



GENETIC ANALYSIS FOR PRODUCTION TRAITS IN WHEAT USING LINE X TESTER COMBINING ABILITY ANALYSIS

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SUMMARY

The knowledge of genetic variability, combining capability, and gene activity are vital in enhancing wheat productivity. Six diverse wheat genotypes, Anmol91, Fatehjung16, Khattakwal, Auqab2000, PR128, Abaseen 2021, and KT06, crossed with three strip rust-resistant wheat lines, i.e., YR5, YR10, and YR15, employed line × tester hybridization. The analysis determined that the general combining ability (GCA) and specific combining ability (SCA) variances were significantly different for examined parameters ($p < 0.05$). Parental lines Auqab2000 and Fatehjung16 emerged as better general combiners for earliness and yield-related attributes; however, Auqab2000 × YR5, KT06 × YR5, Khattakwal × YR10, PR128 × YR5, Khattakwal × Auqab, and KT06 × YR10, proved the top particular cross combinations for contributing features of grain yield per plant. Results also showed that lines import sufficient variety to manifest the traits under investigation. For almost all tested qualities, the value of $\sigma^2_{gca} / \sigma^2_{sca}$ demonstrated a non-additive gene effect, except for days to maturity, which the additive gene action influenced. The selection of superior plants should take time until later segregation generation when non-additive gene activities dominate. The genotypes chosen for the current study are crucial genetic resources for wheat's continued gene development.

Keywords: Combining ability, tester analysis, parental lines, heritability, YR-5, YR-10

Key findings: The wheat genotypes Anmol91, Fatehjung16, Khattakwal, Auqab2000, PR128, Abaseen2021, and KT06, crossed with three strip rust-resistant wheat lines, i.e., YR5, YR10, and YR15, showed their GCA and SCA variances significantly ($p < 0.05$) for examined traits. Parental lines Auqab2000 and Fatehjung16 resulted as better general combiners for earliness and yield-related attributes. Likewise, Auqab2000 × YR5, KT06 × YR5, Khattakwal × YR10, PR128 × YR5, Khattakwal × Auqab, and KT06 × YR10 demonstrated the best particular cross combinations for contributing features of grain yield per plant.

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INTRODUCTION

The bread wheat (*T. aestivum* L.) is a valuable cereal, consumed by 36% of people worldwide as a staple food. Wheat is also an essential source of carbohydrates, protein, and significant minerals, including zinc and copper (Kumar *et al.*, 2014). Cultivating around 216 million ha of land grow the 766 million t of wheat produced worldwide. The population, predicted to increase to almost 9 billion by 2050, poses a severe danger to global wheat production. However, climate change severely hogs wheat productivity (Younas *et al.*, 2020). Ensuring the demands of an expanding population, breeders have generated hybrid lines with high productivity.

The ability of parental lines to combine in a program of hybridization, complicating the genetic variation in the production of calculable and qualitative features of economic value, needs attention instead of increasing wheat yield (Pal *et al.*, 2015; Khan *et al.*, 2022). Therefore, the selection of genetically superior lines critically depends on phenotypic variation and high heritability in the hybrid population. Making decisions about the next stage of a breeding program requires an extensive understanding of the GCA and SCA consequences. Breeders might develop productive genotypes by crossing superior lines in favor of yield and choosing transgressive segregates from hybrid lines (Putri *et al.*, 2020; Araghi *et al.*, 2022).

The genetic variability ratio is a key prerequisite in selecting hybrid lines with high productivity and yield. One of the crucial breeding techniques is line \times tester mating, in which a tester refers to the male parent and a line to the female (Kempthorne, 1957). This frequently used method reveals how line by a tester, GCA, and SCA affect the F_1 generation (first filial). Breeders can choose a cultivar/variety for the hybridization process based on its GCA outcome, with the average performance coming out by mean parental genotype output in the pattern of cross-combination renewed as GCA (Griffing, 1956). Since the GCA effects for the characteristics play a significant part in genotype selection for boosting yield attributing traits, breeders' primary objective is to develop a different and proficient genotype by intersecting a genotype with a high GCA of the required trait (Sing and Chaudhary, 1985).

