



EVALUATION OF F₄ WHEAT LINES FOR GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND CORRELATION STUDIES

Farhan Ahmad Shah¹, Amir Sohail¹, Hidayatur Rahman¹, Ghulam Hassan¹, Shahzad Ali² and Manzoor³

¹Department of Plant Breeding and Genetics, The University of Agricultural, Peshawar, Pakistan

²College of Agronomy, Northwest A&F University, Yangling, Shaanxi, China

³Department of Agronomy, the University of Agriculture, Peshawar, Pakistan

E-Mail: amirsohail@aup.edu.pk

ABSTRACT

To check genetic variability, heritability and genetic advance in F₄ wheat lines a field experiment was designed at the University of Agriculture Peshawar, during 2015-16. Eleven genotypes (10 F₄ lines and one check) were studied in randomized block design using three replications. Data noted on parameters included 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 and harvest index. Significant difference was statistically detected for all the traits. 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 exhibited positively genotypic and phenotypic correlation with 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 and harvest index. Strong correlation of grain yield plant⁻¹ with these traits showed that these traits could be safely used in future breeding program.

Keywords: F₄ wheat lines, heritability, genetic advance, genotypic, phenotypic correlation.

1. INTRODUCTION

Wheat (*Triticumaestivum* L.) is a hexaploid species having chromosome number 2n=6x=42, belong to family gramineae. Wheat is a staple diet of Pakistan and override all the crops in area and production. In Pakistan wheat account for 70% of the cereals and over 36% of country acreage is devoted to wheat cultivation. Pakistan is the 4th wheat producer in Asia and stood 11th worldwide (PAR, 2016). During 2015-16 the world's wheat production was 733.8 million tan, while in Pakistan the production was 27.52 million tan (FAOSTAT, 2016).

Heritability estimates provide a message that how much a character is controlled genetically. Knowledge of heritability of the characters lead the breeder to prognosticate the behavior of generation and helps the breeder in doing selection. Breeding program success reckon on the amount of genetic variation in breeding material available. Improvement in 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 nature and magnitude of variation in breeding material. Crop improvement depends on the existence of genetic variability in germplasm. 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. Heritability 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 expected gain is the function of heritability, high heritability coupled with high selection response is desired for selection (Larik *et al.*, 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 direct effect on yield as criteria of selection.

2. MATERIALS AND METHODS

A set of 10 F₄ wheat lines along with check cultivar i.e. Barsat×Siren, TataraxSiren, Tataraxanbaz, Barsat×Janbaz, AUP-5008×Siren, Salim-2000×Siren, Salim-2000×Janbaz, AUP-5008×Janbaz, TataraxPS-2005, AUP-5008×PS-2005 and Tatarax (check) were evaluated in randomized block design using three replications during 2014-15 at The University of Agriculture Peshawar. Each line was sown in three rows with 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 are recorded on 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 and harvest index (%). Standard cultural practices including soil



fertilization, irrigation, hoeing, weeding etc. were practiced during whole cropping season.

2.1 Statistical analysis

Data taken on each traits were exposed to analysis of variance (ANOVA) technique as determined by Steel and Torrie (1980). Means separation using LSD comparison test was used at probability level of 5%. Broad sense heritability for F4 populations was computed using the general formula:

$$h^2_{B,S} = \frac{V_g}{V_g + V_e + V_p}$$

Where, $h^2_{B,S}$ = broad sense heritability and V_g , V_e and V_p are the genotypic, environmental and phenotypic variances of 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, genotypic and phenotypic correlation among the characters were calculated following Singh and Chaudhery (2005).

3. RESULTS AND DISCUSSIONS

3.1 Days to heading

Mean squares revealed significant differences ($P \leq 0.01$) among F4 wheat lines for days to heading (Table-1). Coefficient of variation was 0.95% and coefficient of determination was 0.89. Mean data ranged from 112 to 121 among F4 wheat lines. Minimum (112) days to heading was recorded for TataraxSiren while maximum (121) days to heading was recorded for TataraxPS2005 (Table-2). Our findings are in favor of Ali *et al.* (2007), who also noted significant differences in wheat genotype for days to heading. High heritability (0.83) and low genetic advance (3.90%) was recorded for days to heading (Table-3). Rahman *et al.* (2016) also noted high heritability and stated that days to heading is genetically controlled and taken into consideration. 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 days to heading with biological yield plant⁻¹ and grain weight spike⁻¹.

