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HERITABILITY AND GENETIC ADVANCE STUDIES IN F_2 POPULATION OF BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

The present experiment was conducted at Barley and Wheat Research Institute, ARI, Tandojam during 2016-2017 in order to study the inheritance pattern of various agronomic traits in nine F_2 segregating populations of bread wheat including nine parents and their six F_2 progenies for nine morphological attributes. The mean squares of genotypes for all the traits were significantly different ($P \leq 0.05$), while mean squares for majority of the traits were also highly significantly different ($P \leq 0.05$) in parents except tillers plant^{-1} and seed index. Similarly, the mean squares for most the traits in F_1 hybrids were also significantly different ($P \leq 0.05$). The analysis of variance for all the genotypes showed higher genetic variability among the genotypes which can further be exploited for various breeding programs to improve bread genotypes. Considering the F_2 hybrids, the progenies Benazir x Sarang and Benazir x Anmol-92 gave desirable results for yield and its associated traits, indicating that above mentioned genotypes may be proved reliable genetic resources. With regards to heritability percentage in broad sense, the F_2 progeny, Benazir x Sarang articulated high heritability for almost all studied traits, with the exception of grain yield plant^{-1}. The present findings suggested that most of the yield associated traits have been successfully transmitted. The information generated will be helpful for better understanding and selection of desirable material especially in advance generations.

Key words: Heritability, Genetic advance, F_2 population, Bread wheat

INTRODUCTION

It is mostly said that the wheat was the first crop domesticated by the human being on this planet (Sootaher *et al.,* 2020). Wheat (*Triticum aestivum* L.*)* belongs to family Poaceae, and it is one of the most important species grown throughout the world for the purpose of human consumption like bread making and bakery products (Debasis and Khurana, 2001). In recent studies, it is proved that approximately 95% of wheat grown in the world is hexaploid type ($2n = 6x = 42$). Among cereals, wheat is the second most important crop next to rice in production. The average global grain yield of major cereal crops was 2520 million tons in 2013-14, of which wheat contributed about 715.5 million tons. Being one of the most important food crops of the world, it occupies one-sixth (17%) of wheat acreage world over, feeding nearly half of the world population and providing one-fifth of total food calories and protein in human diet (Singh *et al*., 2016).

To obtain superior yield with potential resistance against biotic and abiotic stresses in Pakistani wheat cultivars, many breeding efforts had been done in the recent past; consequently, due to its bidirectional breeding approaches a number of promising cultivars with better adaptability have also been released. For the improvements of wheat crops, the assessment and isolation of promising breeding materials from introduced crop materials is the primarily step. Nonetheless, an efficient hybridization program may be a reasonable approach.

To evaluate the modern wheat varieties and advanced genotypes is very important for the further advancement of wheat. The efforts taken through plant breeding have been resulted in the development of numerous bread wheat cultivars possessing improved yield and grain characters. Modern cultivars and advanced genotypes with distinct agro-morphological and economic traits are now available as breeding materials (Zalewski, 2001).

Heritability information for an attribute accurately guides a plant breeder in its transmission from one generation to the next (Larik *et al*., 1989). Heritability is used to measure the phenotypic variance and it is connected with the influence of environment and heredity (Degewione *et al*., 2013). It explains the architecture of population and tell about a given character that up to which extent it could be transmitted to the next generations (Khan *et al.,* 2008). Heritability itself plays a very great role in helping a plant breeder, because it foresees the next progeny performance. It is beneficial and easy for a selection procedure when it is higher which results in a greeter response to the character selection.

Knowing about the degree of heritability, genetic variation, genetic diversity and genetic relationships in between the genotypes is an important task that makes wheat breeding programme more successful. Through knowledge about the existing genetic variability is required in order to develop bread wheat genotypes with desirable characters (Maniee *et a*l., 2009' Kahrizi *et al*., 2010). Comprehensive knowledge on the design, nature and extent of genetic variability helps plant breeders to pick up more diverse parental lines for crossing and hybridization (Shekhawat *et al*., 2001).

