



Analysis of combining ability and gene action studies for grain yield and its component traits in bread wheat utilizing line x tester mating design

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ARTICLE INFO	ABSTRACT
<p>Received : 01 July 2021 Revised : 20 August 2021 Accepted : 31 August 2021</p> <p>Available online: 19 December 2021</p> <p>Key Words: Bread wheat General combining ability Grain yield Line x tester cross Specific combining ability</p>	<p>The present research investigation was conducted in order to analyze combining ability and nature of gene actions in 33 F₁s of bread wheat (<i>Triticum aestivum</i> L. em. Thell) developed by crossing eleven lines with three testers in a line x tester mating design in terms of grain yield and associated traits. The hybrids along with the parental lines and two check varieties were planted in a randomized block design in three replications. Variance ratio between general and specific combining ability was found to be less than unity which indicated the prevalence of non-additive gene actions involved in the inheritance of these characters. Parental lines QLD 75 (3.164), followed by SOKOLL (2.888) and QLD 65 (2.819) exhibited significant GCA for grain yield, while another line PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... was observed to be the better general combiner for most other traits including maturity. Among the hybrids cross combination NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/...x HD 3237 showed significant higher positive SCA for grain yield and biological yield per plant, whereas, F₁ QLD 75 x HI 1621 was a good specific combiner for harvest index (%) and number of grains per spike. The cross combination VORB/4/D67.2/PARANA66.270 x PBW 725 was observed with significant higher positive SCA for days to 75% heading, days to maturity and plant height, and another hybrid VORB/4/D67.2/PARANA 66.270 x HI 1621 exhibited significant positive SCA for 1000 grain weight and spike length.</p>

Introduction

Wheat is one of the most extensively cultivated crops among all the food grains throughout the world ensuring the food security to nearly 35% of the global population (Bonjean *et al.*, 2001). India holds the position of second largest producer of bread wheat globally after China having an acreage of 30.55 million hectares of land to register the all-time highest output of 107.18 million tonnes with an average national productivity hovering around 3508 kg/ha during rabi 2019-20 (Singh *et al.*, 2019). With the ongoing expansion of population in the nation, there will be requirement of more than 140 million tons of wheat grain to be produced by 2050, which is about 40% increase from our present production scenario (Singh *et al.*, 2019). Therefore, there is an urgent requirement for development superior high yielding varieties which can exploit heterosis to break the yield ceiling. Proper

identification of superior parents is an essential prerequisite for the development of superior high yielding varieties (Prasad, 2014). Therefore, for initiating any successful breeding programme requires the breeder to be aware of the nature of gene action and genetic system controlling the inheritance of those desired characters (Ismail, 2015). Combining ability analysis is frequently used by the breeders for evaluation of different lines in terms of their genetic value and their suitability for utilization as parents in a hybridization programme (Tabassum *et al.*, 2017). It also assists in characterization of gene actions involved in the inheritance of various complex quantitative traits including grain yield. The knowledge of general combining ability provides the guidance to the breeder for the identification of superior performing parents which will perform better than the rest of population while utilized in a hybridization programme, whereas, measure of specific combining ability enables a breeder to select higher yielding crosses for exploitation of heterosis and non-additive portion of genetic variance.

Keeping all the previously mentioned aspects into consideration our present research experiment was aimed at investigating the general and specific combining ability variances and effects and to study the nature and magnitude of gene actions involved for yield and yield attributing characters. The analysis has been carried out as per Kempthorne (1957). Combining ability analysis in wheat has been performed earlier by Thakre *et al.* (1996), Kalhoro *et al.* (2015), Jatav *et al.* (2017) and Younas *et al.* (2020).

Material and Methods

Our present research experiment was conducted at Norman E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar (29°N, 79.3° E and 243.84 m above mean sea level) during rabi season of 2018-19 and 2019-20. Eleven genotypes of wheat were used as lines for hybridization with three male testers to produce 33 F₁s during rabi season of 2018-19 (Table 1). These 33 F₁s along with their parents and two standard checks viz., UP 2855 and HD 2967 were then evaluated during rabi season of 2019-20. The experiment was laid out in a randomized complete block design with three

replications. Each plot within a replication consisted of two rows. Each row was one meter in length and the plants were spaced at 20 cm between row to row and 10 cm between plant to plant. Recommended cultural practices were provided accordingly to the plants. Observations were recorded on thirteen characters viz., days to 75% heading, days to maturity, number of productive tillers per plant, plant height, peduncle length, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, 1000 grain weight, biological yield per plant, grain yield per plant and harvest index (%).

