RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
56 (2) 505-518, 2024
http://doi.org/10.54910/sabrao2024.56.2.5
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

GENETIC VARIABILITY, HERITABILITY, AND GENETIC GAIN IN F_3 POPULATIONS OF BREAD WHEAT (*TRITICUM AESTIVUM* L.) FOR PRODUCTION TRAITS

A. ALI[1*], M. JAVED[2], M. ALI[3], S.U. RAHMAN[4], M. KASHIF[2], and S.U. KHAN[1]

[1]Department of Plant Breeding and Genetics, University of Agriculture, Peshawar, Pakistan
[2]Department of Agronomy, University of Agriculture, Peshawar, Pakistan
[3]Department of Agronomy, College of Agriculture, University of Sargodha, Sargodha, Pakistan
[4]Department of Horticulture, College of Agriculture, University of Sargodha, Sargodha, Pakistan
Corresponding author email: akbaragrian@gmail.com
Email addresses of co-authors: mansoor92@aup.edu.pk, m.alipk77@gmail.com, saeedhorticulturist@gmail.com, m.kashifaup1@gmail.com, saifullahkhan066@gmail.com

SUMMARY

Wheat is a globally dominant staple food and one of the highest-consumed products because of its taste, texture, and bread quality. Genetic variability, heritability, and genetic advancement are essential to learning about the yield potential of crops. Finding out wheat's heritability and genetic advance led to this study's design at the research area of the Department of Plant Breeding and Genetics, the University of Agriculture, Peshawar, in 2021–2022. The experiment began using 27 wheat genotypes comprising nine parents and 18 F_3 populations evaluated in a random complete block design (RCBD) with three replications. Highly significant variations observed came from analysis of variance among parents and F_3 populations for days to heading, plant height, tillers plant^{-1}, flag leaf area, spikelet's spike^{-1}, the number of grains spike^{-1}, a thousand-grain weight, and biomass yield. The highest heritability estimates of 0.82, 0.87, 0.88, 0.89, 0.86, 0.76, 0.88, 0.86, 0.89, 0.87, 0.86, and 0.84 emerged from Watan × Janbaz, Fakhr-e-Sarhad × AUP-5008, Pirsabak-2005 × AUP-5008, Barsat × Tatara, Fakhr-e- Sarhad × Tatara, Pirsabak-2005 × Tatara, Watan × Tatara, Watan × AUP-5008, AUP-4008 × Janbaz, Barsat × Tatara, Watan × AUP-5008, and Barsat x Janbaz, respectively, for productive traits. The highest values of genetic advance were 32.71, 20.33, 35.08, and 34.24 for Fakhr-e-Sarhad × AUP-5008, Fakhr-e-Sarhad × Janbaz, Pirsabak-2005 × Tatara, and Watan × Tatara, respectively. The parental genotypes Janbaz and AUP-5008 were the most promising genotypes recommended for further evaluation in upcoming breeding schemes.

Key words: Wheat (*Triticum aestivum* L.), F_3 populations, genetic variability, heritability, genetic gain, production traits

Communicating Editor: Prof. Dr. Z.A. Soomro

Manuscript received: September 9, 2023; Accepted: November 29, 2023.
© Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2024

Citation: Ali A, Javed M, Ali M, Rahman SU, Kashif M, Khan SU (2024). Genetic variability, heritability, and genetic gain in F_3 populations of bread wheat (*Triticum aestivum* L.) for production traits. *SABRAO J. Breed. Genet.* 56(2): 505-518. http://doi.org/10.54910/sabrao2024.56.2.5.

Key findings: The analysis of variance showed highly prominent variation among genotypes, parents, and F_3 populations for most traits observed. The parental genotypes, Janbaz and AUP-5008, and F_3 populations, Watan × Janbaz, Fakhr-e-Sarhad × AUP-5008, and Pirsabak-2005 × AUP-5008, exhibited the shortest plants, lengthiest spikes, highest spikelet's spike^{-1}, higher grains spike^{-1}, early maturing, and remarkably high thousand-grain weight. Saleem-2000 × Janbaz hybrid was smaller and early ripening, with the highest grain yield spike^{-1}, biological, and 1000-grain weight. The hybrid, Watan × Tatara, showed shorter plants, long spikes, a broader flag leaf, the shortest days to heading and maturity, the highest grain yield spike^{-1}, maximum 1000-grain weight, and higher biological yield. Therefore, these genotypes have the potential to benefit future breeding programs.

INTRODUCTION

Bread wheat (*Triticum aestivum* L.), having 42 chromosomes and a hexaploid, belonged to the family Poaceae. An annual, self-pollinating crop, it is also a long-day plant based on photoperiodism. It basically originated in South-East Asia. It is the second-largest source of nutrients, including food, feed, fodder, and energy, and is the global staple food for many populations. Wheat provides 36% food to the whole world and 20% of energy and is a staple used almost worldwide, which accounts for approximately 240 million ha compared with other cultivated crops (Babar *et al*., 2022).

Wheat cultivation in irrigated and rainfed conditions totaled about 8.74 million ha, while in Khyber Pakhtunkhwa, the total cultivated area was 0.74 million ha, yielding 1.36 million tons and producing about 1,860 kg ha^{-1} (Babar *et al*., 2022). One of the chief causes of wheat yield decline is cultivating low-genetic potential varieties (Prasad *et al*., 2021). According to an estimate, more than 60% of Pakistan's people entirely depend on wheat for their daily diet (Shah *et al*., 2017). Wheat has multiple uses as the staple food of the masses and the main ingredient in animal feeds. The recorded wheat cultivation in the country occurred on an area of 8.74 million ha during 2018–2019, indicating a 0.6% decrease in area for this crop over the preceding year (GOP, 2019).

For any breeding program, the vital prime parameter is genetic variability, which provides the knowledge for selecting diverse parents that can benefit future hybridization programs. The genetic potential of varying genotypes' distinct morphological yield traits is essential for a successful breeding program. (Babar *et al*., 2022). Genetic variability is the basis for enhancing plant breeding and varietal improvement activities. The breeder should identify the variation in desired characteristics and skillfully select the desired crop's improvement. Genetic progress is a primary tool to develop high-yielding and drought-tolerant varieties (Seyoum and Sisay, 2021). Heritability is the transfer of phenotypic and genotypic traits from parents to offspring, and it is the best indication for breeders to evaluate penetrance and expressivity by calculating the variance by crossing the parental genotypes.

Genetic gain is the improvement of crops in the mean genetic value of the selected plants per breeding cycle. Genetic advance shows the breeder's progress in the experimental operation and makes them decide the research's right direction. Therefore, heritability and genetic advance are the tools researchers widely apply. Considering these, an effort has begun in the presented study to evaluate a set of promising genotypes, with the objectives of estimating the variability, heritability, and genetic advance for yield and yield-component traits.

Heritability accompanied by high genetic gain would be a more beneficial tool for predicting the ensuing effect in genotype selection for yield and yield-related traits. Many authors have reported the presence of variability, heritability, and genetic gain in different yield-related features of bread wheat improvement (Dabi *et al*., 2019; Seyoum and Sisay*,* 2021). With these traits' importance in mind, a promising study transpired to evaluate the genetic variability, heritability, and genetic advances among F_3 populations for productive traits of bread wheat.