MATERIALS AND METHODS

Experimental Site, Material and Experimental Plan

The present research was conducted at the experimental station of Barley and Wheat Research Institute, ARI, Tandojam during 2016-2017 in order to study the inheritance in F_2 segregating populations of bread wheat in RCBD with three replications. There were total 15 genotypes including 9 parents and 6 progenies. The parents were Khirman, TD-1, Anomol-91, Marvi-2002, Kiran-95, Benazir, Sarang, Imdad, SKD-1, whereas Khirman x TD-1, Khirman x Anmol-91, Marvi-2002 x Kiran-95, Benazir x Sarang, Imdad x SKD-1 were the F2 hybrids in the experiment. The following nine important quantitative characters were studied whose methodology has been explained below.

1. Plant height (cm): Plant height was measured in centimeters from the ground level to the tip of the spike excluding awns at maturity.

2. Tillers plant^{-1}: The total number of tillers was counted randomly at the time of maturity. For this character, total fertile tillers from each plant in each replication were counted.

3. Spike length (cm): Length of the spike of main tiller was measured in centimeters from the base of the spike to the upper most spikelet excluding awns.

4. Spikelets spike^{-1}: The spikelets of main spikes from each tagged plant were counted and used as average spikelet spike^{-1} of each genotype.

5. Grains spike^{-1}: The total numbers of grains spike^{-1} of ten randomly tagged spikes were counted and average numbers of seeds spike^{-1} were calculated.

6. Grain yield plant^{-1} (g): After harvesting each plant was threshed separately with single plant, wheat thresher and cleaned seeds were obtained in the laboratory. Weight of grains was measured on electronic balance and yield plant^{-1} was recorded in grams.

7. 1000-grain weight (g): Thousand seed were counted and weighted in gram with the help of electronic balance in laboratory. The procedure was carried out after manual threshing of spikes and grains counted in thousand were placed in bags.

8. Biological yield plant^{-1} (g): Biological yield was recorded by weighing the total dry matter of the selected plants along with spike with the help of electronic digital balance in laboratory.

9. Harvest index (%): The harvest index was taken by the ratio of grain yield to biological yield. Harvest index was calculated according to following formula:

$$\mathbf{H.I.} = \frac{\text{Grain yield plant}^{-1}}{\text{Biological yield plant}^{-1}} \text{ x } 100$$

Statistical analysis

The collected data were subjected to the statistical analysis of variance according to the statistical methods described by Gomez and Gomez (1984), mean performance and LSD of all genotypes were calculated for the comparison of means according to Steel and Torrie (1980), heritability estimates were determined according to Falconer (1989) and genetic advance was calculated as suggested by Johnson (1955).

Formulae

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

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 p$ = VF_2 or Vp

$\sigma^2 e$ = Environmental variance

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

$\sigma^2 g$ = Genetic variance

$\sigma^2 g$ = VF_2 - Ve or Vp – Ve

h^2 = Heritability

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

G. A = Genetic advance

G. A = k x σ^2p x h^2

RESULTS

Analysis of Variance

Table 1 represents the analysis of variance for all the traits were studied. The result showed that the genotypes were significantly different for all the traits viz. plant height, no of tillers, main spike length, spikelets spike-^{1,} grains spike-^{1,} grain yield plant-^{1}, seed index, biological yield plant^{-1} and harvesting index. While parents and F_2 populations were significant like spikelets spike, grains yield and seed index while non-significant like plant height, number of tillers, spike length, grains spike and biological yield The results were depicted that considerable genetic variability exists in parents and their F_2 populations; therefore, data was further evaluated for estimating genetical parameters such as phenotypic variance, environmental variance, genetic variance, heritability.

Mean Performance of Parents and F_2 Hybrids

The means performance of nine characters of wheat genotypes are presented in the Table 2.

Plant height (cm): Plant height is a quantitative trait effecting other yield parameters. The results revealed that the highest value for height among parents was obtained for Khirman (104.81cm). however, the lowest value for plant height was shown by TD-1 (68.05cm). Among the hybrids, the cross Benazir x Sarang produced tallest plant height (93.83cm) and the shortest height was recorded for Khirman x TD-1 (75.26cm).

