

# Correlation Analysis and Heritability of Yield Characters in Hexaploid Wheat (*Triticum Aestivum* L.)

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**Abstract:** This study was carried to analysis correlation in six wheat (*Triticum aestivum* L.) genotypes such as TJ-83, Kiran-95, NIA-Sundar, Benazir, Hamal and Sehar-2006 for nine different traits viz., plant height (cm), tillers plant<sup>-1</sup>, spike length(cm), spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, seed index (1000-grain weight, g), grain yieldplant biological yield plant<sup>-1</sup> (g) and harvest index (%). The results revealed that genotypes differed significantly ( $P \leq 0.01$ ) for plant height, tillers plant<sup>-1</sup>, spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index. The varieties Kiran-95 and Sehar-2006 showed maximum values in mean performance for different traits. The traits such as spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup> and seed index showed positive and significant correlations with grain yield plant<sup>-1</sup>; hence these traits may be given priority in selection. High heritability estimates were observed for plant height, tillers plant<sup>-1</sup>, spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index.

**Keywords:** correlation, heritability, yield, characters hexaploid, wheat.

## Introduction

Wheat is the world's most important crop that excels all other cereal crops both in area and production, thereby providing about 20.0 per cent of total food calories for the people of the world. Nearly 95% of wheat grown today is hexaploid, used for the preparation of bread and other baked products (Debasis and Khurana, 2001). The husk bran and germ are rich sources of vitamins, minerals and protein (David and Adams, 1985). Since ages, wheat has been playing an important role in the economy several countries (Singh *et al.*, 2010). To obtain superior yield with potential resistance against biotic and abiotic stresses in Pakistani wheat cultivars, many breeding efforts had been done in the recent past; consequently, due to its bidirectional breeding approaches a number of promising cultivars with better adaptability have also been released. Wheat has a unique position among cereal crops, mostly attributable to the reason that grains retain protein with exceptionally good chemical and physical properties (Ali *et al.*, 2013).

As the world population is increasing day by day so the production of the cereals should increase in order to meet the requirement of food in future. Increasing area under cultivation, effective cultural practices, and using genetically improved cultivars are some methods to increase the production of cereal crops (Hannachi *et al.*, 2013). Since independence in 1947, population of the country has increased manifold; while increase in cultivated area is just 40% (Ahmed and Farooq, 2010).

Yield is a complex trait which is influenced by both genetic and climatic factors. Interaction among both these factors makes the selection procedure tough. For obtaining desirable cotton genotypes information regarding interaction between yield and related components assist the breeders in the choice of desirable genotypes. The association analysis provides a good guide to envisage the corresponding change which occurs in one parameter at the expense of the proportionate change in the other (Ahmad *et al.*, 2008). For the purpose of information about genetics of yield and its components is of great worth for breeders for selection of parents to develop new and high yielding varieties. This is the reason for which breeding skill and successful manipulation of genetic makeup involved for expression of traits under selection has gained extreme importance. In wheat grain yield and related parameters are greatly influenced by environment (Anwar *et al.*, 2011).

Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be great importance in planning a successful breeding program (Mary and Gopalan, 2006). Evolution of varieties with high yield potential accompanied with desirable combination of traits

has always been the major objective of wheat breeding programme. It is also widely recognized that genetic architecture of yield can be resolved better by studying its component characters. This enables the plant breeder to breed for high yielding genotypes with desired combinations of traits. The correlations are very important in plant breeding, because of its reflection in dependence degree between two or more traits. If there is genetic correlation between traits, in the case of direct selection of one trait can cause change in other trait. Correlations between traits are depending of genetic and environmental factors (Falconer, 1981). Environmental condition scan variability,

Not only of some trait but interrelationship between its. The objective of this study was to establish the inter-relationship of various wheat components among themselves and with yield. Correlation are very important in plant breeding, because of its correlation is useful in disclosing the magnitude and direction of the relationship between various yield contributing traits and yield. Positive correlation between desirable traits are supposed to be favorable and help to breeder in selection whereas, negative correlations hinders the recovery of the combinations in both characters. Correlation studies provide a better understanding of the association of different characters with grain yield (Dixet and Dubey, 1984). Heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is understood that only the phenotypic value can be measured directly while breeding values of individuals are derived from appropriate analyses. It is the breeding value, which determine show much of the phenotype would be passed onto the next generation (Larik *et al.*, 2000).

