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GENERAL AND SPECIFIC COMBINING ABILITY ANALYSIS IN LINES, TESTERS, AND HYBRIDS (F_1/F_2) OF *TRITICUM AESTIVUM* L.

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Abstract

Most of the wheat breeding programs aim to develop new disease-resistant and widely adopted high-yielding genotypes to enhance food security. The current research work was conducted using the line-by-tester method to investigate genetic divergence, combining ability and inheritance pattern for important traits. Eight wheat lines (PR-137, PR-138, PR-139, Inqilab-91, Auqab-2000, SKD-1, Tajaban, and Benazir-13) and five testers (T-11, Borluog-100, Pirsabaq-15, Zarghoon-21 and Taskeen-22), and their resultant 40 F_1 and F_2 generations were grown in a randomized complete block design (RCBD) with three replications. Highly significant ($p \leq 0.01$) differences were observed among genotypes for all the traits. For the earliness trait, the best general combiner in parental genotypes was PR-137 and T-11. Moreover, the best specific F_1 combinations were PR-13×Zarghoon-21and SKD-1×Borlaug-100, whereas Inqilab-91×T-11 was the best specific combiner in the F_2 generation. Wheat genotype PR-137 was the best general combiner for spike length, whereas PR-139×T-11 and Tajaban×Pirsabak-15 cross combinations were good specific combiners in F_1 and F_2 populations, respectively. For 1000-grain weight, Tajaban was the best general combiner, while cross Tajaban×Taskeen-22 had the best SCA in the F_1 cross. However, cross combinations PR-137×Borlaug-100 had the best SCA in the F_2 cross. For grain yield, parental genotype, i.e. PR-137, had the best GCA, while F_1 cross combinations, i.e. Inqilab-91×Borlaug-100, along with F_2 cross Tajaban×Borlaug-100, were reported with promising SCA. However, for spikelets spike^{-1} wheat cultivars, i.e., PR-139 was the best general combiner, while Tajaban×Borlaug-100 and SKD-1×Pirsabak-15 were promising specific combiners in F_1 and F_2 generation, respectively. Likewise, for biological yield, PR-137 was a promising general combiner. Moreover, cross combinations Benazir-13×Zarghoon-21 among F_1 hybrids and Auqab-2000×T-11 in F_2 populations were the best specific combiners for biomass yield. The ratios of GCA to SCA variances and degree of dominance showed that the inheritance of all traits except days to heading was controlled by non-additive gene action. Therefore, selection for these traits could be done in later generations for better results.

Key words: Additive and dominant gene; Degree of dominance; F_1 and F_2 populations; Genetic variability; GCA and SCA variances

Introduction

Triticum aestivum L. is a self-pollinated annual cereal crop. It is a hexaploid having a chromosome number of 42. It has perfect hermaphrodite flowers and a sexually autonomous crop. Its domestication started from the fertile crescent of the Middle East and later became an important food crop across the globe (Sabit *et al.*, 2017). Wheat is one of the most important staple foods, and the crop is widely grown to meet the food requirements of the growing population of Pakistan. To meet the food demand of the country for the fast-growing population, wheat has largely been imported. The fast-growing population of Pakistan (257.103 million-Worldometer-2025) has resulted in the conversion of valuable agricultural land to urbanisation and consequently low availability of land for cultivation. To keep the equilibrium between food and population (rising at 2.07% per year), it is essential to enhance wheat production further (Afridi *et al.*, 2019). Therefore, all wheat breeders are trying to produce sound genotypic and high-yield varieties, both for irrigation and rain-fed conditions. Wheat is nutritionally an important cereal, essential for food security, poverty mitigation, and livelihood (Govindan *et al.*, 2022; Khokhar *et al.*, 2019). *T aestivum* L. represents a vital source of carbohydrate, protein and rich in fats, riboflavin, thiamin, niacin, and vitamin E as well as essential substances like copper, zinc and magnesium (Sabit *et al.*, 2017; Hama-Amin & Towfiq, 2019), while the total consumption of the crop is approximately 36% globally and greatly in Asian countries (Govindan *et al.*, 2022). Similarly, gluten protein is predominantly found in wheat grain (Shewry *et al.*, 1995; Gautam *et al.*, 2013). Wheat needs good, windy, irrigated, and fertile soil for higher production. There are around 743 million tonnes of wheat cultivated in Russia, Canada, Germany, India, France, and Pakistan (Anon., 2018). Production of wheat crops in 2024 is officially estimated at a record level of 31.4 million tonnes in Pakistan, reflecting large sowings and excellent yields, supported by an adequate supply of irrigation water and widespread use of high-yielding seed varieties (Anon., 2024). Assessment of general combining ability (GCA) effects for yield components has great potential in

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the selection of desirable parents (Bhateria *et al.*, 2006; Arif *et al*., 2023). Therefore, the work of Griffing (1956) and Kempthorne (1957) on the genetic combining ability of wheat, followed by other workers, was of tremendous importance for creating new desirable wheat traits (Rashid *et al.*, 2012; Fasahat *et al.*, 2016). The cumulative effect of dominant and minor recessive genes creates various wheat types (Kumar *et al.*, 2018; Farooq *et al.*, 2019). Combining ability indicates the good genetic potential of various wheat varieties (Afridi *et al.*, 2017).

Line×tester techniques have been used to determine the combining ability for the improvement of wheat varieties (Tiwari *et al.*, 2017; Rajput, 2019; Wajid *et al.*, 2022; Khan *et al.,* 2023). In wheat, the combining ability is studied for two aspects, i.e., the general combining ability (GCA), which is due to the additive type of genes, while specific combining ability (SCA) is due to the dominant type of genes (Sprague and Tatum, 1942; Younas *et al.*, 2020; Rauf *et al.,* 2023). The plant breeders prefer wheat varieties with the best and most desirable traits and disease resistance in the segregating population (Minhas *et al.*, 2014; Ahmad *et al.*, 2017; Sadiq *et al.*, 2025). Combining ability and genetic analysis have a significant role in the selection of parental genotypes and their offspring for improved wheat varieties (Istipliler *et al.*, 2015; Rajput and Kandakar, 2018; Rauf *et al.*, 2023). The analysis is performed by various statistical and genetic techniques to determine the best productive wheat varieties (Khattab *et al.*, 2010; Hei *et al.*, 2015; Ahmad *et al.*, 2017). Selection of wheat for the next generation is based on GCA and SCA after proper crosses with the best traits (Istipliler *et al.*, 2015; Mandal & Madhuri, 2016). Therefore, the GCA and SCA of F_1 and F_2 with the desirable genotype of respective parents for onward generations are selected (Rabbani *et al.*, 2009; Tiwari *et al.*, 2017; Sattar *et al.*, 2018). The general combining ability and specific combining ability are particularly important in parental genotypes for grain production in the F_1 generation in wheat (Rahul, 2017; Hama-Amin & Towfiq, 2019). Development of new productive genotypes by hybridizing the genotypes with good GCA for the traits of interest and selecting the vigorous hybrids remained the main objective of the breeders. Information about diallel analysis and various gene actions is essential to promote a standard breeding program, as it provides a basis for the genetic pattern of inheritance controlling different traits in wheat (Murugan & Kannan, 2017; Dhoot *et al.*, 2020; Sinare *et al.*, 2024). Earlier research enunciated that grain yield, and its component traits were controlled by additive gene action in wheat (Khiabani *et al.*, 2015; Kandil *et al.*, 2016; Rahul, 2017; Adhikari *et al.*, 2020). However, some investigations revealed that grain yield and other agronomic traits, i.e., days to maturity, plant height and spike traits, were managed by non-additive gene action in wheat (Saeed & Khalil, 2017; Ingle *et al.*, 2018; Farooq *et al.*, 2019; Parveen *et al.*, 2019). Taking the above facts in mind, the current study was planned to determine the potential parental lines and testers and their F_1 and F_2 populations by estimating their GCA and SCA effects, respectively and to estimate the nature and degree of gene action for maturity and yield-related traits in a line×tester mating design in wheat.

Table 1. Parental genotypes (Lines & Testers) and hybrids (F_1 & F_2) resulted from line-by-tester crosses, used in the study.

