



RESEARCH PAPER

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Evaluation of bread wheat genotypes for yield and its associated traits

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Abstract

Wheat (*Triticum aestivum* L.) is the most widely adapted crop to various agro climatic conditions, consequently, has got a major place among the cereal crops in the world. In wheat development programs, the evaluation and identification of superior lines from introduced plant materials, is the first and leading step in a crop improvement program. The experiment was planted at Mountain Agricultural Research Center, Juglot, Pakistan during 2014-15 following randomized complete block design with three replications. The current research was carried out to evaluate 10 bread wheat accessions for yield and its associated characters. The analysis of variance, mean performance, correlation and cluster analysis were computed. The analysis of variance exhibited that all the genotypes performed significantly ($P \leq 0.05$) variable for plant height, days to flowering, days to 50% maturity, grain per spike, straw weight, Total grain weight, registering the significant genetic variability among the genotypes for further evaluation. With regards to mean performance, the AC-4, AC-6 and AC-8 showed better performance for various traits. Cluster analysis revealed two accessions AC-4 and AC-5 as most diverse among all members. So, these accessions can be further used in breeding programme to achieve better yield. Also molecular studies on these accessions can point out many novel gene sources in these accessions.

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Introduction

Wheat (*Triticum aestivum* L.) is the most widely adapted crop to various agro climatic conditions, consequently, has got a major place among the cereal crops in the world, both in area and production. It is the chief cereal crop of the temperate region of the world; however, it is also cultivated on huge areas in the tropics. Worldwide, it occupies 218.46 million hectares with annual production of 749.3 million tones and average production of 2900 kg ha⁻¹. In Pakistan, it contributes 2.1 % to GDP area under wheat cultivation was 9180 million hectares during 2014-15 with a production of 25.478 million tons and average production of 2775 kg per hectare (PBS, 2016).

In Pakistan, efforts on wheat breeding have been focused on superior yields and development of cultivars showing resistance and tolerance to various biotic and abiotic stresses. In this bidirectional breeding efforts of the past, many potential cultivars of bread wheat have been evolved. Wheat is supreme among grain crops, mainly due to the reason that grains possess protein with exceptional chemical and physical properties (Ali *et al.*, 2013). In wheat development programs, the evaluation and identification of superior lines from introduced plant materials, is the first and leading step in a crop improvement program. Promising genotypes with high yielding, good adaptation and agronomically desirable characteristics could reliably be exploited for commercial cultivation. Nevertheless, an efficient and immense hybridization program would be a feasible approach and for the success of such hybridization programs, the evaluation of the important traits and pattern of genetic variability of the existing germplasm keeps a promise (Sanghera *et al.*, 2014). Genetic variability is an important aspect for the successful breeding programs in any population. A wide range of variability will augment the chances of selection for a desirable genotype. For this fact, heritability is a good sign of the transfer of characters from generation to generation (Baloch *et al.*, 2014a). Keeping in view the fact of genetic variability, in the current study, the germplasm was assessed for a variety of yield and its associated traits.

Materials and methods

Plant material for the study comprised of 10 accessions of bread wheat (Table 1). The experiment was planted at Mountain Agricultural Research Center, Juglot, Pakistan during 2014-15 following randomized complete block design with three replications. Each plot consists of rows, 5m long and 25 cm apart. Fertilizer was applied at the rate of 90:90kg NP respectively with no irrigation.

The recommended dose of fertilizer, number of irrigations, weedicide and inter-culturing was applied at appropriate time. For the recording of observations, per exotic bread wheat genotype, ten plants were randomly selected and labeled from each replication.

Parameters studied

The data recorded were plant height, days to flowering, days to 50% maturity, grain per spike, straw weight, total grain weight, total weight per plot.

Statistical analysis

Analysis of variances was done by Statistix 8.1 computer software, while the means were compared using Duncan's Multiple Range Test as suggested by Duncan (1955). The combined data of grain yield and its components were then subjected to analysis to estimate the simple statistic i.e., simple correlation. Quantitative traits were analyzed by cluster and principal component analysis with the help of software program 'Past' for windows. Cluster analysis identifies variable which are further clustered into main group and subgroups using Ward's method. The genotypes in each cluster were also analyzed for basic statistics. Mean value of each variable were standardized prior to cluster and principal component analysis to avoid the effects due to difference in scale.

