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Estimation of Heritability and Genetic Advance in F₂ Populations of Wheat

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Abstract:

Estimation of heritability and genetic advance plays a pivotal role in selection. A set of 19 wheat genotypes comprised of seven parents and 12 F₂ populations were evaluated at The University of Agriculture-Peshawar during 2013-14 in a randomized complete block design (RCBD) with three replications. Data were recorded on days to 50% heading, days to maturity, plant height, flag leaf area, productive tillers plant⁻¹, spike length, biological yield plant⁻¹, spikelet spike⁻¹, grains spike⁻¹, grain yield plant⁻¹, and harvest index. Analysis of variance showed significant differences among genotypes, parents, and F₂ populations for all the studied traits while parent vs. F₂ population also revealed significant genetic variability for all the studied traits except plant height, spike length, and spikelet spike⁻¹. Low to moderate broad-sense heritability coupled with low genetic advance was observed for almost all the traits studied. Among Parents, Janbaz was the highest in productive tillers plant⁻¹, spikelet spike⁻¹, grains spike⁻¹, and grain yield plant⁻¹. Among F₂ population, Saleem-2000 × Barsat had the earliest 50% heading and maturity, Saleem-2000 × Watan, Tatara × Barsat, AUP-5008 × Fakhre Sarhad, and Janbaz × Barsat showed the shortest plant, large flag leaf area, long spikes, more productive tillers plant⁻¹, grain yield plant⁻¹, harvest index, biological yield plant⁻¹, and spikelet spike⁻¹. Saleem-2000 × Watan, Tatara × Barsat, AUP-5008 × Fakhre Sarhad and Janbaz × Barsat having a better performance for most of the traits and hence could be utilized in future wheat breeding programs.

Keywords: F₂ population, genetic advance, heritability, parents.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the world's major cereal crops and staple food of many regions, grown under both irrigated and rain-fed conditions (Asad *et al*., 2016). It belongs to the family Graminae. Wheat is one of the first cereals known to have been domesticated, and wheat's ability to self-pollinate greatly facilitated the selection of many distinct domesticated varieties. Wheat usually needs 150-180 days between planting and harvest, depending upon climate, seed type, and soil condition. It is one of the most widely grown crops in the world. In Pakistan and Khyber Pakhtunkhwa, low yield of wheat as a whole is attributed to various factors such as unavailability of good quality seed of high yielding cultivars, delayed planting, unavailability of required soil moisture at critical growth stages (Fatima *et al.*, 2018) and higher prices of chemical fertilizers. Various factors are considered in the selection of highest yield genotypes and are suggested for further crop renovation programs (Kamran *et al.*, 2016).

Genetic manipulation is the best way to boost up wheat production. Therefore, it is necessary to estimate and study the genetic variation and mode of inheritance in different plant parameters to initiate productive wheat breeding programs (Ijaz and Khan, 2009). Achievement of any crop improvement depends upon the presence of genetic variability and heritability as well as genetic gain in selection (Khan *et al.,* 2006). A fundamental aspect of plant breeding is to estimate the fraction of the total variance among plants of a population that may be attributed to genetic differences between them. This ratio is called heritability, which is one of the essential components of the breeder's equation that aims to predict the expected response to selection. In general, the higher the heritability of a trait, the greater the expected genetic gain since artificial selection can be carried out more efficiently (Mazurkievicz *et al.,* 2019). Plant traits having satisfactory variability, high heritability, and genetic advance would be an effective tool for crop improvement (Aytaç and Kinaci, 2009).

In wheat breeding programs, the main aim is to develop genotype for the improvement of yield under adverse conditions. The scope of crop improvement by breeding is determined by the amount of heritable or genetic variation to that of non- heritable. Therefore, efforts were made in the present study to determine the extent of heritability, genetic advance, and desirable high yielding genotypes in F_2 populations of wheat for the agronomic traits as a basis for selection.

MATERIALS AND METHODS

The present research was carried out at The University of Agriculture-Peshawar during 2013-14. Nineteen genotypes, including seven parents and 12 F_2 populations (Table 1) were evaluated in a randomized complete block design (RCBD) with three replications. The randomized complete block (RCB) design is one of the most widely used experimental designs in agricultural research. The design is especially suited for field experiments, where the number of treatments is not large, and the experimental area has a predictable productivity gradient. The primary distinguishing feature of the RCB design is the presence of blocks of equal size, each of which contains all the treatments (Shieh and Jan 2004). Data was recorded on the following parameters. Ten plants in parents and 20 plants in F_2 populations were randomly selected for data analysis.

Days to 50% heading: Days to 50% heading were counted from the date of sowing till the date when spike emerged from the sheath of the flag leaves in 50% plants in a plot.

Days to maturity: Numbers of days to maturity were counted from date of sowing to the date of physiological maturity of the genotype.

Plant height (cm): Plant height was taken from the base to tip of the spike, excluding awns at the time of the physiological maturity of randomly selected plants.

Table 1. List of genotypes utilized in the experiment

Parents	F_2 populations
1. Janbaz (UOA)	1. Janbaz x Barsat
2. AUP-5008 (UOA)	2. Janbaz x Fakhre Sarhad
3. Saleem-2000 (CCRI)	3. Janbaz x Watan
4. Tatara (NIFA)	4. Saleem 2000 x Barsat
5. Watan (Punjab)	5. Saleem 2000 x Fakhre Sarhad
6.Fakhre Sarhad (NIFA)	6. Saleem 2000 x Watan
7. Barsat (NIFA)	7. Tatara x Barsat
	8. Tatara x Fakhre Sarhad
	9. Tatara x Watan
	10. AUP- 5008 x Barsat
	11. AUP-5008 x Fakhre Sarhad
	12. AUP-5008 x Watan

Flag leaf area (cm^2): At the time of physiological maturity, the length of the flag leaf lamina was measured from the base of the lamina to the extreme tip, while the width was measured at its broadest place. The flag leaf area was determined according to the formula (Francis *et al.,* 1969). Flag leaf area = Leaf length x Leaf width x 0.75

Productive tillers plant^{-1}: Productive tillers were counted on randomly selected plants.

