



## ESTIMATION OF GENETIC PARAMETERS OF YIELD AND YIELD TRAITS IN WHEAT GENOTYPES UNDER RAINFED CONDITIONS

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### Abstract

Development of superior crop varieties is the prime objectives of all plant breeding programs. To determine genetic variability, heritability and genetic advance, 24 elite bread wheat lines were planted in randomized complete block design with three replications at the University of Agriculture, Peshawar under rainfed conditions. Data were recorded on days to heading, days to maturity, plant height (cm), flag leaf area (cm<sup>2</sup>), spike length (cm), grain yield (kg ha<sup>-1</sup>), biological yield (kg ha<sup>-1</sup>), 1000 grain weight (g), grains spike<sup>-1</sup>, grain weight spike<sup>-1</sup>(g), and harvest index (%). Analysis of variance revealed significant differences among genotypes for all the traits studied. Broad sense heritability was high for days to heading (0.89), grain weight spike<sup>-1</sup>(0.61g), spike length (0.70 cm), 1000-grain weight (0.62g), grain yield (0.78 kg ha<sup>-1</sup>) and harvest index (0.62%); and was moderate for days to maturity (0.52), plant height (0.38 cm), and grains spike<sup>-1</sup> (0.49), while low heritability was estimated for spike weight (0.25g), flag leaf area (0.28 cm<sup>2</sup>) and biological yield (0.25 kg ha<sup>-1</sup>). The values of genetic advance for days to heading, days to maturity, plant height, spike length, grains spike<sup>-1</sup>, grain weight spike<sup>-1</sup>, 1000-grain weight, grain yield, biological yield, flag leaf area, and harvest index were; 5.47, 1.88, 4.01, 6.42, 0.16, 5.02, 0.71, 418.83, 379.64, 2.89 and 3.92, respectively. Genotype PR 105 surpassed all other genotypes in grain yield (3144.33 kg ha<sup>-1</sup>) and hence it can be recommended for rainfed area.

Keywords: Wheat, genetic variability, heritability, genetic advance, drought

**Abbreviations:** DH=Days to heading, DM=days to maturity, PH=plant height, FLA=flag leaf area, SL=spike length, GSP =grains spike<sup>-1</sup>, GWS=grain weight spike<sup>-1</sup>, TGW=1000 grain weight, GY=grain yield, BY=biological yield, HI=harvest index

## **Introduction**

Wheat (*Triticum aestivum* L.) is the staple food for a large part of the world population including Pakistan. Wheat is one of the most important cereal crops in terms of production and utilization. It is a source of energy, protein and dietary fiber in human diet (Kalimullah et al., 2010). Wheat is the leading food crop in Pakistan and is cultivated both under irrigated and un-irrigated regions of the country (Shehzad et al., 2005). Heritability, is a measure of the phenotypic variance attributable to genetic causes, has predictive function in breeding crops (Songsri et al., 2008). It provides an estimate of the genetic advance a breeder can expect *from* selection applied to a population under certain environment. The higher the heritability estimates, the simpler are the selection procedures (Khan et al., 2008). High genetic advance coupled with high heritability estimates offer the most effective selection criteria for selection (Larik et al., 2000). The magnitude of genetic inheritance and expected genetic advance are important for the prediction of response to selection in diverse environments and provide the basis for planning and evaluating breeding programs (Ahmad et al., 2006). The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program (Shukla et al., 2004). In plant breeding program, direct selection for yield as such could be misleading. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. To attain maximum crop yield is the major objective in most breeding programs and the major emphasis in wheat breeding is on the development of improved varieties (Abdullah et al., 2002). Grain yield is a complex trait, which is highly influenced by genetic as well as environmental factors. Grain yield in wheat has low heritability showing the greater role of environment and hence, selection becomes more difficult in a given environment. Therefore, there is a need to improve wheat yield potential on per unit area basis to feed ever increasing population of Pakistan (Maqbool et al., 2010). The objectives of the present study were to find out the extent of genetic variation, broad sense heritability, genetic advance, and to identify superior genotypes for general cultivation in rainfed area.

