RESEARCH PAPER

Estimation of heritability and genetic advance in F₂ populations of bread wheat (*Triticum aestivum* L.) genotypes

Mitho Kachi[1], Tanweer Fatah Abro[1]*, Jay Kumar Sootaher[1], Tarique Ahmed Baloch[4], Mazhar Ali Mastoi[1], Tanveer Ali Soomro[1], Kirshan Kumar Menghwar[1], Gul Muhammad Jadgal[1], Muhammad Saleem Chang[3], Waqar Hussain Shah[2]

[1]*Department of Plant Breeding & Genetics, Sindh Agriculture University, Tandojam, Sindh, Pakistan*

[2]*Department of Soil Science, Sindh Agriculture University, Tandojam, Sindh, Pakistan*

[3]*Department of Agronomy, Subcampus Umerkot, Sindh Agriculture University, Tandojam, Sindh, Pakistan*

[4]*Directorate of Agriculture Research (Dates), Kech, Turbat, Balochistan, Pakistan*

Abstract

The current research study was conducted to determine the heritability and genetic advance of six F₂ bread wheat populations obtained from eight parental varieties for vital diversified yield contributing attributes. The experiment was carried out in a randomized complete block design with three replications. Among genotypes, parents were highly significant at 0.01 probability level for plant height (cm), spike length (cm), grains spike⁻¹, grain weight of main spike (g), grain yield plant⁻¹ (g), seed index (1000 grain weight, g) and biological yield plant⁻¹ (g), whereas in parents, tillers plant⁻¹, spikelets spike⁻¹ and harvest index (%) were non-significant. In case of hybrids, all the traits were highly significant at 0.01 probability level. Among the F₂ hybrids, Khirman x Benazir was best in heritability for plant height (87.48%), spike length (84.74%), grain weight of main spike (85.70%) and harvest index (92.29%); Kiran-95 x TD-1 for tillers plant⁻¹ (73.28%); SKD x Blue silver for spikelets spike⁻¹ (91.76%); Moomal x Benazir had the best performance in heritability for grains spike⁻¹ (78.50%) and grain yield plant⁻¹ (77.80%); NIA-Sundar x TD-1 was the best heritability contributor for seed index (96.91%) and biological yield plant⁻¹ (80.21%). These hybrids might be the best choices for the utilization of hybrid crop improvement in bread wheat for the selection of desirable plants from later segregating generations.

* **Corresponding Author:** Tanweer Fatah Abro ✉ fatahtanweer@yahoo.com

Introduction

The hexaploid wheat comes from the family named Poaceae which is also known as Gramineae. There are many species of this crop, but the most vital one is hexaploid, because this is cultivated all over the globe for the purpose of human consumptionin a wide range of forms (Debasis and Khurana, 2001). Recently, it has been proved that about 95% of the wheat species on the earth is bread wheat ($2n = 6x = 42$). A wide range of foods such as, chapaties, bread noodles crackers, cakes, breakfast food, cookies biscuits, and a number of confectionary items are being globally prepared from wheat (Laghari *et al.,* 2012).

Many steps are being taken by the breeders, researchers and scientists of wheat for the betterment and development of yield potential by bringing an evolution in new cultivars entailing promising genetic makeup so as to cope with the utilization pressure of over increasing world population (Memon *et al.,* 2007).

The genetic analysis, heritability is of a huge vitality as it assists a plant breeder in predicting the performance of the subsequent generation and making alluring choices. Heritability is undertaken for the measurement of phenotypic variance and is linked with the environmental and hereditary effect (Degewione *et al.,* 2013). The architecture of a population is also explained with the aid of heritability for a given attribute to know about the extent of the transmission (Khan *et al.,* 2008).

High heritability estimates associated with high genetic advance can increase the chances of success from selection in cultivar development. High yield is one of the prime objectives in any breeding program. Heritability estimates take the breeding process on the way towards genotypic variance (Bhateria *et al.,* 2006). In the evaluation of heritability, low heritability is observed when an attribute is more and more governed by the environment, but high heritability is seen owning to more contribution of genotypic constitution than the environment.

