Full Length Article

Line × Tester Analysis for Combining Ability and Identification of Gene Action in F₂ Populations of Bread Wheat

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Abstract

Classical breeding has a long-term foundation in the current era of molecular breeding, and molecular marker applications are verified by classical breeding. The present research was carried out on bread wheat to determine the genetic variability, combining ability effects among F₂ populations and gene action for yield traits. Five lines Shafaq-06, SKD-1, TD-1, Benazir-13 and Khyber-87 and three testers IBWSN-24, IBWSN-192, IBWSN-205 were initially crossed during spring 2017–2018 in a line × tester fashion design. After advancing the generation the parental lines, testers and their fifteen F₂ populations were grown during the wheat season 2019-2020 in randomized complete block design with 3 replications. Significant (*P ≤ 0.01*) variation was recorded among genotypes and lines for all the tested characters. Means squares for lines × testers interactions/F₂ populations and testers exhibited significant differences (*P ≤ 0.01*) for most traits except plant height. The studied parental lines Shafaq-06, TD-1, Benazir-13 and Khyber-87, testers IBWSN-192(17–18) and IBWSN-205(17–18) and F₂ populations Shafaq-06 × IBWSN-24(17–18), Shafaq-06 × IBWSN-192(17–18), SKD-1 × IBWSN-205(17–18), TD-1 × IBWSN-192(17–18), Benazir-13 × IBWSN-192(17–18) and Benazir-13 × IBWSN-205(17–18) revealed significant (*P ≤ 0.01*) GCA and SCA effects and appeared as best general and specific combiners for numerous traits. In percent contribution to the total variance, the lines and L × T F₂ populations had a maximum share for most of the characters. Ratios of GCA to SCA variances and degree of dominance showed that all the traits were managed by dominant gene action. Non-additive gene action indicated the selection of desirable genotypes should be postponed to later segregating generations for further improvement. The said outstanding populations could be used in the future breeding program to develop high production wheat varieties for commercial cultivation. © 2022 Friends Science Publishers

Keywords: Combining ability; Gene action; Yield productive traits; F₂ population; Bread wheat

Introduction

Wheat (*Triticum aestivum* L.) is a bisexual, self-pollinated crop with chromosomal numbers of $2n = 6x = 42$ that belongs to the Poaceae family. Wheat is a major cereal crop in many countries throughout the world and it is the most widely consumed cereal food in Pakistan (Akram *et al.* 2008). Similarly, it is believed that wheat was primarily originated in the Southeast regions of the Asian continent. It adds 8.9% to the agricultural value-added and 1.6 percent to Pakistan's GDP (PBS 2018). Therefore, wheat provides food to 36% of the global population and contributes 20% of the food calories required for healthy growth (Khan and Naqvi 2011; Bhanu *et al.* 2018). Wheat is the most significant and widely adapted grain crop in Pakistan. Wheat is produced as a rain-fed crop on more than 52% of the land in Khyber Pakhtunkhwa. Its average yield is comparably poor due to a lack of acceptable wheat cultivars for the area's climatic conditions and a proper time of sowing (Ali and Akmal 2016).

Wheat production on a global level must continue to increase 2% annually until 2030 to meet future demands of the growing population and maintain prosperity growth (Anonymous 2015). The worldwide wheat cultivated area was 215.47 million hectares which producing 731.28

million metric tons (USDA 2019). Similarly, China, India, Russia, the United States, France, Canada, Germany and Pakistan are indeed the world's top wheat producers, releasing 126, 95, 60, 55, 39, 29, 28 and 26 million metric tons of wheat annually (Food Outlook 2017). Pakistan is one of the top ten wheat-producing nations on this planet, and the fourth-largest producer in Asia. Bread wheat was sown on 8.74 million hectares across the country in 2018–19, yielding 25.19 million tons with an average yield of 2883 kg ha^{-1} (PBS 2018). Wheat crop in Pakistan grew at a pace of 0.5 percent every year (Pakistan Economic Survey 2018–2019). Similarly, in Khyber Pakhtunkhwa (KPK), bread wheat was grown on 0.74 million hectares and yielded 1.36 million tons with a total production of 1860 kg ha^{-1} (PBS 2017). Furthermore, wheat was cultivated on 0.38 million hectares in the rainfed area, yielding 0.57 million tons, while the irrigated range produced 0.79 million tons in KPK (Agriculture statistics Khyber Pakhtunkhwa, Peshawar 2016–2017). Similarly, Punjab supplied 76% of total production, Sindh 16%, KP 5% and Baluchistan 3% (Laghari *et al.* 2016).

Selection of best parents and choice of good mating design is the key to success of plant breeding programs. In any crop, line × tester is used by plant breeders and geneticists to make new populations and provide a base for additional selection and develop new potential genotypes with desirable traits (Akbar *et al*. 2009). Line × tester analysis, also known as the modified version of the top cross scheme, is an evaluation technique developed by Kempthorne (1957). In the top cross, only one tester is used, whereas several testers are used in line × tester mating. The first stage in determining the efficacy of new lines is to cross them with a common parent (tester) and compare their hybrid performance (test cross or top cross). Knowing how combining ability (CA) influences yield and its components can help you identify genotype variations and the nature and intensity of gene acts (Fasahat *et al.* 2016). Previous studies on combining ability and genetic architecture in wheat using the line × tester mating techniques revealed that parental cultivars were substantial for specific combining ability (SCA) and general combining ability (GCA) effects in grain yield and yield association traits in bread wheat among and with their F$_2$ population, respectively (Murugan and Kannan 2017; Rahul 2017; Hama-Amin and Towfiq 2019).

Information of GCA and SCA influencing yield and its components has become increasingly important for plant breeders to select appropriate parents while, developing high-yielding synthetic and hybrid cultivars (Aslam *et al*. 2014). Besides other available techniques to improve the existing cultivar or develop a new line, Line × tester analysis is one of the most dominant tools for estimating the GCA of parents and selecting right parents and crosses with high SCA (Rashid *et al*. 2007). Assessing the effects of GCA for yield components is very powerful in parental selection of self-pollinated crops including wheat (Bhateria *et al.* 2006). Grain yield, like most attributes, has been

reported to be influenced by non-additive gene effects. (Sulayman and Akguni 2007). On the other hand, Tambe *et al.* (2013) found that the number of tillers plant^{-1} is controlled by additive gene action.

Given the preceding, the current investigation was designed to identify possible parental lines and testers, and their F$_2$ populations by evaluating their GCA and SCA effects. With all of these philosophies in mind, this study was conducted for the estimation of genetic parameters with production traits in selected lines and to identify general and specific combining ability of genotype for future breeding program and to study the gene action and gene magnitude among the selected lines and F$_2$ populations.