Statistical Analysis

Combining ability analysis in line x tester design was carried out as per the method proposed by Kempthorne (1957), which was later modified by Arunachalam (1974). Significance of combining ability is tested in terms of 't' test as proposed by Fisher and Yates in 1938. Covariance between full sibs and covariance between half sibs were calculated from the expectations of mean squares as follows,

$$\begin{aligned} \text{Cov. H. S.}_{(\text{line})} &= \frac{M_1 - M_{1t}}{rt} \\ \text{Cov. H. S.}_{(\text{testers})} &= \frac{M_t - M_{1t}}{lt} \\ \text{Cov. H. S.}_{(\text{average})} &= \frac{1}{r(2lt-1)} \left[\frac{(l-1)(M_1) + (t-1)(M_t)}{1+t-2} - M_{1t} \right] \end{aligned}$$

$$\text{Cov. (F.S.)} = \left[\frac{(M_1 - M_e) + (M_t - M_e)}{3r} \right] + \left[\frac{6r \text{Cov. H.S.} - r(1+t) \text{Cov. H.S}}{3r} \right]$$

Where,

M_1 = MS line (female)

M_t = MS tester (male)

M_{1t} = MS due to line x tester

M_e = error mean sum of square

$$\text{Var. gca} = \text{Cov. H.S} \left[\frac{(1+F)}{4} \right] \text{Var. A}$$

Therefore,

$$\text{Var. A.} = \text{Cov. H.S}; \text{ if } F = 0$$

$$\text{Var. A.} = 2 \text{Cov. H.S}; \text{ if } F = 1$$

$$\text{Var. D.} = \text{Var. sca}; \text{ if } F = 1$$

Combining ability analysis is carried out utilizing 'INDOSTAT' statistical software developed at INDOSTAT Services, Hyderabad (<http://indostat.software.informer.com/>). ANOVA was also carried out utilizing the same software.

Table 1: Lines, Testers and Checks utilized for the study

SN	Lines	Testers	Checks
1.	QBP 12-11	HD 3237	UP 2855
2.	SOKOLL	PBW 725	HD 2967
3.	WH 1182	HI 1621	
4.	QLD 75		
5.	PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//...		
6.	QLD 65		
7.	NW 6036		
8.	K 1402		
9.	VORB/4/D67.2/PARANA 66.270		
10.	HPBW 01		
11.	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5//...		

Results and Discussion

Components of variance for combining ability

Analysis of variance is carried out for all the thirteen characters at 5% significance level. ANOVA was carried out using ‘INDOSTAT’ statistical software and results are tabulated in table 2. Analysis of variance revealed that mean sum of squares due to lines was significant for days to 75% maturity while mean sum of squares due to testers was found significant for number of spikes per plant. The mean sum of squares due to line x testers were significant for days to 75% heading, days to maturity, number of tillers per plant, spike length, biological yield per plant, number of grains per spike, 1000 grain weight, grain yield per plant, grain weight per spike and harvest index.

Analysis for genetic components of variance displayed that variance ratio between general and specific combining ability was estimated to be less than unity for all the traits under investigation except for number of spikelets per spike. This was an indicative of prevalence of nonadditive gene action involved in the inheritance of these traits, while only one trait number of spikelets per spike was governed by additive gene action. Further, the dominance ratio was revealed to be less than one for the traits days to 75% heading and number of spikelets per spike indicating these traits to be governed by partial dominance, whereas, traits like number of tillers per plant, days to maturity and spike length were having dominance ratio of one and, therefore, these traits seemed to be governed by dominance. Inheritance of rest of the traits were

observed to be under the control of over dominance. The similar results were observed in the earlier experimental findings of Jatav *et al.* (2017), Sarwar (2016) and Saeed *et al.* (2016).

Combining ability effects

Days to 75% heading

GCA effects for the trait days to 75% heading varied between -2.990 to 2.677. Out of fourteen parental lines six lines showed significant amount of GCA effects. PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... (-2.990) followed by K 1402 (-2.101) were observed to possess highly significant negative GCA effects for the trait.