Therefore, this investigation was made to estimate the heritability and genetic advance of bread wheat genotypes of various traits so that the selection can expose positive results, in case wider the scale of heritable differences, the more the effective will be the selection.

Materials and methods

Experimental design

The experiment was conducted to make an estimation of heritability and genetic advance for grain yield and its related traits in F_2 populations of bread wheat during the year 2017-2018 at Southern Wheat Research Station, Tandojam.

The plot was laid out in Randomized Complete Block Design with three replications. The plot was comprised of 4 rows and each row was 6 feet long. The distance between rows to row was put 20 centimetres and the distance between plants to plant was made 5 centimetres. The seed of eight wheat varieties along with their six cross combinations of F_2 populations were sown. The parents were Kiran-95, NIA-Sundar, Khirman, Moomal, SKD, TD-1, Benazir and Blue silver, while the F_2 populations were Kiran-95 x TD-1, NIA-Sundar x TD-1, Khirman x Benazir, Moomal x Benazir, and SKD x Blue silver and TD-1 x Blue silver. The calculations were analyzed according to the following methods.

Statistical analysis

The collected data were brought under the statistical analysis of variance according to the statistical methods using the software Statistix 8.1 created by Gomez and Gomez (1984), DMRT (Duncan's Multiple Range Test) was calculated for the comparison of means according to Duncan (1955) and heritability estimates in broad sense were determined according to Mahmud and Kramer (1951).

Formulae

$$\text{Variance} = \frac{\sum x^2 - \frac{(\sum x)^2}{N}}{N-1}$$

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 p$ = VF_2 or Vp

σ²e = Environmental variance

$$\sigma^2 e = \frac{(VP1 + VP2)}{2}$$

σ²g = Genetic variance

σ²g = VF₂ - Ve or Vp − Ve

h² = Heritability

$$h^2 (\%) = \frac{Vg}{Vp} \times 100$$

G. A = Genetic advance

G. A = k x σ²p x h²

Results

Analysis of variance

The analysis of variance was carried out for ten different traits recorded from fourteen genotypes with eight parents and their six F₂ populations of bread wheat as presented in Table 1 and 2. Pertaining to the analysis of variance, all the genotypes were highly significant and significant for all the traits at 0.01% and 0.05% probability level. Among genotypes, the parental lines were highly significant at 0.01% probability level for plant height (cm), spike length (cm), grains spike⁻¹, grain weight of main spike (g), grain yield plant⁻¹ (g), seed index (1000-grain weight, g) and biological yield plant⁻¹ (g), however non-significant at 0.05% probability level for tillers plant⁻¹, spikelets spike⁻¹ and harvest index (%). In terms of F₂ populations, all the hybrids for all the attributes i.e. plant height (cm), tillers plant⁻¹, spike length (cm), spikelets spike⁻¹, grains spike⁻¹, grain weight of main spike (g), grain yield plant⁻¹ (g), seed index (1000-grain weight, g), biological yield plant⁻¹ (g), and harvest index (%).were highly significant at 0.01% probability level.

Table 1. Mean squares for different morphological traits of bread wheat.

SOV	D. F	Plant height	Tillers plant⁻¹	Spike length	Spikelets spike⁻¹	Grains spike⁻¹
Replications	2	1.19	1.40	0.39	51.20	8.94
Genotypes	13	410.12**	0.72*	16.17**	56.14*	361.82**
Parents	7	405.04**	0.46ᴺˢ	15.37**	4.98ᴺˢ	126.39**
Hybrids	5	141.42**	1.50**	17.32**	116.05**	287.47**
Error	26	4.85	0.60	0.26	50.02	27.70
Total	40	-	-	-	-	-

Table 2. Mean squares for different morphological traits of bread wheat.

