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Characterization of Bread Wheat Genotypes Using Spike Related Traits for Sustainable Yield Potential

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Abstract

Wheat is a cereal that is majorly consumed around the world. There is a dire need for the advancement of wheat cultivars that are producing high yield. The experiment was conducted to characterize the spike related traits of wheat genotypes. Twenty wheat genotypes comprising three replications were experimented using randomized complete block design. The difference was significant among the studied twenty genotypes revealed by analysis of variance. Correlation Pearson's revealed that the number of grains per spike (GPS) has positive relationship among all the studied traits such as the number of tillers per plant (NTP), spike weight (SWT), spike length (SL), and grain yield per plant (GYP). The GYP has a strong positive association with GPS (0.81**), GYS (0.78**), and SL (0.68**). The biological yield had a non-significant association with GYS (0.28) and GPS (0.13). All studied attributes have variations in the mean values which were represented by Radar analysis. The genotype Sadiq-21 was the best performing genotype among the SWT, GYS and BY followed by genotype Nawab-21 which performed best among the NTP, GYS and GPS and genotype Ghazi-19 which performed good among BY, SWT and GPS. The genotypes that were among the worst performing were Suren-10, Galaxy-13 and Borluag-16. The results of our study showed grain yield was mainly affected by NTP, GYS and GPS. For the improvement of wheat yield, these attributes must be improved for selection so that the yield of the wheat can be increased because these have a strong association with the grain yield.

Keywords: Yield; Wheat; Correlation; Grain; Tillers; Spike; Genotypes

Introduction

The widely consumed cereal which is of utmost importance for the people and is considered as staple food of Pakistan is bread wheat. In the world, Pakistan is major producer of wheat crop. In the year 2007-08, with the total of 683 million tons production with an average yield calculated to be around 2750 kg per hectare with the total area under the cultivation throughout the world was 221 million hectares with (Anwar *et al.*, 2009). In the year 2020-21, the total area 9,178 thousand hectares was under cultivation with an increased by 4.2% over the last cropping season of about 8,805 thousand hectares. This year had a unexceptional high production of wheat producing 27.293 M tons by uplift of 8.1% from the previous year (Bilal *et al.*, 2021).

There is a huge gap between the average yield of Pakistan, to fulfill this loss a severe demand exists for high reproductive cultivars in the country as the population of the country and the world is increasing drastically. Wheat is most demanding crop which is cultivated on the large area and contribute greatly in the world's trade. The wheat is basic source of food for the population of the Pakistan. As most of the population use wheat as staple food to fulfill their demands. So, the demand of food is continuously increasing. The gap of the potential varieties must be fulfilled, there is a need of new genotypes to be developed that produces more yield per hectare and have the potential to resist against many biotic and a-biotic diseases. Variation in the genetic variability which is important in plant breeding