Spike length (cm): Ten spikes in parents and 20 in crosses were randomly selected from each plot, and their length was measured from the base of the first spikelet to the tip of spike and finally averaged for data analysis.

Biological yield plant^{-1}(g): Each selected plant of each genotype was harvested individually, and its biological yield was determined.

Spikelet spike^{-1}: Number of spikelet spike^{-1} was counted for randomly selected spike and then was averaged for the final analysis.

Grains spike^{-1}: Numbers of grains spike^{-1} was counted for each randomly selected spike and then were averaged for final data analysis.

Grain yield plant^{-1}: Grain yield plant^{-1} was obtained by weighing total grain yield plant^{-1} after threshing of each genotype and then was averaged for data analysis.

Harvest Index (%): Harvest index was determined as the ratio of grain yield plant^{-1} to biological yield plant^{-1} by the following formula;

$$\text{Harvest index (\%)} = \frac{\text{Grain yield plant}^{-1}}{\text{Biological yield plant}^{-1}} \times 100$$

Data Analysis

To estimate variation among parents and F_2 populations, the data were subjected to statistical analysis by using the analysis of variance technique (Steel and Torrie, 1960) Least significant differences (LSD) test was used for mean separation of parents and F_2 populations. Broad sense Heritability was calculated using the formula described (Mahmud and Kramer, 1951) as follows:

$$h^2(B.S.) = \frac{VF_2 - \sqrt{VP_1 \times VP_2}}{VF_2} \times 100$$

Where, h^2 = heritability of a trait, V_{F2}= variance of F_2's, V_{P1} = variance of female parent in a cross, V_{P2} = variance of male parent in a cross. Whereas, for days to 50% heading and days to maturity, heritability in broad sense was estimated as the ratio of genotypic to phenotypic variance (Singh and Ceccarelli, 1996).

$$h^2 (BS) = \frac{Vg}{Vp}$$

Where, Vg = Genetic variance of a trait, Vp = Phenotypic variance of a trait

The heritability was categorized as low, moderate, and high, as indicated (Robinson *et al.,* 1951).

0-30% = Low, 31- 60% = Moderate, 61% and above = High

The genetic advance was calculated according to (Allard, 1999) with the following formula:

$$GA = i\delta_p h^2$$

Where; GA = genetic advance, δ_p = phenotypic standard deviation, h^2 = heritability in broad sense, í = selection intensity. The value of í = 1.40 (at 20% selection pressure) was used in this study.

The genetic advance was categorized as low, moderate, and high as given (Johnson *et al.,* 1955).

G.A < 10%: Low, 10% < G.A < 20%: Moderate, G.A > 20%: High

RESULTS

Analysis of variance (ANOVA):

Mean square values of 11 yield and component traits are presented in (Table 2). Highly Significant variability among genotypes, parents and F_2 population were recorded for days to 50% heading, days to maturity, plant height, flag leaf area, productive tillers plant^{-1}, spike length, biological yield plant^{-1}, spikelet spike^{-1}, grains spike^{-1}, grain yield plant^{-1}, and harvest index. Among parents vs. F_2, significant variability was observed as well for all the traits except plant height, spike length, and spikelet spike^{-1}.

Table 2. Mean squares for various parameters of 19 wheat genotypes.

Traits	Replications df = 2	Genotypes df = 18	Parents df = 6	F_2 df = 11	P vs F_2 df = 1	Error df = 36	CV (%)
Days to 50% heading	3.02	26.68**	12.00**	35.06**	22.61**	2.33	1.25
Days to maturity	4.79	22.09**	29.33**	18.17**	21.65**	2.36	0.92
Plant height	6.10	50.67**	73.39**	40.34*	27.95	17.21	4.58
Flag leaf area	8.88	29.50**	26.46**	20.62**	145.50**	6.42	10.13
Productive tillers Plant^{-1}	4.00	25.89 **	15.33*	20.87 **	144.55 **	6.41	14.71
Spike length	0.89	1.37**	2.21**	0.98*	0.67	0.41	5.12
Biological yield plant^{-1}	13.98	133.67**	139.26**	120.35**	246.69*	38.47	15.38
Spikelet spike^{-1}	1.74	3.02**	3.58**	2.97**	0.16	0.94	4.67
Grains spike^{-1}	24.88	42.95**	34.84**	38.11**	144.89**	10.17	5.06
Grain yield plant^{-1}	5.26	20.82**	17.19*	20.86**	42.25*	6.48	14.31
Harvest index	29.86	161.67**	215.07**	102.87*	488.11**	50.00	15.72

* = Significant at 1% and **** =** 5% level of probability

Range and mean values:

Range and mean values are presented in figure-1. Days to 50% heading ranged from 113.0 to 125.7 days. Among parental lines, the maximum number of days (125.0 days) was recorded for Saleem-2000, while minimum (119.3 days) were recorded for Janbaz. While among the F_2 population, the maximum number of days to 50% heading (125.7 days) was recorded for cross Janbaz × Barsat, while the minimum number of days (113.0 days) was recorded for Saleem-2000 × Barsat. Variability for the number of days to maturity showed a range from 162.3 to 171.3 days. Parental line 'Tatara' took more (171.3 days) days to maturity, while less (164.33 days) number of days to maturity was recorded for AUP-5008 and Saleem-2000. Maximum variance (169.7 days) for days to maturity among F_2 population was recorded for crosses Janbaz × Barsat, Janbaz × Fakhre Sarhad, and AUP-5008 × Watan, while minimum (162.3) days to maturity was noticed for Saleem-2000 × Barsat. Plant height is a quantitative trait affecting other yield parameters. Mean values for plant height ranged from 82.6 to 97.2 cm.   The parental line 'Tatara' had maximum plant height (97.2 cm) while Saleem-2000 had minimum plant height (82.6 cm). Maximum plant height (95.9 cm) was recorded for the F_2 population Tatara × Watan, while minimum plant height (83.5 cm) was recorded for Saleem-2000 × Watan. A high extent of variability 17.3 to 29.6 cm^2 was observed for the flag leaf area. Among parental lines, the maximum flag leaf area (26.1 cm^2) was recorded for Saleem-2000, and a minimum (17.3 cm^2) was recorded for AUP-5008. Among the F_2 population, the maximum flag leaf area (29.6 cm^2) was recorded for cross Tatara × Barsat while the minimum flag leaf area (20.9 cm^2) was recorded for AUP-5008 × Watan. Mean values for productive tillers $plant^{-1}$ ranged from 11 to 22.8.   Among parental lines, maximum productive tillers $plant^{-1}$ (18.7) were recorded for Janbaz, while minimum (11) were recorded for Watan. F_2 population AUP-5008 × Fakhre Sarhad showed maximum productive tillers

$plant^{-1}$ (22.8), while minimum (13.7) were recorded for Saleem-2000 × Barsat. Spike length is a quantitative trait, and it is concerning other yield components (Madić *et al.,* 2005; Zecevic *et al.,* 2004), and broader knowledge about the influence of genetic and environmental variability will contribute to the successfulness of breeding programs.

Variances for spike length ranged from 11.3 to 13.7 cm. Among parental lines, maximum spike length (13.7 cm) was recorded for parental line Barsat, while minimum (11.3 cm) was recorded for parental line Saleem-2000. Among F_2 populations, maximum spike length (13.5 cm) was recorded for Tatara × Barsat, while minimum (11.8 cm) was recorded for AUP-5008 × Watan. Mean values for biological yield ranged from 31.3 to 52.1 g. Maximum biological yield $plant^{-1}$ (52.1 g) was recorded for parental line Tatara, while minimum (31.3 g) for parental line AUP-5008. Maximum biological yield $plant^{-1}$ (51.9 g) was recorded for cross combination, Janbaz × Barsat, while minimum (33.9 g) was recorded for Saleem-2000 × Barsat. Mean values for spikelet $spike^{-1}$ ranged from 19.3 to 22.7. Maximum spikelet $spike^{-1}$ (22.7) was noted for parental line Janbaz while minimum (19.7) was recorded for AUP-5008. Maximum spikelet $spike^{-1}$ (22.3) was recorded for cross combination Janbaz × Barsat, while minimum (19.3) was recorded for Saleem-2000 × Barsat, and Saleem-2000 × Watan. Mean values for the number of grains $spike^{-1}$ ranged from 55.7 to 71.2. Parental line Janbaz had the maximum number of grain $spike^{-1}$ (66.2), while minimum numbers (55.7) for Barsat. The maximum number of grain $spike^{-1}$ (71.2) was recorded for cross combination, Janbaz × Barsat, while minimum numbers (57.9) were recorded for Janbaz × Watan. Mean values for grain yield $plant^{-1}$ ranged from 12.3 to 22.8 g. Among parental lines, maximum grain yield $plant^{-1}$ (19.6 g) was recorded for Janbaz, while minimum grain yield $plant^{-1}$ (12.3 g) was recorded for Watan. Among the F_2 population, maximum grain yield $plant^{-1}$ (22.8 g) was recorded for AUP-5008 × Fakhre Sarhad, while minimum