SOV	D. F	Main spike yield	Grain yield plant⁻¹	Seed index	Biological yield plant⁻¹	Harvest index
Replications	2	0.11	0.26	7.66	3.68	7.90
Genotypes	13	0.39**	4.92**	24.70**	28.97**	154.51**
Parents	7	0.31**	5.89**	16.89**	23.97**	0.79ᴺˢ
Hybrids	5	0.38**	4.39**	39.02**	25.98**	308.30**
Error	26	0.03	1.16	3.23	5.50	17.56
Total	40	-	-	-	-	-

** = Highly significant at P ≤ 0.01 probability level

* = Significant at P ≤ 0.05 probability level

NS = Non-significant at P ≤ 0.05 probability level.

Mean performance

Mean performance for parents and hybrids is depicted in Table 3 and 4. The results showed that, the maximum plant height (106.20 cm) was expressed by the cross Khirman x Benazir, followed by the cross NIA-Sundar x TD-1 (102.47 cm). In terms of tillers plant⁻¹, the maximum tillers plant⁻¹ (7.40) were shown by the cross TD-1 x Blue silver, followed by the cross SKD x Blue silver (7.26). The longest spikes (13.22 cm) were observed in the cross-combination NIA-Sundar x TD-1, followed by the parent Kiran-95 (12.53 cm).

Table 3. Mean performance of parents and different cross combinations for yield and its traits in bread wheat.

Genotypes	Plant height	Tillers plant[-1]	Spike length	Spikelets spike[-1]	Grains spike[-1]
Kiran-95	84.00 gh	6.73 ab	12.53 ab	18.93 bcd	44.93 defg
NIA-Sundar	94.74 c	6.26 ab	11.60 abc	16.60 ef	42.20 efgh
Khirman	92.13 cde	6.20 ab	10.80 bcd	20.46 ab	48.20 bcde
Moomal	92.73 cd	7.00 a	10.86 bcd	20.26 ab	49.60 bcd
SKD	72.20 i	6.53 ab	9.13 cde	15.80 fg	37.60 j
TD-1	60.73 j	6.80 ab	8.60 def	15.15 fg	38.53 hi
Benazir	80.53 h	6.86 a	9.73 cde	16.80 ef	39.00 ghi
Blue silver	86.13 fg	6.40 ab	10.33 bcd	17.40 cde	43.00 efg
Kiran-95 x TD-1	95.40 c	7.06 a	10.86 bcd	19.26 abc	66.86 a
NIA-Sundar x TD-1	102.47 b	6.26 ab	13.22 a	20.93 a	62.20 ab
Khirman x Benazir	106.20 a	5.53 b	11.20 abc	17.80 cde	62.80 ab
Moomal x Benazir	88.67	6.60 ab	10.93 bcd	14.61 g	41.80 fgh
SKD x Blue silver	90.87 de	7.26 a	11.60 abc	19.33 abc	47.66 cdef
TD-1 x Blue silver	92.93 cd	7.40 a	11.66 abc	20.66 ab	58.86 abc

Table 4. Mean performance of parents and different cross combinations for yield and its traits in bread wheat.

Genotypes	Main spike yield	Grain yield plant[-1]	Seed index	Biological yield plant[-1]	Harvest index
Kiran-95	2.35 def	10.44 abc	44.06 abcd	23.28 abc	44.81 cde
NIA-Sundar	2.29 ef	10.63 abc	45.90 abc	23.62 abc	45.06 bcd
Khirman	2.52 bcde	10.21 bc	45.66 abc	22.95 abcd	44.00 de
Moomal	2.58 bcde	10.25 bc	44.86 abcd	22.78 abc	45.02 bcd
SKD	2.44 cdef	9.66 d	45.16 abc	21.99 cde	44.04 cde
TD-1	2.46 cde	10.85 ab	46.90 a	23.22 abc	46.75 abc
Benazir	2.51 bcde	10.43 abc	46.26 ab	23.43 abc	44.50 cde
Blue silver	2.48 cde	11.11 ab	46.46 ab	23.72 abc	46.81 abc
Kiran-95 x TD-1	2.76 abc	10.40 bc	45.00 abc	22.62 abcd	45.98 bcd
NIA-Sundar x TD-1	2.87 ab	11.58 a	45.73 abc	24.60 ab	47.08 ab
Khirman x Benazir	2.97 a	10.58 abc	46.06 ab	22.44 abcd	47.16 a
Moomal x Benazir	2.08 f	10.67 abc	45.03 abc	23.85 abc	44.76 cde
SKD x Blue silver	2.23 ef	11.24 ab	46.30 ab	24.16 ab	46.51 abc
TD-1 x Blue silver	2.69 abcd	11.27 ab	41.93 bcde	24.76 a	45.58 bcd

