

Estimation of Genetic Parameters and Interrelationship among Important Traits in Bread Wheat

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ABSTRACT: In the present studies wheat genotypes along with their F₃ populations were evaluated to estimate variability, heritability, genetic advance and correlation among yield and yield related traits. The experiment was conducted in the experimental field of Nuclear Institute for Food and Agriculture, Peshawar during 2015-16. Eight F₃ populations namely, Barsat × NR 395, Lalma × Barsat, Lalma × NR 397, Marvi × RIL 0815, NRL 0707 × Barsat and NRL 1107 × Lalma along with their parents were evaluated in a randomised complete block design with three replications. Highly significant differences were observed for the target traits indicating the existence of variability and potential for improvement through selection. Greater magnitude of heritability coupled with high genetic advance for most of the traits suggest that improvement of these characters could be faster. Selection on the basis of these traits would be more fruitful as they are least influenced by the environment due to additive gene affects. The most promising cross combinations were Barsat × NR 395, Marvi × NRL 1107, NRL 1107 × Lalma, NR 0707 × Barsat and RIL 0815 × Barsat. These crosses deserve more attention in future wheat improvement programs for development of high yielding wheat cultivars. Fertile tillers plant⁻¹, biological yield plant⁻¹, 100-grain weight and harvest index had significant positive relation with grains yield plant⁻¹ pointing out their utility as direct selection criteria for isolation of superior genotypes from genetically mixed populations.

Keywords: Genetic Parameter, Bread Wheat, Genotypes

INTRODUCTION

Wheat (*Triticum aestivum* L.) is an important cereal and serves as a staple food for more than one-third of the world population. In Pakistan it is one of the leading food grain and accounts for 37.1% of the total cropped area. It contributes 10.3% to value added in agriculture and 2.2% to GDP. The crop is grown on both irrigated and rainfed areas of the country. About 70% of the wheat is grown on irrigated land while 30% is grown under rainfed conditions. It occupied an area of 9.19 million hectare with annual production of 25 million tonnes and average productivity of 2775 kg ha⁻¹ during 2014-15 (PBS 2014). The low wheat yield in Pakistan is due to unavailability of quality seed, delayed planting, unavailability of required soil moisture content at critical growth stages and higher prices of fertilizers.

The ultimate goal of any crop improvement program is to develop high yielding cultivars with consistent performance over diverse environments. The study of genetic variability is the pre-requisite for such programs. Hybridization is the basic technique for creation of variation. Genetic variability is important for breeding and in

selecting desirable genotypes. Heritability of a trait is very important in determining the response to selection. It was reported that genetic improvement for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program (Akinwale *et al.*, 2011). Heritability indicates the effectiveness with which selection of genotypes could be based on phenotypic performance. Plant attributes with high heritability can be selected in earlier generations to accelerate the process of cultivar development. Heritability estimates would help to predict about the possible progress that can be attained by making the selection process effective and in predicting the performance of further generations (Cooper *et al.*, 2013). However, high heritability does not always indicate high genetic gain. Heritability coupled with genetic advance is used in predicting the ultimate effect for selecting superior varieties (Ali *et al.*, 2002). Estimates of heritability and genetic advance will help in knowing the nature of gene action affecting the target traits (Sravan, 2012). Higher heritability estimates coupled with better genetic advance confirms the scope of selection in developing new genotypes with desirable characteristics in early segregating generations (Ajmal *et al.*, 2009). Genetic advance gives clear picture and precise view of segregating generations for possible selection.

Breeding strategy in wheat depends upon degree of associated traits as well as its magnitude and nature of variation. Therefore, information about the yield contributing traits is of great importance to breeders for development of high yielding varieties. The knowledge of association of target traits with yield helps in their selection with more precision and accuracy. The degree of relationship of these components with yield can be directly measured and expressed as correlation coefficients. This can help in yield improvement since grain yield is a complex trait and is highly influenced by several component traits. The present research studies were undertaken to elucidate information on genetic variability, heritability, and genetic advance and traits associations in F₃ populations of wheat and to identify desirable wheat genotypes for future wheat improvement programs.

