Research Article

Assessment of genetic variability and heritability for grain yield and its associated traits in F₂ populations of bread wheat (*Triticum aestivum* L.)

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Abstract

The current research was carried out to determine the genetic variability and heritability for grain yield and its associated traits of six F₂ bread wheat segregating populations originated from seven parental varieties at the experimental field of Southern Wheat Research Station, ARI, Tandojam, Sindh. The experiment was carried out in randomized complete block design with three replications for 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 (g), biological yield plant⁻¹ (g) and harvest index (%). Many variation were observed in all the studied traits giving an evidence of the crop improvement. The result regarding analysis of variance, all the genotypes, parents and hybrids displayed highly significant and significant differences for the all the attributes at 0.01% and 0.05% probability level. Among the F₂ hybrids, the cross Khirman x TD-1 was best (92.76%) in the contribution of heritability for plant height. Kiran-95 x Marvi-2000 performed notably for tillers plant⁻¹ (83.51%), spike length (88.69%), spikelets spike⁻¹ (95.62%), grains spike⁻¹ (87.90%), grain weight of main spike (91.99%), grain yield plant⁻¹ (94.13%), seed index (88.03%) and harvest index (89.12%). In case of biological yield plant⁻¹ (85.21%), the cross Bakhar-2002 x TD-1 (85.21%) was the highest heritability contributor. It is concluded that these hybrids may be the best choices for the exploitation of heritability and hybrid crop development in bread wheat or selection of desirable plants from later segregating generation.

Keywords: Bread wheat; F₂ populations; Genetic variability; Genetic advance; Heritability

Introduction

Wheat is one of the premier crops of the whole world. It is almost said that this crop was the first crop which was domesticated by the human being on the earth. The wheat has higher protein content, about 14% than any other the grain crop. It approximately accounts for 20% of nutritional sources of the people all over the world [1]. The basic goal of wheat breeders is to develop such

wheat varieties that are genetically more stable, high yielding than existing ones and well adapted to a wide range of environments.

Genetic variability is the basic utensil of breeding tactics which could be achieved through hybridization of diversified genetic material. The exploration of genetic variation in breeding material is of major interest to plant breeders and helpful in achieving higher return per unit area in any crop plant. Heritability isolates the amount of genotypic variation from phenotypic one. There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. The expected response to selection is also called genetic advance. Heritability with value of genetic advance helps the plant breeder predict the gain under selection. The highest heritability in any trait demonstrates its highest transmitting ability to the next generation [2]. The heritability was categorized as low, moderate and high as by [3].

Genetic advance as percent mean was categorized as low, moderate and high as given by [4]. High genetic advance coupled with high heritability estimates offers the most effective condition for selection [5]. The heritability also gives the information about the structure of a population and the percentage of trait transmission from one generation to the next as well. The higher value of heritability will make the selection process effective, which will result in higher response. Therefore, the main aim of this study is to determine heritability and genetic advance of the characters of wheat genotypes among the various agro-morphological to identify the traits that may be useful in selection.

Materials and methods

The experiment was conducted to assess heritability and genetic advance for grain yield and its associated 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 one of them was 6 feet long. The distance between row to row was 20 centimetres and the distance between plant to plant was 5 centimetres. Seven parental lines along with their six cross combinations of F_2 populations were grown. The parents were Bakhar-2002, Khirman, Sahar-2006, Benazir, Kiran-95, TD-1 and Marvi-2000, while the F_2 populations were Bakhar-2002 x TD-1, Khirman x TD-1, Sahar-2006 x TD-1, Benazir x Marvi-2000, Kiran-95 x Marvi-2000 and Khirman x Marvi-2000. The data were analyzed according to the following methods.

Statistical analysis

The collected data were subjected to the statistical analysis of variance according to the statistical methods developed by [6] Gomez and Gomez (1984), DMRT (Duncan's Multiple Range Test) was calculated for the comparison of means according to [7] Duncan (1955) and genetic variability and heritability estimates were determined according to [8] Falconer (1989).

