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GENETIC POTENTIAL AND HERITABILITY ESTIMATES OF YIELD TRAITS IN F₃ SEGREGATING POPULATIONS OF BREAD WHEAT

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Abstract

An experiment comprising of 24 wheat genotypes was undertaken during 2011-12, at New Developmental Research Farm, The University of Agriculture Peshawar, to elucidate information on the nature and magnitude of genetic variability, index of transmissibility and assessing the level of genetic improvement of the quantitative characters. The experimental material comprising 19 F₃ populations along with their 5 parents of bread wheat were evaluated in randomized complete block design (RCBD) with three replications. Analysis of variance exhibited highly significant ($P \leq 0.01$) differences among genotypes for all the traits studied. F₃ population Ghaznavi-98 x Pirsabak-05 showed maximum mean value for 1000-grain weight (47.3 g) and biological yield (11474.9 kg ha⁻¹), whereas, maximum values for grain yield (4027.3 kg ha⁻¹), and harvest index (48.1%) were observed for Pirsabak-05 x AUP-4006. Moreover, maximum spike length (11 cm) was recorded for cross combination Pirsabak-05 x Pirsabak-04 and Janbaz x Pirsabak-05, respectively. In addition, Pirsabak-04 showed maximum value for number of grains spike⁻¹(55.0). Genetic variances were of greater magnitude than environmental variances for all the traits except for spike length and 1000-grain weight. Heritability estimates were of higher magnitude ranged from 0.64 to 0.92 for harvest index, biological yield, grain yield, and grains spike⁻¹. Moderate to low heritability (0.40-0.46) was observed for 1000-grain weight, and spike length, respectively. Genetic gain was for spike length (0.48 cm), grains spike⁻¹ (8.57), 1000-grain weight (2.93 g), grain yield (639.87 kg ha⁻¹), biological yield (1790.03 kg ha⁻¹), and harvest index (5.32 %). From high values of heritability and genetic advance, it could be concluded that selection for traits like grains spike⁻¹ suggested good selection criteria and could be effective for future breeding programs.

Keywords: Genetic variability, wheat, heritability, segregating populations

Introduction

Due to increase in the world's population, the demand for more food is still a critical issue worldwide. According to FAO estimates, over 200 million hectare of crop land will be needed in the next thirty years to feed the world's population (Amin, 2002). In spite of documented impact of green revolution, 2 billion people still lack reliable access to nutritionist food, and 800 million of them are chronically malnourished (Fresco and Baudoin, 2002). Over the next half century, it is estimated that global demand for cereals will increase by approximately 60% (Rosegrant and Coline, 2003).

For bringing improvement in heritable characters, estimation of genetic parameters is of prime importance in any breeding program. Heritability estimates provide the information about index of transmissibility of the quantitative characters of economic importance and are essential for an effective crop breeding strategy. The magnitude of heritability also helps in predicting the behavior of succeeding generations by devising the appropriate selection criteria and assessing the level of genetic improvement. Heritability is the extent to which the variation in the successive generations is predictable and reflects the extent to which a given character would be transmitted to next generation. Heritability estimates thus provide much needed confidence in selection procedures. Heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is understood that only the phenotypic value can be measured directly while breeding values of individuals are derived from appropriate analyses. It is the breeding value, which determines how much of the phenotype would be passed onto the next generation (Chowdhry *et al.*, 1994). The present study was thus designed to evaluate twenty four wheat genotypes comprising parents and F₃ populations to find out the extent of genetic variability, heritability and genetic advance for various yield and yield associated traits in F₃ segregating populations.

