



**Full Length Article**

## Wheat Assessment through Line by Tester Combining Ability Analysis for Maturity and Yield Traits

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### Abstract

To feed the rising population of Pakistan, there is an awful need of improving wheat genotypes for better yield potential per unit area. Therefore, development of productive wheat cultivars by crossing good general combining lines and selecting transgressive segregants is a prerequisite. The present study aims to determine the hereditary variation, general (GCA) and specific combining ability (SCA) effects, gene action and proportional contribution of parental lines, testers, and line × tester F<sub>2</sub> populations for maturity and yield variables. Seven lines *i.e.*, Seher-06, Pirsabak-85, Shahkar-13, Galaxy-13, Ghaznavi-98, TD-1 and Inqalab-91 and three testers *i.e.*, Parula, Yr-5 and Yr-10 were crossed during 2017–18 in a line × tester mating fashion at Cereal Crop Research Institute (CCRI), Nowshera, Pakistan. The generation was advanced during the summer season of 2018 at Summer Agricultural Research Station (SARS), Kaghan, Pakistan. After advancing the generation, 21 F<sub>2</sub> populations with their ten parents were grown during crop season 2018–2019 with three replications in a randomized complete block design at the University of Agriculture, Peshawar, Pakistan. Parental lines, testers and their line by tester F<sub>2</sub> derivatives exhibited significant ( $p \leq 0.01$ ) variations for almost all the traits. Parental lines Galaxy-13 and Shahkar-13 were considered as best general cultivars by having the highest GCA for grains spike<sup>-1</sup>, thousand-grain weight, biological and grain yield plant<sup>-1</sup>. The F<sub>2</sub> populations TD-1 × Parula, Pirsabak-85 × YR-5 and Shahkar-13 × Yr-5 revealed the best SCA effects for the majority of the parameters and were recognized as best specific combiners. In proportional contribution, the line by tester F<sub>2</sub> derivatives share was the highest by comparing with lines and testers for all of the variables. The ratios of GCA to SCA variances, and degree of dominance authenticated that all the variables were influenced by dominant gene effects. Due to non-additive gene effects, the F<sub>1</sub> hybrids could be selected in F<sub>1</sub> generation, however, for segregating populations the selection could be delayed for above promising populations in terms of maturity and yield variables. © 2021 Friends Science Publishers

**Keywords:** L × T combining ability; Genetic variability; GCA and SCA variances; F<sub>2</sub> populations; Maturity and yield variables; *Triticum aestivum*

### Introduction

Wheat (*Triticum aestivum* L.) being the world largest cereal crop, secured a prominent position because of its larger acreage and high productivity (Shah *et al.* 2020). In Pakistan, wheat accounts for 9.2 percent of the value added in agriculture and 1.8 percent of the gross domestic product (Pakistan Economic Survey 2020–2021). Wheat is a staple food crop and more than 40% of the world population consumed wheat (Afridi *et al.* 2017a). The world population is increasing day by day which increases the cereal grain demand. However, this increasing wheat demand cannot be fulfilled because in many regions the wheat production facing several challenges like climatic change, drought and heat stress and evolution of new races of rust (Din *et al.*

2020; Dhoot *et al.* 2020).

In Pakistan wheat is cultivated on a larger area and falls in ten major wheat producing countries of the world (Ishaq *et al.* 2018). In comparison to advanced countries like Australia, USA, China, France and Brazil, the average wheat yield is very low in Pakistan (Afridi *et al.* 2019). In Pakistan, the major factors of low yield are the susceptibility of available germplasm to new races of rust, improper time of rainfall, scarcity of irrigation water and abiotic stresses (Ahmad *et al.* 2017; Farooq *et al.* 2019). To overcome these problems, it is a dire need to develop new high-yielding wheat genotypes with disease resistance. In Pakistan wheat was cultivated on 8.805 million hectares, and the total production was 25.248 million tones with 2867 kg ha<sup>-1</sup> (Pakistan Economic

Survey 2020–2021). In comparison to last year, the wheat area under cultivation increased by 1.5% with increased production of 3.7%, followed by a 2.2% increase in yield per hectare. In wheat breeding, the breeder's main objective is to develop the genotypes with better yield potential and desirable trait combinations. Many breeding strategies including hybridization between different parental genotypes for the accumulation of favorable allele's resulted in useful segregations in wheat (Ahmed *et al.* 2017; Din *et al.* 2021).

Line by tester analysis is an important mating design for predicting the combining ability and choosing the appropriate parental cultivars, their subsequent F<sub>1</sub> and F<sub>2</sub> derivatives and knowledge regarding genetic control of various variables in wheat (Usharani *et al.* 2016; Murugan and Kannan 2017). Information on GCA and SCA effecting maturity and yield variables has become progressively significant to plant breeders to select suitable parents for evolving hybrids and cultivars in different crop plants (Jain and Sastry 2012; Din *et al.* 2020, 2021). Identification of superior parents is an important prerequisite for the improvement of genetically superior wheat cultivars with maximum yield. Yield and yield contributing parameters are expressed by using GCA and SCA values in the parental genotypes and their line by tester F<sub>1</sub> and F<sub>2</sub> derivatives, respectively in wheat (Saeed and Khalil 2017). To determine the nature and extent of diverse gene values and to assess the performance of different populations, line by tester combining ability analysis could be successfully used for better results in wheat (Din *et al.* 2018).

For development of potential hybrids in different crops, the knowledge of GCA and SCA has become progressively significant to the breeders. In commercial hybrid seed production, the desirable SCA values could be easily subjugated in self and cross-pollinated crops. If parental genotypes are good general combiners, then the line by tester populations with the highest SCA can be used in self-pollinated crops like wheat by choosing transgressive segregates (Murugan and Kannan 2017; Sharma *et al.* 2019). To study the gene action, GCA and SCA effects, and genetic makeup of wheat hybrid populations, the diallel and line by tester analyses have been used for improving yield attributing parameters in F<sub>1</sub> and F<sub>2</sub> populations (Abro *et al.* 2016; Ahmed *et al.* 2017; Din *et al.* 2018, 2020, 2021). Past studies revealed that over-dominant type of gene effects controlled the yield and its allied variables in F<sub>1</sub> and F<sub>2</sub> derivatives of wheat (Singh *et al.* 2012; Saeed and Khalil 2017; Afridi *et al.* 2017a, 2019). Combining ability is very obliging in the recognition of promising populations for best hybrids and insight of genetics concerned with various parameters in wheat (Afridi *et al.* 2017b). The current study aims to determine the genetic variation, GCA and SCA effects, gene action, and proportional contribution of parental lines, testers and line by tester F<sub>2</sub> derivatives for maturity and yield variables in wheat.