Formulae

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

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 p$ = VF₂ or Vp

$\sigma^2 e$ = Environmental variance

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

$\sigma^2 g$ = Genetic variance

$\sigma^2 g$ = VF₂ - Ve or Vp – Ve

h^2 = Heritability

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

G. A = Genetic advance

G. A = k x $\sigma^2 p$ x h^2

Results

Analysis of variance

The analysis of variance was carried out for ten different traits recorded from thirteen genotypes with seven parents and their six F_2 populations of bread wheat as presented in table 1 & 2. The data were recorded for the ten characters i.e. plant height (cm), tillers plant⁻¹, spike length (cm), spikelet 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 (%). Regarding 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 parents were highly significant at 0.01% probability level for plant height (cm), spikelets spike^{-1}, grains spike^{-1}, seed index (1000 grain weight, g), biological yield plant^{-1} (g) and harvest index (%), whereas significant at 0.05% probability level for spike length (cm), grain weight of main spike (g) and grain yield plant^{-1} (g) and non-significant for tillers plant^{-1} only. In case of F_2 populations, the hybrids were highly significant at 0.01% probability level for plant height (cm), grain weight of main spike (g), seed index (1000 grain weight, g) and harvest index (%), while significant at 0.05 probability level for spike length, spikelets spike^{-1}, grain yield plant^{-1} (g) and biological yield plant^{-1} (g) and non-significant for tillers plant^{-1} and grains spike^{-1}.

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

SOV	D. F	Plant height (cm)	Tillers plant^{-1}	Spike length (cm)	Spikelets spike^{-1}	Grains spike^{-1}
Replications	2.0	9.17	1.70	0.00	1.58	29.92
Genotypes	12.	271.87**	17.37**	2.79**	95.05**	30.34*
Parents	6.0	282.04**	0.61 NS	0.71*	16.05**	50.98**
Hybrids	5.0	264.04**	2.02NS	1.45*	4.54*	11.64 NS
Error	24	2.50	5.44	0.20	1.76	15.97
Total	37	-	-	-	-	-

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	0.06	0.49	3.19	0.40	29.26
Genotypes	12	0.09*	6.44*	70.06**	20.86**	75.19**
Parents	6	0.08*	7.63*	25.72**	33.97**	37.60**
Hybrids	5	0.12**	6.26*	104.92**	8.15*	120.81**
Error	24	0.03	2.22	9.82	3.86	16.76
Total	37	-	-	-	-	-

** = Highly significant at P≤ 0.01 probability level, * = Significant at P≤ 0.05 probability level, **N.S** = Non-significant at P≤ 0.05 probability level

Mean performance

Mean performance for parents and hybrids is presented in table 3 & 4. The results indicated that, maximum plant height (102.20 cm) was taken by the cross Kiran-95 x Marvi-2000 followed by the cross Khirman x Marvi-2000 (100.53 cm). In case of tillers plant^{-1}, the maximum tillers plant^{-1} (9.26) were displayed by the cross Bakhar-2002 x TD-1 followed by the cross Kiran-95 x Marvi-2000 (9.20). The longest spikes (13.25 cm) were produced in the cross Bakhar-2002 x TD-1 followed by the cross Kiran-95 x Marvi-2000 (13.05 cm). The maximum spikelets spike^{-1} (20.13) were counted in the cross Kiran-95 x Marvi-2000 followed by the variety TD-1 (19.88). For grains spike^{-1}, the cross Bakhar-2002 x TD-1took the first position (65.26) followed by the cross Khirman x TD-1 (63.73). According to grain weight of main spike, the first (4.50 g) was ranked by the cross Benazir x Marvi-2000 followed by the cross Khirman x Marvi-2000 (4.41 g). For grain yield plant^{-1}, the variety Khirman occupied the first position (11.40 g), while the second place was taken by the variety Sahar-2006 (11.34 g). The maximum seed index (46.66 g) was expressed by the variety Khirman followed by the variety Benazir (46.13 g).

While, the maximum biological yield planl⁻¹ (25.59 g) was obtained by the variety TD-1 followed by the variety Kiran-95 (25.03 g). In terms of harvest index (%), the variety Khirman (46.91) was on the top followed by the variety Marvi-2000 (46.22).