SCA effects for days to 75% heading were observed varying from -2.929 to 2.525. Three, out of thirty three combinations possessed significant SCA effects. Hybrid VORB/4/D67.2/PARANA66.270 x PBW 725 (-2.929) followed by HPBW 01 x HI 1621(-2.152) showed significant negative SCA effects for the trait.

Days to maturity

GCA effects for days to maturity were observed in a range from -2.455 to 2.101. Parental lines PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... (-2.455) followed by QBP 12-11 (-2.101) had high significant negative GCA effects for the trait.

For days to maturity SCA effects ranged from -4.404 to 3.717. Three cross combinations expressed significant SCA effects for the trait. The cross combination VORB/4/ D67.2/PARANA66.270 x PBW 725 (-4.404) was observed with highest significant negative SCA effects.

Number of tillers per plant

In terms of number of tillers per plant GCA effects ranged between -2.212 to 2.876. GCA effect values were observed significant for six parents out of fourteen. Parental line QLD 65 (2.876) followed by QBP 12-11 (1.438) were observed to have high significant positive GCA effects.

SCA effects were observed from -3.368 to 3.009 for number of productive tillers per plant. Six cross combinations exhibited significant SCA effects for the trait. Hybrids HPBW 01 x HI 1621 (3.009) followed by NW 6036 x HD 3237 (2.834) and QLD 75 x PBW 725 (1.979) exhibited significant positive SCA effects.

Plant height (cm)

Range of GCA effects for plant height was observed from -4.046 to 3.345. QBP 12-11 (-4.046)

Table 2: Analysis of variance for combining ability for different characters

Source of variation	d. f.	D75H	DM	NTPP	PH	PL	SL	NSPS	NGPS
Replication	2	17.707**	21.586*	18.338**	180.908**	18.932*	1.234*	11.235**	53.287**
Crosses	32	12.968**	16.698**	14.523**	30.526	9.083	0.773**	1.745**	102.852**
Line	10	28.321**	21.277	17.796	42.51	12.381	1.043	1.951	147.982
Tester	2	6.495	32.131	35.34	6.545	8.833	1.357	6.956**	60.801
Line x Tester	20	5.939*	12.865**	10.805**	26.932	7.459	0.580*	1.121	84.492**
Error	64	3.009	4.825	2.162	21.303	5.877	0.291	0.837	8.867
Total	98	6.561	9.044	6.528	27.572	7.19	0.467	1.346	40.463

Source of variation	d. f.	GWPS	GW	BYPP	GYPP	HI
Replication	2	0.001	1.757	300.949**	73.614**	6.074
Crosses	32	0.168**	24.692**	381.425**	85.311**	12.551**
Line	10	0.274	25.914	384.902	73.583	8.128
Tester	2	0.109	5.953	527.856	128.513	12.124
Line x Tester	20	0.121**	25.955**	365.043**	86.855**	14.806**
Error	64	0.007	0.807	48.888	7.814	2.375
Total	98	0.059	8.626	162.616	34.462	5.773

was observed with significant high negative GCA effects for the trait. Parental line NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... (3.226) possessed significant higher positive GCA for the trait.

SCA effects for plant height varied from -4.255 to 6.694. Significant positive SCA effects were observed in the cross VORB/4/D67.2/PARANA66.270 x HI 1621 (6.694). None of the cross exhibited significant negative SCA effects for the trait.

Peduncle length (cm)

In terms of peduncle length the GCA effect values ranged from -1.625 to 1.810. Significant negative GCA effects were observed in the line QLD 75 (-1.625), whereas, the parental line PRL/2*PASTOR*2/FH6-1-7/3/KINGBIRD#1//... (1.810) was observed with highest significant positive GCA for the trait.

SCA effects for peduncle length varied from -2.089 to 3.260 among the crosses. Out of thirty three F₁s, only one cross combination VORB/4/D67.2/PARANA66.270 x HI 1621 (3.260) exhibited significant positive SCA effect.

Spike length (cm)

GCA effects for spike length varied from -0.457 to 0.557. Parental lines NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... (0.557) and PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... (0.482) exhibited significant

positive GCA effects.