### Materials and Methods:

The present research was carried out at the Experimental Field, Southern Wheat Research Station, Tandojam. The experiment was laid-out in randomized complete block design with three replications during rabi season, 2022-23. The sowing was done by dibbling, keeping 20 cm space between plants and 30 cm between rows. Ten plants were randomly selected and tagged from each replication.

Genotypes=06

1. TJ-83
2. Kiran-95
3. NIA-Sundar
4. Benazir
5. Hamal
6. Sehar-2006

The detail of studied traits is mentioned in following paragraphs:

Plant height(cm)

The height of each selected plant was measured in centimeters from the surface of soil to the tip of the ear head including awns and the mean plant height per genotype was calculated.

Tillersplant<sup>-1</sup>

When crop was matured, the number of fertile tillersplant<sup>-1</sup> were counted And recorded from each selected plant.

Spike length (cm)

Length of spike was measured in centimeter from the base of spike to the upper most spikelet excluding awns and was averaged.

Spikeletsspike<sup>-1</sup>

Spike lets spike<sup>-1</sup> of selected plants was counted after harvest in the laboratory.

#### Grainsspike<sup>-1</sup>

The total number of seeds spike<sup>-1</sup> of randomly selected spike was counted and the average number of seeds spike<sup>-1</sup> was calculated.

#### Grain yield plant<sup>-1</sup>(g)

After harvesting, each plant was threshed separately by hand and grains were weighed on electronic digital balance and yield plant<sup>-1</sup> was weighed in grams.

#### Seed index(1000-grainweight,g)

Thousand seeds were counted at random and weighed in grams in the laboratories with the help of electronic digital balance.

#### Biological yield plant<sup>-1</sup>(g)

Biological yield plant<sup>-1</sup> was recorded as the plants harvested at maturity and weighed along with grains and the straw.

#### Harvest index(%)

Harvest index in percentage was calculated from following formula: HI (%)  
 = 
$$\frac{\text{Grain yield plant}^{-1}}{\text{Biological yield plant}^{-1}} \times 100$$

#### Biological yield plant<sup>-1</sup>

### Statistical analysis

Data was statistically analyzed using analysis of variance according to Gomez and Gomez (1984), while least significant differences test (LSD) was used to compare the mean differences. Correlation coefficient and path analysis between different traits was computed according to Snedecor and Cochran (1987), while heritability in broad sense was estimated as suggested by Allard (1960).

### RESULT:

#### Analysis of variance

The analysis of variance for all the characters is given in Table 1. The obtained results revealed that genotypes differed significantly ( $P \leq 0.01$ ) for plant height, tillers plant<sup>-1</sup>, spike length, spike lets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index.

#### Mean performance and correlations

Mean performance of all genotypes correlation and heritability results of each character is given below.  
 Plant height(cm)

Among the genotypes, NIA-Sundar showed maximum plant height (84.16 cm), while the Kiran-95 showed dwarf plants with the minimum plant height of 72.46 cm. Correlations results indicated that plant height showed negative and significant association with tillers plant<sup>-1</sup> ( $r = -0.75^{**}$ ); while also showed positively significant correlation with biological yield plant<sup>-1</sup> ( $r = 0.56^*$ ). Furthermore, plant height revealed positive and but non-significant correlations with spike lets spike<sup>-1</sup> ( $r = 0.13$ ), grains spike<sup>-1</sup> ( $r = 0.06$ ), grain yield plant<sup>-1</sup> ( $r = 0.07$ ) and seed index ( $r = 0.40$ ), whereas also showed negative but non-significant associations with spike length ( $r = -0.01$ ) and harvest index ( $r = -0.40$ ). The genetic variance ( $\delta^2_g$ ) was 27.32 and phenotypic variance ( $\delta^2_p$ ) was 30.65, which reflected higher heritability estimates ( $h^2 = 89.16\%$ ) for plant height in wheat genotypes.