Materials and Methods

Experimental site and conduct of experiment

The study entitled "line × tester analysis for combining ability and identification of gene action in F2 populations of bread wheat" was carried out at the Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera (Pakistan) located at 34^0 North Latitude, 72^0 East longitudes and 28^0 altitudes under normal conditions during 2019–2020. Five wheats (hereafter referred to as female lines) *i.e.,* SKD-1, Khyber-87, Shafaq-06, Benazir-13, TD-1 and three wheat genotypes (hereafter referred to as male testers) *i.e.*, IBWSN-24(17–18), IBWSN-192(17–18), IBWSN-205(17–18), [acquired from International Bread Wheat Screening Nursery (IBWSN), CIMMYT, Mexico], were initially crossed during 2017–2018 in at CCRI in line × tester fashion. Therefore, during 2019–2020 wheat season, the five lines, three testers and 15 F$_2$ populations were assessed under normal conditions. The preceding experimental material, which included overall 23 genotypes (8 parents and 15 F$_2$ populations) was sown in randomized complete block design having three replications, every single genotype was sown in four rows of two meters length, with spacing of 30 cm and 15 cm between rows and plants, respectively.

Cultural practices

All agronomic cultural procedures were completed before planting, and the experimental area was properly irrigated for ideal seedbed conditions. Therefore, the soil was loose, fine, levelled and crushed each time the experimental sowing area was ploughed with a deep plough and then harrowed with planking. The fertilizer was applied at the rate of 120:90:60 NPK kg ha^{-1}. Sowing was carried out during 3rd week of November by hand sowing machine, after germination, thinning was done for maintaining plant to plant distance while, dominant weeds and roughing (to maintain the variety purity) was done manually without application of insecticide, pesticide during entire crop growing season. Data was recorded on fourteen parameters by using ten randomly selected plants in each plot.

Data recorded on quantitative traits to be measured

Ten plants were selected from every single entry and data were noted on the consequent traits at proper time. In almost all breeding or selection trials, prime importance is given to the heading of wheat genotypes. This trait is important for isolating the early, moderate or late genotypes for wide or narrow adaptation. Days to heading was noted on or after the date of sowing till the date of spike appearance in every single plot. The third important yield related trait is the plant height or length of the tiller. Plant height was measured in centimeters as the distance from the plant root of the soil surface to the tip of the spike excluding awns, after detecting the physiological maturity. Plant height is an equally significant for breeders and farmers as it is an absolute indicator of whether to recommend the taller or dwarf wheat variety for a specific area. Suppose for the dwarf varieties are good for regions with heavy wind flow. Similarly, the tall genotypes were good for preserving the moisture in the soil. Number of leaves and area of leaf is equally important just like days to maturity, heading and height while dealing with wheat crop. Flag leaf area is an indirect metric for identifying photosynthetically active genotypes in a given area. Normally, the genotypes with broader leaf area are selected and recommended for irrigated regions whereas, the genotypes with narrow leaf area, assembled vertically are recommended or selected for drought or low-rainfall regions. The following formula was used to calculate the flag leaf area, as described by Francis *et al*. (1969). Flag leaf area = Leaf length × Leaf width × 0.75.

Number of tillers plant[-1] is utilized for direct selection of bread wheat genotypes. More quantity of tillers plants[-1] is directly proportional with the grain yield. Using ten arbitrary plants and taking an average was count the quantity of productive tillers of every single genotype. These ten arbitrarily selected plants were counted for numbers of tillers plant[-1] and the sample extent and accurate demonstrative of the complete plot. Spike length is a direct selection criterion once more. A long, extended spike with compacted grains or spikelets can hold a large number of grains. As a result, the space between the bottom of the wheat plant spike and the tip of the ending spikelet, excluding awns, was determined as the wheat plant spike length of every single entry utilizing ten spikes and the mean score value was determined. Grain yield is the end product, and in many situations, breeders rely on grain yield to choose appropriate and fixed genotypes due to a lack of funds. At harvest, each experimental entry was threshed individually and grain yield was calculated in kilograms for each variety. After that, the data was transformed to kg per hectare. Harvest index is also regarded as a supplementary yield-contributing factor. The grain fraction and biomass of bread wheat were determined using the harvest index ratio. Harvest index was calculated by dividing grain yield by biological yield for each genotype and then converting it to a percentage using the formula below:

$$Harvest\ index\ (\%) = Grain\ yield/Biological\ yield \times 100$$

Statistical analysis

The data collected on different agronomic and yield-related characteristics was statistically evaluated using excel sheet, a computer program designed for RCBD. To assess genetic progress the means were separated using the LSD test at a 5% level of probability was estimated from the mean squares of ANOVA.

Combining ability effects

To filter out significant differences, the data were run *via* an analysis of variance (Steel *et al*. 1997). Characters with considerable variances were more likely to be subjected to Kempthorne (1957) line × tester examination to approximate general and specific combining ability.

Genetic components

Genetic components were calculated, according to the Singh and Chaudhary (1985).

Gene action and degree of dominance

When the value of general combining ability variance to specific combining ability variance (σ^2GCA/σ^2SCA) was smaller than one, were taken as preponderance of non-additive type of gene action, and more than one as additive gene action. In addition, equivalent to one were taken as equal effects of additive and non-additive type of gene action (Singh and Chaudhary 1985). Likewise, inferior than one $(\sigma^2D/\sigma^2A)^{1/2}$, were taken as preponderance of additive gene effects, more than one as non-additive, and equal to one was taken as equality of additive and non-additive effects.

Proportional contribution of populations to total variance

Singh and Chaudhary (1985) looked at the proportional contribution of maternal lines, paternal testers and their lines × testers interactions to overall variance in percentage.

Results

Analysis of Variance

The results obtained through ANOVA stated that the variations observed enough for the successful selections for suitable material used in this experiment because selection and variation are the base pillars for improvement in plant breeding. The female parent (lines) exhibited highly significant variations (*P ≤ 0.01*) for all the traits. Moreover, the male parent (Tester) also showed highly significant differences (*P ≤ 0.01*) for flag leaf area, tillers plant[-1], spike length, grain yield and harvest index. Interactions of lines ×

Table 1: List of breeding materials of 23 wheat genotypes were studied for selected morphological and production traits during the year 2019–2020 at CCRI, Pirsabak Nowshera

S. No	Parental genotypes	S. No	F$_2$ Populations
1	Shafaq-06	4	SKD-1 × IBWSN-24(17-18)
2	SKD-1	5	SKD-1 × IBWSN-192(17-18)
3	TD-1	6	SKD-1 × IBWSN-205(17-18)
4	Benazir-13	7	TD-1 × IBWSN-24(17-18)
5	Khyber-87	8	TD-1 × IBWSN-192(17-18)
Testers		9	TD-1 × IBWSN-205(17-18)
1	IBWSN-24(17-18)	10	Benazir-13 × IBWSN-24(17-18)
2	IBWSN-192(17-18)	11	Benazir-13 × IBWSN-192(17-18)
3	IBWSN-205(17-18	12	Benazir-13 × IBWSN-205(17-18)
F$_2$ Populations		13	Khyber-87 × IBWSN-24(17-18)
1	Shafaq-06 × IBWSN-24(17-18)	14	Khyber-87 × IBWSN-192(17-18)
2	Shafaq-06 × IBWSN-192(17-18)	15	Khyber-87 × IBWSN-205(17-18)
3	Shafaq-06 × IBWSN-205(17-18)		