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

Genotypes	Plant height	Tillers plant⁻¹	Spike length	Spikelets spike⁻¹	Grains spike⁻¹
Bakkhar-2002	82. g	6.73 d	12.57 bc	17.83 bcd	61.40 abcd
Khirman	98.13 bc	6.73 d	12.57 bc	19.78 ab	61.26 abcd
Sahar-2006	92.40 ef	7.06 d	12.58 bc	16.57 de	55.73 de
Benazir	93.93 de	7.86 bcd	12.60 bc	17.30 bcd	62.73 abc
Kiran-95	83.67 g	6.60 d	12.82 abc	17.16 bcd	53.46 e
TD-1	74.07 h	6.80 d	12.55 bc	19.88 ab	58.20 bcde
Marvi-2000	95.87 cd	6.86 d	12.52 c	16.84 cde	57 cde
Bakhar-2002 x TD-1	95.07 de	9.26 a	13.25 a	18.99 abc	65.26 a
Khirman x TD-1	89.87 f	8.53 abc	12.96 abc	17.31 bcd	63.73 ab
Sahar-2006 x TD-1	82.60 g	8.60 abc	12.90 abc	18.08 abc	60.86 abcd
Benazir x Marvi-2000	93.80 de	8.86 abc	12.74 bc	18.67 abc	62.60 abc
Kiran-95 x Marvi-2000	102.20 a	9.20 ab	13.05 ab	20.13 a	60.13 abcd
Khirman x Marvi-2000	100.53 ab	7.53 cd	12.88 abc	19.56 ab	62.53 abc

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

Genotypes	Main spike yield	Grain yield plant⁻¹	Seed index	Biological yield plant⁻¹	Harvest index
Bakkhar-2002	3.26 de	10.81 bc	45.66 abc	23.99 bcd	45.06 abc
Khirman	3.20 e	11.40 a	46.66 a	24.30 abc	46.91 a
Sahar-2006	3.70 bc	11.34 ab	45.73 abc	24.80 abc	45.72 abc
Benazir	3.67 bc	10.41 bcde	46.13 ab	24.05 abc	43.28 cde
Kiran-95	3.52 cd	10.59 bcde	44.53 bc	25.03 ab	42.30 def
TD-1	3.32 de	10.26 cde	45.53 abc	25.59 a	40.09 fg
Marvi-2000	3.76 bc	10.60 bcd	45.33 abc	22.93 cde	46.22 ab
Bakhar-2002 x TD-1	3.36 de	10.45 bcde	45.93 abc	23.99 bcd	43.55 cde
Khirman x TD-1	4.34 ab	10.39 bcde	45.13 abc	23.40 bcd	44.40 bcd
Sahar-2006 x TD-1	3.55 cd	10.95 bc	45.13 abc	24.17 abc	45.30 abc
Benazir x Marvi-2000	4.50 ac	10.03 efg	45.46 abc	23.65 bcd	42.41 def
Kiran-95 x Marvi-2000	3.92 bc	10.85 bc	44.93 abc	24.44 abc	44.39bcd
Khirman x Marvi-2000	4.41 ab	10.08 def	44.13 c	23.32 bcd	43.22 cde

Heritability estimates and genetic advance

Heritability performs a great role in the transmission of attributes from one organism to the next due to genes. So, the heritability parameters like environmental variance, genetic variance and phenotypic variance, broad sense heritability and genetic advance for a wide range of traits are depicted in from table 3 to 12.

Plant height (cm)

The results regarding plant height in table 5 showed that, the cross Khirman x TD-1 exhibited the highest heritability (92.76%) followed by the cross Sahar-2006 x TD-1 (88.27%), while the minimum heritability was observed by the cross Khirman x Marvi-2000 (74.77%). The results about genetic advance indicated that, the cross Khirman x TD-1 (70.35) demonstrated the highest genetic advance, while the minimum genetic

advance was manifested by the cross Khirman x Marvi-2000 (19.31) for this particular trait.

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

F$_2$ populations	σ^{2}e	σ^{2}g	σ^{2}p	h^2% (B.S)	G. A
Bakhar-2002 x TD-1	1.89	10.18	12.07	84.33	20.96
Khirman x TD-1	2.67	34.17	36.84	92.76	70.35
Sahar-2006 x TD-1	3.21	24.19	27.40	88.27	49.78
Benazir x Marvi-2000	5.24	20.50	25.74	79.65	42.20
Kiran-95 x Marvi-2000	4.58	29.30	33.89	86.48	60.31
Khirman x Marvi-2000	3.17	9.39	12.55	74.77	19.31

Tiller plant^{-1}

The results for tillers plant^{-1} are given in table 6. The data revealed that the cross Kiran-95 x Marvi-2000 manifested the maximum heritability (83.51%) followed by the cross Bakhar-2002 x TD-1 (82.31%) and the minimum heritability was displayed by the cross Khirman x Marvi-2000 (59.75%). For genetic advance, the cross Kiran-95 (9.13) manifested the maximum genetic advance, while the minimum genetic advance was demonstrated by the cross Khirman x Marvi-2000 (1.37).

