RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
56 (6) 2295-2305, 2024
http://doi.org/10.54910/sabrao2024.56.6.11
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

GENETIC VARIABILITY AMONG WHEAT GENOTYPES UNDER AGROECOLOGICAL CONDITIONS OF DISTRICT DIAMER, GILGIT-BALTISTAN, PAKISTAN

R. KABIR[1], I. AHMED[2*], M.N. TAHIR[2], U. ARIF[3], M. ABBAS[4], M. ZAKRIYA[5], A. ULLAH[6], S. KHALID[7], A. SUBHANI[7], and S.O. JAVED[7]

[1]PARC-Mountain Agricultural Research Station, Chilas, District Diamer, Pakistan
[2]PARC- Arid Zone Research Centre, Umerkot, Pakistan
[3]Horticultural Research Institute, National, National Agricultural Research Centre, Islamabad, Pakistan
[4]Vegetable Research Station, Karor, Pakistan
[5]Department of Agronomy, University of Poonch, Rawalakot, Pakistan
[6]Department of Agriculture Extension, Chilas, District Diamer, Pakistan
[7]Department of Plant Breeding and Molecular Genetics, University of Poonch, Rawalakot, Pakistan
*Corresponding author's email: Israr.rush@gmail.com
Email addresses of co-authors: rehmatk1972@gmail.com, naumanuaar@gmail.com, uzmaarif47@gmail.com, abbasmudassir51@gmail.com, Zakriya141@gmail.com, atifsubhani80@gmail.com, abadullah39@yahoo.com, shagufta0800@gmail.com,okashasyed@yahoo.com

SUMMARY

Wheat (*Triticum aestivum* L.) belongs to the Poaceae family and serves as a staple in many portions worldwide, as well as, in Pakistan. Wheat yield in Gilgit-Baltistan is comparatively low versus other parts of the country because cultivars developed suited other regions globally. Moreover, the country performs less due to unique agroecological conditions. This study progressed on 20 wheat accessions at the PARC-Mountain Agricultural Research Station, Chilas, District Diamer, Gilgit-Baltistan, in 2018–2019. It used a randomized complete block design (RCBD) with three replicates to assess the genetic variability and trait association in wheat. High phenotypic and genotypic coefficient of variation (%) was evident for characteristics, i.e., spike length, flag leaf area, tillers plant^{-1}, spikelets spike^{-1}, yield plot^{-1}, yield hectare^{-1}, and straw yield hectare^{-1}. Estimates of heritability were high for all traits under consideration. Estimated high broad-sense heritability (H^2) tied with high genetic advance percent over means for spikelets spike^{-1}, flag leaf area, tillers plant^{-1}, seeds spike^{-1}, spike length, thousand-grain weight, yield plot^{-1}, straw yield plot^{-1}, yield hectare^{-1}, and straw yield hectare^{-1}. It indicated a simple selection based on phenotype would be effective for improvement during early generations.

Communicating Editor: Dr. Tonette P. Laude

Manuscript received: September 13, 2023; Accepted: September 04, 2024.

Citation: Kabir R, Ahmed I, Tahir MN, Arif U, Abbas M, Zakriya M, Ullah A, Khalid S, Subhani A, Javed SO (2024). Genetic variability among wheat genotypes under agroecological conditions of district Diamer, Gilgit-Baltistan, Pakistan. *SABRAO J. Breed. Genet.* 56(6): 2295-2305. http://doi.org/10.54910/sabrao2024.56.6.11.

Estimating correlation coefficients for various traits revealed that plant height, days to maturity, harvest index, straw yield plot-^{1}, and thousand-grain weight exhibited positively significant correlations with yield hectare^{-1}. Meanwhile, plant height, thousand-grain weight, days to maturity, and yield plot^{-1} showed relevant correlations with straw yield plot^{-1}.

Keywords: Accession, coefficients of variation, correlation, genetic variability, heritability, and genetic advance

Key findings: The genotypes AC-12, AC-13, AC-5, and AC-15 emerged as high-grain yielders, and AC-15, AC-23, and AC-12 proved as better straw-yielding genotypes. These wheat genotypes may benefit the development of new wheat varieties of the future for the agroecological condition of Gilgit-Baltistan.

INTRODUCTION

Wheat (*Triticum aestivum* L.) belongs to the family Poaceae and serves as a staple in a large part of the world (Haleem *et al.,* 2022). Global wheat production stood at 779 million tons during 2021–2022 (Wysocka et al. 2024). In Pakistan, wheat is the largest food grain crop based on area and production. During the cropping season of 2022–2023, wheat crop planting reached 9,043,000 hectares, which was 0.7% higher than 8.977 million hectares of wheat-cultivated area in the previous year (Pakistan Economic Survey, 2022–2023). Wheat contributed 8.9% to the agricultural value addition and 1.8% to the national GDP (ESP, 2022). The livestock totally depends on wheat straw, maize stalk, and hay due to long and dry winters. Therefore, cultivating wheat is also for kernel and for chaff in Gilgit-Baltistan.

