



Exploring the genetic variability in F₂ intraspecific crosses of bread wheat

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Abstract

The wheat breeders are being focused to improve the yield potential of bread wheat by evolving new varieties with desirable genetic makeup in order to overcome the consumption pressure of ever increasing human population. For resolving this situation, a research was carried out on ten F₂ populations along with their five parents grown in the Experimental Field, Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam during the growing season of 2017-18. The experiment was carried-out in a randomized complete block design with four replications. The analysis of variance revealed significant differences among genotypes, parents and F₂ crosses for all the traits studied. Such results signify the worth of breeding materials for further exploitation. Based on average performance, the parent AS-2002 and F₂ cross Sehar-2006 × Kiran-95 showed promising performance for majority of studied traits including grain yield plant⁻¹, showing their importance for future breeding programs. The genetic parameters indicated that from ten F₂ progenies, Benazir × Sehar-2006 displayed higher heritability estimates coupled with more genetic gain for maximum number of traits, showing a good parental combination for effective selection to improve wheat productivity in subsequent segregating generations.

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Introduction

Wheat (*Triticum aestivum* L.) belongs to family poaceae, which is a large family and constituted by out-standing group of food plants. The wheat breeders are concentrating to improve the yield potential of wheat by developing new varieties. Wheat is a self-pollinated crop and can be grown successfully in both tropical and subtropical areas. Wheat attains unique prominent position in agriculture and economic perspective of our country because of being second most important food crop after rice (Bhushan *et al.*, 2013). Pakistan is also one of the principle wheat growing country and its diverse consumptions in the human nutrition leads to present as the most important among the cereals (Farzi and Bigloo, 2010). The wheat breeders are concentrating to improve the yield potential of bread wheat by developing new varieties with desirable genetic makeup in order to overcome the consumption pressure of ever increasing population (Degewione *et al.*, 2013). Wheat provides more energy as compared to other cereals. It is also the main source of staple food. Genetic improvement in wheat is taking place both by slow process of nature and rapid process by selection of main since the earliest time the wheat has been cultivated (Soshm *et al.*, 2015). Improvement of wheat is main goal of prehistoric time to present breeding programs in increasing the production and grain yield ha^{-1} . The wheat has capacity for improvement, maximum utilization of gene pool in hybridization of wheat to fulfill food need of day by day increasing population. Genetic manipulation is the best way to boost up wheat production (Yadawad *et al.*, 2015).

Grain yield is a polygenic trait; hence selection of genotypes based on grain yield alone is not very efficient therefore, to increase breeding efficiency identification of traits by wheat breeder contributing to final yield is of grater important (Saeed *et al.*, 2016). Modern wheat breeding emphasis on development of new high yielding varieties suited best diversified agro-climatic conditions. This requires

information about genetic diversity existed in the available germplasm, inheritance mechanisms operative for the yield and its contributing traits. It can be achieved by breeders through identification/selection of superior germplasm and crossed them with each other using different crossing pattern to generate new variability and wheat plants with elevated levels of genetic diversity and/or recombination (Ishaq *et al.*, 2018). Heritability studies provide valuable genetic information to the breeders to predict the interaction of genes in segregating generations. Heritability is the estimation of genetic portion of physical appearance. Heritability and genetic advance values help us in making selection more effective and estimation of response to selection (Ijaz *et al.*, 2015). Genetic variability in a population can be partitioned into heritable and non-heritable variation with the aid of genetic parameters such as variance, genotypic coefficient of variation, heritability and genetic advance, which serve as a basis for selection of some outstanding genotypes from existing ones (Tsegaye *et al.*, 2012). High heritability coupled with high genetic advance for plant height, peduncle length, days to heading and grain yield (Ijaz *et al.*, 2014). The current study was planned to estimate genetic variability and genetic gain in segregating populations of bread wheat F_2 progenies.

