

Research Article

Evaluation of wheat genotypes on the basis of morphological characters in bread wheat

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Abstract

An experiment was performed in the experimental field of Cereal Crops Research Institute (CCRI) Pirsabak, Nowshera, Khyber Pakhtunkhwa, Pakistan during the year 2015-2016 to evaluate wheat genotype based on morphological characters. Twenty wheat genotypes were evaluated under normal conditions using a randomized complete block design. Days until heading, thousand grain weight, plant height, grain yield, spike length, spikelets per spike, biological yield, and harvest index were all substantially different ($P \leq 0.05$). Days to heading varied from 108.6 to 114.6 days, plant height from 84.0 to 100.6 cm, spike length from 8.43 to 10.63 cm, spikelet's spike⁻¹ from 15.9 to 20.4, 1000-grains weight from 58.3 to 70.80 g, the biological yield from 4333.3 to 8666.7 kg ha⁻¹, grain yield from 2043.0 to 3713.3 kg ha⁻¹ and harvest index from 18.63 to 29.30 %. The early heading genotype was CT-13052 (108.6 days), minimum plant height was shown by DN-120 (84.0 cm) and maximum spike length was exhibited by genotype DN-122 (10.63 cm). Similarly, check cultivar Pakhtunkhwa-2015 showed maximum spikelet's spike⁻¹ (20.4 no) and the highest 1000-grains weight was recorded in genotype AUP-07014 (70.80 g). Maximum grain yield was exhibited by genotypes PS-35 (3713.3 kg ha⁻¹) followed by other genotypes CDRI-SA-12 (3180.0 kg ha⁻¹), CT-13052 (3066.7 kg ha⁻¹), PS-28 (3000.0 kg ha⁻¹) and DN-120 (2949.3 kg ha⁻¹). Heritability estimates were moderate for most of the traits due to the influence of environmental conditions than the genetic make-up of plants. Genotypes expressed a high heritability estimate for biological yield. This study is done to play a vital role as a food security in society and provided resistant lines or genotypes to future breeding programme. Eventually, for yield and yield-related attributes, the genotypes AUP-07014, PS-35, CT-13052, and Pirsabak-13 were recommended, and they might be employed in future breeding projects to improve grain production in bread wheat.

Keywords: Heritability; Morphological characters Wheat; Grain yield

Introduction

Hexaploidy wheat is a grass belonging to the Poaceae family and tribe Triticeae. Since Linnaeus' original nomenclature in 1753, there have been numerous revisions in the taxonomic description of Triticum

and its associated taxa. There is no consensus that the genus *Aegilops*, which is closely related to wheat, should be united with *Triticum* [1]. Diploid, tetraploid, and hexaploidy species make up the genus

Triticum. As a result, polyploidy has a significant impact on wheat evolution.

In case of taking majority of the world regions hexaploidy wheat gaining the top position in whole cereal crops. Hexaploidy wheat is very important as a stable source food for approximately 36% populations of the world which is equal to 2 billion people, and the world's main civilizations for the last 8000 years, and has been used to produce bread, chapattis, cakes, cookies, and confectionary items. Wheat is Pakistan's major food crop, accounting for 13.7 percent of agricultural value added and 3% of GDP [2]. Wheat accounts for almost 55 percent of carbs and 20 percent of food calories and protein consumed around the world [3].