#### Tillers plant<sup>-1</sup>

For the character tillers plant<sup>-1</sup>, Kiran-95 produced maximum number of Tillers plant<sup>-1</sup> (12.30), where as the TJ-83 produced minimum number of tillers plant<sup>-1</sup> of 5.20. Correlations results showed that tillers plant<sup>-1</sup> showed negative and non-significant associations with all traits such as spike length ( $r = -0.29$ ), spikelets spike<sup>-1</sup> ( $r = -0.44$ ), grains spike<sup>-1</sup> ( $r = -0.42$ ), grain yield plant<sup>-1</sup> ( $r = -0.43$ ), seed index ( $r = -0.12$ ), biological yield plant<sup>-1</sup> ( $r = -0.10$ ) and harvest index ( $r = -0.03$ ). The genetic variance for tillers plant<sup>-1</sup> was  $\delta^2_g = 72.18$  and phenotypic variance was  $\delta^2_p = 73.72$ , which disclosed high heritability estimates of 97.91 % for the character tillers plant<sup>-1</sup>.

**Spike length (cm)**

Regarding spike length, TJ-83 produced the longer length of spike (12.66 cm), whereas the Sehar-2006 produced shorter length of spike (7.56 cm). Correlations results displayed that spike length showed positive and significant associations with spikelets spike<sup>-1</sup> ( $r= 0.84^{**}$ ), grains spike<sup>-1</sup> ( $r= 0.92^{**}$ ) and grain yield plant<sup>-1</sup> ( $r= 0.73^{**}$ ). However, showed negative and non-significant correlations with seed index ( $r= -0.23$ ), biological yield plant<sup>-1</sup> ( $r= -0.12$ ) and harvest index ( $r= -0.44$ ). In case of spike length, genetic variance ( $\delta^2g = 51.91$ ) was somewhat lower to its phenotypic variance ( $\delta^2p = 52.59$ ), revealed high heritability estimates ( $h^2=98.51\%$ ).

**Spikeletsspike<sup>-1</sup>**

About spikelets spike<sup>-1</sup>, TJ-83 produced the maximum number of spikelets spike<sup>-1</sup> (20.30), whereas the Sehar-2006 produced minimum number of spikeletsspike<sup>-1</sup> (14.43). Correlations results exhibited that spikeletsspike<sup>-1</sup> showed positive and significant associations with grains spike<sup>-1</sup> ( $r= 0.80^{**}$ ) and grain yield plant<sup>-1</sup> ( $r=0.87^{**}$ ). However, showed positive but non-significant correlations with seed index ( $r= 0.40$ ), biological yield plant<sup>-1</sup> ( $r= 0.10$ ) and harvest index ( $r= 0.01$ ). In case of spikelets spike<sup>-1</sup>, genetic variance ( $\delta^2g = 35.05$ ) was somehow lower to its phenotypic variance ( $\delta^2p=35.75$ ), revealed high heritability estimates ( $h^2=98.06\%$ ).

**Grainsspike<sup>-1</sup>**

For the character grains spike<sup>-1</sup>, TJ-83 produced the maximum number of grains spike<sup>-1</sup> (70.63); however the NIA-Sundar produced minimum number of grains spike<sup>-1</sup> (33.66). Correlations results exhibited that grains spike<sup>-1</sup> showed positive and significant associations with grain yield plant<sup>-1</sup> ( $r= 0.78^{**}$ ). However, showed negative and non-significant correlations with seed index ( $r= -0.15$ ), biological yield plant<sup>-1</sup> ( $r= -0.02$ ) and harvest index ( $r= -0.42$ ). Grains spike<sup>-1</sup> expressed a modest difference in genetic variance ( $\delta^2g = 68.07$ ) and phenotypic variance ( $\delta^2p = 72.67$ ), which showed high heritability estimates ( $h^2= 93.66\%$ ).