Wheat yield is comparatively lower in Gilgit-Baltistan versus other parts of Pakistan. Therefore, a need to develop cultivars with high grain and straw yield is a requirement (Kabir *et al*., 2017a). In Gilgit-Baltistan, the cultivated land mostly consists of small valleys, with a large portion of land falling into mono-crop areas. Owing to unique agroecological conditions, wheat cultivars developed are more suitable for other regions worldwide, and the country does not perform better. Therefore, before cultivation, these cultivars require testing for adaptability in the region (Alam *et al.,* 2006).

Improvement of local cultivars is an essential strategy of the wheat-breeding program. According to a widely accepted theory, extensive plant breeding and intense selection have further decreased genetic diversity among cultivars, limiting the germplasm base accessible for more advancements in breeding (Reif *et al.,* 2005). Therefore, the identification of better-performing genotypes from local landraces and old cultivars is necessary for direct cultivation or use as a parent in a hybridization program. Local genotypes are well-adapted varieties of native environments, and they are essential tools for developing high-yielding and suitable cultivars for the region (Sabaghnia *et al*., 2014).

Kernel production is the principal characteristic of a cereal crop, with the yield controlled by several genes affected by many associated characteristics. For that reason, selecting superior genotypes does not depend on production alone, but considering other correlated features is also necessary (Degewione *et al*., 2013). Variation in a population is a prerequisite for the success of crop improvement, and it is proportional to the heritable genetic variations in the existing material. Variability in the population offers different choices for the breeders to select genotypes of their choice. Selection will be successful if heritable variation occurs in existing populations (Cheruiyot *et al*., 2015).

The heritability estimates determine the behavior and nature of variability in a population. High heritability indicates variations are genetic and transmissible to the next generation, and selecting desirable genotypes could be easy. Knowledge of genetic advances informs about the nature of variation and expected progress through selection in successive generations (Tiwari *et al*., 2017). Correlation studies are essential to determine the extent to which different yield-contributing traits connect. Identification of nature and level of association among various characteristics is necessary to select desirable genotypes (Singh *et al*., 2002; Khan *et al*., 2015). This study commenced to evaluate the differences among wheat genotypes for diversity in yield and other important associated traits for identifying suitable genotypes in agroecological conditions of Gilgit-Baltistan.

MATERIALS AND METHODS

The experimental site was the PARC-Mountain Agricultural Research Station, Chilas, District Diamer, Gilgit-Baltistan (Latitude 35° 27′ 0″ North, Longitude 74° 18′ 0″ East) located 1166.55 meters above sea level. It falls in a cold semi-arid region with 87.73 mm precipitation annually. Summers are hot and dry, while winters are freezing cold and partially cloudy. Temperatures range from 5.6 °C in January to 28.2 °C in July. The texture of the soil is silt loam in the surface soil and silt clay loam in the subsoil. Soil is non-calcareous, nearly neutral soil. Their organic matter content in the surface soil is 0.6% and 0.5% to 9.8% in the soil surface. The pH of the soil is 7 to 7.6. Plant material comprised 20 accessions collected from the MARC Chilas, District Diamer, Gilgit-Baltistan (Table 1).

Each accession’s planting began on November 11, 2018, in a plot size of 6 m × 1.5 m in RCBD with three replicates, with harvesting done in the first week of June 2019. All agronomic and cultural practices, including land preparation, weed management, and fertilizer application proceeded for all accessions during the cropping season, as recommended by Sohail *et al*., (2013). Irrigating the crop was according to the crop's need. Data of 14 plant characteristics came from 10 random plants of each accession from all three replications. These data are flag leaf area, spike length, plant height, tillers plant^{-1}, spikelets spike^{-1}, grains spike^{-1}, days to heading, days to plant maturity, yield plot^{-1}, thousand-grain weight, harvest index, straw yield plot^{-1}, straw yield hectare^{-1}, and grain yield hectare^{-1}. The straw yield computation comprised subtracting the seed yield from the biological yield. Determining the grain and straw yield hectare^{-1} from each plot reached subsequent conversion to yield tons hectare^{-1}. Harvest index percentage calculation used the formula: HI (%) = Grain yield/ Biological yield × 100.

The data collected sustained analysis of variance using Microsoft Excel (2007), following the method of Steel and Torrie (1980). Genotypic and phenotypic variance (Vg and Vp) and coefficient of variability (GCV and PCV) estimation employed the method suggested by Burton and Devane (1953), with broad sense heritability (H^2) computed using the method by Singh and Chaudhary (1985). Estimating genetic advance as percent over means used the formula designed by Allard (1960). Correlation coefficients among various traits reached computation with the IBM-SPSS v. 22, following the procedure outlined by Singh and Chaudhary (1999).

RESULTS AND DISCUSSION

Analysis of variance helped assess the variation among the wheat genotypes. The results revealed highly significant differences among genotypes for all the traits, indicating a relevant amount of variability existed among the bread wheat genotypes (Table 2).