Materials and Methods

Ten F_2 cross combinations along with their five respective parents were grown in the Botanical Garden, Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam during the growing season of 2017-18. The experiment was carried out in randomized complete block design with four replications. At maturity, five plants per genotype per replication were selected and tagged as index plants for recording data on yield and its related traits. The five parents were; TD-1, Benazir Sehar-2006, Kiran-95 and AS-2002, while ten F_2 crosses were; TD-1 x Benazir, TD-1 x Sahar-2006, TD-1 x Kiran-95, TD-1 x AS-2002, Benazir x Sehar-

2006, Benazir x Kiran-95, Benazir x AS-2002, Sehar-2006 x Kiran-95, Sehar-2006 x AS-2002 and Kiran-95 x AS-2002. Regarding data analysis, the analysis of variance was applied to the data according to the method suggested by Gomez and Gomez (1984) and the means were compared using least significant difference test. The genetic, environmental and phenotypic variances, broad sense heritability (h^2) and expected response to selection was estimated according to Robinson *et al.* (1949).

Results and Discussion

The present research was designed to assess the genetic parameters of F_2 populations for different traits of bread wheat. The genetic parameters studied were: genetic variance (σ^2_g), phenotypic variance (σ^2_p), environmental variance (σ^2_e), heritability in broad sense (h^2 .b.s.) and genetic advance (GA) at 20% selection intensity. The trait wise interpretations with respect to genetic parameters are given in the following paragraphs.

Analysis of variance

The analyses of variance for all the studied characters are shown in Table 1. Results indicated that genotypes, parents and their F_2 populations differed significantly ($P < 0.05$) in the mean performance for all the traits *viz.* spike length, spikelets spike⁻¹, grains spike⁻¹, grain yield plant⁻¹ and seed index. These results suggested that considerable genetic variability among the parents and their F_2 progenies was present. Therefore, data need further evaluation for the estimation of genetic parameters.

Spike length (cm)

The mean performance for spike length is given in Table 2. The longest spike (11.23 cm) among the F_2 progenies was observed in TD-1 x Sehar-2006 and the shortest spike (9.60 cm) was recorded in Sehar-2006 x AS-2002. Among the parents, the longest spike (10.78 cm) was measured in Kiran-95, while shortest spike (8.06 cm) was measured in Benazir. The heritability (h^2) for the character spike length

varied from 6.01 to 83.86%, while genetic advance varied from 0.12 to 4.54 (Table 3). The cross TD-1 x Sehar-2006 expressed high heritability (h^2 83.86%) with low genetic advance (GA=0.12). This shows that this trait is more under genetic control than environment and may be improved at ease. Formerly researchers, Soshma *et al.* (2015) found similar results for the trait spike length. Furthermore, Sharaan *et al.* (2017) referred that heritability was greater than 80% for all studied traits, including trait spike length, whereas genetic advance as a percentage of mean ranged from 0.14 to 4.54.

Spikelets spike⁻¹

The wheat breeding studies have been reported that spikelets spike⁻¹ may directly contribute towards grain yield. The mean performance for spikelets spike⁻¹ is given in Table 2. Considering the crosses, the maximum (19.40) spikelets spike⁻¹ was noticed in Benazir x Sehar-2006 and minimum (16.86) number of spikelets spike⁻¹ was observed in Sehar-2006 x AS-2002. Among the parental genotypes, the maximum (18.73) number of spikelets spike⁻¹ was found in Kiran-95, whereas minimum (15.00) was recorded in TD-1. The heritability percentage (h^2) for the character spikelets spike⁻¹ ranged from 6.20 to 68.82% in the F_2 populations of Benazir x Sehar-2006 and Kiran-95 x AS-2002, respectively (Table 4). While, genetic advance varied from 0.32 to 5.36 in the F_2 populations of Benazir x Sehar-2006 and Kiran-95 x AS-2002, respectively (Table 4). Most of the crosses low to moderate heritability, indicating the improvement of this trait is not easy through phenotypic selection in early segregation population; however, selection may be delayed for further generations. In contrast to these results, Gandahi *et al.* (2016) reported high heritability in broad sense in many F_2 progenies for this trait.