Materials and methods

To study genetic variability and heritability an experiment was conducted at New Developmental Research Farm, The University of Agriculture, Peshawar during 2011-12 season. The experimental material was 19 F₃ populations along with their 5 parents that were evaluated in randomized complete block design (RCBD) with three replications. All the F₃ populations were developed by crossing five parents during 2009-10. Seeds from each F₁ hybrid were collected to raise F₂ populations and collected in bulk to produce F₃ plants of each populations. Pedigree of the parents used in the crossing scheme to produce 14 F₃ populations are given below in Table A. The size of plot was 5 m by 1.8 m. Each plot was having six rows with row length and row-row distance of 5 m and 30 cm, respectively. All other cultural practices were carried out uniformly in all plots. Fifty spikes (50) were randomly selected in each plots for measuring spike length and counting number of grains spike⁻¹. Furthermore, selected spikes were threshed and seeds were counted to calculate 1000-grain weight. At maturity, all the plants were harvested to record biological yield (kg ha⁻¹), and then threshed

to calculate grain yield (kg ha⁻¹) and harvest index (%).

Table A. List of five parents and their pedigree used in hybridization program

Genotypes	Pedigree
AUP- 4006	Gen/Buc/Filk/Buchin
Pirsabak-04	KAUZ/STAR
Pirsabak-05	MUNIA/CHTO//AMSEL
Ghaznavi-98	JUP/Bjyy/Ures
Janbaz	Gen*2//Buc/Filk/3/Buchin

Statistical analysis

Analysis of Variance

The data recorded on each parameter was subjected to analysis of variance (ANOVA) techniques appropriate for a randomized complete block design through MSTATC computer program. The mean differences among wheat genotypes for different yield and yield related traits was determined by using Least Significant Differences (LSD) test at 5% level of probability as suggested by Steel and Torrie (1980).

Heritability (B.S)

The genotypic, phenotypic, and environmental variances, and heritability were calculated by the following formula proposed by Singh and Chaudhery (1997);

$$\text{Genotypic Variance } (\delta^2_g) = \frac{GMS - EMS}{r}$$

$$\text{Phenotypic Variance } (\delta^2_p) = \delta^2_g + \delta^2_e$$

$$\text{Environmental Variance } (\delta^2_e) = EMS$$

$$h^2_{(BS)} = \frac{\delta^2_g}{\delta^2_p}$$

δ^2_g = Genotypic variance for a trait.

δ^2_p = Phenotypic variance for a trait.

$h^2_{(BS)}$ = Broad sense heritability for a trait.

Genetic advance (GA)

Genetic advance (GA) for important traits was predicted using 20% selection intensity ($i = 1.40$) as follow:

$$\text{Genetic advance} = \text{GA} = i \times \sqrt{V_{px}} \times h^2_x$$

Where: i = a constant value at specific selection intensity ($i = 1.40$ for 20% selection intensity); V_{px} = Phenotypic variance for a specific trait x ; h^2_x = Heritability for a specific trait x .

Results and Discussion

Spike length (cm)

Analysis of variance for spike length showed highly significant differences ($P \leq 0.01$) among wheat genotypes (Table 1). Spike length of 24 wheat genotypes ranged from 8.9 cm for genotypes Pirsabak-04 x Ghaznavi-98 to 11 cm for Janbaz x Pirsabak-05 with the mean value of 10.2 cm (Table 3). These results are in agreement with those of Afridi and Khalil (2007), Laghari *et al.* (2010), and Eid (2009), who also reported significant differences among wheat genotypes for spike length.

Genetic and environmental variances, broad-sense heritability and estimates for expected genetic advance for spike length are given in Table 2. The magnitudes of genetic and environmental variances for spike length were 0.24 and 0.34, respectively. Moderate broad-sense heritability (0.41) was observed for spike length. Using 20% selection intensity, the expected genetic advance for spike length was 0.48 (Table 2). The present findings are in close conformity with the research work of Ahmad *et al.*, (2007) who also observed low magnitude of heritability for spike length. On the other hand, Memon *et al.*, (2007), Ullah *et al.*, (2007), Laghari *et al.*, (2010), Eid (2009), and Ajmal *et al.*, (2009), reported high heritability for spike length.

