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Short Communication

Combining ability and gene action for grain yield and its components under high temperature environment in bread wheat [*Triticum aestivum* (L.) em. Thell]

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Bread wheat (*Triticum aestivum* L.) is a thermo-sensitive crop and adapted best to temperate climate. However, it is predominantly produced and consumed in tropical and sub tropical regions of the world, where it is exposed to high temperature stress during later stages, resulting in tremendous yield losses. Wheat crop grown in Northern India under late sown conditions is exposed to low temperature up to booting stage where it has to face higher temperature, which enables grain development under high temperature conditions leading to poor yield. Cultivars differ in their relative adaptation to hot environments irrespective of their yield performance in cool environments [1]. For development of high yielding genotypes under stress environments, information on genetic control of grain yield and associated characters under heat stress and identification of good general combiner parents/crosses are the primary requirements. This study was therefore, undertaken to identify desirable parents and crosses and to elucidate the gene action for grain yield and yield components in bread wheat using diallele mating approach under normal (N) and high temperature (HT) environments.

Material for the present investigation comprised of eight genetically diverse bread wheat varieties with varying degree of heat tolerance namely Raj 3777, Raj 3765, Raj 3077, PBW 373, Raj 1482, HD 2329, WH 147 and Lok 1. These varieties were crossed in all possible combinations excluding reciprocals to produce 28 crosses. All crosses along with eight parents were evaluated in randomized block design with three replications in each of two environments *viz.*, normal [N, temperature- maximum: 32.4°C and minimum: 12.9°C (21st November, 2004) sowing and temperature-maximum: 34.1°C and minimum: 16.9°C at maturity] and high temperature [HT, temperature- maximum: 26.3°C and minimum: 8.6°C (15th December, 2004) at sowing and temperature- maximum: 38.3°C and minimum: 19.9°C at maturity]. The high temperature (at maturity) under late sown condition leads to enforced maturity. Plot size was single row with 30 cm row spacing and plant to plant spacing 10 cm. The data were recorded for traits such as, days to maturity, number of effective tillers per plant, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight, biological yield per plant, harvest index and grain yield per plant. Estimation of genetic parameters for traits under study was done following Hayman [2]. Combining ability analysis was performed following Griffing's [3] Method II Model I.

The estimates of components of genetic variance (Table 1) indicated that both additive and dominance gene actions were involved in the expression of most the traits under study in normal (N) and high temperature (HT) environments, except for spike length (HT), where only additive component (D) seemed to be significant. It was only in case of days to maturity (HT), number of effective tillers (HT), spike length (N), biological yield per plant (N) and grain yield per plant (N & HT), where overdominance effect of heterozygous loci (h^2) was found to be significant. Degree of dominance $[(H_1/D)^{1/2}]$ ranged from over dominance for all the characters to partial dominance in case of spike length (HT). The value of $H_2/4H_1$ indicated that for loci exhibiting dominance, frequency of positive alleles was predominant for number of effective tillers per plant (HT), spike length (N & HT), biological yield per plant (N) and grain yield per plant (HT). Positive and significant value of coefficient of co-variance (F) for days to maturity and grain yield per plant (N), indicated predominance of dominant genes in parents. Prevalence of dominant genes for majority of the traits could also be seen from the ratio $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$.

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Singh *et al.* [4] have also made such observations for gene behavior. Effect of environmental variation associated with individual means (E) seemed to be significant for most of the traits, in normal (N) environment. These results were in conformity with the earlier results [5, 6, 7] in which both additive and dominance effects were important in controlling various metric characters studied with preponderance for dominance gene actions.

Narrow sense heritability estimates obtained in component analysis ranged from low to high for different characters (Table 1). This was 0.326 for days to maturity in N environment, 0.265 for number of effective tillers per plant in HT environment, 0.245 and 0.463 for spike length in N and HT environments, 0.263 for biological yield per plant in N environment, 0.256 and 0.344 for grain yield per plant in HT and N environments, respectively. The lower values of heritability for above mentioned characters clearly indicated that these were mainly under the control of non-additive gene action.