MATERIALS AND METHOD

The present research studies were conducted at the Nuclear Institute for Food and Agriculture (NIFA) Peshawar, during 2015-16. Eight F₃ populations namely, Barsat × NR 395, Lalma × Barsat, Lalma × NR 397, Marvi × RIL 0815, NRL 0707 × Barsat and NRL 1107 × Lalma along with their parents were sown in the field according to randomised complete block design (RCBD) with 03 replications. Each entry was grown in a 4-row plot having row length of 3 m. The plant to plant and row to row distance was kept as 15 cm and 30 cm, respectively. All other agronomic practices were uniformly adopted for the whole experiment.

Data were recorded for plant height, fertile tillers plant⁻¹, spike length, spikelets spike⁻¹, grains spike⁻¹, grain weight spike⁻¹, 100-grain weight, biological yield plant⁻¹, grains yield plant⁻¹ and harvest index. Ten plants in each parent and 20 plants in each F₃ population were randomly selected for recording data.

The data were subjected to statistical analysis by using the analysis of variance technique as outlined by Steel and Torrie (1980). Heritability estimates in broad sense were computed using the formula described by Mahmud and Kramer (1951) given as:

$$h^2(\text{B.S}) = \frac{VF_3 - \sqrt{VP_1 \times VP_2}}{VF_3} \times 100$$

Where, h² = heritability of a trait, VF₃ = variance of F₃, VP₁ = variance of P₁, VP₂ = variance of P₂

Genetic advance was calculated according to Allard (1960):

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

Where GA = genetic advance, σ_p = phenotypic standard deviation, h² = heritability in broad sense

i = selection intensity

Value of i = 1.40 (at 20% selection pressure) was used in this study.

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences (P ≤ 0.01) among genotypes, parents, F₃ population and parents versus F₃ population for all the studied traits indicating the presence of sufficient genetic variability among the genotypes (Table 1). Similar findings have also been reported by Narwal *et al.*, 1999 and Tazeen *et al.*, 2009. Fertile tillers plant⁻¹, biological yield plant⁻¹, grains spike⁻¹, grain weight spike⁻¹, 100-grain weight, grain yield plant⁻¹ and harvest index had high coefficient of variability indicating a wide range of variation in these characters. Similarly plant height, spike length and spikelets spike⁻¹ had low coefficient of variability suggesting that these characters had little variation (Table 2).

Broad sense heritability for fertile tillers plant⁻¹ ranged from 0.70 to 0.94%. The highest value of heritability (0.94%) was observed for cross combination, Marvi × RIL 0815, while the lowest value (0.70%) was observed for Barsat × NR 395. The expected genetic advance for fertile tillers plant⁻¹ ranged from 4.46 to 9.3, with the highest

genetic advance (9.32) recorded for population, Barsat x NR 395 and the lowest (4.46) was recorded for Marvi x RIL 0815 (Table 3). These results are in agreement to the findings of Waqas *et al.* (2014), Kumar *et al.* (2014), Rashid *et al.* (2013), Subhashchandra *et al.* (2009) and Iftikhar *et al.* (2013). Fertile tillers plant⁻¹ revealed positive and significant association with biological yield plant⁻¹ (0.676**) and grain yield plant⁻¹ (0.310*) whereas it expressed non-significant correlation with spike length and spikelets spike⁻¹ (Table 4). These results are in line with the findings of Subhashchandra *et al.*, 2009, Munir *et al.*, 2007 and Khaliq *et al.*, 2004.

