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(Original Article)

Genetic Components and Combining Ability for Grain Yield and Yield Components Using Line × Tester Analysis in Bread Wheat (*Triticum aestivum L.*)

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Abstract

Eight bread wheat (*Triticum aestivum L.*) genotypes included 6 lines and 2 testers were crossed in a line × tester mating design. The 12 F_1's and their parents were evaluated for grain yield/plant and 9 agronomical traits. The results indicated highly significant genetic variability for all studied traits. Line Q8 was the best combiner for early flowering date, grains/spike, grain weight/spike and 1000-kernel weight traits. While line Q10 was the best parent for tallness and grain yield/plant. The T1 (PI330456) was a potential tester parent for spike length, spikelets/spike, stem diameter, grains/spike, and grain yield/plant. While T2 (PI330458) was good combiner for earliness and 1000-kernel weight. Several hybrids showed highly significant positive specific combining ability (SCA) for some studied traits. Mother lines played a positive influential role towards plant height, spike length, tillers/plant and grain weight/spike. While paternal testers influence was predominant for days to flowering, spikelets/spike, stem diameter, grains/spike, 1000-kernel weight and grain yield/plant. Additive gene action was found for plant height, spikelets/spike, stem diameter grains/spike and grain weight/spike. While, for days to flowering, spike length, tillers/plant, 1000-kernel weight and grain yield/plant, non-additive gene action was predominant. High estimates of broad- and narrow-sense heritability for grains/spike, grain weight/spike, plant height and 1000-grain weight. Maximum genetic advance along with high narrow-sense heritability were observed for grains/spike and plant height reflecting that a reliable selection for these traits can be made on the basis of phenotypic performance in early generations. Highly significant positive correlations were observed between most studied traits.

Keywords: *Wheat; Combining ability; Heritability; Genetic advance and correlation.*

Introduction

Common bread wheat (*Triticum aestivum L.*) is one of the main crops widely cultivated not only in Egypt but also all over the world as a major food cereal. it is a highly self-pollinated and annual cereal crop. Recently in Egypt, cereal crops production in 2022 season is estimating an average 23.8 million tons. Six percent (9.5 million tons) of this total was increased in 2022 above the average wheat produced in 2021 (FAOSTAT, 2021). Wheat production for growing population

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under changing conditions has some accompanying problems, which can be compensated by genome modifications using crossbreeding. A successful breeding program is based on the selection of good parents, and their progenies in the breeding program. The best selection of the parents provides genetic variability and their combining ability effects leads to achieve the targets (Akbar *et al.*, 2009; Abro *et al.*, 2021).

The role of combining ability is to determine the parents, crosses, and the appropriate breeding program to be followed to select the desired segregates (Salgotra *et al.*, 2009). General combining ability (GCA) can determine superior combiner parents where Specific combining ability (SCA) effect helps in identifying good cross combinations that may eventually lead to the development of the hybrids (Krystkowiak *et al.*, 2009; Abro *et al.*, 2016) Various breeding approaches have been used to select parents and crosses in breeding programs. Line × tester analysis provided by Kempthorne (1957) is a powerful tool available for estimating GCA and SCA to select the best parents and crosses (Salgotra *et al.*, 2009; Abro *et al.*, 2021). It is important to predict the response to selection in the early generations.

Additive gene actions are fixable while non-additive gene actions cannot be reliably fixed (Xiang and Li, 2001; Iqbal *et al.*, 2007). Line × tester analysis was used to study combing ability and genetic analysis for grain yield and its associated traits in wheat by several researchers (Gupta and Ahmed 1995, Saeed *et al.*, 2001; Fellahi *et al.*, 2013 and Farooq *et al.*, 2018). In several studies on wheat, Gupta and Ahmed (1995), Ahmed and Khaliq (2016) and Joshi *et. al.* (2003) noticed that mostly of genetic variances in grain yield as well as yield components were under the control of additive gene effects. While, Suleyman and Akguni (2007) reported that grain yield and most of the traits were under the control of non-additive gene action.

Heritability which in broad-sense ($H^2{}_{bs}$) include both additive and non-additive gene effects and in narrow-sense ($H^2{}_{ns}$) included additive effects (Saleem *et al.*, 2016; Kumar *et al.*, 2022) heritability estimate for a particular trait helps breeders to determine the best selection program to be followed under a particular condition. Thus, increasing the yield. Estimates of heritability combined with expected genetic advance are more useful than the value of heritability alone in predicting the resulting effect of selecting the superior genotypes (Mangi *et al.*, 2008; Verma *et al.*, 2007 and Saleem *et al.*, 2016).

The correlation coefficient provides information about the associations between plant traits, hence the selection of traits that are positively correlated with yield can help the breeder to obtain lines with high yield (Ali *et al.*, 2008; Saleem *et al.*, 2016).

The present study was conducted to evaluate wheat lines and their hybrids in terms of combining ability, heritability and genetic advance by a line × tester analysis, and correlations for yield and its contributed characters in bread wheat (*Triticum aestivum L.*).

