

Research Article



Heritability and Correlation Studies of Yield and Yield Related Traits in Bread Wheat

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Abstract | A set of 27 genotypes were tested for estimation of heritability, genetic advance and association of yield and yield related traits in wheat. For all the studied traits, mean squares showed the presence of significant variation ($p \leq 0.01$) among the genotypes. Heritability estimates were observed high ($h^2 > 0.60$) for all the traits. The highest heritability (0.93) was noticed in plant height followed by flag leaf area (0.89). The values of genetic advance were recorded low to moderate for all parameters. Grain yield was observed to have positive significant association with most of the important yield related traits such as fertile tillers, spike length, 1000-grain weight and grains per spike. These results suggest that all the traits showing significant correlation with grain yield needs better attention in future wheat breeding programs for increasing yield.

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Introduction

Wheat belongs to family Gramineae and is the main cereal crop of Pakistan. It covers the largest area under any crop in the country. During 2014-15, the area under wheat cultivation in Pakistan was 9.1 million ha having total production of 25.48 million tons (GoP, 2014-15).

For a successful plant breeding program, the genetic variation present in the breeding material used in the program is of prime importance. The observed variation is combination of genetic and environmental factors. For improving any plant character through selection, first the estimation of genetic parameters must be made. There are various techniques through which genetic parameters and the level of transmissibility of a trait can be computed. Heritability plays a predictive

role regarding improvement in a desirable trait and determines the effectiveness of selection for different traits. High values of heritability will mean simpler selection procedures (Khan et al., 2008). But heritability estimates alone do not give information regarding expected gain in the next generation. Expected genetic gain resulting from selection can be estimated through genetic advance. For an effective plant improvement program, information regarding heritability estimates and genetic advance for different traits is important (Haq et al., 2008). It is also important to obtain information about correlation of yield with other yield related characters, before the starting of any crop breeding program. Correlation studies are useful for improving yield through indirect selection of yield related traits. The present study was carried out with the objectives to assess heritability estimates, genetic advance and find the correlations among the

yield and its components to find the suitable criteria for yield improvement.

Materials and Method

This experiment was conducted during cropping season 2012-13 at Peshawar, Pakistan in a RCB design with three replicates. Twenty seven genotypes (18 F₁ hybrids and 9 parents) were included in this experiment. Two rows of five meter row length were allotted to each genotype and row-row distance was 30 cm. Data was recorded on twenty plants both in parents and F₁'s progenies. All the recommended agronomic practices were adopted during the entire growing season. The data was collected on plant height, fertile tillers, flag leaf area, grains per spike, spike length, 1000-grain weight and grain yield.

Statistical analysis

The data were analyzed statistically according to Steel and Torrie (1980) using M-STATC software.

Measurement of heritability and genetic advance

Heritability estimates (h^2) were computed as follow:

$$h^2_{(b.s)} = \frac{\sigma_g^2}{\sigma_p^2}$$

σ_g^2 : Genotypic variance; σ_p^2 : Phenotypic variance
Genetic advance was computed as (Falconer and Mackey, 1996):

$$GA = K \times \sigma_p \times h^2$$

$$GA (\%) = \frac{GA}{GM} \times 100$$

GM = Grand Mean

Results and Discussion

Analysis of variance, heritability and genetic advance (%)

Plant height: Short stature plants are desirable in wheat. The genotypes showed highly significant variations for plant height (Table 1). The value of genetic variance for plant height was 25.49 and environmental variance was 2.01 (Table 2). Heritability estimates were observed high (0.93) while genetic advance was

recorded low (7.42%) in case of plant height, which indicates the preponderance of non-additive gene action. Ahmad et al. (2016) also observed highly significant variations among wheat genotypes and also high heritability estimates (>0.90) in a study evaluating six genotypes and their 30 crosses. Similarly for plant height, high heritability estimates in wheat were also noticed by Farshadfar et al. (2013) and Kumar and Kerkhi (2015).