Grains spike⁻¹

The mean performance for grains spike⁻¹ is mentioned in Table 2. Among the F_2 progenies, the

maximum (56.86) number of grains spike⁻¹ were set in TD-1 × Sehar-2006, whereas minimum (46.46) grains spike⁻¹ were set in Sehar-2006 × AS-2002. Among the parental genotypes, the maximum grains spike⁻¹(57.2) was found in AS-2002; however, minimum (51.06) grains spike⁻¹ was recorded in TD-1. The heritability percentage (h²) for the character grains spike⁻¹ was moderate to high (34.22 to 96.31%), while genetic advance was low to high in all F₂ combinations, ranging from 5.91 to 32.73 (Table 5). The crosses Sehar-2006 × AS-2002 (h²=96.31) and Benazir × Sehar-2006 (h²=88.22%) showed high heritability with high genetic advance of 32.73 and 24.89, respectively, indicating the improvement of this trait is quite possible through phenotypic selection in early segregation population. Earlier scientist like Khilawat *et al.* (2014) and Arya *et al.* (2018) also reported high heritability estimates for grains spike⁻¹.

Grain yield plant⁻¹ (g)

Grain yield is a complex character, which is controlled by many genes; thus requires a special attention. The potential of wheat cultivar is determined by the grain associated characters (Sultana *et al.*, 2012). Among F₂ populations, the maximum (40.40 g) grain yield plant⁻¹ was achieved in Benazir × Sehar-2006, while the minimum (12.01 g) grain yield plant⁻¹ was produced by the cross TD-1 × Kiran-95. Considering the parents, the maximum (13.34 g) grain yield plant⁻¹ was observed in AS-2002; while minimum (10.64 g) grain yield plant⁻¹ was noticed in TD-1 (Table 2). The extent of heritability percentage (h²) and genetic advance for the character grain yield plant⁻¹ was ranged from 21.60 to 91.18% and 1.55 to 7.35, respectively (Table 6). The cross Benazir × Sehar-2006 expressed high heritability estimates of 91.18%. High heritability estimate indicates that more genetic components are involved. Selection will be suitable for the improvement of grain yield. Sharaan *et al.* (2017)

referred that heritability was greater than 80% for all studied traits, including grain yield plant⁻¹

Seed index (1000-grain weight, g)

1000-grain weight is the main yield contributing trait. The highest 1000-grain weight (46.48 g) in F₂ population was recorded in Benazir × Kiran-95, while the cross Kiran-95 × AS-2002 showed the lowest 1000-grain weight (37.13 g). Among the parental lines, TD-1 stands first with the maximum 1000-grain weight of (43.78 g) and Sehar-2006 stands at the bottom with minimum 1000-grain weight (40.32 g). The heritability percentage (h²) for the character 1000-grain weight varied from 29.12 to 97.23%, while genetic advance varied from 5.79 to 28.53 and the progeny TD-1 × AS-2002 showed high heritability (h²= 97.23%) with high genetic advance (GA=25.64) among the crosses (Table 7). It denotes the existence of genetic variability in F₂ populations for seed index is quite high hence such crosses may be exploited for the promising progress of wheat genotypes.

Conclusion

The genotypes, parents and F₂ crosses differed significantly (P<0.05) in the mean performance for all the characters under investigation, suggesting that evaluated materials retained useful genetic resources; hence these plant materials may be utilized in further breeding programs. Based on average performance, the parent AS-2002 and F₂ cross Sehar-2006 × Kiran-95 showed promising performance for majority of studied traits including grain yield plant⁻¹, showing their importance for future breeding programs. The genetic parameters indicated that from ten F₂ progenies, Benazir × Sehar-2006 displayed higher heritability estimates coupled with more genetic gain for maximum number of traits, showing a good parental combination for effective selection to improve wheat productivity in subsequent segregating generations.

