

Research Article

Genetic variability, heritability and genetic advancement in F₃ population of wheat

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Abstract

An experiment was conducted to study genetic variability, heritability and genetic advancement for twenty four (24) wheat genotypes including eight (08) parents and sixteen (16) F₃ progenies. Study indicated existence of significant amount of genetic variability, heritability and advancement for all the traits used in experiment. Among parental genotypes NR-397 produced longer plants (109.0 cm), Lalma, NR-397 and RIL-0815 gave more fertile tillers plant⁻¹ (FTP⁻¹) (10), Lalma produced lengthy spikes (13.3 cm), more grains spike⁻¹ (GS⁻¹) (74) and higher grain yield plant⁻¹ (GYP⁻¹) (27.2 g), Barsat gave more spikelets spike⁻¹ (SS⁻¹) (22.0) and higher biological yield plant⁻¹ (BYP⁻¹) (59 g). Similarly, among F₃ populations Marvi x NIFA-Insaf produced longer plants (107.4 cm), NIFA-Insaf x NR-397, Marvi x NR-1107, Marvi x Barsat and NIFA-Insaf x Lalma gave more FTP⁻¹ (10), Marvi x NRL-1107 produced lengthy spikes (13.5 cm), higher BYP⁻¹ (60.9 g), and more GYP⁻¹ (27.9 g), Lalma x NR-397 gave more SS⁻¹ (22.5) and Barsat x NR-397 gave more GS⁻¹ (79). Higher heritability accompanied higher genetic advancement for plant height (0.87, 15.59), FTP⁻¹ (0.84, 4.22), spike length (0.61, 1.04), SS⁻¹ (0.79, 18.22), GS⁻¹ (0.93, 18.22), BYP⁻¹ (0.95, 28.64) and GYP⁻¹ (0.92, 13.48) respectively. It is concluded that F₃ population Marvi x NRL-1107, Lalma x NR-397, Barsat x NR-397 and Marvi x NIFA-Insaf performed better and surpassed their parents all the studied traits. Moreover, NIFA-Insaf x Lalma, Marvi x NIFA-Insaf and Lalma x NR-397 and Marvi x NIFA-Insaf showed higher heritability and more genetic advancement.

Keywords: Bread wheat; Heritability; Plant breeding; Variability; Wheat

Introduction

Wheat (*Triticum aestivum* L.) is the world's most broadly adapted crop, providing one-

third of the world population with more than half of their calories and nearly half of their protein [1]. Wheat is the dominant crop in

temperate countries, and plays promising role in the nutritional security of Pakistan [2]. In Pakistan, wheat being the main staple food cultivated on the largest acreages. Pakistan falls in ten major wheat-producing countries of the world in terms of area under wheat cultivation, total production and yield per hectare [3].

Almost one sixth of the entire cultivable land in the world is under wheat [3]. Globally wheat was cultivated on an area of 222 million hectares with overall production of 750 million tons and average yield of 3.4 metric tons ha⁻¹ during 2017-18 [4]. Similarly, in Pakistan 9.2 million hectares land was under wheat cultivation with total wheat production of 25.6 million tonnes and an average yield of 2780 kg ha⁻¹, in which Khyber Pakhtunkhwa contributed 0.77 million hectares land and 1.4 million tonnes production with average yield of 1814 kg ha⁻¹ during 2016-17 [5].

The earliest and original cultivated form of bread wheat was essentially landraces. These landraces were selected by the farmers from wild and diverse populations on the basis of their superior performance probably in yield and other characteristics [6]. This was an early and obviously the non-scientific form of plant breeding. However, domestication and introduction of new forms to local environments were also concomitant with the selection of genetic characters that isolated them from their wild-relatives [7]. Therefore to meet the enhancing food requirements of the rapid increase in population, invention of new improved varieties which have maximum resistance to biotic (disease, insect or pest resistance) and abiotic (moisture, mineral and heat tolerance) stresses became essential [8].

