

RESEARCH ARTICLE

Correlation studies for yield and yield attributing characters in the commercial wheat cultivars

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Abstract

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 (RCBD) with three replications during rabi season, 2016-17. The study was carried to analysis correlation in ten wheat (*Triticum aestivum* L.) genotypes for eight different traits. The results revealed that genotypes differed significantly for plant height, tillers plant⁻¹, spike length, spikelets spike⁻¹, grains spike⁻¹, grain weight spike⁻¹, grain yield plant⁻¹ and seed index, demonstrating that evaluated materials retain enough variations for different quantitative traits. The variety TD-1 produced desirable short plants; maximum number of tillers plant⁻¹, longer spike length, maximum number of spikelets spike⁻¹, maximum number of grains spike⁻¹, heavier spike weight, higher grain yield plant⁻¹ and more seed index hence may be given priority in future breeding programs. The traits such as tillers plant⁻¹, spike length, spikelets spike⁻¹, grains spike⁻¹ and grain weight spike⁻¹ showed positive and significant associations with grain yield

plant⁻¹ hence these traits may be given priority in selection.

Key words: Correlation, genotype, wheat, yield

Introduction

Bread wheat, botanically named as *Triticum aestivum* L., is principal cereal grain cultivated worldwide (Belderok *et. al.*, 2000). It contributes proteins and calories to human diet (Ahmad *et. al.*, 2019). More than 60 percent of people in Pakistan are entirely dependent of wheat for their daily diet (Shah *et. al.*, 2017). The plant belongs to poaceae family, originates in the Ethiopian highlands (Ortiz *et. al.*, 2008), is leading cereal and staple food of almost half of the world population offers more than 20.00 percent of the total energy required by humans in food (Dupont *et. al.*, 2006). Its adaptation and diverse consumption in human diet proves its vital importance among cereals in Pakistan; and the average per capita utilization of wheat is 125 kg (Khan and Habib, 2003). 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). 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% (Ahmad 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 expanse of the proportionate change in the other (Ahmad *et al.*, 2008). 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. Keeping in view the present study was carried out to assess mean performance of bread wheat genotypes for yield traits and its related traits and to determine correlations between yield and yield components.

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, 2016-17. 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.

The observations were recorded as follows-

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.

Tillers plant⁻¹: When crop was matured, the number of fertile tillers plant⁻¹ 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.

Spikelets spike⁻¹: Spikelets spike⁻¹ of selected plants was counted after harvest in the laboratory.

Grains spike⁻¹: The total number of seeds spike⁻¹ of randomly selected spike was counted and the average number of seeds spike⁻¹ was calculated.

Grain weight spike⁻¹ (g): Randomly selected five spikes from each replication of each genotypes were threshed and weighed in grams with the help of electronic digital balance.

Grain yield plant⁻¹ (g): After harvesting, each plant was threshed separately by hand and grains were weighed on electronic digital balance and yield plant⁻¹ was weighed in grams.

Seed index (1000-grain weight) (g): Thousand seeds were counted at random and weighed in grams in the laboratories with the help of electronic digital balance.

Statistical Analysis

Data was statistically analyzed using analysis of variance according to Gomez and Gomez (1984), while least significant differences (LSD) test was used to compare the mean differences. Correlation coefficient analysis between different traits was computed according to Snedecor and Cochran (1987).

Results and discussion

The analysis of variance for all the characters is given in Table 1. The obtained results revealed that genotypes differed significantly ($P \leq 0.05$) for plant height, tillers plant⁻¹, spike length, spikelets spike⁻¹, grains spike⁻¹, grain weight spike⁻¹, grain yield plant⁻¹ and seed index. In connection of these results, a number of workers also obtained similar kind of findings, namely, Zeeshan *et al.* (2013), Baloch *et al.* (2014a), Baloch *et al.* (2014b), Soomro (2018). These researchers also found the significant genetic variance for the number of traits, such as, plant height, tillers plant⁻¹, spike length, grain yield plant⁻¹ and seed index.

