

**Correlation analysis for grain and its contributing traits in wheat (*Triticum aestivum* L.)**Syed Ahtisham Masood<sup>1</sup>, Shoaib Ahmad<sup>1</sup>, Muhammad Kashif<sup>1</sup> and Qurban Ali<sup>1,2</sup><sup>1</sup>. Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan<sup>2</sup>. Centre of Excellence in Molecular Biology, University of the Punjab Lahore, PakistanCorresponding author E-mail: [s.ahtisham01@gmail.com](mailto:s.ahtisham01@gmail.com), [saim1692@gmail.com](mailto:saim1692@gmail.com)

**Abstract:** Among the parents, genotypes; 9595, 9703, AARI-11 and Millat-11, had the most desirable mean value for number of spikelets/spike, awn length, plant height, grain yield/plant and spike length respectively. On the other hand cross combination 9703 × AARI-11 was the best one, based upon the mean performance, having maximum mean value for grain yield/spike, awn length, flag leaf area and yield/plant. For plant height and number of spikelets/spike cross; 9705 × Pb-11 showed the most desirable mean value having minimum mean for height and maximum mean number of spikelets/spike. Whereas, crosses 9554 × AARI-11, 9703 × Millat-11, 9595 × Pb-11, 9705 × Millat-11, 9554 × Millat-11 and 9554 × Pb-11 had the maximum mean value for tillers/plant, peduncle length, grains/spike, spike length, 1000-grain weight and extrusion length. All the morphological traits exhibited normal trend of association with grain yield/plant, the ultimate focus of breeders, except peduncle length which had a negative association with it at both genotypic and phenotypic levels while, extrusion length and spike length were negatively associated to grain yield/plant at phenotypic level only. So results of correlation for spike length, extrusion length and peduncle length were opposite to the normal association previously reported, indicating the effect of environment which resulted in the change of association for these studied traits. It was concluded that the selection of suitable parents on the basis of higher 1000-grain weight and grain yield/plant be used for the development of synthetic and hybrids.

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**1. Introduction**

Wheat (*Triticum aestivum* L.) is regarded as one of the most imperative crop, extensively cultivated throughout the world, with main purpose of human consumption, supporting approximately 35% of the world's population and 95% of wheat grown today is hexaploid (2n=6x), which is used in bread making and other bakery products (Debasis and Khurana, 2001). Being a Rabi crop, it plays an important role in meeting food and nutritive requirements of the country, used for making chapatti, bread, biscuits, pastries, cake and other bakery goods. The protein found in wheat is called gluten which renders wheat a multipurpose crop, and is a primary protein source for world's inhabitants. It is also regarded as an important food and feed crop based upon its production, utilization, nutritive value, and adaptation (Hogg *et al.*, 2004). Due to these facts wheat deserves special attention. Area under its cultivation was 8.69 Mha during 2012-13 and its production was 24.30 M tonnes, sharing about 12.5% in agri. sector and 2.6% in GDP of Pakistan (Pakistan Economic survey, 2012-13). So far, an enormous research work has been done in the field of wheat breeding using conventional and modern technologies. However, rapid increasing population and environmental fluctuation necessitate the breeders to bring further breakthrough in production and nutritive value of wheat. It is dire need

of time to enhance wheat production to ensure the food security in developing countries. Sustainable increase in production of wheat requires breeders to explore possible ways to achieve the objectives. So, the main objective of breeders is to develop wheat cultivars with high yielding ability (Ehdaie and Waines, 1989). It is prerequisite to have proper knowledge of genetic architecture of yield, yield-related traits and nature of gene action for a successful breeding program. Selection based upon these estimates helps to improve complex associated traits related to yield (Sokoto *et al.*, 2012; Mohammadi *et al.*, 2012; Ahmad *et al.*, 2010; Anwar *et al.* 2014; Ali *et al.* 2013; Khan *et al.* 2014; Tariq *et al.* 2014; Muhammad *et al.* 2013). Correlation analysis provides any opportunity to select genotypes for higher yield (Ali *et al.* 2014; Qamar *et al.* 2014ab; Ali *et al.* 2014abc; Azam *et al.* 2014; Jahangir *et al.* 2014).