MATERIALS AND METHODS

The study to evaluate the genetic diversity in F_3 populations of bread wheat commenced in November 2021–2022 at the University of Agriculture Peshawar at an experimental block located at a longitude of 34.026° N, a latitude of 71.4814° E, and an altitude of 359 m above sea level. The soil class was loam (32.6% sand, 42.56% silt, and 20% clay). According to 30-year climatic data, Peshawar has a warm to hot, semi-arid, and subtropical climate, with a mean annual temperature of 22.7 °C (72.9 °F) and an annual rainfall of 445 mm. The experimental materials came from the University of Agriculture, Peshawar (UAP); the Cereal Crops Research Institute (CCRI), Nowshera; the Nuclear Institute of Food and Agriculture (NIFA), Peshawar; and the Pakistan Agriculture Research Centre (PARC), Islamabad, Pakistan (Table 1). Allocating the wheat genotypes in an RCBD with three replications to minimize environmental influences comprised a plant-to-plant distance of 15 cm and a row-to-row distance of 30 cm in four rows with a length of 3 m. Data sampling ensued on 10 randomly selected plants from each entry. All agronomic cultural practices require uniform applications to prevent environmental errors. For proper computation, data recording included days to heading, days to maturity, plant height, tillers plant^{-1}, flag leaf area, spikelet's spike^{-1}, spike length, grains spike^{-1}, a 1000-grain weight, grain yield spike^{-1}, biological yield, and harvest index at their proper time.

Statistical analysis

Analysis of variances to test the significance for each trait had estimates as per methodology given by Panse and Sukhatme (1967).

Heritability

Broad sense (h^2) calculations employed the formula by Burton and Vane (1953):

$$H^{B.S} = \frac{VG}{VP} X\ 100$$

Where: VG = Genotypic variance and VP = Phenotypic variance.

Genetic advance

Computation for the genetic advance comprised of taking the percent of the mean using the following formula:

$$GAM = \frac{GA}{\bar{x}}\ X\ 100$$

Where: GAM = the genetic advance as the percent of the mean, GA = the genetic advance, and $\bar{x}$ = the grand mean. Genetic advance categories comprised low (0% to 10%), medium (10% to 20%), and high (>20%) rates, as suggested by Falconer *et al.* (1996).

Table 1. List of wheat genotypes including nine parents and 18 F_3 populations used in the experiment.

Parental cultivars	Research Institutes	F_3 populations	
Janbaz	UAP	AUP-4008 × Janbaz	Saleem-2000 × Janbaz
Pirsabak-2005	CCRI	Fakhr-e-Sarhad × Tatara	Watan × AUP-5008
Saleem -2000	NIFA	AUP-4008 × AUP-5008	Saleem-2000 × AUP-5008
Fakhr-e-Sarhad	NIFA	Pirsabak-2005 × Janbaz	Watan × Janbaz
Barsat	NIFA	Pirsabak-2005 × Tatara	Pirsabak-2005 × AUP-5008
AUP-5008	UAP	Fakhr-e-Sarhad × AUP-5008	Barsat × AUP-5008
AUP-4008	UAP	Fakhr-e-Sarhad × Janbaz	Barsat × Janbaz
Tatara	NIFA	AUP-4008 × Tatara	Watan × Tatara
Watan	PARC	Barsat × Tatara	Saleem-2000 × Tatara

UAP: University of Agriculture, Peshawar, Pakistan; CCRI: Cereal Crops Research Institute, Nowshera, Pakistan: NIFA: Nuclear Institute of Food and Agriculture, Peshawar, Pakistan; PARC: Pakistan Agriculture Research Centre, Islamabad, Pakistan.

RESULTS AND DISCUSSION

Days to heading

Days to heading mean squares exhibited the highest variance ($P \leq 0.01$) for parents, F_3 populations, and parents vs. F_3 populations (Table 2). The mean value for headings was 118.85 days for parents, while for F_3 populations, it was 120.93 days. The mean values for days to headings ranged from 114.33 to 123.33 (Table 3). In parents, the maximum number of days to heading (123.33) was apparent for genotype AUP-4008, while the lowest (114.00) emerged for genotype Watan. Among F_3 populations, the maximum days to heading (125.67) were evident for Pirsabak-2005 × AUP-5008, while the minimum days to heading (115.00) were notable for Watan × Tatara. Almost similar mean values and ranges for days to heading have also resulted from the work by Prasad *et al*. (2021).

The broad sense of heritability for days to heading varied in estimates from 0.31 to 0.88. The highest heritability (0.88) appeared from a cross combination, Watan × Tatara, followed by AUP-4008 × AUP-5008 (0.87) and Barsat × Tatara (0.83), with the lowest heritability (0.31) arising from Watan × Janbaz (Table 5). The highest genetic progress (35.08 days) was notable for Pirsabak-2005 × Tatara, followed by AUP-4008 × AUP-5008 (33.40 days) and Saleem-2000 × Tatara (32.57 days). Meanwhile, the lowest genetic advance (0.06 days) was apparent for the cross combination, Watan × Tatara (Table 6). The highest heritability shows less environmental influence on days to heading. Taneva *et al.* (2019) showed low genetic advance and high heritability for most wheat crosses. Similar agreements were also prominent from previous researchers for plant height (Bazai *et al*., 2020), while the observed days to heading, grain filling period, and spike length by Meles *et al*. (2017) slightly differed from the above findings.

Days to maturity

Analysis of variances for days to maturity exhibited considerable variation ($P \leq 0.01$) for parents and F_3 populations (Table 2). The mean number of days to maturity for parents was 153.22 days, and for F_3 populations, it was 153.98 days. The mean numbers for days to maturity ranged from 151.33 to 156.67 days (Table 3). In parents, the maximum days to reach maturity was 156.67 days, documented for genotype AUP-4008, with the minimum recording of 150.67 days for genotype Barsat. Days to maturity trait were highest (156.33 days) among F_3 populations for the crosses Fakhr-e-Sarhad × Janbaz and Saleem-2000 × Janbaz, closely followed by Pirsabak-2005 × Janbaz (156.00 days), and the least days to maturity (150.67 days) showed for Watan × Tatara.

The estimates of heritability for days to maturity ranged from 0.24 to 0.87 (Table 5). The highest heritability (0.87) was noticeable for Watan × AUP-5008, followed by AUP-4008 × Janbaz (0.86), AUP-4008 × AUP-5008 (0.86), and Pirsabak-2005 × AUP-5008 (0.84). The lowest heritability (0.24) was evident for Barsat × Tatara. The utmost genetic advance (34.24 days) resulted in cross Watan × Tatara, followed by Saleem-2000 × AUP-5008 (33.58 days) and Saleem-2000 × AUP-5008 (33.57 days). However, the lowest genetic advance (0.35) surfaced for Barsat × Janbaz (Table 6). Differences among genotypes, parents, and crosses having moderate to high heritability for days to reach physiological maturity with low genetic advance have also been outcomes of a study (Khan and Hassan, 2017). In contrast with the presented results, the findings of Zerga *et al*. (2016) recorded high heritability with less genetic advance for this trait, probably due to environmental influences.