Table 2: Mean squares for various traits of 8 parents and 15 F$_2$ populations, were evaluated in lines 5 × 3 testers mating design of bread wheat during the year 2019–2020 at CCRI, Pirsabak Nowshera

Source of variation	DF	DH	PH	FLA	Tp^{-1}	SL	GYLD	HI
Replications (r)	2	4.45	35.49	0.21	0.45*	0.12	9553.39	2.87
Genotypes (g)	22	57.51**	265.32**	4.56**	0.65**	2.03**	550399.65**	10.87**
Parents (p)	7	12.42*	97.76**	4.39**	0.53**	0.90*	428285.38**	4.16**
Parents *vs.* Crosses	1	615.22**	3873.14**	26.57**	2.48**	4.46**	3150680.39**	21.68**
Crosses (c)	14	40.21**	91.40**	3.08**	0.58**	2.43^{NS}	425722.44**	13.46**
Lines (l)	4	99.02**	223.74**	3.40**	0.61**	2.51**	1132910.49**	34.86**
Testers (t)	2	28.16*	19.36^{NS}	6.01**	0.85**	5.55**	325140.43**	3.87*
Lines × Testers	8	13.82*	43.24^{NS}	2.18**	0.50**	1.60**	97273.92**	5.15**
Error	44	5.16	24.30	0.53	0.14	0.27	19975.06	1.07
C.V.%		1.97	5.44	2.40	3.44	4.51	5.32	3.08

*: significant at 0.05%; **: significant at 0.01%; NS: Non-significant at 5 and 1% level of significance

testers accounted highly significant variations ($P \leq 0.01$) for traits *i.e.,* flag leaf area, tillers plant^{-1}, spike length, grain yield and harvest index of the characters except plant height while, bearing of heading on the other hand, showed significant ($P \leq 0.05$) variations (Table 1 and 2).

Genetic changeability among parental genotypes and line × tester F$_2$ populations

No. of days to heading

In parental lines, the days to heading ranged between 107.00 days (Shafaq-06) to 112.33 days (Benazir-13), testers ranged between 111.67 days (IBWSN-24(17–18)) to 113.33 days (IBWSN-192(17–18)) while in F$_2$ population ranged between 112.67 days (SKD-1) × (IBWSN-24(17–18)) to 124.00 days (Khyber-87) × (IBWSN-192(17–18)). Among all the tested wheat genotypes, the maximum numbers of days to heading (124.00) were detected in following two F$_2$ populations *i.e.,* (Khyber-87) × (IBWSN-192(17–18)) and (Khyber-87) × (IBWSN-205(17–18)). However, in lines, minimum numbers of days to heading (107.00) was observed in (Shafaq-06), in tester least numbers of days to heading (IBWSN-192(17–18)) (111.67 days). Overall, the F$_2$ population means ranged is high than the parental genotypes (Table 3).

Plant height

In maternal lines, the plant height ranged between 71.67 cm

(Shafaq-06) to 84.67 cm (Benazir-13) and paternal testers ranged between 80.00 cm (IBWSN-24(17–18)) to 86.00 cm (IBWSN-205(17–18)). In F$_2$ populations, for plant height ranged between 86.67 cm (Shafaq-06) × (IBWSN-24(17–18)) to 106.67 cm (Khyber-87) × (IBWSN-205(17–18)). In female lines *i.e.,* short stature genotype was Shafaq-06 (71.67 cm) and TD-1 (72.67 cm). In F$_2$ generations minimum plant height was recorded by (Shafqat-06) × (IBWSN-24(17–18)) (86.67 cm), followed by (Shafqat-06) × (IBWSN-192(17–18)) (89.33 cm) (Table 3).

Flag leaf area

In parental lines, mean value for flag leaf area ranged between 27.35 cm^2 (SKD-1) to 31.28 cm^2 (Khyber-87), testers ranged between 28.68 cm^2 (IBWSN-24(17–18)) to 30.65 cm^2 (IBWSN-192(17–18)) (Table 3). And the F$_2$ populations the average value for flag leaf area ranged between 28.59 cm^2 (Shafaq-06) × (IBWSN-192(17–18)) and 32.25 cm^2 (Khyber-87) × (IBWSN-24(17–18)). However, the highest average area was observed in F$_2$ populations *i.e.,* (Khyber-87) × (IBWSN-24(17–18)) (32.25 cm^2) accompanied by F$_2$ populations (Benazir-13) × (IBWSN-205(17–18)) (31.66 cm^2). Moreover, the minimum average area was observed in maternal line (SKD-1) (27.35 cm^2) for flag leaf area (Table 3).

Tillers per plant

In maternal lines, mean values for tillers plant^{-1} ranged

Table 3: Mean performance of lines, testers, and F_2 population for various traits were evaluated in lines 5 × 3 testers mating design of bread wheat during the year 2019–2020 at CCRI, Pirsabak Nowshera