**2. Material and methods**

The present study was carried to access correlation among yield traits in wheat by parents and F1 hybrids develop through line×tester design in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experimental material consisted of nine wheat genotypes, six wheat elite lines viz. 9546, 9554, 9595, 9703, 9704 and 9705 (Female parent) and

three testers viz. AARI-11, Millat-11 and Pasban-11. These wheat genotypes were crossed in line  $\times$  tester fashion during the 1<sup>st</sup> crop season in 2012-13. germplasm was sown in three replications. Each replication consisted of nine varieties (Parents) and 18 F<sub>1</sub> crosses with one meter long single row for treatment. Plant to plant and row to row distance were 15 and 30 cm, respectively. Two seeds per hole were sown with the help of dibbler and later thinned to one seedling per hole after germination. The experimental populations were kept under normal condition from sowing to maturity. Moreover, efforts were done to implement proper production technology. At maturity well-guarded plants from each line were selected to record the data on the traits including plant height, number of tillers/plant, flag leaf area, spike length, peduncle length, extrusion length, awn length, spikelets/spike, number of grains/spike, 1000-grain weight and grain yield/plant. Data was analyzed by using Steel *et al.* (1997) analysis of variance technique and correlation was estimated by using Know and Torre (1964) technique.

### 3. Results and discussions

#### Study of Mean Values of Morphological traits

Phenotype is not merely the result of its genetic composition it is actually the blend of genotype influenced by the environment. Both macro and micro environment of the plant are responsible to produce a specific expression of a genotype. A bunch of variation exists within the genome of wheat plants but different genes require different circumstances, elaborated as the environment of plant, to get expressed in its normal form. Genotypes utilized in the present research as parents had a broad spectra of phenotype expressions from highest to lowest levels. Various genotypic expressions produced by these genotypes, in the form of their averages, show the large amount of variation hidden in the wheat genome. (Table 2 and 3)

#### 3.1 Plant height

Genotypes utilized as parents in the contemporary research differ in their phenotypic expression in terms of plant height from medium to dwarf ones. Significant variation was revealed from the analysis of the mean data of the genotypes. Plant height varied from 98.43 cm in line 9703 to 69.40 cm in tester AARI-11. Plant height for lines ranged from 88.67 cm to 98.43 in 9705 and 9704 respectively. Plant height reduced in the different cross combinations exhibiting hybrid vigor in term of plant height. Almost all the cross combinations exhibited medium plant height plant height ranging from 92.43 cm to 74.95 cm in crosses 9704  $\times$  AARI-11 and 9705  $\times$  Pasban-11 sequentially. Crosses of tester Pasban-11 had lesser plant height than other ones. The genotypes

with short plant stature may be used for the development of higher yield varieties (Dogan (2009), Mahmood *et al.* (2006); Ali *et al.* (2014abc); Farooq *et al.* (2011ab)).

#### 3.2 Flag leaf area

Flag leaf area plays vital part in grain development and grain filling because it is responsible for the photosynthetic activity. With an increase in the flag leaf area greater amount of light is absorbed by the plant which results in greater photosynthates accumulation which helps in grain filling and its development. Due to its contribution to the grain yield, our main objective is the selection of genotypes with large flag leaf area. A mixed trend was observed for flag leaf area in both line and tester genotypes. Flag leaf area was maximum for genotype 9554 (29.63 cm<sup>2</sup>) and minimum for genotype 9546 (18.32 cm<sup>2</sup>). Flag leaf area was maximum for cross 9703  $\times$  AARI-11 (48.91 cm<sup>2</sup>) and minimum for cross 9703  $\times$  Millat-11 (17.97 cm<sup>2</sup>). Higher leaf area suggested that the amount of organic compounds increased in the plant body and increased grain yield Anwar *et al.* (2013); Dogan (2009), Mahmood *et al.* (2006); Ali *et al.* (2014abc); Farooq *et al.* (2011ab).