Plant height

Data regarding mean square revealed ($P \leq 0.01$) significance among the genotypes, parents, and F_3 populations for plant height. The plant height averages expanded from 72.6 to 92.33 cm (Table 2). Highly significant differences in plant height were present among parents, F_3 populations, and parents vs. F_3 populations (Table 3). Selecting tall plants could be helpful for biological yield. The maximum plant height (91.60 cm) was visible

Table 2. Analysis of variance of different characteristics of wheat genotypes.

SOV	DF	DH	DM	PH	TPP	FLA	SLPS	SL	GPS	TGW	GYS	BY	HI
Reps	2	62.31	42.12	52.34	0.05	68.03	1.73	2.16	6.57	10.15	0.02	0.3	56.57
Genotypes	26	29.74**	9.31*	95.18**	5.99**	74.43**	4.83**	1.25**	63.79**	36.33**	0.06**	0.45**	89.85**
Parents	8	33.51**	11.08*	130.50**	5.53**	118.08**	7.34**	1.34**	39.53**	31.39**	0.01	0.35**	127.93**
F_3	17	25.16**	8.41*	86.47**	6.15**	44.11**	2.94**	1.02*	69.43**	36.95**	0.09**	0.52**	76.26*
P vs. F_3's	1	77.43**	10.38	3.21	6.80**	240.78**	25.92**	4.43**	162**	65.23**	0.01	0	16.17
Error	52	9.36	5.15	15.51	0.56	17.92	1.14	0.44	10.98	5.23	0.01	0.06	41.55
CV (%)	--	2.54	1.48	4.8	10.93	10.94	5.23	6.31	5.75	6.39	15.54	18.59	15.16

*, ** = significant at 5% and 1% probability, respectively.

Abbreviations: DH - days to heading, DM - days to maturity, PH - plant height, TPP - tillers plant^{-1}, FLA - flag leaf area, SLPS - spikelet's spike^{-1}, SL - spike length, GPS - grains spike^{-1}, TGW - 1000-grain weight, GYS - grain yield spike^{-1}, BY - biological yield, HI -harvest index.

Table 3. Mean values for days to heading, days to maturity, plant height, tiller plant^{-1}, flag leaf area, and spikelet's spike^{-1} of wheat genotypes.

Genotypes	DH	DM	PH	TPP	FLA	SLPS
Parents						
AUP-4008	123.33	156.67	84.33	6.47	35.46	21.93
Pirabak-2005	119.33	154.67	91.60	5.53	50.23	18.73
Fakhr-e-Sarhad	120.67	151.33	86.47	10.40	33.62	20.20
Saleem-2000	114.33	151.67	74.27	7.13	29.75	18.20
Barsat	118.67	150.67	76.27	7.13	40.32	19.67
Watan	114.00	152.33	72.73	6.40	32.14	17.40
Janbaz	120.67	154.67	83.13	7.93	31.36	21.53
Tatara	116.33	153.67	84.80	7.40	34.3	19.40
AUP-5008	122.33	153.33	82.53	7.07	39.15	19.53
Means	118.85	153.22	81.79	7.27	36.25	19.62
F_3 populations						
AUP-4008 × Janbaz	123.33	152.00	86.53	7.40	41.83	22.47
AUP-4008 × Tatara	119.33	155.00	84.27	6.93	39.25	21.13
AUP-4008 × AUP-5008	122.33	153.33	84.00	6.87	38.46	20.60
Pirsabak-2005 × Janbaz	121.33	156.00	92.33	5.53	44.64	21.80
Pirsabak-2005 × Tatara	123.33	154.67	90.67	6.67	44.87	20.87
Pirsabak-2005 × AUP-5008	125.67	155.00	82.53	4.73	49.80	22.73
Fakhr-e-Sarhad × Janbaz	122.67	156.33	80.13	6.53	36.13	21.27
Fakhr-e-Sarhad × Tatara	122.33	155.33	82.33	8.00	38.10	19.93
Fakhr-e-Sarhad × AUP 5008	125.33	154.00	78.87	7.80	42.77	20.07
Saleem-2000 × Janbaz	119.33	156.33	72.60	4.73	37.24	21.80
Saleem-2000 × Tatara	118.67	153.67	80.07	8.40	40.29	20.47
Saleem-2000 × AUP-5008	118.00	151.33	87.00	9.80	35.99	20.07
Barsat × Janbaz	121.00	154.33	80.40	6.07	39.60	21.40
Barsat × Tatara	119.67	153.67	77.07	5.93	39.82	19.67
Barsat × AUP-5008	116.67	151.67	78.47	5.07	40.31	19.53

Table 3. (cont’d).

Genotypes	DH	DM	PH	TPP	FLA	SLPS
Watan × Janbaz	119.33	154.33	74.20	5.07	33.34	19.67
Watan × Tatara	115.00	150.67	90.00	8.40	37.71	20.07
Watan × AUP-5008	123.33	154.00	78.40	5.93	38.37	21.27
Means	120.93	153.98	82.22	6.65	39.91	20.82
LSD $_{(0.05)}$	5.012	3.72	6.45	3.37	6.94	1.75

Table 4. Mean values for spike length, grains spike$^{-1,}$ grain yield spike^{-1}, thousand grain weight, biological yield, and harvest Index of wheat genotypes.

Genotypes	SL	GPS	GYS (g)	TGW (g)	BY (kg)	HI
Parents						
AUP-4008	10.67	56.93	0.50	33.10	1.15	44.95
Pirsabak-2005	10.93	52.67	0.53	36.17	1.70	32.47
Fakhr-e-Sarhad	9.80	54.47	0.60	41.30	2.05	29.51
Saleem-2000	9.40	53.67	0.50	34.57	1.13	44.96
Barsat	11.13	58.40	0.52	37.90	1.28	41.75
Watan	9.33	56.13	0.52	39.13	1.17	44.98
Janbaz	9.80	49.87	0.64	41.67	1.52	42.93
Tatara	10.00	62.60	0.58	36.47	1.22	48.66
AUP-5008	10.67	55.73	0.44	33.00	0.95	46.78
Means	10.19	55.60	0.54	37.03	1.35	41.887
F$_3$ populations						
AUP-4008 × Janbaz	10.80	55.73	0.54	37.50	1.47	37.19
AUP-4008 × Tatara	10.87	60.87	0.65	34.97	1.44	46.09
AUP-4008 × AUP-5008	10.27	50.60	0.64	37.30	1.45	44.91
Pirsabak-2005 × Janbaz	11.27	65.00	0.35	36.87	0.92	37.55
Pirsabak-2005 × Tatara	10.93	60.27	0.53	37.57	1.29	42.27
Pirsabak-2005 × AUP-5008	12.27	57.80	0.26	24.87	0.70	37.93
Fakhr-e-Sarhad × Janbaz	10.80	56.93	0.42	38.10	1.03	40.57
Fakhr-e-Sarhad × Tatara	10.13	59.67	0.59	33.83	1.43	42.08
Fakhr-e-Sarhad × AUP-5008	10.40	57.87	0.74	37.40	1.81	40.63
Saleem-2000 × Janbaz	10.60	68.00	0.32	31.67	0.77	41.50
Saleem-2000 × Tatara	9.80	55.80	0.63	37.53	1.85	34.56
Saleem-2000 × AUP-5008	10.67	62.20	0.82	38.33	1.98	42.09
Barsat × Janbaz	11.47	53.20	0.45	36.10	1.00	45.74
Barsat × Tatara	10.67	56.67	0.67	32.93	1.16	57.74
Barsat × AUP-5008	10.93	66.27	0.47	35.73	1.02	45.96
Watan × Janbaz	10.27	50.73	0.50	31.57	1.13	44.45
Watan × Tatara	10.07	59.87	0.97	38.37	2.20	44.40
Watan × AUP-5008	10.20	57.20	0.63	31.70	1.42	45.37
Means	10.69	58.59	0.57	35.13	1.33	42.83
LSD $_{(0.05)}$	1.09	12.51	0.33	9.11	0.82	74.42