grain yield plant^{-1} (13.7 g) was recorded for Saleem-2000 × Barsat. Harvest index reflects the partitioning of photosynthate between the grain and the vegetative plant, and improvements in harvest index emphasize the importance of carbon allocation in grain production. Mean values for harvest index ranged from 32.8 to 53.7%. Among parental lines, the maximum harvest index (53.7%) was recorded for Janbaz, while minimum (32.8%) recorded for Tatara. Among F$_2$ populations, the maximum harvest index (52.4%) was recorded for cross combination, Janbaz × Watan, while minimum (33.1%) was recorded for Janbaz × Barsat.
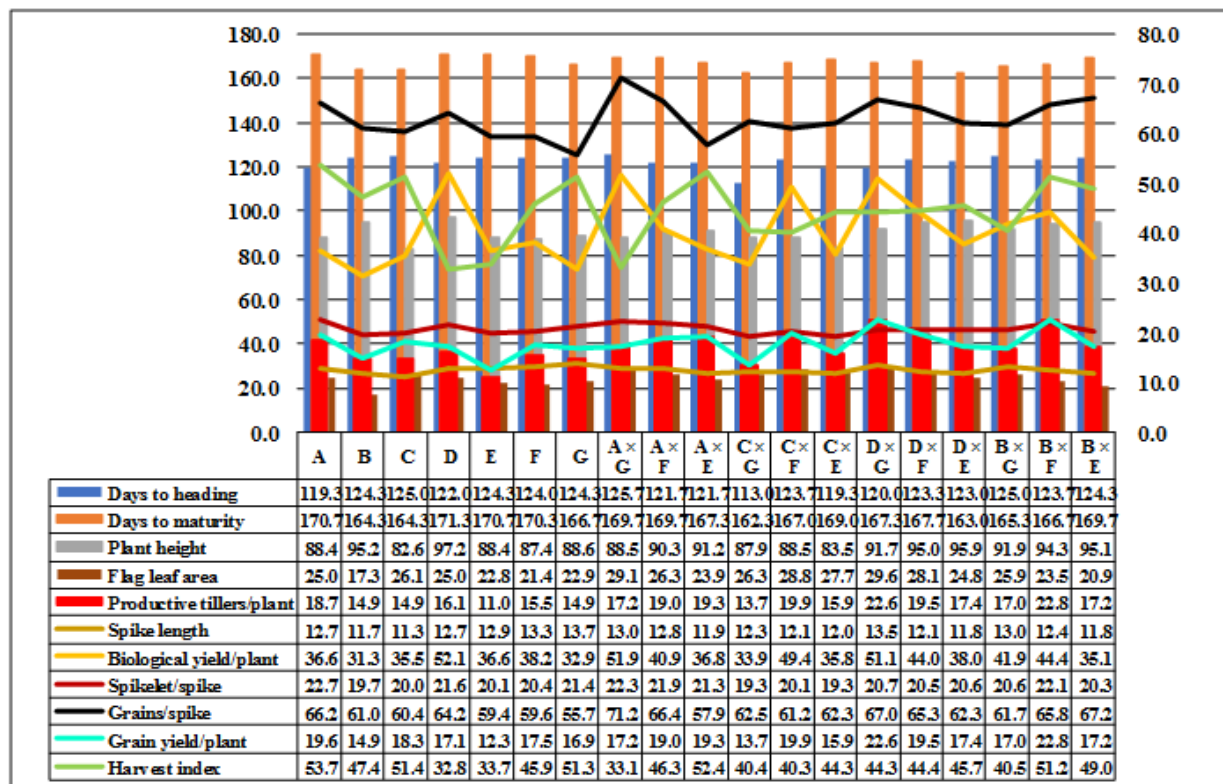
	A	B	C	D	E	F	G	A× G	A× F	A× E	C× G	C× F	C× E	D× G	D× F	D× E	B× G	B× F	B× E
Days to heading	119.3	124.3	125.0	122.0	124.3	124.0	124.3	125.7	121.7	121.7	113.0	123.7	119.3	120.0	123.3	123.0	125.0	123.7	124.3
Days to maturity	170.7	164.3	164.3	171.3	170.7	170.3	166.7	169.7	169.7	167.3	162.3	167.0	169.0	167.3	167.7	163.0	165.3	166.7	169.7
Plant height	88.4	95.2	82.6	97.2	88.4	87.4	88.6	88.5	90.3	91.2	87.9	88.5	83.5	91.7	95.0	95.9	91.9	94.3	95.1
Flag leaf area	25.0	17.3	26.1	25.0	22.8	21.4	22.9	29.1	26.3	23.9	26.3	28.8	27.7	29.6	28.1	24.8	25.9	23.5	20.9
Productive tillers/plant	18.7	14.9	14.9	16.1	11.0	15.5	14.9	17.2	19.0	19.3	13.7	19.9	15.9	22.6	19.5	17.4	17.0	22.8	17.2
Spike length	12.7	11.7	11.3	12.7	12.9	13.3	13.7	13.0	12.8	11.9	12.3	12.1	12.0	13.5	12.1	11.8	13.0	12.4	11.8
Biological yield/plant	36.6	31.3	35.5	52.1	36.6	38.2	32.9	51.9	40.9	36.8	33.9	49.4	35.8	51.1	44.0	38.0	41.9	44.4	35.1
Spikelet/spike	22.7	19.7	20.0	21.6	20.1	20.4	21.4	22.3	21.9	21.3	19.3	20.1	19.3	20.7	20.5	20.6	20.6	22.1	20.3
Grains/spike	66.2	61.0	60.4	64.2	59.4	59.6	55.7	71.2	66.4	57.9	62.5	61.2	62.3	67.0	65.3	62.3	61.7	65.8	67.2
Grain yield/plant	19.6	14.9	18.3	17.1	12.3	17.5	16.9	17.2	19.0	19.3	13.7	19.9	15.9	22.6	19.5	17.4	17.0	22.8	17.2
Harvest index	53.7	47.4	51.4	32.8	33.7	45.9	51.3	33.1	46.3	52.4	40.4	40.3	44.3	44.3	44.4	45.7	40.5	51.2	49.0

Fig. 1. Mean performance of wheat F$_2$ population for yield and component traits.

A = Janbaz, B = AUP-5008, C = Saleem-2000, D = Tatara, E = Watan, F = Fakhre Sarhad, G = Barsat, A x G = Janbaz x Barsat, A x F = Janbaz x Fakhre Sarhad, A x E = Janbaz x Watan, C x G = Saleem-2000 x Barsat, C x F = Saleem-2000 x Fakhre Sarhad, C x E = Saleem-2000 x Watan, D x G = Tatara x Barsat, D x F = Tatara x Fakhre Sarhad, D x E = Tatara x Watan, B x G = AUP-5008 x Barsat, B x F = AUP-5008 x Fakhre Sarhad, B x E = AUP-5008 x Watan

Estimation of heritability and genetic advance:

Estimates of heritability and genetic advance are given in (Tables 3, 4, 5). High broad-sense heritability (0.77) was observed for days to 50% heading with the genetic advance value of 3.48. Days to maturity also showed high heritability (0.73), while the value for the genetic advance was 3.05 (Table 3). The estimates of broad-sense heritability for plant height varied from 0.37 to 0.62 (Table 4). Whereas, expected genetic advance ranged from 2.92 to 6.08. The highest value of heritability (0.62) was estimated

for cross combination, Saleem-2000 × Watan, while the lowest value of heritability (0.37) was estimated for cross combination, Tatara × Barsat. Similarly, the highest value of genetic advance (6.08) was observed for cross combination, Saleem-2000 × Watan, while the lowest value of genetic advance (2.92) was observed for cross combination, Tatara ×

Barsat. Broad sense heritability for flag leaf area varied from 0.45 to 0.65. Whereas, expected genetic advance ranged from 2.84 to 4.97. Saleem-2000 × Watan showed a high value of heritability (0.65), while the lowest value of heritability (0.45) was estimated for cross combination, AUP-5008 × Barsat.

Table 3. Genotypic variance (V_g), environmental variance (V_e), phenotypic variance (V_p), heritability (h^2), and genetic advance (GA) for days to 50% heading and days to maturity.