Mean performance of the genotypes

Mean performances of different wheat genotypes for flag leaf area, tillers-plant^{-1}, plant height (cm), days to heading, spike length (cm), days to maturity, and spikelets spike^{-1} are in Table 3a. The means of grains spike^{-1}, yield plot^{-1} (kg), thousand-grain weight (g), the yield of straw plot^{-1} (kg), harvest index percentage, straw yield hectare^{-1} (tons), and yield hectare^{-1} (tons) appear in Table 3b.

Highest tillers plant^{-1} were evident in genotype AC-04, while AC-10 emerged as the lowest tillering genotype. The shortest plant height resulted in AC-01 (60.3 cm). On the

Table 1. Wheat genotypes used in the present study.

No.	Accessions	No.	Accessions
1	AC-1	11	AC-11
2	AC-2	12	AC-12
3	AC-3	13	AC-13
4	AC-4	14	AC-14
5	AC-5	15	AC-15
6	AC-6	16	AC-16
7	AC-7	17	AC-17
8	AC-83	18	AC-18
9	AC-95	19	AC-19
10	AC-108	20	AC-20

AC = Accession

Table 2. Analysis of variance for yield and yield-related traits in wheat genotypes.

S.O.V.	TP	FLA	PH	DH	DM	SL	SPS	GS	GW	YP	SYP	HI	SYH
Replications	2.6	14.135	8.7485	22.816	7.55	1.89	6.391	20.058	4.593	0.028	0.009	2.203	0.0106
Genotypes	12.721**	104.537**	167.337**	92.262**	73.237**	12.159**	38.260**	150.812**	115.46**	0.797**	2.126**	21.160**	2.624**
Error	0.995	1.678	4.201	4.378	5.006	0.391	2.072	7.98	5.418	0.0102	0.0327	2.064	0.0404
Total	4.825	35.226	56.891	33.305	27.065	4.232	13.872	54.386	40.829	0.264	0.706	8.219	0.871
CV	11.46	5.52	2.79	1.74	1.44	7.27	8.45	6.13	6.2	4.02	4.54	3.79	4.54

SOV: Source of variation, TP: TIllers-plant^{-1}, FLA: Flag leaf area (cm^{2}), PH: Plant height (cm), DH: Days heading, SL: Spike length (cm), DM: Days to maturity, SPS: Spikelets spike^{-1}, GW: Thousand-grain weight (g), GS: Grains spike^{-1}, YP: Yield plot^{-1} (kg), SYP: Straw yield plot^{-1} (kg), HI: Harvest index (%), SYH: Straw yield hectare^{-1} (tons), GYH: Grain yield hectare^{-1} (tons).

other hand, the tallest plants manifested in genotype AC-20 (85.4 cm). The accession AC-17 signified maximum days to maturity (163 days). Meanwhile, AC-2 proved as an early maturing genotype among tested accessions, with 144 days to maturity. The AC-5 indicated a maximum 1000-grain weight (49 g), while AC-7 provided the lowest 1000-grain weight genotype (24.3g). Genotype AC-12 produced the ultimate grain yield plot-1 (3.4 kg) and yield hectare-1 (3.7 t), followed by AC-13's yield plot-1 at 3.3 kg and yield hectare-1 at 3 t. The lowest yield produced occurred with AC-01 at yield plot-1 of 1.7 kg and yield hectare-1 of 1.8 t.AC-15 performed best among tested genotypes for straw yield, producing 6.4 t of straw hectare^{-1}. Inversely, AC-1 had a minimum straw yield of 2.9 t hectare^{-1}. The highest harvest index was evident for AC-04 (43%), followed by AC-07 (42%). The least harvest index resulted from AC-15 (33%).

Table 3a. Mean performance of wheat genotypes for morphological characters.

Genotypes	T/P	FLA (cm^2)	PH (cm)	DH	DM	SL(cm)	SPS
AC-1	7	16.8	60.3	118	148	5.6	11
AC-2	9	19.2	63.7	112	144	6.6	13
AC-3	11	18.3	68.3	115	156	9.1	17
AC-4	13	16.2	63.5	123	155	10.7	17
AC-5	6	23.4	77.1	119	157	7.4	11
AC-6	6	17.8	75.7	128	159	5.9	15
AC-7	8	20.8	80.2	116	151	7.5	17
AC-8	9	19.8	70.8	112	152	8.7	11
AC-9	10	18.2	72.5	114	154	7.5	17
AC-10	5	27.3	78.4	127	158	9.3	18
AC-11	10	24.5	63.4	111	154	11.5	21
AC-12	8	26.4	71.7	122	160	5.3	11
AC-13	7	22.5	82.7	120	149	7.4	17
AC-14	12	19.5	65.6	125	159	8.8	19
AC-15	10	23.12	80.6	125	161	9.1	19
AC-16	9	35.8	76.4	124	155	10.8	18
AC-17	8	23.8	74.5	126	162	8.1	19
AC-18	9	29.4	77.3	126	163	12.2	21
AC-19	7	29.8	83.4	120	152	11.3	24
AC-20	11	36.5	85.4	125	153	8.9	19
$LSD_{0.05}$	1.65	2.14	3.39	3.46	3.70	1.03	2.38
Means	9	24	73.6	120	155	8.6	17

FLA: Flag leaf area (cm^2), TP: Tillers plant^{-1}, PH: Plant height (cm), DH: Days to heading, SL: Spike length (cm), DM: Days to maturity, SPS: Spikelets spike^{-1}.