Table 5. Heritability estimates for various characteristics of wheat genotypes.

F$_3$ populations	DH	DM	PH	TPP	FLA	SLPS	SL	GPS	THW (g)	GYS (g)	BY (kg)	HI
AUP-4008 × Janbaz	0.80	0.86	0.81	0.29	0.25	0.45	0.81	0.44	0.79	0.72	0.83	0.47
AUP-4008 × Tatara	0.56	0.33	0.62	0.48	0.25	0.73	0.81	0.37	0.45	0.88	0.85	0.49
AUP-4008 × AUP-5008	0.87	0.86	0.54	0.76	0.23	0.41	0.67	0.20	0.85	0.55	0.54	0.58
Pirsabak 2005 × Janbaz	0.37	0.36	0.43	0.45	0.33	0.24	0.23	0.50	0.73	0.86	0.79	0.52
Pirsabak-2005 × Tatara	0.57	0.58	0.66	0.57	0.52	0.39	0.85	0.76	0.79	0.48	0.39	0.56
Pirsabak 2005 × AUP-5008	0.51	0.84	0.46	0.18	0.54	0.87	0.76	0.73	0.85	0.51	0.61	0.39
Fakhr-e-Sarhad × Janbaz	0.57	0.59	0.79	0.55	0.81	0.35	0.67	0.60	0.68	0.83	0.47	0.62
Fakhr-e-Sarhad × Tatara	0.75	0.51	0.46	0.86	0.83	0.50	0.79	0.62	0.55	0.70	0.70	0.30
Fakhr-e-Sarhad × AUP-5008	0.37	0.27	0.36	0.37	0.50	0.73	0.88	0.64	0.76	0.87	0.77	0.41
Saleem-2000 × Janbaz	0.52	0.58	0.43	0.30	0.49	0.43	0.41	0.28	0.84	0.85	0.85	0.43
Saleem-2000 × Tatara	0.49	0.78	0.80	0.67	0.63	0.60	0.83	0.28	0.22	0.83	0.50	0.29
Sal 2000 × AUP-5008	0.54	0.44	0.44	0.75	0.86	0.79	0.84	0.63	0.76	0.73	0.68	0.55
Barsat x Janbaz	0.72	0.69	0.40	0.47	0.23	0.70	0.38	0.35	0.87	0.23	0.42	0.84
Barsat × Tatara	0.83	0.24	0.42	0.71	0.89	0.35	0.50	0.53	0.39	0.89	0.41	0.52
Barsat × AUP-5008	0.51	0.66	0.72	0.34	0.34	0.46	0.67	0.43	0.68	0.23	0.39	0.38
Watan × Janbaz	0.31	0.65	0.82	0.50	0.39	0.72	0.66	0.63	0.46	0.78	0.78	0.82
Watan × Tatara	0.88	0.70	0.46	0.20	0.85	0.26	0.75	0.53	0.45	0.84	0.58	0.44
Watan × AUP-5008	0.76	0.87	0.75	0.65	0.87	0.76	0.86	0.33	0.76	0.74	0.86	0.42

Abbreviations: DH - days to heading, DM - days to maturity, PH - plant height, TPP - fertile tillers plant^{-1}, FLA - flag leaf area, SLPS - spikelets spike^{-1}, SL - spike length, GPS - grains spike $^{-1}$, TGW - 1000-grain weight, GYS - grain yield spike^{-1}, BY - biological yield, and HI - harvest index.

Table 6. Genetic advance values in percent of means for various characteristics of wheat genotypes.

F$_3$ populations	DH	DM	PH	TPP	FLA	SLPS	SL	GPS	THW(g)	GYS(g)	BY(kg)	HI
AUP-4008 × Janbaz	10.98	0.43	8.93	1.26	2.23	4.79	0.08	6.74	2.24	0.12	0.41	4.63
AUP-4008 × Tatara	7.15	2.54	13.18	4.86	5.18	2.31	1.75	5.16	1.92	0.16	0.32	0.23
AUP-4008 × AUP-5008	33.40	13.94	10.54	1.43	2.00	5.22	0.54	1.01	3.78	0.08	0.30	5.76
Pirsabak-2005 × Janbaz	13.70	7.68	0.29	2.39	2.19	0.44	0.33	1.98	4.25	0.14	0.62	4.69
Pirsabak-2005 × Tatara	35.08	9.74	7.48	0.61	3.51	0.14	0.73	4.25	2.03	0.07	0.01	8.26
Pirsabak-2005 × AUP-5008	9.18	13.79	0.13	0.19	12.63	3.13	2.87	4.22	5.62	0.05	0.21	3.84
Fakhr-e-Sarhad × Janbaz	1.83	2.17	7.37	0.60	20.33	0.74	1.61	3.39	3.27	0.21	0.23	7.67
Fakhr-e-Sarhad × Tatara	22.99	1.38	3.65	3.21	16.84	0.82	0.73	2.73	3.60	0.10	0.47	3.46
Fakhr-e-Sarhad × AUP-5008	18.37	0.96	32.71	0.26	4.00	0.79	3.47	2.27	4.63	0.38	0.45	4.26
Saleem-2000 × Janbaz	28.35	4.11	0.45	0.37	7.23	0.80	2.08	0.93	3.53	0.17	0.03	3.29
Saleem-2000 × Tatara	32.57	13.18	4.94	1.17	3.70	0.88	2.51	0.74	0.41	0.12	0.16	4.01
Sal × AUP-5008	4.99	33.58	2.17	0.45	9.97	1.94	3.36	0.33	4.28	0.12	0.02	7.81
Barsat × Janbaz	0.56	0.35	4.96	0.00	2.27	0.00	0.00	0.16	0.13	0.00	0.00	0.70
Barsat × Tatara	16.97	0.66	12.30	1.43	10.04	0.37	1.73	2.63	2.31	0.20	0.19	5.40
Barsat × AUP-5008	4.66	2.44	22.72	0.25	1.95	0.68	0.54	3.76	3.06	0.03	0.14	3.37
Watan × Janbaz	1.90	4.59	10.83	6.19	3.13	1.92	4.66	3.19	2.35	0.10	0.00	0.29
Watan × Tatara	0.06	34.24	4.55	2.95	10.75	0.28	0.12	2.12	10.91	0.10	0.38	12.40
Watan × AUP-5008	30.45	11.51	13.50	3.08	11.5	5.56	7.33	7.09	11.15	0.47	0.72	5.99

Abbreviations: DH - days to heading, DM - days to maturity, PH - plant height, TPP - tillers plant^{-1}, FLA - flag leaf area, SLPS - spikelet's spike^{-1}, SL - spike length, GPS - grains spike^{-1}, TGW - 1000-grain weight, GYS - grain yield spike^{-1}, BY - biological yield, and HI -harvest index.

in parent Pirsabak-2005, whereas the smallest (72.73 cm) was prominent in Watan. Among F_3 populations, the tallest plants (92.33 cm) were evident for Pirsabak-2005 × Janbaz, and the shortest plant (72.60 cm) was distinct for Saleem-2000 × Janbaz. Similar findings came from Ahmad and Gupta (2023) for plant height.