In 2018, worldwide production of wheat was 757.9 million tonnes, a 2.2 percent decrease from the 2016 record. In 2017, data recorded about wheat top producer country list, Pakistan was in eight positions in whole world and 4th in all Asians country. China (126metric tonnes) was the first followed by India (95metric tonnes), Russia (60metric tonnes), United States (55metric tonnes), France (39metric tonnes), and Canada (29metric tonnes) Germany (28metric tonnes) and Pakistan (26metric tonnes), accordingly [4]. Pakistan is Asia's fourth-largest wheat grower, which is one of the top ten wheat-producing states in the world. Hexaploidy wheat was grown on 8.73 million ha in Pakistan, yielding 25.4 metric tons with a mean return of 2919 kg ha⁻¹, while wheat was grown on only 0.76 million hectares in Khyber Pakhtunkhwa, yielding (1.4 million tonnes) with a mean yield of (1860 kg ha⁻¹). In (Khyber Pakhtunkhwa) total irrigated area was recorded 0.270 (million hectares) producing (0.603 million tonnes), while non-irrigated area was 0.361 million hectares producing (0.441 million tonnes) [5]. Likewise, Punjab, Sindh, KPK, and Baluchistan generated 76 percent, 16 percent, 5 percent, and 3 percent of total production, accordingly [6].

Germplasm enhancement and genetic diversity are essential for ensuring the stable and long-term production of food crops. Measurement of the extent of accessible genetic diversity is most important for effective evaluation and exploitation of germplasm in winter wheat on the base of pedigree information, morphological features, and final quality factors to estimate genetic diversity [7]. In wheat, morphological features have been used in conjunction with multivariate approaches to estimate genetic distance [8, 9].

The effectiveness of a breeding effort is largely determined by the selection and use of possible parental genotypes for hybridization, followed by gene combination selection. The breeder's knowledge of genetic diversity and heritability provides a reliable tool for improvement. Genetic variability is a measure of a population's likelihood for individual genotypes to differ for certain qualities of interest, and it is the foundation of crop development [10]. Quantitative attributes can be used to determine genetic variability among wheat genotypes. In a population, there are two types of genetic variation: heritable and non-heritable variance. In general, heritability is defined as the proportion of genetic variance to overall variance (phenotypic variance). The term "heritability" refers to the degree to which heredity and environment interact. Plant breeders can use heredity knowledge to forecast the behaviour of subsequent generations and make favourable selections, which is an important technique in crop development.

Over the previous three decades, Agriculture has been improved due to use of efficient fertilizers and development of highly varieties. Since the introduction of semi dwarf wheat cultivars, wheat output has increased in all main cropping systems, representing various and variable agro-ecological settings.

Given the preceding facts and figures, first and main aim of this research was to

evaluate wheat genotypes based on their performance and morphological characteristics. Second important objective was to estimation of genetic variability and heritability. Finally, identification of relevant genotypes for use in future wheat breeding programs.

Materials and Methods

Materials and target research site

This research was done in between 2015-2016 year at Cereal Crops Research Institute (CCRI) Pirsabak-Nowshera, Pakistan under irrigated conditions (placed at 340 North Latitude, 720 East Longitudes,

and 2880 Altitude). Twenty wheat genotypes (Table 1) were used in the study, including eighteen advanced lines and two control cultivars (Pakhtunkhwa-2015, Pirsabak-13). Each genotype was sown in 3 replications under randomized complete block design. Each genotype was planted using row to row distance is twenty-five centimeters with row length is 5 meters. From each replication, ten plants were chosen at random. To make data collection easier, a single row between adjacent plots was left empty.

Table 1. List of 20 wheat genotypes studied for morphological traits at CCRI during 2015-16

S. No.	Genotypes	S. No	Genotypes
1	Inq-91/FS(f8)	11	PS-33
2	SRN-13121	12	PS-34
3	CT-13052	13	PS-35
4	CT-13169	14	AUP-05814
5	DN-120	15	AUP-07014
6	DN-122	16	CDRI-PV-1
7	DN-123	17	CDRI-PV-2
8	PS-22	18	CDRI-SA-12
9	PS-23	19	Pakhtunkhwa-2015 (Check)
10	PS-28	20	Pirsabak-13 (Check)