Lines, testers and F_2 populations	DH	PH	PL	FLA	Tp^{-1}	SL	GYLD	HI
Lines								
Shafaq-06	107.00	71.67	31.33	28.99	10.17	11.07	1972.22	32.84
SKD-1	111.67	78.00	27.68	27.35	10.10	11.32	1972.22	34.96
TD-1	110.00	72.67	31.63	29.08	11.40	10.91	2294.44	32.55
Benazir-13	112.33	84.67	34.32	29.50	10.20	11.14	2283.33	32.96
Khyber-87	112.00	84.33	34.46	31.28	10.20	10.17	2277.78	31.87
Means	110.60	78.27	31.88	29.24	10.41	10.92	2160.00	33.03
Testers								
IBWSN-24(17-18)	111.67	80.00	29.53	28.68	10.40	11.59	2244.44	34.13
IBWSN-192(17-18)	113.33	85.00	29.76	30.65	10.53	11.14	2802.78	32.10
IBWSN-205(17-18)	113.00	86.00	32.98	28.95	10.53	12.07	3047.22	31.44
Means	112.67	83.67	30.76	29.43	10.49	11.60	2698.15	32.56
F_2 populations								
Shafaq-06 × IBWSN-24(17-18)	114.33	86.67	31.59	31.03	10.50	11.24	2430.56	30.78
Shafaq-06 × IBWSN-192(17-18)	115.67	89.33	35.06	28.59	10.03	11.73	2866.67	31.58
Shafaq-06 × IBWSN-205(17-18)	118.00	94.00	37.23	30.59	10.97	11.27	2650.00	31.77
SKD-1 × IBWSN-24(17-18)	112.67	97.33	39.59	28.92	10.20	11.16	2308.33	34.42
SKD-1 × IBWSN-192(17-18)	117.00	100.67	37.41	29.60	10.33	10.57	2458.33	33.47
SKD-1 × IBWSN-205(17-18)	117.00	92.67	38.63	31.51	11.47	13.57	2550.00	34.61
TD-1 × IBWSN-24(17-18)	117.33	95.00	31.91	31.28	11.37	11.08	2280.56	36.32
TD-1 × IBWSN-192(17-18)	112.67	94.67	34.47	29.84	10.77	10.34	3061.11	33.68
TD-1 × IBWSN-205(17-18)	114.00	92.67	33.62	30.45	11.17	11.83	2519.44	34.43
Benazir-13 × IBWSN-24(17-18)	117.33	98.67	33.45	31.01	11.17	12.69	2975.00	31.17
Benazir-13 × IBWSN-192(17-18)	118.33	97.00	32.15	30.40	10.87	12.31	2970.83	34.39
Benazir-13 × IBWSN-205(17-18)	122.33	90.67	36.51	31.66	10.53	12.50	3136.11	33.82
Khyber-87 × IBWSN-24(17-18)	120.00	99.33	35.46	32.25	11.33	11.31	3240.28	36.52
Khyber-87 × IBWSN-192(17-18)	124.00	105.00	38.43	31.00	10.87	11.24	3305.56	35.11
Khyber-87 × IBWSN-205(17-18)	124.00	106.67	38.41	31.06	11.03	12.82	3404.17	38.40
Means	117.64	96.02	35.59	30.61	10.84	11.71	2810.46	34.03
Over all mean	115.46	90.55	34.16	30.16	10.70	11.52	2654.41	33.62
$LSD_{0.05}$	3.74	8.11	2.46	1.19	0.61	0.86	232.57	1.70

between 10.10 (SKD-1) to 11.40 (TD-1), besides paternal testers mean values ranged 10.40 (IBWSN-24(17–18)) to 10.53 (IBWSN-192(17–18)). In F_2 populations for tillers plant^{-1} average value ranged between 10.03 (Shafaq-06) × (IBWSN-192(17–18)) to 11.47 (SKD-1) × (IBWSN-205(17–18)). The F_2 populations showed more numbers of tillers plant^{-1} (SKD-1) × (IBWSN-205(17–18)) followed by (TD-1) × (IBWSN-24(17–18)) (11.37). Over all means, of tillers plant^{-1} in F_2 population is greater than both lines and tester (Table 3).

Spike length

Minimum (10.17 cm) and maximum values (11.32 cm) for spike length was found in lines Khyber-87 and (SKD-1), paternal testers average value for spike length ranged between (IBWSN-192(17–18)) (11.14 cm) to (IBWSN-205(17–18)) (12.07 cm). In F_2 generations the mean value for spike length starting from 10.34 cm (TD-1) × (IBWSN-192(17–18)) to 13.57 cm (SKD-1) × (IBWSN-205(17–18)). F_2 populations had the longest average value for spike length *i.e.,* (SKD-1) × (IBWSN-205(17–18)) (13.57 cm) and (Khyber-87) × (IBWSN-205(17–18)) (12.82 cm). In the future the F_2 populations (Khyber-87) × (IBWSN-205(17–18)) and (SKD-1) × (IBWSN-205(17–18)) will be used to improve spike length in wheat breeding projects (Table 3).

Grain yield

In maternal lines, the mean value for grain yield ranged between Shafaq-06 and SKD-1 (1972.22 kg ha^{-1}) to TD-1 (2294.44 kg ha^{-1}) while, the paternal testers ranged between 2244.44 kg ha^{-1} (IBWSN-24(17-18) to 3047.22 kg ha^{-1} (IBWSN-205(17-18)) (Table 3). In F_2 populations, the mean value for grain yield ranged between 2280.56 kg ha^{-1} (TD-1) × (IBWSN-24(17-18)) to 3404.17 kg ha^{-1} (Khyber-87) × (IBWSN-205(17-18)). In F_2 populations, the maximum mean for grains yield were observed in F_2 generations *i.e.,* (Khyber-87) × (IBWSN-205(17–18)) (3404.17 kg ha^{-1}) followed by (Khyber-87) × (IBWSN-192(17–18)) (3305.56 kg ha^{-1}). Therefore, the F_2 populations, *i.e.,* (Khyber-87) × (IBWSN-192(17–18)) and (Khyber-87) × (IBWSN-205(17–18)) were recommended for selection and use in next wheat breeding initiatives aimed at increasing grain yield.

Harvest index

Harvest index of wheat parental genotypes *i.e.,* In lines the average for harvest index ranged between 31.87% (Khyber-87) to 34.96% (SKD-1) while, the testers ranged between 31.44% (IBWSN-205(17-18)) to 34.13% (IBWSN-24(17–18)). In F_2 populations, the average for harvest index ranged between 30.78% (Shafaq-06) × (IBWSN-24(17–18)) and

38.40% (Khyber-87) × (IBWSN-205(17–18)). F_2 populations, the highest average for harvest index was observed in F_2 populations *i.e.,* (Khyber-87) × (IBWSN-205(17–18)) (38.40%) followed by (Khyber-87) × (IBWSN-24(17–18)) (Table 3).

Combining ability analysis

Greater genetic changes in the mating material allows for a more detailed examination and partitioning of combining ability into its components, such as general and specific combining ability impacts in lines, testers, and line by tester interactions (Table 1 and 2). According to GCA and SCA impacts, Positive values are desirable for most crop plants characteristics, such as growth and yield yield-related attributes. Negative GCA and SCA impacts, on the other hand, are desirable for characters where minimum values are essential and appealing, such as early flowering.

General and specific combining ability effects

In maternal lines, for days to heading GCA effects ranged between -2.09 to 5.02. As a good general combiner, maternal line (TD-1) (-2.98) had highly significant ($P ≤ 0.01$) and highest negative desired GCA effects, and female line (SKD-1) -2.09 had significant ($P ≤ 0.05$) negative GCA effects. Similarly, highly significant ($P ≤ 0.01$) and highest positive GCA effects were found in line (Khyber-87) (5.02) followed by line (Benazir-13) (1.69). The GCA effects for days to heading ranged from -1.31 to 1.42 in the situation of paternal testers. Therefore, significant ($P ≤ 0.05$) maximum positive GCA effects was detected in male tester (IBWSN-205(17–18)) (1.42) and the maximum negative GCA effects were exhibited in the following paternal testers *i.e.,* (IBWSN-24(17–18)) (-1.31) and (IBWSN-192(17–18)) (-0.11) (Table 4).