The maximum spikelets spike[-1] (20.93) were counted in the hybrid NIA-Sundar x TD-1, followed by the cross TD-1 x Blue silver (20.66). For grains spike[-1], the maximum grains spike[-1] (66.86) were exhibited by the cross, Kiran-95 x TD-1, followed by the cross, Khirman x Benazir (62.80).

Table 5. Heritability estimates for different F$_2$ segregating populations for plant height.

F$_2$ populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h^2% (B.S)	G. A
Kiran-95 x TD-1	10.25	61.02	71.27	85.61	102.17
NIA-Sundar x TD-1	11.87	62.34	74.21	84.01	128.42
Khirman x Benazir	7.41	51.76	59.17	87.48	106.62
Moomal x Benazir	6.42	43.67	50.10	87.18	89.97
SKD x Blue silver	11.43	50.95	62.38	81.67	104.62
TD-1 x Blue silver	12.24	35.11	47.35	74.16	72.33

The maximum grain weight of main spike (2.97 g) was weighed by the cross Khirman x Benazir, followed by the cross NIA-Sundar x TD-1 (2.87 g). Regarding grain yield plant[-1], the maximum grain yield planl[-1] (11.58 g) was displayed by the cross NIA-Sundar x TD-1, followed by the cross TD-1 x Blue silver (11.27 g). The maximum seed index (46.90 g) was manifested by the variety TD-1, followed by the variety Blue silver (46.46 g). However, the maximum biological yield planl[-1] (24.76 g) was obtained by the cross TD-1 x Blue silver, followed by the cross NIA-Sundar x TD-1 (24.60 g). In case of harvest index, the maximum harvest index was recorded by the cross Khirman x Benazir (47.16%), followed by the cross NIA-Sundar x TD-1 (47.08).

Table 6. Heritability estimates for different F_2 segregating populations for tillers plant[-1].

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	0.63	1.72	2.35	73.28	3.54
NIA-Sundar x TD-1	0.66	1.69	2.35	71.86	3.47
Khirman x Benazir	0.62	1.65	2.27	72.69	3.39
Moomal x Benazir	0.58	1.40	1.98	70.91	2.89
SKD x Blue silver	1.03	2.06	3.10	66.62	4.25
TD-1 x Blue silver	0.80	1.98	2.78	71.23	4.07

Heritability estimates and genetic advance
Heritability performs an important role in the transmission of attributes from one generation to the next owing to genes. Hence, the parameters of heritability such as environmental variance, genotypic variance and phenotypic variance along with genetic advance for different traits are appeared in Tables 5 to 14.

Table 7. Heritability estimates for different F_2 segregating populations for spike length.

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	1.90	7.67	9.57	80.15	15.80
NIA-Sundar x TD-1	1.38	6.60	7.98	82.76	13.60
Khirman x Benazir	1.29	7.17	8.46	84.74	14.76
Moomal x Benazir	1.22	3.48	4.70	74.04	7.16
SKD x Blue silver	1.37	6.61	7.98	82.88	13.62
TD-1 x Blue silver	1.48	4.22	5.70	74.08	8.69

Plant height (cm)
The results concerning plant height in Table 5 for different cross combinations and their heritability estimates and genetic advance showed that, the cross Khirman x Benazir manifested the maximum heritability (87.48%) followed by the cross Moomal x Benazir (87.18%), while the minimum heritability was detected in the cross TD-1 x Blue silver (74.16%). The results about genetic advance indicated that, the cross NIA-Sundar x TD-1 (128.42) demonstrated the maximum genetic advance, whereas the minimum genetic advance was displayed by the cross TD-1 x Blue silver (72.33).