Heritability for plant height ranged from 0.48 to 0.83 while its expected genetic advance ranged from 3.50 to 11.81. Highest broad sense heritability (0.83) coupled with maximum genetic advance was observed for F₃ population, Lalma x NR 397 while low heritability with minimum genetic advance was noticed for Barast x NR395 (Table 3). Maximum heritability and the higher genetic advance manifested for plant height in the present studies are in conformity with the judgments of Kumar *et al.* (2014), Khan *et al.* (2013) and Rashid *et al.* (2013) who also reported high heritability and higher genetic advance for plant height. Correlation studies regarding plant height manifested significant but negative relationship with spikelets spike⁻¹ (-0.501*) whereas, positive and non-significant associations were found with fertile tiller plant⁻¹, biological yield plant⁻¹, grain spike⁻¹, grain weight spike⁻¹ and 100-grain weight (Table 4). The association between plant height and grain yield plant⁻¹ was negative and non-significant. These results are in agreement with the finding of Akram *et al.*, 2008 who also reported negative and non-significant association of plant height with grain yield.

The estimates of broad-sense heritability for grains spike⁻¹ varied from 0.37 to 0.90 whereas its expected genetic advances ranged from 4.22 to 17.91. High broad sense heritability of 0.90, 0.89 and 0.87 were observed for F₃ populations, Lalma x NR 397, Marvi x NRL 1107 and Marvi x RIL 0815, respectively. The highest estimate of genetic advance (17.91) for grains spike⁻¹ was observed for Barsat x NR 395 and the lowest value of genetic advance (4.22) was noticed for Lalma x NR 397 (Table 3). These results are supported by the findings of Baloch *et al.*, 2013, Waqas *et al.*, 2014 and Hussain *et al.*, 2013. Grains spike⁻¹ revealed positive and non-significant association with plant height, grain weight spike⁻¹, 100-grain weight and harvest index. The current findings are in conformity with the findings of Waqas *et al.*, 2014 and Khan *et al.*, 2013, while contrary to the findings of Iftikhar *et al.*, 2013.

Estimates of heritability for biological yield plant⁻¹ ranged from 0.66 to 0.94 whereas its expected genetic advance varied between 17.83 and 39.16. The lowest value of heritability for biological yield plant⁻¹ (0.66) was noticed for population, Lalma x Barsat, whereas, the highest value (0.94) was authenticated by NR 0707 x Barsat. Maximum value of genetic advance (39.16) was unveiled for NRL 1107 x Lalma, while, the lowest value of genetic advance (17.83) was uncovered for Lalma x Barsat (Table 3). The current findings are companionable with the judgment of Kumar *et al.* (2014) who also reported high heritability coupled with high genetic advance for biological yield plant⁻¹. Biological yield plant⁻¹ had positive and significant association with fertile tillers plant⁻¹ (0.676**) and grain yield plant⁻¹ (0.465*) while negative and significant association was found with harvest index (-0.494) whereas, its association was positive but non-significant with plant height, spike length and spikelets spike⁻¹. Khan *et al.* (2012) also reported significant contribution of biological yield towards grain yield plant⁻¹. Almost similar results were documented by Baloch *et al.*, 2013 and Abinasa *et al.*, 2011.

Spike length is an important character as it contributes to the grain yield. As the spike length increases the number of grains per spike also increases, ultimately increasing the yield. Broad-sense heritability for spike length varied from 0.18 to 0.75, whereas, its estimates of expected genetic advance ranged from 0.26 to 1.85. The highest heritability (0.75) was observed for population, RIL 0815 x Barsat, while Lalma x NR 397 had the lowest estimate (0.18) heritability for the this trait. Maximum genetic advance (1.85) for spike length was noticed for RIL0815 x Barsat, while the lowest value of 0.26 for this trait was observed for Lalma x NR 397 (Table 3). The current results are well-matched with judgments of Rashid *et al.* (2013) and Hussain *et al.* (2013). However our judgments are contradictory to the findings of Khan *et al.* (2013) who reported non-significant differences among segregating populations regarding spike length. Spike length exhibited highly significant and positive association with spikelets spike⁻¹ (0.748**), a significant and negative association with harvest index (-0.587*) and non-significant and positive correlation with biological yield plant⁻¹ and fertile tillers plant⁻¹. These results are in contrast to the findings of Subhashchandra *et al.*, 2009 and Baloch *et al.*, 2013 who reported significant contribution of spike length towards grain yield plant⁻¹.