In the F_2 population, the SCA impacts for days to heading ranged from -2.09 to 3.98. Sixty percent of the F_2 populations showed negative and desirable SCA effects ranged between -2.09 to -0.09 while, the other six F_2 populations revealed positive SCA effects ranged between 0.02 to 3.98 for days to maturity. The significant ($P ≤ 0.05$) positive SCA effects were detected in F_2 population (TD-1) × (IBWSN-24(17–18)) (3.98*). Therefore, the following F_2 population had the highest negative and desirable SCA effects *i.e.,* (TD-1) × (IBWSN-205(17–18)) (-2.09) followed by (TD-1) × (IBWSN-192(17–18)) (-1.89) (Table 5).

For plant height, in lines the GCA effects ranged between -6.02 and 7.64. Therefore, the highly significant negative and desirable GCA impacts were recognized in female line (Shafaq-06) (-6.02**), whereas highly significant and highest positive GCA impacts were detected in maternal line (Khyber-87) with the value of 7.64**. In state of testers, the GCA effects ranged between -0.69 and 1.31 for plant height. In three testers, there are no significant GCA effects were observed for plant height. As

a result, in maternal lines and paternal testers, the maximum negative value and desirable GCA effects were distinguished in line (Shafaq-06) because highly significant which is more contributed and recognized as good general combiners for plant height (Table 4).

In F_2 populations, SCA effects calculated for plant height varied from -4.09 to 4.69. Therefore, 46% F_2 generations exhibited negative and desirable SCA effects exhibited ranged between -4.09 and -0.76. For plant height, the remaining eight F_2 generations had positive SCA effects between 0.02 and 4.69. For the said character, there are no substantial SCA consequences. However, in F_2 populations the negative SCA impacts on plant height were seen in (Benazir-13) × (IBWSN-205(17–18)) with highest SCA effects value of -4.09; whereas, the highest positive SCA effects were manifested in F_2 population (Shafaq-06) × (IBWSN-205(17–18)) with highest SCA effects value of 4.69 for plant height (Table 5).

The general combine ability (GCA) influences on flag leaf area in (females) lines ranged from -0.58 to 0.83. Maternal line (SKD-1) (-0.58*) showed significant negative GCA consequences whereas, maternal line (Khyber-87) (0.83**) showed highly significant ($P ≤ 0.01$) beneficial GCA effects for flag leaf area. In state of paternal testers, the GCA impacts for flag leaf area starting from -0.73 to 0.45. Therefore, highly significant ($P ≤ 0.01$) negative GCA impacts were manifested by paternal tester 'IBWSN-192(17–18)' (-0.73**) whereas (IBWSN-205(17–18)) (0.45*) displayed the maximum significant ($P ≤ 0.05$) positive GCA impacts for for flag leaf area. Overall, female line 'Khyber-87' and 'IBWSN-205(17–18)' was known as the good general connecters for the said character (Table 4).

Specific combination ability (SCA) effects on flag leaf area ranged from -1.38 to 1.05 in F_2 populations. 33% F_2 generations revealed negative SCA impacts ranged between -1.38 and -0.83 whereas, the eight F_2 generations had positive SCA impacts on flag leaf area (0.04 to 1.05). Therefore, in the F_2 generation (SKD-1) × (IBWSN-24(17–18)) (-1.38**) was seen highly significant ($P ≤ 0.01$) adverse SCA effects. Furthermore, the significant ($P ≤ 0.05$) and highest positive SCA impacts was recorded in F_2 generation (SKD-1) × (IBWSN-205(17–18)) (1.05*) and identified as good specific combiner for flag leaf area (Table 5).

In parental lines, for tillers plant^{-1} the general combine ability (GCA) effects ranged between -0.34 and 0.26. Highly significant ($P ≤ 0.01$) negative GCA impacts were attained by maternal line (Shafaq-06) (-0.34**). Whereas, the significant ($P ≤ 0.05$) and maximum positive useful GCA impacts were noted maternal line (TD-1) (0.26*) and (Khyber-87) (0.24*) for tillers plant^{-1}. In state of paternal testers, for tillers plant^{-1} the GCA impacts ranged between -0.27 and 0.19. The paternal tester (IBWSN-192(17–18)) (-0.27**) achieved highly significant ($P ≤ 0.01$) negative GCA influences whereas was paternal tester (IBWSN-205(17–18)) (0.19*) achieved significant maximal positive GCA influences for tillers plant^{-1}. Overall, female lines (TD-1), (Khyber-87) and male tester (IBWSN-205(17–18))

Table 4: General combine ability (GCA) effects among lines and testers for various traits were evaluated in lines 5 × 3 testers mating design of bread wheat during the year 2019–20 at CCRI, Pirsabak Nowshera

Parental genotypes	DH	PH	FLA	Tp^{-1}	SL	GYLD	HI
Lines							
Shafaq-06	-1.64	-6.02**	-0.54	-0.34**	-0.28*	-161.51**	-2.65**
SKD-1	-2.09*	0.87	-0.58*	-0.17	0.04	-371.51**	0.14
TD-1	-2.98**	-1.91	-0.10	0.26*	-0.62**	-190.07**	0.77
Benazir-13	1.69	-0.58	0.39	0.02	0.78**	216.82**	-0.90*
Khyber-87	5.02**	7.64**	0.83**	0.24*	0.08	506.27**	2.65**
S.E.	0.89	1.90	0.28	0.11	0.12	45.72	0.38
S.E (gi - gj) lines	1.26	2.68	0.39	0.15	0.17	64.66	0.54
$CD_{0.05}$	2.59	5.50	0.81	0.31	0.35	132.55	1.11
$CD_{0.01}$	3.48	7.41	1.09	0.42	0.47	178.46	1.49
Testers							
IBWSN-24(17-18)	-1.31	-0.62	0.28	0.07	-0.21*	-163.44**	-0.19
IBWSN-192(17-18)	-0.11	1.31	-0.73**	-0.27**	-0.47**	122.02**	-0.38
IBWSN-205(17-18)	1.42*	-0.69	0.45*	0.19*	0.69**	41.42	0.57
S.E.	0.69	1.47	0.22	0.08	0.09	35.42	0.30
S.E (gTi - gTj) testers	0.98	2.08	0.31	0.12	0.13	50.09	0.42
$CD_{0.05}$	2.00	4.26	0.63	0.24	0.27	102.68	0.86
$CD_{0.01}$	2.70	5.74	0.84	0.33	0.36	138.24	1.16

S.E (gi - gj) lines = Standard error between lines, S.E (gTi - gTj) testers = Standard error between testers, and CD = Critical difference.