Table 3b. Mean performance of wheat genotypes for yield and yield-contributing traits.

Genotypes	GS	GW (g)	YP (kg)	SYP (kg)	HI %	GYH (t)	SYH (t)
AC-1	37	37.7	1.7	2.6	38	1.8	2.9
AC-2	41	37	1.7	2.9	37	1.9	3.3
AC-3	52	34.3	2.4	3.6	40	2.7	3.9
AC-4	47	37	2.6	3.5	43	2.9	3.9
AC-5	32	49	3.4	3.8	39	3.8	4.2
AC-6	45	28.3	1.9	3.3	35	2.1	3.7
AC-7	46	24.3	1.82	2.58	42	2	2.9
AC-8	43	41.3	2.6	4.8	35	2.9	5.3
AC-9	52	36	2.7	4.4	37	2.9	4.9
AC-10	54	34.7	2.5	4.1	37	2.8	4.7
AC-11	57	35.7	2.3	4.6	35	2.6	5.1
AC-12	37	47.6	3.4	4.9	40	3.7	5.5
AC-13	47	44.7	3.3	5.4	35	3.7	6
AC-14	49.	35.7	2.3	3.7	40	2.6	4.1
AC-15	40	47.3	3.1	5.8	33	3.4	6.4
AC-16	43	40.7	2.3	4.1	36	2.6	4.5
AC-17	47	34.3	2.54	4.45	37	2.8	4.9
AC-18	49	33	2.7	3.7	40	3	4.1
AC-19	61	34.7	2.26	3.5	38	2.5	3.9
AC-20	45	37.3	2.44	3.8	39	2.7	4.2
$LSD_{0.05}$	4.67	3.85	0.17	0.29	2.37	0.16	0.33
Means	46.09	37.5	2.51	3.9	38	2.8	4.4

GW: Thousand-grain weight (g), YP: Yield plot^{-1} (kg), SYP: Straw yield plot^{-1}, GS: Grains spike^{-1}, YP: Yield plot^{-1} (kg), HI: Harvest index (%), SYH: Straw yield hectare^{-1} (tons), GYH: grain yield hectare^{-1} (tons).

These findings reveal all tested accessions are significantly different for all traits under examination. It means that a substantial amount of genetic variation exists among genotypes, and this variation can be helpful for future wheat breeding. The existence of genetic variation is a primary need for initiating improvement or new varietal development. The greater the amount of variation, the better chances of enhancement. Early investigators, such as Kabir *et al.* (2017b) and Gebrie *et al.* (2020), obtained noteworthy differences for traits in wheat during their investigations. Peymaninia *et al.* (2012) and Tahmasebi *et al*. (2013) also described similar findings for grain weight, spike length, grains per spike, and spikelets spike^{-1}. Kaddem *et al*. (2014) found highly significant variations in straw yield, grain yield, plant height, and days to heading and maturity. Tiwari *et al*. (2017) reported remarkable variations among wheat genotypes for tillers, thousand-grain weight, flag leaf area, and spike length.

Variability components

Genotypic and phenotypic coefficients of variations (GCV and PCV), broad sense heritability (H^2), and genetic advance (G.A.) over means were fundamental indicators of the nature of gene action involved and guide the breeder's future progress of a breeding population (Table 4) (Nasarullah *et al*., 2017; Ali *et al*., 2024; Anwar *et al*., 2024).

Genetic parameters

High GCV and PCV estimates for the flag leaf area (25% and 26%), spike length (23% and 24%), tillers plant^{-1} (23% and 25%), straw yield hectare^{-1} (21% and 22%), yield plot^{-1} (20% and 20%), spikelets spike^{-1} (20% and 22%), and yield hectare^{-1} (20% and 21%) indicated a vast amount of genetic variation existed for these traits among genotypes. The selection for breeding with these attributes could be successful. Studies of genetic variations, diversity, and relationship of quantitative traits with grain yield have come from Kumar *et al.* (2009), Ali *et al*. (2008), and Rudra *et al.* (2015). Yield traits in wheat and significant genotypic differences were evident for similar traits under study. Moderate GCV and PCV were apparent for traits, i.e., straw yield plot^{-1} (18.25% and 19.5%), thousand-grain weight (16.13% and 17.28%), grains spike^{-1} (14.97% and 16.18%), and plant height (10.02% and 10.4%). Meanwhile, low GCV and PCV percentage appeared for harvest index (6.66% and 7.66%), days to heading (4.5% and 4.82%), and days to maturity (3.08% and 3.4%). These characters indicated limited scope for simple phenotypic selection, and manipulating genotype could be through hybridization. PCV values are higher than GCV for all traits, which shows variations are genetic. Levels of PCV and GCV above 20% proved high, whereas levels below 10% are seemingly low, with values between 10% and 20% deemed medium. Bekele (2020) and Mengistu Biru (2020) reported low GCV and PCV for days to 50% heading, straw yield, grain weight, and grains spike^{-1}. Other investigators, Ali *et al.* (2008), Abinasa *et al.* (2011), and Tiwari *et al.* (2017) also described similar results regarding plant height and the kernels per spike, noting greater GCV and PCV values (>10%). Low PCV and GCV (<5%) in test weight, days to maturity, and the spikelets per spike, indicate difficulty in controlling these features through plant breeding. Despite the slight variations, PCV values remained generally higher than GCV values.