Table 1. Mean squares of different traits of bread wheat genotypes.

Source of variation	D.F.	Spike length	Spikelets spike ⁻¹	Grains spike ⁻¹	Grain yield plant ⁻¹	Seed index
Replications	3	0.01	2.05	35.93	0.31	19.77
Genotypes	14	3.18**	6.02**	30.25*	7.56**	25.33*
Parents	4	3.49**	6.77**	16.35*	25.04*	3.80*
F ₂ crosses	9	1.81**	4.00**	37.32*	4.93*	56.48*
Error	42	0.29	0.87	12.61	1.75	10.25

** ,* indicate significant level at 1 and 5% of probability levels, respectively

Table 2. Mean performance of parents and their F₂ populations for different traits in bread wheat genotypes.

Genotypes (Parents and hybrids)	Spike length (cm)	Spikelets spikes ⁻¹	Grains spikes ⁻¹	Grain yield plant ⁻¹ (g)	Seed index (g)
Parents					
TD-1	8.57	15	51.06	10.64	43.78
Benazir	8.06	18.46	55.33	12.87	42.45
Sehar-2006	9.56	17.4	54.33	11.26	40.32
Kiran-95	10.78	18.73	56.06	11.6	42.79
AS-2002	9.91	18.06	57.2	13.43	45.12
LSD (5%)	0.56	0.68	2.43	1.01	2.04
F₂ populations					
TD-1 × Benazir	10.93	19.26	58	12.87	45.92
TD-1 × Sehar-2006	11.23	20.33	56.86	15.22	43.13
TD-1 × Kiran-95	10.06	17.8	55.4	12.01	44.58
TD-1 × AS-2002	10.2	18.86	48.93	14.39	43.8
Benazir × Sehar-2006	12	19.4	54.13	12.2	40.4
Benazir × Kiran-95	11.06	19.4	52.53	13.96	42.56
Benazir × AS-2006	9.73	19.2	51.53	14.85	43.16
Sehar-2006 × Kiran-95	11.56	20.46	56.6	15.7	46.48
Sehar-2006 × AS-2002	9.6	16.86	46.46	13.36	39.15
Kiran-95 × AS-2002	10.76	18.06	53.6	13.06	37.13
LSD (5%)	1.03	1.64	5.02	1.56	3.01

Table 3. Heritability and genetic advance estimates for spike length.

F₂ populations	Genotypic variance (σ^2g)	Environmental variance (σ^2e)	Phenotypic variance (σ^2p)	Heritability (b.s. %)	Genetic advance (GA)
TD-1 × Benazir	0.09	0.66	0.75	11.87	0.27
TD-1 × Sehar-2006	3.64	0.70	4.34	83.86	4.54
TD-1 × Kiran-95	0.23	0.43	0.66	35.54	0.75
TD-1 × AS-2002	0.04	0.58	0.62	6.01	0.12
Benazir × Sehar-2006	0.87	0.70	1.57	55.43	1.81
Benazir × Kiran-95	1.21	0.43	1.57	74.91	2.76
Benazir × AS-2006	1.21	0.43	1.64	73.91	2.46
Sehar-2006 × Kiran-95	1.49	0.65	2.14	69.71	2.65
Sehar-2006 × AS-2002	0.38	0.42	0.80	47.50	1.52
Kiran-95 × AS-2002	0.22	0.53	0.75	29.13	0.65

Table 4. Heritability and genetic advance estimates for spikelets spike⁻¹.

