GENETIC VARIABILITY STUDIES IN BREAD WHEAT (*TRITICUM AESTIVUM* L.) ACCESSIONS

Said Salman*, Shah Jehan Khan*, Javed Khan**, Rehmat Ullah Khan*** and Imran Khan****

ABSTRACT:- Sixty five wheat accessions were evaluated for yield and related traits during winter 2010-2011. Highly significant ($P \leq 0.01$) differences were found for all the traits studied indicating the scope of improvement through simple selection for high mean values of these traits. Maximum genotypic differences were observed for all the studied parameters except chlorophyll concentration index and number of spikelet per spike indicating considerable amount of variation among the accessions for each trait. The genotypic and phenotypic coefficient of variation estimates were higher for all the traits except chlorophyll concentration index and days to physiological maturity. Highest heritability estimates and expected genetic advance were found for all the traits except chlorophyll concentration index, spike length and number of spikelet spike^{-1} which exhibited moderate heritability. Based on Euclidian dissimilarity distance, 65 wheat accessions were classified in to 6 different clusters. Maximum diversity was found in cluster 1 and cluster 4. This maximum diversity explains the better parental selection for future breeding programme.

Key Words: Bread Wheat; Cluster Analysis; Diversity; Drought; Genetic Variability; Pakistan.

INTRODUCTION

Wheat (*Triticum aestivum L.*) is the most widely consumed cereal crop worldwide. Globally, demand for wheat by 2020 is forecasted at around 950mt year^{-1} (Kronstad, 1998). This target will be achieved only, if global wheat production is increased by 2.5% per annum. It is the staple food for a large part of the world population including Pakistan. Wheat is currently grown on 9.0mha with annual production of 23.8 mt. The present per capita consumption of wheat is 37.5 kg annum^{-1} (GoP, 2010).

Wheat production can be enhanced through the development of improved cultivars having wider genetic base capable of producing better yield under various agro-climatic conditions. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development (Manjarrez-Sandoval et al., 1997). New varieties with improved agronomic traits have been the

* Department of Plant Breeding and Genetics, Faculty of Agriculture, Gomal University, Dera Ismail Khan, Pakistan.
** Department of Plant and Environmental Protection, National Agricultural Research Centre, Islamabad, Pakistan.
*** Extension Education and Communication, Faculty of Social Sciences, University of Agriculture, Peshawar, Pakistan.
**** Department of Agriculture Extension, Dera Ismail Khan, Pakistan.
Corresponding author: salmanazoor@hotmail.com

major contributing factor to increase food production. The estimate of genetic diversity and evaluation are useful for facilitating efficient germplasm collection, management and utilization (Nisar et al., 2008). Genetic diversity is a vital source of various disease resistance and high yielding genes hence, crop improvement mainly depends on the extent of heritable diversity existing in crop species. Frequent use of few parents in breeding programme led to genetic erosion. Diverse genetic background provides desirable allelic variation among parental lines to produce new and valuable combinations (Tar'an et al., 2005). To develop high yielding and resistant varieties it is necessary to utilize the various existing genetic resources with maximum genetic diversity.

Considering the importance of genetic diversity as a basic breeding tool for improvement, the present study was conducted to evaluate the genetic variability and selection of suitable diverse parents for yield and related traits in future breeding programme.

MATERIALS AND METHOD

The experiment was carried out at research area of Department of Plant Breeding and Genetics, Faculty of Agriculture, Gomal University Dera Ismail Khan during winter seasons 2010-2011. Seeds of 65 bread wheat accessions differing in their genetic make-up were collected from National Agricultural Research Centre (NARC, PGRI) Islamabad and Agriculture Research Institute (ARI) Ratta Kulachi D.I. Khan (Table 1). The experiment was conducted in three replications in 5m long rows in randomized complete block design (RCBD). The plant to plant and row to row distance was kept 10 cm and 30 cm, respectively. All the recommended cultural practices were performed. At the time of maturity five plants were selected randomly from each plot to collect data on days to 50% heading, days to physiological maturity, chlorophyll concentration index, plant height (cm), number of tillers per plant, flag leaf area (cm^2), spike length (cm), number of grains per spike, number of spikelet per spike, 1000-grain weight (g) and grain yield per plant (g).