The effectiveness of SCA of certain cultivars in a specific mating arrangement with another parent may promote possible hybrids (Khan and Raziuddin, 2019). High GCA

indicates an additive mode of gene activity, whereas high SCA indicates a non-additive type of gene effect (Sprague and Tatum, 1942). The dominant kind of gene action is said to control and regulate the grain yield of plants, as well as, many characteristics. According to numerous geneticists, an epistatic genetic factor effect is particular in some of the genomic differences supporting the concluding grain production, aside from the situation for contributing traits (Masood and Kronsted, 2000).

Given the aforesaid literature, the project's goal was to explore the best parental, testers, and hybrid lines by evaluating their variability and heritability, as well as general and particular combining potential genetic influence on grain yield and yield-contributing characters.

MATERIALS AND METHODS

In year one, the crossing of six diverse wheat genotypes, Khattakwal, PR128, Fatehjung16, Anmol-91, KT06, and Auqab2000, with three (YR5, YR10, and YR15) yellow rust wheat-resistant genotypes used the proposed line \times tester mating (Kempthorne, 1957). In year two, 18 F_1 -hybrid lines plus parental lines underwent assessment in the cropping season in a randomized complete block design (RCBD) in three repetitions for foremost traits. The study followed most of the national practice standards for each treatment at the appropriate time to minimize the environmental effect.

Data collection

Five randomly selected plants proceeded with data analysis from each genotype per replication at the proper time for days to maturity, grain yield per plant, grain per spike, tillers per plant, biological yield per plant (g), plant height (cm), and 1000 grain weight (g).

Statistical analysis

The statistical analysis ensued through ANOVA and Statistical Version 8.1. Observing the recorded facts was according to the method by Steel and Torrie (1980) to verify the null hypothesis of means equality. The relevant data of all parameters advanced to the line \times tester combining ability analysis to estimate GCA and SCA effects by the proposed method (Kempthorne, 1957; Singh and Chaudhary, 1985). The significance of combining ability

effects at the 0.05 and 0.01 levels of probability investigation used a t-test.

Genetic components

In 1985, Singh and Chaudhary examined the genetic components, and they approximated the variance due to GCA and SCA assuming there was no epistasis. According to Singh and Narayanan (2004), using F_1 determined genetic variances of additive (σ^2_A) and dominance (σ^2_D) traits (inbreeding coefficient).

Dominance degree and gene function

The in-between ratio of σ^2_A/σ^2_D and $\sigma^2_{gca}/\sigma^2_{sca}$ is less than unity, which will show non-additive gene action. But if the ratio is greater than one, that will represent an additive gene behavior. When the value of significance was equal to one, then the effectiveness of both additive and non-additive gene impacts will be evenly distributed in the expression of a particular trait. Similar to how additive gene actions are regarded dominant when the degree of dominance ($(\sigma^2_D/\sigma^2_A)^{1/2}$) ratio is less than one, non-additive gene actions are foremost when the ratio is equal to one, and both types of gene impacts are considered equal when the ratio is more than one. The analysis proceeded based on the approach used by Singh and Chaudhary, 1985.

Genetic advance as % of mean and heritability

The operating equation to determine genetic advancements as a percentage of means and broad-sense heritability was according to the formula ($H^2 = V_g/V_p$, where H = Heritability estimate, V_g = Variation in genotype, and V_p = Variation in phenotype). Genetic progress

rating is highest (>20%), medium (10% – 20%), and low (10%) as a percentage of means. Similar to this, dividing heritability into three categories include: moderate (30%–60%), high (more than 60%), and low (less than 30%).

Role of parental lines, testers, and line × tester populations

Using formulas suggested by Singh and Chaudhry (1985), the total variance capacity of parental genotypes and line × tester got determined (Table 1).

RESULTS

The statistical investigation of the data revealed considerable variation ($p \leq 0.01$) for all the mentioned parameters among F_1 -population and line × tester (Table 1). These results indicate sufficient variability in the breeding material, allowing further analysis for GCA, SCA, and gene expression.