Flag leaf area (cm²): Flag leaf area is also an important trait because it play important role in photosynthesis. Means square depicted highly significant variation among the genotypes for flag leaf area (Table 1). Genetic variance in case of flag leaf area was 21.23 while environmental variance was 2.72 (Table 2). High broad sense heritability (0.89) accompanied by moderate genetic advance (12.51%) was observed for flag leaf area. Ashfaq et al. (2016) also noticed highly significant differences in wheat genotypes for flag leaf area. Similarly, Jatoi et al. (2012) also noticed significant differences in wheat varieties and high heritability estimates for leaf area.

Fertile tillers per plant: The genotypes showed highly significant differences for fertile tillers per plant (Table 1). The genetic variance for fertile tillers per plant was 1.34 and environmental variance was 0.36 (Table 2). For fertile tillers, high broad sense heritability estimate (0.79) along with moderate genetic advance was 10.12% observed, indicating that it is controlled by non-additive gene action. The results are in accordance with those of Kumar et al. (2012) and Farshadfar et al. (2013). But contrary to our findings, Kumar and Kerkhi (2015) reported moderate heritability estimates for fertile tillers.

Spike length: Spike length is another important trait, as large spikes are likely to produce more grains which lead to more yield per plant. Mean squares depicted that the genotypes differed significantly for spike length (Table 1). For spike length, the magnitude of genetic variance was 0.52 and environmental variance was 0.14 (Table 2). The heritability estimate was 0.79 and genetic advance was 6.7% for spike length. Baloch et al. (2016) reported highly significant variation among genotypes. They also found high heritability for spike length. However for spike length, Kumar and Kerkhi (2015) observed moderate heritability and genetic advance in their study.

Table 1: Mean squares for yield and yield related traits of 27 wheat genotypes

Sov	df	Plant height	Flag leaf area	Tiller per plant	Spike length	Grains per spike	1000-grain weight	Grain yield per plant
Reps	2	0.29	0.09	0.05	0.24	0.42	1.60	0.28
Genotypes	26	78.49**	66.43**	4.37**	1.69**	60.04**	57.37**	31.22**
Error	52	2.01	2.72	0.36	0.14	5.62	4.68	4.79

*, **: Significance at 1% and 5% level of probability

Table 2: Estimation of heritability and genetic advance (%) for yield and yield related traits in 27 wheat genotypes

Trait	Vg	Ve	Vp	h ² (B.S)	GA (%)
Plant height	25.49	2.01	27.50	0.93	7.42
Flag Leaf Area	21.23	2.72	23.96	0.89	12.51
Fertile Tiller plant ⁻¹	1.34	0.36	1.70	0.79	10.12
Spike length	0.52	0.14	0.65	0.79	6.69
Grains spike ⁻¹	18.14	5.62	23.76	0.76	6.92
1000-grain weight	17.57	4.68	22.24	0.79	13.04
Grain yield plant ⁻¹	8.81	4.79	13.60	0.65	11.14

Vg: Genotypic variance; **Ve:** Environmental variance; **Vp:** Phenotypic variance; **h²(B.S):** Heritability (Broad sense); **GA (%)**: Genetic advance as % of mean

Grains per spike: Grains per spike is a major component of yield and has significant contribution to grain yield. Highly significant differences were recorded for grains per spike among the genotypes (Table 1). The value of genetic variance was 18.14 and environmental variance was 5.62 for grains per spike (Table 2). Broad-sense heritability was observed high (0.76) while low genetic advance (6.92%) was observed for grains per spike. For grains per spike, other researchers also reported highly significant variation among genotypes and high heritability estimates like Kumar et al. (2012) and Baloch et al. (2016). Low genetic advance was also observed for grains per spike by Hussain et al. (2013).

1000-grain weight (g): Thousand grain weight is another major component of grain yield in wheat. Genotypes showed highly significant variations for 1000-grain weight (Table 1). The genetic variance was 17.56 and environmental variance was 4.68 (Table 2). For 1000-grain weight, high broad-sense heritability (0.79) accompanied by moderate genetic advance (13.04%) was recorded. Similar finding were also reported by Farshadfar et al. (2013). They evaluated five parents and 15 F₁ hybrids and noticed high heritability

in case of 1000-grain weight. High heritability was also reported for 1000-grains weight by Baloch et al. (2016).