program which existed in yield and traits that are related with the yield (Arain *et al.*, 2022; Talebi *et al.*, 2009). The interaction of the plants with the environment had drastic effects on their characteristics and the main output of the plant or crop which is yield. The GYS and GPS in wheat are very important attributes that were a major product of many factors contributing together directly or indirectly (Waqar-Ul-Haq *et al.*, 2008). Wheat yield can be increased by screening and developing the genotypes that can produce more grains in every environment with different biotic and abiotic factors. The association among the traits is very essential to determine the association around the different traits with each other having positive or negative effects present in the developing cultivars for the selection of suitable adoptive program (Bnejdi *et al.*, 2010). The yield of the plants can only increase if there is genetic variation present in the cultivars and they have better adaptability for every environment (Ali *et al.*, 2008). Many researchers in the past have studied and analyzed that person's correlation coefficient of different traits that are related to yield are useful for the genetic improvement in wheat (Shahid *et al.*, 2002); (Aycicek *et al.*, 2006); (Akram *et al.*, 2008). Many plant scientists have analyzed that yield attributes such as NTP have significant contributions to the grain yield potential, it was also summarized that GPS, SL, and GYP are the traits which are mainly contributed to the yield in wheat. It's also concluded that the grain yield showed a positive and significant correlation with the NTP (Qasim *et al.*, 2008). The relation between different traits that were needs to improve exhibited the positive correlation. This correlation had a direct effect on the yield. In the earlier experiments from different researchers, the researcher concluded that the SL and spike width observed positive and significant correlation with the yield of grain (Akram *et al.*, 2008), that similar statement was also concluded by (Shahid *et al.*, 2002) that the yield of the grain was positively associated with the spike weight of the wheat. It is also been concluded that the grain yield (GY) exhibits a highly significant and positive association with the NTP and spikelet per spike (SPS) (Sharma *et al.*, 2003). The current experiment was to analyze the information present in the study of the association of the traits that are related to yield in the bread wheat under normal conditions to screen the best performing genotypes as shown in Figure No. 1. The figure showed the performance of the genotypes among the studied traits. The yield-related traits that were significant and positively associated with the yield were the number of tillers per plant as the more the NTP more will be the GPS (number of grains per spike) producing grains and the more will be the yield of the plant and vice versa (D Kumar *et al.*, 2015). Moving towards the SL (length of the spike) which is positively correlated with the GPS, the grains which are present in the middle

of the spike are healthier hence increasing the yield (MJ Baloch *et al.*, 2016). The GPS was also significantly related to yield as the more the number of grains in the spike greater the yield of the plant (MS Baloch *et al.*, 2012). The researchers explained the association of spike density with the other spike-related traits that exhibited a positive association with spike weight, spike length, and the number of grains per spike while, it had a non-significant association with the biological yield but had no effect on the yield of the crop as mentioned by (Yousaf, *et al.*, 2017). In the earlier experiments from different researchers, the researchers concluded that the spike length and spike width showed a significant positive association with the yield of grains of plants (Akram *et al.*, 2008), a similar statement was also revealed by (Shahid *et al.*, 2002) that the yield of the grains is positively correlated with the spike weight of the wheat. It is also been concluded that the grain yield exhibits a positive correlation which is highly significant with the NTP and spikelets per spike (Sharma *et al.*, 2003). The positive association between the yield-related traits helps us to increase the yield. When plants tillers and spikelets were increased, the output of crop also increased. The present experiment was carried out to analyze current knowledge on the association of the components of yield with the yield of the wheat under normal conditions to screen the best-performing genotypes. The objectives of the current experiment were to increase the yield of the wheat crop to assess the genotypes that are performing best and have desirable traits for improving the yield of the wheat crop and to evaluate and screen the given wheat genotypes that have good morphological attributes.

Materials and Methods

Research design: The recent study was carried out in the experimental block area of the department of Plant Breeding and Genetics, The Islamia University of Bahawalpur in the recent cropping season of 2021-22 under non-stressed conditions. Twenty wheat genotypes were screened and evaluated for grain yield along with the yield-related traits. The crop was cultivated in the month of November, 2021 in a plot size of 3 meters single row in triplicated randomized complete block design (Anwar *et al.*, 2009). The varieties were collected from the Regional Agricultural Research Institute, Bahawalpur. The list of varieties were given in table No. 1. The space between the seed and the rows was fixed at 14 and 28 cm, respectively.

Experimental site: The soil was pulverized by rotavating and turned-up followed by planking at the end. The ratio of the fertilizer was applied at the rate of 150:85:50 kg of N: P: K per hectare (Anwar *et al.*, 2009). The seed was planted by a planter at the seed rate of 100 kg per hectare and the field was irrigated after the drilling of the seed. After 30 days of the sowing, the first

irrigation was applied to the wheat crop and three more irrigation were applied to the crop at subsequent critical stages which are of vital importance for the yield (flowering, anthesis, and filling of grains). The field was cleared from weeds physically such that all the nutrients could be taken up by plants. The selection of ten random plants which were strong in vigor was selected at the maturity level, and the data was collected for NTP, SL, SWI, SWT, GYS, GYP, BY, and GPS.

