Original Research Article

ESTIMATION OF COMBINING ABILITYIN BREAD WHEAT USING LINE X TESTER ANALYSIS

Abstract

The present investigation was undertaken to study the combining ability for yield and its components in F_1 generation of wheat through Line × tester analysis. Experiment was conducted with 3 replications and 39 genotypes consisting 9 lines *viz.,* HD 2851, HD 2893, HD 3226, PBW 677, HD 3086, PBW 725, Phule samadhan, Phule unnat, GW 273 and 3 testers *viz.,* Faisalabad 2005, HW 2045, PBW 343 and their 27 crosses made in L × T mating fashion in randomized block design at experimental research farm, Lovely Professional University, Phagwara, Punjab during 2023-24. The genotypes (parents and crosses) exhibited highly significant variation for all traits studied indicating the presence of genotypic differences among these twelve genotypes under investigation. The mean square of parent vs crosses was found to be highly significant for all traits studied expect 1000 grain weight. Further partitioning of crosses mean squares i.e., Line×tester analysis showed highly significant for all traits studied. Line × tester analysis is used in predicting the effects of the general combining ability of parents and specific ability combining of their crossesThe lines PBW 725, GW 273 and tester PBW 343 exhibited significant GCA for grain yield. The lines PBW 725, HD 2893 and Phule unnat which performed good combining ability effects for biological yield per plant were also good combiners. Among the cross combination PBW 725 × PBW 343 showed significant positive SCA for grain yield and biological yield per plant, whereas, PBW 725 × Faisalabad 2005, HD 2893 × HW 2045 and GW 273 × PBW 343 was a good specific combiner for 1000 grain weight.

Keywords: Bread wheat, line × testeranalysis, GCA, SCA, Combining ability

Introduction

Bread wheat (*Triticum aestivum* L. em. Theil)is one of the world's most important cereal crops, providing a major source of dietary energy and protein for millions of people worldwide (FAOSTAT 2021). Bread wheat (*Triticum aestivum* L. em. Theil) belongs to the Poaceae family whose chromosome number 42. This cereal grain is highly nutritious and plays a vital role in ensuring food security, and sustaining livelihoods. Its significance lies in being an essential dietary component that contributes to the well-being and economic stability of populations. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity, nutritive value, and the prominent position it holds in the international food grain trade.It consists of about 55% carbohydrates, 10-18 % protein and 19% of calories required for humans, and it is also used as a straw for feeding animals.

According to the Food and Agriculture Organization of the United Nations (FAO), the worldwide production of wheat in 2022-23 was approximately 806.2 million tonnes (FAO, 2023). The top five wheat producing countries in the world are China, India, Russia, the United States, and Canada. India is the world's second-largest producer of wheat (Jaiswal *et al.*,2010). In India, it is the second most important food crop after rice both in terms of area and production. According to the Ministry of Agriculture and Farmers' Welfare,Production of wheat during

2022-23 is estimated at record 1105.54 Lakh tonnes. It is higher by 28.12 Lakh tonnes than previous year's wheat production of 1077.42 Lakh tonnes and by 48.23 Lakh tonnes than the average wheat production of 1057.31 Lakh tonnes.

Analyzing general combining ability (GCA) and specific combining ability (SCA) is vital for plant breeders when selecting parental lines and hybrid combinations for developing high-yielding cultivars (Fasahat *et al.*,2016). GCA helps identify parents that contribute favorable additive effects for yield and yield components, while SCA estimates reveal hybrid combinations exhibiting superior performance due to non-additive gene action. Understanding the relative contributions of GCA and SCA provides insights into the genetic control of traits, guiding appropriate breeding strategies. Additionally, SCA estimates allow breeders to exploit heterosis by identifying hybrid combinations with high hybrid vigor for yield-related traits, ultimately leading to the development of high-performing hybrid cultivars.

In plant breeding programs, selecting parents with the desired characteristics that have strong general combining ability effects on grain yield and its components, as well as significant estimations for specific combining ability effects, is crucial. These estimations will aid in developing solid, efficient, and successful breeding techniques to achieve quick and deliberate development in this crop. The current study focused to analyze the capacity and genetic makeup of grain yield and yield related traits in wheat crossings using a line × tester design.