Parameter	V_g	V_e	V_p	h^2	GA
Days to 50% heading	8.11	2.33	10.44	0.77	3.48
Days to maturity	6.57	2.36	8.93	0.73	3.05

Table 4. Heritability and genetic advance for various traits of F_2 populations of wheat.

F2 Populations	Plant height (cm)		Flag leaf (cm^2)		Productive tillers plant^{-1}		Spike length (cm)		Biological yield plant^{-1} (g)	
	h2	GA	h2	GA	h2	GA	h2	GA	h2	GA
Janbaz × Barsat	0.57	5.45	0.59	4.22	0.63	4.56	0.38	1.29	0.59	5.78
Janbaz × Fakhre Sarhad	0.51	4.55	0.52	3.43	0.49	3.06	0.49	1.79	0.52	4.79
Janbaz × Watan	0.46	3.92	0.59	4.15	0.54	3.48	0.46	1.71	0.59	5.77
Saleem-2000 × Barsat	0.55	4.97	0.54	3.61	0.36	2.00	0.46	1.63	0.57	5.28
Saleem-2000 × Fakhre Sarhad	0.41	3.19	0.48	2.97	0.46	2.79	0.56	2.08	0.51	4.60
Saleem-2000 × Watan	0.62	6.08	0.65	4.97	0.29	1.51	0.34	1.10	0.58	5.52
Tatara × Barsat	0.37	2.92	0.61	4.49	0.45	2.65	0.51	1.96	0.45	3.67
Tatara × Fakhre Sarhad	0.60	5.86	0.59	4.14	0.40	2.29	0.45	1.58	0.51	4.52
Tatara × Watan	0.58	5.56	0.63	4.69	0.32	1.76	0.40	1.45	0.33	2.50
AUP-5008 × Barsat	0.40	3.19	0.45	2.84	0.38	2.13	0.48	1.78	0.56	5.32
AUP-5008 × Fakhre Sarhad	0.61	5.92	0.57	4.03	0.46	2.82	0.26	0.79	0.46	4.14
AUP-5008 × Watan	0.44	3.62	0.55	3.77	0.41	2.46	0.47	1.81	0.43	3.62

Similarly, the highest value of genetic advance was observed for cross combination, Saleem-2000 × Watan having a value of 4.97, while the lowest value of genetic advance (2.84) was recorded for cross combination AUP-5008 × Barsat. The estimates of broad-sense heritability for productive tillers plant^{-1} varied from 0.29 to 0.63. Whereas, expected genetic advance ranged from 1.51 to 4.56. The highest value of heritability (0.63) was estimated for cross combination, Janbaz × Barsat, while the lowest

value of heritability (0.29) was observed for cross combination, Saleem-2000 × Watan. Similarly, the highest value of genetic advance was observed for cross combination, Janbaz × Barsat having a value of 4.56, while the lowest value of genetic advance (1.51) was observed for cross combination, Saleem-2000 × Watan. The estimates of broad-sense heritability for spike length varied from 0.26 to 0.56, and the expected genetic advance ranged from 0.79 to 2.08. The highest value of heritability (0.56) was

estimated for cross combination, Saleem-2000 × Fakhre Sarhad, while the lowest value of heritability (0.26) was estimated for cross combination, AUP-5008 × Fakhre Sarhad. Similarly, the highest value of genetic advance was observed in cross combination, Saleem-2000 × Fakhre Sarhad having a value of 2.08, while the lowest value of genetic advance (0.79) was observed in cross combination, AUP-5008 × Fakhre Sarhad. The estimates of broad-sense heritability for biological yield plant^{-1} varied from 0.33 to 0.59. Whereas, expected genetic advance ranged from 2.50 to 5.78. The highest value of heritability (0.59) was estimated for cross combinations, Janbaz × Barsat and Janbaz × Watan, while the lowest value of heritability (0.33) was estimated for cross combination, Tatara × Watan. Similarly, the

highest value of genetic advance was observed for cross combination, Janbaz × Barsat having a value of 5.78, while the lowest value of genetic advance (2.50) was observed for cross combination, Tatara × Watan (Table 4). The estimates of broad-sense heritability for spikelet spike^{-1} varied from 0.27 to 0.60. Whereas, expected genetic advance ranged from 1.40 to 4.26. The highest value of heritability (0.60) was estimated for cross combination, Saleem-2000 × Watan, while the lowest value of heritability (0.27) was estimated for cross combination, Tatara × Fakhre Sarhad. Similarly, the highest value of genetic advance was observed for cross combination, Saleem-2000 × Watan having a value of 4.26, while the lowest value of genetic advance (1.40) was observed for cross combination, Tatara × Fakhre Sarhad (Table 5).

Table 5. Heritability and genetic advance for various traits of F_2 populations of wheat.

F2 Populations	Spikelet spike^{-1}		Grain spike^{-1}		Grain yield plant^{-1} (g)		Harvest Index (%)	
	h2	GA	h2	GA	h2	GA	h2	GA
Janbaz × Barsat	0.48	2.97	0.45	6.80	0.39	3.29	0.53	8.04
Janbaz × Fakhre Sarhad	0.53	3.46	0.47	7.36	0.54	5.17	0.52	7.90
Janbaz × Watan	0.43	2.54	0.52	8.26	0.40	3.42	0.58	9.56
Saleem-2000 × Barsat	0.47	2.85	0.53	8.62	0.54	5.10	0.55	8.46
Saleem-2000 × Fakhre Sarhad	0.47	2.87	0.48	7.55	0.64	6.69	0.52	7.79
Saleem-2000 × Watan	0.60	4.26	0.51	8.15	0.53	5.02	0.44	6.24
Tatara × Barsat	0.52	3.34	0.47	7.22	0.33	2.63	0.57	8.99
Tatara × Fakhre Sarhad	0.27	1.40	0.45	6.87	0.52	4.82	0.54	8.11
Tatara × Watan	0.52	3.38	0.52	8.37	0.44	3.91	0.51	7.58
AUP-5008×Barsat	0.56	3.78	0.52	8.32	0.56	5.35	0.55	8.51
AUP-5008 × Fakhre Sarhad	0.42	2.50	0.53	8.83	0.53	4.77	0.51	7.48
AUP-5008 × Watan	0.49	3.10	0.50	7.80	0.56	5.41	0.47	6.76