Materials and methods

Plant materials and procedure

The present investigation was carried out at the genetics Experimental Farm, faculty of agriculture, Assiut University under normal field conditions. The plant material comprises eight bread wheat (*Triticum aestivum L.*) genotypes. Six wheat lines Q7, Q8, Q9, Q10, Q11 and Q12, designated as lines, were used as females, and the two lines PI330456 (T1) and PI330458 (T2) designated as testers, were used as males. The tested genotypes were kindly obtained from the Genetics Department, Faculty of Agriculture, Assiut University. In 2019/2020 season, the parents were crossed to produce twelve F1 hybrids by line × tester mating design (Kempthorne, 1957). In 2020/2021 season, the F_1 seeds along with their parents were sown in the field in a Randomized Complete Block Design (RCBD) with three replications. Recommended cultural practices were followed to raise a good crop.

Data Collection

Five plants from each entry (excluding border plants) were chosen before heading and data were recorded for ten traits viz., the number of days to flowering (days), Plant height (cm), Spike length (cm), number of Spikelets/spike, No. fertile tillers/plant, stem diameter (mm), number of grains/spike, grain weight/spike (g), 1000- kernel weight (g), and grain yield/plant (g).

Statistical analysis

The recorded data of the traits were subjected for analysis of variance (ANOVA) according to (Steel and Torrie, 1980) to test significant differences among genotypes for studied traits. General combining ability (GCA) effects for parents (lines and testers) and specific combining ability (SCA) effects for hybrids were estimated according to (Singh and Chaudhary, 1977). Ratios of GCA/SCA (Kempthorne, 1957) variance were used to determine the additive versus non-additive gene actions (Verma and Srivastava, 2004). Additive and dominance genetic variances were calculated using GCA and SCA variances as described by (Fellahi *et al.*, 2013). Genotypic, phenotypic and environmental variances were calculated by the formula provided by (Uguru, 2005). Broad- and Narrow-sense heritability estimates were calculated from these variances as per (Panse and Sukhatme, 1954), which were rated as low (0-29%), moderate (30-59%) and high (60% or above) heritable. Expected genetic advance with one selection cycle and 5 % selection intensity was calculated by the formula of (Panse and Sukhatme, 1954). All these statistical analyses were performed using the Microsoft Excel 2010 while phenotypic correlation was built under Statistical Package Social Science (SPSS) software.

Table 1. Mean squares from ANOVA for 10 wheat traits derived from line × tester analysis

Source of Variation	d.f.	Days to flowering	Plant height	Spike length	Spikelets per Spike	Tillers per Plant	Stem diameter	Grains per spike	Grain weight per spike	1000-kernel weight	Grain yield / Plant
Replication	2	112.47**	49.89**	0.15^{NS}	1.28^{NS}	1.08^{NS}	0.03^{NS}	0.23^{NS}	0.02^{NS}	21.03**	0.80^{NS}
Genotypes	19	186.05**	1735.79**	8.05**	22.75**	64.17**	0.36**	883.54**	2.37**	95.20**	447.72**
Parents (P)	7	327.05**	3563.17**	19.35**	47.87**	54.51**	0.38**	1144.56**	3.21**	110.56**	90.02**
Parents vs Crosses	1	490.00**	4105.58**	3.47**	49.93**	454.13**	1.17**	471.21**	6.99**	277.06**	6405.75**
Crosses (C)	11	68.70**	357.47**	1.28**	4.29**	34.86**	0.27**	754.93**	1.41**	68.89**	133.71**
Lines (L)	5	36.73^{NS}	735.43**	1.27^{NS}	3.95^{NS}	37.98^{NS}	0.11^{NS}	456.32**	1.69**	18.35^{NS}	53.50^{NS}
Testers (T)	1	498.78**	48.38^{NS}	5.26*	22.99**	20.65^{NS}	2.18**	5881.19**	6.99**	585.80**	523.26^{NS}
Lines × Testers	5	14.64^{NS}	41.33**	0.50**	0.88^{NS}	34.58**	0.04^{NS}	28.29**	0.02^{NS}	16.03**	136.01**
Error	38	6.12	9.05	0.16	0.58	1.00	0.02	7.45	0.02	3.64	8.17

**highly Significant at 0.01 level., * Significant at 0.05 level., ^{NS} non-Significant

Results and discussion

Estimation of mean square values

The analysis of variance revealed to highly significant differences ($p \leq 0.01$) among evaluated genotypes for all studied traits while non-significant differences among replications for all studied traits except three traits viz., NO. days to flowering, Plant height, and 1000- kernel weight which were highly significant (Table 1). These results indicated the presence of sufficient genetic variability among lines, testers as well as in hybrids to assess the genetic analysis and combining ability effects. These results were in agreement with those obtained by (Abro *et al*., 2021).

The results also revealed that lines, testers and their interaction displayed significant differences in some traits while not-significant in the others. Significant differences were found between lines in plant height, grains/spike and weight of grains per spike (Table 1). While testers showed highly significant differences in days to flowering, spikelet/spike, stem diameter, grains/spike, weight of grains/spike and 1000-kernel weight. These results in agreement with those obtained by (Farooq *et al*., 2018).