#### 3.3 Number of tillers/plant

The range of mean values for number of tiller/plant was almost same for both females (lines) and males (testers). Maximum and minimum mean values for number of tillers for lines were observed in 9705 (8.73) and 9595 (7.93). Whereas, mean values for testers were 8.27, 7.67 and 6.8 in genotypes; Millat-11, AARI-11 and Pasban-11, respectively. Number of tillers per plant is directly associated to the number of spikes/plant which is the direct determinant of grain yield in wheat so it has a vital role in enhanced yield production. Different crosses exhibited increased number of tillers toward the better parent and for other cross combinations hybrid vigor was less. Maximum and minimum mean values for number of tillers were observed in 9554  $\times$  AARI-11 (8.53) and 9595  $\times$  Pb-11 (6.07) respectively. Higher number of tillers suggested that the spikes per plant may be increased and hence increased yield per plant (Anwar *et al.* (2013); Dogan (2009), Mahmood *et al.* (2006); Farooq *et al.* (2011ab)).

#### 3.4 Extrusion length

Extrusion lengths were significantly higher for lines (females) than testers (males). Extrusion length showed more variation in means than any other trait. Extrusion length was maximum in 9554 (17.73 cm) and minimum in Millat-11 (7.28 cm). For extrusion length maximum variations in means were observed than any other trait. Peduncle length was maximum in 9703  $\times$  Millat-11 (12.05 cm) and minimum in 9705  $\times$  AARI-11 (7.98 cm). Similar results were reported by Anwar *et al.* (2013); Dogan (2009), Mahmood *et al.*

(2006); Farooq *et al.* (2011ab).

### 3.5 Peduncle length

Peduncle lengths were also significantly higher for lines (females) than testers (males) but were quite stable in both cases. Like extrusion length peduncle length was maximum in 9554 (45.53 cm) and minimum in Millat-11 (33.13 cm). The crosses involving either 9546 or 9703 produced the quite stable and greater values of peduncle length. Peduncle length was maximum in 9704 × Pasban-11 (43.30 cm) and minimum in 9705 × AARI-11 (34.67 cm). results were in accordance with findings of Anwar *et al.* (2013); Dogan (2009), Mahmood *et al.* (2006); Farooq *et al.* (2011ab).

### 3.6 Spike length

Greatest mean value of spike length was 12.49 cm in Millat-11 followed by 9595 (12.36 cm) and 9546 (12.29 cm) with minimum value recorded in 9705 (11.11 cm). Greatest mean value of spike length was 15.96 cm in 9705 × Millat-11 followed by 9705 × AARI-11 (13.69 cm) and 9595 × Pb-11 (13.44 cm) with minimum value recorded in 9705 × Pb-11 (11.25 cm). Mean data indicated that crosses involving Millat-11 with other lines showed the maximum spike lengths. Higher spike length suggested that number of spikes and grains per spike may also be increased (Dogan (2009), Mahmood *et al.* (2006); Farooq *et al.* (2011ab)).

### 3.7 Awn length

Awn length varied in the range of 5.91 to 7.12 for genotyped Millat-11 (tester) and 9703 (lines) sequentially. Overall awn length was less in testers than lines. Awn length varied in the range of 5.64 to 8.07 for genotyped 9704 × AARI-11 (5.64) and 9703 × AARI-11, respectively. Similar results were reported by Dogan (2009), Mahmood *et al.* (2006); Farooq *et al.* (2011ab).

### 3.8 Number of spikelets/spike

Mean values for number of spikelets/spike ranged from 22.27 to 18.40 in lines 9595 and 9546 respectively. Quite stable mean values for number of spikelets/spike were observed in testers whereas it varied significantly for lines. Mean values for number of spikelets/spike ranged from 23.60 to 17.00 in crosses; 9705 × Pasban-11 and 9705 × Millat-11, respectively. Mean values of number of spikelets/spike increased favorably towards the better parent but still a few some had less number of spikelets/spike. Higher spikelets suggested that grain yield may be improved (Dogan (2009), Mahmood *et al.* (2006); Farooq *et al.* (2011ab)).