Estimation of genetic variability and evaluation are beneficial for enabling effective germplasm collection, management and application [9]. Genetic variability is a vital source of high yielding genes therefore;

crop improvement largely depends on the degree of heritable diversity existing in crop species. Regular practice of limited parents in breeding program causes genetic erosion. Diverse genetic background provides desirable allelic variation among parental lines to produce new and valuable combinations [10]. The genetic diversity is the backbone of crop improvement and the traits showing genetic variability can be utilized for further breeding program to synthesize a new wheat variety [11]. Together with heritability, genetic advancement gives estimates of possible gain at a specific selection intensity which is an essential tool in plant breeding for varietal development [12]. High heritability assessments results in high genetic advancement for yield components in wheat offer better opportunity for selection of genotypes in early generations [13].

The success of breeding program depends on type and extent of genetic variation. The larger the genetic variation the bigger the chances for bringing about sustainable improvement through selection. The measurement of genetic variation as well as the mode of inheritance of various genetic characters are thus of primary importance [14]. The present study was aimed to estimate the genetic variability, heritability and genetic advancement correlations for yield and yield-associated traits in F₃ populations of wheat. The information obtained from this study appears to be of great value for the development of such varieties, which are capable of better yield and best adapted to agro-climatic conditions of Peshawar.

Materials and methods

Experimental material and design

A field trail was conducted in the research farm of Plant Breeding and Genetics Department, Agriculture University Peshawar during 2015-16. To evaluate the genetic variability, heritability and genetic advancement Eight (08) parental lines and

their sixteen (16) F₃ progenies were studied (Table 1). Seeds of parental lines along with their selected F₃ crosses were space planted in the field under randomized completed block design (RCBD) replicated three times. Each plot contained four rows per entry of three-meter length with 30 cm row to row and 15 cm plant to plant distance, respectively. All other agronomic practices were done as recommended for wheat production in the area.

Data measurement

Ten (10) guarded plants from parents and twenty (20) plants from F₃ population were randomly selected from the central two rows from each replication for recording data using standard procedures for each parameter. Height (cm) of each selected plant was measured at physiological maturity from ground level to the tip of last spikelet without awns. Productive tillers plant⁻¹ (tillers with spike) were counted at the time of harvest for each parent and F₃ population. The biomass (g plant⁻¹) of the selected plants was taken with electric balance and then their average was worked out. Spike length (cm) of selected plants of each parental line and F₃ population was measured from the base of first spikelet to the tip of last spikelet (without awns). Total number of spikelet on main spike of the selected plants in each replication was counted at the time of maturity and average value was calculated for further analysis. The total numbers of grains were counted from the main spike of each selected plant in each replication and average value was calculated for further analysis. At the time of harvesting each selected plant was threshed individually. The grain yield (g) of each selected plant was recorded separately using electronic balance.

Statistical analysis

To estimate variation among parental lines and F₃ population, the data were subjected to statistical analysis by using the analysis of variance technique as outlined for RCBD by

Singhand Chaudhary [15]. The sum of squares pertaining to genotypes were further split into sum of square due to parents, F₃ population and parents versus F₃ population. For mean comparison of genotypes Least Significant Difference (LSD) test was used. Broad-sense heritability was assessed using the formula described by Mahmud and Kramer [16] as follows:

$$h^2_{B.S} = [V_{F_3} - \sqrt{(V_{P1} \times V_{P2})}] / V_{F_3}$$

Where

$h^2_{B.S}$ = Broad sense heritability

V_{F_3} = F₃ variance

V_{P1} = Parent-1 variance

V_{P2} = Parent-2 variance

Expected genetic advancement was assessed according to Allard's [17] and was estimated from the following formula:

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

Where

GA = Genetic advancement

σ_P = Phenotypic standard deviation

h^2 = Broad sense heritability in fraction

i = Selection intensity

Value of i = 1.40 (at 20% selection intensity).

