



Full Length Article

Assessment of Genetic Diversity in Hexaploid Wheat of Northern Areas of Pakistan (Gilgit Baltistan) using Morphological Marker

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Abstract

Germplasm of bread wheat collected from Gilgit Baltistan (GB) was characterized using morphological markers. One hundred and fifty-seven hexaploid wheat accessions were planted for two growing seasons in GB agro-climatic condition. Accessions showed sufficient genetic differences for all the morphological characters studied. Maximum variability was observed for biological yield followed by harvest index and yield/plant respectively. The strong positive correlation ($p < 0.01$) was recorded among length of spike - total spikelets/spike, seed yield per plant-spike length, total spikelets/spike - plant yield, total spikelets/spike - harvest index and yield/plant - harvest index. Highly significant negative correlation was recorded for number of days to spike emergence - spike length, days to spike emergence - seed yield/plant, plant height - spike length, plant height - total spikelets/spike, plant height - seed yield per plant, plant height -1000 seed weight, plant height - harvest index. The phylogenetic analysis further classified these genotypes into three major groups (A-C). The groups A, B and C contained 61, 48 and 48 genotypes, respectively. The high yielding screened genotypes can be utilized in further breeding programs aimed at improving common wheat cultivars suitable for high altitude area. © 2019 Friends Science Publishers

Keywords: Correlation; Genetic diversity; Gilgit Baltistan; Morphological characters; *Triticum aestivum*; Yield

Introduction

Wheat (*Triticum aestivum* L. genomically AABBDD, $2n=6x=42$) is cultivated worldwide on an area of 600 mha with a total annual production of 220 million tons (FAO, 2014). The hexaploid wheat is cultivated in maximum area of the world and cultivated in 95% of wheat growing areas (Pomeranz and Munk, 1981). In Pakistan, wheat is cultivated in large areas and mostly the hexaploid species is cultivated on 1.8 mha area with total production and yield of 1.8 mha/year and 2.5 tons/ha, respectively (Anonymous, 2014; FAO, 2014).

The cultivation of hexaploid wheat is decreasing in world due to its replacement by high yielding and newly identified landraces and the release of new elite pure lines or varieties (Bhullar *et al.*, 2011). It is the key for wheat improvement to replace the existing low yield wheat varieties with new high yielding landraces; hence its production can be improved many times. To improve both quality and quantity of crop species is the key to know about the morpho-biochemical and molecular processes that control its growth and development (Jan *et al.*, 2016; Jan *et al.*, 2017a; Afzal *et al.*, 2018; Ibrar *et al.*, 2018) The new and novel wheat genotypes can be produced by testing in various agro-

climatic condition and stress environments to check its stability. The high yielding genotypes can be selected if maximum divergence exists among the testing germplasm (Ali *et al.*, 2008). Agro-morphological based diversity is important to identify elite wheat genotypes. The presence of no genetic divergence among Pakistani wheat genotypes is a key cause of stagnant yield (Ijaz and Khan, 2009).

Gilgit-Baltistan contained maximum diverged plant species including the hexaploid wheat type. Different areas of this province have different hexaploid wheat landraces showing varying level of morphological response. Hence, it is a prerequisite to elaborate genetic structure and estimate existing genetic diversity in the landraces. In early studies few morphological markers have been utilized to screen novel genotypes. These markers though used successfully in wheat breeding and genetics studies, but can be affected by the environment (Islam and Shepherd, 1992).

To date no report is available on the genetic diversity study from GB in the identification and characterizing of novel high yielding genotype. Keeping in views these gaps, the current experiment was conducted to identify and characterize elite genotypes from the collected wheat germplasm from GB province using morphological markers under the specific agro-climatic conditions of Gilgit Baltistan.

Materials and Methods

Area Description

Northern areas of Pakistan (mainly Gilgit Baltistan) are important mountainous area including world famous mountains like Pamir, Himalaya, Hindukush and Karakoram (Anonymous, 2014). The soils are relatively low in organic matter, very free-draining, contain virtually no clay and have low natural fertility. The climate is basically Himalayan, though modified by location and altitude. At lower altitudes the main crop is winter wheat followed by maize. At altitude barley and wheat are the major crops (Hashmi and Shafiullah, 2003).

Plant Materials and Experimental Details

In present study, 157 accessions of common wheat collected from GB were acquired from Plant Genetic Resources Institute, National Agricultural Research Centre, Islamabad, Pakistan. These genotypes belong to altitude from 1500 meters to 2500 meters above sea level (Table 1).