The data collected was subjected to analysis of variance to test the level of significance among the genotypes for different characters according to Steel et al. (1997). Various descriptive parameters (mean, standard error of means, range and mean squares) were calculated. Genotypic and phenotypic variances, genotypic and phenotypic coefficient of variability, broad sense heritability and expected genetic advance were computed according to the method suggested by Singh and Chaudhary (1985). Using the Statistica software, cluster analysis according to Ward method was performed to separate the genotypes into distinct groups and clusters.

RESULTS AND DISCUSSION

Genetic Variability

Highly significant differences ($P \leq 0.01$) were observed for all the traits studied among genotypes (Table 2). Maximum genotypic (Vg) and phenotypic variation (Vp), genotypic (GCV) and phenotypic coefficient of variability (PCV) were found for all the parameters showing a considerable range of variation among genotypes (Table 3). The PCV values in all the

Table 1. Description and source of 65 bread wheat accessions grown in 2010-2011

S. No	Accession	Source	S. No	Accession	Source
1	010718	S-1319	34	010788	SVP-37
2	010724	TANOORI	35	010789	SVP-40
3	010726	S-1406	36	010790	SVP-40
4	010728	23584/NAI-310 299,61	37	010791	SVP-39
5	010730	SOFTYXTOB'S'	38	010792	SVP-38
6	010731	C-273	39	010795	SVP-44
7	010736	Moncho-S	40	010796	SVP-50
8	010737	V-1319	41	010797	SVP-50
9	010738	S.A. 75	42	010798	SVP-50
10	010739	C-228	43	010799	SVP-40
11	010740	Indus, 79	44	010800	SVP-40
12	010741	S-347	45	010801	SVP-39
13	010743	Maxi-Pak	46	010802	SVP-38
14	010744	S-1538	47	010803	SVP-44
15	010748	S-57	48	010804	SVP-50
16	010749	S-33	49	010805	SVP-50
17	010750	PM.HARI'S VIREOS	50	010806	SVP-86
18	010751	DIRK	51	010807	SVP-67
19	010752	ZA-77	52	010809	SVP-74
20	010753	S-415	53	011809	002463(01)
21	010754	WL-711	54	011860	Zarghoon-79
22	010775	SVP-64	55	011861	Pari-73
23	010777	SVP-4	56	011862	Punjnad-88
24	010778	SVP-4	57	011864	Khyber-79
25	010779	SVP-9	58	011865	Chakwal-86
26	010780	SVP-22	59	011866	Sindh-81
27	010781	SVP-33	60	011867	Sutlaj-86
28	010782	SVP-12	61	011868	5-42
29	010783	SVP-25	62	ZAM 04	27th IBWSN-1994/95 E#334
30	010784	SVP-26	63	GOMAL 08	RBWYT-MR-1999/00 E#5
31	010785	SVP-29	64	HASHIM 08	BWON-SA-1997/98 E#52
32	010786	SVP-24	65	DERA 98	5th WAWSN-1991/92 E#41
33	010787	SVP-24	65	DERA 98	5th WAWSN-1991/92 E#41

Table 2. Various descriptive statistics of important traits of bread wheat accessions

Parameter	Mean	Mean Square	S.E. of Mean
Flag leaf area (cm^2)	15.51	33.29332 **	0.413201
Chlorophyll concentration index	42.73	10.36408 **	0.230541
Number of fertile tiller $plant^{-1}$	9.22	3.23635 **	0.128828
Plant height (cm)	84.04	277.00630 **	1.191866
Spike length (cm)	11.56	8.73757 **	0.211679
Days to 50% heading	110.35	261.88410 **	1.158877
Days to physiological maturity	149.07	317.56010 **	1.276132
Number of spikelets $spike^{-1}$	20.33	17.64391 **	0.300802
Number of grains $spike^{-1}$	36.53	279.29200 **	1.196773
1000-grain weight (g)	40.95	239.84930 **	1.109052
Grain yield $plant^{-1}$ (g)	13.66	32.73940 **	0.409749

*** Significant at 5% level of probability.*

parameters were higher than GCV values exhibiting the influence of environment over these traits. Heritability estimates of all the studied parameters were higher except chlorophyll concentration index which exhibited slightly moderate heritability. Asif et al. (2010) also recorded high heritability estimates for grain yield per plant, number of tillers per plant which supports these findings. Highest expected genetic