Heritability in the broad sense of the trait varied from 0.36 to 0.82 (Table 5). The uppermost heritability (0.82) was outstanding for cross Watan × Janbaz, followed by AUP-4008 × Janbaz (0.81), Saleem-2000 × Tatara (0.80), and Fakhr-e-Sarhad × Janbaz (0.79). The minimum heritability (0.36) appeared for the cross Fakhr e Sarhad × AUP-5008. Moderate and high values for inheritance related to plant height undermine the role of additive gene and dominant gene action, which better indicate non-environmental influence on the genotypes. The study results support the findings of Bayisa *et al*. (2020) and Bazai *et al*. (2020). The highest genetic advance (32.71 cm) was significant for the cross combination, Fakhr-e- Sarhad × AUP-5008, followed by Barsat × AUP-5008 (22.72 cm) and AUP-4008 × Tatara (13.18 cm), with the lowest genetic advance (0.13 cm) arising for Pirsabak-2005 × AUP-5008 (Table 6). High genetic advances for crosses are evidence of improvement per breeding cycle. A high genetic advance was also an outcome of a study by Kumar and Kerkhi (2015).

Tillers Plant^{-1}

Data regarding tillers plant^{-1} showed highly significant variations at ($P \leq 0.01$) for the parents, F_3 populations, and parent vs. F_3 populations (Table 2). The parents' mean was 7.27, while for the F_3 populations, it was 6.65. Overall means ranged from 4.73 to 10.4 (Table 3). In parents, the maximum number of tillers plant^{-1} (10.4) was visible for Fakhr-e-Sarhad, with the minimum (5.53) observed for Pirsabak-2005. Among F_3populations, the maximum number of tillers plant^{-1} (9.8) surfaced for Saleem-2000 × AUP-5008, and 4.73 emerged for Pirsabak-2005 × AUP-5008. Prasad *et al*. (2021) also mentioned significant variations among F_3 wheat populations.

The heritability estimates for the number of tillers plant^{-1} ranged from 0.18 to 0.86. The utmost heritability (0.86) was apparent for the F_3 population, Fakhr-e-Sarhad × Tatara and the lowest heritability (0.18) occurred in the cross combination, Pirsabak-2005 × AUP-5008 (Table 5). The highest genetic advance value (6.19) manifested for the combination, Watan × Janbaz, followed by AUP-4008 × Tatara (4.84). The lowest genetic advancement (0) resulted from the F_3 cross Barsat × Janbaz (Table 6). High broad-sense heritability and high genetic advance in wheat populations were also outcomes in several reports (Bazai *et al*., 2020; Ullah *et al.,* 2011). Past findings suggested that most of the yield-associated traits had different heritability, implying selection should proceed on the basis of highly heritable attributes (Singh *et al*., 2012; Bhat *et al*., 2018; Qulmamatova *et al*., 2022).

Flag leaf area

Mean squares of the flag leaf area exhibited considerable variations among the genotypes, parents, parents vs. F_3, and F_3 populations at $P \leq 0.01$ (Table 2). The overall mean for the trait was 36.25 cm^2 for parents and 39.91 cm^2 for F_3 populations. The general means of the flag leaf area ranged from 29.75 to 50.23 cm^2 (Table 3). In parental genotypes, the maximum flag leaf area (50.33 cm^2) was plain for Pirsabak-2005, with the minimum (29.75 cm^2) observed for the genotype, Saleem-2000. In the case of F_3 populations, the broader flag leaf (49.48 cm^2) was definite in the cross Pirsabak-2005 × AUP-5008, while the smaller flag leaf area (33.34cm^2) was conspicuous in the cross Watan × Janbaz (Adhikari *et al*., 2018).

The flag leaf area's broad-sense heritability varied from 0.23 to 0.89. The analysis of the data indicated that high heritability (0.89) appeared in the cross, Barsat × Tatara, followed by Watan × AUP-5008 (0.87), Saleem-2000 × AUP-5008 (0.86), and Watan × Tatara (0.85), with the lowest (0.23) resulting in the cross combination AUP-4008 × AUP-5008 (Table 5). The highest genetic advance (20.33 cm^2) occurred for the cross combination Fakhr-e-Sarhad × Janbaz, followed by Fakhr-e-Sarhad × Tatara (16.84 cm^2), while the lowest genetic advance ($1.95cm^2$) was notable for Barsat × AUP-5008 (Table 6). Ahmad *et al*. (2023) have reported medium to high heritability with less genetic advance for the flag leaf area. The slight differences may be due to environmental influences on the genotype.

Spikelets spike^{-1}

Analysis of data for the spikelets spike^{-1} revealed highly considerable variations ($P \leq 0.01$) among the genotypes, parents, F_3, and parents vs. F_3 populations (Table 2). The mean value for parents was 19.62, while it was 20.82 for F_3 populations. The overall means ranged from 17.4 to 22.73. In parents, the maximum spikelets spike^{-1}(21.93) showed for AUP-4008, with the minimum (17.4) occurring for the genotype Watan (Table 3). Among the F_3 populations, the maximum spikelets spike^{-1} (22.73) arose for Pirsabak-2005 × AUP-5008, and the minimum (19.53) cropped up for Barsat × AUP-5008. Highly significant variances among genotypes and crosses for the number of spikelets spike^{-1} have also resulted from a report by Adhikari *et al*. (2018) in wheat genotypes.

Broad-sense heritability for spikelets spike^{-1} ranged from 0.24 to 0.87. The utmost heritability (0.87) emerged for the cross, Pirsabak-2005 × AUP-5008, followed by Saleem-2000 × AUP-5008 (0.79), Watan × AUP-5008 (0.76), and AUP-4008 × Tatara (0.73). However, the lowest heritability (0.24) occurred for the cross Pirsabak-2005 × Janbaz (Table 5). The highest genetic advancement detailed in the figure (5.56) was remarkable for the cross, Watan × AUP-5008, followed by AUP-4008 × Janbaz (4.79), with a zero genetic advance exhibited by Barsat × Janbaz (Table 6). High broad-sense heritability and genetic advancement among F_3 populations indicate the presence of fixable genes, and, hence, selection in early generations would be fruitful. Similar results about the trait were consistent with the study outcomes (Meles *et al*., 2017; Adhikari *et al*., 2018).