Plants were grown in the field for two years at Agricultural Research Center, Gilgit during 2014-2015 and 2015-2016. All the genotypes were planted in RCBD method with three replications of each accession. The plot was design having 3 rows of 3-meter length. The space from one row to other was maintained 30 cm and space between plants were kept 10 cm. Recommended agricultural practices were applied from start to end of experiment. Data for all quantitative traits were measured by taking five random single plants by following descriptor of IBPGR (1985) with minor modification as given below;

Morphological Traits

Days to germination and germination percentage: It was measured visually and the germination was noted from number of days to sowing.

Germination percentage was measured by dividing germinated plants in a row by total seed sown in respective line multiplying by 100.

Number of Days to Spike Emergences

Number of days of spike emergence spike was counted from germination at 2-4 spikelet stage.

Days to 50% Heading

The days to 50% heading (from the sowing date till 50% heading) was visually taken with respect to the whole plot.

Number of days to 90% Maturity

The data for number of days to 90% maturity was conducted when spike matured and its color changed from green to pale yellow.

Plant Height

Plant height was measured in meter from five random selected plants from base to top of apex of the spike (ignoring awns).

Length of Spike

Length of spike of the mother shoot was recorded with help of scale from the base to the tip to the spike (ignoring awns).

Number of Spikelet's per Spike

The number of spikelets/spike was selected randomly and counted from randomly selected five plants.

Yield per Plant

Randomly selected five plants from each plot were threshed manually and grains were weighted by electronic balance.

Thousand Seed Weight

Thousand seeds from each genotype were counted and weighted.

Biological Yield per Plant

The mature plants of each landrace were harvested and whole plant along with leaves and straws were measured.

Harvest Index

The harvest index was measured by using following formula;

$$\text{Harvest Index} = \text{grain yield/biological yield} \times 100$$

Data Analysis

The basic statistics data was recorded for all studied traits and mean, median, minimum, maximum, St. deviation, St. error, coefficient of variation, cluster analyses and Analysis of Variance (ANOVA) were performed by using computational software "PAST" (PAleontological Statistics, version 3.11).

Results

Morphological Diversity

In present study twelve economically important quantitative traits were studied for 157 hexaploid wheat genotypes for two years experiment. Significant level of genetic variability ($p < 0.01$) was recorded for the accessions and accession x year interaction of the studied traits indicating that all germplasm showed maximum variability for yield and its yield related traits (Table 2a and b).

Table 1: Germplasm accessions of hexaploid wheat collected from Northern areas of Pakistan