Statistical analysis: The data were analyzed to get an analysis of variance (ANOVA) according to a method that was given by (Steel *et al.*, 1997). The analysis of variance and Pearson's correlation analysis was evaluated and analyzed by statistix version 8.1 and RADAR were analyzed by Microsoft word 2015. Pearson's correlation association between yield and traits related to it was computed according to given formula

$$r = \frac{n(\sum xy) - (\sum x)(\sum y)}{\sqrt{[n \sum x^2 - (\sum x)^2][n \sum y^2 - (\sum y)^2]}}$$

Results

The results of the analysis of variance of studied attributes were represented in table No. 1. The analysis of studied traits represented significant differences among the given genotypes that showed the presence of high variability among the crop as shown in table No. 1. The analysis showed the mean square of genotypes and replication.

The correlation results of given yield-related traits were represented in table No. 2. The number of tillers had a highly significant mean square value (27.34**) revealed by analysis of variance. A positive highly significant association of NTP with BY was revealed. The correlation was significant and positive between NTP and GYS, GPS, and GYP. The trait NTP observed a non-significant positive association with the SL (0.23), SWI (0.31), and SWT (0.002). Nawab-21 had the highest number of tillers (13.67), the Nawab-21 had the best grain yield per spike as related to other remaining genotypes. The genotypes Azrik Dera, Fakhr-e-Bhakar, Akbar-19, Ihsan-16, and Gold-16, had average grain yield (11.33), while the genotypes Bhakar Star, Zincol-16, and Anaaj-17 had the low number of tillers and minimum grain yield (10.33) as shown in figure No. 1. The number of tillers significantly contribute to the grain yield as more the NTP, more will be the yield of the plant. The given mean values of the yield-related traits showed variability was present among the genotypes.

The SL had a significant and positive association with the SWI (0.26*) and a positively high significant association with the SWT (0.6**), GYS (0.68**), GPS (0.62**), and GYP (0.58**) while the SL had non-significant and positive association with the BY that is

0.21. The mean square value for spike length (2.34**) was shown in table No. 1. The genotype 1 showed maximum length of a spike (19.00cm). The Nawab-21 had (18.46cm) spike length while genotypes Anaaj-17, NARC-9, Jauhar-16, Ihsan-16, and Ujala-16 had the medium spike length (17cm). The minimum length of the spike was revealed by genotype Borlaug-16 (15.58cm). The spike length had a relation with the GPS, more the SL; the greater will be the GPS as shown in figure No. 1.

Spike width revealed a negative association with the biological yield which was non-significant (-0.25) and grain yield per plant (-0.12) and non-significant and positive with spike weight (0.11). The correlation was significantly positive exhibited between two attributes spike width (SWI) and GYS (0.25*) and GPS (0.36*). Maximum spike width showed by the Sadiq-21 (1.24cm). The average spike width showed by the genotypes Jauhar-16, Anaaj-17, Sindhu-16, Tuaban-10, and Gold-16 had a spike width (1.11cm). The minimum spike width had Suren-10 (1.06cm) as shown in figure No. 2. The mean square value of spike width was (0.06**) as shown in table No. 2.

The spike weight (SWT) correlated highly significantly and positively with the GYS (0.56**), GPS (0.63**), and GYP (0.74**) while the spike weight mentioned an on-significant association with biological yield (0.19). In figure No. 2, spike weight showed that Sadiq-21 maximum spike weight (4.00g). The genotypes Zincol-16, Ihsan-16, Gold-16, and Ujala-16 had an average range of spike weight (3.83g) and the Galaxy-16 had a minimum value of spike weight (2.50g). The mean square value of the spike weight was 0.57** shown in the analysis of variance as given in table No. 2.