Data recorded

Data on the following variables were recorded at the appropriate time, as prescribed for each parameter. Counting days between first date of sowing and when fifty percent plants had achieved heading was used to calculate the days to heading. Data recorded on important parameter plant height was took in centimeters at physiological maturity using when all spikes omitting awns from level of soil up-to spike top. Measuring of spike length was done using distance between first spikelet to the top of spikelets excluding awns. Data recorded on using 10 randomly selected plants in each replication for all traits. On the same eight randomly picked spikes from each plot, the number of spikelets with spike⁻¹ was tallied. A thousand grains (g) were randomly selected from each plot's bulk grain production in each replication

and weighed on an electronic scale. At maturity, each entry was harvested separately and weighed with an electronic scale after sun drying for 2-3 days to record biological yield according to the formula below. $(\text{Biological yield plot}^{-1} / \text{plot area } m^2) \times 10,000 m^2 = \text{biological yield (kg ha}^{-1})$ The weight of grains obtained after threshing the full produce of each plot using the technique below was used to estimate grain yield. $(\text{Grain yield plot}^{-1} / \text{plot area } m^2) \times 10,000 m^2 = \text{grain yield (kg ha}^{-1})$. Using the formula below, the harvest index was calculated as the ratio of grain yield to total above-ground biomass. $\text{Harvest index (\%)} = [\text{Grain yield plot}^{-1} / \text{Biological yield plot}^{-1}] \times 100$.

Statistical analysis

The statistical approach (SAS, 2009) was utilized to calculate variation among the population. To estimate broad sense

heredity, using the mean squares, the variability components (V_g , V_e , and V_p) were determined. The averages were parted through using LSD test at a probability level of 5 percent when significant

Where,

$$\text{Genetic variance (} V_g) = \frac{GMS - EMS}{re}$$

$$\text{Phenotypic variance (} V_p) = V_g + G \times EMS - \left(\frac{EMS}{r}\right) + EMS$$

$$\text{Heritability (broad sense)} = \frac{\text{Genetic variance}}{\text{Phenotypic variance}}$$

$$\text{Heritability (broad sense)} = \frac{V_g}{V_g + V_e} = \frac{V_g}{V_p}$$

Stansfield (1986) classified heritability estimates as low, moderate, or high, with less than 20% reported to be low, 20 to 50 % considered moderate, and more than 50 percent called high.

Results

Number of days to heading

Mean squares for days to heading revealed highly significant ($p \leq 0.01$) difference (Table 2). Important trait days to heading show genetic diversity amongst wheat genotypes. Days to heading productivity of wheat cultivars varied from 108.6 to 114.6 days, with genotype CT-13052 having the lowest days to heading (108.6 days) and CDRI-SA-12 (109.0 days) followed by PS-28 (109.3 days) and PS-33 (110 days) while late heading genotypes were AUP-07014 (114.6 days), CDRI-PV-1 and PS-35 (113.3 days each). In (Table 3) average value for overall days to heading was 111.93. Number of days to heading trait had genetic and environmental variations of 1.67 and 2.88, respectively. The increased degree of environmental variations for this attribute indicated that the environment controls a large part of variation. Furthermore, for days to heading, modest heritability values of (37%) were discovered (Table 5).

Plant height (cm)

Mean squares for plant height in ANOVA revealed highly significant differences ($p \leq 0.01$) for each genotype (Table 2). The presence of genetic change amongst cultivars for plant height was shown to have a significant effect. Plant height mean

differences were discovered. (Steel and Torrie, 1980).

Heritability (Broad sense)

For several traits, Singh and Chaudhery technique was used to calculate heritability across environments (1997).

values varied from 84.0cm to 100.6cm in (Table 3), where minimum plant height was recorded for genotype DN-120 (84.0 cm) followed by other genotypes PS-28 (85.6 cm) and AUP-05814 (86.3 cm) while maximum plant height was recorded in CT-13169 (100.6 cm). Average plant heights of 20 genotypes were (91.8 cm). Genetic and environmental variances were 12.8 and 21.1. It means that plant height was more under environment control than genetic. Moderate heritability estimates (38 %) were recorded for plant height (Table 5).