Sr. No.	Accession No.	Site of collection	District	Sr. No.	Accession No.	Site of collection	District	Sr. No.	Accession No.	Site of collection	District
1	PAK0016199	Jutial	Glt	54	PAK0016459	Jutal	Glt	107	PAK0017505	Hushe Valley	Hun
2	PAK0016203	Sultan Abad	Glt	55	PAK0016460	Chalt	Hun	108	PAK0017506	Hushe Valley	Hun
3	PAK0016204	Hunza	Hun	56	PAK0016462	SkandarAbad	Hun	109	PAK0017507	Hushe Valley	Hun
4	PAK0016205	Oshikhandas	Glt	57	PAK0016463	Gulmit	Hun	110	PAK0017508	Hushe Valley	Hun
5	PAK0016206	Oshikhandas	Glt	58	PAK0016464	Murtiza Aabad	Hun	111	PAK0017509	Hushe Valley	Hun
6	PAK0016207	Oshikhandas	Glt	59	PAK0016471	Moorkhund	Hun	112	PAK0017510	Hushe Valley	Hun
7	PAK0016208	Oshikhandas	Glt	60	PAK0016475	Gakuch	Ghz	113	PAK0017511	Hushe Valley	Hun
8	PAK0016209	Oshikhandas	Glt	61	PAK0016476	Tawos	Ghz	114	PAK0017512	Hushe Valley	Hun
9	PAK0016210	Oshikhandas	Glt	62	PAK0016481	Hakis	Ghz	115	PAK0017513	Hushe Valley	Hun
10	PAK0016213	Oshikhandas	Glt	63	PAK0016502	Gazar	Ghz	116	PAK0017514	Hushe Valley	Hun
11	PAK0016214	Oshikhandas	Glt	64	PAK0016521	Gulpur	Ghz	117	PAK0017515	Hushe Valley	Hun
12	PAK0016215	Oshikhandas	Glt	65	PAK0016522	Gulpur	Ghz	118	PAK0017620	Hushe Valley	Hun
13	PAK0016216	Oshikhandas	Glt	66	PAK0016857	Keris	Ghz	119	PAK0017627	Hushe Valley	Hun
14	PAK0016218	Oshikhandas	Glt	67	PAK0016858	Keris	Ghz	120	PAK0017628	Hushe Valley	Hun
15	PAK0016219	Oshikhandas	Glt	68	PAK0016860	Astor	Ast	121	PAK0017629	Hushe Valley	Hun
16	PAK0016221	Oshikhandas	Glt	69	PAK0016861	Astor	Ast	122	PAK0017631	Hushe Valley	Hun
17	PAK0016222	Oshikhandas	Glt	70	PAK0017430	Shysote	Unknown	123	PAK0017632	Hushe Valley	Hun
18	PAK0016223	Oshikhandas	Glt	71	PAK0017431	Singal	Ghz	124	PAK0017633	Hushe Valley	Hun
19	PAK0016225	Gulmit	Hun	72	PAK0017432	Damas	Ghz	125	PAK0017634	Hushe Valley	Hun
20	PAK0016227	Gulmit	Hun	73	PAK0017436	PINGAL	Ghz	126	PAK0017636	Hushe Valley	Hun
21	PAK0016228	Gulmit	Hun	74	PAK0017437	Chashi	Unknown	127	PAK0017637	Hushe Valley	Hun
22	PAK0016229	Gulmit	Hun	75	PAK0017439	RahimAbad	Glt	128	PAK0017758	Hushe Valley	Hun
23	PAK0016230	Gulmit	Hun	76	PAK0017456	Yogo	Unknown	129	PAK0017759	Hushe Valley	Hun
24	PAK0016231	Gulmit	Hun	77	PAK0017461	Lunkha	Unknown	130	PAK0017760	Hushe Valley	Hun
25	PAK0016297	Gulmit	Hun	78	PAK0017463	Saling	Ghizer	131	PAK0017761	Hushe Valley	Hun
26	PAK0016429	Rai Kot	Dia	79	PAK0017465	Kanday	Unknown	132	PAK0017762	Hushe Valley	Hun
27	PAK0016430	Gilgit	Glt	80	PAK0017466	Hushe Valley	Ghn	133	PAK0017763	Hushe Valley	Hun
28	PAK0016431	Sakowar	Glt	81	PAK0017473	Hushe Valley	Hun	134	PAK0017764	Hushe Valley	Hun
29	PAK0016432	Munawar	Glt	82	PAK0017478	Hushe Valley	Hun	135	PAK0017765	Hushe Valley	Hun
30	PAK0016433	Paribangla	Glt	83	PAK0017479	Hushe Valley	Hun	136	PAK0017766	Hushe Valley	Hun
31	PAK0016434	Chamangarh	Hun	84	PAK0017480	Hushe Valley	Hun	137	PAK0017767	Hushe Valley	Hun
32	PAK0016435	Mohammad abbad	Glt	85	PAK0017481	Hushe Valley	Hun	138	PAK0017768	Hushe Valley	Hun
33	PAK0016436	Shil Mish Das	Glt	86	PAK0017482	Hushe Valley	Hun	139	PAK0017769	Hushe Valley	Hun
34	PAK0016437	Nomal Das	Glt	87	PAK0017483	Hushe Valley	Hun	140	PAK0017770	Hushe Valley	Hun
35	PAK0016438	Nomal	Glt	88	PAK0017484	Hushe Valley	Hun	141	PAK0017771	Hushe Valley	Hun
36	PAK0016439	Hurmay	Unknown	89	PAK0017485	Hushe Valley	Hun	142	PAK0017772	Hushe Valley	Hun
37	PAK0016440	Naltar Pine	Glt	90	PAK0017486	Hushe Valley	Hun	143	PAK0017835	Hushe Valley	Hun
38	PAK0016441	Hurmay	Unknown	91	PAK0017487	Hushe Valley	Hun	144	PAK0017836	Hushe Valley	Hun
39	PAK0016442	Hanuchal	Hun	92	PAK0017488	Hushe Valley	Hun	145	PAK0017837	Hushe Valley	Hun
40	PAK0016443	Sassi	Glt	93	PAK0017489	Hushe Valley	Hun	146	PAK0017838	Hushe Valley	Hun
41	PAK0016444	Sassi	Glt	94	PAK0017491	Hushe Valley	Hun	147	PAK0017839	Hushe Valley	Hun
42	PAK0016445	Shengus	Unknown	95	PAK0017492	Hushe Valley	Hun	148	PAK0017840	Hushe Valley	Hun
43	PAK0016446	Yellow	Hun	96	PAK0017494	Hushe Valley	Hun	149	PAK0017841	Hushe Valley	Hun
44	PAK0016447	Talu	Skr	97	PAK0017495	Hushe Valley	Hun	150	PAK0017842	Hushe Valley	Hun
45	PAK0016448	Ajr Port	Glt	98	PAK0017496	Hushe Valley	Hun	151	PAK0017902	Hushe Valley	Hun
46	PAK0016449	Gambus Skadu	Skr	99	PAK0017497	Hushe Valley	Hun	152	PAK0017903	Hushe Valley	Hun
47	PAK0016450	Hussin Aabd	Hun	100	PAK0017498	Hushe Valley	Hun	153	PAK0017904	Hushe Valley	Hun
48	PAK0016451	Hussin Aabd	Hun	101	PAK0017499	Hushe Valley	Hun	154	PAK0017905	Hushe Valley	Hun
49	PAK0016452	Lamsa	Unknown	102	PAK0017500	Hushe Valley	Hun	155	PAK0017906	Hushe Valley	Hun
50	PAK0016454	Shingrela Resor	Skr	103	PAK0017501	Hushe Valley	Hun	156	PAK0017970	Hushe Valley	Hun
51	PAK0016455	Shookha	Unknown	104	PAK0017502	Hushe Valley	Hun	157	PAK0017971	Hushe Valley	Hun
52	PAK0016456	Hajigam	Skr	105	PAK0017503	Hushe Valley	Hun				
53	PAK0016457	Sordas	Unknown	106	PAK0017504	Hushe Valley	Hun				