Table 6. Heritability estimates for different F$_2$ segregating populations for tillers plant^{-1}

F$_2$ populations	σ^{2}e	σ^{2}g	σ^{2}p	h^2% (B.S)	G. A
Bakhar-2002 x TD-1	0.80	3.70	4.50	82.31	7.62
Khirman x TD-1	0.71	2.27	2.98	76.20	4.67
Sahar-2006 x TD-1	0.98	3.57	4.54	78.51	7.34
Benazir x Marvi-2000	0.70	2.29	2.98	76.68	4.70
Kiran-95 x Marvi-2000	0.88	4.44	5.31	83.51	9.13
Khirman x Marvi-2000	0.45	0.67	1.12	59.75	1.37

Spike length (cm)

The results concerning spike length are mentioned in table 7. The cross Kiran-95 x Marvi-2000 proved the highest heritability (88.69%) followed by the cross Khirman x TD-1 (88.29%), while the minimum heritability was observed by the cross Sahar-2006 x TD-1 (60.13%). In case of genetic advance, the cross Khirman x TD-1 (0.78) showed the highest genetic advance, while the lowest genetic advance was manifested by the cross Benazir x Marvi-2000 (0.52) for this character.

Table 7. Heritability estimates for different F$_2$ segregating populations for spike length

F$_2$ populations	σ^{2}e	σ^{2}g	σ^{2}p	h^2% (B.S)	G. A
Bakhar-2002 x TD-1	0.06	0.36	0.42	85.43	0.73
Khirman x TD-1	0.05	0.38	0.43	88.29	0.78
Sahar-2006 x TD-1	0.21	0.31	0.51	60.13	0.63
Benazir x Marvi-2000	0.03	0.26	0.29	88.22	0.52
Kiran-95 x Marvi-2000	0.04	0.29	0.33	88.69	0.60
Khirman x Marvi-2000	0.13	0.35	0.49	72.87	0.73

Spikelets spike^{-1}

In table 8 expressed the results about spikelets spike^{-1}. The highest heritability (95.62%) was expressed by the cross Kiran-95 x Marvi-2000 followed by the cross Khirmanx TD-1 (91.77%), while the minimum heritability was observed by the cross Bakhar-2002 x TD-1 (58.08%). About genetic advance, the cross Khirman x TD-1 (49.98) displayed the maximum genetic advance, while the minimum genetic advance was shown by the cross Bakhar-2002 TD-1 (3.72).

Table 8. Heritability estimates for different F$_2$ segregating populations for spikelets spike^{-1}

F$_2$ populations	σ^{2}e	σ^{2}g	σ^{2}p	h^2% (B.S)	G. A
Bakhar-2002 x TD-1	1.31	1.81	3.12	58.08	3.72
Khirman x TD-1	2.18	24.28	26.46	91.77	49.98
Sahar-2006 x TD-1	1.55	12.80	14.35	89.22	26.36
Benazir x Marvi-2000	1.83	10.09	11.92	84.62	20.77
Kiran-95 x Marvi-2000	0.72	12.71	16.43	95.62	32.35
Khirman x Marvi-2000	2.12	10.80	12.92	83.57	22.22

Grains spike^{-1}

In table 9, the results for grains spike^{-1} were shown. The cross Kiran-95 x Marvi-2000 revealed the highest heritability (87.90%) followed by the cross Khirman x TD-1 (79.83%), while the minimum heritability (75.29%) was manifested by the cross Benazir x Marvi-2000. According to genetic advance, the cross Khirman x TD-1 (113.29) expressed the highest genetic advance, while the lowest genetic advance was manifested by the cross Benazir x Marvi-2000 (29.16) for this trait.