The grains yield per spike (GYS) exhibited a non-significant and positive association with BY (0.28) and had a positive and highly significant association with the GYP (0.68**) and GYS (0.78**). Nawab-21 reported the maximum grain yield per spike (3.5g). The genotypes Jauhar-16, Sindhu-16, Akbar-19, Zincol-16, and Tuaban-10 reported an average value of grain yield per spike (3.00g) as shown in figure No. 2. The Borlaug-16 had the lowest value of GYS (2.00g). The mean square value of analysis of variance showed by grain yield per spike was 0.46** as showed in table No. 2.

The mean square value of grain per spike was 15.54** as shown in the Table No.2. The GPS had a positive highly significant association with the GYP with the value of 0.81** while the biological yield (BY) indicated a positive association while non-significant with GYS (0.13). In the studied genotypes, the Sadiq-21 had the highest GPS (38.23g) as shown in figure No. 1. The genotypes PARS-9, Zincol-16, and Gold-16 had a medium range of GPS (33g) and the Galaxy-13 had the lowest GPS (29.30g).

The mean square revealed by the biological yield was 3.51* as shown in table No. 2. Biological yield had a positive and significant association with GYP (0.27*). In table No. 3, BY recorded positive results with the GYP. BY also had a direct effect on the yield. Nawab-21 had the maximum biological yield (22.37g). The genotypes NARC-9, Akbar-19, Bhakar Star, and Ujala-16 had an average value of biological yield (20.17g) and the Borlaug-16 had a minimum biological yield (18.43g) as shown in figure No. 1. The mean square value showed by the grain yield per plant was 13.78** as showed in

the table No. 2. Data collected for grain yield per plant reported that the Sadiq-21 had the highest range of grain yield (14.23g). The genotypes Jauhar-16, Bhakar Star, and Tuaban-10 had an average scale value of grain yield per plant (10.23g). And the Suren-10 had a minimum range of grain yield per plant (7.10g) as shown in figure No. 1. The mean values of all the studied genotypes that were performing best, and worst are mentioned in table No. 4. These mean values indicated that variability was present in the genotypes.

Table No. 1: List of Genotypes used in current Experiment

Genotypes	Name	Genotypes	Names	Genotypes	Names	Genotypes	Names
G1	Azrik Dera	G6	Galaxy-13	G11	Sadiq-21	G16	Ihsan-16
G2	Fakhr-e-Bhakar	G7	Anaaj-17	G12	Akbar-19	G17	Ghazi-19
G3	Nawab-21	G8	Bhakar Star	G13	Zincol-16	G18	Gold-16
G4	NARC-9	G9	Sindhu-16	G14	Borlaug-16	G19	Suren-10
G5	Jauhar-16	G10	PARS-9	G15	Tuaban-10	G20	Ujala-16

Table No. 2: Analysis of variance of all studied traits of the given wheat genotypes

Source	Df	NTP	SL	SWI	SWT	GYS	GPS	BY	GYP
REP	2	2.2789	0.02511	0.00127	1.55	1.67917	1.0445	3.05267	0.042
GEN	19	27.34**	2.34**	0.06**	0.57**	0.46**	15.54**	3.51*	13.78**
Error	38	1.6104	0.10213	0.00238	0.21667	0.21864	0.3191	1.56302	0.0662
Total	59								

** (highly significant), * (significant), Df (degree of freedom), REP (replication), GEN (genotype), NTP (number of tillers per plant), SL (spike length), SWI (spike width), SWT (spike weight), GYS (grain yield per spike), GPS (number of grains per spike), BY (biological yield) and GYP (grain yield per plant).

Table No. 3: Pearson's Correlation coefficient shows association among all studied traits

	NTP	SL	SWI	SWT	GYS	GPS	BY
SL	0.23ns						
SWI	0.31ns	0.26*					
SWT	0.002ns	0.6**	0.11ns				
GYS	0.31*	0.68**	0.25*	0.56**			
GPS	0.33*	0.62**	0.36*	0.63**	0.78**		
BY	0.51**	0.21ns	-0.25ns	0.19ns	0.28ns	0.13ns	
GYP	0.29*	0.58**	-0.12ns	0.74**	0.68**	0.81**	0.27*

** (highly significant), * (significant), ns (non-significant), NTP (number of tillers per plant), SL (spike length), SWI (spike width), SWT (spike weight), GYS (grain yield per spike), GPS (number of grains per spike), BY (biological yield) and GYP (grain yield per plant).