## **Materials and methods**

This experiment was conducted at New Developmental Research Farm at the University of Agriculture, Peshawar, during 2012-2013. The material comprised 24 elite wheat breeding lines from various wheat breeding programs of the country. This material was supplied by the National Coordinated Wheat Program, Islamabad for routine testing under rainfed conditions as National Uniform Yield Trials. Randomized complete block design with 3 replications was used. Each entry consisted of six rows with row length of 5 meters and row to row distance of 0.3 m. The material was planted on November 17<sup>th</sup>, 2012. Standard agronomic practices were carried out throughout the growing season. Days to heading and maturity was counted as days taken from sowing till 50% heading, whereas maturity as days taken from sowing till yellowing of 80% parts of plants in each plot. Plant height was measured from the base till the tip of the plant excluding awns using meter rod in cm. Flag leaf length and width was measured and was converted to flag leaf area according Francis et al. 1997. Fifty spikes were randomly selected to measure spike length, and then threshed to count grains spike<sup>-1</sup> and weighed to calculate grain weight spike<sup>-1</sup> and 1000 grain weight. Central two rows of each plot was harvested first to calculate biological yield and then threshed to record grain yield and harvest index by dividing grain yield by biological yield.

## **Statistical analysis**

The data collected were subjected to analysis of variance technique appropriate for randomized complete block design according to Singh and Chaudry (1997) using computer software Statix ver 8.1.

## **Heritability**

Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson et al., 1956).

$$\text{Heritability (h}^2\text{)} = V_g / V_p \times 100$$

Where

V<sub>g</sub>= Genetic variance

V<sub>p</sub>= Phenotypic variance

## **Genetic advance**

Genetic advance was calculated following Allard (1990), as follow:

$$G.A = i \times h^2 \times \delta_p$$

G.A= Genetic advance

i = Selection intensity

$h^2$  = Heritability of a trait

$\delta_p$  = Phenotypic standard deviation

## **Results and discussion**

### **Days to heading**

Analysis of variance for days to heading showed significant differences ( $P \leq 0.01$ ) among wheat genotypes (Table 1). Findings in this study for days to heading are in conformity with the results of Anwar et al. (2009) who also reported highly significant differences among wheat genotypes for this trait. Mean value for days to heading ranged from 102 to 121. Genotype PR-105 took maximum days to heading whereas minimum days to heading was observed for genotype Pirsabak-05 (Table 2). Estimates of broad sense heritability and genetic advance (GA) for days to heading were 0.89 and 5.47 respectively, genotypic coefficient of variations (GCV) for days to heading was 3.61 and 3.84 was the value of phenotypic coefficient of variation (PCV) (Table 3). Khan and Naqvi (2011) findings were validated results of the current study who also reported high level of heritability for days to heading.

### **Days to maturity**

Analysis of variance for days to maturity showed highly significant differences ( $P \leq 0.01$ ) among wheat genotypes (Table 1). Anwar et al. (2009) also reported highly significant differences for days to maturity. Mean values for genotypes ranged from 143 to 152 days. Maximum days to maturity were taken by the genotypes V-11183 and 10C033 whereas genotype Pirsabak-05 took minimum days (Table 2). Environmental and genetic variances for days to maturity were 3.23 and 3.48 respectively, with broad sense heritability, and genetic advance (GA) of 0.52 and 1.88 respectively. Genetic variance is slightly higher than

environmental variance resulting into moderate level of heritability. Genotypic and phenotypic coefficients of variations for days to maturity were calculated as 1.25 and 1.73, respectively, (Table 3). Contrary to findings in the current study, Yadav et al. (2011) reported high heritability for days to maturity while in our studies it was moderate.

### **Plant height (cm)**

Statistical analysis of the data for plant height showed significant differences ( $P \leq 0.01$ ) among wheat genotypes (Table 1). Results of this study for plant height are supported by the findings of Hussain et al. (2012), who also reported highly significant differences among genotypes for plant height. Mean values for plant height ranged from 92.53 cm to 115.27 cm. Genotype AUR-0809 was the tallest (115.27 cm) whereas genotype DH-31 was the shortest plant (92.53 cm) (Table 2). Variances due to environment and genetic factors were calculated as 34.28 and 21.38 respectively with broad sense heritability and genetic advance (GA) of 0.38 and 4.01, respectively. Genotypic coefficient of variation for plant height was 4.49 and 7.24 respectively, (Table 3). These results are in agreement with the findings of Aycicek and Yildirim (2006), Gupta and Verma (2000), and Eid (2009) who also reported low heritability coupled with low genetic advance for plant height.