Tillers plant^{-1}: Productive tillers plant^{-1} have a straight impact on grain yield plant. The variety Imdad showed maximum number of tillers plant^{-1} (8.26) followed by Kiran-95 (7.53). In F_2 population, the number of tillers plant was maximum in the cross-combination Benazir x Sarang (9.66) and minimum was found in Marvi x Kiran (8.16).

Spike length (cm): Spike length is one the major traits that affects the grain yield. Longer spikes usually give higher yield of grain. It is obvious from the data that highest value for spike length was given by parent genotype Imdad (10.11cm) and the cross combination Marvi x Kiran (11.54cm) respectively.

Spikelets spike^{-1}: According to the data the genotype Khirman had maximum number of spikelets spike^{-1} (19.96), while minimum value was obtained by Anmol (16.43). Moreover, the cross combination Khirman x TD-1 recorded that maximum number of spikelets spike^{-1} (20.60) as compare to other hybrids.

Grains spike^{-1}: The mean value for grains spike^{-1} was highest (48.03) for TD-1 among parents and the cross combination Khirman x TD-1 (64.70) among crosses, respectively. Whereas as lowest grains spike^{-1} (36.70) were recorded of SKD-1 and the cross combination Imdad x SKD-1 (57.13).

Seed index (g): It is one of the essential characters that determine the actual grain yield. Highest weights for 1000 grains were recorded for TD-1 (5.76) and the lowest weight for 1000 grains was observed for Anmol (4.90). Among the cross combinations Khirman-TD and Khirman x Anmol had greater (5.66) weight for 1000 grains and the lowest was observed for Benazir x Marvi (5.16).

Grain yield plant^{-1} (g): The highest grain yield was observed for Benazir (10.19g) and the lowest (7.69g) amount of grain yield was produced by Sarang. Within the cross combination the cross Khirman x TD-1 revealed more grain yield (15.120 g) and Imdad x SKD-1 showed lowest grain yield value (12.14g) respectively.

Biological yield (g): Biological yield among the parent cultivars ranged from 16.89 g to 22.64. Maximum biological yield was produced by wheat variety Kiran-95 (22.64 g) and minimum yield was recorded for Sarang (14.50 g). Among the F_2 population the biological yield ranges from 24.41 to 30.73 g. The maximum biological yield among wheat hybrid was produced by cross combination Khirman x TD-1 (30.73 g), while Imdad-SKD-1 produced minimum biological yield of 24.41 g respectively.

Harvest index (%): Most of the wheat cultivars revealed good harvest index extending between 51.19 to 52.57%. Although, lowest harvest index of (51.19 %) Within the F_2 population maximum harvest index of 50.72% was observed in Benazir x Sarang, while the lowest harvest index of 49.89 was observed in Imdad-SKD-1.

Broad sense heritability and genetic advance estimates

The genetic variability studies in F_2 indicated that sufficient genetic variability in present in F_2 population. Generally, the phenotypic variance values for all the characters were greater than the genotypic variance values. The difference among both the parameters were small (the smaller differences between both the parameters revealed that the environmental effected was smaller for the traits to be expressed. All cross combinations exhibited moderate to high values for heritability and genetics advance.

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

Characters	Replication D.F.=2	Genotypes D.F.=15	Parents (P) D.F.=8	Hybrids (H) D.F.=5	P x H D.F.=1	Error D.F.=27
Plant height	0.494	385.49**	0.120^{ns}	2.456$^{n.s}$	122.42**	2.64
Tillers plant^{-1}	0.160	4.367**	0.074**	0.00889$^{n.s}$	0.84089**	0.02422
Spike length	0.166	2.843**	0.059^{ns}	0.51962$^{n.s}$	1.13732**	0.43799
Spikelets spike^{-1}	0.027	3.659**	1.051**	3.894**	5.4600**	0.10400
Grain spike^{-1}	0.120	43.264**	0.055**	0.2639$^{n.s}$	23.4339**	0.4419
Grain yield plant^{-1}	0.440	1.402**	0.011$^{n.s}$	0.08976*	4.78308**	0.05395
Seed index	0.001	0.285**	0.007*	0.00667**	0.13600**	0.00267
Biological yield plant^{-1}	15.125	13.825**	10.692**	0.2898$^{n.s}$	20.1336**	0.5095
Harvest index	0.700	0.593**	0.108^{ns}	1.02462**	0.28362**	0.12981

Table 2. Mean performance of parents and F_2 hybrid for yield and its related traits of bread wheat.