Length of spike (cm)

Mean square for length of spike in (Table 2) showed only significant difference ($p \leq 0.05$), strongly associated toward final grain yield. This showed genetic variability among genotypes for this important trait. Spike length averages varied from (8.43 to 10.63 cm), where maximum spike length was observed in genotype DN-122 (10.63 cm) while smallest spike length was expressed in genotype AUP-07014 (8.43 cm). Four other genotypes CDRI-PV-1, CDRI-SA-12 and SRN-13121 and PS-23 also revealed maximum spike length with values of (10.60 cm), (10.43 cm) and (10.16 cm) (Table 3). Spike length differences were 0.22 and 0.67, respectively, due to genetic and environmental factors. For spike, heritability values of (25%) were reported, respectively (Table 5).

Spikelet's per spike (No.)

Mean square due to spikelets per spike described only significant difference

($p \leq 0.05$) for all genotypes (Table 2). Spikelet's per spike mean value vary from 15.9 to 20.4. The genotype Pakhtunkhwa-2015 showed maximum spikelet's spike⁻¹ (20.4 no), other genotypes PS-33 (19.9 no), Pisabak-2013 (19.8 no), PS-28 (19.5 no) and DN-123 (19.1 no) also exhibited maximum spikelet's spike⁻¹, while minimum number of spikelet's per spike was found in genotype AUP-07014 (15.9 no). Overall average mean for spikelet's spike⁻¹ was (18.1 no) (Table 3). Spikelet's spike⁻¹ had 0.88 and 1.96 genetic and environmental variations, respectively. Moreover, moderate heritability (31%) was recorded for spikelet's spike⁻¹ (31%), respectively showing greater influence of environmental factors on this trait (Table 5).

1000-grains weight (g)

ANOVA exhibited significance differences ($p \leq 0.05$) for 1000-grains weight (Table 2). Its mean that genetic variability was detected among genotypes for this vital trait. For thousand grains weight means values differ from 58.3g to 70.80g. For maximum 1000-grains weight the genotypes; AUP-07014 (70.80 g), Pirsabak-2013 (69.8 g), CT-13169 (69.1 g) and PS-34 (67.2 g), similarly 1000-grains weight of 67.0, 66.9 and 66.6 g were recorded in genotypes DN-123, PS-35 and PS-22. Moreover, minimum 1000-grains weight was displayed by genotype DN-120 (58.3 g). For 1000 grains, the genotypes had a mean average weight of 64.90 g (Table 4). The genotypic and environmental variances were 6.19 and 13.14, respectively, which was a lesser size than the environmental variance. Similarly, moderate heritability estimates of (32%) was detected for 1000-grains weight, respectively (Table 5).

Biological Yield kg per hectares

For biological yield ANOVA technique displayed highly significant changes ($p \leq 0.01$) (Table 2). Biological yield ranging from (4333.3 to 8666.7 kg ha⁻¹), where extreme biological yield was found by genotypes AUP-07014 and PS-22 (each contain 8666.7 kg per hectares) followed by

SRN-13121 (6266.7 kg ha⁻¹), Pirsabak-2013 (6200 kg ha⁻¹), CDRI-PV-2 (6133.3 kg per hectares) and Inq-91/FS(f8) (6600.0 kg ha⁻¹) while minimum biological yield was recorded by genotype DN-123 and CT-13169 (4333.3 kg ha⁻¹). Similarly, the genotypes Pakhtunkhwa-2015 and PS-34 also produced same biological yield (5533.3kg ha⁻¹), respectively. For biological yield, the average of all 20 wheat cultivars was (5653.3 kg ha⁻¹) (Table 4). The genetic and environmental variations for biological output kg ha⁻¹ were 14289614 and 1053579, respectively, indicating that the trait was much more genetically controlled than the environment. Moreover, high heritability estimates (93%) were observed for biological yield kg ha⁻¹ (Table 5).