### 3.9 Number of grains/spike

For number of grains/plant highest average value was recorded for female parent 9704 having 63.07 mean and minimum was also female parent 9705 with 44.47 mean. Other genotype having higher mean

value was 9703 (60.53). For number of grains/spike cross combination; 9595 × Pasban-11 (64.33), 9703 × Millat-11 (64.2), 9705 × Pasban-11 (61.3) and 9703 × AARI-11 (60.87) had higher means. Lower mean values were recorded for crosses; 9546 × AARI-11 (48.267), 9703 × Pasban-11 (50.4) and 9554 × Pasban-11 (50.93). Higher number of grains indicated the increase in yield per plant (Dogan (2009), Mahmood *et al.* (2006); Ali *et al.* (2014abc); Farooq *et al.* (2011ab))

### 3.10 Grain yield/spike

Grain yield/spike is an important trait for selection having narrow amount of variation with stable phenotypic expression. Highest mean value exhibited by the testers was 2.64 g closely followed by 2.62 g in the genotypes AARI-11 and Pasban-11 sequentially. While, for lines highest mean values were recorded for 9703 (3.23 g) and 9704 (3.18 g). Minimum grain yield/spike was given by Millat-11 with 2.17 g. Grain yield/spike is an important trait for selection having narrow amount of variation with stable phenotypic expression. Highest mean value exhibited by the cross 9703 × AARI-11 (3.25) closely followed by 9595 × Pasban-11 (3.19) and 9546 × Pasban-11 (3.19), respectively. Lowest mean values were observed in the cross 9703 × Millat-11 (2.42). Similar results were found by Anwar *et al.* (2013); Dogan (2009), Mahmood *et al.* (2006); Ali *et al.* (2014abc); Farooq *et al.* (2011ab).

### 3.11 1000-grain weight

The estimated mean values for 1000-grain weight were significantly different in both male and female parental genotypes. 1000-grain weight was maximum in 9705 (58.48 g) followed by 9703 (54.48) and minimum in 9546 (43.23). 1000-grain weight is a chief trait which determinates the final yield in cereal crops especially wheat. It is considered as a stable trait with some exceptions in it. For 1000-grain weight crosses involving lines 9554 and 9546 produced stable and better means than the other four lines. 1000-grain weight was maximum in 9554 × Millat-11 (58.80 g) followed by 9546 × Pasban-11 (55.42 g) and minimum in 9703 × Millat-11 (37.74 g). As 9554 × Millat-11 outperformed other cross combinations so their parents can be further evaluated to find out the best parental genotypes which can be utilized successfully in future breeding schemes with the ultimate goal to enhance yield/plant. Higher 1000-grain weight suggested that grain yield may be improved by selecting genotypes on the basis of 1000-grain weight (Anwar *et al.* (2013); Dogan (2009), Mahmood *et al.* (2006); Ali *et al.* (2014abc); Farooq *et al.* (2011ab)).

### 3.12 Grain yield/plant

The genotype 9704 (20.25 g) had maximum and 9595 (15.93 g) had minimum grain yield/plant.

Whereas, Pasban-11 (19.1 g) exhibited maximum grain yield and lowest grain yield was observed in Millat-11 (14.24) in case of testers. The cross combination; 9703 × AARI-11 (21.73 g) had maximum grain yield/plant followed by 9705 × AARI-11 (21.39 g) whereas, 9705 × Pasban-11 (11.9 g) had minimum grain yield/plant. Similar findings were reported by Anwar *et al.* (2013); Dogan (2009), Mahmood *et al.* (2006); Ali *et al.* (2014abc); Farooq *et al.* (2011ab).

#### 4. Correlation studies among the morphological traits

The determination of the coefficients of correlation of different yield contributing traits helps us to find out the degree of association/interrelationship among these traits. Phenotypic correlation coefficient value helps us in direct estimation of the association between two characters. On the other hand, genotypic coefficients of correlation express the extent to which the two characters are genetically associated. When improvement of the complex associated traits is looked-for, understanding of association between the component traits benefits in defining which character to choose. Interrelationship between different plant attributes can be figured out by determining their correlation coefficients. Both genotypic and phenotypic correlation of between various agronomic traits helps in the indirect selection of promising plants in crop breeding program. Genotypic and phenotypic coefficients of correlation among the grain yield and yield related components were estimated during study (Table 4).