Broad-sense heritability and expected genetic advance for spikelets spike⁻¹ varied between 0.24 and 0.76 and 0.67 to 2.53, respectively. Maximum heritability (0.76) and genetic advance (2.53) for spikelets spike⁻¹ was observed for population, Lalma x Barsat. The lowest heritability (0.24) and the minimum genetic advance (0.67) were noticed for Lalma x NR 397 (Table 3). Bhushan *et al.* (2103) also reported high heritability coupled with low genetic advance. Ajmal *et al.* (2009) also reported lower genetic advance in the assessment of six wheat varieties

and their twelve F₂ populations. Spikelets spike⁻¹ showed strong positive and significant relationship with spike length (0.75**) and negative significant association (-0.51*) with 100-grain weight (Table 4). This trait had positive and non-significant relationship with fertile tillers plant⁻¹ and biological yield plant⁻¹, and negative and non-significant association with plant height, grains spike⁻¹, grain weight spike⁻¹, grain yield and harvest index (Table 4). The findings of negative effect between spikelets spike⁻¹ with yield in the present study is contradictory to the findings of Kumar *et al.*, 2014 and Akram *et al.*, 2008 who reported the direct effect of spikelets spike⁻¹ on grain yield.

The values of heritability for grain weight spike⁻¹ ranged from 0.19 to 0.78 with expected genetic advance from 0.17 to 1.52. Maximum heritability (0.78) for grain weight spike⁻¹ was observed for Barsat × NR 395 while minimum heritability (0.19) was recorded for Lalma × NR397. Similarly, the highest genetic advance (1.52) for grain weight spike⁻¹ was noticed for Barsat × NR 595 while the lowest genetic advance (0.17 g) was observed for Lalma × NR 397 (Table 3). Almost similar results have been reported by Ijaz *et al.* (2015) and Waqas *et al.* (2014). Grain weight spike⁻¹ showed positive and non-significant association with plant height, grains spike⁻¹, 100-grain weight and harvest index (Table 4), whereas, its association was negative and non-significant with fertile tillers plant⁻¹, spike length, biological yield plant⁻¹, spikelets spike and grain yield plant⁻¹ (Table 4). Our results are contradictory to the judgments of Yagdi, 2009 who reported the direct effect of grain weight spike⁻¹ on grains yield plant⁻¹.

Heritability values for 100-grain weight varied from 0.27 to 0.59. The highest heritability (0.59) was authenticated for Lalma × Barsat coupled with maximum genetic advance (0.82), while the lowest heritability (0.27) was noticed for Marvi × RIL 0815. The lowest estimate of genetic advance (0.32) was noticed for Marvi × NRL 1107 (Table 3). Our results are contradictory to the finding of Majumder *et al.* (2008) who reported high heritability coupled with high genetic advance. Relationship of 100-grain weight with spikelets spike⁻¹ was negative and significant (-0.51*) and with plant height, grain spike⁻¹, grain weight spike⁻¹ and harvest index it was positive and non-significant and negative non-significant with fertile tillers plant⁻¹, spike length, biological yield plant⁻¹ and grain yield plant⁻¹ (Table 4). Our results are in agreement to that of Kumar *et al.*, 2014 who also reported the direct effect of 100-grain weight on grain yield plant⁻¹.