Table No. 4: Best and worst performances of genotypes with their higher and lower mean values

Traits	Genotype number and their higher mean values	Genotype number and their lower mean values
Number of Tillers	G3(13.66), G11(12.22), G17(11.66)	G19(10.33), G6(10.34), G14(10.33)
Spike Length	G11(19), G3(18.45), G17(18.16)	G19(15.57), G14(16.28), G6(16.38)
Spike width	G11(1.24), G17(1.22), G3(1.23)	G14(1.10), G6(1.10), G19(1.06)
Spike weight	G11(4), G3(3.83), G17(3.5)	G6(2.5), G19(2.5), G14(3)
Grain yield per spike	G3(3.5), G11(3.5), G17(3.5)	G14(2), G6(2.5), G19(2.5)
Grain yield per plant	G11(14.23), G3(13.66), G17(13.03)	G19(7.1), G14(7.26), G6(7.53)
Biological yield	G17(22.26), G3(22.3), G11(22.26)	G14(18.43), G6(19.16), G19(19.5)
Grain per spike	G11(38.23), G3(37.46), G17(37.36)	G6(29.3), G19(31.66), G14(32.4)

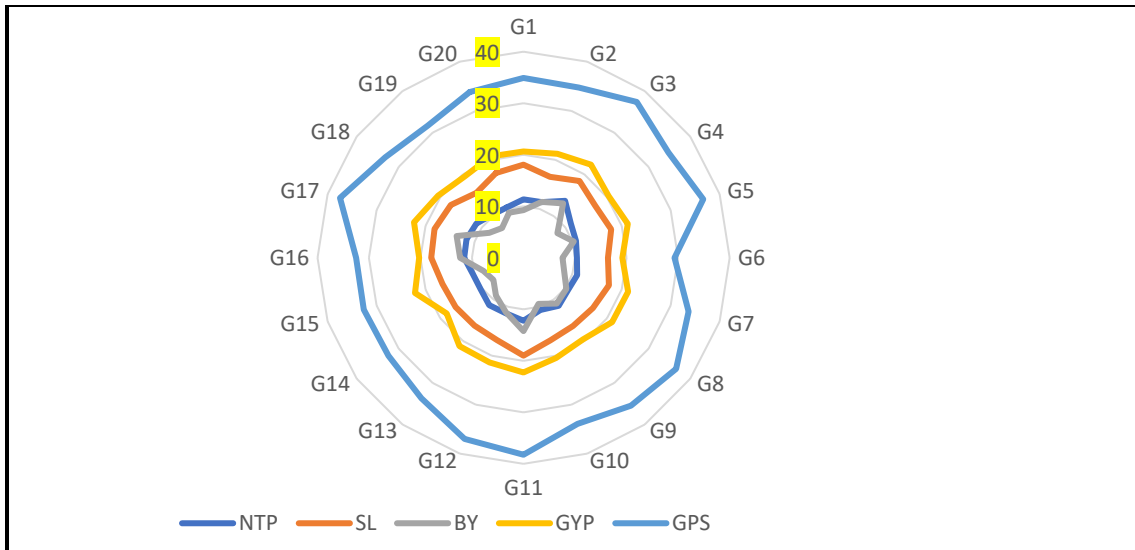


Figure No.1 RADAR graph showing the performance of 20 genotypes for (SL) Spike length, (NTP) Number of tillers, (BY) Biological yield, (GYP) Grain yield per plant, (GPS) Grain yield per spike.