##### 4.1. Correlation studies between plant height and remaining component traits

Plant height exhibited non-significant negative correlation to number of grains/spike at genotypic and phenotypic levels as both phenotypic and genotypic coefficients of correlation were less than one and negative. Negative correlation at both genotypic and phenotypic level was observed between plant height and grain yield/spike. Plant height was positively and significantly correlated to the tillers/plant at both phenotypic and genotypic levels. Correlation between plant height and spikelets/spike was non-significantly and negative showing that increase in the plant height results in decrease of number of spikelets/spike. Awn length was observed to be positively correlated to the plant height at both genotypic and phenotypic level and association was fairly significant. The correlation between plant height and spike length was fairly strong, significant and positive at genotypic as well as phenotypic level. The correlation of plant height with peduncle length and extrusion length was significant and positive at genotypic as well as phenotypic level

showing significant association for these traits. Negative and a non-significant correlation for plant height and flag leaf area was witnessed at both genotypic and phenotypic level. Plant height stood non-significant and positively interrelated to the 1000-grain weight at genotypic plus phenotypic level. Negative and significant association between grain yield/plant and plant height was witnessed in the study. As plant height increases grain yield/plant decreases, so short statured plant will give high yield/plant. The results obtained in current study are in accordance to the Anwar *et al.* (2013); Dogan (2009), Mahmood *et al.* (2006); Ali *et al.* (2014); Farooq *et al.* (2011ab).

##### 4.2. Correlation studies between number of grains/spike and remaining component traits

Positive and significant association for grains/spike and yield/spike was witnessed at both levels of genotype and phenotype. Grains/spike and number of tillers/plant were observed to be negatively correlated at genotypic plus phenotypic levels. Correlation of grains/spike with spikelets/spike was negative and fairly significant at genotypic level but was negatively correlated at phenotypic level. Grains/spike was significant and positively correlated to the awn length at both levels. The association among grains/spike and spike length was significant and positive at level of genotype but it was non-significant at phenotypic level. Grains/spike was positively associated with peduncle length and extrusion length at genotypic plus phenotypic levels. The correlation value in case of grains/spike and flag leaf area was fairly significant and positive at genotype level but was non-significant at phenotype level. Relationship of grains/spike with 1000-grain weight and yield/plant was observed to be significant and positive at both levels of phenotype and genotype which are similar to the results of Dogan (2009) and Mahmood *et al.* (2006).

##### 4.3. Correlation studies between grain yield/spike and remaining component traits

Grain yield/spike was found to be significantly and positively correlated with number of tillers/plant at both genotypic as well as phenotypic level. A significant positive correlation between grain yield/spike and spikelets/spike was observed at genotypic level whereas correlation was non-significant for phenotype. Correlation observed between grain yield/spike and awn length was significant and positive at both levels of genotype and phenotype. Correlation of grain yield/spike with spike length was positive with significant value at genotypic level but it was non-significant at phenotypic level as reported previously by Usman *et al.* (2006). Correlation between grain yield/spike and peduncle length was negative at both levels in the present study.

Grain yield/spike was significant and positive correlated to the extrusion length by the side of genotypic and phenotypic levels. Strong association between grain yield/spike and flag leaf area was observed at genotypic plus phenotypic levels which was positive with significant value significant. Grain yield/spike was found to be significantly and positively associated to the 1000-grain weight at all levels. On the other hand, grain yield/spike was positive at the level of genotype but it was highly significant with positive value at phenotype level. Very comparable results were reported by Aruna and Raghavaiah (1997) previously.