Average days taken to germination ranged from 17.67-25 days and 16.3- 24.3 days, for 1st and 2nd years respectively. The coefficient of variation was higher (7.96) during 2nd year as compared to 1st year (5.05) (Table 2a). However, low level of genetic variability was observed for this trait in both years. The average germination rate among genotypes ranged from 23.3-90.0% and 66.7-100%, for 1st and 2nd year with maximum variability value (26.6) for 1st year (Table 2a).

Average number of days to spike emergence ranged from 62.3-89.3 days and 67-86.67 days, for 1st and 2nd years, respectively. In addition, lower genetic variability (4.6 and 4.8) was recorded for both years respectively (Table 2a). Average number of days to 50% heading in 157 hexaploid wheat accessions ranged from 70.0-98.3 days and 75-102.33, for 1st and 2nd years, respectively. Lower phenotypic variability was recorded for days taken to heading. It means that majority of genotypes showed similar performance for

Table 2a: The morphological response of different wheat landraces in two years experiments at GB

Parameter	Days to germination (days)		Germination (%)		Days spike emergence (days)		Days 50% heading (days)		Days 90% maturity (days)	
	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2
Average	21.6	19.89	64.4	81.8	76.0	77.45	86.4	88.98	127.2	134
Min	19.3	16.3	23.3	66.7	62.3	67	70.0	75	113	123.33
Max	25.0	24.33	90.0	100	89.3	86.67	98.3	102.33	142	149.33
Median	21.67	19.67	70	80.33	76.3	78.33	86.33	88.67	126.67	133.33
St. Error	0.08	0.13	1.47	0.62	0.28	0.33	0.29	0.35	0.40	0.38
St. Dev	1.09	1.58	17.3	7.72	3.48	3.75	3.71	4.35	5.03	4.77
Coeff. Var	5.05	7.96	26.9	9.4	4.59	4.84	4.29	4.88	3.96	3.55
F value accession	303.69**	26.42**	8.59**	4.78**	10.33**	4.97**	171.50**	38.82**	6.35**	12.30**
F value accession * Year		14.47**		7.29**		6.8**		6.79**		18.13**

