ generations.

It is well established that there could be no separate gene system for yield *per se* as yield is an end product of the multiplicative interaction between its various components. Based on heterotic studies, the best direct yield attribute was grains per spike followed by harvest index. Similarly, for grain protein content maximum significant positive heterotic response was recorded in four crosses. In contrast to SCA effects, GCA effect represent additive and additive x additive component of variation which are fixable and contribute tangibly to the improvement of self-pollinated crops. Therefore, in self-pollinated crops more stress should be laid on GCA effects rather than SCA effects. In the present study, an overall appraisal of GCA effects revealed that PBW 502 was good general combiner for spike area and spikelets per spike, while Raj 4037 appeared as most promising for grain protein content. An account of SCA effects indicated that no cross combination was consistently good for all the characters studied. However, Raj 1482 x PBW 502 for days to maturity, Raj 1482 x HD 2687 for spike area and grain protein content were superior combinations on the basis of their SCA effects. Whereas, UP 2338 x Raj 4037 and DBW 17 x PBW 502 were promising for harvest index. For grain protein content crosses *viz*., PBW 343 x DBW 17, PBW 343 x Raj 4083 and HD 2687 x Raj 4037 possessed highly significant SCA effects, high heterotic response and high *per se* performance involving parent with medium x low, medium x low and low x high combination, respectively. These crosses involved HD 2687, Raj 4037 and Raj 4083 with high GCA effects for grain protein content as well as significant GCA effects for spike area and peduncle area. Thus these crosses could throw desirable transgressive segregates giving rise to new populations.

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