**Grainyieldplant<sup>-1</sup>**

For the trait grain yield plant<sup>-1</sup>, Sehar-2006 produced the maximum grain yield plant<sup>-1</sup> (18.53 g); however the NIA-Sundar produced minimum grain yield plant<sup>-1</sup> (12.33 g). Correlations results demonstrated that grain yield plant<sup>-1</sup> was positively and significantly associated with seed index ( $r= 0.54^*$ ), while negative and non-significant correlations with biological yield plant<sup>-1</sup> ( $r= -0.43$ ) and harvest index ( $r= -0.14$ ). The genetic variance ( $\delta^2g$ ) and phenotypic variance ( $\delta^2p$ ) were 43.03 and 46.00, respectively, which estimated high heritability ( $h^2=93.54\%$ ).

**Seed index(1000-grainweight,g)**

The average performance of seed index is given in Table 2, Sehar-2006 produced the maximum weight of 1000 grain (46.38 g), conversely Benazir produced minimum seed index of 32.45g. Correlations results demonstrated that seed index was negatively and significantly associated with seed index with biological yield plant<sup>-1</sup> ( $r= -0.62^{**}$ ) but non-significantly correlated with harvest index ( $r= -0.25$ ). The genetic variance ( $\delta^2g=47.85$ ) and the phenotypic variance ( $\delta^2p=51.37$ ), resulted in high heritability estimates ( $h^2 = 93.14\%$ ).

**Biological yield plant<sup>-1</sup> and harvest index**

The average performance of biological yield plant<sup>-1</sup> and harvest index is given in Table 2. Sehar-2006 produced the maximum biological yield plant<sup>-1</sup> (29.31 g); on the other hand, NIA-Sundar produced minimum biological yield plant<sup>-1</sup> (22.50 g). The highest harvest index was shown by Sehar-2006 (63.22%), while the lowest harvest index was produced by TJ-83 (50.78 %). Correlations results demonstrated that biological yield plant<sup>-1</sup> and harvest index positively and significantly associated with each other ( $r= 0.53^*$ ). For the character biological yield plant<sup>-1</sup>, the genetic variance ( $\delta^2g=120.60$ ) and the phenotypic variance ( $\delta^2p=123.30$ ), resulted in high heritability estimates ( $h^2 = 97.57\%$ ). In case of harvest index, genetic variance ( $\delta^2g = 76.46$ ) was somewhat lower to its phenotypic variance ( $\delta^2p = 78.26$ ), revealed high heritability estimates ( $h^2 = 97.69\%$ ).

Table1.Meansquaresfromanalysisofvarianceforvarioustraitsinbreadwheatgenotypes

Sourceof variance	D.F.	Characters								
		Plant height	Tillers plant <sup>-1</sup>	Spike length	Spikelets spike <sup>-1</sup>	Grains spike <sup>-1</sup>	Grain yield plant <sup>-1</sup>	Seed index	Biological yield plant <sup>-1</sup>	Harvest index
Replication	2	8.27	0.17	0.18	0.36	32.40	2.36	0.92	0.54	1.14
Genotypes	5	76.32**	19.11**	12.12**	18.59**	511.72**	101.42**	107.26**	24.66**	410.01**
Error	10	2.49	0.11	0.23	0.52	7.04	0.67	0.31	0.20	0.03

\*\*=Significantat1%of probabilitylevel

Table2.Mean performance ofvarioustraitsinbreadwheatgenotypes

Genotypes	Plant height (cm)	Tillers plant <sup>-1</sup>	Spike length (cm)	Spikelets spike <sup>-1</sup>	Grains spike <sup>-1</sup>	Grain yield plant <sup>-1</sup> (g)	Seed index (1000 grain weight, g)	Biological yield plant <sup>-1</sup> (g)	Harvest index (%)
TJ-83	83.83	5.20	12.66	20.30	70.63	14.23	45.43	28.02	50.78
Kiran-95	72.46	12.30	11.23	18.16	53.03	16.60	36.45	27.84	59.62
NIA-Sundar	84.16	8.50	7.63	14.13	33.66	12.33	45.23	22.50	54.80
Benazir	75.86	8.06	9.93	17.86	54.06	15.70	32.45	25.71	61.06
Hamal	81.40	7.03	9.26	18.93	44.90	15.06	36.46	28.44	52.95