Materials and Methods:

The experimental material consisted twelve genotypesof bread wheat consisting nine lines*viz.*, HD 2851, HD 2893, HD 3226, PBW 677, HD 3086, PBW 725, Phulesamadhan, Phuleunnat, GW 273 and three testers*viz.*, Faisalabad 2005, HW 2045, PBW 343were crossed in all possible combinations usingline × tester mating design during Rabi 2022-23 at agriculture research farm, Lovely Professional University, Phagwara, Punjab. The 12 parental lines along with 27 F$_1$s were sown inrandomized block design with three replications during*Rabi* 2023-24.Observations were recorded on randomly selected 5 tagged plants and different yield contributing traits viz., days to 50% heading, days to maturity, flag leaf area (cm2), plant height, number of tillers per plant, spike length, 1000-grain weight(g), grain yield per plant(g), number of spikelets per spike, number of grains per spike,biological yield per plant and harvest index.Line x tester analysis wascarried out for determining the effect due to general and specific combining ability as described by Kempthorne adapted by Singh and Chaudhary.

Results and Discussion

Analysis of variance

Significant (P≤0.05 or 0.01) differences were found among the genotypes for all studied traits (Table 1) indicating the presence of sufficient genetic variation among the lines, testers, and their crosses. Obvious differences observed between the minimum and maximum of mean values of the genotypes for the studied traits were 16.00 days, 19.33 days, 22.47cm, 3.53 tillers, 3.07cm, 8.26cm^{2,} 4.07g, 15.8g, 3.46 spikelet, 21.74 grains, 26.86g, and12.08%for DH, DM, PH,

NT/P, SL, FLA, TGW, GY/P, NS/S, NG/S, BY/P, and HI%, respectively (Table 2). Parents and crosses exhibited significant (P≤0.05 or 0.01) differences for all traits. Significant (P≤0.05 or 0.01) differences were found for the contrast parents *vs*. crosses for all traits except days to heading and plant height indicating considerable amount of average heterosis was reflected in their crosses for most traits (Table 1). Partitioning mean squares of crosses (line × tester) revealed that variance due to both of lines and testers were significant for most traits of lines and testers and days to heading of testers. The variance due to line × tester was significant for all traits studied indicating that the nine lines did express effective role with the three testers according to their crosses performance (Table 1). Similar findings were also reported by Abd El-Aty *et al.*,2016, El-Gammaal*et al.*,2019, Abro *et al.*,2021 and Roy *et al.*,2021.

TABLE 1. Mean squares for line × tester design for the studied traits

Sources	Df	Days to 50% heading	Days to maturity	Plant height (cm)	Number of tillers per plant	Spike length(cm)
Rep	2	5.88	7.59	2.04	0.06	0.02
Genotypes	38	41.17**	56.95**	65.80**	2.29**	1.87**
Parents	11	20.18**	64.81**	102.12**	2.56**	2.70**
Crosses	26	6.18**	33.57**	52.46**	1.98**	1.54**
P vs C	1	1181.70**	578.51**	13.33**	7.23**	1.36**
Lines	8	15.41**	67.15**	120.58**	3.03**	2.49*
Testers	2	7.27**	108.79**	164.18**	9.93**	0.68
L x T	16	1.43	7.38*	4.44**	0.47**	1.17**
Error	76	3.02	3.45	1.05	0.12	010

,*significant at 0.05 and 0.01 levels of probability, respectively.

Table1 : Continued…

Sources	Df	Flag leaf area(cm)2	1000-grain weight (g)	Grain yield per plant (g)	Number of spikelets per spike	Number of grains per spike
Rep	2	2.03	0.12	0.35	0.36	3.31
Genotypes	38	11.65**	2.96**	26.04**	2.85**	59.04*
Parents	11	19.45**	3.76**	58.02**	4.95**	115.67**
Crosses	26	4.86**	2.72**	6.79**	1.62**	33.21**
P vs C	1	102.35**	0.36	174.77**	11.49**	107.55**
Lines	8	7.19**	1.89	11.40	1.83	67.06**
Testers	2	16.81**	8.67*	30.69**	2.26	119.16**
L x T	16	2.21**	2.40**	1.49	1.44**	5.54**
Error	76	0.49	0.35	1.13	0.35	1.29

*, ** significant at 0.05 and 0.01 levels of probability, respectively.

Table1 : Continued…

Sources	Df	Biological yield per plant (g)	Harvest index (%)

Rep	2	0.08	1.05
Genotypes	38	73.01**	31.30**
Parents	11	143.77**	62.36**
Crosses	26	26.80**	16.42**
P vs C	1	496.14**	76.43**
Lines	8	46.81**	37.94**
Testers	2	68.24**	34.48**
L x T	16	11.62**	3.40
Error	76	1.54	5.46

*,** significant at 0.05 and 0.01 levels of probability, respectively.