SCA effects among the crosses ranged from -0.889 to 0.618. None of the hybrids exhibited significant positive SCA effects for the trait.

Number of spikelets per spike

GCA effects for the trait number of spikelets per spike ranged from -0.895 to 0.366. None of the lines had significant positive GCA for the trait. Among the testers HD 3237 (0.366) exhibited positive GCA effects.

SCA effects for number of spikelets per spike ranged from -1.068 to 1.229. Hybrid HPBW 01 x PBW 725 (1.229) exhibited significant positive SCA effects for the trait.

Number of grains per spike

The values of GCA effects in terms of number of grains per spike varied from -4.777 to 7.396. HPBW 01 (7.396), followed by NW 6036 (5.919) showed high significant positive GCA effects for the trait.

SCA effects for number grains per spike were varying from -7.003 to 8.289. Among thirty three hybrids seventeen showed significant SCA effects for the trait. The cross combinations QLD 75 x HI 1621(8.289) followed by NW 6036 X HI 1621 (7.034) exhibited high significant positive estimates of SCA effects.

Grain weight per spike (g)

GCA effects for the trait grain weight per spike ranged from -0.165 to 0.325. Among the parental

Table 3. GCA effects of the parents for different characters

Parents	D75H	DM	NTPP	PH	PL	SL	NSPS
1.QBP 12-11	-1.990**	-2.121**	1.438**	-4.046**	-1.067	-0.261	-0.895**
2.SOKOLL	0.566	0.545	-0.029	-0.054	-0.517	0.263	-0.463
3.WH 1182	2.677**	1.879*	0.476	0.056	-1.419	-0.052	0.464
4.QLD 75	2.010**	1.545	0.788	-2.586	-1.625*	-0.24	0.328
5.PRL/2*PASTOR*2/FH6-1-7/3/KINGBIRD#1//...	-2.990**	-2.455**	-0.657	-0.48	1.810*	0.482**	0.07
6. QLD 65	0.677	-0.232	2.876**	0.26	-0.395	-0.424*	0.456
7.NW 6036	1.455*	2.101**	-0.668	0.585	-0.324	-0.457*	0.371
8. K 1402	-2.101**	-1.343	0.135	-1.122	1.407	-0.063	-0.294
9.VORB/4/D67.2/PARANA 66.270	-0.101	-0.566	-2.212**	3.345*	1.374	0.159	0.255
10. HPBW 01	-0.212	0.101	-0.579	0.817	0.429	0.037	0.231
11.NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/...	0.01	0.545	-1.568**	3.226*	0.327	0.557**	-0.524
SE of gi	0.5732	0.7855	0.5414	1.4166	0.7678	0.1786	0.3057
SE of gi- gj	0.8106	1.1109	0.7656	2.0033	1.0859	0.2525	0.4323
12.HD 3237	0.475	0.949*	0	0.257	0.54	0.156	0.366*
13.PBW 725	-0.404	0.071	-1.035**	-0.514	-0.048	-0.229*	-0.515**
14.HI 1621	-0.071	-1.020*	1.035**	0.257	-0.492	0.073	0.149
SE of gi	0.2993	0.4102	0.2827	0.7398	0.401	0.0933	0.1596
SE of gi – gj	0.4233	0.5801	0.3998	1.0462	0.5671	0.1319	0.2258

Table 3. contd...