Results and discussion

The analysis of variance exhibited that all the genotypes performed significantly ($P \leq 0.05$) variable for plant height, days to flowering, days to 50% maturity, grain per spike, straw weight, total grain weight, total weight per plot (Table 2),

signifying that studied materials hold valuable genetic resources for range of characters thus can comprehensively be used for upcoming breeding challenges.

Similar results regarding total grain weight and total weight per plot have also been penned by several other workers, namely, Baloch *et al.* (2014a) and Baloch *et al.* (2014b).

Table 1. List of Genotypes used in the study.

S.N	Genotypes	S.N	Genotypes
1	AC-1	6	AC-6
2	AC-2	7	AC-7
3	AC-3	8	AC-8
4	AC-4	9	AC-9
5	AC-5	10	AC-10

Table 2. Mean squares from analysis of variance for various traits in bread wheat genotypes.

SOV	PH	DFF	DM	GPS	STW	TGW	TWPP
Rep	0.026841	0.05943	0.52573	0.066505	3702.233	0.000163	152.508
Geno	16339.09**	48265.48**	86421.84**	5624.799**	380592.08**	43.00454**	15765316**
Error	21.86821	4.739693	13.39678	31.52511	411013.6	0.0891	40950.22

Where PH= Plant Height, DFF= Days to flowering, DM= Days to 50% maturity, GPS= Grains per spike, STW= Straw weight, TGW= Total Grain weight and TWPP= Total weight per plot.

These researchers also observed the considerable genetic variance for the various yield and its related traits.

Mean performance of ten wheat accessions are given in Table 03. According to plant height, the AC-1 produced the tallest plants with height of 79.1cm, while AC-8 was the shortest accession, having plant height of 61.4cm, indeed it is desirable, thus AC-8 could be utilized in further breeding programs to

achieve short stature plants since these genotypes do not lodge at great scale, consequently more yield is expected. Days to 50% maturity were minimum for AC-3 that was 121.00 and maximum was for AC-5 and AC-10 (165.00). Days to flowering were maximum for AC-1 that was 126.43 and minimum for AC-3 (117.77). Among the yield associated components, grains per spike ranged from 33.9 to 41.2 with an average of 38.1.

Table 3. Means for various traits in 10 bread wheat accessions.

Genotypes	PH	DFF	DM	GPS	STW	TGW	TWPP
AC-1	79.1	126.43	163.78	39.5	3400	3.38	1822.2
AC-2	68.6	117.53	160.22	39.7	3037.887	3.29	1788.9
AC-3	73.3	121.00	157.78	41.2	3933.333	3.32	2211.1
AC-4	69.3	117.77	158.33	41.6	3861.11	3.92	3050.0
AC-5	74.0	122.53	165.00	47.6	3544.443	3.50	2177.8
AC-6	70.4	121.77	161.67	49.7	3803.887	3.60	2300.0
AC-7	70.3	121.77	160.89	40.3	3166.667	3.64	2366.7
AC-8	61.4	117.77	161.89	39.1	2805.553	3.73	2155.6
AC-9	66.3	121.10	163.55	33.9	2711.11	3.75	1788.9
AC-10	69.3	121.43	165.00	38.1	3444.443	3.90	1888.9
LSD	7.80	3.	6.11	9.37	1070.59	0.49	337.9

Where PH= Plant Height, DFF= Days to flowering, DM= Days to 50% maturity, GPS= Grains per spike, STW= Straw weight, TGW= Total Grain weight and TWPP= Total weight per plot.

The AC- 6 produced maximum grains per spike while AC-9 showed minimum grains per spike. Referring that AC-6 may be registered as reliable breeding material, especially while breeding for grain yield. AC- 4 was showing maximum values for thousand

grain weight that is 3.92 while minimum was 3.29 for AC-2. Total weight per plant was maximum for AC-4 that was 3050.0kg and minimum was noticed for AC-2 and AC-9, i.e; 1788.9kg.

Table 4. Correlation among different traits.

	PH	DFF	DM	GPS	STW	TGW	TWPP
PH	1						
DFF	0.98	1					
DM	0.97	1.00	1				
GPS	0.92	0.91	0.91	1			
STW	0.90	0.86	0.85	0.92	1		
TGW	0.92	0.97	0.98	0.87	0.83	1	
TWPP	0.80	0.82	0.82	0.85	0.87	0.86	1

Where PH= Plant Height, DFF= Days to flowering, DM= Days to 50% maturity, GPS= Grains per spike, STW= Straw weight, TGW= 1000- Grain weight and TWPP= Total weight per plot.