Results and discussion

Plant height (cm)

Data analysis showed significant differences ($P \leq 0.01$) for plant height among wheat genotypes (Table 2). Longer plants (109.0 cm) were produced by parental genotype NR-397, whereas shorter plants (90.7 cm) were noted for NIFA-Insaf. Mean squares of parents, F₃ population and parents vs. F₃ population also showed significant differences for plant height of wheat. Among parental genotypes plant height ranged from 90 cm for NIFA-Insaf to 109.0 cm for NR-397 and among F₃ crosses the range was 92.6 cm for NRL-1107 x Lalma to 107.4 cm for Marvi x NIFA-Insaf (Table 3). Our results are in line with [18-20] who reported significant variation in plant height for different varieties. Heritability assessments for plant height was high for most of the F₃ population, indicating that F₃ population had

significant quantity of genetic variability, which means that different height levels can effectively be selected from segregating population. The magnitude of heritability regarding plant height varied from 0.25 to 0.87, while the values of genetic advancement ranged from 2.06 to 15.59. The highest heritability (0.87) accompanied with higher genetic advancement (15.59) was calculated for NIFA Insaf x Lalma and RIL-0815 x Barsat. However cross combination Barsat x NR-395 gave low heritability (0.25) and genetic advancement (2.06) (Table 4). Similar results were obtained by [21-22] who reported maximum heritability and higher genetic advancement for most of the crosses in segregating populations.

Fertile tillers plant⁻¹

Data analysis showed significant differences ($P \leq 0.01$) for fertile tillers plant⁻¹ among wheat genotypes (Table 2). Lalma, NR-397, RIL-0815, Marvi, NIFA-Insaf x Barsat and Marvi x NRL-1107 genotypes gave more fertile tillers plant⁻¹(10.0), whereas fewer fertile tillers plant⁻¹(7.0) were recorded for segregating population Lalma x Barsat (Table 3). Mean squares of parents, F₃ population and parents vs. F₃ population also showed significant differences for fertile tillers plant⁻¹ of wheat. Among parental genotypes more and analogous number of fertile tillers plant⁻¹ (10.0) were produced by Lalma, NR-397 and RIL-0815. Among F₃ crosses the higher fertile tillers plant⁻¹ (10.0) were recorded for NIFA-Insaf x NR-397, Marvi x NRL-1107 and NIFA-Insaf x Lalma. Fewer fertile tillers plant⁻¹ (7.0) were noted for Lalma x Barsat (Table 3). Research showed significant differences for fertile tillers plant⁻¹ in segregating population of wheat [19, 22-24]. However, in contrast to our results, [25] observed non-significant differences for fertile tillers plant⁻¹ in six parental cultivars and their F₃ progenies. Higher heritability and genetic advancement simplifies the selection procedure [26].

Higher heritability (0.84) was noted for F₃ population Marvi x NIFA-Insaf, whereas Barsat x NR-395 gave lower heritability (0.27). Similarly, Marvi x NIFA-Insaf marked more genetic advancement (4.22), whereas Barsat x NR-395 revealed low genetic advancement (0.87) (Table 4). Higher heritability and more genetic advancement indicate high genetic potential for this trait, low environmental effect and the presence of predominant role of additive genes. Hence, selection may be effective for high tillering capacity. Our findings are similar with those of [19, 22-24] who reported high heritability along with higher genetic advancement in early generation of wheat.