#### **4.4. Correlation studies between number of tillers/plant and remaining component traits**

There was non-significant and weak association between tillers/plant and spikelets/spike at genotypic level however these traits were non-correlated at the phenotypic level as correlation coefficient was 0.003. A weak and negative association between tillers/plant and awn length was observed at both genotypic plus phenotypic level. Number of tillers/plant and spike length had significantly strong negative correlation at genotypic level but correlation was fairly significant at phenotypic level. Association between number of tillers/plant and peduncle length was weak but positive at both levels. Number of tillers/plant and extrusion length exhibited weak positive correlation at genotypic level. On the other hand correlation at phenotypic level was negative and weak for the same characters. Number of tillers/plant had positive value of correlation with flag leaf area at genotypic level but was negative at phenotype level. The association at both genotypic plus phenotypic level was very weak. Association between the tillers/plant and 1000-grain yield was negative with non-significant value at genotypic level. At the phenotypic level both traits were non-correlated. In case of tillers/plant and yield/plant the correlation was positive at both phenotypic and genotypic level. Results for number of tiller/plant are in accordance to the results of Anwar (2009).

#### **4.5 Correlation studies between spikelets/spike and remaining component traits**

Spikelets/spike was negatively correlated to the awn length in the experiment at both genotypic and phenotypic levels with fairly weak association. Genotypic correlation for number of spikelets/spike and spike length was negative and significant but phenotypic correlation was negative and non-significant as stated previously by Fellahi *et al.* (2013). Negative and non-significant correlation was observed between the spikelets/spike and peduncle length at both levels. Spikelets/spike was positively correlated with the extrusion length at both levels. Association between spikelets/spike and flag leaf area was

observed to be negative and non-significant. A fragile and negative relationship between the spikelets/plant and 1000-grain weight was established at genotypic plus phenotypic level. Correlation for spikelets/spike and grain yield/plant was positive at level of genotype. Association was positive and significant at phenotypic front as stated previously by Bhutta *et al.* (2006) and Chowdhry *et al.* (2001).

#### **4.6 Correlation studies between awn length and remaining component traits**

Awn length and spike length were significant and positively correlated at genotypic level and was positively correlated at phenotypic level. Positive but weak association was observed for awn length with peduncle length was perceived at both genotype and phenotype levels. Fairly significant and positive correlation was recorded for awn length and extrusion length at these two levels. Awn length with flag leaf area showed the positive correlation between them at genotypic in addition to phenotypic level. The interrelationship between awn length and 1000-grain weight was negative at both genotypic plus phenotypic level. For awn length and grain yield/plant interrelationship observed was fairly positive at genotypic level but was weak association at phenotypic level.

#### **4.7 Correlation studies between spike length and remaining component traits**

Correlation between spike length and peduncle length was significant and positive at both levels. Negative with significant value of association for spike length and extrusion length was observed at genotypic level but negative at level of phenotype. A positive plus significant association between spike length and flag leaf area at genotypic level was observed but weak positive association was witnessed at level of phenotype. A weak positive connection was witnessed for spike length and 1000-grain weight at both levels of estimation. The association of spike length with grain yield/plant was very weak and positive at genotypic level whereas association at phenotypic level was negative in nature. The present results on spike length are very much in resemblance to the ones reported by Khan and Naqvi (2012).

#### **4.8 Correlation studies between peduncle length and remaining component traits**

Highly significant with positive value of correlation between the peduncle length and extrusion length was observed at genotypic level plus phenotypic level. Peduncle length and flag leaf area were reported to be positively correlated at both levels of association study and was considerably weak. The association between peduncle length and 1000-grain weight was significant and negative at both genotype plus phenotype level. Interrelationship of peduncle length with the grain yield/plant was negative and

non-significant at both levels of estimation.

#### 4.9 Correlation studies between extrusion length and remaining component traits

Extrusion length and flag leaf area was significant and positively associated at genotypic (G) level but it was positive at phenotypic (P) level. A weak non-significant and negative association between extrusion length and 1000-grain weight was witnessed at genotypic level whereas, association was non-significant and positive at phenotypic level. Extrusion length and yield/plant were non-correlated at genotypic level but, at the phenotypic level very weak, non-significant and negative association was

observed.

#### 4.10 Correlation studies between flag leaf area and remaining component traits

Association between flag leaf area and 1000-grain weight was observed to be positive and significantly correlated at genotypic level but non-significantly correlated at phenotypic level. On the other front a positive and significant association between flag leaf area plus grain yield/plant was found at genotypic level which was non-significant at level of phenotype. The results of correlation of flag leaf area with other characters were in agreement with the conclusions of Chaudhry *et al.* (1992).