Spike length

From the table of mean squares ($P \leq 0.01$), highly considerable variations were present among the parents and parents vs. F_3, with significant differences in F_3 segregants for spike length (Table 2). The mean spike length was 10.19 cm for parents and 10.69 cm for the F_3 populations (Table 4, Figure 1). The overall

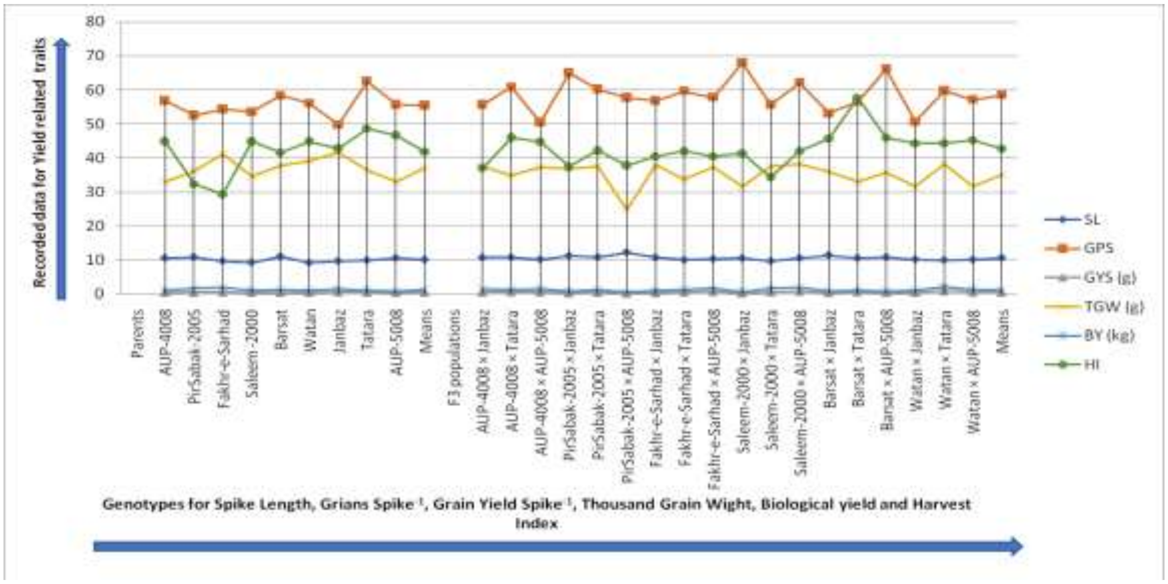

Figure 1. Mean performance of the parental genotypes and F_3 populations for yield-attributing traits.

mean for spike length ranged from 9.33 to 12.27 cm. In parents, the lengthiest spike (11.13 cm) was visible for Barsat, while the shortest (9.33 cm) was apparent for the genotype Watan. Among F_3 populations, the lengthier spike (12.27 cm) manifested in the P.S-2005 × AUP-5008, with the shorter (9.8 cm) documented for the cross S-2000 × Tatara. Highly significant differences among the genotypes are prominent indications of variance in spike length in all genotypes, as observed by Obsa *et al*. (2017).

The broad-sense heritability estimates for spike length ranged from 0.23 to 0.88. The maximum heritability (0.88) was evident in the cross combination, Fakhr-e-Sarhad × AUP-5008, followed by Watan × AUP-5008 (0.86), Pirsabak-2005 × Tatara (0.85), and Saleem 2000 × AUP-5008 (0.84), with the lowest heritability (0.23) notable in the cross combination, Pirsabak-2005 × Janbaz (Table 5). The maximum genetic advance (7.33 cm) was prominent for the cross, Watan × AUP-5008, followed by Watan × Janbaz (4.66), while a zero genetic advance resulted for Barsat × Janbaz (Table 6). A high percentage of heritability and genetic gain provides confidence for selecting better plants even at an early stage, and a high genetic variance reflects the amount of variation and the chance of selection. A study documented a high genetic advance with heritability for spike length (Kumar and Kerkhi*,* 2015). Similar results also came from previous researchers for plant height, days to heading, and spike length (Dargicho *et al.,* 2015).

Grains spike^{-1}

Grains spike^{-1} mean squares data showed considerable variances ($P \leq 0.01$) for the parents and F_3 populations (Table 2). The mean of grains spike^{-1} was 55.60 for parents and 58.59 for F_3 populations. Means of grains spike^{-1} ranged from 49.87 to 68 (Table 4, Figure 1). In parents, the supreme grains spike^{-1} (62.0) was notable for the genotype Tatara, while the smallest (49.87) was for the Janbaz genotype. Among F_3 populations, the maximum number of grains spike^{-1} (68) was available for Saleem-2000 × Janbaz, while the minimum (50.6) was with AUP-4008 × AUP-5008. Mohapatra *et al*. (2019) have also reported comparable ranges for grain yield with high genetic advance and high heritability.

The heritability for grains spike^{-1} varied from 0.20 to 0.76. The highest heritability (0.76) was dominant with Pirsabak-2005 × Tatara. Bazai *et al*. (2022) also observed high heritability for grain spike^{-1}. The lowest heritability (0.20) appeared for AUP-4008 × AUP-5008 (Table 5). Meantime, the highest genetic advance value was 7.09 for the F_3 population Watan × AUP-5008, followed by AUP-4008 × Janbaz (6.74); however, the lowest genetic advance (0.16) occurred for Barsat × Janbaz (Table 6). These observations are in parallel with the findings of Zerga *et al*. (2016). The proper estimate of genetic advancement and heritability could be helpful in the process of desirable trait selection. Adhikari *et al.* (2018) have also reported less genetic advancement and high heritability for most crosses in wheat.

1000-grain weight

Mean squares for a 1000-grain weight exhibited notable variations ($P \leq 0.01$) among the genotypes, parents, F_3 populations, and parents vs. F_3 populations (Table 2). The means observed for parents and F_3 populations were 37.03 and 35.13 g, respectively. The overall means ranged from 24.87 to 41.67 g (Table 4, Figure 1). In parents, the bulkiest weight for a thousand grains (41.67 g) surfaced for Janbaz, while the minimum (33.0 g) emerged for AUP-5008. Among F_3 populations, the heaviest thousand grains (38.37 g) was evident for Watan × Tatara, followed by Saleem-2000 × AUP-5008 (38.33 g), and Fakhr e Sarhad × Janbaz (38.1 g), with the minimum (24.87 g) recorded for Pirsabak-2005 × AUP-5008. Highly significant differences among genotypes, parents, and crosses have also resulted in their research by Elahi *et al.* (2020).

The heritability estimates for 1000-grain weight ranged from 0.22 to 0.87. The supreme heritability (0.87) was distinct for Barsat × Janbaz, followed by AUP-4008 × AUP-5008 (0.85) and Pirsabak-2005 × AUP-5008

(0.85), while the lowest heritability (0.22) was apparent for Saleem-2000 × Tatara (Table 5). The highest genetic advance (11.51 g) appeared for Watan × AUP-5008, followed by Watan × Tatara (10.91), and Pirsabak-2005 × AUP-5008 (5.62), with the lowest (0.13 g) discovered for Barsat × Janbaz (Table 6). An experiment documented the highest rate of heritability and high genetic advance for 1000-grain weight (Taneva *et al*., 2019).