Genotypes	Plant height (cm)	Tillers plant^{-1}	Spike length (cm)	Spikelets Spike^{-1}	Grains spike^{-1}	Grain yield plant^{-1} (g)	Seed index (g)	Biological yield plant^{-1} (g)	Harvest index (%)
Khirman	104.81	5.66	8.52	19.96	46.56	8.62	4.93	16.89	52.12
TD-1	68.05	5.76	7.15	19.43	48.03	9.41	5.76	17.90	51.89
Anmol	98.36	7.16	7.99	16.63	39.10	9.40	4.90	17.90	52.31
Marvi	93.88	5.36	8.79	16.86	39.33	8.87	5.50	17.55	52.46
Kiran-95	82.48	7.53	9.66	17.30	43.50	8.75	5.70	22.64	52.57
Benazir	84.02	6.73	8.54	17.90	40.73	10.19	5.33	19.48	52.00
Sarang	97.44	4.36	7.59	18.06	41.13	7.69	5.46	14.58	52.39
Imdad	95.75	8.26	10.11	18.36	38.54	9.12	5.56	17.93	51.19
SKD-1	82.10	6.60	9.41	18.36	36.70	9.20	5.23	17.74	51.62
Average	**89.65**	**6.38**	**8.64**	**18.09**	**41.51**	**9.02**	**5.37**	**18.06**	**52.06**
F_2 Population									
Khirman x TD-1	75.263	8.9333	9.887	20.600	64.700	15.120	5.6667	30.737	50.323
Khirman x Anmol	88.920	8.5667	10.693	18.600	58.267	14.307	5.6667	28.820	50.697
Marvi x Kiran-95	90.270	8.1667	11.540	17.133	58.167	14.010	5.2333	27.733	50.480
Benazir x Sarang	93.837	9.6667	10.207	18.200	58.400	15.060	5.6333	29.687	50.727
Benazir x Marvi	88.973	9.1667	10.187	17.533	57.767	12.523	5.1667	24.810	50.543
Imdad x SKD-1	88.823	9.2333	9.993	16.933	57.133	12.147	5.5333	24.417	49.893
Average	87.68	8.95	10.41	18.16	59.07	13.86	5.48	27.70	50.44
LSD (5%)	2.957	0.283	1.204	0.586	1.209	0.422	0.042	1.298	0.655

Table 3. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for plant height.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	3152.19	13.59	1338.60	99.57	145.35
Khirman x Anmol	4448.15	16.40	4431.75	99.63	172.77
Marvi x Kiran-95	4529.34	15.77	4513.57	99.65	174.37
Benazir x Sarang	4898.89	5.21	4893.68	99.89	181.79
Benazir x Marvi	4399.26	2323.61	2075.65	47.18	81.37
Imdad x SKD-1	4383.59	1775.12	2608.47	59.57	102.43

Table 4. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for tillers plant^{-1}.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	44.75	8.97	35.78	79.96	13.91
Khirman x Anmol	41.02	16.97	24.05	58.63	9.76
Marvi x Kiran-95	37.73	25.24	12.49	33.10	5.29
Benazir x Sarang	52.11	15.27	36.84	70.70	13.27
Benazir x Marvi	47.23	7.76	39.47	83.57	14.93
Imdad x SKD-1	47.69	13.43	38.26	71.85	12.90

Table 5. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for spike length.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	54.98	16.36	38.62	70.24	13.54
Khirman x Anmol	63.84	12.58	51.26	80.30	16.68
Marvi x Kiran-95	82.49	11.76	70.72	85.74	20.25
Benazir x Sarang	58.08	8.88	49.20	85.71	16.79
Benazir x Marvi	57.95	20.68	37.27	64.31	12.73
Imdad x SKD-1	55.72	23.96	31.77	57.01	11.06