Spike length (cm)

Data analysis showed significant differences ($P \leq 0.01$) for spike length among wheat genotypes (Table 2). Longer spikes (13.5 cm) were recorded for Marvi x NRL-1107 among all genotypes. Parental cultivar Marvi gave shorter spikes (11.0 cm). Similar results were obtained by [20] who reported significant variation in spike length of different varieties. Mean squares of parents, F₃ population and parents vs. F₃ population also showed significant difference for spike length (Table 3). Among parental genotypes the longer spikes (13.3 cm) were recorded for NRL-1107, followed by Lalma (13.2 cm). Among F₃ populations longer spikes were noted for Marvi x NRL-1107 (13.5 cm) and Lalma x Barsat (13.2 cm), whereas shorter spikes (11.3 cm) were given by NIFA x Lalma (Table 3). Significant variations in parental cultivars and their F₃ populations for spike length were reported by various researchers [22, 24, 27]. Overall heritability for spike length was 0.32 (Barsat x NR-397) to 0.61 (NRL-1107 x Lalma and NIFA-Insaf x Lalma), indicating moderately high heritability (Table 4) with moderate genetic advancement of 0.43 (Barsat x NR-297) to 1.04 (NIFA-Insaf x Lalma). Such magnitude of heritability and genetic advancement

showed that selection for spike length should be practiced with care in early segregating generations. Our results are in line with those of [22, 28] who reported that spike length was highly heritable in most of the crosses and showed higher genetic advancement.

Spikelets spike⁻¹

Data analysis showed significant differences ($P \leq 0.01$) for spikelets spike⁻¹ among wheat genotypes (Table 2). More spikelets spike⁻¹ (22.5) were noted for Lalma x NR-397, whereas fewer spikelets spike⁻¹ (18.0) were noted for parental cultivar Marvi. Mean squares of parents, F₃ population and parents vs. F₃ population also showed significant difference for spikelets spike⁻¹ (Table 3). More spikelets spike⁻¹ was noted for segregating populations as compared with parental cultivars. Among F₃ crosses spikelets spike⁻¹ ranged from 19.5 for NIFA-Insaf x Lalma to 22.47 for Lalma x NR-397, whereas for parental cultivars spikelets spike⁻¹ ranged from 18 from Marvi to 21.97 for Barsat (Table 3). Research showed significant difference for spikelets spike⁻¹ in early generation of wheat [28, 29]. High heritability values (0.68-0.93) accompanied by high genetic advancement (9.94-18.22) were recorded for spikelets spike⁻¹, indicating a high response to selection. Higher heritability for Lalma x NR-397, NIFA-Insaf x Barsat and Lalma x Barsat (0.93, 0.91 & 0.91 respectively) indicated that these genotypes can be exploited for varietal development. Genetic advancement ranged from 9.94 to 18.22. Maximum genetic advancement (18.22) was note for Lalma x NR-397, whereas minimum (9.94) was given by Marvi x NIFA-Insaf (Table 5). Our results are in line with those of [22, 29] who recorded higher heritability and more genetic advancement for spikelets spike⁻¹ of wheat.

Grains spike⁻¹

Data analysis showed significant differences ($P \leq 0.01$) for grain spike⁻¹ among wheat genotypes (Table 2). More grain spike⁻¹ (79)

were recorded for segregating population, Barsat x NR-397, whereas less grains spike⁻¹ (69) were noted for Barsat. Mean squares of parents, F₃ population and parents vs. F₃ population also showed significant difference for grains spike⁻¹ (Table 3). F₃ segregating populations gave more grains spike⁻¹ as compared with parental cultivars. Among parental cultivars more grains spike⁻¹ (74) were recorded for Lalma, whereas among segregating populations Barsat x NR-397 gave more grains spike⁻¹ (79) (Table 3). These results are similar with [20, 24, 28, 30] who reported significant variations for grains spike⁻¹ in early generations of wheat. High heritability values (0.68-0.93) accompanied by high genetic advancement (9.94-18.22) were recorded for grains spike⁻¹, showing high response to selection. Among F₃ populations higher heritability (0.93) was noted for Lalma x NR-397, whereas lower heritability (0.68) was recorded for Barsat x NR-395. Similarly, more genetic advancement (18.22) was noted for Lalma x NR-397 whereas, less genetic advancement (9.94) Marvi x NIFA-Insaf. Our results are in line with those of [24, 28] who reported higher heritability and more genetic advancement for grains spike⁻¹ of wheat.