The estimates of broad-sense heritability for the number of grain spike^{-1} varied from 0.45 to 0.53. Whereas, expected genetic advance ranged from 6.80 to 8.83. The highest value of heritability (0.53) was estimated for cross combinations, Saleem-2000 × Barsat, and AUP-5008 × Fakhre Sarhad, while the lowest value of

heritability (0.45) was estimated for cross combination, AUP-5008 × Fakhre Sarhad, while the lowest value of heritability (0.45) was estimated for cross combinations, Janbaz × Barsat, and Tatara × Fakhre Sarhad. Similarly, the highest value of genetic advance was observed for cross combination, AUP-5008 ×

Fakhre Sarhad having a value of 8.83, while the lowest value of genetic advance (6.80) was observed for cross combination, Janbaz × Barsat (Table 5). The estimates of broad-sense heritability for grain yield plant^{-1} varied from 0.33 to 0.64. Whereas, expected genetic advance ranged from 2.63 to 6.69. The highest heritability (0.64) was recorded for cross combination, Saleem-2000 × Fakhre Sarhad, while the lowest value of genetic advance (2.63) was observed for cross combination, Tatara × Barsat. The estimates of broad-sense heritability for harvest index varied from 0.44 to 0.58. Whereas, expected genetic advance ranged from 6.24 to 9.56. The highest value of heritability (0.58) was estimated for cross combination, Janbaz × Watan, while the lowest value of heritability (0.44) was estimated for cross combination, Saleem-2000 × Watan. Similarly, the highest value of genetic advance (9.56) was observed for cross combination, Janbaz × Watan, while the lowest value of genetic advance (6.24) was observed for cross combination, Saleem-2000 × Watan.

DISCUSSION

The understanding of the inheritance of genetic architecture of the important yield component traits is essential for formulating a systematic breeding program for developing variety with the important yield traits. The presence of genetic variability and the extent of heritability in any crop is considered to be necessary for the selection of superior genotypes. In the present experiment, a set of 19 wheat genotypes were studied to assess their genetic variability, heritability, and genetic advance for important yield traits. The wide range of genetic variability estimated for all the traits showed that these traits could be utilized for developing new wheat varieties and thus could respond positively in selection. Several researchers reported significant differences among wheat genotypes studied. (Dabi *et al.,* 2019) studied 30 wheat genotypes at two locations and reported significant genetic variability for different morphological as well as yield traits. A study reported significant differences among 55 genotypes for 12 morphological traits such as days to 75% heading, days to maturity, flag leaf area, plant height, spike length, number of grains spike^{-1}, No. of spikelets spike^{-1}, number of productive tillers plant^{-1}, 1000-grain weight, grain yield plant^{-1}, biological yield plant^{-1}, and harvest index (Joshi *et al.,* 2018). Jamil et al. (2017) also observed significant genetic variability among 60 wheat genotypes for different yield traits. Sanini and Shweta (2017) found a significant amount of genetic variability among 50 wheat genotypes for maturity and yield traits. Significant differences for morphological and yield component traits were also reported by (Kumar *et al.,* 2017). Kalimullah et al. (2012) reported that grains spike^{-1}, No. of tillers plant^{-1}, 1000-grain weight, spike density, and grain yield plant^{-1} showed highly significant differences.

Thus, it indicated that there was sufficient genetic variability and hence could be utilized to develop potential lines in future wheat breeding programs. High heritability estimates, coupled with high genetic advance, indicate that there are more chances that a character is controlled by additive genes. Hence, selection for improvement in the early segregation is more fruitful. Most of the F_2 cross combinations revealed moderate broad-sense heritability for all the studied traits, and thus further improvement for phenotypic selection could be practiced. The heritability estimate is useful when deciding the characters to be considered in the selection process. However, selection based only on heritability can limit progress as it is likely to change with environmental change, materials (Anu *et al.,* 2019). Several earlier researchers (Rathwa *et al.,* 2018; Sohail *et al.,* 2018; Anu *et al.,* 2019; Mishra *et al.,* 2019) observed moderate to high broad-sense heritability coupled with low to high genetic advance while studying different wheat populations. This little contradiction in results was due to the difference in the experimental

environment and experimental breeding materials used in the experiment.

Similarly, other researchers (Hussain *et al.,* 2017a; Ishaq *et al.,* 2017; Hussain *et al.,* 2017b; Aziz *et al.,* 2018; Elmassry and El-Nahas, 2018) also reported low to moderate type of broad-sense heritability for some of the yield components. Various other studies documented significant differences and high heritability with low genetic advance for morphological as well as yield traits (Choudhary *et al.,* 2015; Jan *et al.,* 2015; Harshwardhan *et al.,* 2016; Saleem *et al.,* 2016; Ahmad *et al.,* 2016). Significant differences and high heritability with a low genetic advance in most of the F_2 populations of wheat for days to 50% heading was observed in the previous experiments (Ijaz *et al.,* 2013; Waqas *et al.,* 2014). Khan et al. (2013) reported moderate to high heritability with low genetic advance for flag leaf area. Hokrani et al. (2013) studied moderately to high heritability with low genetic advance for productive tillers plant^{-1} in most of the crosses. Moderate heritability with a low genetic advance in most of the F_2 populations of wheat for spike length was reported by reported moderate to high heritability with a low genetic advance in most of the cross combinations for spikelet spike^{-1}. High heritability with high genetic advance was estimated in most of the cross combinations for biological yield plant^{-1} (Baloch *et al.,* 2013; Jawad *et al.,* 2013). Moderate to high heritability, coupled with a low genetic advance in most of the cross combinations were reported (Zeeshan *et al.,* 2014).