Table 6. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for spikelets spike^{-1}.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	237.85	24.09	213.75	89.87	36.04
Khirman x Anmol	155.02	18.05	136.97	88.36	28.60
Marvi x Kiran-95	169.27	22.96	146.31	88.44	29.24
Benazir x Sarang	183.45	17.27	166.18	90.59	31.90
Benazir x Marvi	43.66	13.52	30.14	69.04	11.86
Imdad x SKD-1	160.73	89.32	71.41	44.43	14.65

Table 7. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for grains spike^{-1}.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	2326.70	166.27	2160.43	92.85	116.45
Khirman x Anmol	1888.16	90.25	1797.91	95.22	107.58
Marvi x Kiran-95	1881.43	21.45	1859.98	98.86	111.49
Benazir x Sarang	1887.39	16.63	1880.76	99.12	112.26
Benazir x Marvi	161.01	53.01	108.00	67.07	22.13
Imdad x SKD-1	1817.09	355.50	1461.59	80.44	89.15

Table 8. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for grain yield plant^{-1}.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	127.59	22.01	105.58	82.75	24.30
Khirman x Anmol	74.15	50.32	23.83	47.37	8.74
Marvi x Kiran-95	66.73	45.28	21.45	47.37	8.29
Benazir x Sarang	51.74	35.11	16.63	47.37	7.30
Benazir x Marvi	87.33	21.51	65.82	75.37	18.31
Imdad x SKD-1	82.26	23.74	58.52	71.14	16.78

Table 9. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for seed index.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	351.02	143.98	207.04	58.98	28.73
Khirman x Anmol	327.09	21.88	305.21	93.31	43.88
Marvi x Kiran-95	289.09	21.48	267.62	92.57	40.92
Benazir x Sarang	334.97	60.16	274.82	82.04	39.04
Benazir x Marvi	281.77	151.25	130.52	46.32	20.22
Imdad x SKD-1	323.19	136.94	186.25	57.63	26.94

Table 10. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for biological yield plant^{-1}.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	184.18	82.10	102.08	55.42	19.56
Khirman x Anmol	464.37	120.87	343.50	73.97	41.44
Marvi x Kiran-95	428.93	156.85	272.08	63.43	34.16
Benazir x Sarang	490.68	145.82	344.86	70.28	40.48
Benazir x Marvi	342.70	81.86	260.84	76.11	36.63
Imdad x SKD-1	332.52	87.34	245.18	73.73	34.96

Table 11. Phenotypic variance, environmental variance, genotypic variance, heritability and genetic advance of F_2 populations for harvest index.

F_2 population	σ^2p	σ^2e	σ^2g	h^2 (%)	G. A.
Khirman x TD-1	1503.83	716.84	786.99	52.33	52.76
Khirman x Anmol	1429.50	81.16	1348.33	94.32	92.72
Marvi x Kiran-95	1416.28	186.49	1229.78	86.83	84.96
Benazir x Sarang	1430.10	83.25	1346.85	94.18	92.60
Benazir x Marvi	1421.19	128.80	1292.39	90.94	89.13
Imdad x SKD-1	1384.07	704.20	679.87	49.12	47.51

Plant height (cm): Table 3 represents the phenotypic, genotypic, heritability and genetic advance estimates for plant height. Among the F_2 population, the phenotypic variance and genotypic variance values were usually high for plant height. The highest values for phenotypic and genotypic variance of 4898.89 and 4893.68 respectively were obtained by the cross combination of Benazir x Sarang. High heritability and genetic advance were noticed for plant height. The maximum heritability and genetic advance were shown by Benazir x Sarang (99.89 and 181.79). While lowest heritability and genetic advance was showing that by Benazir x Marvi (47.18 and 81.37). Thus, these results indicate that high heritability and genetic advance for this trait will be efficient for a better breeding program.