3.2 Plant height (cm)

Mean squares revealed significant differences ($P \leq 0.01$) among F4 wheat lines for plant height (Table-1). CV value was 1.67% and R^2 value was 0.94. Among the

F4 wheat lines plant height ranged from 72.2 to 89.1 cm. mean data revealed that plant height ranged from 72.2 to 89.1 cm. Salim-2000xSiren had minimum (72.2 cm) plant height, while AUP-5008xJanbaz had maximum (89.1 cm) plant height (Table-2). Rahman *et al.*, (2016) also reported similar results in bread wheat. Genetic variance was 9.2 times greater than environmental variance which means that plant height is genetically controlled and resulted in high heritability (0.90) and moderate genetic advance (10.0 %). (Table-3). 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 conform the findings of (Mohtasham *et al.* 2012), Khan *et al.* (2015) and Jamali *et al.* (2008) who also come up with positive genotypic and phenotypic association of plant height with spike length.

3.3 Flag leaf area (cm²)

A significant difference ($P \leq 0.01$) was observed among F4 wheat lines for flag leaf area (Table-1). CV value was 3.56% and R^2 value was 0.95. Means ranged from 21.4-30.0 cm². TataraxSiren showed minimum value (21.4 cm²) for flag leaf area while AUP-5008xJanbaz showed maximum value (30.0 cm²) for flag leaf area (Table-2). Our finding are in correspondence with Ali *et al.* (2012) who, also noted significant differences in bread wheat for flag leaf area. High magnitude of heritability (0.92) and genetic advance (24.72%) were observed for flag leaf area (Table-3). High coefficient of heritability and genetic advance indicated that flag leaf area is genetically controlled and hence selection was effective. Flag leaf area revealed 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 Muniret. *al.* (2007), who also reported positive genotypic and phenotypic relationship between flag leaf area and harvest index.

3.4 Spike length (cm)

Mean squares showed significant differences ($P \leq 0.01$) among F4 wheat lines for spike length (Table-1). CV value was 4.54% and R^2 value was 0.73. Means ranged from 8.7 to 10.6 cm for spike length among F4 wheat lines. Minimum (8.7 cm) spike length was initiated for TataraxJanbaz while maximum (10.6 cm) spike length was noted for check (Tatarax) (Table-2). Ali *et al.* (2008) and Mangi *et al.* (2007) also reported significant difference for 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 is in favor of Ali *et al.* (2012) who stated that moderate heritability indicates environmental influence while low genetic advance indicates that selection is ineffective. Spike length revealed positive genotypic and phenotypic association with 1000 grain weight ($rG = 0.55^{**}$ and $rP = 0.31^{NS}$). On other hand 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 spike length (Table-4). Our findings are in close correspondence with Khan *et al.* (2015) and Khan *et al.* (2007).

3.5 1000-grain weight (g)

F4 wheat lines revealed significant differences ($P \leq 0.01$) for 1000 grain weight (Table-1). CV value for 1000 grain weight was 3.24% and R^2 value was 0.89. Mean values of 1000 grain weight ranged from 36.7 to 45.1 g. Minimum (36.7 g) 1000-grain weight was recorded for Barsat×Janbaz, while maximum (45.1 g) 1000-grain weight was noted for AUP-5008 x PS-2005 (Table-2). Heritability and genetic advance calculated for 1000 grain weight was 0.83 and 13.8% respectively (Table-3). Ali *et al.* (2012) and Yousif *et al.* (2015) also reported high value of heritability and moderate genetic advancement in wheat genotypes. And said that this trait is under greater genetic control and selection was effective. Thousand grain weight expressed significant positive genotypic association with spike length ($rG = 0.55^{**}$), grain weight spike⁻¹ ($rG = 0.77^{**}$) and harvest index ($rG = 0.33^*$). Similarly 1000 grain weight showed significant and positive phenotypic association with grain weight spike⁻¹ ($rP = 0.49^{**}$). While with remaining traits it had non-significant genotypic and phenotypic association (Table-4). Our finding are in argument with Yousif *et al.* (2015) who also showed positive association of 1000 grain weight with grains weight spike⁻¹ and grain yield.

