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Correlation and regression studies of yield and yield associated traits in advance bread wheat (*Triticum aestivum L.*) Lines

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Abstract

The correlation and regression in advanced lines of hexaploid wheat were analyzed for nine yield contributing traits Wheat and Barely Research Institute, Tandojam, Sindh applying four replications in RCBD. The results regarding analysis of variance demonstrated highly significant values in wheat genotypes for all character which were studied resulting in a large amount of genetic variability, hence these genotypes would be extremely beneficial for the future breeding improvement programmes. In case of mean performance among genotypes, Sindhu (Check) manifested dwarf plants (73.25 cm), SAWYT/2 produced shorter peduncle length (30.39 cm), but SAWYT/1 exhibited maximum tillers plant^{-1}(7.23) and grain yield plant^{-1}(12.14 g), while SAWYT/9 articulated the longest spikes (12.60 cm) with maximum grains spike^{-1}(53.45), SAWYT/7 demonstrated more spikelets spike^{-1} (16.52) and SAWYT/4 expressed the most biological yield plant^{-1}(19.50 g) and seed index (48.63 g). The interrelationship results indicated that all the characters grain yield plant^{-1} as a dependent attribute was supported by all the characters very generously which behaved in a highly significant and positive way with the most important traits, grain yield with the correlation coefficient of r = 0.5609**, 0.7999**, 0.6989**, 0.7998**, 0.6998**, 0.5633**, 0.5965** and 0.6994**. The regression coefficient has been observed with the highest variance ingrain yield plant^{-1}with the contribution of 63.98% variation by tillers plant^{-1}, followed by spikelets spike^{-1} (48.97%) and biological yield plant^{-1} (48.91%) which proved the maximum increase in grain yield was made by these three characters. It was concluded that correlation coupled with regression among yield sharing traits articulated that selection of such good expressing characters would be very effective and progress for desirable traits from selection would also be very high. The identified advanced lines could be utilized in future wheat development programmes to improve yield linked characters.

Keywords: Wheat**,** Regression, Correlation, Peduncle, Spike

Introduction

Hexaploid wheat has become the world's most popular cereal crop. It provides about 20% of all food calories for humanity (Nayak *et al*., 2018). Internationally, bread wheat contributes

17% of the yield land offering nourishment for about 40% of the total population (Bhutto *et al*., 2016). Being staple food grain, its straw is also extremely vital as fodder for animals. As a result, it covers a central position in the economy and policies of agriculture (Mahmood and Sheikh, 2006). In Pakistan, the crop wheat is the leading cereal crop in the rabi season. In our country, its contribution in value added is 9.9% and 2% of GDP (Hussain *et al.*, 2017 and Banbhan *et al*., 2024). For the past many years, Pakistan imports wheat largely in the globe. According to population estimates, two billion people feed on wheat, accounting for 36 percent of the world's population, since wheat ranks first in terms of area and demand (Singh *et al*., 2017). Grain yield is the most principal and quantitative attribute which creates a lot of complexity because it is influenced by many yield contributing characteristics and environmental conditions. It is therefore very significant to have a knowledge about correlation different characters with yield. Components of yield correlation coefficients generally articulate a complex interaction chain (Majumder *et al*., 2008). Correlation along with regression would aid in the choice of the best characters whose selection would result in the betterment of a complex attribute such as yield. Correlation in the science of plant breeding is also vital for multiple causes and an improvement of one character is at the same time reflected on the switchover of another trait (Falconer, 1981). The estimates of correlation and degree of association between variables are very fruitful. On the other hand, regression supports for the functional linkage among the dependent and independent attributes (Joshi, 2005). From the genetic aspect, correlation also talks about the interrelationship between genes and the appearance of pleiotropic effects of genes (Djuric *et al.*, 2017). Considering the existing conditions, this study was carried out in order to evaluate the association between grain yield and its elements and to carry out grain yield regression on its other impacting characteristics.

Materials and Methods

The research experiment was conducted to study correlation and regression analysis in ten advanced lines of wheat genotypes for nine yield contributing traits. The experiment was laid out in randomized complete block design (RCBD) with 3 replications during Rabi season 2017-18 at Southern Wheat Research Station, Tandojam. The genotypes were SAWYT/1, SAWYT/2, SAWYT/3, SAWYT/4, SAWYT/5, SAWYT/6, SAWYT/7, SAWYT/8, SAWYT/9 and Sindhu (Check) and the attributes such as plant height, peduncle length, tillers plant^{-1}, spike length, spikelets spike^{-1}, grains spike^{-1}, grain yield plant^{-1}, seed index, biological yield plant^{-1} were analyzed.