Combining ability analysis

The mean squares of combining ability showed that testers were with prime importance ($p \leq 0.01$) for grain yield plant⁻¹, 1000 grain weight, biological yield (biomass) plant⁻¹, and wheat plant height; however, lines had desirable ($p \leq 0.01$) variation for the earlier stated traits. Line × tester and F_1 populations were promising ($p \leq 0.01$) for plant height, grains per spike, and 1000 grain weight (Table 1). Positive values are ideal for most characters based on combining ability impacts, while negative general and particular combining ability effects are ideal for plant height and days to maturity.

Table 1. Analysis of variance showing means squares for agronomic traits among wheat parents and their F_1 progenies.

SOV	DF	DM	PH	TP	GPS	TGW	GYP	BYP
Replication	2	57.79**	7.10	25.92	18.85	3.51	129.54	1019.36**
Genotypes	26	24.17**	281.80**	57.46**	380.09**	104.00**	284.29**	944.18**
Parents	8	24.56**	626.97**	123.96**	516.72**	66.11**	144.27**	625.50**
Parents × Crosses	1	162.00**	20.20	43.40	61.40	445.71**	2484.30**	5447.77**
Crosses	17	15.88**	134.76**	26.99**	334.53**	101.73**	220.77**	829.23**
Lines	5	42.50**	353.16**	53.25**	919.48**	98.59**	486.79**	1260.48**
Testers	2	3.88	65.65**	2.34	170.28**	345.65**	81.47	334.15
Lines × Testers	10	4.98	39.38**	18.78	74.91	54.52**	115.62**	712.62**
Error	52	5.75	10.58	10.58	27.93	14.40	27.27	144.46
C. V. %		1.47	3.24	17.16	6.66	9.70	14.29	13.67

*, ** Significant at p 0.05 and p 0.01, respectively, SOV=Sources of Variation, DF=Degree of Freedom, DM=Days to Maturity, PH=Plant Height, TP=Tillers per Plant, GPS=Grains per Spike, TGW=1000- Grain Weight, GYP=Grain Yield per Plant, BYP=Biological Yield per Plant.

Table 2. General combining ability effects between lines and testers for different traits.

Lines	DM	PH	TP	GPS	TGW	GYP	BYP
Auqab2000	3.00**	-4.10**	2.94*	15.60**	-1.78	13.59**	16.05**
Fatehjung16	1.00	-5.48**	0.66	-2.12	3.93**	0.74	7.61
Anmol-91	-1.33	-2.88*	1.56	6.24**	-5.19**	-4.71*	3.58
Khattakwal	0.83	11.46**	-2.17	-12.44**	-1.01	-7.37**	-18.02**
KT-06	-0.17	-1.64	0.62	-8.27**	2.02	0.65	-3.04
PR-128	-3.33**	2.64*	-3.61**	0.99	2.02	-2.90	-6.18
S.E.	0.80	1.08	1.08	1.76	1.27	1.74	4.01
CD at 5%	1.62	2.20	2.20	3.58	2.57	3.54	8.14
CD at 1%	2.18	2.96	2.96	4.80	3.45	4.75	10.93
Testers							
YR-5	0.42	-1.25	0.30	-3.53**	5.06**	1.71	4.35
YR-10	-0.50	-0.95	-0.40	1.40	-2.58**	-2.38	-0.09
YR-15	0.08	2.20**	0.10	2.13	-2.48**	0.67	-4.26
S.E.	0.57	0.77	0.77	1.25	0.89	1.23	2.83
CD at 5%	1.15	1.56	1.56	2.53	1.82	2.50	5.75
CD at 1%	1.54	2.09	2.09	3.40	2.44	3.36	7.73

*, ** = Significance at 5% and 1% level of probability, SE = Standard Error, CD = Critical Difference, DF=Degree of Freedom, DM=Days to Maturity, PH=Plant Height, TP=Tillers per Plant, GPS=Grains per Spike, TGW=1000-Grain Weight, GYP=Grain Yield per Plant, BYP=Biological Yield per Plant.