Biological yield plant⁻¹ (g)

Data analysis showed significant differences ($P \leq 0.01$) for biological yield plant⁻¹ among wheat genotypes (Table 2). Among all genotypes more biological yield plant⁻¹ (60.9 g) was noted for Marvi x NRL-1107 of F₃ population, whereas less biological yield plant⁻¹ (37.9 g) was recorded for parental cultivar RIL-0815. Mean squares of parents, F₃ population and parents vs. F₃ population also showed significant difference for biological yield plant⁻¹ (Table 3). Means of F₃ population were higher than parental cultivars. Higher biological yield plant⁻¹ (59.0 g) was recorded for Barsat among all parental genotypes. Among segregating populations, Marvi x NRL-1107 gave more biological

yield plant⁻¹ (60.9 g) with the adjoining value tailed by cross combination Marvi x NIFA-Insaf (57.6 g). Less biological yield plant⁻¹ (41.0 g) was recorded for Marvi x RIL 0815 (Table 3). Significant differences were noted for biological yield plant⁻¹ in segregating population of wheat [21, 31]. Heritability plays significant role in deciding the suitability and strategy for selection of a character [32]. Higher heritability of 0.95 was shown by F₃ population NIFA-Insaf x Lalma, followed by Marvi x Barsat (0.94) and Lalma x NR 397 (0.93). Among F₃ populations NIFA x Lalma showed maximum genetic advancement (28.64). Higher heritability indicated that heritability may be due to higher contribution of genetic component. Our results are in line with those of [20, 21] who reported maximum heritability with higher genetic advancement for biological yield.

Grain yield plant⁻¹ (g)

Data analysis showed significant differences ($P \leq 0.01$) for grain yield plant⁻¹ among wheat genotypes (Table 2). More grain yield plant⁻¹ (27.9 g) was noted for Marvi x NRL-1107 whereas, less grain yield plant⁻¹ (13.8 g) was recorded for RIL-0815. Mean squares of parents, F₃ population and parents vs. F₃ population also showed significant difference for grain yield plant⁻¹ of wheat (Table 3). Among parental cultivars more grain yield plant⁻¹ (27.2 g) was noted for Lalma whereas,

less grain yield plant⁻¹ (13.8 g) RIL-0815. Similarly, among F₃ population more grain yield plant⁻¹ noted for Marvi x NRL-1107 whereas, less grain yield plant⁻¹ (16.9 g) was recorded for Marvi x RIL-0815. Our results are in line with the findings of [20, 24, 28] who reported significant differences in grain yield among tested genotypes of wheat. Heritability and genetic advancement assessment provide information about the extent of genetic improvement from generation to generation. Higher heritability and more genetic advancement for grain yield may be helpful in selecting high yielding cross combinations. Higher heritability (0.92) was noted for NIFA-Insaf x NR-397, RIL-0815 x Barsat and NIFA-Insaf x Lalma whereas, lower heritability (0.69) was recorded for Barsat x NR-395. These results showed that these cross combinations can be exploited for varietal development and their selection will be fruitful for grain yield plant⁻¹ of wheat. Among F₃ populations more genetic advancement (13.48) was recorded for NIFA-Insaf x Lalma followed by NIFA-Insaf x NR-397 (12.98) and RIL-0815 X Barsat (12.70) whereas, less genetic advancement (8.96) was noted for NIFA-Insaf x Barsat (Table 5). These results are also similar with [24, 29, 30] who reported higher heritability associated with more genetic advancement among tested genotypes of wheat.