### **Flag leaf area (cm<sup>2</sup>)**

Analysis of variance revealed significant differences ( $P \leq 0.01$ ) among wheat genotypes for flag leaf area (Table 1). Kalimullah et al. (2012) also reported significant differences for flag leaf area. Mean values for flag leaf area ranged between 29.02 cm<sup>2</sup> and 48.31 cm<sup>2</sup>. Genotype AUP-1052 achieved maximum flag leaf area (48.31 cm<sup>2</sup>), whereas genotype PR-105 with minimum flag leaf area (29.02 cm<sup>2</sup>) (Table 2). Genetic variance ( $V_g$ ) and environmental variance ( $V_e$ ) for days to heading were 15.07 and 38.11 respectively. Broad sense heritability estimate for flag leaf area was 0.28 with genetic advance (GA) of 2.89. Genotypic and phenotypic coefficients of variations for flag leaf area were calculated as 10.33 and 19.41, respectively (Table 3). Choudhary et al. (2001) reported low to moderate heritability for this trait, which supports our results.

### **Spike length (cm)**

Analysis of variance for spike length showed highly significant differences ( $P \leq 0.01$ ) among wheat genotypes (Table 1). Our results are in agreement with Anwar et al. (2009) and

Hussain et al. (2012) who also reported highly significant differences among genotypes. Mean values for genotypes ranged from 10.59 cm to 12.62 cm. Genotype V-11183 has the longest spikes (12.62 cm), whereas genotype 06 FJS3013 has the shortest spikes (10.59) (Table 2). Environmental and genetic variances were 12.61 and 9.88 respectively, with broad sense heritability estimates of 0.70 and genetic advance 6.42. Genotypic coefficient of variation was 12.31 and phenotypic coefficient of variation for spike length was 14.68 (Table 3). Our results confirmed the findings of Tefera et al. (2003), Khalil et al. (2010) and Khan and Naqvi (2011), who also reported high heritability for spike length and high genetic advance.

### **Grains spike<sup>-1</sup>**

Genotypes have highly significant differences ( $P \leq 0.01$ ) for grains spike<sup>-1</sup> (Table 1). Mean values for grains spike<sup>-1</sup> ranged from 26.67 to 46.13. Genotype PR-104 produced the highest number of grains spike<sup>-1</sup> (46), whereas genotype V-08314 produced the lowest number for grains spike<sup>-1</sup> (27) (Table 2). Environmental and genetic variances were 13.33 and 21.00 for grains spike<sup>-1</sup>, respectively. Broad sense heritability was 0.61 with genetic advance of 5.02. The values of genotypic and phenotypic coefficients of variations were 12.77 and 16.33 respectively, for grains spike<sup>-1</sup> (Table 3). Results of this study are in agreement with Gupta and Verma (2000), Haq et al. (2008) and Kisana et al. (1982), who reported high heritability for grains spike<sup>-1</sup>.

### **Grain weight spike<sup>-1</sup>(g)**

Analysis of variance showed significant differences ( $P \leq 0.01$ ) for grain weight spike<sup>-1</sup> within wheat genotypes (Table 1). Findings of the present study are in agreement with Kashif and Khaliq (2006), who reported highly significant differences among genotypes for grain weight spike<sup>-1</sup>. Mean values ranged from 1.37 g to 2.16 g. Genotype PR-104 has maximum grain weight spike<sup>-1</sup> (2.16 g), whereas genotype DH-31 has minimum grain weight spike<sup>-1</sup> (1.37 g) (Table 2). Genetic and environmental variances were 0.026 and 0.028, respectively. Broad sense heritability and genetic advance were 0.61 and 5.02 respectively, Genotypic and phenotypic coefficients of variance for grain weight spike<sup>-1</sup> were 12.77 and 16.33 respectively (Table 3). Our results are parallel to the findings of Tefera et al. (2003), who also reported high heritability for grain weight spike<sup>-1</sup>.

### **1000-grain weight (g)**

Genotypes showed significant differences ( $P \leq 0.05$ ) for 1000-grain weight within wheat genotypes (Table 1). Anwar et al. 2009, Hussain et al. (2012) and Kalimullah et al. (2012) also found significant differences among genotypes for 1000-grain weight. Mean values ranged from 35.33 g to 53.50 g. For 1000-grain weight genotype NR-419 has highest value of 53.50 g and genotype PR-105 has the lowest value of 35.33 g (Table 2). Environmental and genetic variances were 12.61 and 29.88 respectively, which resulted into high level of heritability 0.70 and genetic advance 6.42. Genotypic coefficient of variation was 12.31 and phenotypic coefficient of variation for 1000-grain weight was 14.68 (Table 3). Kisana et al. (1982) also reported high heritability for 1000-grain weight