Table 2b: The morphological response of different wheat landraces in two years experiments at GB

parameter	Plant height (cm)		Spike length (cm)		Spikelet / spike (No.)		Yield per plant (g)		1000 grain wt (g)		Biol Yield (g)		Harvest index (%)	
	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2	Year 1	Year 2
Average	76.7	86.32	11.17	13.16	19.19	23.71	17.0	26.1	46.8	49.3	67.05	98.43	25.9	27.16
Min	64.0	70.67	8.6	9.25	15.33	17.92	11.8	14.4	30.0	29.7	50.42	47.2	16.3	18.5
Max	89.0	103.67	13.6	17	23.0	27.9	22.27	35.1	60.3	64.2	132.61	151.29	38.7	38.5
Median	76.33	86.33	11.13	13.2	19.0	23.8	16.57	26.4	47.00	49.9	65.42	94.3	25.00	27.5
St. Error	0.53	0.61	0.09	0.12	1.30	0.16	0.22	0.33	0.58	0.61	0.88	1.69	0.37	0.39
St. Dev	6.67	7.6	1.09	1.53	1.64	2.05	2.72	4.17	7.23	7.54	10.99	21.22	4.63	4.9
Coeff. var	8.70	8.81	9.79	11.61	8.54	8.66	16.01	15.97	15.45	15.28	16.39	21.55	17.80	18.06
F value accession	6.65**	13.33**	7.76**	9.42**	8.26**	33.15**	6.73**	6.95**	7.33**	6.58**	18.15**	6.64**	7.94****	7.79**
F value Accession * year	16.03**		14.67**		20.91**		10.73**		9.62**		6.91**		14.14**	

**=Highly significant at $p < 0.01$

this particular trait in both years' experiments (Table 2a). The average number of days to 90% maturity values ranged from 113-142 days and 123.33-149.33 days, for 1st and 2nd years, respectively. However lower genetic variability was recorded for both years with coefficient values of 3.96 and 3.55 for both years respectively (Table 2a).

The mean plant height values ranged from 64.0-89.0 cm and 70.67-103.6 cm, for the two consecutive years (Table 2b). The level of variability was found very low for both years. Average spike length values ranged from 8.6-13.6 cm and 9.25-17 cm, for the 1st and 2nd year, respectively (Table 2b). Maximum number of spikelets per spike for first year was 23 and for second year maximum number of spikelets per spike was 27.9 (Table 2b).

The grain yield/plant trait showed maximum variability among genotypes and its values ranged from 11.8-22.2 and 14.4-35.1 g, for 1st and 2nd years, respectively. The coefficient of variation values for this trait was found almost similar (16.01 and 15.97) for both consecutive years (Table 2b). Similarly, the thousand grain weight values ranged from 30-60.3 g for first year planting while for second year planting it ranged from 29.7-64.2 g (Table 2b). In addition, the mean biological yield/plant ranged from 50.42-132.6 g and 47.2-151.29 g, for 1st and 2nd year, respectively. The coefficient of variation value was found high (21.55) for 2nd year than 1st year (16.39) (Table 2b). It showed that maximum variability exists among genotypes for this trait in 2nd year than 1st year experiment. The mean harvest index values ranged from 16.3-38.7 and 18.5-38.5, for 1st and 2nd years, respectively with maximum genetic variability values for both years (Table 2b).

Correlation for different Quantitative Traits

Strong positive correlation ($p < 0.01$) was observed among days taken to germination - days to spike emergence, days taken to germination - days to 50% heading, days to spike emergence - days to 50% heading, days to spike emergence - days to 90% maturity, days to 50% heading - days to 90% maturity, spike length - number of spikelets per spike, spike length - seed yield per plant, spike length - 1000 seed weight, spike length - harvest index, number of spikelets per spike - seed yield per plant, number of spikelets per spike - 1000 seed weight, number of spikelets per spike - biological yield, number of spikelets per spike - harvest index, seed yield per plant - 1000 seed weight, seed yield per plant - biological yield, seed yield per plant - harvest index and 1000 seed weight - harvest index (Table 3). However, some studied traits showed negative correlation with one another (Table 3).