## Materials and Methods

### Breeding material and study sites

The breeding material comprising ten wheat genotypes, in which seven cultivars were used as lines *i.e.*, Seher-06, Pirsabak-85, TD-1, Inqalab-91, Ghaznavi-98, Galaxy-13, and Shahkar-13, while three genotypes were used as testers *i.e.*, Parula, Yr-5 and Yr-10 (Table 1). All the genotypes were grown during 2017–2018 and crossed by following the line by tester fashion at the Cereal Crops Research Institute, Nowshera, Pakistan (Kempthorne 1957). At maturity, the crossed spikes were harvested and threshed separately to get the F<sub>1</sub> crosses seed. During summer season 2018, the generation was advanced to F<sub>2</sub> seed at the Summer Agricultural Research Station (SARS), Kaghan, Khyber Pakhtunkhwa, Pakistan. For further evaluation, the parent lines, testers and 21 F<sub>2</sub> populations were sown during crop season 2018–2019 in a randomized complete block design (RCBD) with three replications at the University of Agriculture, Peshawar, Pakistan. All the entries were sown in four rows having five meters of length, with required rows and plants spacing. The recommended cultural practices were used during the crop lifetime.

### Data recorded

Data were recorded for days to maturity, spike length, biological yield, grains spike<sup>-1</sup>, thousand-grain weight, and grain yield by following the standard procedure in lines, testers and their F<sub>2</sub> derivatives. Days to maturity were counted from sowing to complete physiologically maturity. Spike length was measured in centimeters from the spike base to the spike tip apart from awns. Biological yield plant<sup>-1</sup> (g) was recorded with electric balance at maturity after complete sun drying. For grains per spike, the single spike in each entry and replication was threshed and counted and then averaged. The randomly selected plants were harvested separately and threshed with single plant thresher. To record the thousand-grain weight (g), an eloquent sample of thousand grains was used and weighed. For getting grain yield plant<sup>-1</sup> (g), the 20 plant grains in each line, tester and their F<sub>2</sub> derivatives were weighed and then averaged.

### Biometrical analysis

Data pertaining to various variables was analyzed (Steel *et al.* (1997). Genotype means for each trait were further divided and compared by using least significant difference (LSD) test. Upon getting significant variations among the genotypes for various variables in wheat crop and to know about genetic effects and their general and specific combining ability, the data were subjected to line by tester combining ability analysis (Kempthorne 1957; Singh and Chaudhary 1985). Variances due to GCA, SCA and additive and dominance genetic variances, and proportional

contribution to the total genetic variance by lines, testers, and line by tester F<sub>2</sub> derivatives were also calculated.

## Results

All the parental lines and testers were semi-dwarf except TD-1 which was dwarf. Parental line Shahkar-13 and all the testers (Parula, YR-5 and YR-10) were resistant to yellow rust, while six other parental lines (Seher-06, Pirsabak-85, TD-1, Inqalab-91, Ghaznavi-98 and Galaxy-13) were susceptible to yellow rust caused by *Puccinia striiformis* f. sp. *tritici* (Pst). In case of maturity, all the lines and testers were having normal maturity except TD-1 (early maturing) and YR-5 (late maturing). According to grain yield potential, the maximum and same yield potential (6500 kg ha<sup>-1</sup>) presented by the cultivars TD-1, Inqalab-91 and Galaxy-13, followed by Seher-06 and Pirsabak-85 with moderate grain yield (6000 kg ha<sup>-1</sup>), while Ghaznavi-98 and Shahkar-13 were recorded with least grain yield (5500 kg ha<sup>-1</sup>). Lines, testers and line by tester F<sub>2</sub> derivatives were significant ( $P \leq 0.01$ ) for almost all the variables excluding testers for grains per spike (Table 2). The means presentation of the various populations, GCA and SCA effects, variances due to GCA and SCA, degree of dominance, gene action, and proportional contribution of lines, testers, and line by tester F<sub>2</sub> derivatives to total genetic variance are discussed herein.

### Genetic differences among lines, testers and line by tester F<sub>2</sub> populations

#### Days to maturity

Among lines, days to maturity ranged from 156.7 (TD-1) to 170.7 days (Pirsabak-85), testers varied from 161.7 days (Parula) to 173.7 (Yr-5) (Table 3). However, in F<sub>2</sub> derivatives the maturity days varied between 160.7 (Seher-06 × Yr-10 and Pirsabak-85 × Parula) to 177.3 days (Shahkar-13 × Yr-10). Overall, the minimum days to maturity were observed for line TD-1 (156.7 days), followed by F<sub>2</sub> populations Seher-06 × Yr-10 and Pirsabak-85 × Parula (160.7) days. Maximum days to maturity were taken by F<sub>2</sub> populations Shahkar-13 × Yr-10 (177.3 days) and Shahkar-13 × Yr-5 (175.3 days), followed by tester Yr-5 (173.7 days). Therefore, early maturing line TD-1, F<sub>2</sub> populations Seher-06 × Yr-10 and Pirsabak-85 × Parula, and Galaxy-13 × Yr-10 and tester Parula could be utilized for development of early maturing wheat genotypes.