The estimates of broad-sense heritability and genetic advance for grain yield plant⁻¹, respectively ranged between 0.62 and 0.93 and 6.67 to 15.3. The Maximum heritability (0.93) for grain yield plant⁻¹ was observed for NRL1107 × Lalma while the minimum (0.62) was recorded for Marvi × NRL 1107. The highest genetic advance was observed for NRL 1107 × Lalma (15.3 g) while the lowest value was noticed for Marvi × RIL 0815 (Table 3). These results are in line with the judgment of Ijaz *et al.* (2015) and Yadawad *et al.* (2015). Positive and significant association of grain yield plant⁻¹ was found with harvest index (0.51*) and biological yield plant⁻¹ (0.46*). Association between grain yield plant⁻¹ and fertile tillers plant⁻¹ was positive but non-significant. The trait had negative and non-significant association with plant height, spike length, spikelets spike⁻¹, grains spike⁻¹, grains weight spike⁻¹ and 100-grain weight (Table 4). Our results are partially supported by the finding of Baloch *et al.*, (2013) who also reported significant association of grain yield with biological yield and harvest index.

Broad-sense heritability and expected genetic advance harvest index varied from 0.77 to 0.98 and 11.81% to 26.37%, respectively. The highest heritability (0.98%) was observed for Barsat × NR 95 followed by Lalma × Barsat (0.96) and NRL 0707 × Barsat (0.95). The highest genetic advance (26.37%) was observed for Lalma × Barsat, while the lowest (11.81%) was noticed for RIL 0815 × Barsat (Table 3). The present findings get support from earlier findings by Baloch *et al.* (2013) and Jan *et al.* (2015) who reported higher heritability estimates with higher genetic advance. Harvest index revealed positive and significant association with grain yield plant⁻¹ (0.51*) whereas, negative and significant association with spike length (-0.587*) and biological yield plant⁻¹ (0.494*). The studied trait had positive and non-significant association with grains spike⁻¹, grain weight spike⁻¹ and 100-grain weight. These results are in agreement to the findings of Baloch *et al.*, 2013 and Azam *et al.*, 2013.

Table 1. Mean squares for yield and yield related traits in wheat during 2015-16

SOV	DF	FTP	PH	GSP	BY	SL	SSP	GWSP	HGW	GY	HI
Replications	2	1.33	10.25	19.19	1134.86	0.09	0.26	0.008	0.0008	11.70	216.88
Genotypes	15	37.02**	852.92**	97.62**	681.04**	3.08**	4.14**	0.29**	0.86**	123.57**	159.22*
Parents (P)	7	61.55**	1306.14**	99.72**	552.10**	2.42**	2.72**	0.28**	0.53*	102.96*	79.51 ^{NS}
F ₃ Populations	7	6.05**	284.50**	60.00**	554.88**	2.99**	2.87**	0.26**	0.59*	123.29**	250.84**
P vs F ₃	1	82.03**	1659.39**	346.28**	2466.77**	8.28**	22.96**	0.58**	5.12**	269.80**	75.92 ^{NS}
Error	30	1.83	50.95	7.92	1647.10	0.17	0.43	0.075	0.22	34.35	72.43
CV (%)	--	7.81	7.53	4.40	12.93	3.11	2.97	7.18	7.62	16.76	22.64

*, ** Significant at 1% and 5% levels of probability, respectively.

Abbreviations: FTN = fertile tillers plant⁻¹; PH = plant height; GSP = grains spike⁻¹; BY = biological yield plant⁻¹; SL = spike length; SSP = spikelets spike⁻¹; GWSP = grain weight spike⁻¹, HGW = 100-grain weight, GY = grain yield plant⁻¹, HI = harvest index

Table 2. Variance and coefficient of variability for yield and yield related traits in wheat during 2015-16