For line, L3 recorded the earliest line in days to 50% heading by 94.67 days and the lowest line in each of days to maturity (127.33 days), flag leaf area (16.60cm^2), biological yield/plant (48.67g) (Table 2). Moreover, L3 gave the highest values for each of plant height (85.20cm), number of tiller/plant (7.87 tillers), spike length(10.60cm), 1000-grain weight (38.13g), grain yield/plant (20.07g), number of spikelet/spike (18.87 spikelet), number of grains/ spike (56.13 grains) and harvest index (41.21%). The line L7 gave the highest values for each of days to maturity(141.33 days). Line L2recorded the flag leaf area (24.73cm^2), biological yield (73.73g). (Table 2).

For testers,T1 gave the highestvalues for each of days to 50% heading (100.33), number of tiller/plant (9.07 tillers), number of spikelet/spike (19.93 spikelet) (Table2). T2 gave the highest values for eachof days to maturity(137.33 days), spike length (11.27cm), 1000-grain weight (40.27g).T3 recorded the highest values for plant height (85.93cm), flag leaf area(23.20cm^2), grain yield/plant (24.07g), number of grains/ spike (67.07 grains), biological yield (62.53g), harvest index (38.47%) (Table 2). Similar results are in line with conclusions of Abro *et al.*,2021, Roy *et al.*,2021, Baloch *et al.*,2016.

Concerning crosses, cross L3 × T3 recordedthe earliest cross for days to 50% heading(89.33 days). L5 × T3 recordedthe highest values for plant height (91.00cm).L2× T3 gave the highest values for each of flag leaf area(21.33), grain yield/plant (22.40) and biological yield/plant (60.80). L3 × T2 gave the highest values foreach of spike length (11.53) and number of spikelet/ spike (19.80). L8 × T3 recorded the highest number of grains/spike (68.00 grains).L1× T1 recorded the highest tillers/plant (10.00 tillers), L2× T3 gave the highest biological yield (60.80g) and L3 × T3 recorded the highest harvest index (40.05%).

TABLE 2. Mean performance for the studied traits of the 9 lines, 3 testers and their 27 F1s crosses

Genotypes	Days to 50% heading	Days to maturity	Plant height (cm)	Number of tillers per plant	Spike length(cm)	Flag leaf area(cm)2
L1	99.33	137.67	79.40	9.80	10.87	17.80
L2	97.33	135.67	76.33	7.40	10.27	24.73
L3	94.67	127.33	85.20	7.87	10.60	16.60
L4	100.33	130.33	78.47	7.93	8.20	22.53
L5	97.00	130.67	92.80	9.47	11.00	22.07
L6	100.33	140.67	76.93	7.60	9.27	20.80

L7	105.33	141.33	70.33	8.13	10.87	19.80
L8	101.00	131.00	76.27	7.27	9.20	22.27
L9	98.33	136.67	78.67	9.33	11.00	18.07
T1	100.33	131.67	81.87	9.07	10.67	19.40
T2	99.33	137.33	76.80	8.00	11.27	18.00
T3	99.67	129.33	85.93	7.13	11.00	23.20
L1 ×T1	94.67	130.00	81.07	10.00	10.20	16.60
L1 × T2	93.67	133.33	78.33	8.07	11.00	17.13
L1 × T3	94.33	128.67	82.40	7.80	10.47	17.80
L2 × T1	94.33	131.33	76.80	7.40	8.87	18.40
L2 × T2	90.67	132.33	76.33	7.33	10.87	17.67
L2 × T3	92.67	128.67	80.60	6.60	10.40	21.33
L3 × T1	89.67	125.67	83.17	7.80	10.53	17.20
L3 × T2	89.67	127.67	80.00	7.53	11.53	16.47
L3 × T3	89.33	125.00	87.07	6.47	10.67	17.40
L4 × T1	94.00	126.00	79.13	8.47	8.53	18.47
L4 × T2	93.00	126.33	77.07	7.53	9.87	17.87
L4 × T3	93.67	122.00	83.93	8.13	9.60	21.07
L5 × T1	92.33	128.67	89.73	8.73	10.20	19.07
L5 × T2	92.67	128.33	86.27	7.40	10.67	18.13
L5 × T3	91.67	126.33	91.00	7.20	10.00	20.20
L6 × T1	93.33	129.67	78.67	7.60	9.60	18.87
L6 × T2	91.67	130.67	78.93	7.40	8.87	18.07
L6 × T3	92.67	131.00	82.27	6.87	10.07	21.13
L7 × T1	93.67	134.33	78.07	8.47	10.73	18.60
L7 × T2	93.00	137.00	72.87	8.07	9.33	17.40
L7 × T3	93.33	128.00	78.67	7.33	10.27	17.60
L8 × T1	92.67	128.67	77.80	7.60	9.67	18.87
L8 × T2	91.67	129.67	78.40	6.73	9.87	18.40
L8 × T3	93.67	127.00	80.27	6.60	9.60	19.00
L9 × T1	92.67	131.33	78.67	9.20	11.07	17.87
L9 × T2	92.00	135.67	76.93	8.40	10.00	18.53
L9 × T3	91.67	128.33	83.07	7.47	10.67	18.00
LSD 5%	2.83	3.02	1.67	0.57	0.53	1.14
LSD 1%	3.75	4.01	2.22	0.76	0.71	1.52

L1 HD 3226, L2 PBW 725, L3HD 2851, L4 HD 2893, L5 PBW 677, L6 HD 3086, L7 GW 273, L8 Phule Unnat, L9 Phule Samadhan, T1 HW 2045, T2 Faisalabad 2005, T3 PBW 343.