	Lines		
1.	PR-137	5.	Auqab-2000
2.	PR-138	6.	SKD-1
3.	PR-139	7.	Tajaban
4.	Inqilab-91	8.	Benazir-13
	Testers		
1.	T-11	4.	Zarghoon-21
2.	Borlaug-100	5.	Taskeen-22
3.	Pirsabak-15		
	Line × Tester Crosses (Hybrids-F1 & F2)		
1.	PR-137 × T-11	21.	Auqab-2000 × T-11
2.	PR-137 × Borlaug-100	22.	Auqab-2000 × Borlaug-100
3.	PR-137 × Pirsabak-15	23.	Auqab-2000 × Pirsabak-15
4.	PR-137 × Zarghoon-21	24.	Auqab-2000 × Zarghoon-21
5.	PR-137 × Taskeen-22	25.	Auqab-2000 × Taskeen-22
6.	PR-138 × T-11	26.	SKD-1 × T-11
7.	PR-138 × Borlaug-100	27.	SKD-1 × Borlaug-100
8.	PR-138 × Pirsabak-15	28.	SKD-1 × Pirsabak-15
9.	PR-138 × Zarghoon-21	29.	SKD-1 × Zarghoon-21
10.	PR-138 × Taskeen-22	30.	SKD-1 × Taskeen-22
11.	PR-139 × T-11	31.	Tajaban × T-11
12.	PR-139 × Borlaug-100	32.	Tajaban × Borlaug-100
13.	PR-139 × Pirsabak-15	33.	Tajaban × Pirsabak-15
14.	PR-139 × Zarghoon-21	34.	Tajaban × Zarghoon-21
15.	PR-139 × Taskeen-22	35.	Tajaban × Taskeen-22
16.	Inqilab-91 × T-11	36.	Benazir-13 × T-11
17.	Inqilab-91 × Borlaug-100	37.	Benazir-13 × Borlaug-100
18.	Inqilab-91 × Pirsabak-15	38.	Benazi-13 × Pirsabak-15
19.	Inqilab-91 × Zarghoon-21	39.	Benazir-13- × Zarghoon-21
20.	Inqilab-91 × Taskeen-22	40.	Benazir-13 × Taskeen-22

Materials and Methods

Selected diverse wheat lines i.e., PR-137, PR-138, PR-139, Inqilab-91, Auqab-2000, SKD-1, Tajaban, and Benazir-13 were crossed with five testers i.e., T-11, Borlaug-100, Pirsabak-2015, Zarghoon-21 and Taskeen-22, resulted in the production of 40 F_1 and 40 F_2 populations (Tables 1 and 2). These genotypes were cultivated at the Cereal Crops Research Institutes (CCRI), Pirsabak, Pakistan, during 2021-2024. The CCRI Pirsabak is located in Nowshera near the Kabul River, 34-N latitude and 72 E longitudes, having an altitude of 288m. Due to its proximity to the Kabul River, the soil is sandy and loamy, having a pH of 7. The seeds were sown in two rows, two meters long, 25 cm apart from each other in a complete block design with three replications.

Crop husbandry: The soil was deeply ploughed 2 to 3 times, levelled, pulverized, and irrigated, as well as supplemented with green manure of leguminous plants to reclaim the loss of nitrogen and organic matter before sowing. Synthetic fertilizers of Phosphorus, Nitrogen, and Potassium were also added at specific developmental stages in the ratio of 90:120:60. The first irrigation was done in November at the coleoptile stage, while the next irrigation was subsequently carried out according to need.

Data recording and statistical analysis: Observations were noted on 10 plants per plot per replication for days to heading, spike length, number of spikelets per spike, 1000 grain weight, grain yield per plant and biological yield.

Biometric analysis: The data analysis was conducted according to Steel & Torrie (1980), utilizing the least significant difference (LSD, 0.05) test to compare and separate population means for each variable. Upon detecting significant variations among populations, the line tester combining ability analysis was performed, following Kempthorne (1957) and Singh & Chaudhary (1985). This analysis estimated variances due to GCA (σ2gca), variances due to SCA (σ^2SCA), additive (σ^2A) and dominance (σ^2D) components, and proportional contribution of lines, testers, and line×tester interactions of F_1 and F_2 to the total variance, providing insights into gene action and combining ability effects for various traits in wheat.

Results

Days to headings: The data recorded for days to headings showed greater diversity for lines, testers, and their F_1 and F_2 populations. For lines, maximum days to heading were recorded for Auqab-2000 (118 days), followed by Inqilab-91 (116 days), while the minimum days to heading, i.e. 113.5, 114 and 114.5 days were observed for Tajaban, Benazir-13 and PR-139, respectively (Table 3). Similarly, in testers, maximum days to headings were observed for Taskeen-22 (118 days), followed by T-11 (117 days), while the minimum days for heading were recorded for Borlaug-100 (114 days). Moreover, minimum days to heading were noted for F_1 hybrid combinations, i.e., Auqab-2000×T-11 (112.5 days), followed by PR-137×T-11 (113.5 days). Furthermore, maximum days to heading for F_1 were reported for Benazir-13×Taskeen-22 (119 days), followed by Benazir-13×Zarghoon-21, Tajaban×Taskeen-22, Benazir-13×T-11 (118 days), and Benazir-13×Borloung-100 (118.50 days). Similarly, minimum days to heading data were recorded for F_2 cross combinations, i.e. PR-139×T-11 and Inqilab-91×T-11 (112 days), followed by Auqab-2000×T-11 (113 days). In case of the F_2 population, maximum days to heading were recorded for cross combinations, i.e. Benazir-13×Taskeen-22, along with other cross combinations like PR-137×Taskeen-22, PR-138×Borlaug-100, SKD-1 × T-11 and Tajaban × Zarghoon-21, which took 117 days, followed by cross combinations PR-138×Zarghoon-21 (117.50 days).

Table 2. ANOVA analysis of the table of 53 wheat genotypes (13 parents and 40 F_1 and F_2 hybrids).

Sources	Df	Days to heading	Spike length	Spikelet per spike	1000 Grain weight	Grain yield	Biological yield
Replication	2	43.48**	0.14^{NS}	0.01^{NS}	196.78**	8.32NS	2906.72^{NS}
Genotypes	52	6.91**	2.67**	3.85**	42.90**	1658.22**	12040.52**
Parents	12	15.30**	4.96**	7.82**	52.37**	1041.19**	7427.19**
F_1 (Crosses)	39	4.49**	2.02**	2.66**	38.75**	1723.99**	11984.64**
P vs. F_1	1	0.59^{NS}	0.55^{NS}	2.52*	91.42**	6497.58**	69579.62**
Lines	7	6.02**	4.29**	5.94**	79.90**	4941.04**	38082.15**
Testers	4	8.23**	5.36**	10.12**	83.97**	961.61**	5228.44**
L x T	28	3.57**	0.98**	0.77**	22.00**	1028.64**	6425.44**
Error	104	1.56	0.27	0.37	5.49	45.82	1332.91

Spike length: The spike length in cm of lines, testers, F_1 and F_2 populations were also recorded (Table 3). Among the lines, the minimum (12.44cm) spike length was recorded for PR-139, followed by PR-138 (13.30 cm), while the highest spike length was noted for Tajaban (17.00 cm), followed by Benazir-13 (14.78) and Inqilab-91 (14.68 cm), respectively. The testers' highest value was 14.06 cm for Pirsabak-15, followed by T-11, 12.82 cm. In F_1 crosses, minimum spike length was found in SKD-1×T-11 (12.53 cm), followed by SKD-1×Zarghoon-21 and Benazir-13×T-11 (12.75 cm), whereas the highest spike length was recorded for Tajaban×Borlaug-100 (17.29 cm), followed by Inqilab-91×Borlaug-100 (14.93 cm), for Inqilab-91×Pisabak-15 (14.60 cm) and Inqilab-91×T-11 (14.57 cm). Similarly, in the F_2 generation, the lowest spike length was recorded for Tajaban× Zarghoon-21 (12.62 cm), SKD-1×T-11 (12.84 cm), PR-139×Taskeen-22 (12.96 cm), whereas the highest spike length was noted for Tajaban×Pirsabak-15 (17cm) followed by Inqilab-91×Pirsabak-15(15.68 cm), Inqilab-91×Borlaug-100(15.44 cm), Auqab2000×PirsabaK-15 (15.21 cm) and Inqilab-9×Zarghoon-21 (15.19 cm).