Parents	FTN		PH		BY		SL		GSP		SSP		GWSP		HGW		GY		HI		
	Var.	CV%	Var.	CV%	Var.	CV%	Var.	CV%	Var.	CV%	Var.	CV%	Var.	CV%	Var.	CV%	Var.	CV%	Var.	CV%	
Barsat	6.48	8.71	13.27	3.12	52.59	4.39	0.45	3.58	15.96	4.97	0.86	3.02	0.50	12.24	0.38	7.51	2.24	2.42	5.54	4.14	
NR 395	2.45	7.20	30.33	3.87	114.76	6.75	0.81	4.67	30.27	7.03	4.24	6.66	0.34	11.34	0.63	10.20	7.61	5.79	4.39	4.50	
Labna	4.26	9.94	8.08	2.35	246.88	9.19	0.80	5.68	30.92	6.44	2.15	4.96	0.23	8.95	0.47	8.09	19.53	7.32	23.02	8.26	
NR 397	8.00	9.24	26.99	4.45	275.00	10.29	1.13	6.07	46.11	8.48	4.39	7.11	0.50	13.56	0.61	9.13	11.04	6.04	41.48	11.33	
RIL 0815	1.51	5.40	10.06	2.92	265.30	12.89	1.07	5.50	33.12	6.11	2.82	5.48	0.49	13.96	0.47	10.17	8.69	6.58	36.59	11.18	
Maru	5.21	7.76	12.01	2.81	166.31	8.43	0.57	3.95	5.65	2.51	1.71	4.11	0.38	12.62	0.95	11.99	2.91	3.81	14.37	8.28	
NRL 0707	6.26	7.49	10.03	1.78	52.43	4.70	0.63	4.35	30.90	6.76	2.47	5.47	0.22	10.04	0.72	10.20	24.65	8.40	24.19	9.41	
NRL 1107	1.93	8.69	13.80	4.89	52.78	5.02	0.61	3.79	17.98	6.04	2.77	5.10	0.46	13.04	0.39	7.88	3.96	4.86	11.24	6.45	
F₃ population																					
Barsat × NR 95	18.84	28.65	30.37	5.48	658.50	30.11	0.76	6.68	205.30	20.12	3.62	9.34	2.03	36.55	0.79	12.86	57.49	19.79	354.51	33.36	
Labna × Barsat	27.72	34.45	32.44	6.57	343.28	23.91	1.80	11.48	61.78	12.02	5.79	11.36	0.69	22.99	1.01	16.37	86.64	24.35	451.22	34.56	
Labna × NR 397	21.82	32.27	102.85	8.76	665.71	26.34	1.12	8.84	59.96	11.47	3.97	9.55	0.41	18.97	0.89	14.49	113.68	31.62	292.45	35.17	
Maru × RIL 0815	51.01	45.45	36.68	6.37	577.30	30.59	2.32	11.11	105.96	15.28	4.43	9.56	0.85	27.18	0.85	13.27	42.56	24.65	184.73	40.04	
NR 0707 × Barsat	29.80	30.48	23.57	4.44	787.98	25.77	1.27	8.23	81.27	14.62	3.01	7.98	0.53	20.45	0.76	15.35	64.50	24.23	195.33	47.32	
NRL 1107 × Labna	29.28	28.43	35.93	6.34	993.94	30.26	1.16	9.42	54.58	11.78	4.63	10.84	0.39	19.40	0.66	12.82	137.97	29.77	223.79	32.51	
RIL 0815 × Barsat	45.09	40.69	65.43	7.34	818.78	27.82	3.04	12.37	94.87	13.78	5.80	10.65	0.95	26.14	0.81	13.35	41.83	22.37	100.86	34.47	
Maru × NRL 1107	32.64	37.67	28.94	5.47	725.78	27.61	1.03	7.57	88.48	12.76	3.30	8.06	0.83	21.72	0.66	11.71	114.66	23.61	184.84	32.64	

Table 3. Heritability and genetic advance for yield and yield related traits in wheat during 2015-16

