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# EVALUATION OF F4 BREAD WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES FOR GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND CORRELATION STUDIES

**[a]Amir Sohail*, [a]Hidayatur Rahman, [a]Farhat Ullah, [a]Syed M.A. Shah, [b]Tanvir Burni, [c]Shahzad Ali**
[a] *Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Pakistan.*
[b] *Department of Botany, University of Peshawar, Pakistan.*
[c] *College of Agronomy, Northwest A & F University, Yangling, China.*

## ABSTRACT

This research was carried out to check genetic variability, heritability and genetic advance in 11 $F_4$ bread wheat (*Triticum aestivum* L.) genotypes (10 $F_4$ lines and one check) in a randomized block design with three replications at the University of Agriculture Peshawar, Pakistan during 2015-16. Data was/were taken on parameters such as days to heading (days), plant height (cm), flag leaf area ($cm^2$), spike length (cm), grain weight spike$^{-1}$ (g), 1000-grain weight (g), grain yield plant$^{-1}$ (g), biological yield plant$^{-1}$ (g) and harvest index (%). The statistically significant difference(s) was/were detected for the investigated traits. The high magnitude of heritability (>0.62) was noted for all parameters except spike length (0.57) which was moderate. Low expected genetic advance was recorded for days to heading (3.90%) and spike length (8.13%), moderate expected genetic advance was observed for plant height (9.95%), grain weight spike$^{-1}$ (11.54%) and 1000 grain weight (13.41%), while high expected genetic advance was noted for flag leaf area (24.72%), grain yield plant$^{-1}$ (20.45%), biological yield plant$^{-1}$ (23.64%) and harvest index (24%). Grain yield plant$^{-1}$ was non-significantly and positively correlated with days to heading (rG = 0.19$^{NS}$ and rP = 0.07 $^{NS}$), plant height (rG = 0.30 $^{NS}$ and rP = 0.26 $^{NS}$), flag leaf area (rG = 0.25 $^{NS}$ and rP = 0.18 $^{NS}$), spike length (rG = 0.01 $^{NS}$ and rP = 0.07 $^{NS}$), grain weight spike$^{-1}$ (rG = 0.28 $^{NS}$ and rP = 0.22 $^{NS}$) and 1000-grain weight (rG = 0.02 $^{NS}$ and rP = 0.07 $^{NS}$) at both genotypic and phenotypic levels. While significantly and positively correlated with biological yield plant$^{-1}$ (rG = 0.34* and rP = 0.33*) and harvest index (rG = 0.58** and rP = 0.66**) at both genotypic and phenotypic levels. High heritability showed that these traits are under genetic control and single plant selection could be started in $F_5$ generation. The strong correlation of grain yield plant$^{-1}$ with the mentioned traits showed that grain yield could be indirectly improved by improving these traits.

**Keywords**: Wheat (*Triticum aestivcum* L.) genotypes, heritability, genetic advance, genotypic and phenotypic correlation.

## INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is a hexaploid species having chromosome number 2n=6x=42, and it belongs to the family of Gramineae. Wheat is a staple diet of Pakistan and overrides all the crops in area and production. In Pakistan wheat account for 70% of the cereals and over 36% of the country acreage is devoted to wheat cultivation. Pakistan is the 4$^{th}$ wheat producer in Asia continent and stood 11$^{th}$ worldwide (PAR, 2016). During 2015-16 the worlds wheat production was 733.8 million tons, while in Pakistan the production was 27.52 million tons (FAOSTAT, 2016).

Heritability estimates provide a message that how much a character is controlled genetically (Mohtasham *et al.* 2012). Knowledge of heritability of the characters leads the breeder to prognosticate the behavior of generation and helps the breeder in doing the selection. Breeding program success reckon on the amount of genetic variation in breeding material available. Improvement in any characters can be achieved through the knowledge of genetic parameter and heritability. Study of phenotypic, genotypic coefficient of variation, heritability and genetic advance helps in finding the

* Corresponding Author:
Email: amirsohail@aup.edu.pk
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nature and magnitude of variation in breeding material. Crop improvement depends on the existence of genetic variability in germplasm Khan *et. al.* (2015). In any breeding program estimation of genetic parameters are taken into consideration for the improvement in the economic characters (Inamullah *et al., 2006)*.