Sehar-2006	74.60	10.56	7.56	14.43	39.43	18.53	46.38	29.31	63.22
LSD (5%)	2.87	0.60	0.86	1.31	4.83	1.49	1.01	0.82	0.31

Table3. Correlation coefficient (r) between different traits in hexaploid wheat genotypes

Traits	Plant height	Tillers plant <sup>-1</sup>	Spike length	Spikelets spike <sup>-1</sup>	Grains spike <sup>-1</sup>	Grain yield plant <sup>-1</sup>	Seed index	Biological yield plant <sup>-1</sup>
Tillers plant <sup>-1</sup>	-0.75**							
Spike length	-0.01	-0.29						
Spikelets spike <sup>-1</sup>	0.13	-0.44	0.84**					
Grains spike <sup>-1</sup>	0.06	-0.42	0.92**	0.80**				
Grain yield plant <sup>-1</sup>	0.07	-0.43	0.73**	0.87**	0.78**			
Seed index	0.40	-0.12	-0.23	0.40	-0.15	0.54*		
Biological yield plant <sup>-1</sup>	0.56*	-0.10	-0.12	0.10	-0.02	-0.43	-0.62**	
Harvest index	-0.40	-0.03	-0.44	0.01	-0.42	-0.14	-0.25	0.53*

\*\*,\*=significant at 1 and 5% probability levels, respectively.

**Table4.Heritability estimate in broad sense for various trait so fbread wheat genotypes**

Characters	Genotypic variance( $\delta^2g$ )	Phenotypic variance( $\delta^2p$ )	Heritability% (Broad sense)
Plantheight	27.32	30.65	89.16
Tillersplant <sup>-1</sup>	72.18	73.72	97.91
Spikelength	51.91	52.69	98.51
Spikeletsspike <sup>-1</sup>	35.05	35.75	98.06
Grainsspike <sup>-1</sup>	68.07	72.67	93.66
Seedindex	47.85	51.37	93.14
Grainyieldplant <sup>-1</sup>	43.03	46.00	93.54
Biologicalyieldplant <sup>-1</sup>	120.60	123.30	97.57
Harvestindex	76.46	78.26	97.69

## DISCUSSION

Correlation are very important in plant breeding, because of its Correlation is useful in disclosing the magnitude and direction of the relationship between various yield contributing traits and yield. Positive correlation between desirable traits are supposed to be favorable and help to breeder in selection whereas, negative correlations hinders the recovery of the combinations in both characters. Correlation studies provide a better understanding of the association of different characters with grain yield (Dixet and Dubey, 1984). Correlation studies give a clear picture of characters association which is generally due to linkage, pleiotrophy, physiological association in developmental and biochemical pathway. Though, the linkage is a cause of transient correlations particularly in population derived from crosses between two species. Pleiotrophy is simply a property of a gene whereby it affects two or more characters, so that if the gene is segregating it causes variations in those characters. The characters which are correlated are of much interest since change in one character influenced the other one (Chitralkha *et al.*, 2018).

The analysis of variance revealed that all the varieties performed significantly different for plant height, tillers plant<sup>-1</sup>, spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index. This suggests that studied materials possess may be used for upcoming breeding programs. Almost similar results have also been reported by several other workers, namely, Zeeshan *et al.* (2013), Baloch *et al.* (2014a) and Baloch *et al.* (2014b). These researchers found the significant genetic variance for the number of traits, such as, plant height, tillersplant<sup>-1</sup>,spikelength,grainsspike<sup>-1</sup>,grain yieldplant<sup>-1</sup>,seed index, biologicalyieldplant<sup>-1</sup>and harvest index while studying yield and its components.