Tiller plant[-1]
The results for tillers plant[-1] are presented in Table 6 for different cross combinations and their heritability estimates and genetic advance. The data revealed that, the cross Kiran-95 x TD-1 exhibited the most heritability (73.28%) followed by the cross Khirman x Benazir (72.69%) and the lowest heritability was displayed by the cross SKD x Blue silver (66.62%). The result about genetic advance indicated that, the cross SKD x Blue silver (4.25) demonstrated the highest genetic advance, while the lowest genetic advance was manifested by the cross Moomal x Benazir (2.89).

Table 8. Heritability estimates for different F_2 segregating populations for spikelets spike^{-1}.

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	2.62	6.50	9.11	71.26	13.37
NIA-Sundar x TD-1	2.40	6.77	9.17	73.78	13.93
Khirman x Benazir	2.40	6.17	8.57	71.94	12.70
Moomal x Benazir	2.26	22.21	24.47	90.76	45.75
SKD x Blue silver	2.39	26.64	29.03	91.76	54.87
TD-1 x Blue silver	3.71	25.90	29.61	87.47	53.38

Spike length (cm)

For spike length, the results are mentioned in Table 7 for various hybrids and their heritability estimates and genetic advance. The cross Khirman x Benazir proved the maximum heritability (84.74%) followed by the cross SKD x Blue silver (82.88%), while the minimum heritability was found in cross Moomal x Benazir (74.04%). The result about genetic advance indicated that, the cross Kiran-95 x TD-1 (15.80) demonstrated the highest genetic advance, however the lowest genetic advance was expressed by the cross Moomal x Benazir (7.16).

Table 9. Heritability estimates for different F_2 segregating populations for grains spike^{-1}.

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	25.66	84.89	110.55	76.79	174.87
NIA-Sundar x TD-1	22.35	78.74	101.10	77.89	162.21
Khirman x Benazir	35.03	53.71	88.74	60.53	110.65
Moomal x Benazir	21.19	77.36	98.54	78.50	159.34
SKD x Blue silver	25.15	81.98	107.12	76.52	168.85
TD-1 x Blue silver	27.87	80.59	108.46	74.31	166.02

Spikelets spike^{-1}

Table 8 expressed the results about spikelets spike^{-1} of different cross combinations and their heritability estimates and genetic advance. The maximum heritability value (91.76%) was obtained by the cross SKD x Blue silver followed by the cross Moomal x Benazir (90.76%), however the minimum heritability estimate was exposed by the cross Kiran-95 x TD-1 (71.26%). In case of genetic advance, the cross SKD x Blue silver (54.87) demonstrated the maximum value for genetic advance, whereas the minimum value for genetic advance was revealed by the cross Khirman x Benazir (12.70).

Table 10. Heritability estimates for different F_2 segregating populations for grain weight of main spike.

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	0.10	0.34	0.44	77.41	0.70
NIA-Sundar x TD-1	0.17	0.54	0.70	76.54	1.10
Khirman x Benazir	0.08	0.53	0.62	85.70	1.11
Moomal x Benazir	0.16	0.52	0.68	76.40	1.02
SKD x Blue silver	0.12	0.49	0.61	80.40	1.01
TD-1 x Blue silver	0.09	0.37	0.46	79.66	0.75

Grains spike^{-1}

In Table 9, the results for grains spike^{-1} are depicted for various F_2 hybrids and their heritability estimates and genetic advance. The cross Moomal x Benazir revealed the highest heritability estimate (78.50%) followed by the cross NIA-Sundar x TD-1 (77.89%), while the lowest heritability estimate (60.53%) was noted in the cross Khirman x Benazir. The result

about genetic advance showed that, the cross Kiran-95 x TD-1 (174.87) took the highest genetic advance, while the lowest genetic advance was recorded in the cross Khirman x Benazir (110.65).