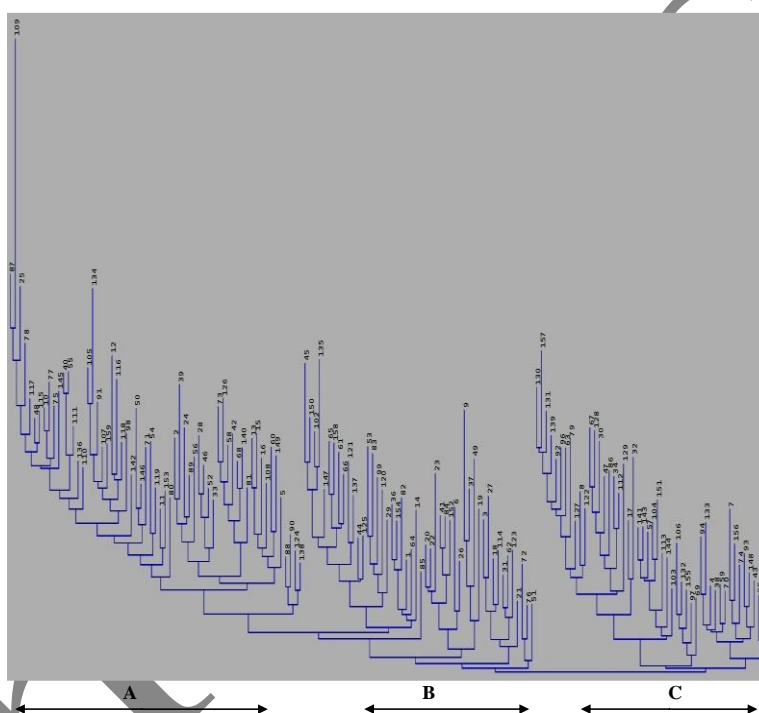
Phylogenetic Relationship

Based on data of 5 phenological and 7 morphological characters, one hindered and fifty-seven hexaploid wheat landraces were clustered in 3 main groups using "neighbor joining cluster analysis" of PAST statistical package (Paleontological Statistics). The total genotypes were clustered into three main groups viz., A, B and C comprised 61, 48 and 48 accessions, respectively (Fig. 1). The first group genotypes had better yield/plant, biological yield and early days to heading and maturity. The second group consisted genotypes having average yield/plant and biological yield, maximum spike length, late maturity and heading and maximum height.

Table 3: Correlation coefficients (lower diagonal) and p value (upper diagonal) regarding 12 morphological characters in 157 accessions of hexaploid wheat

-	A	B	C	D	E	F	G	H	I	J	K	L
A		0.94737	3.4787	1.8805	0.061283	0.34277	0.35198	0.007401	0.03797	0.55094	0.29338	0.20262
B	-0.005311		0.70579	0.36767	0.92439	0.2944	0.39248	0.55465	0.47783	0.74898	0.40993	0.47861
C	0.32401	0.030365		2.4046	7.1529	0.13173	0.034108	0.006321	0.00874	0.02659	0.38351	0.0535
D	0.33427	0.072379	0.77983		1.7268	0.6609	0.61318	0.21323	0.25569	0.27223	0.46265	0.53051
E	0.14971	0.0076354	0.44146	0.5039		0.29138	0.023558	0.16956	0.13021	0.41219	0.18725	0.59087
F	0.076213	-0.084205	0.12082	-0.035274	0.08473		0.004420	0.000276	0.00074	1.5149	0.98584	0.00024
G	-0.074777	-0.068716	-0.16923	-0.040654	-0.18066	-0.22603		5.5023	6.2808	6.85	0.35481	2.0614
H	-0.21299	-0.047504	-0.21706	-0.09989	-0.11017	-0.28642	0.4171		8.8453	4.4134	2.0971	2.1129
I	-0.16579	-0.057058	-0.20862	-0.091253	-0.1213	-0.26653	0.3517	0.75136		5.389	1.2537	5.3924
J	-0.04795	0.025739	-0.17699	-0.08816	-0.065902	-0.40426	0.35036	0.51644	0.55374		0.14289	7.2575
K	-0.084382	-0.066221	-0.070023	-0.059039	-0.1058	-0.0014281	0.074339	0.33248	0.50688	0.11746		3.2247
L	-0.10224	0.056957	-0.15438	-0.050429	-0.043229	-0.2887	0.33276	0.39992	0.44468	0.46667	-0.49798	

Coefficient correlation (r) values among 12 quantitative traits (P<0.01); A= Days taken to germination, B=Germination percentage, C=Days to spike emergence, D=Days to 50% heading, E= Days to 90% maturity, F=plant height, G= spike length, H= number of spikelets per spike, I= seed yield per plant, J= 1000 seed weight, K=biological yield and L=harvest index

**Fig. 1:** Cluster diagram based on 12 morphological characters in 157 accessions of hexaploid wheat collected from Northern areas of Pakistan

In last group majority of genotypes had poor yield response, maximum height, late maturity, maximum spike length and poor% germination. Accessions PAK0017483 and PAK 0017492 were the most distantly related accessions and it is suggested that these accessions should be used in further breeding programs aimed at improving hexaploid wheat cultivars in the area.