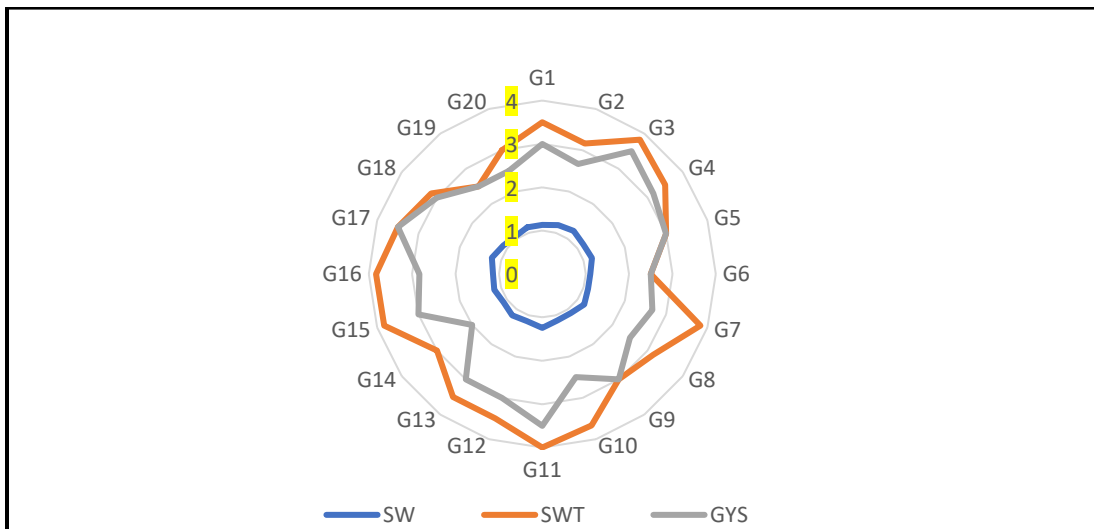


Figure No.2 RADAR graph showing the performance of 20 genotypes for (SW) Spike width, (GYS) Grain yield per spike and (SWT) Spike weight.

Discussion

In the present study, the ANOVA (analysis of variance) observed that all the attributes had positive differences. The traits that had highly significant associations like SL, NTP, SWI, GYS, GPS, SWT, and GYP. The highest value for the mean square revealed the NTP (27.34**) followed by GYP (13.78**) as mentioned in table No. 2. Similar results were also revealed by a researcher that traits showed significant variation among the given traits of the plants (Tripathi et al., 2011).

In the current study, NTP was associated highly significantly with biological yield (0.51**) as mentioned in table No. 2. The number of tillers directly affected the yield of the wheat as the plant had minimum

number of tillers then yield became low. These results were also similar to the researcher (Saxena et al., 2007), the researchers reported that tillers were the main contributor to the yield. Earlier experiment results revealed by (S Kumar et al., 2010); (Muhammad et al., 2010) also mentioned the presence of a positive and significant association between NTP and grain yield (GY). The tillers of plants revealed a non-significant association with SL (0.23), SWI (0.31), and SWT (0.002) which means BY was not affected by these traits. The correlation of NTP with the spike length was non-significant but the yield of the crop was not affected by this association. These results were in confirmation with (Masood et al., 2014). He also observed the non-significant association of NTP with SL.

In our study, the trait spike length had a significant association with the traits like SWI, SWT, GYS, GPS, and GYP such that an increase in these traits will significantly increase the spike length. The same results were mentioned by (Sokoto *et al.*, 2012). He also observed the SL had an association that was positive with GYS and GPS. These results contradict that the genotypes that had long SL give more grain yield than those with short SL (Khan *et al.*, 2017). SL had a non-significant correlation with the BY such that spike length did not affect the biological yield. The association of SL with other studied traits were shown in Figure No. 1. The spike length was strongly associated with GYP, as SL increases the GYP also increases. Spike length was a source of assimilation that was closer to caryopsis and considered an essential trait of the yield. In the current study, the spike width was significantly associated with the GYS and GPS such that they had a direct effect on the spike width. These results were in agreement with (Desheva, 2016). Spikes had remained green and functional with the awns (Sharma *et al.*, 2003). SWT, BY, SL and GPS showed positive and significant associations with the grain yield observed under the normal environment (Peymaninia *et al.*, 2012a).