Grain weight of main spike (g)

The results of heritability estimates and genetic advance for the character main spike yield are given in Table. 10 for different cross combinations which

indicated that, the cross Khirman x Benazir manifested the most value for heritability (85.70%) followed by the cross SKD x Blue silver (80.40%), however the least value for heritability (76.54%) was indicated by the cross NIA-Sundar x TD-1. The result about genetic advance indicated that, the cross Khirman x Benazir (1.11) showed the most genetic advance, whereas the least genetic advance was demonstrated by the cross Kiran-95 x TD-1 (0.70).

Table 11. Heritability estimates for different F_2 segregating populations for grain yield plant[-1].

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	0.58	1.76	2.34	75.20	3.62
NIA-Sundar x TD-1	0.52	1.58	2.10	75.19	3.25
Khirman x Benazir	0.85	2.50	3.35	74.71	5.15
Moomal x Benazir	0.47	1.64	2.11	77.80	3.38
SKD x Blue silver	0.64	1.83	2.48	74.01	3.78
TD-1 x Blue silver	0.65	1.43	2.08	68.74	2.94

Grain yield plant[-1] (g)

The results about heritability estimates and genetic advance of their different cross combinations for grain yield plant[-1] are appeared in Table 11. It showed that, the cross Moomal x Benazir exhibited the maximum heritability (77.80%) followed by the cross Kiran-95 x TD-1 (75.20%). The minimum heritability (68.74%) appeared in the cross TD-1 x Blue silver. The result about genetic advance indicated that, the cross Khirman x Benazir (5.15) disclosed the maximum genetic advance, while the minimum genetic advance was seen in the cross TD-1 x Blue silver (2.94).

Seed index (1000-grain weight, g)

The results for seed index are described in Table 12 of different cross combinations and their heritability estimates and genetic advance.

The findings indicated that, the cross NIA-Sundar x TD-1 had the highest heritability (96.91%) followed by the cross TD-1 x Blue silver (93.63%), nevertheless the lowest heritability (90.24%) was governed by the cross Moomal x Benazir. According to genetic advance, the cross TD-1 x Blue silver (42.35) showed the highest genetic advance, while the cross Kiran-95 x TD-1 (29.26) expressed the lowest genetic advance.

Table 12. Heritability estimates for different F_2 segregating populations for seed index.

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	15.35	142.14	157.49	90.25	29.26
NIA-Sundar x TD-1	6.52	204.71	211.23	96.91	42.15
Khirman x Benazir	14.10	159.23	173.33	91.86	32.79
Moomal x Benazir	20.45	189.11	209.56	90.24	39.94
SKD x Blue silver	18.07	199.56	217.63	91.69	41.09
TD-1 x Blue silver	12.07	177.65	189.72	93.63	42.35

Biological yield plant[-1] (g)

The results for biological yield plant[-1] of various hybrids and their heritability estimates and genetic advance in Table. 13 expressed that, the cross NIA-

Sundar x TD-1 achieved the maximum heritability value (80.21%) followed by the cross SKD x Blue silver (77.23%) and the minimum heritability value (60.16%) was taken by the cross Moomal x Benazir.

The result about genetic advance showed that, the cross SKD x Blue silver (76.54) displayed the highest genetic advance, while the minimum genetic advance was carried by the cross Khirman x Benazir (32.12).

Harvest index (%)

The results for harvest index of different cross combinations and their heritability estimates and genetic advance are manifested in Table 14 which told that, the cross Khirman x Benazir displayed the

maximum heritability (92.29%) followed by the cross NIA-Sundar x TD-1 (86.28%), however the minimum value for heritability (72.32%) was exhibited by the cross TD-1 x Blue silver for harvest index. The result about genetic advance indicated that, the cross Khirman x Benazir (35.00) expressed the maximum genetic advance, whereas the minimum genetic advance was noticed in the cross TD-1 x Blue silver (6.73).