#### Spike length

For spike length, lines ranged from 12.9 (Pirsabak-85 and TD-1) to 16.8 cm (Inqalab-91), testers ranged from 11.9 (Yr-10) to 13.6 cm (Yr-5), while F<sub>2</sub> populations ranged between 10.1 (Galaxy-13 × Parula) and 14.5 cm (Pirsabak-85 × Parula) (Table 3). Overall, the highest spike length was recorded in lines Inqalab (16.8 cm) and Galaxy-13 (16.7

cm), followed by F<sub>2</sub> population Pirsabak-85 × Parula (14.5 cm) and Ghaznavi-98 × Parula and Galaxy-13 × Yr-10 (14.4 cm). However, the least values for spike length were noted in F<sub>2</sub> populations Galaxy-13 × Parula (10.1 cm) and Ghaznavi-98 × Yr-10 (10.8 cm) and Ghaznavi-98 × Yr-5 (11.1 cm). Spike length also contributes to grain yield and therefore, the maximum spike length is favored in plant breeding. Therefore, the parental lines Inqalab and Galaxy-13, followed by F<sub>2</sub> population Pirsabak-85 × Parula, Ghaznavi-98 × Parula and Galaxy-13 × Yr-10 which could be used for the development of new wheat cultivars with enhanced spike length.

#### Grains per spike

For grain spike<sup>-1</sup>, the parental lines ranged from 49.5 (Galaxy-13) to 76.6 (Shahkar-13), testers ranged from 51.9 (Yr-5) to 68.1 (Parula), while in F<sub>2</sub> populations the number of grains per spike varied from 46.3 (TD-1 × Yr-5) to 70.8 (TD-1 × Parula) (Table 3). Overall, the highest number of grains per spike was exhibited by line Shahkar-13 (76.6), followed by F<sub>2</sub> populations TD-1 × Parula (70.8). However, the minimum number of grains was recorded for the F<sub>2</sub> population TD-1 × Yr-5 (46.3) and Ghaznavi-98 × Parula (47.7), followed by line Galaxy-13 (49.5). Grains spike<sup>-1</sup> is a vital yield component and positively correlated to grain yield. Therefore, line Shahkar-13 and F<sub>2</sub> populations TD-1 × Parula and Galaxy-13 × Yr-5 can be utilized for improvement in grains per spike.

#### 1000-grain weight

For 1000-grain weight, lines varied from 10.1 (Galaxy-13) to 30.0 g (Shahkar-13 and Seher-06), testers ranged from 20.1 (Parula) to 30.1 g (Yr-5), while in F<sub>2</sub> populations the 1000-grain weight ranged from 10.1 (Ghaznavi-98 × Parula and Inqalab-91 × Parula) to 40.2 g (Galaxy-13 × Yr-10) (Table 3). Maximum and at par thousand grain weight was recorded in F<sub>2</sub> populations Galaxy-13 × Yr-10 (40.2 g), Ghaznavi-98 × Yr-10 (40.1 g) and Galaxy-13 × Yr-5 (40.1 g), followed by six other F<sub>2</sub> derivatives ranged 30.0 to 30.1 g. Lines Seher-06, Shahkar-13 and testers Yr-5 and Yr-10 also revealed at par 1000-grain weight ranging from 30.0 to 30.1 g. However, the minimum 1000-grain weight was observed in lines Galaxy-13, Inqalab-91 and Ghaznavi-98, followed by F<sub>2</sub> populations TD-1 × Yr-5, Ghaznavi-98 × Parula and Inqalab-91 × Parula ranged from 10.1 to 10.3 g. Thousand-grain weight is associated with grain yield, and therefore, the F<sub>2</sub> populations Galaxy-13 × Yr-10, Ghaznavi-98 × Yr-10 and Galaxy-13 × Yr-5 could be utilized in the advancement of new wheat cultivars with bolder grains.

#### Biological yield per plant

For biological yield, the parental lines varied from 51.0 (Galaxy-13) to 99.1 g (Shahkar-13), testers varied from 69.2 (Yr-10) to 81.8 g (Parula) (Table 3). In F<sub>2</sub> derivatives, the

**Table 1:** Parental lines and testers with parentage and various variables used in line × tester crosses

Cultivars	Pedigree	Plant height	Resistance to Yr	Color	Maturity	Grains spike <sup>-1</sup>	Potential yield (kg ha <sup>-1</sup> )
Lines							
Seher-06	CHILL/2*STAR/4/BOW//BUC/PVN/3/2*VEE#0	Semi-dwarf	Susceptible	Waxy green	Normal	59	6000
Pirsabak-85	KVZ/BUHO//KAL/BB	Semi-dwarf	Susceptible	Green	Normal	60	6000
TD-1	MAIS/NORTENO65/H68	Dwarf	Susceptible	Green	Early	62	6500
Inqalab-91	WL 711/CROW"S	Semi-dwarf	Susceptible	Pale green	Normal	61	6500
Ghaznavi-98	JUP/BJYG//URES	Semi-dwarf	Susceptible	Waxy green	Normal	66	5500
Galaxy-13	PB96/V-87094/ MH97	Semi-dwarf	Susceptible	Waxy green	Normal	56	6500
Shahkar-13	CMH84.3379/CMH78.578 //MILAN	Semi-dwarf	Resistant	Waxy green	Normal	58	5500
Testers							
Parula	FRN1312*FR//KAD/GB/4/BB/CHA	Semi-dwarf	Resistant	Green	Normal	67	-
Yr-5	CX 86.6.1.20	Semi-dwarf	Resistant	Green	Late	52	-
Yr-10	CX93.53.3.1	Semi-dwarf	Resistant	Green	Normal	60	-

**Table 2:** Mean squares for various variables in line by tester combining ability analysis in wheat

Source	d.f.	Days to maturity	Spike length	Grains spike <sup>-1</sup>	1000-grain weight	Biological yield plant <sup>-1</sup>	Grain yield plant <sup>-1</sup>
Replications	2	7.53	0.07	8.95	0.02	20.21	4.56
Genotypes	30	68.46**	6.50**	149.09**	249.79**	943.58**	273.14**
Parents (P)	9	84.06**	8.24**	196.94**	229.69**	734.26**	244.75**
Parents vs. crosses	1	15.04**	27.19**	93.90 <sup>NS</sup>	266.55**	8.76 <sup>NS</sup>	78.98 <sup>NS</sup>
Crosses (C)	20	64.12**	4.68**	130.31**	258.00**	1084.52**	295.62**
Lines (L)	6	130.83**	3.28**	153.26*	295.30**	1298.42**	381.85**
Testers (T)	2	17.44**	0.28**	4.66 <sup>NS</sup>	531.53**	1824.14**	348.07**
L × T	12	38.54**	6.12**	139.78**	193.76**	854.30**	243.77**
Error	60	1.78	0.05	56.24	0.07	247.12	51.31
CV (%)		0.008	0.016	0.12	0.01	0.23	0.27