Table 1. Mean squares of some morphological traits in bread wheat (ANOVA)

SOV	df	Plant	Flag	Number	Extrusion	Peduncle	Spike	Awn	Spikelets/Number	Grain	1000-	
Height	Leaf	of	Length	Length	Length	Length	Spike	of	yield/	grain	yield/	
area	tillers/plant	grains/spike	spike	weight	plant							
Replications	2	11.26**	13.40 <sup>NS</sup>	0.80 <sup>NS</sup>	2.23**	26.58**	2.19**	0.11**	0.52**	25.87**	0.01 <sup>NS</sup>	52.57**
413.06**												
Genotypes	26	166.8**	100.71**	1.59**	16.22**	29.29**	3.06**	0.90**	7.46**	73.91**	0.27 <sup>NS</sup>	
72.81**	17.78**											
Error	52	4.49	40.86	0.45	0.23	1.73	2.01	0.12	1.17	12.14	0.02	14.76
5.69												
Highly significant = **,		Significant = *		Non-significant =		NS						

Table 2. Mean values for parents of some morphological traits in bread wheat

Lines/testers	Plant	Flag	number	Extrusion	Peduncle	Spike	Awn	Spikelets/Number	Grain	1000-		
Height	Leaf	of	length	Length	Length	Length	spike	of	yield/	grain	yield/	
Area	tillers/plant	grains/spike	spike	weight	plant							
<b>Lines</b>												
9546	95.61	18.32	8.40	12.20	40.53	12.29	7.09	18.40	55.73	2.37	43.23	17.59
9554	97.57	29.63	8.00	17.73		45.53		11.16	5.99		18.93	56.80
	2.62	46.51	15.93									
9595	94.57	28.79	7.93	12.55	45.13	12.36	6.68	22.27	55.27	2.55	47.68	18.89
9703	98.43	28.13	8.67	11.27	42.57	11.93	7.12	20.33	60.53	3.23	54.48	19.91
9704	98.07	23.43	8.20	6.93	37.17	11.11	6.60		21.73	63.07	3.18	51.21
	20.25											
9705	88.67	26.20	8.73	8.09	40.80	11.85	6.13		22.07	44.47	2.57	58.48
	18.75											
<b>Testers</b>												
AARI-11	69.40	28.40	7.67	7.45	34.60	11.93	6.15		19.27	55.00	2.64	48.58
	17.32											
Millat-11	71.93	22.25	8.27	7.28	33.13	12.49	5.91		20.60	47.47	2.17	46.87
	14.24											
Pb-11	81.50	22.70	6.80	8.87	37.53	11.31	6.59	19.67	52.87	2.62	50.21	19.10