Spikelets per spike: The highest number of spikelets per spike in lines was observed for Tajaban (24.40), followed by PR-138 (22.70), SKD-1 (20.30) and Inqilab-91 (20.10). Similarly, in testers, maximum spikelets per spike were recorded for Pirsabak-15 (22.3), followed by T-11 & Borlaug-100 (21.5). The F_1 generation showed maximum spikelets per spike for PR-137×Pirsabak-15 and PR-139×Pirsabak-15(23.00), followed by Auqab-2000×T-11 (22.10) and Auqab-2000×Borlaug-100 (22.00). Likewise, minimum spikelets per spike were recorded for cross combination SKD-1×Zarghoon-21 (19.33), Auqab-2000×Zarghoon-21 (19.40), Benazir-13×T-11 (19.55) (Table 2). In the F_2 population, the maximum spikelets per spike was noted for Tajaban×Pirsabak-15 (24.50), followed by PR-139× T-11 (23.80). The minimum spikelets per spike were observed for Tajaban×Zarghoon-21 (18.60), followed by SKD-1× T11 (19.50). Moreover, the maximum number of spikelets per spike was possessed by lines, i.e., Tajaban (24.40) & PR-138 (22.70) and testers, i.e. Pirsabak-15(22.3) (Tables 2 & 3). Furthermore, in F_1 cross combinations, a greater number of spikelets per spike was recorded for F_1 hybrids, i.e. PR-137×Pirsabak-15 and PR-139×Pirsabak-15(23.00). Similarly, in F_2 populations, maximum spikelets per spike were noted for cross combinations, i.e. Tajaban×Pirsabak-15(24.5), followed by PR-139×T-11 (23.80) and PR-137×Pirsaba-15 (23.38) (Table 3).

1000 grain weight (g): Thousand-grain weight of lines, testers, and their F_1 and F_2 presented in Table 3. The data showed that among lines, PR-137 (51.40 g) had the most grains with a greater 1000 grain weight, followed by PR-

138 (44.35g), Inqilab-91 (38.80g) and SKD-1 (37.00g) subsequently. Moreover, Zarghoon-21 (46.60g) had the maximum 1000 grain weight, followed by Taskeen-22 (43.00g). Similarly, the maximum 1000 grain weight for F_1 hybrids was observed for PR-137×Borlaug-100 (55.30g), followed by SKD-1×Pirsabak-15 (51.5g), while the minimum 1000 grain weight was noted for Tajaban×T-11 (34.03 g) (Table 3). Moreover, in F_2 populations, a maximum 1000 grain weight was recorded for PR-137×Borlaug100 (55.30g), followed by PR-138×Taskeen-22 (51.75g). Based on the observations, line PR-137 (51.40g), tester Zarghoon-21 (46.60g), F_1 hybrid, i.e. PR137×Borlaug-100 (53.15g) and F_2 segregating population, i.e. PR-137×Borlaug100 (55.30 g), had bold grain and were best for 1000 grain weight (Table 3).

Grain yield (g): Grain yield is the most important economic component of wheat, and most wheat improvement programs are based on improving yield. In the present research, grain yield showed greater variation for lines, testers, F_1 and F_2 populations. Moreover, in lines, maximum grain yield was recorded for Benazir-13 (120g), followed by PR-138 (110g) and PR-139 (109g). Similarly, in testers, the maximum grain yield was shown by T-11 (88 g), followed by Zarghoon-21 (87g). In F_1 cross combinations, maximum grain yield was recorded for PR-137×Borlaug-100 (119g), followed by PR-137×T-11 (114.00g). However, the minimum grain yield for the first filial generation was noted for Tajaban×Pirsabak-15 (30g). Similarly, maximum grain yield in the second filial generation was recorded for Benazir-13×Borlaug-100 (69g), followed by Iqilab-91×Borlaug-100 (68g), while minimum grain yield per plant was recorded for PR-138×Zarghoon-21 (31g) (Table 3). Among the tested germplasm, the best parental wheat genotypes were Benazir-13, PR-138 and T-11, while in the first filial generation, PR-137×Borlaug100 and in the second filial generation, Benazir-1313×Borlaug-100, showed a maximum grain yield (Table 3).

Biological yield (g): It is the total biomass produced by a crop, including its stem, leaves, branches, inflorescence, spikes, seeds, fruits, and roots. For lines, the minimum biological yield was noted for SKD-1 (200g), for Auqab-2000 (245g), while the maximum biological yield was observed for lines Benazir-13 (329g) and for PR-138 (333g). Similarly, for testers, the minimum biological yield was recorded for semi dwarf cultivar, i.e. Taskeen-22 (197g); however, the maximum biological yield was noted for T-11 (273g) and followed by Pirsabak-15 and Zarghoon-21 (239 g) (Table 2). Moreover, minimum biomass yield was recorded for the F_1 cross combination SKD-1×Pirsbak-15 (84g), followed by the cross of Benazir-13×T-11 (93g). However, maximum biological yield was recorded for the cross between Auqab-2000×T-11 (348g) and PR-137 × Pirsabak-15 (345g). Furthermore, maximum biomass yield was noted for F_2 segregating population PR137×Borlaug-100 (351g), followed by PR139×Borlaug-100 (344 g), respectively. Similarly, the minimum biological yield values were recorded for Tajaban × Taskeen-22 (122 g), followed by Tajaban × Zarghoon-21 (147g).

Combining ability analysis: The greater genetic variation in the breeding material allowed further analysis and partition of combining ability into its components, i.e., general and specific combining ability for lines, testers and their crosses, respectively (Tables 4 & 5). According to GCA and SCA analysis, positive values were found for the majority of the traits, i.e. spike length, spikelets per spike, 1000 grain weight, grain yield and biological yield. However, negative GCA and SCA effects are enviable for those traits where a minimum value is required, i.e. days to heading.

Days to heading: The lines showed negative GCA values in the range of -3.34 to 2.56. Four lines, i.e. PR-137, PR-139, Inqilab-91 and Auqab-2000, showed negative and desirable GCA effect (Table 7). While the other 4 lines, i.e., PR-138, Tajaban and Benazir-13 showed a positive GCA effect. Highly significant ($p \leq 0.01$) negative GCA effects were observed for PR-137 (-3.34), followed by PR-139 (-1.04), Inqilab-91 (-0.84) and Auqab-2000 (-0.74), respectively. However, SKD-1, Tajaban and Benazir-13 showed 0.86, 2.16 and 2.56 GCA values, respectively. Moreover, PR-138(0.36) was statistically non-significant. Furthermore, testers showed GCA values from -0.89 to 1.61. However, testers T-11 (-0.89), Borlaug-100 (-0.70), and Pirsabak-15 (-0.32) showed negative GCA, respectively. In contrast, Zarghoon-21 and Taskeen-22 possessed positive GCA values of 0.30 and 1.61, respectively. In tester, the highly Significant ($p \leq 0.01$) negative GCA effects were observed in T-11, Borlaug-100 and Taskeen-22. Overall, in parental lines and testers, the highest negative and desirable GCA effects were recorded for line PR-137 and tester T-11, and they were considered the best general combiner for days to heading. In F_1 crosses, the SCA effects ranged from -3.3 to 5.09 (Table 4). Twenty-one out of 40 showed negative SCA, ranging from -3.3 to -0.31. However, nineteen F_1 hybrids revealed positive SCA effects (0.09 to 5.09). Moreover, significant ($p \leq 0.01$) negative SCA effects were observed for PR-137×Pirsabak-15 (-2.47), PR-137×Zarghoon-21 (-4.6), Inqilab-91×T-11 (2.91) and SKD-1×Borlaug-100 (-3.3) and identified as the best specific combiner for days to heading. Likewise, in F_2 cross combinations, the SCA effects ranged from -1.99 to 2.61 (Table 4), where 23 out of 40 showed negative SCA ranging from -1.99 to -0.09. However, 17 F_2 populations revealed a positive SCA effect (0.09 to 2.21). Significant ($p \leq 0.01$) negative SCA effects were observed for PR-137×Borlaug-100 (-0.58), Tajaban×Borlaug-100 (-0.68) and Inqilab-91×T-11 (-1.39), which were identified as the best specific combiners for early flowering, which can be used in the development of early maturing wheat genotypes.

Spike length: Lines, i.e. PR-138, PR-139, PR-139, SKD-1 and Benzir-13 showed negative desirable GCA effects ranging from -0.62 to -0.83 (Table 7). However, four lines, i.e. PR-137, Inqilab-91, Auqab-2000 and Tajaban, revealed positive GCA. The highest negative GCA was reported for SKD-1 (-0.62), whereas the highest desirable positive GCA was displayed by Tajban (0.81). Similarly, three testers, i.e. T-11, Zarghoon-21 and Taskeen-22, showed negative GCA ranging from -0.47 to -0.67. However, testers Borlaug-100 and Pirsabak-15 reported positive GCA.