Tillers plant^{-1}: The phenotypic variance and genotypic variance values for number of tillers plant^{-1} was ranged from 37.73-52.11 and 12.49-39.47. The highest phenotypic variance and genotypic variance values were observed for Benazir x Sarang (52.11 and 39.47). All cross combinations exhibited high heritability, while genetic advance was moderate to high except for the cross Khirman x Anmol (9.76). However, maximum heritability and genetic advance were observed for Benazir x Marvi (83.57 and 14.93) respectively (Table 4)

Spike length (cm): All the cross combinations showed low to moderate values for phenotypic variance and genotypic variance, as shown in Table 5, ranging from 54.98-82.49 and 31.77-70.72 respectively. The highest values for phenotypic variance and genotypic variance were observed for Marvi x Kiran-95 (82.49 and 70.72cm). Khirman x TD-1 revealed lowest phenotypic variance (54.98cm) for spike length, whereas the lowest genotypic variance for Benazir x Marvi (37.27). The heritability and genetic advance estimates of main spike ranged from 57.01-85.74 and 11.06-20.25. The highest values recorded of heritability and genetic advance were observed for Marvi x Kirhan-95. According to these findings it is clear that spike length individually cannot be selected for section and selection must be done in early generation.

Spikelets spike^{-1}: The phenotypic variance and genotypic variance values for spikelets spike^{-1} ranged from 43.26-237.85 and 30.14-213.75. The highest phenotypic variance and genotypic variance values were given by the cross Khirman x TD-1 (237.85 and 213.75), whereas the lowest phenotypic variance and genotypic variance were observed in both Benazir x Marvi (43.66 and 30.14). The heritability and genetic advance estimates were high to moderate heritability. The highest heritability and genetic advance were observed for Benazir x Sarang (90.59 and 31.90) while the lowest heritability was recorded Imdad x SKD-1 respectively (Table 6).

Grains spike^{-1}: Table 7 represented moderate to high phenotypic variance and genotypic variance values for grain spike^{-1} in F_2 population. Wheat combination Khirman x TD-1 obtained maximum phenotypic variance and genotypic variance values of 2326.70 and 2160.43 respectively. However, the lowest phenotypic variance and genotypic variance values recorded of 161.01 and 108.00 were recorded in the cross-combination Benazir x Marvi. Highest heritability value of 99.12 was observed for the cross Benazir x Sarang, closely followed by Marvi x Kiran-95 with heritability value of 98.86. Benazir x Sarang gave highest value for genetic advance (112.26) while the lowest value was observed for Benazir x Marvi (22.13).

Grain yield plant^{-1}(g): The phenotypic variance and genotypic variance values for grain yield plant^{-1} were low to high as shown in Table 8. The highest phenotypic variance and genotypic variance values were obtained for Khirman x TD-1 (127.59 and 105.58) respectively. However, the lowest phenotypic variance and genotypic variance values of 51.74 and 16.63 were recorded in the cross-combination Benazir x Sarang. Highest heritability value of 82.75 was observed for the cross Khirman x TD-1, closely followed by Benazir x Marvi with heritability value of 75.37. Khirman x TD-1 gave highest value for genetic advance (24.30) while the lowest value was observed for Benazir x Sarang (7.30).

1000-grains weight (g): The phenotypic variance and genotypic variance values given in Table 9 for seed index were low to moderate. Highest value for phenotypic variance was observed for Khirman x TD-1 (351.02) whereas the genotypic variance was recorded for Khirman x Anmol (305.21). The lowest phonotypic variance and genetics variance values of 281.77 and 130.52 were observed from the wheat cross Benazir x Marvi. The heritability values were usually high for seed index, ranging from 46.32 to 93.31. The highest heritability value was shown by the cross Khirman x Anmol (93.31), while the lowest value was 46.32 which was shown by the cross Benazir x Marvi. The genetic advance estimates were low to moderate for seed index ranging from 20.22-43.88. The highest value of 43.88 was observed for Khirman x Anmol, while the lowest genetic advance value was observed for Benazir x Marvi (20.22).