Table 5: Specific combining ability effects among line × tester/F_2 populations for various traits were evaluated in lines 5 × 3 testers mating design of bread wheat during the year 2019–20 at CCRI, Pirsabak Nowshera

F_2 populations	DH	PH	FLA	Tp^{-1}	SL	GYLD	HI
Shafaq-06 × IBWSN-24(17-18)	-0.36	-2.71	0.67	-0.07	0.05	-54.89	-0.40
Shafaq-06 × IBWSN-192(17-18)	-0.22	-1.98	-0.75	-0.20	0.76**	95.64	0.59
Shafaq-06 × IBWSN-205(17-18)	0.58	4.69	0.07	0.27	-0.81**	-40.76	-0.19
SKD-1 × IBWSN-24(17-18)	-1.58	1.07	-1.38**	-0.54**	-0.37	33.11	0.44
SKD-1 × IBWSN-192(17-18)	1.56	2.47	0.33	-0.07	-0.73**	-102.69	-0.33
SKD-1 × IBWSN-205(17-18)	0.02	-3.53	1.05*	0.61**	1.10**	69.58	-0.12
TD-1 × IBWSN-24(17-18)	3.98*	1.51	0.46	0.19	0.22	-176.33*	1.68*
TD-1 × IBWSN-192(17-18)	-1.89	-0.76	0.04	-0.07	-0.28	318.53**	-0.73
TD-1 × IBWSN-205(17-18)	-2.09	-0.76	-0.50	-0.13	0.06	-142.20	-0.95
Benazir-13 × IBWSN-24(17-18)	-0.69	3.84	-0.29	0.24	0.38	111.11	-1.76*
Benazir-13 × IBWSN-192(17-18)	-0.89	0.24	0.09	0.28	0.29	-178.36*	1.64*
Benazir-13 × IBWSN-205(17-18)	1.58	-4.09	0.21	-0.52*	-0.68**	67.24	0.12
Khyber-87 × IBWSN-24(17-18)	-1.36	-3.71	0.54	0.18	-0.28	87.00	0.03
Khyber-87 × IBWSN-192(17-18)	1.44	0.02	0.29	0.06	-0.04	-133.13	-1.17
Khyber-87 × IBWSN-205(17-18)	-0.09	3.69	-0.83	-0.24	0.32	46.13	1.14
S.E.	1.55	3.29	0.48	0.19	0.21	79.19	0.66
S.E (sij - skl)	2.19	4.65	0.68	0.26	0.30	112.00	0.94
$CD_{0.05}$	4.48	9.53	1.40	0.54	0.61	229.59	1.92
$CD_{0.01}$	6.03	12.83	1.88	0.73	0.82	309.11	2.59

S.E. = Standard error for SCA effects, S.E (sij - skl) = Standard error between Crosses SCA effects, CD = Critical difference

considered to be a major general combiner for boosting tiller capacity (Table 4).

In F_2 generations, for tillers plant^{-1} the specific combine ability (SCA) impacts ranged starting from -0.54 to 0.61. Therefore, for tillers plant^{-1} the positive SCA effects varied from 0.06 to 0.61 in the seven F_2 populations. The highly significant negative SCA impacts were exhibited in F_2 populations (SKD-1) × (IBWSN-24(17–18)) (-0.54**). However, highly significant and highest positive SCA impacts were recorded in F_2 generation (SKD-1) × (IBWSN-205(17–18)) (0.61**) and identified as the best specific combiner, which is more contributed and for enhancement in tillers plant^{-1} (Table 5).

In maternal lines, for spike length, the general combine ability (GCA) influences starting from -0.62 to 0.78. Therefore, significant ($P \leq 0.01$) and highest positive GCA influences were exhibited by maternal line (Benazir-

13) (0.78**), whereas the highly significant and maximum negative GCA influences were recorded by maternal line (TD-1) (-0.62**) for spike length. In case of paternal testers, for spike length, the general combine ability (GCA) effect ranged between -0.47 and 0.69. ($P \leq 0.01$) significant positive GCA influences were showed by male tester (IBWSN-205(17–18)) (0.69**), while the ($P \leq 0.01$) significant and supreme negative GCA influences were recorded by paternal tester (IBWSN-192(17–18)) (-0.47**). In total female lines (Benazir-13) and male tester (IBWSN-205(17–18)) was rated as the finest general combiner for spike length (Table 4).

The SCA influences for spike length in the F_2 generations, starting from -0.81 to 1.10. The 53.33% F_2 populations displayed positive and useful SCA influences ranged between 0.05 and 1.10, whereas remaining 46.67% revealed negative SCA effects (-0.81 and -0.04). Therefore,

for spike length revealed that highly significant and maximum positive SCA influences were recorded in F_2 population (SKD-1) × (IBWSN-205(17–18)) (1.10**) and were discovered to be the most effective specific cross combinations. However, the F_2 population (Shafaq-06) × (IBWSN-205(17–18)) (-0.81**) had the most highly significant ($P \leq 0.01$) and largest negative SCA impacts for spike length (Table 5).

The general combine ability (GCA) influences on grain production in parental lines ranged from -190.07 to 506.27. Highly significant ($P \leq 0.01$) and positive favorable GCA influences were detected in female line (Khyber-87) (506.27**) and (Benazir-130 (216.82**) while, the highly significant ($P \leq 0.01$) and maximum negative undesirable GCA influences were detected in maternal line (SKD-1) (-371.51**) for seed yield (kg ha^{-1}). In state of paternal testers, for grain yield (kg ha^{-1}) the GCA influences ranged between -163.44 and 122.02. The required favorable positive GCA influences were found in paternal tester (IBWSN-192(17–18)) (122.02**) that were highly significant ($P \leq 0.01$) while, ($P \leq 0.01$) significant and maximum undesired negative GCA influences were recorded in paternal tester (IBWSN-24(17–18)) (-163.44**). In total maternal (Khyber-87), (Benazir-13) and male tester (IBWSN-192(17–18)) were regarded as the most effective general combiners in terms of grain yield (Table 4).

The specific combine ability (SCA) impacts on grain yield in F_2 populations ranged from -178.36 to 318.53. In counting of hundred 53.33% F_2 generations were displayed positive and desired SCA impacts ranged between 33.11 and 318.53. Highly significant ($P \leq 0.01$) and favorable positive SCA impacts were noted in F_2 generation (TD-1) × (IBWSN-192(17–18)) (318.53**), which was more suitable as the best specific cross combination for the development of grain yield. Likewise, maximum undesired negative SCA effects were detected in F_2 population (TD-1) × (IBWSN-24(17–18)) (-176.33*) (Table 5).

In parental lines, for harvest index the general combine ability (GCA) effects ranged between -2.65 and 2.65. Highly significant ($P \leq 0.01$) positive and favorable GCA influences were noted in female line (Khyber-87) (2.65**) while the significant ($P \leq 0.01$) and maximum negative undesirable GCA influences were observed in female line (Shafaq-06) (-2.65**). In state of paternal testers, the influences of GCA ranged from -0.38 to 0.57. Therefore, in paternal testers there is no significant positive GCA influences. In total the female line (Khyber-87) for harvest index, was regarded as the best and top general connecters (Table 4).