Statistical analysis

ANOVA was utilized in the information as per the methodology proposed by Gomez and Gomez (1984). Average genotype efficiency was contrasted as indicated by Steel and Torrie (1960) According to Raghavrao (1983), correlation and regression analysis was estimated between various characters.

Results and Discussion

Plant breeders' primary goal is to create wheat varieties that are genetically stable, high yielding, and have other superior qualities. Grain yield in a wheat crop is an incredibly important trait that is the result of several contributing factors that influence yield and grain quality in a direct or indirect way in terms of path analysis. For such a trouble, relationship considers convey a superior comprehension about the relationship of various characters with grain yield (Dixet and Dubey, 1984) and the exploration of linkages among a wide scope of qualities is exceptionally productive to raisers in picking genotypes having gatherings of attractive attributes. Therefore, breeders necessarily want to explore the nature and type of interactions of these properties (Zafarnaderi *et al*., 2013).

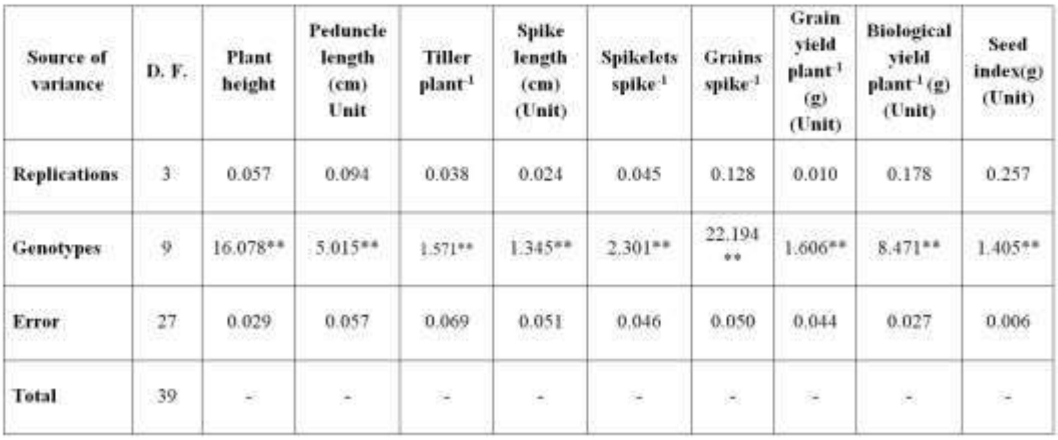
Analysis of variance

The variance analysis was calculated on 9 separate attributes from 10 advanced bread wheat lines as seen in Table 1. With regard to variance analysis, the results have shown that all genotypes are extremely significant for all traits. Khan *et al*. (2015) reported his material was genetically different for all the traits except grain yield plant^{-1}. Bhutto *et al*. (2016) also conducted an experiment with wheat genotypes for various yield and morphological traits and reported that the genotypes were highly significant. Whereas, Rajper *et al*. (2018) also found the genotypes significantly different from one another for all the attributes in his study.