Table 1. Mean squares for various yield traits of 24 wheat genotypes during 2011-12

Traits	Replication (df=2)	Genotypes (df=23)	Error (df=46)	CV (%)
Spike length (cm)	0.200	1.04**	0.34	5.69
Number of grains spike ⁻¹	1.542	101.75**	2.77	4.10
1000 grain weight (g)	32.697	40.65**	13.72	9.00
Grain yield (kg ha ⁻¹)	4226.50	743558.11**	71809.88	8.35
Biological yield (kg ha ⁻¹)	55294.62	6274042.58**	727417.44	9.39
Harvest Index (%)	1.415	62.18**	9.06	8.43

CV= Coefficient of variation and df = Degree of freedom

Number of grains spike⁻¹

Perusal of grains spike⁻¹ data revealed highly significant differences ($P \leq 0.01$) among the tested wheat genotypes (Table 1). Mean number of grains spike⁻¹ for the 24 wheat genotypes ranged from 31.3 for Ghaznai-98 x Pirsabak-05 to 55.0 for Pirsabak-04 with the mean value of 40.6 (Table 3). The present findings are supported by Ali *et al.*, (2007), Memon *et al.*, (2007), and Ajmal *et al.*, (2009), Eid (2009), Khan *et al.*, (2011), who also reported significant differences among wheat genotypes for grains spike⁻¹.

Genetic and environmental variances, broad-sense heritability and estimates for expected genetic advance for grains spike⁻¹ are given in Table 2. The magnitudes of genetic and environmental variances for number of grains spike⁻¹ were 32.99 and 2.77, respectively. High broad-sense heritability (0.92) was observed for number of grains spike⁻¹. It indicates more opportunity for the selection of genotypes with desirable number of grains spike⁻¹. Using 20% selection intensity, the expected genetic advance for number of grains spike⁻¹ was 8.57 (Table 2). The obtained results are in lined with those of and Ajmal *et al.*, (2009), Abinasa *et al.*, (2011), and Rashidi *et al.*, (2011) who also reported high heritability for grains spike⁻¹. Furthermore, Aycicek and Yildirim (2006), Ahmad *et al.*, (2007), and Eid (2009), reported low heritability for number of grains sike⁻¹.

Table 2: Variance components, heritability (BS) and genetic advance for different yield traits of 24 wheat genotypes during 2011-12

Traits	Vg	Ve	Vp	$h^2_{(BS)}$	GA
Spike length (cm)	0.24	0.34	0.57	0.41	0.48
Grain spike ⁻¹	32.99	2.77	35.77	0.92	8.57
1000 grain weight (g)	8.98	13.72	22.70	0.40	2.93
Grain yield (kg ha ⁻¹)	223916.08	71809.88	295725.96	0.76	639.87
Biological yield (kg ha ⁻¹)	1848875.05	727417.44	2576292.49	0.72	1790.03
Harvest Index (%)	17.71	9.06	26.77	0.66	5.32

Vg = Genetic variance, Ve = Environmental variance, Vp = Phenotypic variance
 $h^2_{(BS)}$ = Heritability (broad sense) and G.A = Genetic advance

1000 grain weight (g)

Analysis of variance exemplified highly significant differences ($P \leq 0.01$) among wheat genotypes for 1000 grain weight (Table 1). Mean 1000 grain weight data for the 24 wheat genotypes ranged from 32.8 g for Ghaznavi-98 x AUP-4006 to 47.3 g for Ghaznavi-98 x Pirsabak-05 with the mean value of 41.1 g (Table 3). Our findings are in close agreement

with those of Ahmad *et al.*, (2007), and Tahir *et al.*, (2009), who also reported significant variation for 1000-grain weight among wheat genotypes.

Genetic and environmental variances, broad-sense heritability and estimates for expected genetic advance for 1000 grain weight are presented in Table 2. The magnitudes of genetic and environmental variances for 1000 grain weight were 8.98 and 13.72, respectively. Low broad-sense heritability (0.40) was observed for 1000 grain weight. Using 20% selection intensity, the expected response to selection for 1000 grain weight was 2.93 g (Table 2). These results are in close conformity with the previous observations of Aycicek and Yildirim (2006) who also reported low magnitude of heritability for 1000-grain weight. On the other hand, Eid (2009), had found high magnitude of heritability for 1000-grain weight.