The interaction between lines and testers (L x T) was significant in Plant height, Spike length, No. tillers/plant, No. grains/spike, 1000- kernel weight and grain yield. Significant differences in (Lines × testers) interaction for these traits indicate that SCA is highly related to the expression of these traits and provides the importance of dominance or non-additive variances for all traits (Jayasudha and Sharma, 2009 and Rahimi *et al*., 2010).

Study of mean values among parents and their F_1 crosses

Genetic variations and mean performances can be exploited for genotypic evaluation of parents and hybrids (Fig.1). The overall mean values in the six mother lines were 92.00 days (days to flowering), 131.84 cm (plant height), 16.66 cm (spike length), 27.21 (spikelets/spike), 9.16 (tillers/plant), 4.43 mm (stem diameter), 78.92 (grains/spike), 3.74 g (grain weight/spike), 44.99 g (1000- kernel weight) and 25.25 g (grain yield/plant).

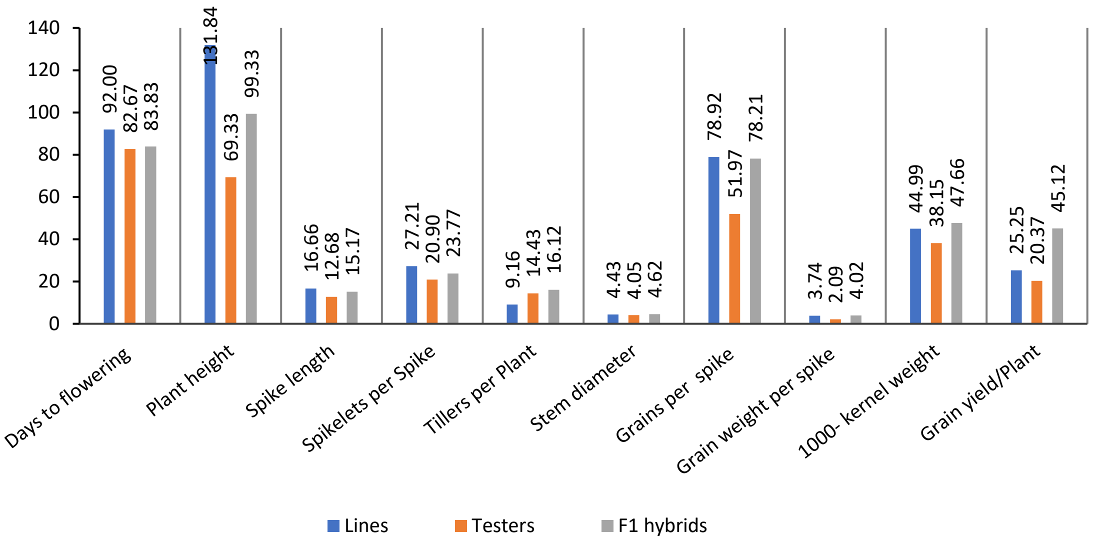

Fig.1. Overall means of lines, testers and F_1 hybrids for ten studied traits

Whereas overall mean values in two parental testers were 82.67 days, 69.33 cm, 12.68 cm, 20.90, 14.43, 4.05 mm, 51.97, 2.09 g, 38.15 g and 20.37 g for Days to flowering, plant height, spike length, spikelet/spike, tillers/plant, stem diameter, grains/spike, grain weight/spike, 1000- kernel weight and grain yield/plant, respectively. The differences between average mean values for lines and testers indicated lines to be the best for all studied traits except No. days to flowering and tillers per plant.

The results of mean performance among eight parents indicated that line Q7 was the best over other parents for spike length (18.87 cm), grain yield/plant (33.65 g) and stem diameter (4.77 mm) while line Q8 was prominent for more of grain characters like grains/spike (93.93), grain weight/spike (4.70 g) and 1000- kernel weight (51.67 g). Lines Q9, Q11 and tester T2 were the best parents for spikelets/spike (29.60), plant height (159.57 cm) and tillers/plant (18.07), respectively. While the T2 tester was superior for earliness and recorded (76.00) days to flowering (Table 2).

Unlike parents, average F_1 hybrids means (Table 3 , Fig.1) were higher than the parental lines for No. of tillers/plant (16.12), stem diameter (4.62 mm), grain weight (4.02 g), 1000-kernel weight (47.66g) and grain yield/plant (45.12). The hybrid (T1 x Q8) observed to have the highest mean values for grains/spike (102.2) and grain weight/spike (5.29 g), while (T1 x Q9) for stem diameter (5.13 mm). The cross (T1 x Q10) showed highest value for spike length (16.10 cm) while, (T1 x Q11) for spikelets/spike (25.56). The hybrid (T1 x Q12) exceeded other hybrids in No. of tillers/plant (25.56) and grain yield (57.12 g). When the tester T2 crossed with Line Q8, the hybrid revealed the highest 1000-grain weight (53.31). The minimum No. days to flowering (77.0 days) was obtained by (T2 x Q9), while (T2 x Q11) showed the maximum plant height (112.83cm)