Heritability

A crucial quantitative parameter called heritability gives proportions of genotype and environment (Table 5) toward the expression of a trait, enabling comparison of proportional contributions of genes and environment to the variance of characteristics within and between populations. Selection in early generations may be effective for the characters with high heritability (Rudra *et al*., 2015). Maximum heritability estimates appeared for grain yield hectare^{-1} (97%), trailed by grain yield plot^{-1} (96%), straw yield hectare^{-1} (95%), flag leaf area (95%), plants height (93%), the spike length (91%), straw yield per plot (88%), thousand-grain weight (87%), days to heading

Table 4. Simple phenotypic correlation coefficient among yield and different associated traits of wheat genotypes.

Traits	T/P	FLA	PH	DH	DM	SL	SPS	GS	GW	YP	SYP	HI	SYH
TP	1											\	
FLA	-0.105	1											
PH	-0.348**	0.590**	1										
DH	-0.170	0.349**	0.394**	1									
DM	0.013	0.156	0.174	0.607**	1								
SL	0.347**	0.432**	0.139	0.103	0.188	1	.						
SPS	0.274*	0.372**	0.341**	0.240	0.198	0.722**	1						
GS	0.174	0.136	0.105	-0.048	0.002	0.561**	0.739**	1					
GW	-0.058	0.140	0.054	0.005	0.075	-0.119	-0.338**	-0.480**	1				
GYP	-0.076	0.197	0.337**	0.156	0.429**	0.038	-0.073	-0.219	0.704**	1			
SYP	0.016	0.198	0.272*	0.083	0.323*	0.118	0.123	0.008	0.600**	0.737**	1		
HI	0.218	-0.078	-0.147	0.057	0.055	0.045	-0.025	0.001	0.273*	0.065	-0.523**	1	
SYH	0.015	0.198	0.271*	0.083	0.323*	0.117	0.122	0.007	0.600**	0.737**	1.000**	-0.524**	1
GYH	-0.076	0.198	0.346**	0.160	0.428**	0.053	-0.062	-0.216	0.705**	0.998**	0.742**	0.301*	0.741**

TP: Tillers plant^{-1}, FLA: Flag leaf area (cm^{2}), DH: Days to heading, PH: Plant height (cm), SL: Spike length (cm), DM: Days to maturity, SPS: Spikelets spike^{-1}, GW: Thousand-grain weight (g), YP: Yield plot^{-1} (kg), SYP: Straw yield plot^{-1} (kg), GS: Grains spike^{-1}, HI: Harvest index (%), SYH: Straw yield hectare^{-1} (tons), GYH: Grain yield hectare^{-1} (tons).

Table 5. Genotypic and phenotypic coefficients of variation, heritability (bs), and genetic advance over mean for yield and contributing traits in wheat genotypes.

Traits	VG	VP	GCV%	PCV%	H^{2}%	GAM%
TP	3.9	4.9	23	25	80	34
FLA	34.3	35.9	25	26	95	45
PH	54.4	58.6	10	10	92	17
DH	29.3	33.8	5	5	87	7
DM	22.7	27.8	3	3	82	5
SL	3.9	4.3	23	24	91	39
SPS	12.1	14.1	20	22	85	33
GS	47.6	55.6	15	16	86	24
GW	36.7	42.1	16	17	87	27
GYP	0.3	0.3	20	21	96	35
BYP	1.4	1.6	18	20	88	30
HI	6.6	8.4	7	8	76	10
GYH	0.3	0.3	20	21	97	35
SYH	0.8	0.9	21	22	95	36

TP: Tillers plant^{-1}, FLA: Flag leaf area (cm^{2}), DH: Days to heading, PH: Plant height (cm), SL: Spike length (cm), DM: Days to maturity, GW: Thousand-grain weight (g), SPS: Spikelets spike^{-1}, YP: Yield plot^{-1} (kg), SYP: Straw plot^{-1}, GS: Grains spike^{-1}, HI: Harvest index (%), SYH: Straw yield hectare^{-1} (tons), GYH: Grain yield hectare^{-1} (tons).