Table 9. Heritability estimates for different F$_2$ segregating populations for grains spike^{-1}

F$_2$ populations	σ^{2}e	σ^{2}g	σ^{2}p	h^2% (B.S)	G. A
Bakhar-2002 x TD-1	9.79	33.85	43.64	77.58	69.67
Khirman x TD-1	13.90	55.02	68.92	79.83	113.29
Sahar-2006 x TD-1	6.80	26.75	33.55	79.72	55.08
Benazir x Marvi-2000	4.65	14.18	18.83	75.29	29.16
Kiran-95 x Marvi-2000	6.78	49.20	55.98	87.90	101.36
Khirman x Marvi-2000	7.66	26.75	34.41	77.73	55.07

Grain weight of main spike (g)

The results of heritability estimates for main spike yield are presented in table 10. The cross Kiran-95 x Marvi-2000 manifested the maximum heritability (91.99%) followed by the cross Khirman x TD-1 (86.13%), while the minimum heritability (71.00%) was indicated by the cross Bakhar-2002 x TD-1). The results about genetic advance indicated that, the cross Kiran-95 x Marvi-2000 (2.38) expressed the highest genetic advance, while the minimum genetic advance was manifested by the cross Sahar-2006 x TD-1 (0.10) for this attribute.

Table 10. Heritability estimates for different F$_2$ segregating populations for grain weight of main spike

F$_2$ populations	σ^{2}e	σ^{2}g	σ^{2}p	h^2% (B.S)	G. A
Bakhar-2002 x TD-1	0.03	0.08	0.11	71.00	0.16
Khirman x TD-1	0.03	0.21	0.25	86.13	0.44
Sahar-2006 x TD-1	0.02	0.05	0.07	71.43	0.10
Benazir x Marvi-2000	0.02	0.10	0.11	85.13	0.19
Kiran-95 x Marvi-2000	0.10	1.16	1.26	91.99	2.38
Khirman x Marvi-2000	0.02	0.06	0.08	73.22	0.12

Grain yield plant^{-1} (g)

The results regarding heritability estimates for grain yield plant^{-1} are appeared in table 11. It showed that, the cross Kiran-95 x Marvi-2000 exhibited the maximum heritability (94.13%) followed by the cross Khirman x Marvi-2000 (88.15%). The minimum heritability (72.95%) was appeared by the cross Khirman x TD-1. The results about genetic advance indicated that, the cross Kiran-95 x Marvi-2000 (2.77) demonstrated the highest genetic advance, while the minimum genetic advance was displayed by the cross Bakhar-2002 x TD-1 (0.22).

Table 11. Heritability estimates for different F$_2$ segregating populations for grain yield plant^{-1}

F$_2$ populations	σ^{2}e	σ^{2}g	σ^{2}p	h^2% (B.S)	G. A
Bakhar-2002 x TD-1	0.02	0.11	0.13	83.46	0.22
Khirman x TD-1	0.30	0.81	1.11	72.95	1.66
Sahar-2006 x TD-1	0.16	0.49	0.65	76.00	1.01
Benazir x Marvi-2000	0.05	0.34	0.39	86.56	0.69
Kiran-95 x Marvi-2000	0.08	1.34	1.43	94.13	2.77
Khirman x Marvi-2000	0.07	0.53	0.60	88.15	1.08

Seed index (1000 grain weight (g))

The results for seed index are described in table 12. The finding indicated that, the cross Kiran-95 x Marvi-2000 had the highest heritability (88.03%) followed by the cross Bakhar-2002 x TD-1 (85.94%). While, the minimum heritability (81.69%) was given by the cross Benazir x Marvi-2000. In terms of genetic advance, the cross Khirman x Marvi-2000 (14.00) gave the highest genetic advance, while the minimum genetic advance was given by the cross Kiran-95x Marvi-2000 (8.15).