### **Grain yield (kg ha<sup>-1</sup>)**

Analysis of variance for grain yield showed significant differences ( $P \leq 0.01$ ) among wheat genotypes (Table 1). Highly significant differences among genotypes for grain yield were also reported by Kalimullah et al. (2012), Hussain et al. (2012) and Anwar et al. (2009). Mean values ranged from 1915.0 kg ha<sup>-1</sup> to 3144.3 kg ha<sup>-1</sup>. Maximum grain yield was observed for genotype PR-105 (3144.4 kg ha<sup>-1</sup>), whereas the lowest grain yield (1915.0 kg ha<sup>-1</sup>) was observed for genotype PR-104 (Table 2). Environmental and genetic variances were 32637.85 and 114917.82 respectively. Estimate of broad sense heritability and genetic advance were 0.78 and 418.83 respectively. Phenotypic and genotypic coefficients of variations were 14.56 and 12.84 respectively (Table 3). Khan and Naqvi (2011) also reported high magnitude of heritability for grain yield.

### **Biological yield (kg ha<sup>-1</sup>)**

Genotypes for biological yield has significant differences ( $P \leq 0.05$ ) (Table 1). Overall mean values ranged from 7996 kg ha<sup>-1</sup> to 11281 kg ha<sup>-1</sup>. Genotype NARC-2009 has the highest value (11281 kg ha<sup>-1</sup>) for biological yield whereas genotype 06 FJS3013 produced the lowest value (7996 kg ha<sup>-1</sup>) for biological yield (Table 2). Genetic and environmental variances were 295599.33 and 892696.00 respectively. Estimate of broad sense heritability and genetic advance for biological yield ha<sup>-1</sup> were 0.25 and 379.6, respectively. Genotypic and phenotypic coefficients of variances for biological yield were 5.70 and 11.43, respectively

(Table 3). These results are contradictory to Khan and Khalil (2007), who reported high heritability for biological yield in wheat.

### Harvest index (%)

Analysis of variance showed significant differences ( $P \leq 0.01$ ) for harvest index within wheat genotypes (Table 1). Mean values for harvest index ranged from 20.37 % to 35.97 %. Genotype 06 FJS3013 has maximum harvest index of 35.97 % while genotype PR-104 has minimum harvest index of 20.37 % (Table 2). Environmental variation for harvest index was 7.98, while genetic variation was 12.75, and the resultant broad sense heritability and genetic advance was 0.62 and 3.92 respectively. Genotypic coefficient of variation and phenotypic coefficient of variation for harvest index in percent were 12.79 and 16.31 respectively (Table 3). Our results are in agreement with the findings of Yadav et al. (2011) and Gupta & Verma (2000), who also reported high heritability for harvest index in wheat.

**Table 1. Mean squares for various morpho-physiological and yield traits of 24 bread wheat genotypes**

Source of Variance	Replication	Genotype	Error	CV(%)
Traits	(df=2)	(df=23)	(df=46)	
Days to heading	11.347	53.853**	2.217	1.30
Days to maturity	3.375	13.676**	3.230	1.20
Plant height (cm)	66.242	98.404**	34.278	5.68
Flag leaf area (cm <sup>2</sup> )	5.043	83.322**	38.111	16.43
Spike length (cm)	0.687	1.518**	0.261	4.39
Grains spike <sup>-1</sup>	41.268	76.322**	13.328	10.18
Grain weight spike <sup>-1</sup> (g)	0.002	0.106**	0.027	9.68
1000 kernel weight (g)	28.948	102.252*	12.615	8.00
Grain yield (kg ha <sup>-1</sup> )	96	377391.3**	32637.85	0.20
Biological yield (kg ha <sup>-1</sup> )	778320	1779494*	892696	9.91
Harvest index (%)	7.776	46.233**	7.975	10.11