Grain yield spike^{-1}

Data analysis showed highly significant variations ($P \leq 0.01$) for grain yield in genotypes and F_3 populations, and no prominent variation among parents and parents vs. F_3 populations occurred (Table 2). The mean values observed for parents were 0.54 g, while for F_3 populations, it was 0.57 g. The mean grain yield spike^{-1} varied from 0.32 to 0.97 g (Table 4, Figure 1). In parents, the higher grain yield spike^{-1} (0.64 g) was evident for Janbaz, while the minimum recorded (0.44 g) was for AUP-5008. In the case of F_3 populations, the maximum grain yield spike^{-1} (0.97 g) was remarkable for Watan × Tatara, followed by Saleem-2000 × AUP-5008 (0.82 g), with the minimum (0.26 g) observed for Pirsabak-2005 × AUP-5008. Highly significant differences among genotypes and crosses have been exhibited in some studies (Muhder *et al*., 2020; Kachi *et al*., 2020).

The heritability for grain yield spike^{-1} varied from 0.23 to 0.89. The highest inheritance rate (0.89) was noteworthy for Barsat × Tatara, followed by AUP-4008 × Tatara (0.88) and Pirsabak-2005 × Janbaz (0.86), while the lowest heritability (0.23) emerged for both cross combinations, Barsat × Janbaz and Barsat × AUP-5008 (Table 5). The highest genetic advance (0.47 g) resulted in Watan × AUP-5008, followed by Fakhr-e-Sarhad × AUP-5008 (0.38 g) and Fakhr-e-Sarhad × Janbaz (0.21 g); however, the lowest genetic advance (0) came for Barsat × Janbaz (Table 6). High heritability estimates coupled with minimum genetic advance indicate non-additive gene action, and, therefore, selection in early generations would be unhelpful and unfruitful; hence, waiting for later generations would be necessary. Alemu *et al*. (2020) also observed the highest heritability and low genetic advance for grain yield.

Biological yield

Significant changes at $P \leq 0.01$ were notable among the genotypes, parents, and F_3 genotypes for biological yield (Table 2). The mean biological yield for parents was 1.35 kg, and for F_3 populations, it was 1.33 kg. The overall means for biological yield ranged from 0.7 to 2.2 kg (Table 4, Figure 1). The maximum biological yield in parents (2.05 kg) was apparent for Fakhr-e-Sarhad, while the minimum (0.95 kg) emerged for AUP-5008. Among F_3 populations, the maximum biological yield (2.20 kg) appeared for Watan × Tatara, followed by Saleem-2000 × AUP-5008 (1.98 kg), Fakhr-e-Sarhad × AUP-5008 (1.81 kg), and Saleem-2000 × Tatara (1.85 kg), with the minimum yield (0.70 kg) recorded for Pirsabak-2005 × AUP-5008. Bazai *et al*. (2020) also reported results of highly significant differences between parents and F_3 populations.

The estimates of heritability for biological yield extended from 0.39 to 0.86. The utmost heritability (0.86) was evident with Watan × AUP-5008, followed by Saleem-2000 × Janbaz, AUP-4008 × Tatara, and Saleem-2000 × Janbaz all at 0.85, and AUP-4008 × Janbaz with 0.83, while the lowest heritability (0.39) occurred for Pirsabak-2005 × Tatara and Barsat × AUP-5008 (Table 5). The supreme genetic advance (0.72 kg) resulted in F_3 Watan × AUP-5008, followed by Pirsabak-2005 × Janbaz (0.62 kg) and Fakhr-e-Sarhad × Tatara (0.47 kg). Meanwhile, Barsat × Janbaz and Watan × Janbaz gave no genetic advance (0) (Table 6). A high broad-sense heritability and high genetic advance for this trait have also materialized in a study by Vaghela *et al*. (2021).

Harvest index

Data and observations regarding the harvest index revealed that mean squares exhibited highly prominent variations ($P \leq 0.01$) in parents and F_3 populations (Table 2). Mean values for the harvest index (41.88) for parental genotypes indicated the lowest mean for PirSabak-2005, while the highest mean value was 48.66, shown by AUP-4008. In F_3 populations, the mean value is 42.83, providing the lowest value in the cross AUP-4008 × Janbaz (37.19) and the highest value from the cross combination Barsat × Tatara (57.74), followed by parental genotype Tatara (48.66), as detailed in Table 4 and Figure 1. The results are consistent with the findings of Baye *et al.* (2020).

The heritability varied from 0.29 to 0.84, with the highest value (0.84) prominent for Barsat × Janbaz, followed by Watan × Janbaz (0.82) and Fakhr-e-Sarhad × Janbaz (0.62) (Table 5). On the other hand, the lowest heritability (0.29) occurred in Saleem-2000 × Tatara. Similarly, the highest genetic advance (12.40%) was evident for Watan × Tatara, followed by Pirsabak-2005 × Tatara (8.26%) and Saleem-2000 × AUP-5008 (7.81%). The lowest genetic advance (0.23 %) emerged in AUP-4008 × Janbaz (Table 6). The study findings were in analogy with those of Adhikari *et al*. (2018).

CONCLUSIONS

The analysis of variance exposed highly considerable variations among genotypes, parents, and F_3 populations for days to heading, tall plants, spikelets spike^{-1}, flag leaf area, tillers plant^{-1}, grains spike^{-1}, a thousand-grain weight, and biological yield. Differences were significant in F_3 populations for spike length, days to maturity, and the harvest index. Meanwhile, nonsignificant variations were evident among parents for grain yield. Based on the highest heritability, maximum genetic advance, and mean squares, the parental genotype Janbaz, AUP-5008, and the cross combinations AUP-4008 × Janbaz, AUP-4008 × AUP-5008, Pirsabaq-2005 × AUP-5008, Saleem-2000 × Janbaz, Barsat x Janbaz, Watan × Tatara, Watan × AUP-5008, AUP-4008 × Tatara, Pirsabak-2005 × AUP-5008, Watan ×Tatara, and Watan × AUP-5008 exhibited supreme figures for yield-contributing traits. The parental genotype AUP-5008 could benefit as a donor parent for high-yielding genotypes in further breeding programs.

REFERENCES

Adhikari BN, Joshi BP, Shrestha Bhatta NR (2018). Genetic variability, heritability, genetic advance and trait association study for yield and yield components in advanced breeding lines of wheat. *Nepalese J. Agric. Sci*. 17 (42): 229-238.

Ahmad A, Gupta RK (2023). Genetic variability, heritability and genetic advance for yield and yield associated traits in bread wheat (*Triticum aestivum* L.). *Ann. Agric. Crop Sci.* 8(1): 1125.

Alemu YA, Anley AM, Abebe TD (2020). Genetic variability and association of traits in Ethiopian durum wheat (*Triticum turgidium* L. var. durum) landraces at Dabat Research Station, North Gondar. *Cogent Food and Agric.* 6(1):1778604.