Correlation studies

Simple correlation coefficient was computed by using PAST software. Table No. 04 shows the values of correlation coefficient. Maximum correlation was found for total days to flowering with plant height (0.98), followed by plant height and days to 50% maturity (0.97), grains per spike and total grain weight with plant height (0.92).

Moderate correlation was noticed among straw weight with plant height (0.90) and days to flowering (0.86), followed by Days to 50% maturity (0.85). Hundred percent correlation was noticed for days to 50% maturity with days to flowering. These findings are in accordance with previous reports of Khodadadi *et al.* (2011), Kaleemullah *et al.* (2015) and Rehman *et al.* (2015).

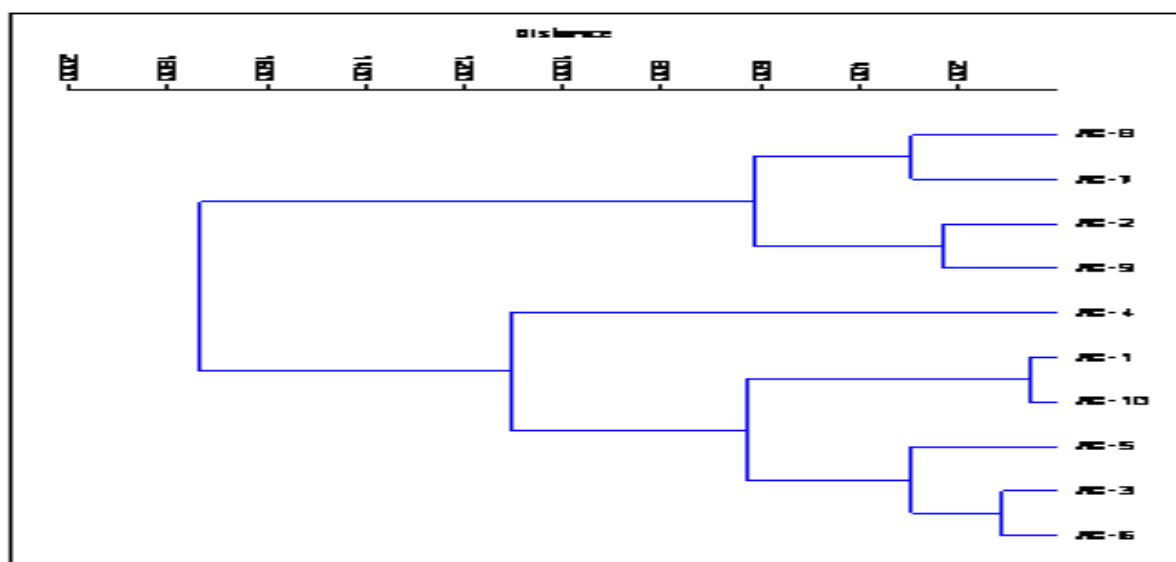


Fig. 1. Dendrogram based on average linkage distance for 10 wheat accessions.

Cluster analysis

Cluster analysis classified accessions of bread wheat into 2 clusters, shared a common node at the linkage distance of near about 1800.

Member of each cluster showed in the dendrogram constructed for different wheat genotypes. To estimate the genetic linkage, seven quantitative traits were scored in the present study.

Cluster I was comprised of four accessions. AC-8 and AC-7, AC-2 and AC-9 were positively correlated to each other at same linkage distance. Cluster II was comprised of total six genotypes. AC-1 and AC-10, AC-3 and AC-6 were significantly correlated to each other at same distance while AC-4 and AC-5 were outliers for this cluster showing maximum diversity from other members.

Conclusion

The analysis of variance exhibited that all the genotypes performed significantly ($P \leq 0.05$) variable for plant height, days to flowering, days to 50% maturity, grain per spike, straw weight, 1000-grain weight, registering the significant genetic variability among the genotypes for further evaluation. With regards to mean performance, the AC-4, AC-6 and AC-8 showed better performance for various traits. Cluster analysis revealed two accessions AC-4 and AC-5 as most diverse among all members.

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