Heritability is the proportion of genetic variation to phenotypic variation. Variation for any trait in a segregation population could be due to genetic and environmental components. As known, the heritability of a trait is used as a tool for the effectiveness of selection response in segregating population following hybridization. It estimates the index of transmissibility of genes controlling the traits. When knowledge of heritability is available then selection for any breeding program can be predicted. Since the expected gain is the function of heritability, high heritability coupled with high selection response is desired for selection (Larik and Joshi, 2004*)*. In selection program selection of superior phenotype is possible only when the phenotype and genotype are correlated. Keeping in view the above-mentioned points the research was conducted to explore the information on genetic variability, heritability, selection response and genotypic as well as phenotypic correlation among the traits for the development of superior genotype by identifying of traits having a direct effect on yield as criteria of selection.

**MATERIALS AND METHODS**

A set of 10 $F_4$ wheat (*Triticum aestivum* L.) lines along with check cultivar i.e. Barsat×Siren, Tatara×Siren, Tatara×anbaz, Barsat×Janbaz, AUP-5008×Siren, Salim-2000×Siren, Salim-2000×Janbaz, AUP-5008×Janbaz, Tatara×PS-2005, AUP-5008×PS-2005 and Tatara (Check) were evaluated in randomized block design with three replications at the University of Agriculture Peshawar, Pakistan during 2014-15. Each line was sown in three rows with a row length of three-meter and row to row distance was 0.3 meter. For data collection ten randomly plants were selected from three rows. Data were recorded on days to heading (days), plant height (cm), flag leaf area ($cm^2$), spike length (cm), grain weight $spike^{-1}$ (g), 1000-grain weight (g), grain yield $plant^{-1}$(g), biological yield $plant^{-1}$ (g) and harvest index (%). Standard cultural practices including soil fertilization, irrigation, hoeing, weeding etc. procedures were applied during the whole cropping season as recommended to growers.

**Statistical Analysis:** Data taken on each trait were exposed to the analysis of variance (ANOVA) technique as determined by Steel and Torrie (1980). Means separation using LSD test was used at a probability level of 5%. Broad-sense heritability for the $F_4$ populations was computed using the general formula:

$$h^2_{B.S} = Vg/Vp$$

Where, $h^2_{B.S}$ = broad sense heritability; Vg and Vp are the genotypic and phenotypic variances of the trait, respectively.

Expected genetic advance (GA) was computed using the following method (Allard, 1960).

$$GA = i \times S \times h^2$$

Where, GA=expected genetic advance, i = selection intensity at 5% i.e 2.06, S= phenotypic standard deviation and $h^2_{B.S}$ = coefficient of heritability (broad sense).

Whereas, the genotypic and phenotypic correlation among the characters were calculated following Singh and Chaudhery (2005).

**RESULTS AND DISCUSSION**

**Days to heading:** Mean squares revealed significant differences (P≤0.01) among $F_4$ wheat lines for days to heading (Table 1). The coefficient of variation was 0.95% and coefficient of determination was 0.89. Mean data ranged from 112 to 121 among $F_4$ wheat lines. Minimum (112) days of heading was recorded for Tatara×Siren while maximum (121) days to heading was recorded for Tatara×PS2005 (Table 2). Our findings are in favor of Ali *et.al. (*2007). who also noted significant differences in wheat genotype for the days to heading. High heritability (0.83) and low genetic advance (3.90%) was recorded for the days to heading (Table 3). Rahman *et. al.* (2016 a) also noted high heritability and stated that days to heading is genetically controlled and taken into consideration. The days to heading exhibited significant genotypic and phenotypic association with spike length (rG = 0.628** and rP = 0.37*), grain weight $spike^{-1}$ (rG = 0.59** and rP = 0.40*) and biological yield $plant^{-1}$ (rG = 0.55** and rP = 0.42*), while non-significant genotypic and phenotypic association was observed with rest of traits studied. (Table 4). The results of our study are in line with results of Khan *et al.,* 2015. Who also noted positive correlation of the days to heading with biological yield $plant^{-1}$ and grain weight $spike^{-1}$.

**Plant height (cm):** Mean squares revealed significant differences (P≤0.01) among $F_4$ wheat lines for the plant height (Table 1).