Parents	NGPS	GWPS	GW	BYPP	GYPP	HI
1. QBP 12-11	-4.777**	-0.165**	-0.459	6.075*	2.730*	0.694
2. SOKOLL	-0.627	-0.142**	1.655**	3.675	2.888**	1.392**
3. WH 1182	-0.648	0.048	-2.029**	-0.925	0.817	0.484
4. QLD 75	-3.121**	0.325**	1.839**	7.325*	3.164**	1.352**
5. PRL/2*PASTOR*2/FH6-1-7/3/KINGBIRD#1//...	-0.522	-0.142**	-1.657**	-0.708	-0.553	-0.354
6. QLD 65	-0.952	-0.210**	1.593**	11.164**	2.819**	-0.652
7. NW 6036	5.919**	-0.102**	-0.436	-2.64	-0.288	0.613
8. K 1402	-2.018*	0.151**	-1.862**	-0.622	-0.216	-0.355
9. VORB/4/D67.2/PARANA 66.270	-4.558**	0.075**	-0.914*	-10.177**	-5.389**	-1.350**
10. HPBW 01	7.396**	-0.048	-0.596	-6.586*	-3.104**	-0.990*
11. NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/...	3.909**	0.210**	2.865**	-6.581*	-2.868**	-0.834
SE of gi	0.908	0.0273	0.3561	2.7619	1.036	0.4669
SE of gi- gj	1.2841	0.0386	0.5036	3.906	1.4652	0.6603
12. HD 3237	1.555**	-0.063**	-0.141	1.796	-0.053	-0.342
13. PBW 725	-0.947	0.049**	0.477*	-4.583**	-1.947**	-0.358
14. HI 1621	-0.608	0.014	-0.336	2.786	1.999**	0.700**
SE of gi	0.4742	0.0143	0.186	1.4424	0.5411	0.2438
SE of gi – gj	0.6706	0.0202	0.263	2.0398	0.7652	0.3448

*, ** significant at 5% and 1% probability levels, respectively. D75H = Days to 75% heading, DM = Days to maturity, NTPP = Number of tillers per plant, PH = Plant height, PL = Peduncle length, SL= Spike length, NSPS = Number of spikelets per spike, NGPS= Number of grains per spike, GWPS = Grain weight per spike, GW= 1000 grain weight, BYPP = Biological yield per plant, GYPP = Grain yield per plant, HI = Harvest index.

Table 4: General and specific combining ability variances

SN	Characters	σ_{GCA}^2	σ_{SCA}^2	$\sigma_{GCA}^2/\sigma_{SCA}^2$	Degree of dominance (H/D) ^{1/2}
1	Days to 75% heading	0.6881**	0.9941*	0.692	0.8499
2	Days to maturity	1.0072**	2.4372**	0.413	1.0999
3	Number of tillers per plant	1.1395**	2.7224**	0.418	1.0929
4	Plant height (cm)	0.308	2.9574	0.104	2.1912
5	Peduncle length (cm)	0.252	0.718	0.351	1.192
6	Spike length (cm)	0.043	0.098	0.439	1.06
7	Number of spikelets per spike	0.172	0.093	1.849	0.521
8	Number of grains per spike	4.618	25.691	0.180	1.668
9	Grain weight per spike (g)	0.009	0.038	0.237	1.47
10	1000 grain weight (g)	0.704	8.271	0.085	2.423
11	Biological yield per plant (g)	18.463	98.796	0.187	1.636
12	Grain yield per plant (g)	4.352	25.732	0.169	1.719
13	Harvest Index (%)	0.389	4.281	0.091	2.347

Table 5: Parental lines and crosses with highest GCA and SCA effects for different characters

SN	Characters	Best general combiner	Best specific combiner
1	Days to 75% heading	PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//...(-2.990)	VORB/4/D67.2/PARANA66.270 x PBW 725 (-2.929)
2	Days to maturity	PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... (-2.455)	VORB/4/D67.2/PARANA66.270 x PBW 725 (-4.404)
3	Number of tillers per plant	QLD 65 (2.876)	HPBW 01 x HI 1621 (3.009)
4	Plant height (cm)	QBP 12-11 (-4.046)	VORB/4/D67.2/PARANA 66.270 x PBW 725 (-4.255)
5	Peduncle length (cm)	PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... (1.810)	VORB/4/D67.2/PARANA 66.270 x HI 1621 (3.26)
6	Spike length (cm)	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5//...(0.557)	QBP 12-11 X HD 3237 (0.614)
7	Number of spikelets per spike	HD 3237 (0.366)	HPBW 01 x PBW 725 (1.229)
8	Number of grains per spike	HPBW 01 (7.396)	QLD 75 X HI1621 (8.289)
9	Grain weight per spike (g)	QLD 75 (0.325)	K 1402 x HD 3237 (0.392)
10	1000 grain weight (g)	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5//...(2.865)	VORB/4/D67.2/PARANA 66.270 x HI 1621 (5.464)
11	Biological yield per plant (g)	QLD 65 (11.164)	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5//... x HD 3237 (18.054)
12	Grain yield per plant (g)	QLD 75 (3.164)	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5//...x HD 3237 (9.237)
13	Harvest Index (%)	SOKOLL (1.392)	QLD 75 x HI1621 (2.806)