(87%), grains spike^{-1} (86%), spikelets spike^{-1} (85%), days to maturity (82%), tillers plant^{-1} (80%), and harvest index% (76%). High heritability estimates emerged for all traits under consideration, indicating that variations in the population are genotypic and heritable to the next generation, and phenotype is a good indicator of genotype. Our results aligned with the early findings of several researchers, such as Khan (2013), Kaddem *et al.* (2014), and Al-Tabbal and Al-Fraihat (2012). They also reported high heritability for important agronomic traits in wheat, such as, fertility percentage and productive tillers per plant, showing moderate heredity. Plant height, number of spikelets per spike, grains per spike, the length of the spike, weight of thousand-grains per spike, and yield per plant all showed high heritability estimates. Ahmed *et al.* (2022) reported high heritability for morphological and fruit traits in hot chilies.

Genetic advance

Genetic advance as percent over means varied from 5% for days to 50% heading and 43% for flag leaf area. High genetic advance as percent over mean reached calculations for flag leaf area (43%), spike length (39%), tillers plant^{-1} (36%), grain yield plot^{-1} (35%), grain yield hectare^{-1} (35%), straw yield hectare^{-1} (35%), spikelets spike^{-1} (33%), straw yield plot^{-1} (30%), thousand-grain weight (27%), and grains spike^{-1} (24%). Heritability alone could not clarify the nature of gene action behind controlling trait and the effectiveness of simple selection for further improvement of the attribute. High heritability along with genetic advance percent over means better explains the gene action involved and scope for phenotype selection. These results are at par with the early results of Ali *et al.* (2008), Kumar *et al.* (2014), and Kyosev and Desheva (2015). Moderate to low genetic advance recording resulted for plant height (17%), harvest index (10%), days to heading (7 %), and days to maturity (5%), revealing that non-additive genes control these characteristics, and simple phenotypic selection may not be essential for trait improvement. A modified selection or hybridization breeding would be helpful for the advancement of the traits. Direct selection based on phenotype would be helpful for the improvement of such features. Study results agreed with the findings of previous wheat crop investigators, i.e., Haq *et al.* (2008) and Kaddem *et al.* (2014). Their results have shown the thousand-grain weight, yield per plant, and grains per spike, among all the examined traits, demonstrated high heritability values along with strong genetic advance, creating favorable selection circumstances.

Correlation

Correlation provides knowledge related to the mutual relationship between different characters and helps in the indirect selection of associated qualities. The correlation between traits is due to the presence of pleiotropic genes, gene linkage, and epistatic effects; in addition to genetic causes, an environmental factor also affects the relationship among traits (Abinasa *et al.,* 2011; Qulmamatova *et al*., 2022). Correlation coefficients estimated for various attributes implied (Table 4) grain yield plot-^{1} showed a highly positively significant relationship with plant height (0.377**), days to maturity (0.429**), and thousand-grain weight (0.704**). However, straw yield plot^{-1} showed significant correlations with plant height (0.272*), days to maturity (0.323*), thousand-grain weight (0.600**), and yield plot^{-1} (0.737**). Grain and straw yields have shown positive nonsignificant correlations with the flag leaf area, tillers plant^{-1}, days to heading, spikelets spike^{-1}, spike length, and grains per spike. Significant correlation among these traits interlinked with each other; selection of a trait may positively affect the improvement of an associated trait indirectly. Hassani *et al.* (2022) also noticed grain yield’s positive correlations with plant height, days to maturity, harvest index, and biological yield. Other searchers, such as Fellahi *et al.* (2013) and Kabir *et al.* (2017b) also noted positive significant seed yield with harvest index, seed weight, plant height, maturity, and straw weight.

Harvest index indicated a significant and positive association with grain weight

(0.273*), while a negative relation with straw yield plot^{-1} (0.523**). It has not shown any significant association with the remaining traits of the study. Similar correlations also came from Wani *et al.* (2011) for harvest index, grain yield per plot, spike length, grains per spike, and thousand-grain weight. Plant height exhibited a negative and significant relationship with tillers (0.348**) and a significant positive relationship with flag leaf area (0.590**). This indicates improvement in tillers will be due to a reduction in height. Thousand-grain weight has shown a negatively significant correlation with spikelets per spike (0.338**) and grains spike^{-1} (0.480**), but a nonsignificant correlation with tillers, area of flag leaf, plant height, heading and maturity, and spike length. It revealed that improvement in spikelets and grains' number in spike could result in a decrease in weight of thousand grains. These findings were in line with previous findings on the genetic variability studies in wheat (Shah *et al.,* 2007; Khan *et al.,* 2015; Singh *et al.,* 2016; Hassani *et al.,* 2022).

CONCLUSIONS

Based on the study, a significant number of variations existed among tested accessions for various traits. Higher values of phenotypic coefficient of variation than genotypic coefficient of variation indicated little influences of environment on the traits. Higher values of heritability (H^2) were notable for all traits, indicating variations are heritable to next generations. High H^2 along with high genetic advance over mean was evident for most plant agronomic attributes. This shows the presence of additive genes for traits and maximum chances of improvement through selection in early generations. Yield was visibly positively associated with plant height, maturity time, grain weight, harvest index, and straw yield. These characteristics can benefit indirect improvement of the yield. During the study, genotypes AC-12, AC-13, AC-5, and AC-15 emerged as better grain yielders, and AC-15, AC-23, and AC-12 served as better for straw-yielding genotypes. These accessions can serve for new cultivars' development of wheat in the future based on the agroecological conditions of Gilgit-Baltistan.