Table 1. Variance analysis results.

| Source | Df | Days to heading | Plant height | Flag leaf area | Spike length | Grain weight spike$^{-1}$ | 1000 grain weight | Grain yield plant$^{-1}$ | Biological yield plant$^{-1}$ | Harvest index (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| Replications | 2 | 0.51 | 4.64 | 1.73 | 0.32 | 0.001 | 1.31 | 0.04 | 1.30 | 10.04 |
| Genotypes | 10 | 18.51** | 52.42** | 32.44** | 0.98** | 0.07** | 25.93** | 4.13** | 20.87** | 125.90** |
| Error | 20 | 1.21 | 1.84 | 0.86 | 0.20 | 0.01 | 1.66 | 0.56 | 1.12 | 14.65 |
| CV (%) | -- | 0.95 | 1.67 | 3.56 | 4.54 | 5.54 | 3.24 | 8.29 | 5.13 | 8.65 |
| $R^2$ value | -- | 0.89 | 0.94 | 0.95 | 0.73 | 0.75 | 0.89 | 0.79 | 0.90 | 0.81 |

*, **= statistically significant at the 1% and 5% probability level, respectively.

Df: degree of freedom, CV: coefficient of variation, R: coefficient of determination.

Table 2. Mean values of the lines.

| F4 wheat lines | Days to heading | Plant height (cm) | Flag leaf area (cm$^2$) | Spike length (cm) | Grain weight spike$^{-1}$ (g) | 1000 grain weight (g) | Grain yield plant$^{-1}$ (g) | Biological yield plant$^{-1}$ (g) | Harvest index (%) |
|---|---|---|---|---|---|---|---|---|---|
| Barsat×Siren | 114 | 80.8 | 24.3 | 9.5 | 1.8 | 37.8 | 9.5 | 19.7 | 48 |
| Tatara×Siren | 112 | 80.0 | 21.4 | 9.4 | 1.9 | 38.4 | 8.3 | 18.3 | 45 |
| Tatara×Janbaz | 114 | 81.2 | 27.0 | 8.7 | 1.8 | 37.5 | 8.1 | 22.0 | 37 |
| Barsat×Janbaz | 115 | 78.7 | 30.7 | 9.3 | 1.9 | 36.7 | 9.1 | 23.1 | 39 |
| AUP-5008×Siren | 115 | 80.2 | 23.0 | 10.3 | 2.0 | 41.2 | 8.0 | 22.0 | 37 |
| Salim-2000×Siren | 115 | 72.2 | 24.0 | 9.4 | 1.9 | 39.8 | 9.0 | 20.5 | 44 |
| Salim-2000×Janbaz | 114 | 78.9 | 25.1 | 9.4 | 1.9 | 38.6 | 8.7 | 20.9 | 42 |
| AUP-5008×Janbaz | 114 | 89.1 | 31.0 | 10.3 | 1.7 | 38.0 | 10.3 | 18.3 | 56 |
| Tatara×PS-2005 | 121 | 78.4 | 22.8 | 10.2 | 2.1 | 37.1 | 10.3 | 26.3 | 39 |
| AUP-5008×PS-2005 | 115 | 84.0 | 27.8 | 9.6 | 2.3 | 45.1 | 11.3 | 21.0 | 54 |
| Tatara (Check) | 118 | 79.4 | 29.0 | 10.6 | 2.0 | 44.5 | 7.7 | 17.0 | 45 |
| Genotypes Mean | 115 | 80.7 | 26.0 | 9.8 | 1.9 | 39.8 | 9.1 | 20.7 | 44 |
| Range | 112-121 | 72.2-89.1 | 21.4-30.1 | 8.7-10.6 | 1.7-2.3 | 36.7-45.1 | 7.7-11.3 | 17.0-26.3 | 37-56 |
| $LSD_{(0.05)}$ | 2.00 | 2.47 | 1.69 | 0.81 | 0.20 | 2.35 | 1.36 | 1.93 | 6.96 |

LSD(0.05) : Least significant differences at the 5% level of probability.

Table 3. Heritability and genetic advance values of the lines.

| Parameters | Vg | Vp | Ve | H(b.s) | GA | GA($\bar{x}$) |
|---|---|---|---|---|---|---|
| Days to heading | 5.77 | 6.97 | 1.21 | 0.83 | 4.50 | 3.90 |
| Plant height | 16.86 | 18.70 | 1.84 | 0.90 | 8.03 | 9.95 |
| Flag leaf area | 10.53 | 11.39 | 0.86 | 0.92 | 6.43 | 24.72 |
| Spike length | 0.26 | 0.46 | 0.20 | 0.57 | 0.79 | 8.13 |
| Grain weight spike$^{-1}$ | 0.02 | 0.03 | 0.01 | 0.62 | 0.22 | 11.54 |
| 1000 grain weight | 8.09 | 9.75 | 1.66 | 0.83 | 5.33 | 13.41 |
| Grain yield plant$^{-1}$ | 1.19 | 1.75 | 0.56 | 0.68 | 1.85 | 20.45 |
| Biological yield plant$^{-1}$ | 6.58 | 7.70 | 1.12 | 0.85 | 4.89 | 23.64 |
| Harvest index (%) | 37.08 | 51.73 | 14.65 | 0.72 | 10.62 | 24.00 |