Table 12. Heritability estimates for different F$_2$ segregating populations for seed index

F$_2$ populations	σ^{2}e	σ^{2}g	σ^{2}p	h^2% (B.S)	G. A
Bakhar-2002 x TD-1	0.75	4.60	5.35	85.94	9.46
Khirman x TD-1	0.86	4.76	5.55	85.68	9.78
Sahar-2006 x TD-1	0.85	4.13	4.98	82.89	8.49
Benazir x Marvi-2000	0.99	4.42	5.41	81.69	9.09
Kiran-95 x Marvi-2000	0.54	3.96	4.50	88.03	8.15
Khirman x Marvi-2000	1.47	6.80	8.27	82.26	14.00

Biological yield plant^{-1} (g)

The results for biological yield plant^{-1} in table 13 expressed that, the cross Bakhar-2002 x TD-1 exhibited the maximum heritability (85.21%) followed by the cross Sahar-2006 x TD-1 (82.37%) and the minimum heritability (67.26%) was displayed by the cross Khirman x Marvi-2000. The results about genetic advance indicated that, the cross Benazir x Marvi-2000 (13.96) displayed the highest genetic advance, while the minimum genetic advance was expressed by the cross Khirman x TD-1 (3.61).

Table 13. Heritability estimates for different F₂ segregating populations for biological yield plant⁻¹

F₂ populations	σ²e	σ²g	σ²p	h²% (B.S)	G. A
Bakhar-2002 x TD-1	0.77	4.42	5.19	85.21	9.10
Khirman x TD-1	0.52	1.76	2.27	77.32	3.61
Sahar-2006 x TD-1	0.48	2.27	2.75	82.37	4.66
Benazir x Marvi-2000	2.15	6.78	8.93	75.96	13.96
Kiran-95 x Marvi-2000	1.29	5.37	6.67	80.63	11.07
Khirman x Marvi-2000	1.53	3.13	4.66	67.26	6.45

Harvest index (%)

The results for harvest index are manifested in table 14 which reported that, the cross Kiran-95 x Marvi-2000 displayed the maximum heritability (89.12%) followed by the cross Khirman x Marvi-2000 (83.68%), while the minimum heritability (71.05%) was exhibited by the cross Khirman x TD-1 for harvest index. The results about genetic advance indicated that, the cross Bskhar-2002 x TD-1 (21.31) demonstrated the highest genetic advance, while the minimum genetic advance was manifested by the cross Khirman x TD-1 (3.17) for this character.

Table 14. Heritability estimates for different F₂ segregating populations for harvest index

F₂ populations	σ²e	σ²g	σ²p	h²% (B.S)	G. A
Bakhar-2002 x TD-1	3.05	10.35	13.40	77.22	21.31
Khirman x TD-1	0.63	1.54	2.17	71.05	3. 17
Sahar-2006 x TD-1	0.78	2.97	3.74	79.26	6.10
Benazir x Marvi-2000	0.70	1.96	2.67	73.57	4.04
Kiran-95 x Marvi-2000	0.27	2.22	2.50	89.12	4.58
Khirman x Marvi-2000	0.74	3.79	4.52	83.68	7.78

Discussion

Genetic improvement of any crop relies on the mode and frequency of the genetic variability and percentage of the relationship of heritable and non-heritable variations between yield and its contributing attributes. In case, desirable variation is not in existence, the plant breeders create genetic variability in the genetic material of crops utilizing a wide range of breeding techniques.

The results regarding mean squares informed that some of the genotypes including parents and hybrids were highly significant and significant for all the traits. Spike length (cm), spikelets spike⁻¹, grains spike⁻¹ and grain yield plant⁻¹ (g) are the characters of more importance. The results of heritability percentage in broad sense for all of the studied attributes reported that the cross Khirman x TD-1 (92.76%) displayed the highest heritability estimates for plant height (cm). The previous researchers such as, [9, 10] observed the similar results from their research. For the parameters tillers plant⁻¹(83.51%), spike length (88.69%), spikelets spike⁻¹ (95.62%), grains spike⁻¹ (87.90%), main spike yield(91.99%), grain yield plant⁻¹ (94.13%), seed index(88.03%) and harvest index(89.12%), the maximum heritability was only manifested by the cross Kiran-95 x Marvi-2000. Finally, for biological yield plant⁻¹, the cross Bakhar-2002 x TD-1 (85.21%) manifested the highest heritability. [11-13] also recorded the highest heritability for the most of the yield traits. Improvement in existing yield status can be acquired by selecting spike length with high heritability [14, 15]. Number of spikelets per spike is also very significant for increasing grain yield. Grains spike⁻¹ is one of the most important yield components which directly affect genetic yield potential. High heritability for grains spike⁻¹ was observed by [16, 17]. These same results for grain yield plant⁻¹ were also gained by [18].