Table 1. List of wheat genotypes including eight parents and sixteen F₃populations

#	Parents	Origin	#	F ₃ Populations	#	F ₃ Populations
1	Barsat	NIFA	1	Barsat x NR-395	9	Marvi x Barsat
2	NR-395		2	Lalma x Barsat	10	NIFA-Insaf x Barsat
3	Lalma		3	Lalma x NR-397	11	Lalma x NR-395
4	NR-397		4	Marvi x RIL-0815	12	Lalma x RIL-0815
5	RIL-0815		5	NIFA-Insaf x NR-397	13	NIFA-Insaf x Lalma
6	Marvi		6	NRL-1107x Lalma	14	Marvi x NIFA-Insaf
7	NIFA-Insaf		7	RIL-0815 x Barsat	15	NRL-1107 x RIL-0815
8	NRL-1107		8	Marvi x NRL-1107	16	Barsat x NR-397

Table 2. Mean squares for various traits

SOV	DF	Plant Height (cm)	Fertile tiller plant ⁻¹	Spike length (cm)	Spikelets spike ⁻¹	Grains spike ⁻¹	Biological yield plant ⁻¹ (g)	Grain yield plant ⁻¹ (g)
Replications	2	23.79	0.26	0.50	1.02	2.6	7.87	1.55
Genotypes	23	69.46**	1.99**	1.39**	2.83**	64.21**	119.28**	37.68**
Parents (P)	7	91.22**	1.61*	1.65**	5.18**	74.39**	193.41**	66.56**
F ₃ population	15	58.99**	1.83**	1.18**	1.69**	61.93**	90.89**	25.86**
P vs. F ₃ s	1	74.21**	7.07**	2.65*	3.61**	27.08**	26.15*	12.86**
Error	46	10.67	0.66	0.46	0.5	2.58	5.31	1.4
C.V (%)	--	3.27	9.07	5.44	3.49	2.36	4.58	5.48

SOV-Source of Variation, DF-Degree of Freedom

Table 3. Mean values for plant height (PH), fertile tillers plant⁻¹ (FTP⁻¹), spike length (SL), spikelets spikes⁻¹ (SS⁻¹), grains spike⁻¹ (GS⁻¹), biological yield plant⁻¹ (BYP⁻¹) and grain yield plant⁻¹ (GYP⁻¹)

Genotypes	PH (cm)	FTP ⁻¹	SL (cm)	SS ⁻¹	GS ⁻¹	BYP ⁻¹ (g)	GYP ⁻¹ (g)
Parental							
Barsat	100.6	9	12.9	22.0	72	59.0	24.8
NR-395	94.7	9	13.0	20.7	61	50.8	21.7
Lalma	100.3	10	13.2	21.5	74	56.9	27.2
NR-397	109.0	10	12.7	18.9	64	58.3	26.1
RIL-0815	94.5	10	12.9	20.0	68	37.9	13.8
Marvi	100.7	9	11.0	18.0	63	46.3	18.8
NIFA-Insaf	90.7	8	12.6	19.8	72	45.0	18.0
NRL-1107	98.4	9	13.3	19.6	64	41.6	17.6
F₃ populations							
Barsat x NR-395	103.8	8	12.9	21.1	71	53.2	22.4
Lalma x Barsat	98.7	7	13.2	20.6	70	46.6	20.4
Lalma x NR-397	94.8	8	12.6	22.5	71	46.0	20.2
Marvi x RIL-0815	100.6	8	12.7	20.4	70	40.7	16.9
NIFA-Insaf x NR-397	103.9	10	12.3	20.5	66	57.0	19.9
NRL 1107 x Lalma	102.3	8	12.2	20.0	66	53.9	22.0
RIL-0815 x Barsat	92.6	9	12.0	20.0	73	50.7	21.7
Marvi x NRL-1107	101.3	10	13.5	20.5	66	60.9	27.9
Marvi x Barsat	107.0	10	12.0	19.9	64	51.5	21.7
NIFA-Insaf x Barsat	101.4	9	11.4	19.7	65	46.0	26.1
Lalma x NR-395	95.9	9	12.0	21.7	64	45.2	18.2
Lalma x RIL-0815	99.7	9	12.8	20.4	62	50.0	21.7
NIFA-Insaf x Lalma	107.1	10	11.3	19.5	72	57.1	24.4
Marvi x NIFA-Insaf	107.4	9	11.7	20.5	65	57.6	25.7
NRL-1107 x RIL-0815	97.0	9	11.8	20.7	73	46.8	19.4
Barsat x NR-397	98.6	9	12.4	20.7	79	48.6	21.6
Mean	100.0	9	12.4	20.4	68	50.3	21.6
LSD (0.05)	5.4	1.3	1.1	1.2	2.6	3.8	1.9