Biological yield plant^{-1}: The phenotypic variance and genotypic variance values for the parameter biological yield plant^{-1} were moderate to high ranging from 184.18-490 and 102.08-344.86. The highest values 490.68 and 344.86 were observed for Benazir x Sarang and lowest values of 184.18 and 102.08 were recorded for Khirman x TD, respectively. The heritability and genetic advance estimates for biological yield plant^{-1} was ranging from 5.42-76.11 and 19.40.48. The results indicate that selection for this trait will be beneficial (Table 10).

Harvest index (%): All the F_2 cross combinations possess moderate values of phenotypic variance and genotypic variance for harvest index as represented in table 11. The highest phenotypic variance value of 1503.83 was recorded from Khirman x TD-1 whereas in the cross Khirman x Anmol produced genotypic variance value of 1348.33. However, the lowest phenotypic variance and genotypic variance was noted from cross Imdad-SKD-1 (1384.07 and 679.87). The heritability and genetic advance estimates were high for the trait harvest index. The maximum values for heritability and genetic advance were given by Khirman x Anmol (94.32 and 92.72). The combinations Imdad-SKD-1 gave the lowest values for heritability and genetic advance (49.12 and 47.51).

DISCUSSION

Genetic variability is the basic utensil of a plant breeder which could be achieved through hybridization of diversified genetic material (Sootaher et al., 2020). It was observed that most of the traits in the genotypes of wheat possessed a large amount of genetic variability which gives the surety of these genotypes for being used for the breeding purposes so as to improve the grain yield and its linked attributes. These results were in paradox with Deoraj et al. (2016), Shah et al. (2016) and Kachi *et al.* (2020).

Plant height is a key trait in bread wheat and it has been well documented that dwarf wheat varieties not only enhance grain yield but are lodging resistance. The heritability and genetic advance for trait plant height showed that high heritability with high genetic advance shown by cross Benazir × Sarang. The high heritability resulted due to lower environmental variance and higher genetic variance for plant height in this cross, referring existence of genetic variability in F_2 population and desirable level of plant height may be effectively selected from this cross. However, rest of the crosses showed low to moderate heritability. Earlier researchers like Memon *et al*. (2007) and Kumar *et al*. (2013) reported higher heritability for plant height. Among yield components, number of tillers plant^{-1} is important plants attribute which increase grain yield in wheat. To evolve high yielding varieties, not only grain yield but yield related traits like number of tillers plant^{-1} also required a special attention. The results regarding the heritability and genetic advance for trait tillers plant^{-1} demonstrated that moderate heritability and low genetic advance was exposed by cross Benazir × Marvi. The moderate heritability is due to low environmental variance and low genetic variance for this cross, whereas rest of the crosses revealed low heritability. Previous investigators like Ahmed *et al*. (2013) and Kalimullah *et al*. (2012) informed moderate heritability for trait tillers plant^{-1}, while on contrasting, Kumar *et al*. (2015) found against our results for trait tillers plant^{-1}.

Spike length is a character of most significance, because larger spike is considered to produce more grains resulting in higher yield plant^{-1}. The trait spike length revealed that moderate heritability and low genetic advance was shown by cross Benazir x Sarang. The moderate heritability is due to similar environmental variance and genetic variance for spike length in this cross, while rest of the F_2 progenies displayed low heritability. Previous scientist like Avinashe *et al*. (2015) stated higher heritability for spikelets spike^{-1}, while Khirman × Imdad-05 expressed low heritability and high genetic advance for grains spike^{-1}. The low heritability is due to high environmental variance and low genetic variance for spike length in this cross. Previous workers like Ayciek and Yildrim (2006) and Eid (2009) also reported low heritability for grains spike^{-1}. The wheat breeding studies have been reported that spikelets spike^{-1} may directly contribute towards grain yield. Heritability estimates varied from 7.39 to 51.32% (Table-6), however genetic advance varied between 0.27 and 5.30. The cross Benazir x Sarang showed high heritability (h^2=51.32%) for spikelets spike^{-1}. Whereas, higher genetic advance (GA=5.30) than rest of the crosses was also observed from the same F_2 cross. This indicated that this trait could be improved by direct selection to enhance the grain yield in wheat cultivars. Earlier scientists like Jan *et al.* (2015) reported low heritability for spike length, while Cheema *et al*. (2006) acquired high and moderate heritability, respectively, for spikelets spike^{-1}.