For harvest index, the specific combine ability (SCA) impacts in F_2 generations ranged from -1.76 to 1.68. Therefore, SCA impacts were positive and desired in 46.67 percent of F_2 generations (0.03 to 1.68). On the other hand, the remaining 53.33 percent, had negative SCA

consequences (-1.76 to -0.12). Similarly, the F_2 populations (TD-1) × (IBWSN-24(17–18)) (1.68*) displayed significant ($P \leq 0.05$) positive favorable SCA impacts and were acknowledged as the good specific cross combination for harvest index (Table 5).

Gene action and degree of dominance

Overall, due to the fact that variance of general combining ability (σ^2GCA), was lesser than the variance of specific combining ability (σ^2SCA), indicated of non-additive type gene action was controlled for all the examined traits. The values of additive genetic variance were lower than the dominance genetic variance for all the studied traits. The ratios of variances of GCA also supported these analyses to SCA (σ^2GCA/σ^2SCA) which were less than unity, which is confirmed by the ratio of additive genetics variance to dominant genetics variance (σ^2A/σ^2D) for all the tested traits. While the ratio of the degree of dominant (σ^2D/σ^2A)$^{1/2}$ is greater than unity for all the investigated traits in this experiment. As a result, it was discovered that non-additive gene action governed the inheritance for all the evaluated traits *i.e.,* days to heading, plant height, flag leaf area, tiller plant^{-1}, spike length, grain yield and harvest index. Based on the frequencies of alleles or genes identified in parental genotypes, the varying ratios of GCA to SCA variances (σ^2GCA/σ^2SCA). Therefore, due to their significant GCA effects, the various parental genotypes exhibited a desirable ratio of GCA and SCA variations (Table 6).

Percent contribution of populations to total variance

The proportional contribution of populations to total variance, showed that the maternal lines obtained highly contributed to the total variance compare to tester and lines × testers interactions for majority of the traits *i.e.,* days to heading (70.36), plant height (69.94), grain yield (76.03), and harvest index (74.02), followed by lines × testers interactions. And for flag leaf area (40.49), tillers plant^{-1} (49.17) and spike length (37.76) showed that highest shares to total variance was due to lines × testers interactions followed by lines. The results clearly showed that the paternal lines and lines × testers interactions/F_2 populations had highly contributed to the total variance that played essential role in dealing with the variation in the existing studies (Table 7).

Discussion

Days to heading are an important marker of earliness in crop output. Early heading is desirable and plant growers are keen to create new varieties of wheat genotypes with early maturity. As a result of delayed heading, the short time for grain filling, eventually led to a reduction in grain weight (Ullah *et al.* 2018). In wheat days to heading, is an

Table 6: Estimation of genetic components among lines, testers and line × tester populations for the studied traits in bread wheat during the year 2019–20 at CCRI, Pirsabak Nowshera

Genetic components	DH	PH	FLA	Tp^{-1}	SL	GYLD	HI
σ^2GCA	0.93	1.70	0.03	0.00	0.03	11612.57	0.29
σ^2SCA	2.22	3.61	0.49	0.13	0.47	26126.28	1.26
σ^2A	1.87	3.41	0.06	0.01	0.06	23225.13	0.59
σ^2D	2.22	3.61	0.49	0.13	0.47	26126.28	1.26
σ^2GCA/σ^2SCA	0.42	0.47	0.06	0.02	0.06	0.44	0.23
σ^2A/σ^2D	0.84	0.94	0.13	0.04	0.12	0.89	0.47
$(\sigma^2$D/σ^2A$)^{\frac{1}{2}}$	1.09	1.03	2.79	4.77	2.83	1.06	1.46

Table 7: Proportional contribution of (female) lines, (males) testers and their derived line × tester/F$_2$ population to the total variability for various traits were estimated in lines 5 × 3 testers mating design of bread wheat during the year 2019–20 at CCRI, Pirsabak Nowshera

Studied traits	Lines (%)	Testers (%)	Line × Tester interactions (%)	Total Variability
Days to heading	70.36	10.00	19.64	100
Plant height	69.94	3.03	27.04	100
Flag leaf area	31.58	27.93	40.49	100
Tiller plant^{-1}	29.85	20.98	49.17	100
Spike length	29.58	32.65	37.76	100
Grain yield	76.03	10.91	13.06	100
Harvest index	74.02	4.11	21.87	100

important trait that donate towards high yield and early heading is desirable for wheat breeders because grain filling duration increases which eventually outcomes in high yield Iqbal *et al.* (2017). Overall, there were significant ($P \leq 0.01$) discrepancies between parental genotypes and the F$_2$ population, indicating that genotypes had greater genetic diversity and greater opportunities for improvement through intense selection in subsequent segregating generations. In past combining ability analysis discovered significant variation among F$_2$ populations for various agronomical traits in wheat (Adhikari *et al.* 2020). The capacity of parental genotypes and their F$_2$ populations to combine their desirable alleles in F$_2$ generation after hybridization was investigated using line × tester analysis to assess the capacity of parental genotypes to combine their beneficial genes in F$_2$ generation after hybridization. Combining abilities have two categories *i.e.,* GCA and SCA and both types were calculated in the current study. Therefore, GCA effects are often caused by additive gene effects, whereas SCA impacts are caused by dominant or epistatic gene effects (Griffing 1956; Kempthorne 1957). The general combining ability of a parental genotype in a cross series supports the breeder in identifying potential genotypes for crossing programs based on GCA findings and mean performance (Singh and Chaudhary 1985). Specific combining ability refers to the capacity of one parent genotype to perform well with another parent in a specific cross combination, which might aid in the development of promising hybrids (Mandal and Madhuri 2016). In wheat breeding programs for the said trait, parental genotypes with desirable GCA effects were regarded as the best parental genotypes and good general combiners (Afridi *et al.* 2017, 2018). However, F$_2$ populations with acceptable SCA effects, on the other hand, were deemed the greatest particular combiners for days to heading and plant height in consideration. Moreover, our results are agreement with

Patel *et al.* (2020) who had ($P \leq 0.01$) significant negative and desirable GCA effects in lines and non-additive gene action was primarily involved for days to heading. These assertions imply that doubling the number of days before heading will increase plant height and the quantity of spikelets spike^{-1}, both of which lead to ultimate production (El-Gammaal and Morad 2018).