In the experiment, spike width indicated a positive and significant association with GPS and SWT. Spike width had a positive association with SWT and GPS. The same results were confirmed by (Yousaf *et al.*, 2017). But these findings were not confirmed by (Farooq *et al.*, 2011). Spike density had a negatively non-significant association with the biological yield. But spike density showed a significant association with grain yield per spike. As it observed the positive correlation with spike-related traits, so, spike density had not affected the yield of the crop (Mecha *et al.*, 2017).

In the current experiment, the spike weight had a significant association with the GYS, GPS, and GYP so they had a direct effect on the spike weight and biological yield did not effect on the spike weight. The results were the same as those (Mollasadeghi *et al.*, 2011) that showed spike weight increase then GYS and GYP also increased. Positive association and significant results were observed between SWT and grain yield under normal conditions. The spike weight direct effect the yield of the crop because with the increase in spike weight the yield increases. Under two-thirds irrigation and one-third irrigation, the highest positive and negative indirect impacts on the grain output were likewise connected with spike weight per plant and harvest index (Zare *et al.*, 2017).

The researcher (Abderrahmane *et al.*, 2013) also mentioned the highly positive significant association of GYS with grain yield. According to the simple correlation results, the GYS was a positive and highly significant association with the attributes GYP and GYS

under the normal irrigated condition. As shown in Figure No. 2, the GYS had a strong connection with spike weight. The grain yield per spike positively correlate with spike weight and this association had a positive effect on the yield of the crop.

The GPS positively correlated with SL, GYS, and BY. The number of grain per spike (GPS) had positive relation with grain yield similar findings were revealed by (Ahmad *et al.*, 2016) and another researcher (Fakhar *et al.*, 2015; Sarfraz *et al.*, 2020) also concluded similar results. It has been reported that great effect was indicated in GPS, BY, and SWT had the most positive and direct effect on grain yield (Mollasadeghi *et al.*, 2011). Examining the 19 wheat advanced lines in Gorgan indicated the relationship of yield components and yield exhibited a little direct effect of 1000 grain weight while the number of grains per spike had a high direct effect on yield (Soghi *et al.*, 2006). And the 1000-grain weight and GYS increased the indirect effect of the number of grains per spike. The study of genetic variation of wheat studied traits indicated that the GPS showed positive and a significant association with yield (Akram *et al.*, 2008); (AL-jana *et al.*).

Characters that had a direct association with yield were selected, their association with the other given traits would simultaneously affect indirectly the yield. The correlation of biological yield with other traits affected the yield of the crop (Abro *et al.*, 2022; Ahmed *et al.*, 2022; Bhushan *et al.*, 2013). The biological yield was positively and highly associated with grain yield per plant. These traits were positively related and had a significant correlation between them. These results were confirmed in a research report (Peymaninia *et al.*, 2012b; Soomro *et al.*, 2022). In Figure No. 1, the association of biological yield with the other traits was observed. The BY was directly affected by the NTP in the enhancement of the yield of crops.

Conclusion

In the current study, 20 genotypes were screened at maturity level under the normal irrigated condition using randomized complete block design (RCBD). The results of the studied traits like NTP, SL, SWI, SWT, GYS, BY, GYP, and GPS revealed that for all the studied attributes, the genotypes differed significantly. The genotypes that are performing best among all the genotypes in this condition were considered to have desirable traits and could be selected and used for future breeding programs. These genotypes were Nawab-21, Sadiq-21, and Ghazi-19. By using the selection criteria, genotypes that have desired traits and perform best in the field were selected. A correlation study revealed that number of grains per spike and spike weight had a strong association among all the studied traits, suggesting that more importance should be given to this trait for improving the yield in wheat. The current study

explained the effect of the attributes on the yield which help in examining the traits that had a direct association with the yield. By the present investigation, the best-performing genotypes for the yield attributes can be preferred, which would help in the breeding program in the future.

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