Grain yield (kg ha⁻¹)

Mean square due to grain yield identified as highly significant difference in (Table 2). Grain yield mean varied from 2043.0 to 3713.3kg ha⁻¹, where maximum grain yield was taken by genotype PS-35 (3713.3 kg ha⁻¹) followed by other genotypes CDRI-SA-12, CT-13052, PS-28 and DN-120 which produced (3180.0 kg ha⁻¹), (3066.7 kg ha⁻¹), (3000.0 kg ha⁻¹) and (2949.3kg ha⁻¹). Moreover, minimum grain yield was recorded by genotype CT-13169 (2043.0 kg ha⁻¹). Average mean for grain yield of all 20 wheat genotypes was (2849.5 kg ha⁻¹) (Table 4). Genetic and environmental variance was 227854.3333 and 353705. Heritability estimates for grain yield (kg ha⁻¹) were (39%), respectively (Table 5).

Harvest index (%)

Mean square due to harvest index (%) examined only significant difference for all studied genotypes (Table 2). Mean data for harvest index varied from (18.63 to 29.30 %). The genotype DN-120 showed maximum harvest index (29.30 %) while genotype DN-123 manifested minimum harvest index (18.63%). Similarly, highest harvest index of 26.23, 24.80 and 24.73 % was expressed by the genotype CT-13169, CT-13052 and CDRI-PV-2. The genotypes SRN-13121 and AUP-05814 showed same

harvest index of (24.67%), respectively. Average harvest index for 20 wheat genotypes were (23.28%) (Table 4). Harvest index observed that genetic and environmental variations were 2.35 and 7.37, respectively. The greater magnitude

of environment variance for this trait reflected that major proportion of variation is under environment control. Moreover, heritability estimates of (25%) was detected for harvest index, respectively (Table 5).

Table 2. Mean squares for various eight agronomically traits of 20 wheat genotypes were evaluated at Cereal Crop Research institute (CCRI) Pirsabak, Nowshera Pakistan during 2015-16

SOV	DF	DH	PH	SL	SPS	TGW	BY	GY	HI
Replication	2	0.82	15.05	0.73	0.93	2.43	48667	96275	3.01
Genotypes	19	7.92	59.66	1.35	4.62	31.71	4392421	1037268	14.23
Error	38	2.89	1.16	0.67	1.97	13.14	1053579	353705	7.17
Total	59								
CV		1.52	5.01	8.52	7.73	5.59	18.16	20.87	11.50

Table 3. Means data of Twenty wheat genotypes examined for number of days to heading, length of spike, and spikelets per spike at CCRI in the year of 2015-2016

Genotypes	Days to heading(no)	Stature of plant	Spike length	Spikelet's spike
Inq-91/FS(f8)	110.67	93.67	9.03	17.93
SRN-13121	113.00	89.67	10.43	16.43
CT-13052	108.67	91.00	9.07	17.23
CT-13169	112.33	100.67	9.63	17.93
DN-120	112.33	84.00	10.13	17.80
DN-122	112.33	94.00	10.63	17.53
DN-123	112.67	96.00	10.10	19.13
PS-22	112.67	94.67	8.70	17.37
PS-23	112.00	87.00	10.17	16.37
PS-28	109.33	85.67	9.57	19.57
PS-33	110.00	91.67	9.10	19.93
PS-34	113.00	93.67	8.97	18.63
PS-35	113.33	92.67	9.37	17.13
AUP-05814	113.33	86.33	9.93	18.23
AUP-07014	114.67	100.00	8.43	15.93
CDRI-PV-1	113.33	91.00	10.60	18.03
CDRI-PV-2	111.67	88.33	9.43	18.83
CDRI-SA-12	109.00	89.67	10.43	18.50
Pakhtunkhwa-2015	111.33	90.33	10.00	20.43
Pirsabak-13	113.00	96.00	8.90	19.87
Means	111.93	91.80	9.63	18.14
LSD_(0.05)	2.81	7.60	1.35	2.31

Table 4. Means data for twenty wheat genotypes evaluated for thousand grain weight, biological yield, harvest index and final grain yield