Vg: genotypic variance, Vp: phenotypic variance, Ve: environmental variance, H(b.s): broad sense heritability, GA: genetic advance, GA($\bar{x}$): genetic advance at percentage of mean.

CV value was 1.67% and the $R^2$ value was 0.94. Among the $F_4$ wheat lines the plant height ranged from 72.2 to 89.1 cm. mean data revealed that the plant height ranged from 72.2 to 89.1 cm. Salim-2000×Siren had the minimum (72.2 cm) plant height, while AUP-5008×Janbaz had the maximum (89.1 cm) plant height (Table 2). Rahman *et. al.,* (2016 b) also reported similar results in bread wheat. Genetic variance was 9.2 times greater than environmental variance which means that the plant height is genetically controlled and resulted in high heritability (0.90) and moderate genetic advance (10.0 %). (Table 3). The plant height expressed significant genotypic and phenotypic association with flag leaf area (rG = 0.45** and rP = 0.42*), spike length (rG = 0.33* and rP = 0.20) and harvest index (rG = 0.56** and rP = 0.49**) whereas, non-significant association with rest of traits (Table 4). Our study conforms the findings of (Jamali and Jamali, 2008) who also come up with positive genotypic and phenotypic association of the plant height with spike length.

**Flag leaf area (cm$^2$):** A significant difference (P≤0.01) was observed among $F_4$ wheat lines for flag leaf area (Table 1). CV value was 3.56% and the the $R^2$ value was 0.95. Means ranged from 21.4-30.0 cm$^2$. Tatara×Siren showed minimum value (21.4 cm$^2$) for the flag leaf area while AUP-5008×Janbaz showed maximum value (30.0 cm$^2$) for the flag leaf area (Table 2). Our findings are in correspondence with Ali *et al.* (2012) who, also noted significant differences in bread wheat for the flag leaf area. The high magnitude of heritability (0.92) and genetic advance (24.72%) were observed for the flag leaf area (Table 3). High coefficient of heritability and genetic advance indicated that the flag leaf area is genetically controlled and hence selection was effective. The flag leaf area revealed a significant and positive association with harvest index (rG = 0.41**) only at genotypic level. While with remaining traits it had non-significant genotypic and phenotypic association. (Table 4). Our findings are in line with Munir *et. al.* (2007), who also reported positive genotypic and phenotypic relationship between the flag leaf area and harvest index.

**Spike length (cm):** Mean squares showed significant differences (P≤0.01) among $F_4$ wheat lines for the spike length (Table 1). CV value was 4.54% and the $R^2$ value was 0.73. Means ranged from 8.7 to 10.6 cm for the spike length among $F_4$ wheat lines. Minimum (8.7 cm) the spike length was initiated for Tatara×Janbaz while maximum (10.6 cm) spike length was noted for the check (Tatara) (Table 2). Mangi et al. (2007) also reported significant difference for the spike length in F4 wheat population. Moderate heritability (0.57) and low genetic advance (8.13%) was observed for spike length (Table 3). Our finding are in favor of Ali *et al.* (2012) who stated that moderate heritability indicates environmental influence while low genetic advance indicates that selection is ineffective. The spike length revealed positive genotypic and phenotypic association with 1000 grain weight (rG = 0.55** and rP = 0.31$^{NS}$). On other hand, the spike length had non-significant positive genotypic and phenotypic association with all the traits except biological yield plant$^{-1}$ which showed non-significant negative association with the spike length (Table 4). Our findings are in close correspondence with Khan *et al.* (2015).