Table 2. Mean performance of eight wheat genotypes for 10 different agronomic traits

Genotypes	Days to flowering	Plant height	Spike length	Spikelets per Spike	Tillers per Plant	Stem diameter	Grains per spike	Grain weight per spike	1000- kernel weight	Grain yield /Plant
Q7	99	116.27	18.87	29.33	9.67	4.77	92.53	4.61	45.39	33.65
Q8	79	132.73	15	25.2	5.33	4.53	93.93	4.7	51.67	24.49
Q9	100	112.9	17.77	29.6	7.87	4.6	89.6	3.73	39.7	23.12
Q10	96	157.87	16.17	28.6	7.93	4.3	67.27	3.26	45.78	18.64
Q11	99.67	159.57	18.47	28.47	8.6	4.53	75.4	3.62	44.34	21.91
Q12	78.33	111.73	13.67	22.07	15.53	3.83	54.8	2.53	43.04	29.67
T1	89.33	69.57	12.4	22.87	18.07	4.3	64.73	2.2	30.73	23.86
T2	76	69.1	12.97	18.93	10.8	3.8	39.2	1.98	45.57	16.88

Table 3. Mean performance for twelve F1 hybrids

F1 hybrid	Days to flowering	Plant height	Spike length	Spikelet per Spike	Tillers per Plant	Steam diameters	Grains per spike	Grain weight per spike	1000- kernel weight	Grain yield /Plant
Q7 × T1	86.67	95.23	15.67	24.47	14.87	5.03	89.73	4.56	43.77	44.93
Q8 × T1	83	109.3	15.53	24.2	13.53	4.87	102.2	5.29	48.42	51.78
Q9 × T1	87.33	90.83	15.8	24.93	16.93	5.13	90.8	4.25	43.4	47.13
Q10 × T1	88.67	111.93	16.1	25.27	13.93	4.83	93.27	4.56	43.82	45.48
Q11 × T1	93	105.44	15.22	25.56	16.22	4.56	94.78	4.53	40.4	47.15
Q12 × T1	86.67	90.2	14.97	23	25.6	4.77	77	3.6	41.97	57.12
Q7 × T2	82	89.67	15.4	23.67	16.6	4.37	68.4	3.69	49.87	43.77
Q8 × T2	78	105.7	15.33	23.4	12.93	4.33	80.13	4.49	53.31	41.63
Q9 × T2	77	82.97	14.47	22.13	13.8	4.57	65	3.35	48.42	32.69
Q10 × T2	83.67	110.3	14.9	23.43	18.27	4.3	63.13	3.49	52.43	51.42
Q11 × T2	81	112.83	14.97	23.6	14.87	4.37	63.73	3.57	52.89	41.85
Q12 × T2	79	87.57	13.67	21.6	15.87	4.3	50.33	2.88	53.26	36.48
L.S.D. at 5 %	3.4	4.14	0.55	1.05	1.38	0.19	3.76	0.21	2.63	3.94
L.S.D. at 1 %	4.9	5.97	0.79	1.51	1.98	0.28	5.41	0.3	3.78	5.67

Estimation of GCA and SCA effects

Although mean performance can be used to exploit the genetic variability, but it is not satisfactory to rely on mean values of complex genetic mechanisms of inheritance in nature. These abilities are estimated in terms of the effects of GCA and SCA effects among the hybrids and the parents (Fellahi *et al*., 2013; Farooq *et al*., 2018).

The significance for GCA and SCA effect was estimated by comparison with the t-values to obtain more stable and reliable results. Among lines (Table 4), line Q7 was good combiner for spike length, while line Q8 was the best combiner for earliness flowering, No. grains per spike, grain weight/spike and 1000- kernel weight and good combiner for Plant height. Line Q9 was the best combiner for shortness and stem diameter, while line Q10 was the best combiner parent for tallness, grain yield per plant and good combiner for spike length and spikelets/spike. Line Q11 was the best combiner for spikelets/spike and highly significant combiner for plant height. Line Q12 was prominent combiner for No. tillers/plant and highly significant combiner for shortest plant height. With respect to the testes (Table 4), the tester T1 was a potential tester parent for spike length, spikelets/spike, tillers/plant, stem diameter, grains/spike, grain weight/spike and grain yield/spike. While T2 was good tester combiner for early date of flowering and 1000- kernel weight.