Grain yield (kg ha⁻¹)

Grain yield data showed highly significant differences ($P \leq 0.01$) among wheat genotypes (Table 1). Mean grain yield data of 24 wheat genotypes ranged from 2318.2 kg ha⁻¹ for Pirsabak-05 x Janbaz to 4027.3 kg ha⁻¹ for genotype Pirsabak-05 x AUP-4006 with the overall mean of 3208.7 kg ha⁻¹(Table 4). These results are supported by Afridi and Khalil (2007), Ahmad *et al.*, (2007), Ajmal *et al.*, (2009), Khan *et al.*, (2011), who also reported significant variation for grain yield of different genotypes.

Table 3. Mean performance for various yield traits of 24 wheat genotypes during 2011-12

Genotypes	Spike length (cm)	Grains spike ⁻¹	1000 grain weight (g)
AUP- 4006	9.3	42.9	41.9
Pirsabak-04	10.0	55.0	43.0
Pirsabak-05	10.1	42.0	40.8
Ghaznavi-98	10.0	41.3	40.4
Janbaz	10.7	46.9	36.4
AUP-4006 × Pirsabak-04	9.3	36.9	43.6
AUP-4006 × Pirsabak-05	9.7	46.6	47.1
AUP-4006 × Ghaznavi-98	10.0	37.9	39.8
AUP-4006 × Janbaz	10.9	36.4	41.3
Pirsabak-04 × AUP- 4006	10.6	41.6	41.7
Pirsabak-04 × Pirsabak-05	9.6	31.5	42.4
Pirsabak-04 × Ghaznavi-98	8.9	38.3	34.9
Pirsabak-04 × Janbaz	10.6	31.4	42.2
Pirsabak-05 × AUP- 4006	10.5	44.5	44.9
Pirsabak-05 × Pirsabak-04	10.2	36.6	41.5

Pirsabak-05 × Ghaznavi-98	10.7	42.4	39.4
Pirsabak-05 × Janbaz	10.0	36.0	41.9
Ghaznavi-98 × AUP- 4006	10.8	47.8	32.8
Ghaznavi-98 × Pirsabak-04	10.4	44.4	37.3
Ghaznavi-98 × Pirsabak-05	10.9	31.3	47.3
Ghaznavi-98 × Janbaz	9.4	44.6	39.9
Janbaz × AUP- 4006	10.1	44.2	37.1
Janbaz × Pirsabak-05	11.0	35.0	42.4
Janbaz × Ghaznavi-98	10.6	39.4	47.2
Mean	10.2	40.6	41.1
LSD_{0.05}	1.0	2.7	6.1

Table 4. Mean performance for various yield traits of 24 wheat genotypes during 2011-12

Genotypes	Grain yield (kg ha⁻¹)	Biological yield (kg ha⁻¹)	Harvest index (%)
AUP- 4006	3057.6	10897	28.0
Pirsabak-04	2548.5	7083.1	36.2
Pirsabak-05	2878.8	10264.3	28.2
Ghaznavi-98	3745.5	11201.9	33.4
Janbaz	2839.4	7296.1	39.1
AUP-4006 × Janbaz	3054.5	8745.2	35.1
AUP-4006 × Pirsabak-05	3036.4	8992.8	33.8
AUP-4006 × Ghaznavi-98	3624.2	9957.5	36.5
AUP-4006 × Pirsabak-04	2369.7	7442.1	31.8
Pirsabak-04 × AUP- 4006	2890.9	7264.3	40.0
Pirsabak-04 × Ghaznavi-98	3427.3	9287.2	36.9
Pirsabak-04 × Janbaz	3575.8	8562.3	41.7
Pirsabak-04 × Pirsabak-05	3172.7	10079.1	31.4
Pirsabak-05 × AUP- 4006	4027.3	8383.4	48.1
Pirsabak-05 × Ghaznavi-98	2918.2	8292.9	35.3
Pirsabak-05 × Pirsabak-04	2600.0	6897.5	37.8