CONCLUSION

Parental genotypes and F_2 populations evaluated in the present study expressed significant genetic variability for yield and yield-related traits. Parental lines, like Janbaz, Saleem-2000, Barsat, and Tatara, were exceeding in most of the yield and component traits and, therefore, could be tested further for

the production of high yielding wheat lines. In F_2 populations cross combination, Saleem-2000 × Barsat, Saleem-2000 × Watan. Tatara × Barsat, AUP-5008 × Fakhre Sarhad, Janbaz × Barsat surpassed in most of the characters, hence could be utilized in future wheat breeding programs. Most of the traits like productive tillers plant^{-1}, spike length, spikelet spike^{-1}, and grain yield plant^{-1} showed moderate heritability with low genetic advance for all cross combinations except Janbaz × Barsat which showed high heritability with low genetic advance for productive tillers plant^{-1} indicated that selection for these traits could not be rewarding. Hence selection could be delayed to later generations. The present result is only an indication, and we cannot reach a definite conclusion. Therefore, since the experiment was carried out at one location in one season, it is advisable to continue with this study over several years and locations.

CONFLICT OF INTEREST

The authors declare no potential conflict of interest to the research, authorship, and/or publication of this article.

REFERENCES

Allard, R.W., 1999. Principles of plant breeding. John Wiley & Sons.

Ahmad, W., Ghulam, H., Ali, M., Ghulam Hassan, Murad Ali, Khan, N., Ishaq, M., Afridi, K., Shah, I.A., Adnan, M., Tajudin,

R., Ullah, L., Rehman, A.U., Hussain, B., 2016. Estimates of heritability, genetic advance and correlation in F₃ populations of Wheat. Pure Appl. Biol., 5(4): 1142-1150.

Anu, Singh, V., Yashveer, S., Niwas, R., Malik, P., Arpit., Dey, S., Ahlawat, U., 2019. Assessment of genetic variability, heritability and genetic advance for grain yield and its contributing traits in Wheat (*Triticum aestivum*). Int. J. Curr. Microbiol. Appl. Sci., 8(08): 1169-1174.

Asad, M., Iqbal, M.N., Ashraf, A., Mahmood, Z., Arshad, A., Raza, U., Kashif, M., 2016. Effect of post-emergence herbicides to Control Broad-leaved Weeds in Wheat under Rainfed Conditions. PSM Biol. Res., 1(1): 16-21.

Aytaç, Z., Kinaci, G., 2009. Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.). Afr. J. Biotechnol., 8(15): 3547–3554.

Aziz, T., Khalil, I.H., Hussain, Q., Shah, T., Ahmad, N., Sohail, A., 2018. Heritability and Selection response for grain yield and associated traits in F₃ Wheat populations. Sarhad J. Agric., 34(4).

Baloch, M.J., Baloch, E., Jatoi, W.A., Veesar, N.F., 2013. Correlations and heritability estimates of yield and yield attributing traits in wheat (*Triticum aestivum* L.). Pak. J. Agri., Agril. Engg., Vet. Sci., 29(2): 96-105.

Choudhary, R.C., Sharma, N.K., Kumar, R., Kumar, M., 2015. Genetic variability, heritability and genetic advance in Wheat under different normal and heat-stressed environments. Electron. J. Plant Breed., 6(4): 1082-1087.

Dabi, A., Mekbib, F., Desalegn, T., 2019. Genetic variability studies on bread wheat

(*Triticum aestivum* L.) genotypes. J. Plant. Breed. Crop. Sci., 11(2): 41-54.

Elmassry, E.L., El-Nahas, M.M., 2018. Genetic behavior of some agronomic characters in three bread Wheat crosses under different environmental conditions. Alexandria J. Agric. Sci., 63(5): 313–325.

Fatima, M., Ahmed, Z., Aslam, M., Zaynab, M., 2018. Drought Effect and Tolerance Potential of Wheat: A Mini-Review. Int. J. Nanotechnol. Allied Sci., 2(2): 16-21.

Francis, C.A., Rutger, J.N., Palmer, A.F.E., 1969. A rapid method for plant leaf area estimation in Maize (*Zea mays* L.). Crop Sci., 9(5): 537-539.

Harshwardhan., Kumar, A., Kumar, A., Prasad, B., 2016. Study of variance, heritability and genetic advance for various yield contributing and quality traits in spring wheat (*Triticum aestivum* L.). J. Appl. Nat. Sci., 8(4): 1811-1814.

Hokrani, V., Naik, V.R., Nadaf, H.L., Desai, S.A., Deshpande, S.K., Kalappanavar, I.K., Patil, B.N., 2013. Genetic studies in free threshable advanced segregating population of tetraploid wheat (*Triticum dicoccum*). Karnataka J. Agric. Sci., 26(1).

Hussain, Q., Aziz, T., Khail, I.H., Ahmad, N., Asim, M., Adnan, M., Farooq, M.U., 2017a. Estimation of heritability and selection response for some yield traits in F₃ populations of wheat. Int. J. Agric. Appl. Sci., 9(1): 6-13.

Hussain, I., Mohammad, F., Iqbal, T., Hassan, G., Khattak, S.I., Anwar, F., Nadeem, F., Gao, S., Ahmad, N., Nauman, M., 2017b. Comparative analysis of some production traits in F₅:₉ recombinant inbred lines (RILs) of bread Wheat. 17(2): 148-154.

Ijaz, F., Khaliq, I., Shahzad, M.T., Saleem, B., 2013. Computation of heritability of yield and some morphological traits in F₂

populations of spring wheat (*Triticum aestivum* L). Int. J. Modern Agric., 2(3): 102-107.

Ijaz, S., Khan, I.A., 2009. Molecular characterization of wheat germplasm using microsatellite markers. Genet. Mol. Res., 8(3): 809–815.