3.6 Grain weight spike⁻¹ (g)

Mean squares showed significant difference among the F4 wheat lines for 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 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 grain weight spike⁻¹ (Table-3). Our findings are in contrast to Farshadfar and Estehghari (2014) who noted significant differences for grain weight spike⁻¹ along with moderate broad sense heritability among the wheat lines. Grain weight spike⁻¹ had significant and positive association with 1000 grain weight ($rG = 0.77^{**}$) biological yield plant⁻¹ ($rG = 0.39^*$), similarly it exhibited significant and positive phenotypic association with 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 Muniret *al.* (2007).

3.7 Grain yield plant⁻¹ (g)

F4 wheat lines exhibited Significant differences ($P \leq 0.01$) for grain yield plant⁻¹ (Table-1). CV value was 8.29% and R^2 value was 0.79. Means ranged from 7.7 to 11.3 g. Tatarareveald 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 significant difference in F4 wheat population. Heritability and expected genetic advance for 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 traits is greatly under genetic controlled and less influenced by environment. 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 finding are in agreement with those of Yousif *et al.* (2015) who also noted positive relationships of grain yield with harvest index and biological yield.

3.8 Biological yield plant⁻¹ (g)

Significant ($P \leq 0.01$) differences were revealed among F4 lines for biological yield plant⁻¹ (Table-1). CV and R^2 values for biological yield plant⁻¹ were 5.13% and 0.90 respectively. Among the wheat genotypes check (Tatara) produce minimum (17.0 g) biological yield plant⁻¹ whereas, maximum (26.3 g) biological yield plant⁻¹ was produced by TataraxPS-2005 (Table-2). High heritability (0.85) and genetic advance (23.64%) was recorded for biological yield plant⁻¹ indicated that this traits is under additive gene affect (Table 3). biological yield plant⁻¹ revealed significant genotypic and phenotypic association with days to heading ($rG = 0.55^{**}$ and $rP = 0.42^*$), grain weight spike⁻¹ ($rG = 0.39^*$ and $rP = 0.29^{NS}$), 1000 grain weight ($rG = -0.44^{**}$ and $rP = -0.40^*$) and grain yield plant⁻¹ ($rG = 0.34^*$ and $rP = 0.33^*$). While non-significant association with rest of traits studied (Table-4). Ahmad *et al.* (2010) also observed high heritability and genetic gain among genotypes along with positive association of biological yield with days to heading and grain yield.

3.9 Harvest index (%)

Mean squares expressed a significant difference ($P \leq 0.01$) among the F4 lines for harvest index (Table-1). Our findings are in contrast with Khan *et al.* (2015) who come up with no difference in wheat genotypes. For harvest index coefficient of variation was 8.84% and coefficient of determination was 0.81. TataraxJanbaz and AUP-5008×Siren had minimum (37%) harvest index, while AUP-5008×Janbaz had maximum (56%) harvest index (Table-2). 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. Harvest index expressed significant genetic association with plant height ($rG = 0.56^{**}$), flag leaf area ($rG = 0.41^*$), 1000 grain weight ($rG = 0.33^*$), grain yield plant⁻¹ ($rG = 0.58^{**}$) and biological yield plant⁻¹ ($rG = -0.56^{**}$). Similarly harvest index exhibited significant association with plant height ($rP = 0.49^{**}$), grain yield plant⁻¹ ($rP = 0.66^{**}$) and biological yield plant⁻¹ ($rP = -0.48^{**}$). While with remaining parameters it had non-significant association (Table-3). Ahmad *et al.* (2010) conveyed positive correlation between harvest index and biological yield in contrast to my results.



4. CONCLUSIONS

Significant variability was noted among F4 wheat lines for all the traits studied indicating the need for effective selection. High heritability was observed for all traits except spike length suggested that these traits were genetically controlled. Grain yield, biological yield and

flag leaf area had high expected genetic advance which showed the effectiveness of selection in F4 wheat lines. Grain yield plant⁻¹ had positive genotypic and phenotypic association with all the traits studied therefore these traits could be used for yield improvement in future wheat breeding program.

Table-1. Mean squares of yield related Traits of F4 wheat lines.

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

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

Table-2. Means value of F4 wheat lines evaluating during 2015-16.

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

**Table-3.** Heritability and genetic advance for various traits of F4 wheat 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

Table-4. Genotypic (rG) and phenotypic (rP) correlation among yield related traits in F4. wheat. 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**	—

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

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