The analysis of variance for combining ability revealed that *gca* as well as *sca* effects were highly significant for the characters under study in both the environments. For most of the traits, the magnitudes of *gca* variance were observed to be higher than *sca* variance. This indicated predominance of additive gene effects, being fixable and thereby heritable. These observations were in accordance with the earlier reports [8, 9]. The *gca* estimates of the parents indicated that under heat stress (HT) environment, Raj 3777 was good general combiner for number of effective tillers per plant, spike length, number of spikelets per spike and biological yield per plant (Table 2). Whereas, WH 147 was good general combiner for the number of grains per spike, 1000-grain weight and grain yield per plant. Lok 1 was found as good general combiner for days to maturity, number of effective tiller per plant, 1000-grain weight and biological yield per plant. Since *gca* effect are attributed to additive and additive × additive gene effects, the above mentioned parents have good potential for the improvement of respective characters and may be used in a multiple crossing programmes to synthesize a dynamic population with most of the favourable genes accumulated [3]. In wheat, parents having good general combining ability have also been reported by earlier workers [6, 7]. Cross combinations with significant and high *sca* effects in

Table 1. Estimates of components of genetic variance for some metric characters under normal (N) and high temperature (HT) environments

Components	Days to maturity	No. of effective tiller per plant	Spike length		Biological yield per plant	Grain yield per plant	
	N	HT	N	HT	N	N	HT
D ± SE	2.668* ± 0.356	0.435* ± 0.120	0.617* ± 0.157	0.442* ± 0.095	183.339* ± 22.344	18.944* ± 2.373	1.141* ± 0.411
H_1 ± SE	8.591* ± 0.817	0.637* ± 0.276	1.889* ± 0.361	0.197 ± 0.219	392.593* ± 53.664	42.219* ± 5.455	5.338* ± 0.946
H_2 ± SE	6.317* ± 0.711	0.564* ± 0.240	1.716* ± 0.314	0.161 ± 0.191	314.526* ± 46.688	31.699* ± 4.746	4.684* ± 0.823
h^2 ± SE	22.709* ± 0.477	1.288* ± 0.161	1.766* ± 0.211	0.038 ± 0.128	557.418* ± 31.311	28.009* ± 3.183	3.975* ± 0.552
F ± SE	2.658* ± 0.840	0.319 ± 0.284	0.496 ± 0.371	–0.059 ± 0.226	204.620 ± 55.159	20.802* ± 5.607	0.865 ± 0.972
E ± SE	0.803* ± 0.119	0.122* ± 0.040	0.027 ± 0.052	0.271* ± 0.032	1.088 ± 7.781	0.337* ± 0.791	0.182 ± 0.137
$(H_1/D)^{1/2}$	1.788	1.210	1.750	0.667	1.463	1.493	2.163
$H_2/4H_1$	0.184	0.221	0.227	0.204	0.200	0.188	0.219
$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	1.765	1.869	1.596	0.819	2.233	2.163	1.425
h^2/H_2	3.595	2.285	1.030	0.237	1.772	0.884	0.849
Heritability in narrow sense	0.326	0.265	0.245	0.463	0.263	0.344	0.256

*Significant at 5 % level of significance

Table 2. Promising top two parents and crosses identified for heat tolerance based on *gca* and *sca* effects for various characters

Characters	Parents	Crosses
Days to maturity	Lok 1**	Raj 3765** × PBW 373**
	WH 147**	Raj 3777* × Lok 1**
No. of effective tillers/pl	Lok 1**	Raj 3777** × Lok 1**
	Raj 3765**	Raj 3077 × PBW 373
Spike length (cm)	Raj 3777**	Raj 3777 × HD 2329**
	Raj 3765**	Raj 3077 × Lok 1**
No. of spikelets/ spike	Raj 3777**	Raj 3777 × Lok 1**
Number of grains/spike	Raj 1482**	Raj 3765 × PBW 373**
	WH 147**	Raj 3777 × Lok 1**
1000-grain weight (g)	Lok 1**	Raj 3077 × WH 147**
	HD 2329**	Raj 3765 × PBW 373**
Biological yield/plant (g)	Lok 1**	Raj 3777 × HD 2329**
	Raj 3765**	Raj 1482 × HD 2329**
Grain yield per plant (g)	WH 147**	Raj 3765 × HD 2329**
	HD 2329**	Raj 3077 × WH 147**

both the environments for at least one character were Raj 3077 × WH 147 for 1000-grain weight, Raj 3765 × HD 2329 for grain yield per plant and Raj 3765 × PBW 373 for days to maturity and Raj 3777 × WH 147 for plant height. The cross Raj 3765 × HD 2329 was found to show the highest and significant magnitude of *sca* effect for grain yield in HT environment. The cross combinations which were significant and good in HT environment were Raj 3765 × PBW 373 for days to maturity, number of grains per spike and 1000-grain weight, Raj 3777 × Lok 1 for number of effective tillers per plant, number of spikelets per spike and number of grains per spike.

It may be concluded that for improving wheat for heat tolerance, both additive and dominant gene action have to be exploited by adopting adequate breeding strategies *viz.*, biparental mating, diallel selective mating and reciprocal recurrent selection.

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