Regarding mean performance for different traits, NIA-Sundar showed maximum plant height (84.16 cm), while the Kiran-95 showed dwarf plants with the minimum plant height of 72.46 cm. Kiran-95 produced maximum number of tillers plant<sup>-1</sup> (12.30),whereastheTJ-83 produced longer length of spike(12.66 cm), the maximum number of spikelets spike<sup>-1</sup> (20.30), also produced the maximum number of grains spike<sup>-1</sup> (70.63). For the trait grain yield plant<sup>-1</sup>, Sehar-2006 produced the maximum grain yield plant<sup>-1</sup> (18.53 g); however the NIA-Sundar produced minimum grain yield plant<sup>-1</sup> (12.33 g). Sehar-2006 produced the maximum weight of 1000 grain (46.38 g), maximum biological yield plant<sup>-1</sup> (29.31g) and highest harvest index (63.22%).ThevarietiesKiran-95and Sehar-2006showed good performance and can be evaluated for future breeding programs.

Phenotypic correlations were determined among seed yield and its components in all possible character combinations and are presented in Table 3. Positive correlation between desirable traits are supposed to be favorable and help to breeder in selection whereas, negative correlations hinders the recovery of the combinations in both characters. Correlations results indicated that plant height showed negative and significant association with tillers plant<sup>-1</sup> ( $r = -0.75^{**}$ ); while also showed positively significant correlation with biological yield plant<sup>-1</sup> ( $r = 0.56^*$ ). Spike length showed positive and significant associations with spikelets spike<sup>-1</sup> ( $r = 0.84^{**}$ ), grains spike<sup>-1</sup> ( $r = 0.92^{**}$ ) and grain yield plant<sup>-1</sup> ( $r = 0.73^{**}$ ). Spikelets spike<sup>-1</sup> showed positive and significant associations with grains spike<sup>-1</sup> ( $r = 0.80^{**}$ ) and grain yield plant<sup>-1</sup> ( $r = 0.87^{**}$ ). Grains spike<sup>-1</sup> showed positive and significant associations with grain yield plant<sup>-1</sup> ( $r = 0.78^{**}$ ), while grain yield plant<sup>-1</sup> was also positively and significantly associated with seed index ( $r = 0.54^*$ ). Correlations results demonstrated that seed index was negatively and significantly associated with seed index with biological yield plant<sup>-1</sup> ( $r = -0.62^{**}$ ). Correlations results also demonstrated that biological yield plant<sup>-1</sup> and harvest index positively and significantly associated with each other ( $r = 0.53^*$ ). These results of correlations revealed that there are some characters, which showed positive and significant correlations with grain yield, such as spike length, grains spike<sup>-1</sup>, spikelets spike<sup>-1</sup> and seed index. These characters may be preferred in selection program to introduce high yielding varieties. Chitrlekha *et al.* (2018) reported that plant height had significant positive correlation with spike length (0.632), whereas, significant negative correlation with seed yield per plot (-0.713), harvest index (-0.537), 1000-seed weight (-0.517), biological yield per plot (-0.504) and number of seeds per plant (-0.490). Number of tillers per plant exhibited significant positive correlation with spike length (0.493), whereas, significant negative correlation with 1000-seed weight (-0.470). Spike length, Number of spike lets per spike and number of seeds per spikelet showed positive and negative correlations which all were non-significant whereas, number of seeds per spike had significant positive correlation with number of seeds per plant (0.591) and seed yield per plant (0.538). Parihar *et al.* (2017) reported that seed yield was significantly and positively associated with number of spikelets plant<sup>-1</sup>, followed by number of effective tillers and 1000- seed weight at both phenotypic and genotypic levels. Seed yield showed a significant negative association with number of seeds spikelet<sup>-1</sup> at genotypic level. Among the significant inter-relationships, the association of days to 50 % spike emergence with days to maturity and 100- seed weight were significant and positive, but were negative and significantly associated with number of seeds spikelet<sup>-1</sup> and number of grains spike<sup>-1</sup>. Similarly, the associations of spike length with number of seeds spikelet<sup>-1</sup>, and number of spikelets plant<sup>-1</sup> and number of effective tillers were negative and significant. The association of number of spikelets plant<sup>-1</sup> with number of effective tillers was also positive and highly significant. Singh *et al.* (2017) reported that grain yield plant<sup>-1</sup> shared positive significant association with number of tillers plant<sup>-1</sup>, number of spikelet spike<sup>-1</sup>, number of grain spike<sup>-1</sup>, 1000 grain weight, biological yield plant<sup>-1</sup> and spike length.