Table 4. Genotypic (rG) and phenotypic (rP) correlation among the lines.

| Traits | Days to heading | Plant height | Flag leaf area | Spike length | Grain weight spike$^{-1}$ | 1000 grain weight | Grain yield plant$^{-1}$ | Biological yield plant$^{-1}$ | Harvest index (%) |
|---|---|---|---|---|---|---|---|---|---|
| Days to heading | ___ | -0.20 | -0.03 | 0.62** | 0.59** | 0.12 | 0.19 | 0.55** | -0.30 |
| Plant height | -0.18 | ___ | 0.45** | 0.33* | -0.18 | 0.10 | 0.30 | -0.32 | 0.56** |
| Flag leaf area | 0.02 | 0.42* | ___ | 0.08 | -0.12 | 0.11 | 0.25 | -0.20 | 0.41* |
| Spike length | 0.37* | 0.20 | 0.01 | ___ | 0.22 | 0.55** | 0.01 | -0.26 | 0.26 |
| Grain weight spike$^{-1}$ | 0.40* | -0.11 | -0.12 | 0.26 | ___ | 0.77** | 0.28 | 0.39* | -0.14 |
| 1000 grain weight | 0.13 | 0.12 | 0.10 | 0.31 | 0.49** | ___ | 0.02 | -0.44** | 0.33* |
| Grain yield plant$^{-1}$ | 0.07 | 0.26 | 0.18 | 0.07 | 0.22 | 0.07 | ___ | 0.34* | 0.58** |
| Biological yield plant$^{-1}$ | 0.42* | -0.29 | -0.18 | -0.18 | 0.29 | -0.40* | 0.33* | ___ | -0.56** |
| Harvest index (%) | -0.26 | 0.49** | 0.31 | 0.10 | -0.07 | 0.21 | 0.66** | -0.48** | ___ |

**1000-grain weight (g):** $F_4$ wheat lines revealed significant differences (P≤0.01) for the 1000 grain weight (Table 1). CV value for the 1000 grain weight was 3.24% and the $R^2$ value was 0.89. mean values of the 1000 grain weight ranged from 36.7 to 45.1 g. The minimum (36.7 g) 1000-grain weight was recorded for Barsat×Janbaz, while the maximum (45.1 g) 1000-grain weight was noted for AUP-5008 x PS-2005 (Table 2). Heritability and genetic advance calculated for the 1000 grain weight was 0.83 and 13.8% respectively (Table 3). Ali *et al. (*2012) also reported the high value of heritability and moderate genetic advancement in wheat genotypes. And said that this trait is under greater genetic control and the selection was effective. Thousand grain weight expressed significant positive genotypic association with the spike length (rG = 0.55**), grain weight spike$^{-1}$ (rG = 0.77**) and harvest index (rG = 0.33*). Similarly, the 1000 grain weight showed significant and positive phenotypic association with the grain weight spike$^{-1}$ (rP = 0.49**). While with remaining traits it had non-significant genotypic and phenotypic association (Table 4). Our findings are in an argument with Yousif *et al.* (2015) who also showed a positive association of 1000 grain weight with the grains weight spike$^{-1}$ and grain yield.

**Grain weight spike$^{-1}$ (g):** Mean squares showed significant difference among the $F_4$ wheat lines for the grain weight spike$^{-1}$ (Table 1). CV value was 5.54% and coefficient of determination was 0.75. Means of grain weight spike$^{-1}$ ranged from 1.7 to 2.3 g. Minimum value (1.7 g) for the grain weight spike$^{-1}$ was recorded for AUP-5008×Janbaz, while maximum value (2.3 g) was recorded for AUP-5008×PS-2005 (Table 2). High heritability (0.62) and moderate genetic advance (11.54%) was recorded for the grain weight spike$^{-1}$ (Table 3). Our findings are in contrast to Farshadfar and Estehghari (2014) who noted significant differences for the grain weight spike$^{-1}$ along with moderate broad sense heritability among the wheat lines. The grain weight spike$^{-1}$ had significant and positive association with the 1000-grain weight (rG = 0.77**) biological yield plant$^{-1}$ (rG = 0.39*), similarly it exhibited significant and positive phenotypic association with the thousand grain weight (rP = 0.49**). Whereas, with rest of parameters it had non-significant association at both genotypic and phenotypic level (Table 4). These findings are in agreement with results of Munir *et al. (*2007).