F ₃ population	FTN		PH		BY		SL		GSP		SSP		GWSP		HGW		GY		HI	
	h ²	GA	h ²	GA	h ²	GA	h ²	GA	h ²	GA	h ²	GA	h ²	GA	h ²	GA	h ²	GA	h ²	GA
Barsat × NR 95	0.70	4.46	0.48	3.60	0.87	31.23	0.24	0.29	0.90	17.91	0.47	1.25	0.78	1.52	0.40	0.51	0.93	9.76	0.98	24.21
Labna × Barsat	0.82	6.00	0.68	5.43	0.66	17.83	0.66	1.24	0.59	6.58	0.76	2.53	0.53	0.63	0.59	0.82	0.92	11.98	0.96	26.37
Labna × NR 397	0.75	4.89	0.83	11.81	0.75	26.98	0.18	0.26	0.37	4.22	0.24	0.67	0.19	0.17	0.43	0.56	0.89	13.24	0.77	17.06
Maru × RIL 0815	0.94	9.32	0.64	5.69	0.74	24.40	0.66	1.43	0.87	12.54	0.50	1.47	0.52	0.65	0.27	0.35	0.66	6.67	0.88	16.34
NR 0707 × Barsat	0.78	6.00	0.49	3.50	0.94	37.02	0.54	0.88	0.69	8.86	0.46	1.19	0.34	0.37	0.36	0.43	0.89	9.37	0.95	17.98
NRL 1107 × Labna	0.90	6.57	0.71	3.92	0.90	39.16	0.41	0.62	0.58	5.95	0.49	1.49	0.23	0.19	0.37	0.42	0.93	15.31	0.86	17.42
RIL 0815 × Barsat	0.92	8.59	0.81	9.17	0.87	34.12	0.75	1.85	0.76	10.29	0.73	2.45	0.52	0.68	0.52	0.67	0.87	7.63	0.83	11.81
Maru × NRL 1107	0.90	7.17	0.49	3.92	0.86	28.80	0.40	0.59	0.89	11.57	0.37	0.93	0.47	0.61	0.28	0.32	0.62	9.44	0.87	15.65

Table 4. Phenotypic correlation among yield and yield related traits in wheat during 2015-16.

	PH	FTP	SL	BY	SSP	GSP	GWSP	HGW	GY	HI
PH	-	0.350	-0.175	0.337	-0.501*	0.324	0.054	0.317	-0.056	-0.291
FTP		-	0.105	0.676**	0.004	-0.065	-0.222	-0.194	0.310*	-0.339
SL			-	0.110	0.748**	-0.103	-0.164	-0.354	-0.457	-0.587*
BY				-	0.144	-0.369	-0.355	-0.340	0.465*	-0.494*
SSP					-	-0.194	-0.113	-0.505*	-0.315	-0.50
GSP						-	0.416	0.411	-0.388	0.061
GWSP							-	0.394	-0.035	0.310
HGW								-	0.122*	0.141
GY									-	0.511*

Abbreviations: PH = plant height; FTP = fertile tillers plant⁻¹; SL = spike length; BY = biological yield; SSP = spikelets spike⁻¹; GSP = grains spike⁻¹; GWSP = grain weight spike⁻¹; HGW = 100-grain weight; GY = grain yield plant⁻¹; HI = harvest index.

CONCLUSIONS

Highly significant genotypic variations were perceived among the genotypes for almost all the characters studied offering sufficient genetic variability for effective selection. High estimates of heritability accompanied with high genetic advance were spotted for most of the traits studied. Exercising of selection pressure on these characters will be fruitful in the improvement of the crop for better yield. Fertile tillers plant⁻¹, biological yield plant⁻¹, 100-grain weight and harvest index disclosed significant contribution towards grain yield plant⁻¹, so more importance should be given to these traits for improving grain yield. Among F₃ populations, Barsat × NR 395, Marvi × NRL1107, NRL1107 × Lalma, NRL 0707 × Barsat and RIL0815 × Barsat were found most promising for yield and yield-associated traits suggesting that these populations deserve more attention in further breeding programs to develop high-yielding wheat varieties.

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