Table 3. Mean performance for various traits of 53 wheat genotypes (13 parents and 40 F_1 and F_2 Hybrids).

Genotypes	Days to heading		Spike length		Spikelet per spike		1000 Grain weight		Grain yield		Biological yield	
I. Parents												
PR-137	114.00		13.63		21.60		51.40		93.00		313.00	
PR-138	115.50		13.30		22.70		44.35		110.00		333.00	
PR-139	114.50		12.44		22.50		43.70		109.00		324.00	
Inqilab-91	116.00		14.68		20.10		38.80		80.00		288.00	
Auqab-2000	118.00		13.81		22.30		41.00		71.00		245.00	
SKD-1	114.00		13.83		20.30		37.00		58.00		205.00	
Tajaban	113.50		17.00		24.40		43.20		102.00		305.00	
Benazir-13	113.50		14.78		20.90		41.65		120.00		329.00	
T-11	117.00		12.82		21.50		34.68		88.00		273.00	
Borlaug-100	114.00		13.18		21.50		42.65		71.00		203.00	
Pirsabak-15	114.50		14.06		22.30		42.25		75.00		239.00	
Zarghoon-21	114.50		12.14		17.80		46.60		87.00		239.00	
Taskeen-22	114.92		13.81		21.50		43.00		71.00		200.00	
Parents mean	**118.50**		**12.51**		**20.10**		**42.33**		**87.31**		**268.90**	
II. F_1 / F_2 Generation	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**
PR-137 × T-11	113.50	113.50	13.14	12.60	20.40	21.60	47.63	50.45	114.00	59.00	321.00	313.00
PR-137 × Borlaug-100	114.00	114.00	14.16	13.81	21.70	21.70	55.30	53.15	119.00	55.00	351.00	333.00
PR-137 × Pirsabak-15	114.50	114.00	14.71	15.20	23.00	23.38	46.05	44.23	92.00	43.00	305.00	324.00
PR-137 × Zarghoon-21	114.50	115.00	13.76	14.08	21.10	20.90	47.60	49.60	99.00	42.00	284.00	288.00
PR-137 × Taskeen-22	116.50	117.50	14.04	14.05	21.00	21.30	40.25	40.85	83.00	36.00	263.00	245.00
PR-138 × T-11	116.50	115.50	13.14	13.00	21.50	21.43	43.43	45.05	83.00	43.00	282.00	205.00
PR-138 × Borlaug-100	117.00	117.00	13.70	13.83	21.90	21.30	43.80	46.00	72.00	28.00	278.00	305.00
PR-138 × Pirsabak-15	116.50	116.00	14.23	14.16	22.00	22.90	39.15	47.20	74.00	39.00	210.00	329.00
PR-138 × Zarghoon-21	116.50	117.50	13.15	14.05	20.70	20.70	47.55	44.45	52.00	31.00	238.00	273.00
PR-138 × Taskeen-22	116.50	117.00	13.29	13.58	21.60	21.50	51.75	47.35	118.00	58.00	252.00	203.00
PR-139 × T-11	113.00	112.00	12.96	13.83	21.50	23.80	39.35	45.25	78.00	59.00	306.00	239.00
PR-139 × Borlaug-100	114.00	114.00	13.50	13.72	22.70	22.60	46.63	49.65	79.00	63.00	344.00	239.00
PR-139 × Pirsabak-15	116.00	115.50	14.04	13.41	23.00	22.20	41.13	40.15	56.00	46.00	221.00	200.00
PR-139 × Zarghoon-21	116.00	115.00	13.03	12.86	21.00	21.00	49.35	48.80	87.00	70.00	223.00	321.00

Table 3. (Cont'd.).

Genotypes	**Days to heading**		**Spike length**		**Spikelet per spike**		**1000 Grain weight**		**Grain yield**		**Biological yield**	
I. Parents												
PR-139 × Taskeen-22	115.50	115.50	13.26	12.96	21.60	22.10	48.75	45.70	86.00	34.00	276.00	351.00
Inqilab-91 × T-11	111.00	112.00	14.57	14.58	21.40	22.50	42.10	41.50	52.00	57.50	264.00	305.00
Inqilab-91 × Borlaug-100	116.50	115.50	14.93	15.44	21.00	22.55	42.53	46.88	90.00	68.00	288.00	284.00
Inqilab-91 × Pirsabak-15	113.50	114.00	14.60	15.68	21.40	22.10	40.80	40.50	66.00	68.00	257.00	263.00
Inqalib 91 × Zarghoon-21	116.50	115.50	14.29	15.19	19.80	21.20	39.15	44.80	96.00	53.00	229.00	282.00
Inqilab-91 × Taskeen-22	116.50	117.00	13.98	14.85	20.80	21.90	43.78	44.10	117.00	38.00	303.00	278.00
Auqab-2000 × T-11	113.00	113.00	14.50	14.53	22.10	22.50	36.80	43.10	61.00	48.00	298.00	210.00
Auqab-2000 × Borlaug-100	115.50	116.00	14.47	14.59	22.00	22.40	42.25	42.18	63.00	66.00	232.00	238.00
Auqab-2000 × Pirsabak-15	115.00	115.50	13.54	15.21	21.40	22.40	35.25	38.05	71.00	44.00	207.00	252.00
Auqab-2000 × Zarghoon-21	115.00	116.00	13.32	14.53	19.40	20.90	45.18	45.80	72.00	60.00	152.00	306.00
Auqab-2000 × Taskeen-22	116.00	116.00	13.88	13.50	21.10	20.90	43.45	44.60	47.00	54.00	203.00	344.00
SKD-1 × T-11	116.00	117.00	12.53	12.84	19.80	19.50	43.60	40.05	59.00	36.00	159.00	221.00
SKD-1 × Borlaug-100	112.50	116.00	13.80	14.42	20.30	20.60	44.50	38.35	32.00	41.00	165.00	223.00
SKD-1 × Pirsabak-15	115.00	115.00	13.92	14.60	21.10	22.60	51.50	37.78	53.00	69.00	205.00	276.00
SKD-1 × Zarghoon-21	117.00	116.50	12.75	13.68	19.30	20.60	46.58	43.55	38.00	31.00	238.00	264.00
SKD-1 × Taskeen-22	117.00	116.50	13.76	13.43	20.70	21.20	49.53	42.18	75.00	69.00	194.00	288.00
Tajaban × T-11	115.00	112.50	13.60	14.96	20.60	22.90	34.03	42.18	79.00	57.00	213.00	257.00
Tajaban × Borlaug-100	114.50	115.00	17.29	14.98	22.40	20.50	40.65	43.60	36.00	60.00	187.00	229.00
Tajaban × Pirsabak-15	116.00	116.50	14.73	17.00	22.00	24.50	37.95	39.60	30.00	28.00	154.00	303.00
Tajaban × Zarghoon-21	117.00	117.50	14.03	12.62	20.30	18.60	40.53	48.20	52.00	21.00	147.00	298.00
Tajaban × Taskeen-22	118.00	118.00	14.04	14.65	21.30	22.10	45.80	44.40	33.00	42.00	122.00	232.00
Benazir-13 × T-11	118.00	118.50	12.72	13.15	19.60	20.10	38.03	46.05	52.00	52.00	188.00	207.00
Benazir-13 × Borlaug-100	118.50	116.00	13.62	13.84	20.40	20.70	39.35	44.95	74.00	69.00	264.00	152.00
Benazir-13 × Pirsabak-15	117.00	116.50	14.09	14.82	20.80	21.30	38.60	40.70	74.00	58.00	196.00	203.00
Benazir-13 × Zarghoon-21	118.00	118.00	13.02	13.37	19.70	19.70	44.00	39.70	86.00	55.00	239.00	162.00
Benazir-13 × Taskeen-22	119.00	117.50	13.60	13.49	20.40	20.80	42.85	42.90	72.45	60.00	252.00	165.00
F_1 s and F_2s Mean	**115.76**	**115.70**	**13.81**	**14.13**	**21.10**	**21.50**	**43.41**	**44.09**	**93.00**	**50.20**	**237.80**	**245.80**
LSD 0.05	**3.63**	**1.33**	**0.84**	**0.72**	**0.99**	**0.86**	**3.79**	**3.79**	**10.96**	**16.90**	**59.10**	**65.70**

Table 4. Specific combining ability effect (SCA) for various traits of 53 wheat genotypes (40 F1 and F_2 Hybrids).