GCA and SCA effects

The GCA effects of parental wheat genotypes appear in Table 2. The GCA effects among parental lines ranged from -3.33 to 3.00 for maturity, -5.48 to 11.46 for plant height, -3.61 to 2.94 for tillers plant⁻¹, -12.44 to 15.60 for grains per spike, -5.19 to 3.93 for the 1000 grain weight, -7.37 to 13.59 for grain yield plant⁻¹, and -18.02 to 16.05 for biological yield. Maximum desired negative general combining ability occurred for advance line PR128 (-3.33) for maturity and cultivar Fatehjung16 (-5.48) for plant height. However, desirable positive GCA effect resulted with Auqab2000 (2.94) for tiller plant⁻¹, grains per spike, grain yield plant⁻¹, and biological yield, and Fatehjung-16 for the 1000 grain weight. For the tester, GCA effects ranged from -0.50 to 0.42 for maturity, -1.25 to 2.20 for plant height, -0.40 to 0.30 for tillers plant⁻¹, -3.53 to 2.13 for grains per spike, -2.58 to 5.06 for 1000 grain weight, -2.38 to 1.71 for grain yield plant⁻¹, and -4.26 to 4.35 for biological yield. Noting a negative and significant GCA effect was for line YR10 for maturity and YR5 for plant height. A significant positive GCA effect surfaced for tester (YR5) for tillers plant⁻¹, 1000 grain weight, grain yield plant⁻¹, and biological yield, and YR15 for grains per spike.

The specific combining ability effects ranged from -1.42 to 1.08 for maturity, -3.82 to 5.69 for plant height, -4.56 to 3.10 for tillers plant⁻¹, -6.66 to 7.92 for grains per spike, -

5.71 to 5.48 for 1000 grain weight, -10.58 to 8.48 for grain yield plant⁻¹, and -27.28 to 15.71 for biological yield (Table 3). Notably, a desired negative SCA effect resulted for the cross Auqaab2000 × YR5 for maturity and KT06 × YR10 for plant height, while the promising positive SCA effects exhibited for Khattakwal × YR10 for tillers plant⁻¹, PR128 × YR15 for grains per spike, KT06 × YR5 for 1000 grain weight, Auqab2000 × YR5 for grain yield plant⁻¹, and Khattakwal × Aquaab for biomass yield.

Gene action

The genetic variation shows that σ_{2gca} was modest relative, except days to maturity variance due to a specialized combining ability (σ_{2gca}) in favor of all tested traits, indicating equal importance of additive and dominant gene effects (Table 4). However, dominance gene action plays a more critical role than additive type in producing the traits under study. The values of $\sigma_{2gca} / \sigma_{2sca}$, which is better for days to maturity, although the degree of dominance was less significant for maturity, smaller than unity for the remaining characters, and larger than one for all of the qualities under study, further supported the current findings. Thus, establishing that researched features other than maturity, where the additive gene effect was more significant, were characterized by dominance gene expression.

Table 3. Specific combining ability effects between line × tester interactions for different traits in wheat.

F ₁ Population	DM	PH	TPP	GPS	TSW	GYP	BYP
Auqab2000 × YR-5	-1.42	4.65*	2.59	3.35	-5.71*	8.48**	14.48*
Auqab2000 × YR-10	0.50	-2.53	-1.59	-0.29	2.94	-3.16	-1.16
Auqab2000 × YR-15	0.92	-2.13	-1.00	-3.06	2.77	-5.32	-13.32
Fatehjung16 × YR-5	0.08	2.65	0.82	2.65	-4.73*	4.20	5.67
Fatehjung16 × YR-10	0.50	0.52	-1.23	1.44	3.42	-1.37	-10.88
Fatehjung16 × YR-15	-0.58	-3.17	40	-4.09	1.31	-2.83	5.21
Anmol-91 × YR-5	-0.58	-0.61	2.51	4.41	-0.54	0.49	12.70
Anmol-91 × YR-10	-0.17	2.09	-0.13	2.24	-2.10	1.22	-3.86
Anmol-91 × YR-15	0.75	-1.48	-2.38	-6.66*	2.64	-1.71	-8.85
Khattakwal × YR-5	-0.75	-1.20	-4.56*	-3.66	4.72*	-10.58**	-27.28**
Khattakwal × YR10	-0.33	1.49	3.10	1.29	-1.96	8.30**	11.57
Khattakwal × YR-15	1.08	-0.29	1.46	2.37	-2.76	2.28	15.71*
KT-06 × YR-5	0.25	-1.87	0.31	-2.16	5.48*	0.54	6.64
KT-06 × YR-10	0.67	-3.82*	-0.20	-1.35	-3.43	-4.20	-8.41
KT-06 × YR-15	-0.92	5.69**	-0.11	3.51	-2.05	3.66	1.77
PR-128 × YR-5	2.42	-3.63	-1.66	-4.59	0.78	-3.13	-12.21
PR-128 × YR-10	-1.17	2.26	0.04	-3.34	1.12	-0.79	12.74
PR-128 × YR-15	-1.25	1.37	1.62	7.92*	-1.90	3.92	-0.53
S.E.	1.38	1.88	1.88	3.05	2.19	3.02	6.94
CD at 5%	2.81	3.81	3.81	6.20	4.45	6.12	14.09
CD at 1%	3.77	5.12	5.12	8.32	5.98	8.22	18.92