Table2 : Continued…

Genotypes	1000-grain weight (g)	Grain yield per plant (g)	Number of spikelets per spike	Number of grains per spike	Biological yield per plant (g)	Harvest index (%)
L1	37.47	21.13	16.87	55.87	51.93	40.69
L2	39.27	31.67	18.87	48.93	73.73	42.96
L3	38.13	20.07	18.87	56.13	48.67	41.21

L4	40.80	23.60	17.27	45.33	60.00	39.36
L5	38.07	17.73	18.20	62.80	57.47	30.88
L6	38.33	16.40	16.60	51.47	53.07	30.97
L7	39.13	21.67	16.87	58.40	52.40	41.39
L8	40.27	19.20	16.47	62.13	57.00	33.67
L9	37.67	16.00	16.47	56.27	50.47	31.73
T1	39.80	18.33	19.93	62.13	52.27	35.09
T2	40.27	16.93	19.27	56.53	52.20	32.44
T3	38.33	24.07	19.27	67.07	62.53	38.47
L1 ×T1	38.73	18.00	18.20	55.67	50.67	35.52
L1 × T2	38.40	16.87	18.33	56.67	50.80	33.21
L1 × T3	39.00	19.00	18.87	59.60	51.47	36.93
L2 × T1	38.33	19.00	18.87	55.47	51.67	36.79
L2 × T2	40.20	17.80	19.40	56.93	51.67	34.46
L2 × T3	38.00	22.40	18.87	56.27	60.80	36.85
L3 × T1	37.80	18.33	19.00	61.07	47.13	38.94
L3 × T2	39.73	17.07	19.80	56.40	46.87	36.46
L3 × T3	38.87	18.93	18.87	60.93	47.27	40.05
L4 × T1	39.67	18.33	19.27	56.13	51.87	35.42
L4 × T2	38.67	17.40	16.87	54.93	50.00	34.86
L4 × T3	38.93	20.47	17.80	59.60	57.87	35.46
L5 × T1	38.13	17.00	18.20	62.40	51.53	33.01
L5 × T2	38.60	16.73	18.47	59.07	51.80	32.30
L5 × T3	40.20	17.73	18.07	64.80	54.40	32.60
L6 × T1	37.73	16.40	18.87	55.87	51.33	31.96
L6 × T2	39.07	16.13	17.67	55.60	50.73	31.83
L6 × T3	38.33	16.87	18.33	59.47	51.27	32.88
L7 × T1	36.73	18.73	19.80	57.47	51.80	36.15
L7 × T2	39.40	17.33	18.60	57.33	51.27	33.85
L7 × T3	40.67	20.60	19.00	61.60	51.80	39.80
L8 × T1	38.87	18.27	17.80	62.93	52.27	34.96
L8 × T2	39.73	16.93	18.20	62.67	51.07	33.13
L8 × T3	40.60	18.47	18.73	68.00	55.73	33.17
L9 × T1	37.67	16.33	19.80	58.67	48.73	33.59
L9 × T2	38.53	15.87	17.27	55.73	49.67	31.96
L9 × T3	38.07	16.80	19.00	61.73	49.47	34.01
LSD 5%	0.96	1.73	0.97	1.85	2.02	3.80
LSD 1%	1.28	2.30	1.29	2.45	2.68	5.04

L1 HD 3226, L2 PBW 725, L3HD 2851, L4 HD 2893, L5 PBW 677, L6 HD 3086, L7 GW 273, L8 Phule Unnat, L9 Phule Samadhan, T1 HW 2045, T2 Faisalabad 2005, T3 PBW 343.

Combining ability effects and variances

The general and specific combining ability arethe main criteria of rapid genetic assaying of thetested genotypes under line × tester design.The effects of general combining ability (ĝi)of the parents (lines and testers) are useful toolsfor selecting the cross parents. According to this,the effects of GCA of the parents for the studiedtraits are presented in Table 3.Among the nine parental lines, line L3 showedsignificant negative GCA effects for days to 50%heading, hence it considered a good combiner forearliness. Line L1 showedhighly significant positive GCA effects for DH. For days to maturity, line L3, L4, L5 and tester T3 had significant negative GCA effects.Thetwo lines L3 and L5 and testerT3 showed significant ($P \leq 0.05$ or0.01) positive GCA effects for plant height henceit was a good combiner for tallness that are desiredto straw yield while, the line L2, L7, L8, L9 and tester T2 were a good combiner forshortness that preferred for resistance for lodging.