F_1 Crosses	Days to heading		Grain yield		Spike length		Spikelet perspike		1000 Grain weight		Biological yield	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
PR-137 × T-11	-0.41ns	0.11*	-19.35**	1.67ns	2.41ns	-0.91ns	-0.94**	-0.38**	2.98ns	3.05ns	-67.32**	0.21**
PR-137 × Borlaug-100	2.4**	-0.58**	9.15**	8.59**	-2.2ns	-0.34ns	-0.31ns	-0.03ns	6.19**	6.97**	20.3*	20.88*
PR-137 × Pirsabak-15	-2.47**	-0.51**	18.21**	14.42**	2.39ns	0.37ns	0.85**	0.51*	0.66ns	0.79ns	54.55**	16.71**
PR-137 × Zarghoon-21	-4.6**	-0.51**	-2.79ns	-1.49ns	1.06ns	0.46*	0.64*	0.26**	-0.49ns	-1.34ns	-15.01ns	-1.25ns
PR-137 × Taskeen-22	5.09**	1.49**	-5.23ns	-23.2**	-3.67*	0.42*	-0.25ns	-0.36**	-9.35**	-9.47**	7.49ns	-36.54*
PR-138 × T-11	1.39*	0.31**	6.65*	-6.06**	1.71ns	-0.28*	0.16ns	-0.34*	-1.98ns	1.08ns	-21.73*	14.01ns
PR-138 × Borlaug-100	-1.3*	0.63**	21.15**	9.86**	-4.17*	-0.1ns	-0.1ns	-0.22ns	-1.74ns	-2.3ns	5.9ns	0.68*
PR-138 × Pirsabak-15	0.82ns	-0.31**	-6.79*	-2.97*	0.52ns	-0.45*	-0.14ns	0.25ns	4.99*	-3.88*	20.15*	-25.49ns
PR-138 × Zarghoon-21	0.2ns	0.19**	1.21ns	-14.89**	-0.24ns	0.66ns	-0.29ns	0.27ns	1.15ns	0.84ns	1.09ns	5.55ns
PR-138 × Taskeen-22	-1.11*	-0.81*	-22.23**	14.07**	2.17ns	0.17*	0.36ns	0.05ns	-2.41ns	4.26ns	-5.41ns	5.26**
PR-139 × T-11	-2.21**	-0.99**	18.65**	19.61**	4.63**	0.92**	-0.36ns	1.26ns	-0.02ns	-2.9ns	55.17**	16.01**
PR-139 × Borlaug-100	0.1ns	-0.18ns	0.15ns	7.19**	-1.18ns	0.16ns	0.18ns	0.3ns	3.69ns	0.62ns	-12.2ns	44.68**
PR-139 × Pirsabak-15	1.73**	1.39**	-4.79ns	-11.98**	-1.99ns	-0.83ns	0.33ns	-1.23ns	-2.28ns	-1.81ns	1.05ns	-36.49**
PR-139 × Zarghoon-21	1.1*	-0.11**	-21.79**	-8.23**	-0.42ns	-0.17ns	0.02ns	-0.2ns	0.91ns	2.73ns	-34.51**	-31.45ns
PR-139 × Taskeen-22	-0.71ns	-0.11ns	7.78**	-6.6**	-1.04ns	-0.08ns	-0.17ns	-0.13ns	-2.31ns	1.35ns	-9.51ns	7.26**
Inqilab-91 × T-11	-2.91**	-1.39**	-1.75ns	-0.19ns	1.57ns	-0.13**	0.62*	0.25ns	-0.33ns	3.22ns	32.38**	-20.19**
Inqilab-91 × Borlaug-100	2.4**	0.92*	-22.25**	-19.27**	-0.44ns	0.09ns	-0.44ns	0.54*	-0.69ns	-0.11ns	-45**	-5.52**
Inqilab-91 × Pirsabak-15	-0.98ns	-0.51ns	9.81**	3.23*	1.25ns	-0.35ns	-0.19ns	-1.04ns	1.24ns	1.24ns	15.25ns	5.31**
Inqilab-91× Zarghoon-21	1.4*	-0.01*	-8.19**	2.31ns	-3.08ns	0.37ns	-0.1ns	0.29*	0.3ns	-4.1ns	-16.31ns	-19.65**
Inqilab-91 × Taskeen-22	0.09ns	0.99*	22.38**	13.93**	0.69ns	0.02ns	0.11ns	-0.04ns	-0.52ns	-0.25ns	13.69ns	40.06**
Auqab-2000 × T-11	-1.01ns	-0.89*	19.65**	12.14**	1.79ns	0.5ns	1.5**	0.48**	5.3**	-0.96**	51.77**	63.61**
Auqab-2000 × Borlaug-100	1.3*	0.92ns	-8.85**	-4.61**	-1.52ns	-0.08ns	0.24ns	0.62ns	-3.99*	0.69**	20.4*	-11.73**
Auqab-2000 × Pirsabak-15	0.43ns	0.49ns	-12.79**	7.56**	-0.33ns	-0.15ns	-0.01ns	-0.51**	-2.3ns	-3.24*	-20.35*	5.11*
Auqab-2000 × Zarghoon-21	-0.2ns	-0.01ns	1.21ns	-3.36*	-0.56ns	0.39ns	-1.32**	0.22*	2.09ns	3ns	5.09ns	-46.85*
Auqab-2000 × Taskeen-22	-0.51ns	-0.51ns	0.78ns	-11.73**	0.62ns	-0.66**	-0.41ns	-0.81*	-1.1ns	0.5ns	-56.91**	-10.14ns
SKD-1 × T-11	0.39ns	2.21**	-10.35**	-25.39**	-10.54**	-0.51ns	-0.37ns	-1.6*	0.34ns	-0.75ns	5.07ns	-50
SKD-1 × Borlaug-100	-3.3**	0.02**	9.15**	-16.14**	4.55**	0.42**	-0.53ns	-0.26**	-2.05ns	-3.6*	21.2*	-56.93*
SKD-1 × Pirsabak-15	2.83**	-0.91ns	-2.79ns	9.69**	-1.56ns	-0.08*	0.16ns	0.61**	0.71ns	6.47**	-58.05**	44.24*
SKD-1 × Zarghoon-21	1.2*	-0.41**	3.21ns	22.77**	3.34*	0.22*	0.08ns	0.84**	1.24ns	-2.14*	21.39*	60.95*
SKD-1 × Taskeen-22	-1.11*	-0.91**	0.77ns	9.07**	4.21*	-0.05*	0.66*	0.41**	-0.25ns	0.03ns	10.39ns	1.99ns
Tajaban × T-11	4.09**	-1.99*	-9.35**	11.67**	3.93*	0.56**	-1.24**	0.98**	-5.64**	-2.98*	43.08**	32.41**
Tajaban × Borlaug-100	-2.6**	-0.68**	8.15**	22.59**	4.52**	-0.06**	1.6**	-1.18**	-4.93*	-0.1**	27.2**	-2.92**
Tajaban × Pirsabak-15	-1.47**	0.89*	-0.29ns	-19.58**	-3.29*	1.27**	-0.65*	1.69**	-5.61**	0.27*	-34.05**	5.91**
Tajaban × Zarghoon-21	1.4*	0.89*	21.71**	-1.16ns	-1.92ns	-1.89**	0.74**	-1.98*	-0.35ns	-0.84**	-29.61**	1.95**
Tajaban × Taskeen-22	-1.41*	0.89*	-20.23**	-13.53**	-3.25ns	0.12**	-0.45ns	0.49*	16.53**	3.65ns	-6.61ns	-37.34ns
Benazir-13 × T-11	0.69ns	2.61ns	-4.15ns	-13.46**	-5.5**	-0.14**	0.64*	-0.62*	-0.66ns	0.25ns	-98.43**	-55.79**
Benazir-13 × Borlaug-100	1ns	-1.08ns	-16.65**	-8.21**	0.43ns	-0.1**	-0.62*	0.22*	3.52ns	-2.18ns	-37.8**	10.88**
Benazir-13 × Pirsabak-15	-0.88ns	-0.51ns	-0.59ns	-0.37ns	3.02ns	0.2ns	-0.37ns	-0.31ns	2.58ns	0.14ns	21.45*	-15.29**
Benazir-13 × Zarghoon-21	-0.5ns	-0.01*	5.41ns	4.04**	1.79ns	-0.03*	0.22ns	0.32*	-4.86*	1.86*	67.89**	30.75**
Benazir-13 × Taskeen-22	-0.31ns	-1.01ns	15.98**	18**	0.26ns	0.07ns	0.13ns	0.39ns	-0.58ns	-0.07ns	46.89**	29.46**
SE for SCA effect	**1.29**	**0.47**	**1**	**0.63**	**0.3**	**0.26**	**0.35**	**0.31**	**1.35**	**1.76**	**21.08**	**23.4**

*, **= Significant at $p \leq 0.05$ and $p \leq 0.01$, Respectively, ns= Nonsignificant, S E= Standard error

Table 5. Genetic components of 53 wheat genotypes (13 parents and 40 Hybrids in each F_1 and F_2) for various traits were evaluated at the Cereal Crops Research Institute (CCRI), Pirsabak Nowshera, under irrigated environment during 2021 and 2024.