Mean performance

The findings showed that the genotype SAWYT/1 and the genotype SAWYT/4 were occupied in the list of tallest plants (80.29 and 79.36 cm), but the most dwarf plants were reported b the genotype Sindhu (73.25 cm). In favour of peduncle length, the longest peduncle length (34.35 cm) was achieved by the genotype SAWYT/7 followed by the genotype SAWYT/6 (33.34 cm), whereas the genotype SAWYT/2 discovered the shortest peduncle length (30.39 cm). In case of tillers plant^{-1}, the most tillers plant^{-1} (7.23) were articulated by the genotype SAWYT/1 followed by the genotype SAWYT/8 (6.37), despite the fact the least tillers plant^{-1} (5.34) were detected by the advanced line SAWYT/7. Moreover, the longest spikes (12.60 cm) were produced in the genotype SAWYT/9 followed by the genotype SAWYT/2 (12.43 cm), while the shortest spikes were shaped by the genotype SAWYT/1 (11.13 cm). Furthermore, the maximum spikelets spike^{-1} (16.52) were counted in the genotype SAWYT/7 followed by the advanced line SAWYT/9 (16.32), nonetheless the minimum spikelets spike^{-1} were expressed by the wheat genotype SAWYT/3 (14.21). For grains spike^{-1}, the maximum grains spike^{-1} (53.45) were calculated by the genotype SAWYT/9 followed by the advanced line SAWYT/8 (53.30), but the minimum grains spike^{-1} was found in the genotype SAWYT/2 (45.33). The highest grain yield plant-1 (12.14 g) has been shown to be SAWYT/1 genotype followed by SAWYT/5 (11.74 g), but SAWYT/9 has been investigated for the lowest grain yield (10.17 g). The most biological yield plant^{-1} (19.50 g) was disclosed by the genotype SAWYT/4 followed by the genotype SAWYT/2 (17.68 g), whilst the minimum biological yield plant^{-1} was displayed by the genotype SAWYT/5 (13.86 g). The seed index results obtained overall seed index values of 48,63 g by advanced SAWTY/4 line and advanced SAWYT/2 line (47,77 g), while the least seed index values were seen by advanced SAWYT/1 line (46.57 g). Previous researchers, such as Bhutto *et al*. (2016), obtained positive results and stated that tillers per plant and grains per spike can be used to improve grain yield per plant in the history of bread wheat by using accurate selection criteria. On the other hand, Rajper *et al*. (2018) notified on the basis of their findings that components of yield can be considered as selective tools for bringing progress in wheat grain production of this crop. Ghallab *et al*. (2017) informed that grain yield plant^{-1} would be increased with the help of good building of plant organs and total plant biomass that resulted in improved grain yield plant^{-1}. These variables would work enormously for a stronger genotyping range in order to obtain high yielding genotypes, according to Lodhi *et al*. (2017).

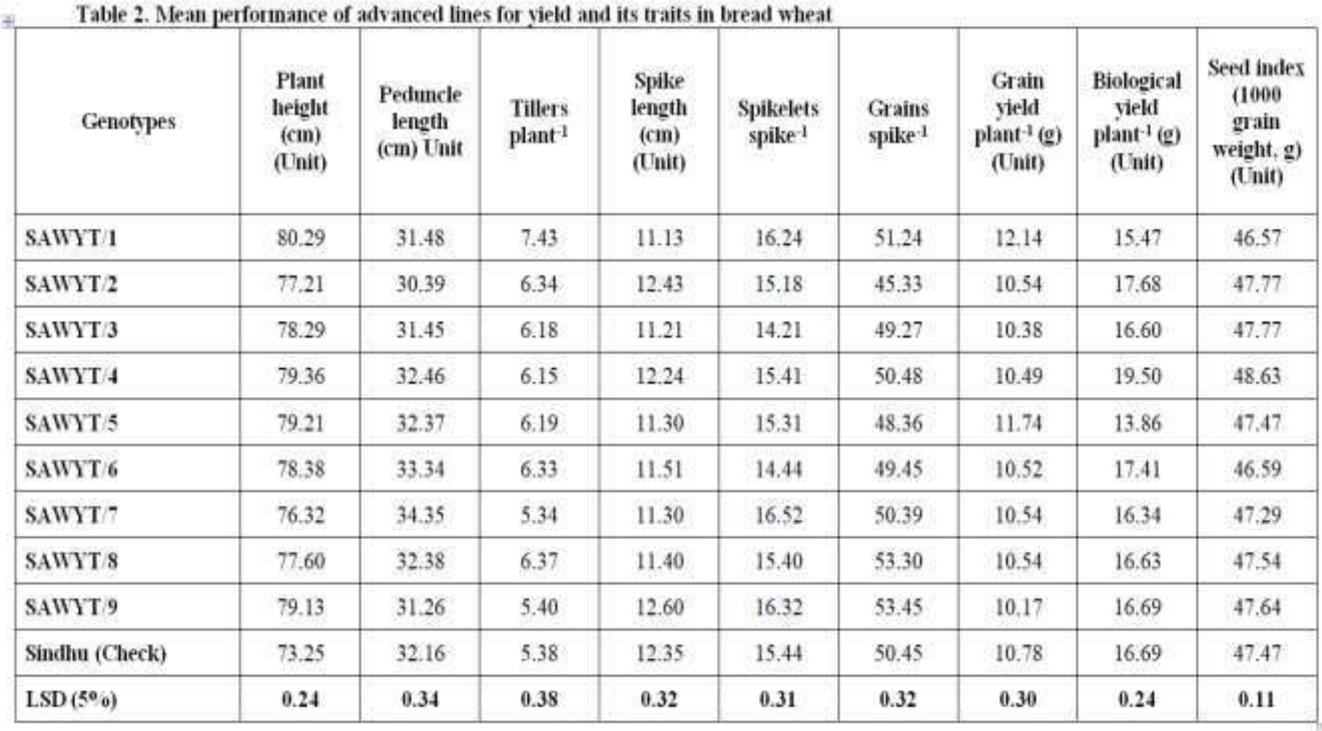
Table 1. Mean squares for different morphological attributes of advanced lines of hexaploid wheat