Table 1: Mean squares from analysis of variance for various traits in bread wheat genotypes

Source of variance and degree of freedom	Plant height	Tillers plant ⁻¹	Spike length	Spikelets spike ⁻¹	Grains spike ⁻¹	Grain weight spike ⁻¹	Grain yield plant ⁻¹	Seed index
Replication (2)	0.32	0.19	0.02	0.66	2.31	0.01	0.13	0.05
Genotype (9)	162.09**	5.70**	6.30**	11.17**	29.85**	0.49**	18.13**	16.17**
Error (18)	0.37	0.18	0.22	0.26	0.78	0.01	0.15	0.49

**= Significant at 1% of probability level

Mean performance (Table 2) of all genotypes and correlation results (Table 3). Among the genotypes, Soghat showed maximum plant height (90.83 cm), while TD-1 showed dwarf plants with the minimum plant height of 66.23 cm. Similar findings were also reported previously by the Mirbahar *et al.* (2009) and Lie *et al.* (2017) they noted variation in plant height in different genotypes. Correlations results indicated that plant height showed negative and significant associations with tillers plant⁻¹ ($r = -0.38^*$), spikelets spike⁻¹ ($r = -0.50^{**}$), seed index ($r = -0.68^{**}$) and grain yield plant ($r = -0.36$), while plant height also showed negative but non-significant correlations with spike length ($r = -0.20$) and grain weight spike⁻¹ ($r = -0.18$). For the character tillers plant⁻¹, TD-1 produced maximum number of tillers plant⁻¹ (12.56), whereas Soghat produced minimum

number of tillers plant⁻¹ of 7.33. Correlations results showed that tillers plant⁻¹ showed positive and significant associations with spike length ($r = 0.41^*$), spikelets spike⁻¹ ($r = 0.53^{**}$), grains spike⁻¹ ($r = 0.36^*$), grain weight spike⁻¹ ($r = 0.41^*$) and grain yield plant ($r = 0.38^*$), nonetheless also showed positive but non-significant associations with seed index ($r = 0.29$). Saharan *et al.* (2007) and Ali *et al.* (2008) also found the similar results. Regarding spike length, TD-1 produced the longer spike (12.83 cm), whereas the NIA-Sarang produced shorter spike (8.96 cm). Correlations results displayed that spike length showed positive and significant associations with spikelets spike⁻¹ ($r = 0.64^{**}$), grain weight spike⁻¹ ($r = 0.50^{**}$) and grain yield plant⁻¹ ($r = 0.86^{**}$). However, also showed positive but non-significant correlations with grains spike⁻¹ ($r = 0.27$) seed index ($r = 0.15$). Our

results are in confirmation with those of Ali *et al.*, (2008); Mollasadeghi *et al.*, (2011) and Junejo (2014). About spikelets spike⁻¹, TD-1 produced the maximum number of spikelets spike⁻¹ (21.50), whereas the NIA-Sunder produced minimum number of spikelets spike⁻¹ (16.06). Correlations results exhibited that spikelets spike showed positive and significant associations with grains spike⁻¹ ($r = 0.36^*$), seed index ($r = 0.38^*$) and grain yield plant⁻¹ ($r = 0.75^{**}$), nevertheless also made positive but non-significant associations with Grain weight spike⁻¹ ($r = 0.21$). Other researchers namely Junejo (2014); Hussain *et al.*, (2014) and Parihar *et al.*, (2017) found the results in similar context. For the character grains spike⁻¹, TD-1 produced the maximum number of grains spike⁻¹ (59.70); however, the Marvi produced minimum number of grains spike⁻¹ (50.00). Correlations results exhibited that grains spike⁻¹ showed positive and significant associations with seed index ($r = 0.39^*$) and grain yield plant⁻¹ ($r = 0.36^*$). However, also showed positive but non-significant correlation with grain weight spike⁻¹ ($r = 0.14$). Our results are in affirmation with