Babar M, Ali S, Akbar F, Ali M, Uzair M, Subhan G, Ali J, Khan H (2022). Study of genetic variability for morphological traits in bread wheat across sowing dates. *Pure. Appl. Biol*. 11(3):843-850.

Baye A, Berihun B, Bantayehu M, Derebe B (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (*Triticum aestivum* L.) lines. *Cogent Food Agric.* 6(1):1752603.

Bayisa T, Tefera H, Letta T (2020). Genetic variability, heritability and genetic advance among bread wheat genotypes at Southeastern Ethiopia. *Agric. For. Fish*. 9(4):128-134.

Bazai KK, Baloch M, Sootaher JK, Baloch T, Naeem M, Abro TF, Chang MS, Menghwar KK (2020). Correlation, heritability and genetic distance analysis in bread wheat (*Triticum aestivum* L.) genotypes. *Pak. Acad. Sci. B. Life Environ. Sci*.57 (1): 75-83.

Bhat JS, Patil BS, Hariprasanna K, Hossain F, Muthusamy V, Mukri G, Mallikarjuna MG, Zunjare R, Singh SP, Mukesh Sankar S, Singhal T, Venkatesh K, Gupta V, Chakraborti M, Chattopadhyay K, Ghagane SC, Hiremath MB, Choudhary AK (2018). Genetic enhancement of micronutrient content in cereals. *SABRAO J. Breed. Genet*. 50(3): 373-429.

Burton GW, Vane de EH (1953). Estimating heritability in tall fescue (*Festuca arundinacea* L.) from replicated clonal material. *Agron. J*. 45(10):478-481.

Dabi A, Mekbib F, Desalegn T (2019). Genetic variability studies on bread wheat (*Triticum aestivum* L.) genotypes. *J. Plant Breed. Crop Sci.* 11 (2): 41-54.

Dargicho D, Sentayehu A, Firdisa E, Ermias A (2015). Genetic variability in bread wheat (*Triticum aestivum* L.) germplasm for yield and yield component traits. *J. Biol. Agric. Healthcare*. 5(17):140-147.

Elahi T, Pandey S, Shukla RS (2020). Genetic variability among wheat genotypes based on agro-morphological traits under restricted irrigated conditions. *J. Pharm. Phytochem*. 9(3): 801-805.

Falconer DS, Mackay TF, Frankham R (996). Introduction to quantitative genetics (4th Ed). *Trends in Genetics*. 12 (7):280.

GOP (2019). Economic Survey of Pakistan. Ministry of Food and Agriculture. Government of Pakistan, Economic Advisory Wing, Finance Division, Islamabad.

Kachi M, Abro TF, Sootaher JK, Baloch TA, Mastoi MA, Soomro TA, Menghwar KK, Jadgal GM, Chang MS, Shah WH (2020). Estimation of heritability and genetic advance in F_2 populations of bread wheat (*Triticum aestivum* L.) genotypes*. Int. J. Bioscience.16* (2): 286-295.

Khan SA, Hassan G (2017). Heritability and correlation studies of yield and yield-related traits in bread wheat. *Sarhad J. Agric*. 33(1):103-107.

Kumar D, Kerkhi SA (2015). Genetic variability, heritability and genetic advance for yield component and quality traits in spring wheat (*Triticum aestivum* L.). *The Bioscan*. 10(4): 2125-2129.

Meles B, Mohammed W, Tsehaye Y (2017). Genetic variability, correlation and path analysis of yield and grain quality traits in bread wheat (*Triticum aestivum* L.) genotypes at Axum Northern Ethiopia. *J. Plant Breed. Crop Sci*. 9(10):175-185.

Mohapatra SS, Priya B, Mukherjee S (2019). Studies on variability, heritability and genetic advance in some quantitative and qualitative traits in bread wheat (*Triticum aestivum* L.) under rain fed condition. *Int. J. Current Microbial. Appl. Sci.* 8(9):1040-1050.

Muhder N, Gessese MK, Sorsa Z (2020). Assessment of genetic variability among agronomic traits and grain protein content of elite bread wheat (*Triticum aestivum* L.) genotypes in the central highlands of Ethiopia. *Asian J. Agric. Res.* 14: 1-12.

Obsa Ch, Wassu W, Firdissa E (2017). Analysis of genetic variability among bread wheat (*Triticum aestivum* L.) genotypes for growth, yield and yield components in bore district, Oromia Regional State. *Agric. Forestry Fish*. 6(6):188-199.

Panse VG, Sukhatme PV (1967). Statistical methods for agricultural workers (2nd ed.), ICAR, New Delhi.

Prasad J, Dashora A, Chauhan A, Rizzardi D, Bangarwa SK, Nesara K (2021). Genetic variability heritability and genetic advance in bread wheat (*Triticum aestivum* L.) genotypes. *Int. J. Cur. Microbial. App. Sci.* 9(10):868-872.

Qulmamatova DE, Baboev SK, Buronov AK (2022). Genetic variability and inheritance pattern of yield components through diallel analysis in spring wheat. *SABRAO J. Breed. Genet.* 54(1): 21-29. http://doi.org/10.54910/sabrao2022.54.1.3.

Seyoum EG, Sisay A (2021). Estimation of genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.). *Int. J. Res. Stud. Agric. Sci*. 7(9):17-26.

Seyoum EG, Sisay A (2021). Genetic variability, heritability and genetic advance study in bread wheat genotypes (*Triticum aestivum* L.). *Adv. Biosci. Bioeng*. 9(3):81-86.

Shah T, Khan AZ, Numan M, Ahmad W, Zahoor M, Ullah M, Jalal A (2017). Nutrient uptake and yield of wheat varieties as influenced by foliar potassium under drought condition. *Cercetari Agronomice in Moldova.* 50 (2): 5-20.

Singh V, Krishna R, Singh L, Singh S (2012). Analysis of yield traits regarding variability, selection parameters and their implication for genetic improvement in wheat (*Triticum aestivum* L.). *SABRAO J. Breed. Genet*. 44(2): 370-381.

Taneva K, Bozhanova V, Petrova I (2019). Variability, heritability and genetic advance of some grain quality traits and grain yield in durum wheat genotypes. *Bulg. J. Agric. Sci*. 25 (2), 288-295.

Ullah K, Khan SJ, Muhammad MIT, Muhammad S (2011). Genotypic and phenotypic variability, heritability and genetic diversity for yield components in bread wheat (*Triticum aestivum* L.) germplasm. *Afr. J. Agric. Res.* 6(23):5204-5207.

Vaghela GK, Patel JM, Rahevar P (2021). Assessment of genetic variability and character association for morpho-chemical traits in bread wheat (*Triticum aestivum*L.). *Emergent Life Sci. Res.*7:14-20.

Zerga K, Mekbib F, Dessalegn T (2016). Estimation of association among growth and yield-related traits in bread wheat (*Triticum aestivum*. L) genotypes at Gurage Zone, Ethiopia. *Int. J. Plant Breed. Crop Sci*. 3(2):123-134.