ACKNOWLEDGMENTS

The authors thank the Mountain Agricultural Research Station, Chilas, District Diamer, for providing plant materials and technical support during the research and data recording.

REFERENCES

Abinasa M, Ayana A, Bultosa G (2011). Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum L. var. durum*) genotypes. *Afr. J. Agric. Res*. 17(6): 3972-3979.

Ahmed I, Nawab NN, Kabir R, Muhammad F, Intikhab A, Rehman AU, Farid MZ, Jellani G, Nadeem S, Quresh W, Ali M, Hussain MM, Ali I (2022). Genetic diversity for production traits in hot chilli (*Capsicum annuum* L). 2022. *Pak. J. Bot*. 54(6): 2157-2166.

Alam Z, Ali Z, Ahmad T, Aabdumanon (2006). Physicochemical characteristics of wheat varieties growing in the same and different ecological regions of Pakistan. *Pak. J. Biol. Sci.* 9(9): 1823-1828.

Ali A, Javed M, Ali M, Rahman SU, Kashif M, Khan SU (2024). Genetic variability, heritability, and genetic gain in F3 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.

Ali Y, Atta BM, Akhter J, Monneveux P, Lateef Z (2008). Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm*. Pak. J. Bot.* 40(5): 2087-2097.

Allard RW (1960). Principles of Plant Breeding. John Wiley and Sons Inc., New York. pp. 485.

Al-Tabbal JA, Al-Fraihat AH (2012). Heritability studies of yield and yield associated traits in wheat genotypes. *J. Agric. Sci.* 4(4): 11-22.

Anwar MT, Chaki T, Sagor GHM (2024). Genetic and stability analyses for the selection of terminal heat stress- tolerant wheat (*Triticum aestivum* L.) genotypes in Bangladesh. *SABRAO J. Breed. Genet.*56 (1) 1-17. http://doi.org/10.54910/sabrao2024.56.1.1.

Bekele Y (2020). Genetic variation and association of yield and yield-related traits in bread wheat (*Triticum aestivum* L.) genotypes under irrigation condition in South Omo, Southern Ethiopia (Doctoral dissertation, Haramaya University).

Burton GW, Devane EM (1953). Estimating heritability in tall fescus from replicated clonal material. *Agron. J.* 45(3): 473-481.

Cheruiyot D, Ojwang PO, Njau PN, Arama PF, Bhavani S (2015). Evaluation of advanced wheat (*Triticum aestivum* L.) lines for stem rust (*Puccinia graminis* f. sp. tritici) resistance and yield. *Int. J. Agron. Agric. Res*. 6(2): 57-70.

Degewione A, Dejene T, Sharif M (2013). Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. *Int. Res. J. Agric. Sci.* 2 (1): 19-29.

Fellahi Z, Hannachi A, Bouzerzour H, Boutekrabt A (2013). Correlation between traits and path analysis coefficient for grain yield and other quantitative traits in bread wheat under semi-arid conditions. *J. Agric. Sustain*. 3(1): 16-26.

Gebrie G, Bitew M, Abebe D, Gudissa T, Wondifraw D (2020). Adaptation and performance evaluation of bread wheat (*Triticum aestivum* L.) varieties in Guagusa-shikudad district of northwestern Ethiopia. *Asian J. Plant Sci*. Res. 10(6):64-68.

Haleem A, Hassan G, Iqbal A, Khan FU, Sajid M, Ahmad F, Khan RU, Ilyas M (2022). Genetic variability and correlation analysis in F_2 wheat populations. *Sarhad J. Agric*. 38(2): 398-408.

Haq WU, Malik MF, Rashid M, Munir M, Akram Z (2008). Evaluation and estimation of heritability and genetic advancement for yield-related attributes in wheat lines. *Pak. J. Bot*. 40(2): 1699-1702.

Hassani I, Nimbal S, Noori A, Singhe V (2022). Genetic variability analysis and correlation studies of bread wheat (*Triticum aestivum* L.) genotypes*. Ekin. J. Crop Breed. Genet.* 8(2):139-145.

IBM Corp. (2013). IBM SPSS Statistics for Windows, Version 22.0. IBM Corp., Armonk, NY.

Kabir R, Ahmed I, Rehman AU, Qamar M, Intikhab A, Rasheed A, Zakriya M, Muneer A, Nisa ZU (2017a). Evaluation of bread wheat genotypes for variability and association among yield and yield-related traits. *Int. J. Biosci.* 11(1): 7-14.

Kabir R, Intikhab A, Ahmed I, Qamar M, Hussain M, Uddin T, Jan R, Shah HA, Nisa ZU (2017b). Adaptability and yield evaluation of different commercial wheat varieties under agroecological of Chilas Diamer. *Int. J. Biosci*. 10(6): 195-201.