those of Akram *et al.*, (2008); Khan and Dar (2009) and Parihar *et al.*, (2017). For the character grain weight spike⁻¹, TD-1 produced the maximum grain weight spike⁻¹ (3.76 g); however, the Hamal produced minimum grain weight spike⁻¹ (2.29 g). Correlations results revealed that grain weight spike⁻¹ showed positive and significant associations with seed index ($r = 0.36^*$) and grain yield plant⁻¹ ($r = 0.40^*$). Saharan *et al.* (2007) also found the same sort of results. For the trait grain yield plant⁻¹, TD-1 produced the maximum grain yield plant⁻¹ (26.57 g); however the NIA-Sundar produced minimum grain yield plant⁻¹ (19.15 g). Correlations results demonstrated that grain yield plant⁻¹ was positively but non-significantly associated with seed index ($r = 0.12$). The average performance of seed index is given in Table 2. The variety TD-1 produced the maximum weight of 1000 grain (49.30 g); on the other hand, Imdad-05 produced minimum seed index of 44.23 g. Our findings are in agreement with those of Singh *et al.*, (2017); Kashif *et al.*, (2007) and Koksai *et al.*, (2007).

Table 2: Mean performance of various traits in bread wheat genotypes

Genotypes	Plant height (cm)	Tillers plant ⁻¹	Spike length (cm)	Spikelets spike ⁻¹	Grains spike ⁻¹	Grain weight spike ⁻¹ (g)	Grain yield plant ⁻¹	1000-grain weight (g)
Imdad-05	90.70	9.46	12.76	21.10	53.13	2.79	23.14	44.23
Benazir	81.50	8.70	11.76	21.33	56.70	2.46	25.70	48.22
Marvi-2000	86.13	9.33	10.76	20.10	50.00	2.70	21.90	46.56
Hamal	88.23	8.50	9.33	17.63	51.33	2.29	20.33	41.96
TD-1	66.23	12.56	12.83	21.50	59.70	3.76	26.57	49.30
NIA-Sarang	87.20	8.66	8.96	19.33	53.06	2.55	19.50	48.56
NIA-Sundar	90.16	8.66	9.16	16.06	55.90	2.65	19.15	46.70
Kiran-95	88.70	8.43	9.46	18.46	55.86	2.47	21.50	44.33
Bhittai	86.46	8.36	10.13	17.46	52.13	2.90	20.16	47.30
Saughat	90.83	7.33	10.76	17.26	50.26	2.60	22.23	44.66
LSD (5%)	1.05	0.74	0.80	0.88	1.52	0.09	0.67	1.20

Table 3: Correlation coefficient (r) between different traits in bread wheat genotypes

Traits	Plant height	Tillers plant ⁻¹	Spike length	Spikelets spike ⁻¹	Grains spike ⁻¹	Grain weight spike ⁻¹	Seed index
Tillers plant ⁻¹	-0.38*						
Spike length	-0.20*	0.41*					
Spikelets spike ⁻¹	-0.50**	0.53**	0.64**				
Grains spike ⁻¹	-0.40*	0.36*	0.27	0.36*			
Grain weight spike ⁻¹	-0.18	0.41*	0.50**	0.21	0.14		
Seed index	-0.68**	0.29	0.15	0.38*	0.39*	0.36*	
Grain yield plant ⁻¹	-0.36*	0.38*	0.86**	0.75**	0.36*	0.40*	0.12

**, * = Significant at 1 and 5% of probability level, respectively

Conclusion

The results revealed that genotypes differed significantly for the traits studies, demonstrating that evaluated materials retain enough variations for different quantitative traits. The variety TD-1 produced desirable short plants; maximum number of tillers plant⁻¹, longer spike length, maximum number of spikelets spike⁻¹, maximum number of grains spike⁻¹, heavier spike weight, higher grain yield plant⁻¹ and more seed index hence may be given priority in future breeding programs.

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