GCA effects for plant height, Consequently, it can be realized that positive or insignificant negative GCA effects increasing the plant height were more than the significant negative effects. It is similar for spike length except the two parents L4, L6, L8 and T2. For spike length, L1, L3, L9 had highly significant positive GCA effects and considered a good combiner for long spike. The three line L1, L4, L9 and tester T1 as good general combiner for NT/P.For flag leaf area, line L2, L4, L5, L6 and tester T3 showed highly significant positive GCA effect and had good combining ability. GCA effect for 1000 GW, line L8 and tester T2, T3 showed highly significant positive effect. Line L2, L4 and L7 was found to be best and showed positive significant GCA effect for GY/P.Line L5, L8 and tester T3 was a good donner for NG/S, where it gave high significant positive GCA effects for them.The three lines, L2, L4, L5, L8 and tester T3 were a good donner for BY/P, where it showed high significant positive GCA effects for these traits. Significant ($P \leq 0.05$ or 0.01) positive GCA effects estimated for HI for lineL3, L7 and tester T3. These consequences are in arrangement with those reported byEl-Gammaal*et al.*,2019, Abro *et al.*,2021, Roy *et al.*,2021, Ijaz *et al.*,2017, Rajput *et al.*,2018, Alhossary*et al.*,2020, Gupta *et al.*,2020 and Chaudhary *et al.*,2022. In self-pollination species, specific combiningability (SCA) effects can be utilizing to selectlines with homozygosity that appear transgressivesegregation in early generations.

TABLE 3. General combining ability GCA effects for the studied traits of the 9lines and 3 testers

Parents	Days to 50% heading	Days to maturity	Plant height (cm)	Number of tillers per plant	Spike length(cm)	Flag leaf area(cm)2
Lines						
L1	1.691**	1.346*	-0.048	0.911**	0.440**	-1.235**
L2	0.025	1.457*	-2.737**	-0.600**	-0.072	0.721**
L3	-2.975**	-3.210**	2.763**	-0.444**	0.795**	-1.390**
L4	1.025	-4.543**	-0.604	0.333**	-0.783**	0.721**
L5	-0.309	-1.543*	8.352**	0.067	0.173	0.721**
L6	0.025	1.123	-0.693*	-0.422**	-0.605**	0.943**
L7	0.802	3.790**	-4.115**	0.244*	-0.005	-0.546*
L8	0.136	-0.877	-1.826**	-0.733**	-0.405**	0.343
L9	-0.420	2.457**	-1.093**	0.644**	0.462**	-0.279
Se (g_l)	0.580	1.187	0.343	0.117	0.108	0.234

Testers						
T1	0.506	0.198	-0.304	0.652**	-0.183**	-0.198
T2	-0.531	1.901**	-2.300**	-0.104	0.106	-0.672**
T3	0.025	-2.099**	2.604**	-0.548**	0.077	0.869**
Se (g_t)	0.334	0.685	0.198	0.067	0.062	0.135

L1 HD 3226, L2 PBW 725, L3HD 2851, L4 HD 2893, L5 PBW 677, L6 HD 3086, L7 GW 273, L8 Phule Unnat, L9 Phule Samadhan, T1 HW 2045, T2 Faisalabad 2005, T3 PBW 343, *, ** significant at 0.05 and 0.01 levels of probability, respectively.

Table 3: Continued…

Parents	1000-grain weight (g)	Grain yield per plant (g)	Number of spikelets per spike	Number of grains per spike	Biological yield per plant (g)	Harvest index (%)
Lines						
L1	-0.128	0.037	-0.123	-1.689**	-0.538	0.402
L2	0.005	1.815**	0.454*	-2.777**	3.195**	1.211
L3	-0.040	0.193	0.632**	0.464	-4.427**	3.665**
L4	0.249	0.815*	-0.612**	-2.111**	1.728**	0.426
L5	0.138	-0.763*	-0.346	3.089**	1.062*	-2.182**
L6	-0.462*	-1.452**	-0.301	-2.022	-0.405	-2.596**
L7	0.094	0.970**	0.543**	-0.200	0.106	1.779*
L8	0.89**	-0.030	-0.346	5.534**	1.506**	-1.069
L9	-0.751**	-1.585**	0.099	-0.289	-2.227**	-1.635*
Se (g_l)	0.197	0.354	0.199	0.378	0.414	0.779
Testers						
T1	-0.654**	-0.096	0.277*	-0.593**	-0.738	0.327
T2	0.309**	-1.015**	-0.301*	-1.740**	-1.086	-1.258**
T3	0.346**	1.111**	0.025*	2.334**	1.825*	0.930*
Se (g_t)	0.113	0.204	0.114	0.218	0.239	0.449