Table 4. Broad-sense heritability and expected genetic advancement for various traits

Genotypes	Plant height (cm)			Fertile tillers plant ⁻¹			Spike length (cm)		
	Var.	h ²	GA	Var.	h ²	GA	Var.	h ²	GA
Parents									
Barsat	24.86	1.75	0.70
NR-395	12.66	2.66	0.41
Lalma	11.12	1.90	0.60
NR-397	22.10	2.20	0.68
RIL-0815	20.43	2.86	0.51
Marvi	30.65	2.07	0.46
NIFA-Insaf	27.68	2.08	0.57
NRL-1107	22.15	2.80	0.61
F₃ populations									
Barsat x NR-395	35.87	0.25	2.06	5.36	0.27	0.87	1.23	0.36	0.55
Lalma x Barsat	48.26	0.43	4.16	5.51	0.65	2.15	1.29	0.56	0.89
Lalma x NR-397	69.79	0.62	7.30	10.43	0.82	3.69	1.25	0.49	0.77
Marvi x RIL- 0815	49.08	0.66	6.46	6.83	0.60	2.20	1.17	0.57	0.87
NIFA-Insaf x NR-397	38.32	0.58	5.03	9.35	0.71	3.02	0.87	0.47	0.62
NRL 1107 x Lalma	151.41	0.87	14.99	7.10	0.67	2.50	1.12	0.61	0.91
RIL-0815 x Barsat	46.48	0.60	5.70	10.61	0.78	3.55	1.09	0.56	0.81
Marvi x NRL-1107	48.95	0.66	6.44	7.53	0.64	2.45	1.11	0.55	0.82
Marvi x Barsat	51.33	0.71	7.09	10.57	0.78	3.55	1.10	0.50	0.73
NIFA-Insaf x Barsat	46.98	0.61	5.83	8.95	0.78	3.26	1.13	0.54	0.81
Lalma x NR-395	46.86	0.63	6.00	7.74	0.74	2.90	1.01	0.42	0.59
Lalma x RIL-0815	29.59	0.47	3.58	8.51	0.73	2.98	1.33	0.55	0.88
NIFA-Insaf x Lalma	163.79	0.87	15.59	10.8	0.77	3.53	1.49	0.61	1.04
Marvi x NIFA-Insaf	145.3	0.82	13.85	12.99	0.84	4.22	1.23	0.55	0.85
NRL-1107 x RIL-0815	102.9	0.76	10.79	9.24	0.77	3.27	1.08	0.43	0.62
Barsat x NR397	51.34	0.57	5.71	10.78	0.77	3.54	0.93	0.32	0.43

Var-Variance, h²-Heritability, GA-Genetic Advancement**Table 5. Broad-sense heritability and expected genetic advancement for various traits**