Source of variance	D. F.	Plant height	Peduncle length (cm) Unit	Tiller plant^{-1}	Spike length (cm) (Unit)	Spikelets spike^{-1}	Grains spike^{-1}	Grain yield plant^{-1} (g) (Unit)	Biological yield plant^{-1} (g) (Unit)	Seed index(g) (Unit)
Replications	3	0.057	0.094	0.038	0.024	0.045	0.128	0.010	0.178	0.257
Genotypes	9	16.078**	5.015**	1.571**	1.345**	2.301**	22.194 **	1.606**	8.471**	1.405**
Error	27	0.029	0.057	0.069	0.051	0.046	0.050	0.044	0.027	0.006
Total	39	-	-	-	-	-	-	-	-	-

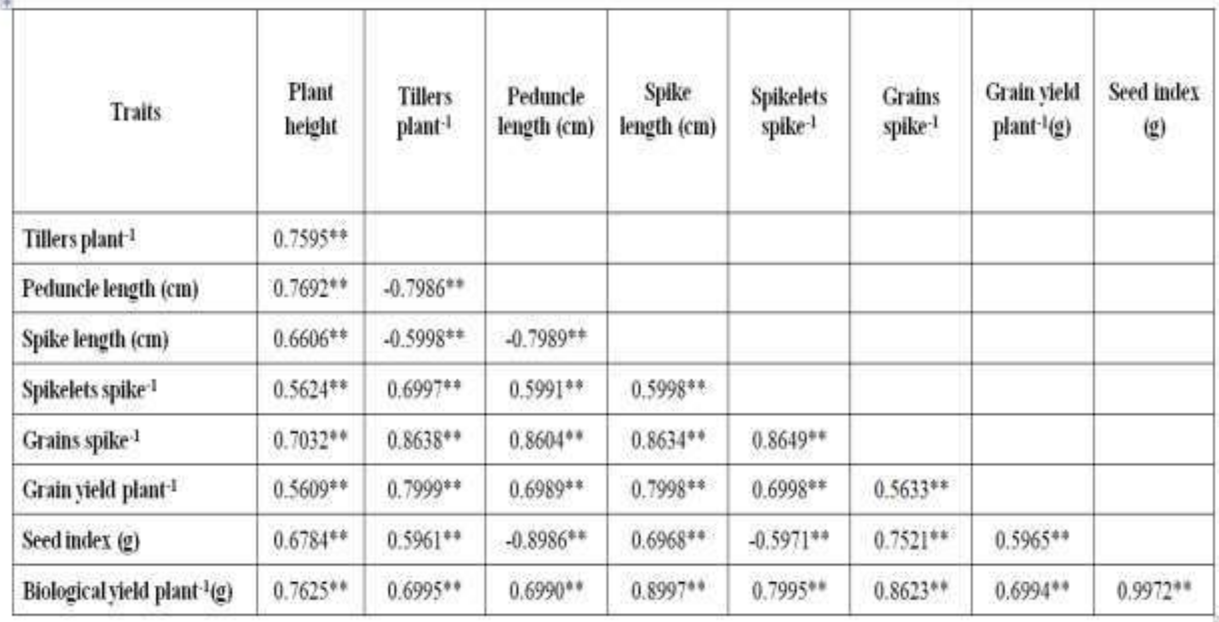
** = Highly significant at P ≤ 0.01% probability level

Table 2. Mean performance of advanced lines for yield and its traits in bread wheat