L1 HD 3226, L2 PBW 725, L3HD 2851, L4 HD 2893, L5 PBW 677, L6 HD 3086, L7 GW 273, L8 Phule Unnat, L9 Phule Samadhan, T1 HW 2045, T2 Faisalabad 2005, T3 PBW 343, *,** significant at 0.05 and 0.01 levels of probability, respectively.

Table 4 showed the effects of specific combining ability (Sij) of the twenty-seven crosses for the studied traits. Only one cross L7 × T3 showed significant negative (desirable) SCA for days to maturity, indicating this cross could be used to select early maturity lines. Four crosses, L4 × T3, L6 × T2, L7 × T1 and L8 × T2 showed significant positive ($P \leq 0.05$ or 0.01) SCA effects for plant height, it could be considered a good combiner for high straw yield. Two crosses, L1 × T1 and L4 × T3 showed significant positive effect. These crosses is highly desirable for effective selection. Six crosses, L2 × T2, L3 × T2, L4 × T2, L6 × T3, L7 × T1 and L9 × T1 significant positive SCA effects for spike length. For flag leaf area, five crosses L2 × T3, L4 × T3, L6 × T3, L7 × T1 and L9 × T2 performed best with both parents involved in the cross having good SCA effect. Two crosses, L2 × T3 and L3 × T1 exhibited highly significant positive SCA effects for biological yield/plant. For number of spikelets/spikes, three crosses L3 × T2, L4 × T1 and L9 × T1 had significant positive ($P \leq 0.05$ or 0.01) SCA effects. So, these crosses could be used for selecting high tillering ability lines.

Regarding grain yield per plant, L2 × T3 exhibitedsignificant positive(0.01) SCA effects. Thiscross could be a good combiner for high yieldingof grain. For number of grains/spikes, two crosses L2 ×T2 and L3 × T1 had significantpositive (P≤0.05 or 0.01) SCA effects. Four crossesL2 ×T2, L4 × T1, L5 × T3 and L7× T3 for 1000 grains weightshowed significant positive(P≤0.05 or 0.01) SCA effects, they considered agood donor for these traits. These results are in line with those reported by El-Gammaal*et al.*,2019,Ijaz *et al.*,2017, Rajput *et al.*,2018, Alhossary*et al.*,2020, Gupta *et al.*,2020, Ranjitha *et al.*,2018, Dhoot *et al.*,2020 and El Nahas *et al.*,2021.

TABLE 4. Specific combining ability SCA for the studied traits of the 27F1's crosses

Crosses	Days to 50% heading	Days to maturity	Plant height (cm)	Number of tillers per plant	Spike length(cm)	Flag leaf area(cm)2
L1 ×T1	-0.062	-0.864	0.770	0.726**	-0.173	-0.380
L1 × T2	-0.025	0.765	0.033	-0.452*	0.338	0.627
L1 × T3	0.086	0.099	-0.804	-0.274	-0.165	-0.247
L2 × T1	1.272	0.358	-0.807	-0.363	-0.995**	-0.536
L2 × T2	-1.358	-0.346	0.722	0.326	0.716**	-0.795
L2 × T3	0.086	-0.012	0.085	0.037	0.279	1.331**
L3 × T1	-0.395	-0.642	0.059	-0.119	-0.195	0.375
L3 × T2	0.642	-0.346	-1.111	0.370	0.516**	0.116
L3 × T3	-0.247	0.988	1.052	-0.252	-0.321	-0.491
L4 × T1	-0.062	1.025	-0.607	-0.230	-0.617**	-0.469
L4 × T2	-0.025	-0.346	-0.678	-0.407*	0.427*	-0.595
L4 × T3	0.086	-0.679	1.285*	0.637**	0.190	1.064*
L5 × T1	-0.395	0.691	1.037	0.304	0.094	0.131
L5 × T2	0.975	-1.346	-0.433	-0.274	0.272	-0.328
L5 × T3	-0.580	0.654	-0.604	-0.030	-0.365	0.198
L6 × T1	0.272	-0.975	-0.985	-0.341	0.272	-0.291
L6 × T2	-0.358	-1.679	1.278*	0.215	-0.751**	-0.617
L6 × T3	0.086	2.654*	-0.293	0.126	0.479*	0.909*
L7 × T1	-0.173	1.025*	1.837**	-0.141	0.805**	0.931*
L7 × T2	0.198	1.988	-1.367*	0.215	-0.884**	0.205
L7 × T3	-0.025	-3.012**	-0.470	-0.074	0.079	-1.136**
L8 × T1	-0.506	0.025	-0.719	-0.030	0.138	0.309
L8 × T2	-0.469	-0.679	1.878**	-0.141	0.049	0.316
L8 × T3	0.975	0.654	-1.159*	0.170	-0.188	-0.625
L9 × T1	0.049	-0.642	-0.585	0.193	0.672**	-0.069
L9 × T2	0.420	1.988	-0.322	0.148	-0.684**	1.072**
L9 × T3	-0.469	-1.346	0.907	-0.341	0.012	-1.002*
Se (sij)	1.004	2.056	0.594	0.203	0.188	0.405