Table 4. General combining ability (GCA) effects for six lines and two testers of wheat in the studied traits

Genotypes (Parents)	Days to flowering	Plant height	Spike length	Spikelets per Spike	Tillers per Plant	Stem diameter	Grains per spike	Grain weight per spike	1000-kernel weight	Grain yield /Plant
Q7	0.50	-5.60**	2.22*	0.95	-0.87	1.42	1.04	1.64	-1.08	-0.66
Q8	-3.30**	6.65**	1.61*	0.09	-7.40**	-0.32	11.76**	14.23**	4.11**	1.36
Q9	-1.65	-10.12**	-0.23	-0.77	-1.77*	4.03**	-1.50	-3.74**	-2.25**	-4.46**
Q10	2.31*	9.60**	2.12*	1.87*	0.02	-0.90	0.27	0.02	0.59	2.86**
Q11	3.14**	7.99**	-0.47	2.60**	-1.34	-2.74**	1.21	0.42	-1.31	-0.53
Q12	-0.99	-8.51**	-5.25**	-4.74**	11.37**	-1.48	-12.78**	-12.57**	-0.06	1.44
T1	6.39**	1.64	4.07**	4.46**	3.21**	7.43**	19.87**	12.50**	-8.97**	5.66**
T2	-6.39**	-1.64	-4.07**	-4.46**	-3.21**	-7.43**	-19.87**	-12.50**	8.97**	-5.66**
Lines S.E.	1.01	1.23	0.16	0.31	0.41	0.06	1.11	0.06	0.78	1.17
Testers S.E.	0.58	0.71	0.09	0.18	0.24	0.03	0.64	0.04	0.45	0.67

**highly Significant at 0.01 level., * Significant at 0.05 level. (1-tailed)

Singh *et al*., (2005) reported that the better performance of a specific cross combination can be achieved in wheat by combining dominant alleles from the good combiners and the recessive alleles from the poor combiners. In other crops, Verma and Srivastava (2004) found in rice that the effects of SCA were positively correlated with hybrids where one parent is common as a good general combiner.

Likely, Tiwari *et al*., (2011) reported that the better performance of a specific cross combination can be achieved in wheat by combining the dominant alleles from the good combiners whereas the recessive alleles from the poor combiners. In rice, Verma and Srivastava (2004) showed that the effects of SCA had positive correlation with hybrids, where one parent is common as a good general combiner.

However, the effects of SCA are not remarkably supportive in improving self-pollinating crops, except in cases where exploitation of heterosis is feasible, potent homozygous lines can be selected in transgressive segregants, which can only be possible by selecting the best hybrids (Fellahi *et al*., 2013). Highly significant SCA values were observed by hybrid (T1 x Q12) and (T2 x Q10) for tillers/plant and grain yield/plant, (T2 x Q7) for tillers/plant, (T2 x Q11) for tallest plants (Table 5).

Table 5. Specific combining ability effects (SCA) for F_1 hybrids

F_1 Hybrids	Days to flowering	Plant height	Spike length	Spikelets per Spike	Tillers per Plant	Stem diameter	Grains per spike	Grain weight per spike	1000-kernel weight	Grain yield /Plant
T1 x Q7	-0.97	0.94	-1.08	-0.91	-2.81**	1.07	-1.34	-0.07	0.89	-1.96*
T1 x Q8	-0.86	0.37	-1.23	-0.91	-0.5	0.25	-1.22	-0.47	1.44	0.77
T1 x Q9	1.01	1.6	1.23	1.37	1.4	0.46	-0.98	0.13	1.38	2.06*
T1 x Q10	-0.86	-0.2	1.02	0.27	-5.06**	0.25	1.45	1.06	-0.25	-4.11**
T1 x Q11	1.6	-2.80**	-1.11	0.41	-0.14	-1.87*	1.74*	0.44	-2.01*	-0.71
T1 x Q12	0.08	0.09	1.16	-0.23	7.11**	-0.16	0.35	-1.1	-1.46	3.94**
T2 x Q7	0.97	-0.94	1.08	0.91	2.81**	-1.07	1.34	0.07	-0.89	1.96*
T2 x Q8	0.86	-0.37	1.23	0.91	0.5	-0.25	1.22	0.47	-1.44	-0.77
T2 x Q9	-1.01	-1.6	-1.23	-1.37	-1.4	-0.46	0.98	-0.13	-1.38	-2.06*
T2 x Q10	0.86	0.2	-1.02	-0.27	5.06**	-0.25	-1.45	-1.06	0.25	4.11**
T2 x Q11	-1.6	2.80**	1.11	-0.41	0.14	1.87*	-1.74*	-0.44	2.01*	0.71
T2 x Q12	-0.08	-0.09	-1.16	0.23	-7.11**	0.16	-0.35	1.1	1.46	-3.94**
S.E. (SCA)	1.43	1.74	0.23	0.44	0.58	0.08	1.58	0.09	1.1	1.65
S.E.(gi-Gj) for lines	1.43	1.74	0.23	0.44	0.58	0.08	1.58	0.09	1.1	1.65
S.E.(gi-Gj) for Tester	0.82	1	0.13	0.25	0.33	0.05	0.91	0.05	0.64	0.95
S.E.(S_{ij} - S_{kj})	2.02	2.46	0.33	0.62	0.82	0.11	2.23	0.12	1.56	2.33

**highly Significant at 0.01 level., * Significant at 0.05 level. (1-tailed)

The hybrid T1 x Q11 showed highly significant negative value for shortness trait. Significant positive values for SCA were also recorded for "T1 x Q9" (grain yield/plant), "T1 x Q11" (grains/spike), "T2 x Q7" (grain yield/plant), and "T2 x Q11" in stem diameter and 1000-kernel weight (Table 5). Ahmad and Khaliq (2016) found significant SCA effect for grain yield and 1000-kernel weight.