CV= Coefficient of variation and df= Degree of freedom

\*\*, \* = Significant at 1% and 5 % level of probability, respectively

**Table 2. Mean performance for yield and yield related traits of the 24 bread wheat genotypes**

Traits	DH	DM	PH	FLA	SL	GSP	GWS	TGW	GY	BY	HI
Genotypes											
PR-104	113	150	99.33	46.70	12.57	46	2.16	46.33	1915.0	9518.5	20.34
PR-105	121	151	109.20	29.02	12.36	37	1.59	35.33	3144.33	10596.3	39.81
AUR-0809	113	151	115.27	29.32	12.30	38	1.88	52.00	2281.33	10956.6	20.87
AZRC-2	112	148	106.33	35.70	11.92	24	1.69	47.67	2988.67	8985.2	33.46
NRL-0707	110	148	98.27	31.85	10.75	34	1.70	48.33	3062.67	9414.8	32.56
DN-84	111	148	101.60	36.44	12.47	33	1.72	40.00	1880.67	8563.0	22.04
VO*BT022	113	147	104.27	43.77	12.41	37	1.84	51.00	2089.0	8948.1	23.38
V-11183	119	152	112.33	39.09	12.62	42	1.71	40.33	2592.67	9544.4	27.80
V-08314	117	151	104.33	36.51	10.93	27	1.81	44.00	2611.0	9722.2	26.88
NR-399	117	149	99.27	37.69	11.05	35	1.50	37.83	3081.67	9818.5	31.50
NR-400	112	148	109.33	39.00	11.53	30	1.44	43.50	2556.33	9729.6	26.39
9C037	119	151	100.13	46.56	11.79	41	1.77	39.00	2563.00	9759.3	26.41
DH-31	116	149	92.53	38.28	11.22	36	1.37	36.33	2166.67	8685.2	25.14
10C033	117	152	107.00	41.68	11.48	39	1.60	39.50	2940.67	10170.4	28.95
06 FJS3013	118	151	93.80	31.48	10.59	35	1.41	39.33	2874.33	7996.3	35.99
NR-419	119	151	96.47	41.31	11.62	33	1.73	53.50	3077.67	9785.2	31.46
NR-420	115	150	102.80	31.89	12.41	31	1.73	53.00	2577.67	8633.3	29.98
NIA-MB-2	112	151	103.47	37.10	10.90	39	1.72	44.33	3006.67	10263.0	29.33
NR-403	116	149	101.40	34.76	11.05	39	2.11	51.67	2622.33	9537.0	28.41
AUP-1052	120	151	111.93	48.31	12.35	43	1.89	35.83	2974.33	9737.0	30.60
AUP-1059	111	145	101.67	39.80	12.50	37	1.70	45.33	2677.67	8929.6	30.56
Pirsabak-05	102	143	101.20	35.56	10.77	31	1.77	43.00	2414.67	9114.8	26.56
NARC-2009	118	150	101.33	36.65	10.83	37	1.67	47.33	2959.33	11281.5	26.64
Janbaz(check)	115	151	98.47	33.34	11.03	36	1.80	52.00	2281.33	9140.7	25.10
<b>Mean</b>	<b>115</b>	<b>149</b>	<b>102.99</b>	<b>37.58</b>	<b>11.64</b>	<b>36</b>	<b>1.72</b>	<b>44.40</b>	<b>2639.15</b>	<b>9535</b>	<b>27.92</b>
<b>LSD<sub>0.05</sub></b>	<b>2.45</b>	<b>2.96</b>	<b>9.62</b>	<b>10.15</b>	<b>0.84</b>	<b>6.00</b>	<b>0.27</b>	<b>0.27</b>	<b>8.87</b>	<b>1552.8</b>	<b>4.64</b>

**Table 3. Genetic variance ( $V_g$ ), error variance, ( $V_e$ ) phenotypic variance ( $V_p$ ), heritability ( $h^2_{BS}$ ), and genetic advance (GA) as percentage of 20 % selection intensity for different traits**

Traits	$V_g$	$V_e$	$V_p$	$h^2_{BS}$	GA
Days to heading	17.212	2.217	19.429	0.89	5.47
Days to maturity	3.482	3.230	6.712	0.52	1.88
Plant height (cm)	21.376	34.278	55.653	0.38	4.01
Flag leaf area (cm <sup>2</sup> )	15.070	38.111	53.182	0.28	2.89
Spike length (cm)	29.879	12.615	42.494	0.70	6.42
Grains spike <sup>-1</sup>	0.026	0.028	0.054	0.49	0.16
Grain weight spike <sup>-1</sup> (g)	20.998	13.328	34.326	0.61	5.02
1000 grain weight (g)	0.419	0.261	0.680	0.62	0.71
Grain yield (kg ha <sup>-1</sup> )	114917.819	32637.847	147555.666	0.78	418.83
Biological yield (kg ha <sup>-1</sup> )	295599.333	892696.000	1188295.333	0.25	379.64
Harvest index (%)	12.752	7.976	20.728	0.62	3.92

### Conclusion

Significant differences were observed among genotypes for all the traits. This indicates that there is existed genetic variability to have an effective selection. High broad sense heritability coupled with high genetic advance for days to heading (0.89), grain weight spike<sup>-1</sup> (0.61 g), spike length (0.70 cm), 1000 grain weight (0.62 g), grain yield (0.78 kg ha<sup>-1</sup>) and harvest index (0.62) warrant effective selection. Genotype PR 105 surpassed all other genotypes in yield and could be recommended for general cultivation in rainfed area.

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