\*\* , \* : Significant at 1% and 5% level of probability, NS: Non-Significant, C.V.: Coefficient of variation

**Table 3:** Mean performance of lines, testers and line by tester F<sub>2</sub> populations for various variables in wheat

Genotypes	Days to maturity	Spike length	Grains spike <sup>-1</sup>	1000-grain weight	Biological yield plant <sup>-1</sup>	Grain yield plant <sup>-1</sup>
Lines						
Seher-06	165.7	13.3	57.2	30.0	55.1	19.9
Pirsabak-85	170.7	12.9	61.0	20.1	77.1	29.5
TD-1	156.7	12.9	53.3	20.0	54.8	19.1
Inqalab-91	161.7	16.8	63.5	10.2	57.3	18.5
Ghaznavi-98	165.3	14.7	58.0	10.3	56.2	17.2
Galaxy-13	166.0	16.7	49.5	10.1	51.0	11.5
Shahkar-13	169.3	13.5	76.6	30.0	99.1	43.1
Testers						
Parula	161.7	12.7	68.1	20.1	81.8	29.4
Yr-5	173.7	13.6	51.9	30.1	77.0	30.8
Yr-10	172.0	11.9	61.9	30.0	69.2	24.2
F <sub>2</sub> populations						
Seher-06 × Parula	165.0	12.1	56.0	20.1	57.3	23.3
Seher-06 × Yr-5	162.3	12.3	62.0	20.3	51.7	17.3
Seher-06 × Yr-10	160.7	12.5	52.8	20.2	72.3	26.5
Pirsabak-85 × Parula	160.7	14.5	51.0	20.1	39.8	14.3
Pirsabak-85 × Yr-5	165.0	12.4	62.5	20.1	79.4	32.1
Pirsabak-85 × Yr-10	163.7	14.3	51.0	30.1	57.1	16.1
TD-1 × Parula	165.3	13.4	70.8	30.0	91.7	37.6
TD-1 × Yr-5	166.3	11.9	46.3	10.2	41.6	12.7
TD-1 × Yr-10	167.3	11.6	65.6	20.1	68.4	24.3
Inqalab-91 × Parula	165.0	13.4	55.1	10.1	38.8	12.7
Inqalab-91 × Yr-5	164.3	14.2	55.0	30.0	66.2	22.2
Inqalab-91 × Yr-10	168.7	12.6	59.8	30.1	80.6	33.2
Ghaznavi-98 × Parula	167.3	14.4	47.7	10.1	49.7	12.6
Ghaznavi-98 × Yr-5	171.0	11.1	58.6	20.1	60.7	23.8
Ghaznavi-98 × Yr-10	169.7	10.8	51.0	40.1	78.9	33.0
Galaxy-13 × Parula	172.7	10.1	63.3	30.1	73.7	30.1
Galaxy-13 × Yr-5	172.3	13.1	68.1	40.1	103.3	42.6
Galaxy-13 × Yr-10	161.7	14.4	63.6	40.2	100.7	42.0
Shahkar-13 × Parula	168.0	12.2	60.5	20.1	58.3	23.4
Shahkar-13 × Yr-5	175.3	13.6	56.9	30.1	88.4	39.7
Shahkar-13 × Yr-10	177.3	12.5	59.3	30.0	80.1	35.2
F <sub>2</sub> Means	166.8	13.1	58.6	23.7	68.3	25.7
Parental means	166.3	13.9	60.1	21.1	67.8	24.3
LSD <sub>0.05</sub>	2.18	0.36	12.25	0.44	25.67	11.70

biological yield plant<sup>-1</sup> varied from 38.8 (Inqalab-91 × Parula) to 100.7 g (Galaxy-13 × Yr-10). Overall, the maximum biological yield was recorded in F<sub>2</sub> populations Galaxy-13 × Yr-10 (100.7 g), Galaxy-13 × Yr-5 (103.3 g),

followed by line Shahkar-13 (99.1 g). However, the lowest biological yield plant<sup>-1</sup> was exhibited by F<sub>2</sub> populations Inqalab-91 × Parula (38.8 g) and line Pirsabak-85 (39.8 g). Other populations presented moderate values for biological

yield. The highest biological yield is favored when the breeder likes to get more green and dry foliage for livestock. For an increase in fodder yield, the F<sub>2</sub> populations Galaxy-13 × Yr-10, Galaxy-13 × Yr-5 and line Shahkar-13 could be used for enhancement in biological yield.

### Grain yield per plant

For grain yield, the lines ranged from 11.5 (Galaxy-13) to 43.1 g (Shahkar-13) while testers varied from 24.2 (Yr-10) to 30.8 g (Yr-5) (Table 3). For F<sub>2</sub> derivatives, the grain yield ranged between 12.6 (Ghaznavi-98 × Parula) to 42.6 g (Galaxy-13 × Yr-5). Generally, the highest and at par grain yield was recorded in line Shahkar-13 (43.1 g) and F<sub>2</sub> populations Galaxy-13 × Yr-5 (42.6 g) and Galaxy-13 × Yr-10 (42.0). However, the minimum grain yield plant<sup>-1</sup> was recorded in line Galaxy-13 (11.5 g), followed by F<sub>2</sub> population Ghaznavi-98 × Parula (12.6 g). The leftover genotypes revealed moderate values for grain yield. The promising genotypes like line Shahkar-13, and F<sub>2</sub> populations Galaxy-13 × Yr-5 and Galaxy-13 × Yr-10 could be used for sustainable improvement in grain yield.

Overall, the line Shahkar-13 performed best for yield-related variables under study. Among testers, the Parula was identified as a good contributor in the improvement of spikelets and grains per spike, whereas tester Yr-5 performed better for thousand-grain weight and grain yield. In F<sub>2</sub> populations, the best performing genotypes were Galaxy-13 × Yr-5, Galaxy-13 × Yr-10, Ghaznavi-98 × Yr-10, TD-1 × Parula and Shahkar-13 × Parula for grain yield and its contributing variables. Therefore, the above promising genotypes could be used for further improvement in wheat.