Genetic components	Days to heading		Spike length		Spikelet perspike		1000 Grain weight		Grain yield per plant		Biological yield	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
σ^2gca= $[(1+F)/4]\sigma^2$A	0.05	0.03	0.04	0.25	15.45	13.90	15.45	13.90	0.25	0.15	113.94	48.79
σ^2sca=$[(1+F)/2]2\sigma^2$D	-0.26	0.62	0.60	5.50	327.60	173.90	327.61	173.90	5.50	5.58	1697.51	1443.00
σ^2gca/σ^2sca	-0.20	0.04	0.06	0.05	0.05	0.08	0.05	0.08	0.05	0.03	0.07	0.03
h^2 (bs)	-0.03	0.33	0.33	0.52	0.89	0.65	0.89	0.65	0.52	0.59	0.59	0.86
k (20%)	1.46	1.46	1.46	1.46	1.46	0.30	1.46	0.30	1.46	1.46	1.46	1.46
Grand Mean	117.00	161.50	13.78	40.70	74.00	56.00	74.00	56.00	40.70	47.78	206.00	168.00
Genetic Advance	-0.01	0.08	0.09	0.16	0.36	0.28	0.36	0.28	0.16	0.15	0.23	0.29
GA (%)	-0.01	0.05	0.68	0.39	0.48	0.51	0.48	0.51	0.39	0.31	0.11	0.17
GCV	2.07	0.92	3.17	3.67	7.87	13.95	7.87	13.95	3.67	2.93	25.44	12.19
PCV	0.13	0.13	0.52	1.00	0.68	0.52	1.00	0.68	0.33	0.25	0.18	0.18

Table 6. Proportional contribution of lines, testers and Line×Tester population in F_1 and F_2 generations.

% Proportional contribution	Days to heading		Spike length		Spikelet per spike		1000 Grain weight		Grain yield per plant		Biological yield	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Lines	42.9	34.0	38.1	39.6	40.1	23.2	37.0	39.2	51.44	23.15	57.0	59.9
Tester	23.3	31.4	27.2	28.4	39.0	37.4	22.2	19.7	5.72	37.43	4.5	10.5
Line x Tester	33.8	34.6	34.7	32.1	20.8	39.4	40.8	41.1	42.84	39.42	38.5	29.6

Table 7. General combining ability effect (GCA) for various traits of 13 parents.

Genotypes	Days to heading	Spike length	Spikelet per spike	1000 grain weight	Grain yield	Biological yield
I. Lines						
PR-137	-3.34 **	0.25*	0.18ns	3.35**	22.48**	73.2**
PR-138	0.36 ns	-0.38**	0.18ns	2.92**	0.47ns	31.6**
PR-139	-1.04 **	-0.52**	0.7**	1.15ns	5.47**	28.7**
Inqilab-91	-0.84 **	0.83**	-0.38**	-2.23*	1.88ns	45.5**
Auqab-2000	-0.74 **	0.07ns	0.44**	-1.13ns	-2.53*	-18.9**
SKD-1	0.86 **	-0.62**	-1.02**	-4.41**	-22.52**	-75.2**
Tajaban	2.16 **	0.81**	0.68**	3.71**	-1.52ns	-52.2**
Benazir-13	2.56 **	-0.44**	-0.8**	-3.37**	-3.72**	-32.7**
S E of GCA for lines	**0.65**	**0.15**	**0.18**	**0.68**	**0.32**	**10.54**
II. Tester						
T-11	-0.89**	-0.47**	-0.1ns	-0.68ns	9.35**	21.23**
Borlaug-100	-0.7**	0.67**	0.57**	0.01ns	-4.15**	-1.4ns
Pirsabak-15	-0.32ns	0.4**	0.71**	-3.31**	1.79ns	-2.65ns
Zarghoon-21	0.3ns	-0.46**	-0.98**	1.93**	-4.21**	-18.09**
Taskeen-22	1.61**	-0.14ns	-0.19*	2.05**	-2.78**	0.91ns
S E of GCA for testers	**0.46**	**0.11**	**0.12**	**0.48**	**0.34**	**7.45**

*,**= Significant at $p \leq 0.05$ and $p \leq 0.01$, Respectively, ns= Non-significant, S E= Standard error

For spike length, in F_1 cross combinations, the SCA effects ranged from -10.54 to 4.63 (Table 4). Nineteen out of 40 showed negative SCA, ranging from (-0.10 to -0.59). In F_1 generations, the SKD-1×T-11 had the highest negative SCA effect (-10.54), followed by Benazir-13×T-11 (-5.5), and the maximum positive SCA was reported for the F_1 hybrid, i.e. PR-139×T-11 (4.63). Similarly, in F_2 populations, the SCA effects ranged from -1.89 to 1.27 (Table 4). Fifteen out of 40 showed negative SCA, ranging from -1.89 to -0.06. Moreover, in the F_2 population, the Tajaban×Zarghoon-21 had the highest negative SCA effect (-1.89) followed by PR-139×T-11 (-0.92) and the maximum positive SCA was reported for Tajaban×Pirsabak-15 (1.27) (Table 4).

Spikelets per spike: For spikelets per spike, the lines showed negative GCA values ranging from -1.02 to 0.7 (Table 7). Three lines, i.e., Inqilab-91, SKD-1 and Benazir-13, showed a negative GCA effect. However, 5 lines, i.e. PR-137, PR-138, PR-139, Auqab-2000 and Tajaban, revealed a positive and desirable GCA. Likewise, testers showed a GCA value from -0.98 to 0.71 (Table 7). Three testers, i.e. T-11, Taskeen-22 and Zarghoon-21, had negative GCA, while two testers, Borlaug-100 and Pirsabak-15, had a positive GCA, i.e. 0.57 and 0.71, respectively. The maximum negative GCA was reported for Zarghoon-21(-0.98). Overall, in parental lines and testers, the highest positive GCA effects were recorded for line PR-139 (0.7) and tester Pirsabak-15 (0.71), which proved to be the best general combiners for spikelet per spike. Similarly, for spikelet per spike, in the F_1 population, the SCA effects ranged from -1.32 to 1.6. Moreover, nineteen out of 40 showed positive SCA, ranging from 0.02 to 1.6, as shown in Table 4. Moreover, in F_1 generations, Tajaban×Borlaug-100 had the highest positive (1.6) SCA effect, followed by Auqab-2000×T-11 (1.5), whereas the maximum negative SCA was recorded for Auqab-2000×Zarghoon-21 (-1.32). Similarly, in F_2 segregants, the SCA effects ranged from -1.32 to 1.6 (Table 4). Moreover, nineteen cross combinations showed positive SCA ranging from 0.08 to 1.6. In F_2 populations, the cross combination, i.e. Tajaban×Borlaug-100, had the highest positive SCA (1.6), followed by Auqab-2000×T-11 (1.5), and the maximum negative SCA was reported for Auqab-2000×Zarghoon-21 (-1.32) (Table 4).