Discussion

The morphological based diversity helped in the identification improved wheat genotypes for further breeding programs. In present study the intra-specific divergence among 157 hexaploid wheat landraces were evaluated under climatic conditions of GB and maximum variability was

observed for twelve important quantitative traits. However, the level of variability was found higher for key yield related traits *i.e.*, harvesting index, biological yield, yield/plant, 100 grain weight and spike length. The yield and yield related trait response varied with type of genotype and in different years experiment (Table 2a and b). These high yielding elite genotypes can be used for further improvement of this plant species. Ali *et al.* (2008) reported maximum genetic variability in 70 hexaploid Pakistani wheat genotypes for important quantitative traits including length of spike and total tillers/plant, plant yield and 1000 weight of grain and for height of plant. Kalhoro *et al.* (2015) also recorded significant diversity for important quantitative traits of wheat. The present study findings are verified with findings of Niaz *et al.* (2014) and

Gashaw et al. (2007), who also recorded maximum diversity in studied wheat germplasm.

The correlation analysis was also performed for all 12 important quantitative traits. These traits showed both positive and negative correlation with one another. The spike traits, days to early maturity, 1000 grain weight, biological yield showed positive correlation with yield/plant (Table 3). Like present study, previously Raut et al. (1995), Mondal et al. (1997) and Sinha et al. (2006) also found strong positive relationship between 1000 grain weights with plant yield in hexaploid wheat. Ali et al. (2008) observed that plant yield in wheat had strong positive correlations with number of spikelets and number of grains per spike and significant positive correlations with spike length. In light of present and past findings, it may be useful to select short stature bold grained hexaploid wheat genotypes to develop high yielding varieties (Ali et al., 2008).

The cluster analysis is a method that classifies genotypes into different groups and sub-groups on the basis on similarity exist among them. Cluster analysis is helpful for understanding the trend of evolution and choosing genetically diverse genotypes (Jan et al., 2017b; Zhu et al., 2018). The genotypes cluster in one group, are in close relation with one another. The results of present study the 157 genotypes were clustered into three main groups on the basis on 12 important quantitative traits. Our results shows similarity with the findings of Ali et al. (2013) who recorded two major groups in 12 wheat genotypes studied. In similar study conducted by Gurcan et al. (2017) who classified 70 Turkey wheat genotypes into three major wheat populations i.e., diploid, tetraploid and hexaploid wheat. They recorded two major groups (A and B) on the basis of molecular markers. The group A consisted diploid *T. monococcum* and tetraploid *T. dococcum* populations and *T. durum* check cultivars. While group B included fully hexaploid wheat tir genotypes. In similar study, Meng et al. (2018) classified 69 maize landraces from Tibet, China into 4 major groups on the basis of some important quantitative traits.

Conclusion

Present results highlighted for the first time that genotypes of hexaploid wheat collected from GB, Pakistan processes maximum morphological based diversity for yield and other economically quantitative traits. The yield and yield related response varied among genotypes. These diverged wheat landraces are recommended for future breeding/hybridization programs to increase yield and quality of elite wheat genotypes in the area. However, we also recommend, testing these genotypes in other areas of country to check its stability.