### Combining ability analysis

Significant genetic variation among the populations for various variables allows further analysis of the combining ability and its constituents *i.e.*, GCA and SCA in lines, testers, and line by tester F<sub>2</sub> derivatives, respectively. Positive combining ability values denote importance for yield and yield associated parameters, while negative values are enviable for variables like heading and maturity variables.

For maturity, in lines the GCA values varied between -4.46 to 6.43 (Table 4). Negative and desired GCA effects were recorded in four lines *i.e.*, Seher-06, Pirsabak-85, TD-1 and Inqalab-91, while three lines *i.e.*, Ghaznavi-98, Galaxy-13 and Shahkar-13 exhibited positive GCA values. The highest negative and significant ( $p \leq 0.01$ ) GCA values owned by lines Seher-06 (-4.46), Pirsabak-85 (-4.02), and Inqalab-91 (-1.13), while the highest positive GCA values were recorded for line Shahkar-13 (6.43), followed by Ghaznavi-98 (2.21) and Galaxy-13 (1.76). In testers, the GCA values varied from -0.84 to 0.97 for maturity. Negative and significant ( $p \leq 0.01$ ) GCA values were possessed by tester Parula (-0.84), followed by Yr-10

(-0.13). However, positive and significant ( $P \leq 0.01$ ) GCA effects were observed for tester Yr-5 (0.97). Overall, the lines Seher-06, Pirsabak-85 and Inqalab-91 and tester Parula revealed significant ( $P \leq 0.01$ ) negative GCA values which could be used as best general combiners for early maturity.

For days to maturity, the SCA values varied between -7.10 to 4.62 in line by tester F<sub>2</sub> derivatives (Table 5). The 10 F<sub>2</sub> derivatives were noted with negative SCA values, while eleven F<sub>2</sub> populations revealed positive SCA values. Significant and negative SCA values were observed for five F<sub>2</sub> populations *i.e.*, Galaxy-13 × Yr-10 (-7.10), Shahkar-13 × Parula (-4.71), Inqalab-91 × Yr-5 (-2.63), Seher-06 × Yr-10 (-1.87) and Pirsabak-85 × Parula (-1.60), followed by five other F<sub>2</sub> populations with non-significant negative SCA values. Significant positive SCA values were observed in five F<sub>2</sub> populations, followed by six other F<sub>2</sub> populations with non-significant positive SCA values. The maximum positive SCA values were obtained for Galaxy-13 × Parula (4.62). F<sub>2</sub> populations Galaxy-13 × Yr-10, Shahkar-13 × Parula and Inqalab-91 × Yr-5 were recognized as the best specific combiners that could be synthesized in the development of early maturing wheat cultivars.

For spike length, the GCA values ranged from -0.63 to 0.97 among the parental lines (Table 4). Positive and desired GCA values were recorded for three lines *i.e.*, Pirsabak-85 (0.97), Inqalab-91 (0.67) and Shahkar-13 (0.04). However, negative GCA values were recorded in four lines *i.e.*, Ghaznavi-98 (-0.63), TD-1 (-0.43), Seher-06 (-0.42), and Galaxy-13 (-0.19). Positive and significant ( $P \leq 0.01$ ) GCA values owned by lines Pirsabak-85 and Inqalab-91, while four lines possessed negative and significant ( $P \leq 0.01$ ) GCA values. In testers, the GCA values varied from -0.07 to 0.13 for spike length. Among testers, the Parula showed significant positive GCA values, while two testers Yr-5 and Yr-10 presented non-significant negative GCA values. Overall, the lines Pirsabak-85 and Inqalab-91 were considered as paramount general cultivars for future use and improvement.

For spike length, in F<sub>2</sub> populations the SCA values ranged from -2.58 to 2.13 (Table 5). Ten F<sub>2</sub> populations revealed positive while eleven populations enunciated negative SCA values. Positive and significant ( $P \leq 0.01$ ) SCA values were noted in F<sub>2</sub> derivatives *i.e.*, Ghaznavi-98 × Parula (2.13), Galaxy-13 × Yr-10 (1.92), TD-1 × Parula (1.00) and Shahkar-13 × Yr-5 (0.92), followed by four other populations ranged from 0.63 to 0.87. However, ten F<sub>2</sub> populations revealed significant negative SCA values for spike length.

For grains spike<sup>-1</sup>, the GCA values varied from -5.51 to 7.07 among lines (Table 4). Three lines *i.e.*, TD-1, Galaxy-13 and Shahkar-13 exhibited positive GCA values, however, four lines *i.e.*, Seher-06, Pirsabak-85, Inqalab-91, and Ghaznavi-98 presented negative GCA values. Significant ( $P \leq 0.01$ ) GCA values were recorded for line Galaxy-13 (7.07), while Ghaznavi-98 (-5.51) revealed significant negative GCA values. Among testers, the Yr-5

**Table 4:** General combining ability (GCA) values for lines and testers for various variables in wheat

Genotypes	Days to maturity	Spike length	Grains spike <sup>-1</sup>	1000-grain weight	Biological yield plant <sup>-1</sup>	Grain yield plant <sup>-1</sup>
Lines						
Seher-06	-4.46**	-0.42**	-0.99	-4.67**	-8.11	-4.03
Pirsabak-85	-4.02**	0.97**	-3.11	-1.45**	-9.76	-5.58*
TD-1	-0.79	-0.43**	2.92	-4.77**	-1.26	-1.56
Inqalab-91	-1.13*	0.67**	-1.33	-1.49**	-6.62	-3.73
Ghaznavi-98	2.21**	-0.63**	-5.51**	-1.41**	-5.43	-3.28
Galaxy-13	1.76**	-0.19*	7.07**	11.94**	24.06**	11.82**
Shahkar-13	6.43**	0.04	0.95	1.84**	7.12	6.36**
S.E.	0.45	0.07	2.50	0.09	5.24	2.39
C.D <sub>0.05</sub>	0.89	0.14	5.00	0.18	10.48	4.78
C.D <sub>0.01</sub>	1.18	0.19	6.65	0.24	13.94	6.35
Testers						
Parula	-0.84**	0.13*	-0.17	-4.78**	-10.04**	-4.40**
Yr-5	0.97**	-0.07	0.53	-0.47**	1.66	0.77
Yr-10	-0.13	-0.07	-0.37	5.25**	8.38*	3.63*
S.E.	0.29	0.05	1.64	0.06	3.43	1.56
C.D <sub>0.05</sub>	0.58	0.09	3.27	0.12	6.86	3.13
C.D <sub>0.01</sub>	0.77	0.13	4.35	0.16	9.12	4.16