Grain yield per plant (g): The mean squares for grain yield are shown in Table 1. The genotypes differed significantly for grain yield. The value of genetic variance was 8.81 while environmental variance was 4.79 (Table 2). Broad-sense heritability estimates were high (0.65) while genetic advance were moderate (11.14%) for grain yield. Beche et al. (2013) and Baloch et al. (2016) supported our results by reporting significant variations in wheat genotypes and high values of heritability for grain yield. Similarly, high heritability was also observed by Kumar et al. (2012) for grain yield. However, Kahrizi et al. (2010) reported low heritability estimates for grain yield. Moderate genetic advance was observed by Hussain et al. (2013) for grain yield.

Table 3: Phenotypic correlation coefficients of yield and yield related traits

Traits	FLA	TPP	SL	GPS	TGW	GYP
PH	0.78**	0.27**	0.46**	-0.14 ^{NS}	0.58**	0.50**
FLA		0.19 ^{NS}	0.33**	-0.11 ^{NS}	0.53**	0.44**
TPP			0.13 ^{NS}	0.09 ^{NS}	0.10 ^{NS}	0.51**
SL				-0.13 ^{NS}	0.42**	0.31**
GPS					0.22*	0.23*
TGW						0.57**

PH: Plant height; **FLA:** Flag leaf area; **TPP:** Tillers per plant; **SL:** Spike length; **GPS:** Grains per spike; **TGW:** Thousand grain weight; **GYP:** Grain yield per plant

Correlation coefficients

The phenotypic correlations of different parameters are shown in Table 3. The yield and related traits expressed different trends of relationship among themselves. Grain yield showed significant positive association with plant height (0.50), flag leaf area (0.44), spike length (0.31), tillers plant⁻¹ (0.51), 1000-grain weight (0.57) and grains per spike (0.23). Similar

ly, significant positive relationship was noticed between 1000-grain weight and leaf area (0.53), plant height (0.58), spike length (0.42), grain yield (0.57) and grains per spike (0.22). Tillers plant⁻¹ exhibited highly significant phenotypic association with plant height (0.27) and grain yield (0.51). Spike length was positively associated to height (0.46), leaf area (0.33), 1000-grain weight (0.42) and yield (0.57) while negatively associated to grains per spike (-0.13). Similarly, grains per spike were found to have positive relationship with 1000-grain weight (0.22) and grain yield (0.23). Other researchers also reported similar results like Ahmad et al. (2016), reported significant and positive association between grain yield and flag leaf area, tillers per plant and 1000-grain weight. Uddin et al. (2015) also reported significant and positive association between grain yield and flag leaf area, plant height, 1000-grain weight and grains spike. Significant positive association of grain yield with tillers per plant and plant height was previously noticed by Masood et al. (2014). Similarly, Iftikhar et al. (2013) also noticed positive association of yield with flag leaf area, grains per spike and 1000-grain weight. Similarly, significant positive relationship of grain yield and flag leaf area was also observed by Hussain et al. (2013). Rehman et al. (2015) also reported positive association between 1000-grain weight and plant height, spike length, grains spike⁻¹ and grain yield. Gelalcha and Hanchinal (2013) also noticed significant positive association between tillers per plant and spike length, grains per spike and grain yield per plant.

Conclusion

The results of the study showed that for all the traits the genotypes differed significantly. Heritability values were observed high for all the traits while genetic advance were observed low to moderate, which is an indicator that non-additive gene action was controlling the expressions of these characters. So, selection is suggested to be delayed to later segregating generations. Furthermore, phenotypic correlation revealed positive correlation of grain yield with leaf area, plant height, spike length, fertile tillers, 1000-grain weight and grains per spike, suggesting that more importance should be given to these traits for improving the yield in wheat.

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Author's Contribution

Sheraz Ahmad Khan conducted this study, collected and analyzed the data and wrote this article while Ghulam Hassan designed the study and supervised it.

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