L1 HD 3226, L2 PBW 725, L3HD 2851, L4 HD 2893, L5 PBW 677, L6 HD 3086, L7 GW 273, L8 Phule Unnat, L9 Phule Samadhan, T1 HW 2045, T2 Faisalabad 2005, T3 PBW 343, *,** significant at 0.05 and 0.01 levels of probability, respectively.

Table 4: Continued…

Crosses	1000-grain weight (g)	Grain yield per plant (g)	Number of spikelets per spike	Number of grains per spike	Biological yield per plant (g)	Harvest index (%)
L1 ×T1	0.677	0.141	-0.543	-1.051	0.427	-0.028
L1 × T2	-0.620	-0.074	0.168	1.096	0.909	-0.750
L1 × T3	-0.057	-0.067	0.375	-0.045	-1.336	0.778
L2 × T1	0.143	-0.637	-0.454	-0.162	-2.306**	0.428
L2 × T2	1.047**	-0.919	0.657	2.451**	-1.958**	-0.315
L2 × T3	-1.190**	1.556*	-0.202	-2.289**	4.264**	-0.113
L3 × T1	-0.346	0.319	-0.499	2.187**	0.783	0.125
L3 × T2	0.625	-0.030	0.879*	-1.323*	0.864	-0.764
L3 × T3	-0.279	-0.289	-0.380	-0.864	-1.647	0.639
L4 × T1	1.232**	-0.304	1.012**	-0.162	-0.640	-0.155
L4 × T2	-0.731*	-0.319	-0.810*	-0.215	-2.158**	0.869
L4 × T3	-0.501	0.622	-0.202	0.377	2.798**	-0.714
L5 × T1	-0.190	-0.059	-0.321	0.904	-0.306	0.045
L5 × T2	-0.686*	0.593	0.523	-1.282	0.309	0.920
L5 × T3	0.877*	-0.533	-0.202	0.377	-0.002	-0.964
L6 × T1	0.010	0.030	0.301	-0.518	0.960	-0.595
L6 × T2	0.380	0.681	-0.321	0.363	0.709	0.867
L6 × T3	-0.390	-0.711	0.020	0.155	-1.669	-0.273
L7 × T1	-1.546**	-0.059	0.390	-0.740	0.916	-0.777
L7 × T2	0.158	-0.541	-0.232	0.274	0.731	-1.491
L7 × T3	1.388**	0.600	-0.158	0.466	-1.647*	2.268
L8 × T1	-0.212	0.474	-0.721*	-1.007	-0.017	0.882
L8 × T2	-0.309	0.059	0.257	-0.126	-0.869	0.632
L8 × T3	0.521	-0.533	0.464	1.133	0.886	-1.514
L9 × T1	0.232	0.096	0.83*	0.549	0.183	0.076
L9 × T2	0.136	0.548	-1.121**	-1.237	1.464*	0.032
L9 × T3	-0.368	-0.644	0.286	0.689	-1.647*	-0.108
Se (sij)	0.341	0.614	0.344	0.655	0.718	1.349

L1 HD 3226, L2 PBW 725, L3HD 2851, L4 HD 2893, L5 PBW 677, L6 HD 3086, L7 GW 273, L8 Phule Unnat, L9 Phule Samadhan, T1 HW 2045, T2 Faisalabad 2005, T3 PBW 343, *,** significant at 0.05 and 0.01 levels of probability, respectively.

Conclusion

Line × tester analysis is used in predicting the effects of the general combining ability of parents and specific abilitycombining of their crosses. The lines PBW 725 and tester PBW 343were a good donor for biological yield/plant, number of spikelets / spikes and grain yield/ plant. Also, HD 2893 and Phule unnatwere found to be the best and good general combiner for BY/P. Tester Faisalabad 2005 and PBW 343were good donors for these traits in addition to 1000 grains weight. One cross, PBW 725 × PBW 343 exhibited excellent combiners for specific combining ability for grain yield per plant and biological yield per plant, whereas, PBW 725 ×

Faisalabad 2005, HD 2893 × HW 2045 and GW 273 × PBW 343 was a good specific combiner for 1000 grain weight.It's recommended to use these genotypes in wheat breeding programs by selection to achieve transgressive segregation.