1000 grain weight: The GCA values for 1000 grain weight ranged from -4.41 to 3.71; four lines, i.e. PR-137, PR-138, PR-139 and Tajaban, revealed positive and desirable GCA effect (Table 7). However, 4 lines, i.e. Inqilab-91, Auqab-2000, SKD-1 and Benazir-13, revealed a negative GCA. The highest negative GCA was recorded for SKD-1 (-4.41), whereas the highest positive GCA was observed for Tajaban (3.71). Likewise, testers showed GCA values ranged from -3.31 to 2.05 (Table 7). However, two testers, i.e. Pirsabak-15 and T-11, had negative GCA, while 3 testers, Taskeen-22, Borlaug-100 and Zarghoon-21 showed a positive GCA of 2.05, 0.01 and 1.93, respectively. The maximum positive GCA was reported for Taskeen-22 (2.05). Overall, in parental lines and testers, the highest positive GCA effects were recorded for line Tajaban (3.71) and tester Taskeen-22 (2.05) and were considered the best general combiner for 100 grain weight. Similarly, for 1000 grain weight, in F_1 hybrids, the SCA effects ranged from -9.35 to 16.53. Seventeen out of 40 showed positive SCA, ranging from 0.02 to 16.53 (Table 4). The F_1 cross combination, i.e., Tajaban×Taskeen-22, had the highest positive (16.53) SCA effect, followed by PR-137×Borlaug-100 (6.19), and the maximum negative SCA was recorded for Tajaban×Pirsabak-15 (-5.61). Moreover, in the F_2 population, the SCA effects were -9.47 to 6.97 (Table 4). Twenty out of 40 F_2 segregants showed positive SCA ranging from 0.03 to 6.97. The PR-137×Borlaug-100 had the highest positive (6.93) SCA effect, followed by SKD-1×Pirsabak-15 (6.47) and the maximum negative SCA was reported by PR-137×Taskeen-22 (-9.47).

Grain yield per plant: The lines showed positive GCA values in the range of 1.88 to 22.88 (Table 7). Four lines, i.e. PR-137, PR-138, PR-139 and Inqilab-91, showed positive and desirable GCA effect. However, 4 lines, i.e. Auqab-2000, SKD-1, Tajaban and Benazir-13 showed a negative GCA effect. Whereas, PR-138, Inqilab-91 and SKD-1 showed 0.47, 1.88, respectively. Similarly, testers showed that GCA values ranged from -4.15 to 9.35. Wheat testers, i.e. T-11 and Pirsabak-15, showed positive GCA (9.35) and (1.79), respectively. However, Borlaug-100, Zarghoon-21 and Taskeen-22 possessed negative GCA values ranging from -4.15, 4.21 and -2.78, respectively. Overall, in parental lines and testers, the highest positive and desirable GCA effects were recorded in line PR-137 and tester T-11 and were found to be the best general combiner for grain per plant (Table 7). For grain yield per plant in F_1 cross combinations, the SCA effects ranged from -20.23 to 22.25 (Table 4). Twenty-one F_1 hybrids out of 40 showed positive and desirable SCA ranging from 0.15 to 22.25. In F_1 cross combinations, i.e. PR-138×Taskeen-22 had the highest negative SCA effect (22.25), followed by PR-138×Taskeen-22(22.23) and the maximum negative SCA was noted by Tajaban×Taskeen-22(-20.23). Highly significant ($p \leq 0.01$) positive SCA was observed in Inqilab-91×Borlaug-100 (22.25), followed by PR-138×Taskeen-22 (22.23) and PR-138×Borlaug-100 (21.15) (Table 4). Similarly, in F_2 segregants, the SCA effects ranged from -25.39 to 22.77 (Table 4). Moreover, eighteen F_2 populations out of 40 showed positive SCA ranging from 1.67 to 22.77. Furthermore, in the F_2 population, SKD-1×Zarghoon-21 had the highest negative SCA effect (22.77), followed by Tajaban×Borlaug-100 (22.59) and the maximum negative SCA was reported for SKD-1×T-11 (-25.39) (Table 4).

Biological yield: For the biological yield of the plants, the GCA effect values ranged from 75.2 to 73.2 (Table 7) among parental genotypes. Four lines, i.e. PR-137, PR-138, PR-139 and Inqilab-91, revealed positive and desirable GCA effect. While four lines, i.e. SKD-1, Tajaban, Auqab-2000 and Benazir-13, revealed a negative GCA. The highest negative GCA was recorded in SKD-1 (-75.2), whereas the highest positive GCA was revealed in PR-137 (73.2). Similarly, testers showed GCA values ranging from -18.09 to 21.23. Three testers, i.e. Pirsabak-15, Borlaug-100 and Zarghoon-21, had negative GCA; however, two testers, T-11 and Taskeen-22, reported a positive desirable GCA value of 21.23 and 0.91, respectively. Overall, in parental lines and testers, the highest positive GCA were recorded for PR-137, PR-138, PR-139, Inqilab-91 and testers T-11, so they are the best general combiners for the biological yield of the plants. In the F_1 population, the SCA effects were noted to range from -98.43 to 67.89 (Table 4). Twenty-three out of 40 cross combinations showed positive SCA in the range of 1.05 to 67.89. Benazir-13×Zarghoon-21 had the highest positive (67.89) SCA effect followed by PR-137×Pirsabak-15 (54.55) and the maximum negative SCA was reported by Benazir-13×T-11 (-98.43) highly Significant ($p \leq 0.01$) positive SCA was observed in cross combinations i.e. PR-137×Pirsabak-15, PR-139×T-11, Inqilab-91×T-11, Auqab-2000×T-11, Tajaban×T-11, Benazir-13×Zarghoon-21 and Benazir-13×Taskeen-22 so these crosses could be used as a best specific combiner for the biological yield of the plants in F_1 generation. Similarly, in the F_2 population, the cross combination, i.e. Auqab-2000×T-11, had the highest positive (63.61) SCA effect, followed by SKD-1×Zarghoon-21 (60.95), and the maximum negative SCA was reported by Benazir-13×T-11 (-55.79), as shown in Table 4. In the F_2 generation, highly Significant ($p \leq 0.01$) positive SCA was observed in the cross of Auqab-2000 × T-11, Tajaban× T-11, PR-139×T-11, Inqilab-91×T-11, Inqilab-91×Taskeen-22, Tajaban×T-11, PR-139×Borlaug-100 and Benazir-13×Taskeen-22, PR-137×Pirsabak-15, so these genotypes could be used as the best specific combiner for the biological yield of the plants.

Gene action: Variances due to σ^2sca in F_1 generation were greater than the σ^2gca for traits, i.e. spike length, spikelet per spike, 1000 grain weight, grain yield per plant and biological yield, suggesting dominant or non-additive gene action (Table 5). Likewise, in F_2 generation variances due to σ^2sca were also greater than the σ^2gca for traits spike length, spikelet per spike, 1000 grain weight, grain yield per plant and biological yield were controlled by non-additive gene action. However, the present study revealed that the variance due to σ2gca was greater than that due to σ2sca for days to heading in both the F1 and F2 generations, indicating that this trait was controlled by additive gene action. The findings were supported by the ratios of the variances for spike length, spikelets per spike, 1000-grain weight, grain yield per plant, and biological yield, which were less than unity. Therefore, it appeared that the inheritance of all traits except days to heading was controlled by additive gene action.

Proportional contribution of genotypes to total variance: In proportional contribution to the total variance in F_1, the lines had a maximum share for traits, i.e., days to heading (42.9%), Spike length (38.1%), spikelet per spike (40.1%), grain yield per plant (51.44%) and biological yield (57.0%), shown in Table 6. Similarly, for 1000 grain weight (40.8%), the share of line-by-tester cross combinations was greater than that of lines and testers. Moreover, in the F_2 generation, the lines had maximum share for traits, i.e. spike length (38.1 %), grain yield per plant (56.47%) and biological yield (59.0%) (Table 6). Furthermore, for days to heading (34.6%), spikelet per spike (39.4%), and 1000 grain weight (41.1%), the contribution of line-by-tester populations was higher compared to lines and testers.

Discussion

The genotypes (parental lines, testers, F_1 and their F_2 populations) exhibited significant ($p \leq 0.01$) differences for earliness, morphological and yield traits, confirming that genotypes had larger genetic variation and more chances of improvement through intensive selection. Days to heading are an important Parameter for earliness in grain yield. Early heading is desirable, and plant architects are keen to create new varieties of wheat with early maturity. As a result of days to heading, the short time for grain filling eventually led to a reduction in grain weight (Ullah *et al.*, 2018). Similarly, in wheat, days to heading is an important trait that contributes towards high yield, and early heading is desirable for wheat breeders because grain filling duration increases, which eventually increases yield (Iqbal *et al.*, 2021). In the present study, the parental cultivars Tajaban, Benazir-13 and PR-139 exhibited significant ($p \leq 0.01$) differences for earliness. In testers, the minimum value for days to heading 114 was recorded in Borlaug-100. The minimum days to heading were reported for Inqilab-91×T-11(F_1 generation) and PR-139×T-11 (F_2 population), which could be used in future breeding programs for earliness.