F₂ populations	Genotypic variance (σ^2g)	Environmental variance (σ^2e)	Phenotypic variance (σ^2p)	Heritability (b.s. %)	Genetic advance (GA)
TD-1 × Benazir	1.51	2.48	3.99	37.86	1.97
TD-1 × Sehar-2006	0.91	2.63	3.54	25.6	1.25
TD-1 × Kiran-95	0.33	2.31	2.64	12.5	0.56
TD-1 × AS-2002	0.52	2.73	3.25	16.04	0.81
Benazir × Sehar-2006	4.88	2.2	7.09	68.82	5.36
Benazir × Kiran-95	3.5	2.71	6.21	56.36	3.81
Benazir × AS-2006	3.87	2.98	16.85	56.53	3.85
Sehar-2006 × Kiran-95	1.62	3.13	4.75	34.04	1.93
Sehar-2006 × AS-2002	1.08	1.88	2.96	36.48	2.05
Kiran-95 × AS-2002	0.25	3.74	3.99	6.2	0.32

Table 5. Heritability and genetic advance estimates for grains spike⁻¹.

F₂ populations	Genotypic variance (σ²g)	Environmental variance (σ²e)	Phenotypic variance (σ²p)	Heritability (b.s. %)	Genetic advance (GA)
TD-1 × Benazir	81.99	35.89	117.88	69.56	19.64
TD-1 × Sehar-2006	15.09	29.02	44.12	34.22	5.91
TD-1 × Kiran-95	33.1	21.22	54.32	60.93	16.6
TD-1 × AS-2002	36.57	28.34	64.91	56.34	11.8
Benazir × Sehar-2006	103.87	13.86	117.74	88.22	24.89
Benazir × Kiran-95	51.48	11.47	62.95	81.81	18.48
Benazir × AS-2006	51.48	14.47	65.94	78.08	16.48
Sehar-2006 × Kiran-95	17.86	7.6	25.46	70.15	9.2
Sehar-2006 × AS-2002	164.59	6.31	170.91	96.31	32.73
Kiran-95 × AS-2002	28.71	6.91	35.62	80.59	19.51

Table 6. Heritability and genetic advance estimates for grain yield plant⁻¹.

F₂ populations	Genotypic variance (σ²g)	Environmental variance (σ²e)	Phenotypic variance (σ²p)	Heritability (b.s. %)	Genetic advance (GA)
TD-1 × Benazir	6.14	4.54	10.67	57.5	4.88
TD-1 × Sehar-2006	4.15	4.79	8.94	46.4	3.61
TD-1 × Kiran-95	1.65	5.99	7.64	21.6	1.55
TD-1 × AS-2002	4.59	4.61	9.2	49.9	3.94
Benazir × Sehar-2006	8.57	0.82	9.4	91.18	7.27
Benazir × Kiran-95	7.93	2.03	9.95	79.61	6.53
Benazir × AS-2006	7.93	2.03	9.95	79.61	6.53
Sehar-2006 × Kiran-95	9.85	2.28	12.14	81.19	7.35
Sehar-2006 × AS-2002	7.39	0.9	8.3	89.1	6.67
Kiran-95 × AS-2002	5.25	2.1	7.36	71.4	5.04

Table 7. Heritability and genetic advance estimates for seed index.

F ₂ populations	Genotypic variance (σ^2_g)	Environmental variance (σ^2_e)	Phenotypic variance (σ^2_p)	Heritability (b.s. %)	Genetic advance (GA)
TD-1 × Benazir	124.33	4.03	128.36	96.86	28.53
TD-1 × Sehar-2006	17.01	41.41	58.42	29.12	5.53
TD-1 × Kiran-95	48.63	3.54	52.17	93.21	17.50
TD-1 × AS-2002	100.05	2.85	102.91	97.23	25.64
Benazir × Sehar-2006	35.00	5.90	40.90	85.57	20.01
Benazir × Kiran-95	42.01	3.50	45.51	92.30	23.21
Benazir × AS-2006	40.47	3.04	43.51	93.01	24.01
Sehar-2006 × Kiran-95	50.55	8.90	59.45	85.02	19.95
Sehar-2006 × AS-2002	14.63	25.10	39.73	36.82	7.59
Kiran-95 × AS-2002	25.46	1.86	27.32	93.20	23.90

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