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References

- Afzal, M., S.S. Alghamdi, H.M. Migdadi, M.A. Khan and M. Farooq, 2018. Morphological and molecular genetic diversity analyses of chickpea genotypes. *Intl. J. Agric. Biol.*, 20: 1062–1070
- Ali, A., N. Ali, I. Ali, M. Adnan, N. Ullah and Z.A. Swati, 2013. Morphological and genetic diversity of Pakistani wheat germplasm under drought stress. *Intl. J. Adv. Res. Technol.*, 2: 186–192
- Ali, Y., B.M. Atta, J. Akhter, P. Monneveux and Z. Lateef, 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pak. J. Bot.*, 40: 2087–2097
- Anonymous, 2014. Agricultural Statistics of Pakistan. Pakistan Bureau of statistics, Islamabad, Pakistan
- Bhullar, N., K. Streel, M. Mackay, N. Yahiaoui and B. Keller, 2011. Unlocking wheat genetic resources for the molecular identification of previously undescribed functional alleles at *Pm3* resistance locus. *Proc. Nat. Acad. Sci.*, 108: 7727–7732
- FAO, 2014. Food and Agriculture Organization. www.fao.org
- Gashaw, A., H. Mohammed and H. Singh, 2007. Genetic divergence in selected durum wheat genotypes of Ethiopian germplasm. *Afr. Crop Sci. J.*, 15: 67–72
- Gurcan, K., F. Demirel, M. Tekin, M.S. Demirel and T. Akar, 2017. Molecular and agro-morphological characterization of ancient wheat landraces of turkey. *BMC Plant Biol.*, 17: 171
- Hashmi and Shafiqullah, 2003. NASSD Background Paper: Agriculture and Food Security. IUCN Pakistan, Northern Areas Programme, Gilgit. 1–136
- IBPGR, 1985. Descriptors of wheat (revised) Rome: IBPGR Secretariat
- Ibrar, D., M.A. Khan, T. Mahmood, M. Ahmad, I.A. Hafiz, S.A. Jan and R. Ahmad, 2018. Determination of heterotic groups among sunflower accessions through morphological traits and total seed storage proteins. *Intl. J. Agric. Biol.*, 20: 2025–2031
- Ijaz, S. and I.A. Khan, 2009. Molecular characterization of wheat germplasm using microsatellite markers. *Genet. Mol. Res.*, 8: 809–815
- Islam, A.K.M.R. and K.W. Shepherd, 1992. Production of wheat-barley recombinant chromosomes through induced homoeologous pairing. 1. Isolation of recombination involving barley arms 3HL and 6HL. *Theor. Appl. Genet.*, 83: 489–494
- Jan, S.A., Z.K. Shinwari, M.A. Rabbani, I.A. Niaz and S.H. Shah, 2017a. Assessment of quantitative agro-morphological variations among *Brassica rapa* diverse populations. *Pak. J. Bot.*, 49: 561–567
- Jan, S.A., Z.K. Shinwari, M.A. Rabbani, H. Khurshid, M.I. Ibrahim, M. Adil and M. Ilyas, 2017b. Comparison of electrophoretic protein profiles of *Brassica rapa* sub-species brown sarson through SDS-PAGE method. *Genetika*, 49: 95–104
- Jan, S.A., Z.K. Shinwari and M.A. Rabbani, 2016. Determining genetic divergence among *Brassicarapa* ecotypes through electrophoretic mobility of total seed proteins. *J. Anim. Plant Sci.*, 26: 1758–1764
- Kalhor, F.A., S.A. Rajpar, S.A. Kalhor and Z.A. Baloch, 2015. Heterosis and combing ability in *F1* population of hexaploid wheat (*Triticum aestivum* L.). *Amer. J. Plant Sci.*, 6: 1011–1026
- Meng, Z., F. Song and T. Liu, 2018. Genetic diversity and genetic structure analysis of maize (*Zea mays*) landraces in Tibet. *Intl. J. Agric. Biol.*, 20: 791–798
- Mondal, A.B., D.P. Sadhu and K.K. Sarkar, 1997. Correlation and path analysis in bread wheat. *Environ. Ecol.*, 15: 537–539
- Niaz, S., H. Ahmad, I.A. Khan, A.H. Shah and I. Rahman, 2014. Molecular and agronomic characterization of durum wheat. *Intl. J. Biosci.*, 4: 270–275
- Pomeranz, Y. and L. Munck, 1981. Cereals, a renewable resource: theory and practice. In: *International Symposium on Cereals, a Renewable Resource, Theory and Practice, Copenhagen (Denmark), 1981*. American Association of Cereal Chemists
- Raut, S.K., J.G. Manjaya and P.W. Khorgade, 1995. Selection criteria in wheat (*Triticum aestivum* L.). *Punjab. Krishi Vid. Res. J.*, 19: 17–20
- Sinha, A.K., S. Chowdhury and A.K. Singh, 2006. Association among yield attributes under different conditions in wheat (*Triticum aestivum* L.). *Ind. J. Genet.*, 66: 233–234
- Zhu, S., X. Zhang, Q. Liu, T. Luo, Z. Tang and Y. Zhou, 2018. Phenotypic variation and diversity of cauliflower (*Brassica oleracea* var. botrytis) inbred lines. *Intl. J. Agric. Biol.*, 20: 1041–1048