**Table 3. Mean values of crosses for some morphological traits in bread wheat**

Crosses	Plant Height	Grains/ spike yield/ area	Grain of weight	Number Spike plant	Spikelets/ Length	Awn Length	Spike Length	Extrusion Length	Peduncle leaf	Flag grain	1000-Grain yield/	Grain
9546 × AARI-11	13.65	84.57	48.26	2.55	6.53	23.13	6.47	11.59	8.01	40.13	25.46	53.44
9546 × Millat-11	16.41	84.73	55.27	2.97	7.27	21.13	6.24	13.37	9.27	41.40	28.36	54.25
9546 × Psb-11	17.85	86.93	58.47	3.19	6.47	23.00	6.05	11.99	8.06	41.40	28.29	55.42
9554 × AARI-11	18.66	88.80	53.13	2.80	8.53	21.67	6.25	11.99	10.24	36.23	26.24	53.64
9554 × Millat-11	15.76	81.90	54.60	3.13	7.47	20.93	5.91	11.98	9.72	40.87	33.58	58.80
9554 × Psb-11	15.48	76.40	50.93	2.55	7.80	22.47	6.03	11.27	10.77	42.43	29.07	50.56
9595 × AARI-11	15.81	82.97	54.13	2.52	8.47	21.93	6.40	11.97	6.99	37.21	25.64	47.00
9595 × Millat-11	15.47	83.47	52.87	2.59	8.07	19.80	5.96	11.93	9.67	36.50	24.64	49.95
9595 × Psb-11	14.27	87.07	64.33	3.19	6.07	20.13	6.95	13.44	10.39	37.30	30.46	49.99
9703 × AARI-11	21.73	87.93	60.87	3.25	8.27	20.47	8.07	12.15	11.72	41.03	48.91	53.77
9703 × Millat-11	16.27	89.27	64.20	2.42	7.06	21.87	6.99	12.64	12.05	41.77	17.97	37.74
9703 × Psb-11	15.05	83.20	50.40	2.67	7.80	19.67	6.47	11.29	10.60	41.47	32.79	54.54
9704 × AARI-11	19.12	92.43	56.00	2.93	7.87	19.40	5.64	11.79	9.57	41.33	34.22	52.84
9704 × Millat-11	16.08	86.50	55.27	2.96	7.40	22.40	6.22	12.04	8.27	39.87	24.72	54.66
9704 × Psb-11	15.18	89.90	58.20	2.71	7.90	21.80	6.45	12.58	10.81	43.30	26.47	46.68
9705 × AARI-11	21.39	83.80	53.13	2.81	7.13	20.47	5.76	13.69	7.98	34.67	24.08	54.02
9705 × Millat-11	14.77	87.77	58.73	3.15	6.60	17.00	7.36	15.96	8.25	39.90	26.98	54.09
9705 × Psb-11	11.92	74.95	61.30	2.52	8.10	23.60	6.47	11.25	11.82	39.05	28.43	42.28

**Table 4. Genotypic (G) and phenotypic (P) correlation of some morphological traits**

Characters	r	Grains/s pike	Grain yield/spike	Tillers /plant	spikelet s/spike	Awn length	Spike length	Peduncle length	Extrusion length	Flag Leaf Area	1000-Grain weight	Grain Yield/Plant
Plant height	G	-0.410	-0.360	0.199	-0.015	0.345	0.046	0.428	0.574	-0.108	0.044	-0.520
	P	-0.320	-0.350	0.128	-0.013	0.279	0.018	0.398	0.519	-0.060	0.060	-0.370
Grains/ spike	G		0.563	-0.263	-0.121	0.614	0.354	0.317	0.220	0.209	0.280	0.114
	P		0.452	-0.167	0.010	0.393	0.122	0.277	0.125	0.039	0.450	0.051
Grain yield/ spike	G			-0.375	0.160	0.302	0.420	-0.119	0.141	0.730	0.630	0.441
	P			-0.169	0.060	0.272	0.196	-0.111	0.128	0.347	0.581	0.291
Tillers/ plant	G				0.086	-0.005	-0.681	0.221	0.072	0.095	-0.188	0.299
	P				-0.003	-0.066	-0.315	0.143	-0.005	-0.059	-0.005	0.230
spikelets/ spike	G					-0.230	-0.856	-0.175	0.104	-0.104	-0.020	0.230
	P					-0.170	-0.190	-0.128	0.112	-0.157	-0.030	0.210
Awn length	G						0.499	0.237	0.233	0.243	-0.235	0.281
	P						0.188	0.183	0.158	0.265	-0.092	0.029
Spike length	G							0.340	-0.291	0.310	0.133	0.006
	P							0.120	-0.035	0.040	0.071	-0.090
Peduncle length	G								0.683	0.182	-0.426	-0.070
	P								0.624	0.113	-0.353	-0.056
Extrusion length	G									0.236	-0.025	0.005
	P									0.121	0.027	-0.012
Flag Leaf Area	G										0.640	0.436
	P										0.289	0.052
1000-Grain weight	G											0.396
	P											0.245

#### 4.11 Correlation studies between 1000-grain weight and remaining component traits

The association of 1000-grain weight with grain yield/plant was observed to be positive plus significant at level of genotype but it was significant plus positive at phenotypic level which is in harmony to the results achieved by Anwar *et al.* (2013); Tila *et al.* (2005); Dogan (2009), Mahmood *et al.* (2006); Ali *et al.* (2014abc).

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