Genotypes	Plant height (cm) (Unit)	Peduncle length (cm) Unit	Tillers plant^{-1}	Spike length (cm) (Unit)	Spikelets spike^{-1}	Grains spike^{-1}	Grain yield plant^{-1} (g) (Unit)	Biological yield plant^{-1} (g) (Unit)	Seed index (1000 grain weight, g) (Unit)
SAWYT/1	80.29	31.48	7.43	11.13	16.24	51.24	12.14	15.47	46.57
SAWYT/2	77.21	30.39	6.34	12.43	15.18	45.33	10.54	17.68	47.77
SAWYT/3	78.29	31.45	6.18	11.21	14.21	49.27	10.38	16.60	47.77
SAWYT/4	79.36	32.46	6.15	12.24	15.41	50.48	10.49	19.50	48.63
SAWYT/5	79.21	32.37	6.19	11.30	15.31	48.36	11.74	13.86	47.47
SAWYT/6	78.38	33.34	6.33	11.51	14.44	49.45	10.52	17.41	46.59
SAWYT/7	76.32	34.35	5.34	11.30	16.52	50.39	10.54	16.34	47.29
SAWYT/8	77.60	32.38	6.37	11.40	15.40	53.30	10.54	16.63	47.54
SAWYT/9	79.13	31.26	5.40	12.60	16.32	53.45	10.17	16.69	47.64
Sindhu (Check)	73.25	32.16	5.38	12.35	15.44	50.45	10.78	16.69	47.47
LSD (5%)	**0.24**	**0.34**	**0.38**	**0.32**	**0.31**	**0.32**	**0.30**	**0.24**	**0.11**

Table 3. Correlation of coefficient (r) between morphological and yield traits bread wheat genotypes



Traits	Plant height	Tillers plant^{-1}	Peduncle length (cm)	Spike length (cm)	Spikelets spike^{-1}	Grains spike^{-1}	Grain yield plant^{-1}(g)	Seed index (g)
Tillers plant^{-1}	0.7595**							
Peduncle length (cm)	0.7692**	-0.7986**						
Spike length (cm)	0.6606**	-0.5998**	-0.7989**					
Spikelets spike^{-1}	0.5624**	0.6997**	0.5991**	0.5998**				
Grains spike^{-1}	0.7032**	0.8638**	0.8604**	0.8634**	0.8649**			
Grain yield plant^{-1}	0.5609**	0.7999**	0.6989**	0.7998**	0.6998**	0.5633**		
Seed index (g)	0.6784**	0.5961**	-0.8986**	0.6968**	-0.5971**	0.7521**	0.5965**	
Biological yield plant^{-1}(g)	0.7625**	0.6995**	0.6990**	0.8997**	0.7995**	0.8623**	0.6994**	0.9972**

** = Highly significant at $P \leq 0.01\%$ probability level

Table 4. Coefficient of correlation (r), coefficient of determination (r^2) and coefficient of regression (b) of yield components on grain yield plant^{-1}

Characters	Correlation (r)	Coefficient of determination (r^2)	Coefficient of regression (b)
Plant height (cm)	0.5609**	0.3146	0.3491
Peduncle length (cm)	0.6989**	0.4884	0.2792
Tillers plant^{-1}	0.7999**	0.6398	0.0212
Spike length (cm)	0.6968**	0.4855	0.5185
Spikelets spike^{-1}	0.6998**	0.4897	0.8230
Grains spike^{-1}	0.5633**	0.3173	0.0401
Seed index (g)	0.5965**	0.3558	0.0795
Biological yield plant^{-1} (g)	0.6994**	0.4891	0.0001