Table 6: SCA effects of crosses for different characters

Crosses	D75H	DM	NTPP	PH	PL	SL	NSPS
QBP 12-11 X HD3237	0.414	-2.061	-1.472	-2.231	0.009	0.614	-0.295
QBP 12-11 x PBW725	-0.374	3.152*	0.662	1.4	-0.56	0.276	0.58
QBP 12-11 X HI1621	-0.04	-1.091	0.809	0.832	0.551	-0.889**	-0.285
SOKOLL X HD3237	-0.141	-1.061	1.062	0.282	0.37	-0.15	0.755
SOKOLL X PBW725	-0.596	-0.848	-1.538	-2.603	-0.322	-0.324	-0.509
SOKOLL X HI1621	0.737	1.909	0.476	2.321	-0.048	0.474	-0.245
WH1182 X HD3237	-0.586	-1.394	-2.144*	0.203	-0.962	-0.179	-0.287
WH1182 XPBW725	0.96	0.818	0.89	3.171	0.259	-0.293	-0.126
WH1182 X HI1621	-0.374	0.576	1.254	-3.374	0.703	0.472	0.413
QLD75 X HD3237	0.747	0.273	-0.555	-3.4	-0.322	-0.057	-0.076
QLD75 X PBW725	-1.04	-0.848	1.979*	0.006	-1.785	-0.088	-0.31
QLD75 X HI1621	0.293	0.576	-1.424	3.393	2.106	0.145	0.386
PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... X HD3237	-0.253	1.939	-0.444	0.752	-0.816	0.188	0.078
PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... X PBW725	-0.04	-1.515	-0.91	-0.431	1.125	0.007	-0.076
PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... X HI1621	0.293	-0.424	1.354	-0.321	-0.309	-0.195	-0.002
QLD65 X HD3237	0.414	1.051	-0.144	1.102	1.225	-0.006	0.73
QLD65 X PBW725	0.293	0.263	-1.51	1.684	0.962	-0.171	-0.522
QLD65 X HI1621	-0.707	-1.313	1.654	-2.786	-2.187	0.177	-0.208
NW6036 X HD3237	-1.697	0.051	2.834**	1.804	-0.007	0.077	-0.728
NW6036 X PBW725	0.515	0.929	0.535	1.317	1.78	0.046	0.103
NW6036 X HI1621	1.182	-0.98	-3.368**	-3.121	-1.774	-0.123	0.625
K1402 X HD3237	-1.808	-0.505	0.874	1.4	1.273	-0.15	-0.286
K1402 X PBW725	1.737	1.04	0.465	0.826	0.817	-0.131	-0.387
K1402 X HI1621	0.071	-0.535	-1.338	-2.226	-2.089	0.282	0.673
VORB/4/D67.2/PARANA 66.270 X HD3237	2.525*	3.717**	-0.055	-2.439	-0.968	0.027	0.228
VORB/4/D67.2/PARANA 66.270 X PBW725	-2.929**	-4.404**	0.812	-4.255	-2.292	-0.121	-0.313
VORB/4/D67.2/PARANA 66.270 X HI1621	0.404	0.687	-0.757	6.694**	3.260*	0.094	0.085
HPBW01 X HD3237	1.303	0.051	-1.855	0.572	0.108	-0.684*	-0.161
HPBW01 X PBW725	0.848	1.596	-1.154	0.91	-0.38	0.351	1.229*
HPBW01 X HI1621	-2.152*	-1.646	3.009**	-1.482	0.272	0.333	-1.068*
NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5//... X HD 3237	-0.919	-2.061	1.900*	1.954	0.089	0.321	0.042
NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5//... X PBW725	0.626	-0.182	-0.232	-2.025	0.397	0.449	0.331
NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5//... X HI1621	0.293	2.242	-1.668	0.071	-0.486	-0.770*	-0.373
CD95%SCA	1.983	2.718	1.873	4.902	2.657	0.618	1.058
SE of SCA	0.9928	1.3605	0.9377	2.4536	0.3093	0.5294	4.7838
SE(s_{ij} - s_{kl})	1.404	1.9241	1.3261	3.4699	0.4374	0.7488	6.7654
SE(s_{ij} - s_{ik})	2.8081	3.8482	2.6522	6.9398	0.8748	1.4975	13.5307

Table 6 contd...