In the current study, first filial generation, i.e. PR-137×Pirsabak-15, PR-137×Zarghoon-21 and F_2 populations, i.e., PR-137×Borlaug-100, Tajaban×Borlaug-100 and Inqilab-91×T-11 Lines PR-137, PR-139, Inqilab-91, Auqab-2000 were found to produce early flowers and were believed to be specific and general combiners for earliness. Combining ability studies conducted earlier also revealed significant variability among the parental cultivars and their F_1 and F_2 populations for various agronomic parameters in wheat (Adhikari *et al.*, 2020; Dhoot *et al.*, 2020). The parental cultivars and F_1 and F_2 populations revealed significant differences for earliness and yield traits by evaluating through LinexTester mating design in wheat (Aslam *et al.*, 2014; Rauf *et al.*, 2023). Similarly, wheat genotypes with the least days to flowering and maturity could be used as a gene source for developing early-maturing wheat genotypes in future breeding programs (Murugan & Kannan, 2017; Rahul, 2017). The current study identified promising general combiners for grain yield per plant among parental genotypes, including lines PR-137, PR-139, Pirsabak-15 and T-11. The best specific combiner in F_1 cross combinations were Inqilab-91×Borlaug-100 and PR-138×Taskeen-22, whereas, in F_2 populations, SKD-1×Zarghoon-21, Tajaban×Borlaug-100 and PR-139×T-11 were the best specific populations. These findings are consistent with previous research, which has shown that grain yield in wheat is significantly influenced by traits such as tillers, spike characteristics and seed index (Ingle *et al.*, 2018). Additionally, studies have reported substantial variations in F_1 and F_2 populations resulting in increased grain yield compared to parental genotypes (Afridi *et al.*, 2019). Furthermore, grain yield is positively correlated with harvest index, with genotypes exhibiting higher harvest indices tending to have increased grain yields (Jain & Sastry, 2012). Combining ability analysis has also revealed that lines and testers can exhibit positive general combining ability for grain yield and its components, while F_1 and F_2 populations can display positive specific combining ability (Aslam *et al.*, 2014). Moreover, significant positive general combining ability for grain yield and harvest index has been observed in parent cultivars and some F_1 populations (Saeed & Khalil, 2017).

Results showed that lines (PR-138, PR-139, PR-139 and SKD-1), Testers (T-11, Zarghoon-21 and Borlaug-100), F_1 hybrids (SKD-1×T-11) and F_2 population (Tajaban×Zarghoon-21) were the best general and specific combiners for spike length. A similar result of the dominance of gene action in spike length was also published by Guo *et al.*, (2024). For spike length, an over-dominance type of gene action was also recorded by Rabbani *et al.* (2009) and Ullah *et al.* (2011), while Zeyu *et al.*, (2024) reported partial dominance gene action in wheat genotypes. Guo *et al.*, (2024) and several other researchers reported both additive and dominant gene action for spike length in bread wheat. In spikelets per spike, the best general and specific combiners were PR-139, in lines, Pirsabak-15 in tester, Tajaban×Borlaug-100 in F_1 and SKD-1×Pirsabak-15 in F_2 crosses. The spikelets per spike showed dominant gene action. Metwali *et al.*, (2014) conducted a 5×5 diallel mating experiment to investigate the genetic structure of 5 barley cultivars, their F1 and F2 progenies, and to assess these genotypes under both normal and salinity stress conditions. “significant” “additive” and “dominance” effect of genes were observed for spikelets per spike, spikes per plant, spike length, grains per spike, chlorophyll a, b contents, calcium and magnesium content. These findings were in accordance with those of Ullah *et al.*, (2011), who also reported an equal proportion of dominant and recessive genes for spikelet spike^{-1} in bread wheat. The present findings were also supported by the study of Nazir *et al.*, (2014), which conducted an experiment using 5×5 diallel crosses in wheat and reported that hybrid plants showed significant effects on spikelet per spike and other parameters.

Similarly, in 1000-grain weight, the best general combiners were PR-137 and PR-138 among lines; Tajabanand, Zarghoon, Taskeen among testers;

Tajaban×Taskeen-22 among F_1 crosses and PR-137×Borlaug100, SKD-1×Pirsabak-15 in F_2 crosses. Similar results of line by testers of different wheat varieties were also reported by Ahmad *et al*., (2017) for 1000-grain weight in bread wheat. Ljubičić *et al*., (2017) also studied economic and grain-related traits using 5×5 diallel crosses involving wheat cultivars/lines viz., Millat-11, Punjab-11, 9466, 9469 and 9459-1. Results showed that some quantitative traits, such as peduncle length, 100-grain weight, and grain yield, were significant. Similar results of dominant genes for 1000-grain weight were also reported by Ullah *et al*., (2011) in different bread wheat genotypes under rainfed conditions. Similar results with dominant and recessive gene distribution in wheat were also published by Rabbani *et al*., (2009). Overall, there were significant ($p \leq 0.01$) variations 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).

PR-137, PR-138, PR-139, Inqilab-91 and testers T-11 were regarded to be the best general combiners and PR-137×Pirsabak-15, PR-139×T-11, Inqilab91×T-11, Auqab-2000×T-11, Tajaban×T-11, Benazir-13×Zarghoon-21 and Benazir-13×Taskeen-22 were the best specific combiners in F_1 cross combinations. Similarly, F_2 populations Auqab-2000×T-11, Tajaban× T-11, PR-139×T-11, Inqilab-91×T-11, Inqilab-91×Taskeen-22, Tajaban×T-11, PR-139×Borlaug-100 and Benazir-13×Taskeen-22, PR-137×Pirsabak-15 were the best specific combiners for biological yield. Our present results were also supported by the study of Akbari *et al*., (2013) in a 6 × 6 diallel of 30 F_2 populations along with their parents to estimate genetic parameters for grain yield and biological yield. In wheat breeding programs for the said traits, parental genotypes with desirable GCA effects were regarded as the best parental genotypes and good general combiners (Afridi *et al.,* 2017). However, F_2 populations with significantly acceptable effects, on the other hand, were deemed the greatest combiners for biological yield. Moreover, our results were in agreement with Patel *et al*., (2020) & Elmyhun *et al*., (2020), who reported a significant negative GCA effect with a desirable p-value ($p \leq 0.01$) in lines and non-additive gene action, which was primarily involved for biological yield.

Conclusion

Our findings reflect incremental improvements across generations for various earliness and yield-related traits in parental lines and their F_1 and F_2 offspring. The maximum 1000-grain weight was reported for PR 137×Borlaug-100 (53.15 g and 55.30 g) in both generations. Similarly, Benazir-13 revealed a maximum grain yield per plant (120g). Regarding combining ability analysis for 1000-grain weight, the promising GCA was reported in Tajaban, while the promising SCA was reported for Tajaban×Taskeen-22 in F_1 and PR-137×Borlaug-100 in F_2 generation. Moreover, for grain yield per plant, the promising general combiners were PR-137 and PR-139, while the best specific combiner was Inqilab-91×Borlaug-100 (F_1) and SKD-1×Zarghoon-21 (F_2). The ratios of GCA to SCA variances and degree of dominance showed that the inheritance of all traits except days to heading was controlled by non-additive gene action. This suggests that selection for improvement should be delayed to later generations for better results. Thus, the above crosses are considered the best wheat varieties and could be used in the next generation to release the best wheat varieties.

Novelty Statement: The wheat genotypes PR-137, PR-139×T-11 and Tajaban×Pirsabak-15 were the best general combiners for spike length. Tajaban and Tajaban × Taskeen-22 were the best general combiners and SCA, respectively, for 1000-grain weight. Genotypes PR-137, Inqilab-91×Borlaug-100 and Tajaban×Borlaug-100 had the best GCA and SCA. The genotypes PR-139, Tajaban×Borlaug-100 and SKD-1×Pirsabak-15 were the best general combiners for spikelets of spike^{-1}.

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Data Availability: All data generated during this study are mentioned in this article.

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