Ishaq, M., Ahmad, G., Afridi, K., Ali, M., Ullah, S., Rahman, H.U., Khan, T.U., Qureshi, M.A., Shah, I.A., Saleem, A., Saeed, M., 2017. Genetic potential and variability for phenological and yield attributes in facultative winter wheat. Pure Appl. Biol., 6(2): 619-626.

Jan, S., Muhammad, F., Khan, F.U., 2015. Genetic potential and heritability estimates of yield traits in F_3 segregating populations of bread Wheat. Int. J. Environ., 1(1): 9-19.

Jamil, A., Khan, S., Sayal, O.U., Waqas, M., Qudratullah., Ali, S., 2017. Genetic variability, broad-sense heritability and genetic advance studies in bread wheat (*Triticum aestivum* L.) germplasm. Pure Appl. Biol., 6(2): 538-543.

Jawad, R., Fareeha, A., Ihsan, K., 2013. Estimation of heritability for some polygenic traits in hexaploid wheat (*Triticum aestivum* L.). Int. J. Agric. Crop Sci., 6(8): 458–463.

Johnson, H.W., Robinson, H.F., Comstock, R.E., 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., 47(7): 314.

Joshi, A., Kumar, A., Budhlakoti, V., Bhatt, N., Tabassum., 2018. Estimation of genetic variability parameters for yield and its components in bread wheat (*Triticum aestivum*). Adv. Agric. Nat. Sci. Sustain. Agric., 87–90.

Kamran, M., Inamullah, Iqbal, M.S., 2016. Yield Performance and Factor Analysis for Superior Cultivars Identification in Wheat (*Triticum aestivum* L.). PSM Biol. Res., 1(1): 11-15.

Kumar, D., Kumar, A., Srivastava, R.K., Kumar, A., 2017. Studies on variability, heritability and genetic advance in some quantitative characters in bread Wheat (*Triticum Aestivum* L). Int. J. Bot. Res., 7(4): 7–40.

Kalimullah, Khan, S.J., Irfaq, M., Rahman, H.U., 2012. Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. J. Anim. Plant Sci., 22(2): 330–333.

Khan, M.A.U., Mohammad, F., Malik, T., Khan, A., Abbas, S.J., 2013. Genetic divergence in $F_{4:6}$ wheat lines for yield and its contributing traits. J. Plant Breed. Genet., 1(3): 169-175.

Khan, A.K., Ali, S., Shakeel, A., Saeed, A., Abbas, G., 2006. Genetic variability and genetic advance analysis for some morphological traits in *Brassica napus* L. J. Agric. Res., 44(2): 83-87.

Madić, M., Paunović, A., Đurović, D., Knežević, D., 2005. Correlations and path coefficient analysis for yield and yield components in winter barley. Acta Agric. Serbica., 10(20): 3-9.

Mahmud, I., Kramer, H.H., 1951. Segregation for yield, height, and maturity following a soybean cross. Agron. J., 43(12): 605-609.

Mazurkievicz, G., Ubert, I.D.P., Krause, F.A., Nava, I.C., 2019. Phenotypic variation and heritability of heading date in hexaploid oat. Crop Breed. Appl. Biotechnol., 19(4): 436–443.

Mishra, U., Sharma, A.K., Chauhan, S., 2019. Genetic variability, heritability and genetic advance in bread Wheat (*Triticum aestivum* L.). Int. J. Curr. Microbiol. Appl. Sci., 8(07): 2311-2315.

Rathwa, H.K., Pansuriya, A.G., Patel, J.B., Jalu, R.K., 2018. Genetic variability, heritability and genetic advance in durum Wheat. Int. J. Curr. Microbiol. Appl. Sci., 7(1): 1208-1215.

Robinson, H.F., Comstock, R.E., Harvey, P.H., 1951. Genotypic and phenotypic correlations in Corn and their implications in selection. Agron. J., 43: 282-287.

Saini, M., Shweta, S., 2017. Genetic variability, heritability, correlation coefficient and path analysis of yield and yield contributing traits in bread wheat (*Triticum aestivum* L.). Int. J. Plant Sci., 12(2): 173-180.

Saleem, B., Khan, A.S., Shahzad, M.T., Ijaz, F., 2016. Estimation of heritability and genetic advance for various metric traits in seven F_2 populations of bread wheat (*Triticum aestivum* L.). J. Agric. Sci. 61(1): 1–9.

Shieh, G., Jan, S. L., 2004. The effectiveness of randomized complete block design. Stat. Neerl., 58(1): 111-124.

Singh, M., Ceccarelli, S., 1996. Estimation of heritability of crop traits from variety trial data. ICARDA.

Sohail, A., Rahman, H., Ullah, F., Shah, S.M.A., Burni, T., Ali, S., 2018. Evaluation of F_4 bread Wheat (*Triticum aestivum* L.)

genotypes for genetic variability, heritability, genetic advance and correlation studies. J. Plant Breed. Genet., 6(1): 01–07.

Steel, R.G.D., Torrie, J.H., 1960. Principles and procedures of statistics. New York: McGraw.

Waqas, M., Faheem, M., Khan, A.S., Shehzad, M., Ansari, M.A.A., 2014. Estimation of heritability and genetic advance for some yield traits in eight F_2 populations of Wheat (*Triticum aestivum* L). Sci. Lett., 2(2): 43-47.

Zecevic, V., Knezevic, D., Micanovic, D., 2004. Genetic correlations and path-coefficient analysis of yield and quality components in wheat (*Triticum aestivum* L.). Genetika., 36(1): 13-21.

Zeeshan, M., Arshad, W., Khan, M.I., Ali, S., Nawaz, A., Tariq, M., 2014. Heritability, trait association and path coefficient studies for some agronomic characters in synthetic elite lines of wheat (*Triticum aestivum* L.) under rainfed conditions. J. Agric. and Allied Sci., 3(4).