Crosses	NGPS	GWPS	GW	GYPP	BYPP	HI
QBP 12-11 X HD3237	-4.483**	-0.083	2.689**	-0.8	-8.969	2.096*
QBP 12-11 x PBW725	3.976*	0.192**	-2.270**	-2.22	1.994	-2.596**
QBP 12-11 X HII621	0.507	-0.109*	-0.419	3.02	6.975	0.5
SOKOLL X HD3237	1.401	0.214**	3.071**	2.331	4.831	0.314
SOKOLL X PBW725	5.603**	-0.158**	-2.181**	-7.095**	-9.740*	-2.907**
SOKOLL X HII621	-7.003**	-0.057	-0.891	4.763*	4.908	2.592**
WH1182 X HD3237	2.746	-0.162**	-0.021	-7.250**	-10.152*	-3.358**
WH1182 XPBW725	-1.203	0.076	2.057**	4.763*	8.177	2.251**
WH1182 X HII621	-1.543	0.085	-2.036**	2.487	1.975	1.107
QLD75 X HD3237	-2.719	-0.202**	-1.464*	-4.907**	-1.785	-2.412**
QLD75 X PBW 725	-5.570**	0.001	1.001	3.871*	10.010*	-0.394
QLD75 X HII621	8.289**	0.201**	0.463	1.037	-8.225	2.806**
PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... X HD3237	-1.03	0.028	-3.223**	-2.943	-9.335	-0.053
PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... X PBW725	-1.188	-0.181**	2.865**	-1.324	-6.323	0.839
PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... X HII621	2.218	0.152**	0.358	4.267*	15.658**	-0.785
QLD65 X HD3237	4.531**	0.131**	1.820**	-1.706	-4.208	-0.57
QLD65 X PBW725	-0.412	-0.073	0.445	2.294	1.755	1.527
QLD65 X HII621	-4.118*	-0.057	-2.265**	-0.588	2.453	-0.957
NW6036 X HD3237	-6.476**	-0.250**	4.114**	5.707**	16.993**	-0.307
NW6036 X PBW725	-0.558	0.056	-3.316**	1.354	-0.208	1.275
NW6036 X HII621	7.034**	0.195**	-0.798	-7.061**	-16.785**	-0.969
K1402 X HD3237	0.586	0.392**	-1.234*	4.175*	2.611	2.140*
K1402 X PBW725	-6.567**	-0.077	2.000**	-0.744	2.45	-1.18
K1402 X HII621	5.981**	-0.315**	-0.766	-3.431	-5.062	-0.96
VORB/4/D67.2/PARANA 66.270 X HD3237	5.425**	-0.089	-2.739**	0.425	1.45	0.781
VORB/4/D67.2/PARANA 66.270 X PBW725	-1.603	0.248**	-2.725**	2.841	1.663	1.588
VORB/4/D67.2/PARANA 66.270 X HII621	-3.822*	-0.159**	5.464**	-3.266	-3.113	-2.369**
HPBW01 X HD3237	0.998	-0.019	-2.811**	-4.270*	-9.491	-1.295
HPBW01 X PBW725	4.262**	0.015	3.627**	-1.549	-3.845	-0.24
HPBW01 X HII621	-5.260**	0.004	-0.816	5.819**	13.336**	1.534
NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... X HD3237	-0.979	0.04	-0.202	9.237**	18.054**	2.663**
NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... X PBW725	3.260*	-0.099*	-1.504*	-2.192	-5.934	-0.165
NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... X HII621	-2.281	0.06	1.706**	-7.045**	-12.120*	-2.499**
CD95%SCA	3.142	0.095	1.232	3.585	9.557	1.616
SE of SCA	1.5727	0.6168	1.7945	0.0473	0.8087	1.3299
SE(s_{ij} - s_{ik})	2.2242	0.8723	2.5378	0.0669	1.1437	1.8808
SE(s_{ij} - s_{ik})	4.4484	1.7446	5.0756	0.1338	2.2874	3.7615

lines QLD 75 (0.325) followed by K 1402 (0.151) exhibited significant positive GCA for the trait.