*, ** = Significant at 5% and 1% level of probability, SE=Standard Error, CD=Critical Difference DF=Degree of Freedom, DM=Days to Maturity, PH=Plant Height, TP=Tillers per Plant, GPS=Grains per Spike, TGW=1000-Grain Weight, GYP=Grain Yield per Plant, BYP=Biological Yield per Plant.

Table 4. Genetic components analysis for important traits in wheat.

Genetic component	DM	PH	TP	GPS	TGW	GYP	BYP
Σ^2_{gca}	0.327	2.860	0.246	7.784	1.416	3.153	3.496
Σ^2_{sca}	-0.258	9.598	2.735	15.659	13.371	29.450	189.388
Σ^2_A	0.654	5.719	0.492	15.568	2.831	6.305	6.992
Σ^2_D	-0.258	9.598	2.735	15.659	13.371	29.450	189.388
$\Sigma^2_{gca}/\sigma^2_{sca}$	-1.268	0.298	0.090	0.497	0.106	0.107	0.018
Σ^2_A/σ^2_D	-2.536	0.596	0.180	0.994	0.212	0.214	0.037
$[\sigma^2_D/\sigma^2_A]^{1/2}$	-0.628	0.456	0.855	0.357	0.387	0.261	0.103
H2(bs)	0.517	0.895	0.596	0.808	0.675	0.759	0.649
GA%	1.590	13.095	23.519	17.924	16.751	32.223	21.840

σ^2_{gca} = GCA variance, σ^2_{sca} = SCA variance, σ^2_A = Additive variance, σ^2_D = Dominant variance, $\sigma^2_{gca}/\sigma^2_{sca}$ = Average degree of dominance, h2(bs) = Broad-sense heritability, GA% = Genetic advance as percent of mean, DF=Degree of Freedom, DM=Days to Maturity, PH=Plant Height, TP=Tillers per Plant, GPS=Grains per Spike, TGW=1000-Grain Weight, GYP=Grain Yield per Plant, BYP=Biological Yield per Plant.

Genetic advance as % of the mean

The estimated genetic advance revealed that grains per spike (17.92%), tillers per plant (23.57%), and biological yield (21.84%) all showed the highest genetic progress as a percentage of means (Table 4). The percent means for 1000 grain weight (16.75%) and plant height (13.09%) showed a moderate range of genetic improvement. Days to maturity (1.590%) showed a low genetic advance range as a percentage of averages.

Broad-sense heritability

Tillers plant⁻¹ (0.596) and days to maturity (0.517) showed a moderate range, whereas for plant height (0.895), 1000 grain weight (0.675), biological (biomass) yield plant⁻¹ (0.649), grain yield plant⁻¹ (0.759), and grains per spike (0.808), the estimate of broad-sense heritability showed a higher range (Table 4).

Table 5. The proportional contribution of lines, testers, and line × tester interaction.