\*\* , \* : Significant at 1% and 5% level of probability, S.E.: Standard error, CD: Critical difference

**Table 5:** Specific combining ability (SCA) values among line by tester F<sub>2</sub> populations for various variables in wheat

F <sub>2</sub> populations	Days to maturity	Spike length	Grains spike <sup>-1</sup>	1000-grain weight	Biological yield plant <sup>-1</sup>	Grain yield plant <sup>-1</sup>
Seher-06 × Parula	3.17**	-0.31*	-0.76	4.71**	6.91	5.37
Seher-06 × Yr-5	-1.30	0.09	4.52	0.54**	-10.41	-5.89
Seher-06 × Yr-10	-1.87*	0.22	-3.75	-5.25**	3.49	0.52
Pirsabak-85 × Parula	-1.60*	0.63**	-3.63	1.49**	-8.96	-2.14
Pirsabak-85 × Yr-5	0.92	-1.27**	7.10	-2.88**	18.95**	10.50*
Pirsabak-85 × Yr-10	0.68	0.63**	-3.47	1.39**	-9.99	-8.36*
TD-1 × Parula	-0.16	1.00**	10.06*	14.68**	34.52**	17.15**
TD-1 × Yr-5	-0.97	-0.33*	-15.14**	-9.46**	-27.33**	-12.94**
TD-1 × Yr-10	1.13	-0.67**	5.09	-5.22**	-7.18	-4.21
Inqalab-91 × Parula	-0.16	-0.13	-1.36	-8.53**	-13.04	-5.61
Inqalab-91 × Yr-5	-2.63**	0.87**	-2.14	7.06**	2.67	-1.27
Inqalab-91 × Yr-10	2.79**	-0.73**	3.50	1.47**	10.37	6.88
Ghaznavi-98 × Parula	-1.16	2.13**	-4.56	-8.54**	-3.37	-6.11
Ghaznavi-98 × Yr-5	0.70	-0.93**	5.62	-2.88**	-4.08	-0.14
Ghaznavi-98 × Yr-10	0.46	-1.20**	-1.06	11.43**	7.45	6.25
Galaxy-13 × Parula	4.62**	-2.58**	-1.51	-1.93**	-8.79	-3.73
Galaxy-13 × Yr-5	2.48**	0.66**	2.54	3.80**	9.07	3.60
Galaxy-13 × Yr-10	-7.10**	1.92**	-1.03	-1.86**	-0.28	0.13
Shahkar-13 × Parula	-4.71**	-0.74**	1.78	-1.87**	-7.27	-4.93
Shahkar-13 × Yr-5	0.81	0.92**	-2.50	3.83**	11.13	6.14
Shahkar-13 × Yr-10	3.90**	-0.18*	0.73	-1.96**	-3.87	-1.21
S.E.	0.77	0.13	4.33	0.15	9.08	4.14
C.D <sub>0.05</sub>	1.54	0.25	8.66	0.31	18.15	8.27
C.D <sub>0.01</sub>	2.05	0.33	11.52	0.41	24.14	11.00

\*\* , \* : Significant at 1% and 5% level of probability, S.E.: Standard error, CD: Critical difference

showed positive GCA values while Parula and Yr-10 exhibited negative GCA values. For grains per spike, all the testers revealed non-significant GCA values. Overall, the lines TD-1, Galaxy-13 and Shahkar-13 and tester Yr-5 were considered as best general combiners for grains spike<sup>-1</sup>.

Among F<sub>2</sub> derivatives, the SCA values varied from that of -15.14 to 10.06 for grains spike<sup>-1</sup> (Table 5). Positive SCA values were observed in nine F<sub>2</sub> populations varied from 0.73 to 10.06, while the leftover twelve F<sub>2</sub> populations showed negative SCA values. Significant ( $P \leq 0.05$ ) positive SCA values were recorded for TD-1 × Parula (10.06), while significant ( $P \leq 0.01$ ) negative SCA values were observed by TD-1 × Yr-5 (-15.15). The highest positive SCA values were owned by F<sub>2</sub> populations *i.e.*, TD-

1 × Parula, Pirsabak-85 × Yr-5, Ghaznavi-98 × Yr-5 and TD-1 × Yr-10 with SCA values of 10.06, 7.10, 5.62 and 5.09, respectively. However, the F<sub>2</sub> populations TD-1 × Yr-5 (-15.14) and Ghaznavi-98 × Parula (-4.56) revealed the uppermost negative SCA values for grains per spike.

In lines, the GCA values varied from -4.77 to 11.94 for 1000-grain weight (Table 4). Parental lines *i.e.*, Galaxy-13 and Shahkar-13 shown positive GCA values, however, five lines presented negative GCA values. Among testers, the positive GCA values were recorded for Yr-10, while Parula and Yr-5 indicated negative GCA values. Significant ( $P \leq 0.01$ ) GCA values were possessed by two lines Galaxy-13 (11.94) and Shahkar-13 (1.84), while five other lines were recorded with significant ( $P \leq 0.01$ ) negative GCA

values. Among testers, significant ( $P \leq 0.01$ ) positive GCA values were observed for Yr-10 (5.25), while negative and significant ( $P \leq 0.01$ ) GCA values were noted for testers *i.e.*, Parula (-4.78) and Yr-5 (-0.47). Therefore, lines Galaxy-13 and Shahkar-13 and tester Yr-10 were believed to be the best general genotypes for thousand-grain weight.

For 1000-grain weight, the SCA values varied between -9.46 to 14.68 among  $F_2$  populations (Table 5). Significant ( $P \leq 0.01$ ) positive SCA values were noted for 10  $F_2$  populations while the remaining eleven populations enunciated significant ( $P \leq 0.01$ ) negative SCA values. The highest positive and significant ( $P \leq 0.01$ ) SCA values owned by  $F_2$  population TD-1 × Parula (14.68), followed by Ghaznavi-98 × Yr-10 (11.43), Inqalab-91 × Yr-5 (7.06) and Seher-06 × Parula (4.71). However, significant ( $P \leq 0.01$ ) negative SCA was acquired by  $F_2$  population TD-1 × Yr-10 (-9.46). Overall, the  $F_2$  population TD-1 × Parula and Ghaznavi-98 × Yr-10 (11.43) revealed desirable SCA values for thousand-grain weight.