In terms of SCA effects, values for the trait ranged between -0.315 to 0.392. Seventeen hybrids were observed to possess significant SCA effects. The cross combinations K 1402 x HD 3237 (0.392) and VORB/4/D67.2/PARANA66.270 x PBW 725 (0.248) expressed high significant positive SCA effects for the trait.

1000 grain weight (g)

GCA effects for 1000 grain weight among the parental lines were varying from -2.029 to 2.865. Significant positive GCA effects were observed in the line NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... (2.865) followed by QLD 75 (1.839).

Whereas, SCA effects for the trait varied from -3.316 to 5.464 among the crosses. Twenty-two exhibited significant SCA effects for the character. The highest significant positive SCA effects were observed in the hybrid VORB/4/D67.2/PARANA66.270 x HI 1621 (5.464) followed by NW 6036 x HD 3237 (4.114).

Biological yield per plant (g)

GCA effects for the trait biological yield per plant ranged from -10.177 to 11.14. Seven parental lines expressed significant GCA effects for the trait. Parental lines QLD 65 (11.164) followed by QLD 75 (7.325) and QBP 12-11 (6.075) showed significant positive GCA for the trait.

For biological yield per plant SCA effects ranged from -16.785 to 18.054, Nine out of thirty-three F1s expressed significant SCA effects. The cross combination NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... x HD 3237 (18.054) followed by NW 6036 X HD 3237 (16.993) exhibited high significant positive SCA effects for the trait.

Grain yield per plant (g)

GCA effects for grain yield per plant ranged from -5.389 to 3.164. Five parental lines out of fourteen were observed with high significant positive GCA effects. The line QLD 75 (3.164), followed by SOKOLL (2.888), QLD 65 (2.819), QBP 12-11 (2.73) and HI 1621 (1.999) exhibited high significant positive GCA effects for the trait.

In terms of SCA effects the values for the trait observed between -7.250 to 9.237. Fourteen out of thirty-three crosses were observed to possess

significant SCA effects for the trait. The cross combination

NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... x HD 3237 (9.237), followed by HPBW 01 x HI 1621 (5.819), SOKOLL x HI 1621 (4.763), WH 1182 x PBW 725 (4.763) and QLD 75 x PBW 725 (3.781) exhibited significant positive SCA effects.

Harvest Index

Parental lines varied in a range from -1.35 to 1.392 for the trait harvest index. Five parental lines showed significant GCA effects for the character. Lines SOKOLL (1.392) followed by QLD 75 (1.352) were observed to possess significant positive GCA for the trait.

SCA effects among the crosses ranged from -3.358 to 2.806 for harvest index. Twelve F1s showed significant SCA effects. The highest significant positive SCA effects were demonstrated by the cross QLD 75 x HI 1621 (2.806) followed by NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/... x HD 3237 (2.663). The results presented here are in accordance with earlier observations of Singh *et al.* (2013), Barot *et al.* (2014), Arya *et al.* (2018) and Patel *et al.* (2020).

The results highlighted from the present research investigation are in close confirmation with the earlier observations of Singh *et al.* (2013), Din *et al.* (2020) and Patel *et al.* (2020) for maturity traits; Kalhoro *et al.* (2015), Arya *et al.* (2018) and Patel *et al.* (2020) for tillers per plant, spikelets per spike, biological yield, spike length and grain yield per plant and Lohithaswa *et al.* (2014), Kalhoro *et al.* (2015) and Jatav *et al.* (2017) for harvest index (%), grains per spike and grain weight per spike.

Conclusion

The present research investigation revealed that there is ample opportunity to exploit the genotypes in terms of combining ability. The parental lines VORB/4/D67.2/PARANA66.270, NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/..., PRL/2*PASTOR*2//FH6-1-7/3/KINGBIRD#1//... and QBP 12-1 were observed to be the superior parents for most of the traits including grain yield based on overall performance along with GCA and are recommended for further utilization in the future breeding programmes. In

terms of cross combinations VORB/4/D67.2/PARANA66.270 x PBW 725 was observed to be the superior hybrid for most of the traits, while, the cross combination NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/

2*PASTOR/5/..... x HD 3237 was showing better performance for grain yield. Therefore, these cross combinations may be further exploited for the isolation of suitable transgressive segregants in a breeding programme.

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