Table 13. Heritability estimates for different F_2 segregating populations for biological yield plant^{-1}.

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	6.14	18.88	25.02	75.48	38.90
NIA-Sundar x TD-1	8.78	35.61	44.40	80.21	73.36
Khirman x Benazir	9.95	15.6	25.55	61.04	32.12
Moomal x Benazir	13.44	20.3	33.74	60.16	41.81
SKD x Blue silver	10.95	37.16	48.11	77.23	76.54
TD-1 x Blue silver	9.95	15.4	25.50	61.02	32.08

Discussion

High heritability is not only enough to make sufficient improvement through selection generally, but also the values of heritability can serve in measuring the degree of association between parents and their descendants (Memon *et al.*, 2007). The degree of heritable inheritance is very essential for the prophecy of comeback to the assortment in varied surroundings which delivers the foundation of for scheduling and assessing breeding programmes. The search for identification and selection of plants that possess variability of immense importance may be multiplied further to serve masses is the prime goal of each breeding program pertaining to crop improvement.

The results regarding mean squares notified that some of the genotypes including parents and hybrids were highly significant and significant for all the traits. Most of the attributes namely, plant height (87.48% and 128.42, respectively), tillers plant^{-1} (73.28% and 4.25, respectively), spike length (84.74% and 15.80, respectively), spikelets spike^{-1} (91.76 and 54.87, respectively), grains spike^{-1} (78.50% and 174.87, respectively), grain weight of main spike (85.70% and 1.11, respectively), grains spike^{-1} (77.80% and 5.15, respectively), 1000-grain weight (96.91% and 42.35, respectively), biomass plant^{-1}(80.21% and 76.54, respectively) and harvest index (92.29% and 35.00, respectively)displayed high heritability values coupled with genetic advance.

Table 14. Heritability estimates for different F_2 segregating populations for harvest index.

F_2 populations	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 p$	h²% (B.S)	G. A
Kiran-95 x TD-1	1.37	8.70	10.43	83.42	17.92
NIA-Sundar x TD-1	1.43	8.98	10.41	86.28	18.50
Khirman x Benazir	1.42	16.99	18.41	92.29	35.00
Moomal x Benazir	1.82	4.96	6.78	73.17	10.21
SKD x Blue silver	1.61	8.80	10.41	84.49	18.11
TD-1 x Blue silver	1.25	3.27	4.52	72.32	6.73

Similar findings were also taken by Khan (2013) for plant height and tillers plant[-1]. Ijaz *et al.* (2015) also got the same result for spike length and spikelets spike[-1]. Hussain *et al.* (2013) found high heritability values and genetic advance for 1000-grain weight and grains spike[-1]. High values for heritability and genetic advance in grain weight of main spike were expressed by Waqas *et al.* (2014).

The same results for grain yield plant[-1] and biological yield plant[-1] were also reported by Haq *et al.* (2016). Negasa *et al.* (2016) displayed high heritability and genetic advance for harvest index.

The cross which has high heritability with high genetic advance shows the additive x additive and additive x non-additive additive gene action and also cooperative for yield donating character (Rashid *et al.*, 2013). High heritability along with high genetic advance recommended that these traits and diversified genotypes must be reputed in selection programs to get better grain yield (Rehman *et al.*, 2015).

Conclusion

The results regarding heritability and genetic advance showed that, Kiran-95 x TD-1 showed the highest values of heritability for tillers plant[-1] (73.28%). NIA-Sundar x TD-1 manifested the highest heritability for, seed index (96.91%) and biological yield plant[-1] (80.21%). Khirman x Benazir was best in heritability for plant height (87.48%), spike length (84.74%), grain weight of main spike (85.70%) and harvest index (92.29%). Moomal x Benazir became best in the contribution of heritability for, grains spike[-1] (78.50%) and grain yield plant[-1] (77.80%). SKD x Blue silver was the best contributor of heritability for spikelets spike[-1] (91.76%). TD-1 x Blue silver had the best heritability only for seed index (93.63%). It was concluded that parents and hybrids were having significant and highly significant genetic differences for most of the traits which were studied. All the parameters exposed a clear indication that these parents and hybrids along with these traits can be used as selection conditions in early generation for

further perfection to conquer the maximum level of yield potential in the breeding programmes.