References

1. Jaiswal, K. K., Pandey, P., Marker, S., & Anurag, P. J. (2010). Heterosis studies for improvement in yield potential of wheat (Triticum aestivum L.). *Advances in Agriculture &Botanics*, *2*(3), 273-278.
2. Fasahat, P., Rajabi, A., Rad, J. M., &Derera, J. J. B. B. I. J. (2016). Principles and utilization of combining ability in plant breeding. *Biometrics & Biostatistics International Journal*, *4*(1), 1-24.
3. Kempthorne, O. (1957). An introduction to genetic statistics.
4. Singh, R. K., & Chaudhary, B. D. (1977). Biometrical methods in quantitative genetic analysis. *Biometrical methods in quantitative genetic analysis.*
5. Abd El-Aty, M. S. M., Kamara, M. M., & Abdo, M. S. M. (2016). Genetic analysis of some bread wheat crosses under normal and water stress conditions. *Egyptian Journal of Plant Breeding*, *20*(6), 907-928.
6. El-Gammaal, A. A. (2019). Evaluation of Bread Wheat Crosses via Line X Tester Mating Design. *East African Scholars Journal of Agriculture and Life Sciences*, *2*(3), 171-178.
7. Abro, S. A., Baloch, A. W., Baloch, M., Baloch, G. A., Baloch, T. A., Soomro, A. A., ... & Ali, M. (2021). 35. Line× tester analysis for estimating combining ability in F1 hybrids of bread wheat. *Pure and Applied Biology (PAB)*, *5*(3), 647-652.
8. Roy, A., Kumar, A., Rawat, V., & Singh, A. (2021). Analysis of combining ability and gene action studies for grain yield and its component traits in bread wheat utilizing line x tester mating design. *Environment Conservation Journal*, *22*(3), 289-298.
9. Baloch, M., Baloch, A. W., Siyal, N. A., Baloch, S. N., Soomro, A. A., Baloch, S. K., &Gandahi, N. (2016). Heterosis Analysis in F1Hybrids of Bread Wheat. *Sindh University Research Journal-SURJ (Science Series)*, *48*(2).
10. Ijaz, S., & Kaukab, S. (2017). Exploitation of heterosis and combining ability effects in wheat breeding. *Journal of Agricultural Research (03681157)*, *55*(2).
11. Rajput, R. S., &Kandalkar, V. S. (2018). Combining ability and heterosis for grain yield and its attributing traits in bread wheat (Triticum aestivum L.). *Journal of Pharmacognosy and Phytochemistry*, *7*(2), 113-119.
12. Alhossary, A. A. (2020). Estimation of combining ability and gene action by using line x tester procedure in bread wheat (Triticumastivum., L). *Annals of Agricultural Science, Moshtohor*, *58*(4), 923-930.
13. Gupta, V. K., Agrawal, A. P., Yadav, R. K., Parihar, R., Meshram, P., Banjare, A. K., ... & Singh, N. (2020). Combining ability studies on terminal heat tolerance in wheat (Triticum aestivum L.) under late sown irrigated condition using Line X Tester analysis. *IJCS*, *8*(5), 774-778.

14. Chaudhary, D., Swati, Nagar, K., & Dhyani, R. (2022). Genetic analysis of yield and its attributes in bread wheat (Triticum aestivum L. em. Theil) under irrigated and rainfed conditions. *Euphytica*, *218*(9), 135.
15. Ranjitha, K. M., Biradar, S. S., Desai, S. A., Naik, V. R., Singh, S. K., Satisha, T. N., ... & Uday, G. (2018). Combining ability of six wheat genotypes and their F1 diallel crosses for nitrogen use efficiency (NUE) and related traits under 50 per cent nitrogen condition. *Int. J. Curr. Microbiol. App. Sci*, *7*(1), 1237-1243.
16. Dhoot, M., Sharma, H., Dubey, R. B., Badaya, V. K., & Dhoot, R. (2020). Combining ability analysis for yield and some of its associated characters in late sown condition in bread wheat (Triticum aestivum L. em. Thell). *Journal of Pharmacognosy and Phytochemistry*, *9*(2), 283-286.
17. El Nahas, M. M., & Ali, O. A. (2021). Estimation of combining ability and heterosis for wheat yield and its components under water stress conditions. *Egyptian Journal of Agronomy*, *43*(2), 277-293.