Genotypes	Thousand grain weight	Biological yield	Grain yield	Harvest index
Inq-91/FS(f8)	64.77	6600.00	2606.67	23.10
SRN-13121	61.07	6266.67	2460.00	24.65
CT-13052	62.47	5466.67	3066.67	24.83
CT-13169	69.13	4333.33	2043.00	26.21
DN-120	58.30	4600.00	2949.33	29.30
DN-122	65.43	5466.67	2726.67	20.47
DN-123	67.00	4333.33	2813.33	18.64
PS-22	66.60	8666.67	2562.67	23.06
PS-23	61.70	5000.00	2606.67	23.28
PS-28	61.23	5733.33	3000.00	23.47
PS-33	65.77	5000.00	2496.00	22.57
PS-34	67.23	5533.33	2273.33	22.47
PS-35	66.93	5200.00	3713.33	21.75
AUP-05814	60.97	4666.67	2674.67	24.68
AUP-07014	70.80	8666.67	2358.67	22.19
CDRI-PV-1	64.83	4933.33	2946.67	22.88
CDRI-PV-2	63.57	6133.33	2306.67	24.73
CDRI-SA-12	64.93	4933.33	3180.00	22.78
Pakhtunkhwa-2015	65.53	5333.33	2647.33	22.16
Pirsabak-13	69.87	6200.00	2429.67	22.40
Means	64.91	5653.33	2693.07	23.28
LSD (0.05)	5.99	983.04	20.87	4.43

Table 5. Evaluation of variance due to genetic and environmental also finding of heritability for all studied parameters

Traits	GMS	EMS	VG	VE	VP	Heritability (%)
D2H	7.91	2.88	1.68	2.88	4.56	37%
PH	59.66	21.15	12.84	21.15	33.99	38%
SL	1.35	0.67	0.23	0.67	0.90	25%
SPS	4.62	1.96	0.89	1.96	2.85	31%
TGW	31.71	13.14	6.19	13.14	19.33	32%
BY	43922421	1053579	14289614.00	1053579	15343193.00	93%
GY	1037268	353705	227854.33	353705	581559.33	39%
HI	14.22	7.17	2.35	7.17	9.52	25%

D2H = Days to heading, PH = Plant height, SL = length of spike, SPS = number of spikelets per spike, TGW = Thousand grains weight, BY = Biological yield, GY = Grain yield, HI = Percent harvest index

Discussion

Plant breeders are eager in developing new genotypes that yield earlier heading since it is desirable. Early heading genotypes provide two major advantages over late heading genotypes. Early-heading genotypes have a longer grain filling

period, which allows them to complete more grains loading early last season while air temperatures are cooler and even more favourable [11]. Plant breeding relies heavily on heritability estimation. It is the inheritance of character from one population to the next, and it is a very useful

tool for determining genetic gain of a parameter when combined with other parameters [12].

Plant height is important in breeding programmes because breeders prefer small stature plants since they help reduce lodging and respond quickly to fertiliser [13]. In all wheat breeding programme plant stature is important parameter since it is linked to lodging, seedling productive capacity of the economy, and weed management [14]. The experimental data revealed highly significant differences in plant height between genotypes; this is in line with [15] which demonstrated significant variation in height of plant between wheat genotypes.

Long spikes are of particular interest to plant breeders because they can boost yield per unit area [16]. Spike length had strongly positive correlation towards grain weight per spike and final grain yield. With awns that boost photosynthetic rate, length spikes stay green and functional for a long time [17]. Length of spike showed only significant differences in ANNOVA table. These findings back up those of [18], who discovered a lot of variation among wheat genotypes. Spike can account for 20–30% of the dry materials deposited in the seeds on average, thus according [19].