On the other hand, plant height is the key morpho-physiological character. Plant breeders are attracted to low height homogeneous plants because shorter plants are more sensitive to manures and are unaffected by lodging in wheat breeding programs during storms. Plant breeders select short stature cultivars for the region with high chances of lodging and tall varieties for regions with drought conditions (Khan *et al.* 2010). Therefore, in the present research except for testers and lines × testers interactions for plant height, extremely significant differences were seen across the genotypes studied. Similarly, Kumar *et al.* (2018) found highly significant variations in plant height across the investigated crosses and lines. In wheat, lines × testers design worked as a rapid measure of screening of genetic stocks based on GCA/SCA effects, rather than their variances and revealed that dominant gene activity was discovered for plant height (Nazeer *et al.* 2013). Previous studies revealed and our results are agreed to El-Gammaal and Morad (2018) had the highly significant negative and desirable GCA effects for the plant height and the negative are useful for breeder who are interested for short stature plant in bread wheat. Moreover, non-additive type of gene action is observed for the said trait and supported by (Shah *et al.* 2019). Furthermore, our results are agreement with Ali and Abdulkhaleq (2019) had the highest percent shares to total variance was due to the fact of lines followed by lines × testers interactions for plant height.

Similarly, due to the facts of its vital function in

photosynthesis, flag leaf area is regarded as the most important yield contributing characteristic (Al-Tahir 2014). Breeders want broad flag leaf area because broad leaves provide a wider surface area for sunlight to catch, resulting in more photosynthates being produced, which enhances grain output (Iqbal *et al.* 2017). Overall, our findings are similar to (Khan *et al.* 2020) who reported significant differences among lines × testers interactions for flag leaf area. Combining ability demonstrated that significant positive GCA and SCA impacts are desirable for wheat in flag leaf area, tillers plant⁻¹, spike length, grain yield and harvest index. Therefore, our finding is supported by (Saeed and Khalil 2017) who estimated significance positive GCA and significance positive SCA were reported for flag leaf area. Similarly, Ishaq *et al.* (2018) was validated to our finding that non-additive gene action is involved for flag leaf area in wheat and also found that lines × testers interactions contributed the most percent shares to overall variation, which is vital point for the development of wheat varieties and hybrid.

To begin with tillers plant⁻¹ is a significant yield boosting characteristic that contributes to increased grain output in wheat (Tilley *et al.* 2019). Tillering determines the extent of the plant canopy, photosynthetic area, and, most critically, the number of spikes carrying grains at maturity (fertile shoots), all of which are important factors in production (Xie *et al.* 2016). Tillers plant⁻¹ is frequently linked to the number of productive spikes as well as the resulting grain production. The genetic makeup of bread wheat frequently differs in terms of tillering potential. A higher number of tillers plant⁻¹ confirms optimal plant populations and as a result higher grain yield. Our findings are consistent with those of (Khan *et al.* 2020) who stated significant ($P \leq 0.01$) differences in tillers plant⁻¹ across bread wheat genotypes. Therefore, the past studied for tillers plant⁻¹ (Rashmi *et al.* 2020) had significantly extensive favorable GCA and SCA impacts in maternal lines, paternal testers, and combinations. Likewise, our findings align with those of Saira *et al.* (2019) had that σ^2GCA is less than σ^2SCA, indicating that non-additive gene action was implicated for tillers plant⁻¹ and had the highest shares to total variance was due to lines × testers interactions, this was good impact in F₂ populations.

In addition, the major yield component is spike length, which adds to the final yield of more grains. Spikes with longer spikes are more willing to enable more spikelets to form Iqbal *et al.* (2017). Spike length and grain yield unit⁻¹ area have a direct relationship. Using lines × testers examinations (Hama-Amin and Towfiq 2019) displayed ($P \leq 0.01$) significant variation for spike length amongst wheat genotypes. Similarly, our finding is supported by Sharma *et al.* (2019) observed positively significant ($P \leq 0.01$) SCA effects on spike length in F₂ populations. Consequently, our findings are consistent with those of (Soni *et al.* 2018), who discovered non-additive kind of gene action and (Hakeem *et al.* 2020) had the highest

percent shares to total variance was due to the fact of lines × testers interactions (70%) for spike length.

Likewise, the grain yield is a multipart character. Plant breeders are generally interested in developing high yielding cultivars to meet the country's food requirement by directly or indirectly enhancing this characteristic. The final grain yield is the significant wheat production trait and the contribution of many components makes the nature of grain yield more complex. In the present study, our results are strongly in agreements with Farooq *et al.* (2019) who concluded highly significant discrepancies in grain yield among wheat cultivars, maternal lines, paternal testers, and lines × testers interactions. In wheat the earlier studies of Farooq *et al.* (2018) and Din *et al.* (2021) shown ($P \leq 0.01$) significant positive GCA and SCA influences these investigations are agreements with our results for grain yield. Therefore, our findings are in accordance with Sarfraz *et al.* (2020) revealed that non-additive gene acts were primarily governed for grain yield.

To begin with harvest index is an important wheat crop feature directly related to biological yield and grain production. For harvest index (Khan *et al.* 2020) revealed that lines × testers analysis observed significant ($P \leq 0.01$) variations across wheat treatments and lines × testers interactions and it means that the selections are desirable. The earlier premeditated of Dhoot *et al.* (2020) discovered highly positively significant GCA and SCA influences in wheat F₂ populations; this research agrees with our harvest index findings. Therefore, our finding is in line with Baranda (2020) revealed that SCA variance was more than GCA variance in macaroni wheat, the variance of GCA to SCA variance was smaller than unity, indicating that non-additive gene activity was primarily involved in the genetic development of the characteristic. Furthermore, our discoveries are contract with Din *et al.* (2021) who observed that the maximum percent share to total genetic variance was due to lines, which indicates that a strong maternal influence for harvest index in studied wheat crop.

Conclusion

Parental lines *i.e.,* TD-1, SKD-1, Benazir-13, Khyber-87, testers IBWSN-192(17–18) and IBWSN-205(17–18) and their F₂ populations Shafaq-06 × IBWSN-192(17–18), TD-1 × IBWSN-192(17–18), Benazir-13 × IBWSN-192(17–18), SKD-1 × IBWSN-205(17–18) and TD-1 × IBWSN-24(17–18) was observed as the best general and specific combiners, respectively and showed outstanding performance for yield productive traits and found better mean performance. Therefore, for all of the parameters the ratio of variances of GCA to SCA were less than unity and additive variance was smaller than dominance variance it means that non-additive type of gene actions. In contrast, degree of dominance was greater than unity which confirmed that all the characters were controlled by non-additive type of gene actions. Therefore, non-additive gene action implies that populations

selection in yield productive traits should be postponed to the later segregating generations for further improvement in these tested selective traits of bread wheat. Therefore, these F_2 populations could be used in future wheat breeding programs to develop outstanding production traits and high yielding wheat genotypes.

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Author Contributions

Contributed materials and planned the experiments HU and KA. In addition, HR, SA, MA, GS, JK and HK contributed in the data collections of this research, however the analysis/ tools: Wrote the paper MB.

Conflicts of Interest

All authors declare no conflicts of interest.

Data Availability

Data presented in this study will be available on a fair request to the corresponding author.

Ethics Approval

Not applicable in this paper.

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