Proportional contribution of lines and testers

The corresponding proportion of lines, testers as well as their interactions for the studied traits is shown in (Fig.2). Lines played a positive influential role towards plant height (93.51%), spike length (45.01%), tillers/plant (49.52%) and grain weight/spike (54.46 %), which indicate that maternal effect was predominant for these traits, these results are in harmony with the findings of Rashid *et al.* (2007).

While paternal influence was predominant for days to flowering (66.01%), spikelets/spike (48.74%), stem diameter (73.94%), grains/spike (70.82%), 1000-kernel weight (77.31%) and grain yield/plant (35.58%). The proportional contribution of paternal and maternal influence was very high in the interaction (line × tester) for tillers/plant (45.09%) and grain yield/plant (46.24%). High proportional contribution of (LxT) was observed for spike length (17.63%) followed by 1000-kernel weight (10.58%), days to flowering (9.69%) and spikelets/spike (9.35%). These results indicated that lines, testers and hybrids contribute most of the genetic variation in the expression of these traits. Similar conclusion was also reached by Fellahi *et al*., (2013).

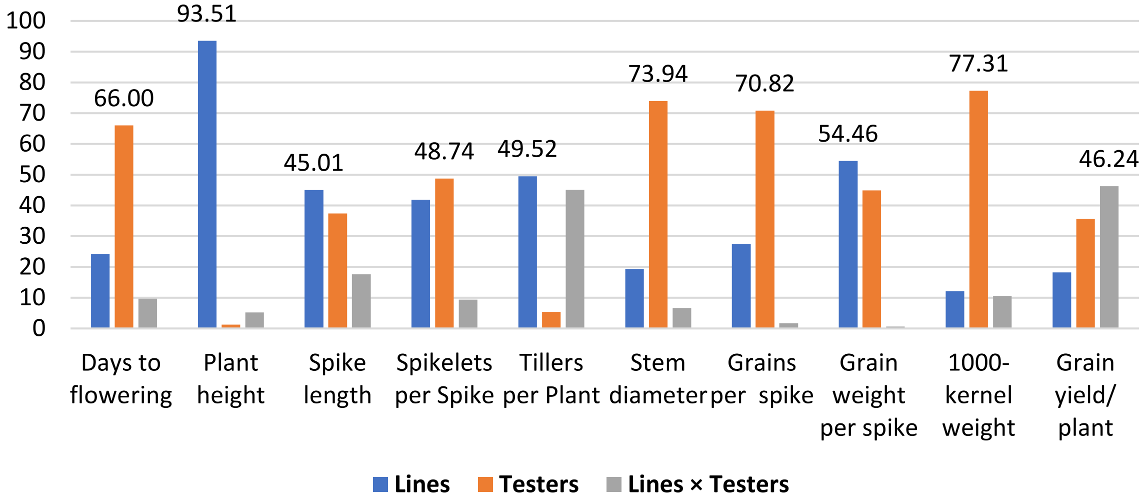

Fig. 2. Proportional contribution of lines, testers and their interaction towards total genetic variation

Genetic components

Line by Tester design is used to determine the nature of gene action by ratio GCA/SCA effects, rather than their variances (Table 6). for plant height, spikelets/spike, stem diameter, grains/spike and grain weight/spike, the GCA variance $(\sigma^2 GCA)$ was higher than SCA variance $(\sigma^2 SCA)$, this indicating additive gene action for these traits. Observed additive gene action for (plant height and days to flowering) and spikelets/spike traits by (Shah *et al.*, 2019) and by (Roy *et al.*, 2021), respectively. In the same direction, Borghi and Perenzin (1994) suggested additive effects for yield traits in wheat. Unlike the other studied traits viz, Days to flowering, spike length, tillers/plant, 1000-kernel weight and grain yield displayed the predominant of non-additive gene action. Similarly, (Fellahi *et al.*, 2013; Farooq *et al.*, 2019; Din *et al.*, 2021), they observed non-additive effect for spike length, tillers/plant, grain yield and 1000-kernel weight. Also, Gnanasekaran *et al.,* (2006) they exhibited additive gene action for grain 1000-grain weight and height of plant. The high multitude of non-additive gene action indicated that the selection of superior plants should be postponed to a later generation (Fellahi *et al.*, 2013).