Grains spike^{-1} is a yield related trait. It relies on some other traits like spike density, spike length and spikelet spike^{-1}. The higher heritability percentage (h^2=31.95%) among the F_2 progenies was recorded in Benazir x Sarang coupled with high genetic advance of 28.27. Similar results were also found by Sial *et al.* (2007) and Khan et al. (2015). These results showed that grains spike^{-1} could be used in direct selection criteria for grain yield improvement. However, grain yield is very important for development of crop varieties for farmer's point of view. However, weight of grains should also be considered while working on grain spike^{-1} because only healthy grains with proper weight can contribute to high yield. Yield is a character controlled by polygenes and is the result of interplay between many genetic and non-genetic components. Grain yield plant^{-1} showed that high heritability and high genetic advance displayed by cross Khirman x TD-1. The high heritability is due to low environmental variance and high genetic variance for this cross, while rest of the crosses displayed low heritability. Earlier worker like Waqar *et al.* (2008), Iftikhar *et al*. (2013) and Kumar *et al*. (2014) testified higher heritability for grain yield plant^{-1}; however, found the results against this research for the trait yield plant^{-1}.

1000-grain weight revealed significant difference among the genotypes. The heritability and genetic advance for trait 1000-grain weight exhibited that moderate heritability and low genetic advance was exposed by cross Khirman × Anmol. The moderate heritability is due to similar environmental variance and genetic variance for this cross, where other crosses showed moderate and low heritability. These estimates of phenotypic and genotypic variances were similar to the results of Sharma *et al.* (2006) and Saleem et al. (2016). The crosses having higher values for variances also showed high heritability and genetic advance values. Higher heritability estimates were also reported by Rasal *et al.* (2008) while Gupta and Verma (2000) and Mandal *et al.* (2008) reported for high heritability value. The phenotypic variance and genotypic variance values for the parameter biological yield plant^{-1} were moderate to high ranging from 184.18-490 and 102.08-344.86. The highest values 490.68 and 344.86 were observed for Benazir x Sarang and lowest values of 184.18 and 102.08 were recorded for Khirman x TD, respectively. The heritability and genetic advance estimates for biological yield plant^{-1} were ranging from 5.42-76.11 and 19.40.48. Analysis of variance revealed important differences as suggested by Bergale *et al.* (2001), Dwidvedi *et al.* (2004) and Asif *et al.* (2004). The highest phenotypic variance value of 1503.83 was recorded from Khirman x TD-1 whereas in the cross Khirman x Anmol produced genotypic variance value of 1348.33. However, the lowest phenotypic variance and genotypic variance was noted from cross Imdad-SKD-1 (1384.07 and 679.87). The heritability and genetic advance estimates were high for the trait harvest index. The maximum values for heritability and genetic advance were given by Khirman x Anmol (94.32 and 92.72). The combinations Imdad-SKD-1 gave the lowest values for heritability and genetic advance (49.12 and 47.51). Ali *et al.* (2013), Ijaz et al. (2015) and Khan and Hassan (2017). and also reported that high heritability values for most of the characters in wheat.

CONCLUSION

The analysis of variance for all the varieties (include nine parents and their six F_2 progenies) showed that all the characters under study differed significantly ($P \leq 0.05$), offering the higher genetic variability among the genotypes which can more to be exploited for different breeding programs to progress bread genotypes. Considering the F_2 hybrids, the progenies Benazir × Sarang and Benazir × Anmol gave desirable results for yield and its associated traits, indicating that above mentioned genotypes may be proved reliable genetic resources. With regards to heritability percentage in broad sense, the F_2 progeny Benazir x Sarang expressed high heritability for almost all studied traits, with the exception of grain yield plant. The present findings suggested that most of the yield associated traits have been successfully transmitted. The information generated will be helpful for better understanding and selection of desirable material especially in advance generations.

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