Correlation

The results regarding correlation indicated that plant height has been found to have highly important and positive associations with tillers plant^{-1} (0.7595**), grain yield plant^{-1} (0.8609**), seed index (0.6784**), and biological yield plant^{-1} (0.7625**).It formulated strongly important and negative relationships with peduncle length (-0.7692**), spike length (-0.6606**), spikelets spike^{-1} (-0.5624**), and grains per spike (-0.7032**).With the correlation coefficient of r = 0.6997**, 0.5638**, 0.7999**, 0.5961** and 0.6995**, tillers plant^{-1} was also extremely significantly and positively associated with spikelets spike^{-1}, grains spike^{-1}, grain yield plant^{-1}, seed index and biological yield plant^{-1}. Peduncle length (-0.7986**) and spike length (-0.5998**) had strongly important and negative relations with this attribute. Khan et al. (2015) have discovered a significant and favourable relationship between plant height and grains per spike. Sandhu and Mangat (1985) discovered a positive relation between grain yield and grains per spike, plant height, and seed index. With the correlations of r = 0.5991**, 0.8604**, 0.6989**, and 0.6990**, peduncle length was found to have favourable and strongly important correlations with spikelets spike^{-1}, grains spike^{-1}, grain yield plant^{-1} and biological yield plant^{-1}. While, it manifested negative, but significant connections with spike length (-0.7989**) and seed index (-0.8986**). Spike length had highly significant and positive associations with all of the traits having the coefficients of r = 0.5998**, 0.8634**, 0.7998**, 0.6968** and 0.8997**. Akhtar *et al.* (2011) reported about the strong correlations between grain yield and other characters. Mohamed *et al.* (2005) tested that the trait fertile tillers per plant is one of the main attributes which have an effect on the final grain yield. Positively meaningful coefficients of r = 0.8649**, 0.6998**, and 0.7995** were noted for spikelets spike^{-1} with grains spike^{-1}, grain yield plant^{-1} and biological yield plant^{-1}. It exposed negative but significant correlation with only seed index (-0.5971**). Bhutto et al. (2016) found the same finding and proposed these yields could be used as reliable selection criterion for increasing wheat production. Similar results were also observed by Bhushan *et al.* (2013).The relationships between grains per spike and grain yield per plant (0.5633**), seed index (0.7521**) and biological yield per plant (0.8623**) were found to be highly variable and optimistic. Grain yield per plant, on the other hand, was highly important and favourably related to seed index and biological yield per plant, with correlation coefficients of 0.5965** and 0.6994**, respectively. Desheva *et al.* (2016) observed that spikelets spike^{-1} had positive significant correlation with grains spike^{-1}. Ghafoor *et al.* (2013) achieved the same results of this trait for correlation with the other traits. Such discoveries had also been made by Chowdhry *et al.* (2000) in which he finalized that yield and its linked characters are premier contributors to grain yield. Gupta *et al.* (1999) testified correlation investigations and got the similar conclusions. Naghavi *et al.* (2015) revealed significant relationship between grain yield and number of spikes plant^{-1}.It was suggested by Tian *et al.* (2012) that grain yield is dependent attribute because it relies upon the others. With correlation coefficient values of r = 0.9972**, the seed index had only a strongly important and favourable relationship with biological yield plant^{-1}. Rajper *et al*. (2018) stated that hence components of yield can be considered as selective tool for bringing progress in wheat grain production of this crop. The interrelationship between total biomass and grain yield was expressed by Fellahi *et al*. (2013). Tsegaye *et al*. (2012) also looked at biological yield, which showed strong predictions in conjunction with grain yield.

Regression

To promote grain yield, the substantiality of the impressing characters that support yield is demarcated by regression (Farshadfar, 2004). The results indicated that (Table-4), between grain yield per plant and tillers per plant had the strongest association (r = 0.7999**), followed by spikelets per spike (r = 0.6998**) and biological yield per plant (r = 0.6994**). According to coefficient of determination, grain yield per plant is most affected by changes in tillers per plant (63.98%), spikelets per spike (48.97%), and biological yield per plant (48.91%). On the other hand, coefficient of regression displayed that increase in yield components simultaneously increase or decrease the grain yield per plant. The highest increase was identified ingrain yield per plant with the increase in tillers per plant (0.0212) followed by biological yield per plant(0.0001), whereas the maximum decrease in grain yield per plant was seen due to increase in spikelets spike^{-1} (0.8230). The features called peduncle length, tillers plant^{-1}, grain yield and biomass per plant were indicated by Kumar *et al*. (2018) as those parameters that are used in regression analysis in relation to over dominance genetic effect type. Fellahi *et al*. (2013) presented his results and suggested, the traits containing biological yield had approximately justified 99.7% variation in seed yield. Bhutto *et al*. (2016) also concluded that more height in plants will automatically will bring about more yield in related characters.

Conclusion

All genotypes were highly significant at 0.01 level of probability for all the studied attributes. The genotypes like Sindhu (Check), SAWYT/2, SAWYT/1, SAWYT/9, SAWYT/7 and SAWYT/4 demonstrated desirable results in all attributes. Grain yield was positively, negatively, significantly and non-significantly linked with all the characteristics. Regression coefficient indicated that the supreme dissimilarity in grain yield plant^{-1} was observed due to variation in tillers per plant followed by biological yield per plant and seed index. The highest increase was identified in grain yield with the increase in tillers plant^{-1} followed by biological yield plant^{-1}.

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