Parameters	Line (%)	Testers (%)	Line × Testers (%)
Days to maturity	78.70	2.87	18.43
Plant height	77.08	5.73	17.19
Tillers plant ⁻¹	58.03	1.02	40.95
Grains spike ⁻¹	80.84	5.99	13.17
1000 grain yield	28.50	39.97	31.52
Grain yield plant ⁻¹	64.85	4.34	30.81
Biological yield plant ⁻¹	44.71	4.74	50.55

The proportional contribution of lines, testers, and line × tester to the total variance

According to the line × tester combining ability investigation, biological yield plant⁻¹ benefits more from the line × tester populations by comparing with the parental lines and testers (50.55%) (Table 4). For nine features, including plant height (77.08%), grains per spike (80.84%), grain yield per plant (64.85%), tillers plant⁻¹ (58.03%), and maturity (78.70%), the portion of the lines presents admirable and dominant. Comparing testers' contribution to lines and the line × tester interaction, the 1000 grain yield contribution from testers was excellent (39.97%) (Table 5). These findings demonstrated that lines contribute adequate variety in expressing the features under evaluation.

DISCUSSION

Inadequate selection and development of genotypes suited for production caused low wheat crop yield genetic gains and yield potential. The objective to reverse this is to create wheat genotypes with high yields that are well-adapted and have physiological and agronomic traits to increase harvest. When choosing appropriate parental genotypes for breeding to develop novel crosses for advancement and further selection, the present study indicated significant effects ($p \leq 0.01$) for the studied attributes among parental genotypes and their F₁ generations. Previous combining ability studies on wheat showed significant variability among some parental genotypes with their F₁ and F₂ offspring for several agronomic parameters.

Significant changes in earliness and yield attributes were revealed in wheat by analyzing parental cultivars, F₁ and F₂ generations, and line by tester mating design. Meanwhile, a significant SCA effect showed non-additive gene action influencing trait

expression, a significant GCA effect suggested additive gene action. In terms of combining ability, the study of several kinds of wheat (hexaploid) lines revealed highly required ($p \leq 0.01$) variations for the examined features, while testers and line by tester interaction revealed substantial ($p \leq 0.01$) variations in the bulk of yield-attributing elements. In wheat, similar effects resulted for various parental genotypes and the F₁ population (Bibi *et al.*, 2013); however, research on various diallel hybrids showed no substantial differences between populations for wheat yield-related components (Ljubicic *et al.*, 2014).

Early maturity is the desired key characteristic in wheat breeding projects that enables plants to avoid terminal stress in drought conditions and produce a reasonable yield (Mondal *et al.*, 2016). Current investigation results are consistent with the assertion that none of the F₁ groups exhibits undesirable and undesirable SCA consequences (Barot *et al.*, 2014). The study also determined that PR128 was a superior general combiner and needs usage in wheat breeding projects for early maturity. However, a prior study revealed that lines, testers, and cross populations took the fewest days to mature in wheat and had favorable negative GCA and SCA effects (Esmail, 2007). Wheat cultivars with short statures are ideal because dwarf genotypes are less likely to lodge and have higher harvest indices (Din *et al.*, 2020). The F₁ population's KT06 × YR10 and Auqab × YR5 genotypes, which showed a desired adverse SCA effect, proved the best specific cross combinations for plant height. Fatehjung16 among the parental lines had preferable negative GCA effects on plant height.

Moreover, lines, testers, and their line × tester generation showed preferred negative GCA and SCA effects in earlier research (Hei *et al.*, 2016). Auqab2000 is regarded as the finest general combiner for tillering ability because it had a suitable and favorable GCA influence on the number of tillers per plant among its parents, although none of the first filial

generation. Prior observations have also reported similar outcomes in wheat (Akbar *et al.*, 2009). Previous research also concluded that the optimal parents for wheat tillers were lines and testers, confirming positive and strong GCA effects (Abro *et al.*, 2021). According to the study, Abaseen 2021 × YR15 emerged as the best particular combiner and parental line for grains per spike. The best general combiners, confirmed as Auqab2000 and Anmol91, require use for increased yield. These results are consistent with the high parental line (Saeed *et al.*, 2005). The values of lines displayed to be greater than testers concerning GCA impact, and wheat showed the same results in favor of grains per spike (Saeed *et al.*, 2001).