Spikelet spike⁻¹ is more abundant in wheat genotypes with longer spikes. Spikelet spike⁻¹ increased, resulting in increased output [20]. Grain yield is increased by selecting plants with a higher number of spikelet spike⁻¹ [21]. Significant changes in flag leaf area were discovered between genotypes in this study. [22] confirmed these findings, revealing significant variance among genotypes for this feature. The 1000-grain weight is a critical parameter in wheat production. One of the contributing qualities to yield is 1000-grain weight, which might be employed as a selection criterion for high output. The yield is proportional to the weight of 1000 seeds. The heavier grains are made heavier by the build-up of dry materials. For this key 1000-grain weight feature, our

experiment revealed significant variation. Our result was contradictory in past research by [23, 24] in thousand grain weight.

In terms of biological yield, there were considerable differences between genotypes. Similar findings were observed by [25], who revealed only significant difference in biological yield amongst cultivars. The level of heritability for biological yield was high, showing that the traits are more genetically regulated than environmental. Our discoveries are comparable to those of [26] that biological yield heritability is considerable.

Grain yield is the most critical and crucial feature in the wheat crop and breeders place a premium on improving it. This parameter is strongly correlated parameter with other parameters (spike length, grain weight, spikelets per spike etc...) either it is affected directly or indirectly. Grain yield differences amongst wheat genotypes were significantly significant in a recent experiment. [27] had previously shown significant changes between genotypes. Current research was similar with those of [28], who found significant heterogeneity in grain production among genotypes. For grain yield, there was moderate heredity.

Conclusion

The following conclusions were taken from the current study based on the findings: Days to heading, stature of plant, biological yield, length of spike, number of spikelets per spike, thousand-seed weight, final yield of grain and harvest index all showed significant variances. Except for biological yield, all traits had moderate heritability (high heritability). CT-13052 and CDRI-SA-12 genotypes had the shortest days to heading. The genotype DN-122 showed maximum spike length. Maximum spikelet's spike was recorded for genotype Pakhtunkhwa-2015. Grain yield was found to have a strong relationship with length of spike, yield of biological, spike per meter and number of grains per spike in both settings. The genotypes AUP-07014, Pirsabak-13, PS-35 and CT-13169

exhibited maximum 1000-grains weight. Highest grain yield was produced by genotypes PS-35, CDRI-SA-12 and PS-28. The genotypes AUP-07014, PS-35, CT-13052 and Pirsabak-13 were recommended for morphological and yield related traits and could be employed in future breeding programmes to improve bread wheat grain output.

Authors' contributions

Conceived and designed the experiments: F Akbar, Performed the experiments: M Ali & M Dalil, Analyzed the data: N Ullah, Contributed materials/ analysis/ tools: A Khan & N Khan, Wrote the paper: M Babar.