For biological yield, the GCA values ranged from -9.76 to 24.06 among the parental lines (Table 4). Positive GCA values were detected in two lines *i.e.*, Galaxy-13 and Shahkar-13 while the remaining five lines showed negative GCA effects. The positive and significant GCA values possessed by line Galaxy-13 (24.06) for biological yield per plant. However, the maximum negative GCA values were observed for line Pirsabak-85 (-9.76), followed by Pirsabak-85 (-9.76) and Seher-06 (-8.11). Except Galaxy-13, all other lines showed non-significant SCA values for biological yield per plant. Among testers, significant ( $P \leq 0.05$ ) positive GCA values were recorded for Yr-10 (8.38), while Parula revealed negative and significant ( $P \leq 0.01$ ) GCA values (-3.35). However, the tester Yr-5 (1.66) owned non-significant positive GCA values for biological yield. Overall, lines Galaxy-13, Shahkar-13, and tester Yr-10 were observed as good general combiners for biological yield.

Among  $F_2$  derivatives, the SCA values varied between -27.33 to 34.52 for biological yield plant<sup>1</sup> (Table 5). Nine  $F_2$  genotypes were noted with positive SCA values, while 12  $F_2$  populations revealed negative SCA values for the said trait. Significant ( $P \leq 0.01$ ) positive SCA values were exhibited by  $F_2$  derivatives *i.e.*, TD-1 × Parula and Pirsabak-85 × Yr-5 with values of 34.52 and 18.95, respectively. However,  $F_2$  population TD-1 × Yr-5 revealed significant negative SCA values (-27.33) for biological yield per plant. Overall, the  $F_2$  populations TD-1 × Parula and Pirsabak-85 × Yr-5 were recognized as the best specific combiners for biological yield.

In parental lines, the GCA values varied between -5.58 to 11.82 for grain yield per plant (Table 4). Positive and desirable GCA values were recorded for two lines *i.e.*, Galaxy-13 and Shahkar-13, while negative GCA values were recorded in five other lines *i.e.*, Seher-06, Pirsabak-85, TD-1, Inqalab-91 and Ghaznavi-98. Significant ( $P \leq 0.01$ ) GCA values were recorded for lines Galaxy-13 (11.82) and Shahkar-13 (6.36), while negative and significant ( $P \leq 0.05$ )

GCA values were noticed for line Pirsabak-85 (-5.58). Among testers, the GCA values varied from -4.40 to 3.63 for grain yield. Tester Yr-10 revealed positive and significant ( $P \leq 0.05$ ) GCA values (3.63), followed by Yr-5 with non-significant positive GCA values. However, tester Parula showed negative and significant ( $P \leq 0.01$ ) GCA values (-4.40) for grain yield. The lines Galaxy-13, Shahkar-13 and tester Yr-10 were considered as best general combiners for grain yield.

For grain yield, the SCA values varied from -12.94 to 17.15 in  $F_2$  populations (Table 5). Nine  $F_2$  populations revealed positive SCA effects, while twelve  $F_2$  populations enunciated negative SCA values for grain yield. The significant positive SCA values were recorded in  $F_2$  populations *i.e.*, TD-1 × Parula (17.15) and Pirsabak-85 × Yr-5 (10.50).  $F_2$  populations TD-1 × Yr-5 (-12.94) and Pirsabak-85 × Yr-10 (-8.36) revealed significant negative SCA values for grain yield. Overall, the  $F_2$  populations TD-1 × Parula and Pirsabak-85 × Yr-5 were established as the best specific combinations for grain yield.

### Gene action

Overall, the GCA variances were smaller than SCA for all the variables under the study, signifying the predominance of dominance gene effects (Table 6). The dominance genetic variances were also greater than additive for all characters under consideration. Furthermore, the ratios of GCA to SCA variances and ratios of the degree of dominance were found smaller and greater than unity, respectively which also authenticated that the dominant gene action prevails in the management of these variables. Therefore, results indicated that the inheritance in all the traits was controlled by non-additive gene effects.

### Proportional contribution of populations

Line by tester  $F_2$  derivatives were recorded with the highest share to total genetic variance for the variables *i.e.*, spike length (78.42%), grains per spike (64.36%), grain yield per plant (49.48%), biological yield per plant (47.26%) and thousand-grain weight (45.06%). However, the lines contribution was the highest for days to maturity (61.22) as compared to line by tester  $F_2$  populations (36.06%) and testers (2.72%) (Table 7). Testers showed minimum contribution for all the variables compared to the line by tester  $F_2$  populations and lines. Results indicated that line by tester  $F_2$  populations and lines played a key role in handling the variation in the maturity and yield related traits.

### Discussion

Although  $F_1$  hybrids might be high yielder than parental cultivars due to heterosis, however, that  $F_1$ s performance has no sustainability, and better to make the selection at  $F_2$  level after segregation (Koemel *et al.* 2004; Longin *et al.*

**Table 6:** Genetic components for various variables in the wheat

Genetic Components	Days to maturity	Spike length	Grains spike <sup>-1</sup>	1000-grain weight	Biological yield plant <sup>-1</sup>	Grain yield plant <sup>-1</sup>
$\sigma^2$ GCA	0.666	0.037	0.247	1.673	5.995	1.350
$\sigma^2$ SCA	12.252	2.025	27.847	64.562	202.392	64.153
$\sigma^2$ A	1.332	0.075	0.493	3.346	11.991	2.701
$\sigma^2$ D	12.252	2.025	27.847	64.562	202.392	64.153
$\sigma^2$ GCA / $\sigma^2$ SCA	0.054	0.018	0.009	0.026	0.030	0.021
$\sigma^2$ A / $\sigma^2$ D	0.109	0.037	0.018	0.052	0.059	0.042
$(\sigma^2$ D / $\sigma^2$ A) <sup>1/2</sup>	3.033	5.19	7.483	4.393	4.108	4.874