Kaddem WK, Marker S, Lavanya GR (2014). Investigation of genetic variability and correlation analysis of wheat (*Triticum aestivum* L.) genotypes for grain yield and its component traits. *Eur. J. Sci. Res*. 11(1): 6529-6538.

Khan SA (2013). Genetic variability and heritability estimates in F_2 wheat genotypes. *Int. J. Agric. Crop Sci*. 9(5): 983-986.

Khan WU, Mohammad F, Khan FU, Zafar FZ, Ghuttai G (2015). Correlation studies among productions traits in bread wheat under rainfed conditions. *Am-Eur. J. Agric. Environ. Sci*. 15(10): 2059-2063.

Kumar B, Lal GM, Ruchi, Upadhyay A (2009). Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). *Asian J. Agric. Sci*. 1(1): 4-6.

Kumar N, Markar S, Kumar V (2014). Studies on heritability and genetic advance in timely sown bread wheat (*Triticum aestivum* L.). *Bio. Disc.* 5:64-69.

Kyosev B, Desheva G (2015). Study on variability, heritability, genetic advance, and associations among characters in emmer wheat genotypes (*Triticum dicoccon* Schrank). *J. BioSci. Biotechnol*. 4(1): 221-228.

Mengistu Biru H (2020). Genetic variability of durum wheat (*Triticum turgidum* var. durum L.) genotypes for yield, yield-related and grain-quality traits under irrigated conditions of Middle Awash, Ethiopia (Doctoral dissertation, Hawassa University).

Microsoft Corporation (2018). Microsoft Excel (2007). Retrieved from https://office.microsoft.com/excel.

Nasarullah R, Uddin F, Jamal M (2017). Interpreting wheat genotypes for grain yield under different regimes of Khyber Pakhtunkhwa. *Pak. J. Agric. Res*. 30(1): 107-121.

Pakistan Economic Survey (2022-2023). Finance Division, Ministry of Finance and Revenue, Government of Pakistan, Islamabad, Pakistan.

Peymaninia Y, Valizadeh M, Shahryari R, Ahmadizadeh M (2012). Evaluation of morpho-physiological responses of wheat genotypes against drought stress in presence of a leonardite derived humic fertilizer under greenhouse condition. *J. Anim. Plant Sci*. 22(4): 1142-1149.

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

Reif JC, Zhang P, Dreisigacker S, Warburton ML, Van-Ginkel M, Hoisington D, Melchinger AE (2005). Wheat genetic diversity trends during domestication and breeding. *Theor. Appl. Genet.* 110: 859-864.

Rudra V, Naik S, Biradar S, Yadawad A, Desai SA, Veeresha BA (2015). Study of genetic variability parameters in bread wheat (*Triticum aestivum* L.) genotypes. *J. Agric. Sci.* 6(1): 123-125.

Sabaghnia N, Jonmohammadi M, Segherloo AE (2014). Evaluation of some agro-morphological traits diversity in Iranian bread wheat genotypes. *Ann. Uni Maria Cure-Sklodoweska Lublin- Polonia* 19(1): 79-92.

Shah Z, Shah SMA, Hassnain A, Khalil IH, Munir I (2007). Genotypic variation and correlation studies in bread wheat. *Sarhad J. Agric*. 23(3): 633-636.

Singh K, Punia MS, Singh V (2016). Inter-relationship between grain yield and its component characters in F2 generation of bread wheat (*Triticum aestivum* L.). *Int. J. Curr. Adv. Res.* 5(4): 749-751.

Singh RK, Chaudhary BD (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publ. New Delhi.

Singh VK, Sharma BB, Dwivedi BS (2002). The impact of diversification of a rice–wheat cropping system on crop productivity and soil fertility. *J. Agric. Sci.* 139(4): 405-412.

Sohail M, Hussain I, Abbas SH, Qamar M, Noman M (2013). Effect of split N fertilizer application on physio-agronomic traits of wheat (*Triticum aestivum* L.) under rainfed conditions. *Pak. J. Agric. Res.* 26(2): 71-78.

Steel RGD, Torrie JH (1980). Principles and Procedures of Statistics. McGraw Hill Book Co. New York. pp. 107-109.

Tahmasebi G, Heydarnezhadian J, Aboughadareh AP (2013). Evaluation of yield and yield components in some promising wheat lines. *Int. J. Agric. Crop. Sci.* 5(2): 2379-2384.

Tiwari A, Mishra DK, Shukla RS (2017). Genetic analysis of yield components and physiological characters under changing climate in wheat. *Int. J. Curr. Microbiol. Appl. Sci*. 6(9) 3525-3530.

Wani BA, Ram M, Yasin A, Singh E (2011). Physiological traits in integration with yield and yield components in wheat (*Triticum aestivum* L.) study of their genetic variability and correlation. *Asian J. Agric. Res*. 5(3): 1-7.

Wysocka K, Cacak-Pietrzak G, Feledyn-Szewczyk B, Studnicki M (2024). The baking quality of wheat flour (*Triticum aestivum* L.) obtained from wheat grains cultivated in various farming systems (organic vs. integrated vs. conventional). *Appl. Sci*. 14(5): 1886-1905.