Heritability estimates are helpful in deciding the characters to be considered while making selection. High heritability estimates were observed for plant height, tillers plant, spike length, spikelets spike, grain spike, seed index, grain yield plant and biological yield plant<sup>-1</sup> and harvest index. High heritability values for these traits indicated that the variation observed was mainly under genetic control. Similar to our findings, Rind (2016) also estimated high heritability in broad sense for number of traits, such as High heritability estimates were observed for days to 75% flowering, days to 75% maturity, plant height, peduncle length, spike length, spike lets spike, grains spike, grain weight spike, tillers/m, Seed index, biological yield plot, grain<sub>1</sub> yield plot and harvest index. Beside it, other researchers including Khodadadi *et al.* (2011) and Baloch *et al.* (2014b) also found high heritability estimates for quantitative traits in bread wheat genotypes.

#### SUMMARY AND CONCLUSIONS

This research was carried out to study correlation in six commercial bread wheat genotypes by studying nine traits (plant height, tillers plant<sup>-1</sup>, spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index). The analysis of variance revealed that all the varieties performed significantly different for plant height, tillers plant<sup>-1</sup>, spike length, spike lets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index.

NIA-Sundar showed maximum plant height (84.16 cm), while the Kiran-95 showed dwarf plants with the minimum plant height of 72.46 cm. Kiran-95 produced maximum number of tillers plant<sup>-1</sup> (12.30), whereas the TJ-83 produced longer length of spike (12.66 cm), the maximum number of spikelets spike<sup>-1</sup> (20.30), also produced the maximum number of grains spike<sup>-1</sup> (70.63). For the trait grain yield plant<sup>-1</sup>, Sehar-2006 produced the maximum grain yield plant<sup>-1</sup> (18.53 g); however the NIA-Sundar produced minimum grain yield plant<sup>-1</sup> (12.33 g). Sehar-2006 produced the maximum weight of 1000 grain (46.38 g), maximum biological yield plant<sup>-1</sup> (29.31 g) and highest harvest index (63.22 %).



Correlations results indicated that plant height showed negative and significant association with tillers plant<sup>-1</sup> ( $r = -0.75^{**}$ ); while also showed positively significant correlation with biological yield plant<sup>-1</sup> ( $r = 0.56^*$ ). Spike length showed positive and significant associations with spikelets spike<sup>-1</sup> ( $r = 0.84^{**}$ ), grains spike<sup>-1</sup> ( $r = 0.92^{**}$ ) and grain yield plant<sup>-1</sup> ( $r = 0.73^{**}$ ). Spikelets spike<sup>-1</sup> showed positive and significant associations with grains spike<sup>-1</sup> ( $r = 0.80^{**}$ ) and grain yield plant<sup>-1</sup> ( $r = 0.87^{**}$ ). Grain spike<sup>-1</sup> showed positive and significant associations with grain yield plant<sup>-1</sup> ( $r = 0.78^{**}$ ), while grain yield plant<sup>-1</sup> was also positively and significantly associated with seed index ( $r = 0.54^*$ ). Correlations results demonstrated that seed index was negatively and significantly associated with seed index with biological yield plant<sup>-1</sup> ( $r = -0.62^{**}$ ). Correlations results also demonstrated that biological yield plant<sup>-1</sup> and harvest index positively and significantly associated with each other ( $r = 0.53^*$ ). High heritability estimates were observed for plant height, tillers plant<sup>-1</sup>, spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index.

### Conclusions

The following conclusions were drawn from the current research:

- The results revealed that genotypes differed significantly ( $P \leq 0.01$ ) for plant height, tillers plant<sup>-1</sup>, spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index.
- The varieties Kiran-95 and Sehar-2006 showed maximum values for different traits.
- The traits such as spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup> and seed index showed positive and significant correlations with grain yield plant<sup>-1</sup>; hence these traits may be given priority in selection.
- High heritability estimates were observed for plant height, tillers plant<sup>-1</sup>, spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, grain yield plant<sup>-1</sup>, seed index, biological yield plant<sup>-1</sup> and harvest index.
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