Conclusion

It is concluded that parents and hybrids were having significant and highly significant genetic variation for most of the traits which were studied. The cross Kiran-95 x Marvi-2000 proved to be the most effective cross combination for most of the traits as showed higher heritability values for many characters. For that reason, selection of this cross would be very fruitful. Some of the cross combinations expressed a specific response for some of the traits as the crosses manifested better performance for many traits. Therefore, these hybrids would be useful in making betterment of these specific characters in cross breeding programmes. Similarly, those cross combinations which proved to be better for specific traits must be chosen for further refinement in the breeding programmes.

Authors' contributions

Conceived and designed the experiments: TF Abro & JK Sootaher, Performed the experiments: JK Sootaher, M Kachi, MA Mastoi & KK Menghwar, Analyzed the data: ZA Soomro & TA Baloch, Wrote the paper: MK Soothar & TA Soomro.

References

1. Khabiri, E, AA Imani & H Shahbazi (2012). Studying the grain yield and yield components in advanced rainfed wheat genotypes. *Biol Res* 3(12): 5647-5650.
2. Subhani, GM & MA Choudhry (2000). Correlation and path coefficient analysis in bread wheat under drought stress and normal conditions. *Pak J Biol Sci* 5(3): 72-77.
3. Robinson, HF, RE Comstock & PH Harvey (1949). Genotypic and phenotypic correlation in corn and their implications in selection. *Agron J* 43: 282-287.
4. Johnson, HW, HF Robinson & RE Comstock (1955). Estimates of genetic and environmental variability in soybean. *Agron J* 47: 314-318.
5. Larik, AS, SI Malik, AA Kakar & MA Naz (2000). Assessment of heritability and genetic advance for yield and yield components in upland cotton (*Gossypium hirsutum* L.). *Sci Khyber* 13(2): 39-44.
6. Gomez, KA & AA Gomez (1984). Statistical procedures for agricultural research (Second Edition). New York: John Wiley and Sons.
7. Duncan, DB (1955). Multiple range and multiple F tests. *Biometrics* 11(1):1-42.
8. Falconer, DS (1989). Introduction to quantitative genetics. Longman Scientific and Technical, 3rd Edition, New York, USA. 187-192.
9. Asif, M, MY Mujahid, NS Kisana, SZ Mustafa & I Ahmed (2004). Heritability, genetic variability and path coefficient of some traits in spring wheat. *Sarhad J Agric* 20(1): 87-91.
10. Awan, SI, MFA Malik & M Siddique (2005). Study on seedling traits for drought tolerance in wheat under moisture stress conditions. *J Agric* 3(6): 247-254.
11. Sial, MA, MA Arain, MH Naqvi, AM Soomro, S Laghari, NA Nizamani & A Ali (2003). Seasonal effects and genotypic responses for grain yield in semi-dwarf wheat. *Asian J Pl Sci* 2(15): 1091-1101.
12. Saifullah, A, N Zakir & MY Mujahid (2009). Estimation of genetic parameters and character association in wheat. *J Agric Biol Sci* 1(1): 15-18.
13. Mangi, SA, MA Sial, BA Ansari, MA Arain, KA Laghari & AA Mirbahar (2010). Heritability studies for grain yield and yield components in F_3 segregating generation of spring wheat. *Pak J Bot* 42(3): 1807-1813.
14. Khan, AS, I. Saleem and Z. Ali (2003). Heritability of various morphological traits in wheat. *Int J Agric Biol* 5(2): 138-140.
15. Ahmed, N, MA Chowdhury, I Khaliq & M Maekawa (2007). The inheritance of yield and yield components of five wheat hybrid populations under drought conditions. *Indonesian J Agric Sci* 8(12): 53-59.
16. Riaz, R & MA Chowdhry (2003). Genetic analysis of some economic traits of wheat under drought conditions. *Asian J Pl Sci* 2(3): 790-796.
17. Singh, SP, PB Jhang & DN Singh (2001). Genetic variability in polygenic traits in late sown wheat genotypes. *Ann Agric Res* 22(8): 34-36.
18. Yousaf, A, B Atta, M Akhtar & Z Lateef (2008). Genetic variability, association and diversity studies in wheat. *Pak J Bot* 40(5): 2087-2097.