References

Bhateria S, Sood SP, Pathania A. 2006. Genetic analysis of quantitative traits across environments in linseed (*Linum usitatissimum* L.). Euphytica **150,** 185-194.

Degewione A, Dejene T, Sharif M. 2013. Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. International Research Journal of Agricultural Sciences **1(2),** 19-29.

Duncan DB. 1955. Multiple range and multiple F tests. Biometrics **11(1),** 1-42.

Debasis P, Khurana P. 2001. Wheat biotechnology: A minireview. Electronic Journal of Biotechnology **4(2),** 76-102.

Gomez KA, Gomez AA. 1984. Statististical procedures for agricultural research (Second Edition). New York: John Wiley and Sons.

Haq MM, Hassan G, Fakharuddin, Khalil Z, Iqbal N, Ullah U, Attaullah. 2016. Estimation of Heritability and Genetic Advance in F_3 Populations of Wheat. Pure and Applied Biology **5(4),** 773-781. http://dx.doi.org/10.19045/bspab.2016.50097

Hussain F, Rafiq M, Iqbal Z, Iqbal J, Chowdhry MA. 2013. Estimates of heritability and genetic advance for grain yield and its components in different segregating populations of wheat. Journal of Agricultural Research **51(4),** 349-360.

Ijaz F, Khaliq I, Shahzad MT. 2015. Estimation of heritability for some yield contributing traits in F_2 populations of bread wheat (*Triticum aestivum* L.). Journal of Agricultural Research **53(2),** 157-164.

Khan H, Rahman H, Ahmed H, Ali H. 2008. Magnitude of heterosis and heritability in sunflower

over environments. Pakistan Journal of Botany **1,** 301-308.

Khan SA. 2013. Genetic variability and heritability estimates in F₂ wheat genotypes. International Journal of Agriculture and Crop Sciences **5(9),** 983-986.

Laghari KA, Sial MA, Arain MA. 2012. Effect of high temperature stress on grain yield and yield components of wheat (*Triticum aestivum* L.). Science, Technology and Development **31(2),** 83-90.

Memon S, Din MU, Qureshi MB, Sial MA. 2007. Genetic heritability for grain yield and its related characters in spring wheat (*Triticum aestivum* L.). Pakistan Journal of Botany **39(5),** 1503-1509.

Mahmud I, Kramer HH. 1951. Segregation of yield, height and maturity following soybean crosses. Agronomy Journal **43(12),** 605-609.

Negasa D, Chauhan DK. 2016. Variability, heritability and genetic advances in wheat (*Triticum aestivum* L.) breeding lines grown at Horro Guduru Wollega Zone, Western Ethiopia. International Journal of Advanced Scientific Research and Management **1(1),** 23-28.

Rashid J, Anwar F, Abdullah, Khaliq I. 2013. Estimation of heritability for some polygenic traits in hexaploid wheat (*Triticum aestivum* L.) development. International Journal of Agriculture and Crop Sciences **34(4),** 260-264.

Rehman SU, Ali M, Bilal M, Ashraf J, Liaqat S, Ahmed RI, Qanmber G. 2015. Genotype by trait analysis and estimates of heritability of wheat (*Triticum aestivum* L.) under drought and control conditions. Basic Research Journal of Agricultural Science and Review **4(4),** 127-134.

Waqas M, Faheem M, Khan AS, Shehzad M, Ansari MAA. 2014. Estimation of heritability and genetic advance for some yield traits in eight F₂ populations of wheat (*Triticum aestivum* L.). Science Letters **2(2),** 43-47.