Pirsabak-05 × Janbaz	2318.2	7079.3	32.8
Ghaznavi-98 × AUP- 4006	3527.3	10291.8	34.4
Ghaznavi-98 × Pirsabak-04	2881.8	8259.3	34.9
Ghaznavi-98 × Janbaz	3581.8	11474.9	31.5
Ghaznavi-98 × Pirsabak-05	3872.7	9079.7	42.6
Janbaz × AUP- 4006	3536.4	9987.0	35.4
Janbaz × Pirsabak-05	3578.8	10867.4	32.9
Janbaz × Ghaznavi-98	3945.5	10414.6	38.5
Mean	3208.7	9087.5	35.7
LSD_{0.05}	440.4	1401.7	5.0

Genetic and environmental variances, broad-sense heritability and expected genetic advance for grain yield are given in Table 2. The magnitudes of genetic and environmental variances for grain yield were 223916.08 and 71809.88, respectively. High broad-sense heritability (0.76) was observed for grain yield. Using 20% selection intensity, the expected selection response was 639.87 (Table 2). These outcomes are supported by the research work of Memon *et al.*, (2007), Ajmal *et al.*, (2009), and Mangi *et al.*, (2010), who also observed high heritability for grain yield in wheat. In contrast, Rashidi (2011) reported low heritability for grain yield.

Biological yield (kg ha⁻¹)

Analysis of variance for biological yield revealed significant differences ($P \leq 0.05$) among wheat genotypes (Table 1). Mean biological yield for the 24 wheat genotypes ranged from 6897.5 kg ha⁻¹ for Pirsabak-05 x Ghaznavi-98 to 11474.9 kg ha⁻¹ for Ghaznavi-98 x Pirsabak-05 with the mean value of 9087.5 kg ha⁻¹ (Table 4). These results are in agreement with the findings of Wajid *et al.*, (2004), Afridi and Khalil (2007), and Khan *et al.*, (2011), who also reported significant variation for biomass in wheat.

Genetic and environmental variances, broad-sense heritability and expected genetic advance for biological yield are given in Table 2. The magnitudes of genetic and environmental variances for biological yield were 1848875.05 and 727417.44, respectively. High broad-sense heritability (0.72) was observed for biological yield. Expected genetic advance for biological yield was 1790.03 kg ha⁻¹ (Table 2). The present results are in close agreement with the findings of Ajmal *et al.*, (2009), and Mangi *et al.*, (2010), who also observed high heritability for biological yield in wheat. In contrast, Rashidi *et al.*, (2011) reported low heritability for biological yield.

Harvest index (%)

Perusal of harvest index data elucidated highly significant differences ($P \leq 0.01$) among the wheat genotypes (Table 1). Mean harvest index of 24 wheat genotypes ranged from 28.0% for genotype AUP-4006 to 48.1% for genotype Pirsabak-05 x AUP-4006 with

the mean value of 35.7 % (Table 4). The obtained results are supported by Afridi and Khalil (2007), Khan *et al.*, (2011), and Rashidi *et al.*, (2011), who also reported significant difference among wheat genotypes for harvest index.

Genetic and environmental variances, broad-sense heritability and estimates for expected genetic advance for harvest index are given in Table 2. The magnitudes of genetic and environmental variances for harvest index were 171.71 and 9.06, respectively. High broad-sense heritability (0.66) was observed for harvest index. The expected genetic advance for harvest index was found 5.32% (Table 2). Memon *et al.*, (2007), Ajmal *et al.*, (2009), and Mangi *et al.*, (2010), who also observed high heritability for harvest index in wheat. In contrast, Rashidi *et al.*, (2011), observed low to medium heritability for harvest index.

Conclusion

Significant differences were observed among wheat genotypes for all the traits studied, showing that there is sufficient variability to have an effective selection. Similarly, high broad sense heritability estimates associated with high genetic advances were observed for most the traits studied, indicating that there is more genetic control and selection should lead to quick improvement. F₃ populations Ghaznavi-98 x Pirsabak-05 and Pirsabak-05 x AUP-4006 showed maximum value for important yield component and could be emphasized in future breeding program.

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