Table 6. Genetic components, heritability and genetic advance for ten wheat traits

Genetic Variation	Days to flowering	Plant height	Spike length	Spikelets per Spike	Tillers per Plant	Stem diameter	Grains per spike	Grain weight per spike	1000-kernel weight	Grain yield / Plant
$\sigma^2 GCA$	2.06	12.07	0.03	0.13	0.01	0.01	27.75	0.05	2.02	-0.09
$\sigma^2 SCA$	2.84	10.76	0.11	0.10	11.19	0.01	6.95	0.001	4.13	42.61
GCA/SCA	0.73	1.12	0.27	1.28	0.001	1.32	3.99	69.49	0.49	-0.002
σ^2_A	4.13	24.15	0.06	0.26	0.02	0.02	55.51	0.11	4.04	-0.18
σ^2_D	2.84	10.76	0.11	0.10	11.19	0.01	6.95	0.001	4.13	42.61
σ^2_g	6.97	34.91	0.17	0.36	11.22	0.02	62.45	0.11	8.17	42.44
σ^2_e	6.12	9.05	0.16	0.58	1.00	0.02	7.45	0.02	3.64	8.17
σ^2_p	13.09	43.96	0.33	0.94	12.22	0.04	69.90	0.13	11.81	50.61
h^2_{bs} %	53.27	79.42	51.98	38.54	91.80	54.95	89.35	82.70	69.19	83.85
h^2_{ns} %	31.55	54.94	18.06	27.71	0.17	39.87	79.41	82.11	34.19	-0.35
GA (5%)	3.97	10.85	0.62	0.77	6.61	0.24	15.39	0.61	4.90	12.29

σ^2GCA : variance due to GCA, σ^2SCA : variance due to SCA, σ^2GCA /σ^2SCA : GCA/SCA variance ratio, σ^2_A: additive variance, σ^2_D: dominance variance, σ^2_g : genetic variance, σ^2_e: environmental variance (= M.Se), (σ^2_P): phenotypic variance, (h^2_{bs}): broad sense heritability, (h^2_{ns}): narrow sense heritability and GA (5%): genetic advance with 5% intensity of selection**.**

The results in (Table 6) showed that the genotypic variance (σ^2_P) was higher than its corresponding environmental variance, displaying high estimates of broad- and narrow-sense heritability (H^2_{bs} = 89.35, H^2_{ns} = 79.41 %) for grains/spike, (h^2_{bs} = 82.70, h^2_{ns} = 82.11 %) for grain weight/spike followed by (H^2_{bs} = 79.42, H^2_{ns} = 54.94 %) in plant height and (H^2_{bs} = 69.19, H^2_{ns} = 34.19 %) in 1000-grain weight. High broad-sense heritability along with very low narrow-sense were found for number of tillers/plant (H^2_{bs} = 91.80, H^2_{ns} = 0.17 %) and grain yield/plant (H^2_{bs} = 83.85, H^2_{ns} = -0.35 %), which may be due to the very low amount of additive genetic variance (Table 6). Moderate heritability was perceived for stem diameter (H^2_{bs} = 54.95, H^2_{ns} = 39.87 %) and days to flowering (H^2_{bs} = 53.27, H^2_{ns} = 31.55 %). Moderate H^2_{bs} along with low H^2_{ns} were found for spike length (H^2_{bs} = 51.98, H^2_{ns} = 18.06 %) and spikelets/spike (H^2_{bs} = 38.55, H^2_{ns} = 27.71 %).

Heritability estimates are useful to help in deciding which characters to consider during selection, but the selection based on heritability alone may be limited the progress, as it is subject to changes with environment and materials (Athwal and Gain Singh, 1966; Farooq *et al.*, 2018).

In other words, estimates of heritability along with genetic advance are more advantageous than the value of heritability alone in predicting the resulting effect for selecting the best genotypes (Johnson *et al.*, 1955 and Falconer 1996). In addition, heritability and genetic advance (GA %) are very necessary measure to improve any character of wheat as this will help in knowing if the desired objective of the material can be achieved or not (Fellahi *et al.*, 2013). The effectiveness of selection further strengthens in case high broad-sense heritability with high genetic advance which has been documented by many researchers like, (Ghosh and Gulati, 2001; Akbar *et al.*, 2003; Igbal *et al.*, 2003; Iqbal *et al.*, 2017).

Maximum genetic advance (assuming 5% intensity of selection) along with high narrow-sense heritability were observed for No. of grains/spike (GA = 15.39, H^2_{ns} = 79.41 %) followed by plant height (GA = 10.85, H^2_{ns} = 54.94 %) reflecting the preponderance of additive gene action in controlling these traits (Table 6). The other traits showed low genetic advance (GA from 0.24 to 4.90%) with moderate or very low broad-sense heritability (0.17 – 39.87%), except grain yield/plant showed 12.29% genetic advance and -0.35% narrow-sense heritability (Table 6). These results suggested a low scope in the improvement of these traits and could not be improved by direct selection, but through indirect selection of other correlated characters.

Phenotypic correlation

The results of phenotypic correlation between ten wheat traits revealed that several traits exposed highly significant positive correlations and others showed significant values (Table 7). Highly significant correlations were observed between spike length with days to flowering and plant height. Spikelets/spike showed highly significant association with days to flowering, plant height and spike length traits. The assessments of correlation clearly manifested that association of grains/spike with spike length, spikelets/spike and stem diameter was positive and highly significant. Highly significant positive relationships were also observed between grain weight/spike and each of spike length, stem diameter and grains/spike as well as between grain yield/plant and tillers/plant (Table 7). Significant positive correlations were also observed between plant height and days to flowering, stem diameter and spikelets/spike, grains/spike and days to flowering, grain weight/spike and spikelets/spike, as well as between grain yield and each of stem diameter and grain weight/spike (Table 7). While, significant negative correlation was found between days to flowering and 1000-kernel weight which reflects that selection for early flowering plants including high kernel weight.