**Grain yield plant$^{-1}$ (g):** $F_4$ wheat lines exhibited significant differences (P≤0.01) for the grain yield plant$^{-1}$ (Table 1). CV value was 8.29% and the $R^2$ value was 0.79. Means ranged from 7.7 to 11.3 g. Tatara had the minimum (7.7 g) grain yield plant$^{-1}$ while AUP-5008×PS-2005 produced maximum (11.3 g) grain yield plant$^{-1}$ (Table 2). Ajmal *et al.* (2009) also observed a significant difference in $F_4$ wheat population. Heritability and expected genetic advance for the grain yield plant$^{-1}$ was 0.68 and 20.45% respectively (Table 3). These results are in accordance with Kaleemullah *et al.* (2015). Who said that this trait are greatly under genetic controlled and less influenced by environment. The grain yield plant$^{-1}$ had significant and positive genotypic and phenotypic association with biological yield plant$^{-1}$ (rG = 0.34* and rP = 0.33*) and harvest index (rG = 0.58** and rP = 0.66**). While with remaining traits it had non-significant genotypic and phenotypic association (Table 4). Our findings are in agreement with those of Yousif *et al.* (2015) who also noted positive relationships of grain yield with harvest index and biological yield.

**Biological yield plant$^{-1}$ (g):** Significant (P≤0.01) differences were revealed among $F_4$ lines for the biological yield plant$^{-1}$ (Table 1). CV and $R^2$ values for the biological yield plant$^{-1}$ were 5.13% and 0.90 respectively. Among the wheat, genotypes check (Tatara) produce the minimum (17.0 g) biological yield plant$^{-1}$ whereas, the maximum (26.3 g) biological yield plant$^{-1}$ was produced by Tatara×PS-2005 (Table 2). High heritability (0.85) and genetic advance (23.64%) was recorded for the biological yield plant$^{-1}$ indicated that this trait are under additive gene affect (Table 3). The biological yield plant$^{-1}$ revealed significant genotypic and phenotypic association with days to heading (rG = 0.55** and rP = 0.42*), the grain weight spike$^{-1}$ (rG = 0.39* and rP = $0.29^{NS}$), the 1000 grain weight (rG = -0.44** and rP = -0.40*) and the grain yield plant$^{-1}$ (rG = 0.34* and rP = 0.33*). While the non-significant association with rest of traits studied (Table 4). Joti *et al.* (2012) also observed high heritability and genetic gain among genotypes along with the positive association of the biological yield with the days to heading and the grain yield.

**Harvest Index (%):** Mean squares expressed a significant difference (P≤0.01) among the $F_4$ lines for harvest index (Table 1). Our findings are in contrast with Khan *et al.* (2015) who come up with no difference in used wheat genotypes. For the harvest index coefficient of variation was 8.84% and coefficient of determination was 0.81. Tatara×Janbaz and AUP-5008×Siren had a minimum (37%) the harvest index, while AUP-5008×Janbaz had maximum (56%) the harvest index (Table 2). The harvest index expressed high heritability (0.72) coupled with high genetic advance (24.0%) (Table 3). Ali *et al.* (2012) also come up with high heritability and genetic advance. It was expressed significant genetic association with the plant height (rG = 0.56**), the flag leaf area (rG = 0.41*), the 1000 grain weight (rG = 0.33*), the grain yield plant$^{-1}$ (rG = 0.58**) and biological yield plant$^{-1}$ (rG = -0.56**). Similarly, the harvest index exhibited significant association with the plant height (rP = 0.49**), the grain yield plant$^{-1}$ (rP = 0.66**) and the biological yield plant$^{-1}$ (rP = -0.48**). While with remaining parameters it had a non-significant association (Table 3). Ahmad *et al.* (2010) conveyed positive correlation between the harvest index and biological yield in contrast to our results.

## CONCLUSIONS AND RECOMMENDATIONS

Significant variability was noted among $F_4$ wheat lines for all the traits studied indicating the need for effective selection. High heritability shows that there is a comparatively less environmental influence and the selection was efficient for the traits studied High heritability also indicates that the traits are genetically controlled and single plant selection could be started in $F_5$ generation. The grain yield, the biological yield and the flag leaf area agronomic traits had high expected genetic advance which showed the effectiveness of selection in $F_4$ wheat lines. One the other hand, the grain yield plant$^{-1}$ had shown positive genotypic and phenotypic association with all the investigated traits therefore mainly this trait, and other examined traits could be used safely for yield improvement in the future wheat breeding program(s). The present study showed that significant differences in $F_4$ genotypes indicate the presence of greater genetic variability. High heritability indicates that the studied traits are under genetic control and single plant selection could be started in $F_5$ generation. The strong correlation of grain yield plant$^{-1}$ with the mentioned traits showed that grain yield could be indirectly improved by improving these traits.

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