**Table 7:** Proportional contribution of lines, testers and line by tester F<sub>2</sub> populations for various variables in wheat

Variables	Lines (%)	Testers (%)	Line by Tester F <sub>2</sub> Populations (%)
Days to maturity	61.22	2.72	36.06
Spike length	20.98	0.60	78.42
Grains spike <sup>-1</sup>	35.28	0.36	64.36
1000-grain weight	34.34	20.60	45.06
Biological yield plant <sup>-1</sup>	35.92	16.82	47.26
Grain yield plant <sup>-1</sup>	38.75	11.77	49.48

2015). Therefore, in the present study, the generation has been advanced and F<sub>2</sub> derivatives in comparison to parental line and testers have been studied for maturity and yield traits to make further selection for promising F<sub>2</sub> populations. Significant differences among the genotypes, lines, testers, and their line by tester F<sub>2</sub> derivatives for the majority of the traits confirmed the greater genetic variability among the wheat populations. Previous investigations also exhibited significant variations among parental lines, testers and their F<sub>1</sub> and F<sub>2</sub> derivatives in line by tester combining ability studies in wheat (Ahmad *et al.* 2017; Rahul 2017). The development of new wheat genotypes with early maturity can play a key role and to cope with abiotic stresses during the wheat crop life (Ahmed *et al.* 2017; Farooq *et al.* 2019). Lines Seher-06, Pirsabak-85, Inqalab-91, tester Parula, and their F<sub>2</sub> populations Galaxy-13 × Yr-10, Shahkar-13 × Parula and Inqalab-91 × Yr-5 revealed significant negative GCA and SCA effects and considered as best general and specific combiners for early maturity. Studies on the line by tester combining ability in wheat also identified the parent lines and testers and their F<sub>1</sub> and F<sub>2</sub> derivatives as general and specific combiners for early maturity (Afridi *et al.* 2017a, b; Ishaq *et al.* 2018; Afridi *et al.* 2019).

Parental lines Pirsabak-85, Inqalab-91, and tester Parula were identified as the best general combiners for spike length, while lines Galaxy-13, Shahkar-13 and tester Yr-5 were recognized as best cultivars for grains spike<sup>-1</sup>, thousand-grain weight, biological, and grain yield. Line by tester F<sub>2</sub> populations TD-1 × Parula, Pirsabak-85 × Yr-5 and Shahkar-13 × Yr-5 were considered as best specific combinations for grains spike<sup>-1</sup>, thousand-grain weight, biological and grain yield. Past studies on combining ability also identified the lines, testers, and their line by tester F<sub>1</sub> and F<sub>2</sub> derivatives with desirable GCA and SCA values for yield contributing variables in wheat (Khaliq *et al.* 2004; Istiqliler *et al.* 2015; Dhoot *et al.* 2020). Enhanced biological yield is of great importance when the breeder likes to get more green and dry foliage for the livestock.

Grain yield is a complex trait and is dependent upon many yield-related variables. Therefore, assortment based on component variables could be more consistent than assortment on the grain yield alone (Zare-Kohan and Heidari 2012; Fasahat *et al.* 2016).

Selection should be based both on GCA and phenotypic performance of the populations for various variables in wheat (Zare-Kohan and Heidari 2012; Shamsabadi *et al.* 2020). Observations on the performance of different populations and based on SCA values, the inferences can be made about the gene action. Greater SCA values resulting from F<sub>2</sub> populations having both parents as best general combiners may be credited to additive-by-additive gene effects. The highest SCA effects in F<sub>2</sub> populations having high × low GCA parents may be credited to promising additive and epistatic effects. High SCA effects revealed by populations with low × low GCA parents which might be due to non-allelic interaction of genes creating over dominance (Fasahat *et al.* 2016; Murugan and Kannan 2017; Din *et al.* 2021).

The present outcomes were also supported by the ratios of GCA to SCA variances and degree of dominance for all the studied parameters. Hence, it seemed that the characters were controlled by dominant gene effects. The proportions of GCA to SCA variances and degree of dominance were lesser and larger than unity, respectively for the majority of the variables in wheat which also supported the current observations (Singh *et al.* 2012; Jatav *et al.* 2017; Din *et al.* 2021).

In proportional contribution, line by tester F<sub>2</sub> derivatives contributed more compared to parental lines and testers individually for all the variables. Past studies also reported a greater share of the line by tester F<sub>1</sub> and F<sub>2</sub> populations compared to lines and testers for numerous variables in wheat (Istipliler *et al.* 2015; Jatav *et al.* 2017; Ishaq *et al.* 2018). Hence, line × tester interactions provided more genetic variability and controlled the yield and its components in wheat. Overall, the F<sub>2</sub> populations had higher



values than their parental genotypes for almost all the traits. Results also showed that SCA variances were greater than GCA and confirmed the prevalence of dominant gene action. The existence of non-additive gene action in the management of yield and its components variables in wheat was consistent with the past studies in wheat (Singh and Yadav 2011; Singh *et al.* 2012; Shamsabadi *et al.* 2020).

Hybrid varieties in self-pollinated crops (particularly cereals) have not been very successful (Koemel *et al.* 2004; Longin *et al.* 2013). In case of hybrid wheat, despite the earlier failures, renewed efforts in recent years have been made and it's still at the experimental basis (Longin 2016). Therefore, through conventional breeding the hybrid development could not be recommended in wheat.

## Conclusion

The lines Galaxy-13 and Shahkar-13 and F<sub>2</sub> populations TD-1 × Parula, Pirsabak-85 × Yr-5 and Shahkar-13 × Yr-5 were considered as best general and specific combiners for yield related traits. In the development of F<sub>2</sub> populations with best mean performance and auspicious specific combining ability effects, the high and low general combiners were found involved.

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## Author Contributions

SS and NUK planned and conducted the experiments, managed the resources, analyzed the data and made the write up. IHK help in managing the experiments and data analysis. SA and KA help in providing the breeding material and data compilation. All the authors have read and agreed to the submitted version of the manuscript.

## Conflicts of Interest

The authors declare no conflict of interest.

## Data Availability

The data included in this paper will be made available on a reasonable request.

## Ethics Approval

Ethical approval is not applicable in this study.

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