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References

1. Athwal DS (1968). Concept of plant type and disease resistance in rice breeding. Presidential address delivered at annual general meeting. *Soc Genet Plant Bree Jan 3*: 1968.
2. Pakistan Bureau of Statistics. 2017-18.
3. Breiman A Graur D (1995). Wheat evolution. *Isr J Plant Sci* 43(2): 85-98.
4. Food outlook (2017). Food and Agricultural Organization Statistics Agriculture statistics Khyber Pakhtunkhwa, Peshawar (2014-15).
5. Laghari AH, Talpur MGH, Laghari GM, Leghari SJ, Rajput RM, Sanjrani IN & Laghari AH (2016). Statistical survey on analysing market and environmental factors influencing wheat crop. *Adv Envi Biol* 10(9): 242-245.
6. Fufa H, Baenziger PS, Beecher BS, Dweikat I, Graybosch RA & Eskridge KM (2005). Comparison of phenotypic and molecular marker-based classifications of hard red winter wheat cultivars. *Euphytica* 145(1-2): 133-146.
7. Zeven AC & Schachl R (1989). Groups of bread wheat landraces in Austrian alps. *Euphytica* 41(3): 235-246.
8. Roy O (2004). Globalized Islam: The search for a new ummah. Columbia University Press.
9. Chimdesa B (2014). Genetic variability among bread wheat genotypes for growth characters, yield and yield components in bore district, Oromia regional state (doctoral dissertation, haramaya university).
10. Tewolde H, Fernandez CJ & Erickson CA (2006). Wheat cultivars adapted to post-heading high temperature stress. *J Agron Crop Sci* 192(2): 111-120.
11. Memon S, Qureshi M, Ansari BA & Sial MA (2007). Genetic heritability for grain yield and its related characters in spring wheat (*Triticum aestivum* L.). *Pak J Bot* 39(5): 1503-1509.
12. Khan MI, Mohammad T, Subhan F, Amin M & Shah ST (2007). Agronomic evaluation of different bread wheat (*Triticum aestivum* L.) genotypes for terminal heat stress. *Pak J Bot* 39(7): 2415-2425.
13. Donald CM & Hamblin J (1976). The biological yield and harvest index of cereals as agronomic and plant breeding criteria. *Adv Agron* 28: 361-405.
14. Akhtar MZ, Khan MA, Ahmad K & Alam M (2001). Evaluation of wheat varieties for their potential grain yield under their agroecological conditions of DI Khan. *J Biol Sci* 19(4): 185-188.
15. Khan AJ, Hamblin Azam F & Ali A (2010). Relationship of morphological traits and grain yield in recombinant inbred wheat lines grown under drought conditions. *Pak J Bot* 42(1): 259-267.
16. Sharma SN, Sain RS & Sharma RK (2003). Genetics of spike length in durum wheat. *Euphytica* 130(2): 155-161.
17. Hamam KA & Khalid A (2009). Stability of wheat genotypes under different environments and their

- evaluation for yield traits. *J Basic Sci* 3(1): 206-207.
18. Thorne GN (1965). Photosynthesis of ears and flag leaves of wheat and barley. *Ann Bot* 29(3): 317-329.
 19. Akram Z, Ajmal SU, & Munir M (2008). Estimation of correlation coefficient among some yield parameters of wheat under rainfed conditions. *Pak J Bot* 40(4): 1777-1781.
 20. Mohammadi M, Karimizadeh R, Shefazadeh MK & Sadeghzadeh B (2011). Statistical analysis of durum wheat yield under semi-warm dry land condition. *Aust J Crop Sci* 5(10): 1292-1297.
 21. Kashif M & Ihsan K (2004). Heritability, correlation and path coefficient analysis for some metric traits in wheat. *Int J Agri Biol* 6(1): 138-142.
 22. Abbasi MK, Kazmi RH & Khan MQ (2003). Growth performance and stability analysis of some wheat genotypes subjected to water stress at Rawalakot Azad Jammu Kashmir. *Archi Agro Soi* 49: 415-426.
 23. Ahmad MZ, Akram, Munir M & Rauf M (2006). Physiomorphic response of wheat genotypes under irrigated and rainfed condition. *Pak J Bot* 38(50): 1697-1702.
 24. Kamal AMA, Islam MR, Chowdhury BL & Maleque MA (2003). Yield performance and grain quality of wheat varieties grown under rainfed and irrigated conditions. *Agric Water manage* 2(3): 358-360.
 25. Mecha B, Alamerew S, Assefa A & Dustom D (2016). Genetic variability, heritability and genetic advance for yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes. *Global J Sci Frontier Res* 16(7): 8-18.
 26. Bhushan B, Gaurav SS, Kumar R, Pal R, Panday M, Kumar A, Bharti S, Nagor SS & Rahul VP (2013). Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.). *Environ & Ecology* 31(2): 405-407.
 27. Khayantnezhad M (2010). Evaluation of the reaction of wheat genotypes to drought conditions using various stress tolerance indices. *African J Mic Bio Res* 6(200): 4315-4323.
 28. Talebi R, Fayaz F & Naji AM (2009). Effective selection criteria for assessing drought stress tolerance in wheat. *Gen Appl Plant Physiol* 35(2): 64-74.