The unfavorable correlation between thousand-kernel weight and high grain number has prevented the combination of these two features. The line Fatehjung16 and tester YR5 are viewed as an excellent general combiner for 1000 grain weight and requires application to increase yield in future wheat breeding programs, yet KT06 × YR5 and Khattakwal × YR5 showed desirable and positive SCA effects, hence, thought as the best cross combination. Earlier discoveries also stated similarities for the thousand-grain weight (Farooq *et al.*, 2006). Several factors control grain yield, which is regarded as a crucial economic characteristic. For boosting wheat production in the current study's F_1 population, Auqab-2000 × YR5 and Khattakwal × YR10 proved to be the best particular combiners, with the line Auqab-2000 deemed as the best general combiner.

Previous research has shown that numerous characters greatly influence grain yield. Enhancing these yield-contributing qualities will increase wheat's overall grain yield (Ingle *et al.*, 2018). The resulting F_1 individuals displayed more grain than their progeny, which is noteworthy given the variations between the parental genotypes and their F_1 hybrids (Jatav *et al.*, 2014). Additionally, wheat cultivars with the most growth and foliage will produce more cattle fodder. The F_1 populations Khattakwal × YR15, Auqab × YR5, and Auqab × YR 2000 provided to be the best genotypes with significantly favorable SCA and GCA effects and entail usage in the future to generate wheat populations with greater biological yield. Overall, earlier results have demonstrated that F_1 and F_2 generations with considerable SCA effects outperform parental genotypes based on biological yield in wheat. The biological yield of wheat genotypes varied significantly; a

larger biological yield is typically viewed favorably from the perspective of feed (Yadav and Sirohi, 2011).

The dominant gene governed all the investigated parameters except days to maturity, impacted by additive gene action, differences due to GCA and SCA, and the degree of dominance. It means the involvement of both gene actions in the manifestation of maturity. Similarly, both dominant and additive gene actions influenced the transmission of different traits (Abro *et al.*, 2021). However, other studies revealed that the additive gene effect governed traits linked to earliness and yield (Mandal and Madhuri, 2016). Selection should take time to a later generation because genetic changes caused by GCA and SCA showed that the dominance gene effect regulates the inheritance of numerous factors (Ingle *et al.*, 2018).

In terms of genotypes' contribution to overall variation, parental lines and testers have the highest shares. Similar findings indicated lines managed the majority of the variance in the analyzed traits (Nour *et al.*, 2011). For the six qualities of earliness, plant height, tillers plant-1, grains per spike, and grain yield plant-1, the proportion of parental lines was good instead of the tester and line × tester interaction. The testers' contribution to the 1000 grain yield was outstanding, whereas the line tester had the largest part of the biological yield plant-1. However, the influence of lines and testers together was far greater than their contributions to overall variances (Istipliler *et al.*, 2015). Earlier studies discovered that line × tester handled the variances for most yield-related variables and that line × tester shares in total variance were higher than parental genotypes (Akbar *et al.*, 2009). The level to which particular features are passed down from one generation to the next is known as heritability.

Genetic progress and heritability are crucial selection criteria. According to recent research, selection will likely succeed because of strong heritability and genetic progress supporting the traits grain and biological yield, grains per spike, 1000-grain weight, and plant height. Early life demonstrated a low genetic advance, high heritability was taken advantage of due to the supportive effect of external circumstances rather than genotypes, and choosing alleged qualities may not always be advantageous. These findings are consistent with parental genotypes (Rahul, 2017). In earlier studies, high heritability and minimal genetic progress appeared for earliness (Iqbal *et al.*, 2017).

CONCLUSIONS

Generally, the wheat genotype Auqab2000, Fatehjung16, and YR5 were inveterate good overall combiners and respond progressively to maturity and other yield-related traits. However, the first filial generation of Auqab2000 × YR5, KT06 × YR5, Khattakwal × YR10, PR128 × YR5, Khattakwal × YR15, and KT06 × YR10, resulted as best specific crosses for grain yield per plant along with some other yield contributing traits. Therefore, the recommendation for these lines' use needs attention in future late-sowing breeding programs.

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