These results were in agreement with those obtained by (Iqbal *et al.*, 2017), They also found high positive phenotypic correlation for grains/spike with grain weight/spike and spike length with grains/spike. In a correlation study, Desheva and Kyosev (2017) found that 1000-kernel weight, spike length, grain weight/spike and number of grains/spike showed significant and valuable contribution in grain yield. Also, (Gerema et al., 2020) observed positive highly significant correlation for plant height with spike length and tillers with grain yield per hectare.

Table 7. Phenotypic correlations among ten wheat traits

Traits	Days to Flowering	Plant height	Spike length	Spikelets per Spike	Tillers per Plant	Stem diameter	Grains per spike	Grain weight per spike	Grain yield / Plant
Days to Flowering	1								
Plant height	0.506*	1							
Spike length	0.748**	0.649**	1						
Spikelets per Spike	0.883**	0.724**	0.886**	1					
Tillers per Plant	-0.261	-0.583-**	-.446-*	-0.505*	1				
Stem diameter	0.386	0.071	.520*	0.449*	0.106	1			
Grains per spike	.0.453*	0.304	0.596**	0.613**	-0.168	0.817**	1		
Grain weight per spike	0.217	0.333	0.577**	0.473*	-0.165	0.757**	0.910**	1	
Grain yield /Plant	-0.177	-0.254	-0.0002	-0.174	0.711**	0.520*	0.381	0.524*	1
1000-kernel weight	-.522-*	0.195	0.033	-0.198	-0.170	-0.124	-0.147	0.247	0.218

**. Correlation is significant at the 0.01 level , *. Correlation is significant at the 0.05 level.

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المكونات الوراثية والقدرة على الائتلاف لمحصول الحبوب ومكوناته باستخدام تحليل (Line x Tester) في قمح الخبز(*Triticum aestivum L.*)

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الملخص

تم التهجين بين ثمانية تراكيب وراثية من قمح الخبز (*Triticum aestivum L.*) اشتملت على 6 سلالات كأم و2 سلالة اختبار كأب باستخدام نظام التزاوج (line × tester). هذا ولقد تم تقييم الاباء و12 هجين F_1 لصفات محصول الحبوب/النبات و9 صفات محصوليه اخرى. لقد أشارت النتائج إلى وجود تباين وراثي عالي المعنوية في جميع الصفات المدروسة. كانت السلالة Q8 الافضل في القدرة العامة على الائتلاف (GCA) للتزهير المبكر عدد الحبوب/سنبلة وزن الحبوب/سنبلة ووزن 1000 حبة. بينما كانت السلالة Q10 الافضل لصفة ارتفاع النبات ومحصول الحبوب/نبات. كانت سلالة الاختبار الابوية (T1= PI330456) الافضل لطول السنبلة عدد السنيبلات/السنبلة، قطر الساق، عدد الحبوب/السنبلة ومحصول الحبوب/نبات بينما كان الأب (T2= PI330458) ذو GCA جيدة لتاريخ الإزهار المبكر ووزن الالف حبة. كما أظهرت عدة أنواع من الهجن وجود قدرة خاصة على الائتلاف SCA موجب وعالية المعنوية لبعض الصفات المدروسة. لعبت السلالات الأمية دورًا مؤثرًا إيجابيًا في طول النبات، طول السنبلة، عدد الافرع/النبات ووزن الحبوب/سنبلة. بينما كان لسلالات الاباء الأثر الاكبر في تاريخ التزهير، عدد السنيبلات/سنبلة قطر الساق، عدد الحبوب/سنبلة، وزن 1000 حبة ومحصول الحبوب/نبات.

كذلك وجد ان الفعل الجيني المضيف هو المؤثر الرئيسي في طول النبات، عدد السنيبلات/سنبلة، قطر الساق، عدد الحبوب/سنبلة ووزن الحبوب/السنبلة. بينما كان الفعل السيادي غير الإضافي هو المؤثر الرئيسي في مواعيد التزهير، طول السنبلة، عدد الافرع/نبات، وزن 1000 حبة ومحصول الحبوب للنبات. كما لوحظ تقديرات عالية من درجات التوريث بالمعنى الواسع والضيق لصفات عدد الحبوب/سنبلة، وزن الحبوب/سنبلة، ارتفاع النبات ووزن الالف حبة. أيضا لوحظ اقصى تقدم وراثي إلى جانب اعلى معامل توريث بالمعنى الضيق لصفات عدد الحبوب/السنبلة وطول النبات والذي يعكس امكانية الانتخاب الحقيقي لهذه الصفات في الاجيال المبكرة. لوحظ وجود ارتباط موجب عالي المعنوية بين معظم الصفات المدروسة.