Genotypes	Spikelets spike ⁻¹			Grains spike ⁻¹			Biological yield plant ⁻¹			Grain yield plant ⁻¹		
	Var.	h ²	GA	Var.	h ²	GA	Var.	h ²	GA	Var.	h ²	GA
Parents												
Barsat	15.90	11.58	14.79	8.03
NR-395	16.94	16.71	32.94	8.49
Lalma	18.97	12.77	23.34	7.92
NR-397	17.80	15.72	23.69	9.87
RIL-0815	18.01	15.43	25.97	8.65
Marvi	18.68	17.84	38.72	9.18
NIFA-Insaf	14.39	17.24	54.20	7.38
NRL-1107	22.13	16.13	36.38	8.14
F₃ populations												
Barsat x NR-395	58.38	0.69	11.85	153.59	0.68	11.85	334.63	0.72	18.48	90.64	0.69	9.21
Lalma x Barsat	47.77	0.68	15.00	142.07	0.90	15.00	213.82	0.89	18.18	71.64	0.88	10.43
Lalma x NR-397	36.73	0.35	18.22	196.64	0.93	18.22	380.01	0.93	25.26	87.06	0.91	11.91
Marvi x RIL- 0815	67.47	0.65	15.10	147.38	0.89	15.10	300.23	0.88	21.46	81.44	0.90	11.34
NIFA-Insaf x NR-397	41.93	0.51	11.20	93.37	0.83	11.20	317.18	0.91	22.63	102.33	0.92	12.98

NRL 1107 x Lalma	73.27	0.77	14.83	144.76	0.88	14.83	377.71	0.91	24.64	97.85	0.91	12.60
RIL-0815 x Barsat	64.22	0.70	11.78	101.98	0.83	11.78	379.09	0.89	24.22	97.49	0.92	12.70
Marvi x NRL-1107	45.47	0.60	12.00	103.70	0.84	12.00	304.25	0.89	21.64	88.51	0.91	11.93
Marvi x Barsat	48.55	0.48	11.77	96.71	0.85	11.77	402.86	0.94	26.38	83.84	0.90	11.55
NIFA-Insaf x Barsat	54.19	0.70	16.71	171.27	0.91	16.71	232.53	0.87	18.59	56.72	0.85	8.96
Lalma x NR-395	80.74	0.79	15.08	144.18	0.90	15.08	243.84	0.85	18.67	55.74	0.86	9.02
Lalma x RIL-0815	74.82	0.76	17.28	179.93	0.92	17.28	324.14	0.91	22.94	77.18	0.90	11.02
NIFA-Insaf x Lalma	47.49	0.61	13.25	118.68	0.87	13.25	466.75	0.95	28.64	110.40	0.92	13.48
Marvi x NIFA-Insaf	58.38	0.69	9.94	80.44	0.79	9.94	398.97	0.92	25.84	94.09	0.90	12.21
NRL-1107 x RIL-0815	47.77	0.68	14.43	137.21	0.88	14.43	258.92	0.86	19.41	72.21	0.88	10.49
Barsat x NR-397	36.73	0.35	11.17	92.77	0.83	11.17	321.75	0.91	22.82	88.29	0.90	11.82

Var-Variance, h^2 -Heritability, GA-Genetic Advancement

Conclusion

It is concluded that F_3 population Marvi x NRL-1107, Lalma x NR-397, Barsat x NR-397 and Marvi x NIFA-Insaf performed better and surpassed their parents all the studied traits. Moreover, NIFA-Insaf x Lalma, Marvi x NIFA-Insaf and Lalma x NR-397 and Marvi x NIFA-Insaf showed higher heritability and more genetic advancement. Hence, these crosses could be helpful in selection of suitable genotypes for wheat improvement programs to get high yielding genotypes of wheat and can be exploited for varietal development in the agro-climatic condition of district Peshawar.

Authors' contributions

Conceived and designed the experiments: A Shah, J Amin, S Ali & MR Khan, Performed the experiments: A Shah, F Azam, F Ghani, A Ali & Z Wahab, Analyzed the data: A Rab, G Hassan, M Zakir, A Ali & S Hayat, Contributed reagents/materials/analysis tools: A Rab, S Hayat, S Ali, G Hassan & Z Wahab, Wrote the paper: A Rab, A Shah & J Amin.

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