Table 3. Various genetic components of important traits of bread wheat accessions

Parameter	Vg	Ve= Vp-Vg	Vp	Heritability %	PCV	GCV	Exp. GA
Flag leaf area (cm^2)	32.27	3.06	35.33	91.33	38.32	36.62	11.18
Chlorophyll conc. index	9.09	3.80	12.90	70.48	8.40	7.05	5.21
Number of tiller $plant^{-1}$	3.14	0.26	3.41	92.30	20.02	19.24	3.51
Plant height (cm)	276.77	0.68	277.46	99.75	19.81	19.79	34.22
Spike length (cm)	8.04	2.09	10.13	79.36	27.52	24.52	5.20
Days to 50% heading	260.34	4.63	264.92	98.25	14.75	14.62	32.94
Days to physio. maturity	317.03	1.58	318.61	99.50	11.97	11.94	36.58
No. of spikelets $spike^{-1}$	16.58	3.18	19.76	83.88	21.86	20.02	7.68
Number of grains $spike^{-1}$	277.98	3.92	281.90	98.60	45.95	45.63	34.10
1000-grain weight (g)	233.07	20.33	253.40	91.97	38.86	37.27	30.16
Grain yield $plant^{-1}$ (g)	31.38	4.06	35.44	88.54	36.86	34.69	12.47

Ve = Environmental variance

Table 4. Grouping based on different clusters for 65 bread wheat accessions evaluated during winter 2010-2011

Parameters	Cluster					
	1	2	3	4	5	6
Flag leaf area (cm^2)	15.30 ± 1.10	14.62 ± 1.27	16.15 ± 1.2	14.25 ± 1.2	16.44 ± 0.6	13.13 ± 0.7
Chlorophyll conc. index	42.66 ± 0.70	42.18 ± 0.60	43.14 ± 0.7	43.30 ± 0.6	42.88 ± 0.3	41.59 ± 0.9
Number of tiller plant^{-1}	8.46 ± 0.58	9.04 ± 0.28	9.40 ± 0.2	9.04 ± 0.2	9.42 ± 0.2	9.61 ± 0.3
Plant height (cm)	83.35 ± 3.30	77.25 ± 1.91	89.54 ± 4.1	91.06 ± 4.1	84.86 ± 1.8	79.02 ± 2.3
Spike length (cm)	10.85 ± 0.40	11.25 ± 0.64	12.81 ± 0.6	12.17 ± 0.9	11.84 ± 0.3	10.38 ± 0.7
Days to 50% heading	106.12 ± 3.40	112.50 ± 1.62	114.70 ± 0.9	111.80 ± 3.6	112.40 ± 0.7	97.71 ± 7.6
Days to Physio. maturity	144.37 ± 5.80	147.75 ± 4.00	153.70 ± 1.3	154.00 ± 2.4	150.50 ± 1.8	137.85 ± 2.8
No. of spikelets spike^{-1}	20.67 ± 1.32	20.92 ± 0.60	20.68 ± 0.4	20.76 ± 0.4	20.56 ± 0.3	17.49 ± 1.3
Number of grains spike^{-1}	42.82 ± 4.28	35.60 ± 2.26	39.10 ± 2.6	31.14 ± 2.6	37.06 ± 1.9	30.41 ± 2.6
1000-grain weight (g)	41.78 ± 2.69	40.64 ± 1.25	39.51 ± 2.4	40.57 ± 3.9	42.31 ± 2.0	38.32 ± 2.8
Grain yield plant^{-1} (g)	14.48 ± 1.06	13.09 ± 0.90	14.48 ± 1.3	11.69 ± 2.1	14.60 ± 0.9	11.28 ± 1.3

advance was found for days to heading, physiological maturity, 1000-grain weight and number of grains spike^{-1}. The remaining traits showed moderate to low expected genetic advance. Heritability and expected genetic advance is normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson et al., 1955).

High heritability accompanied with high expected genetic advance for most of the traits indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. The findings of higher heritability and expected genetic advance are in line with the findings of Munir et al. (2007), who also reported higher heritability coupled with expected genetic advance. Higher heritability with low expected genetic advance for number of tillers plant^{-1}, spike length and number of spikelets spike^{-1} indicates non additive gene effects and there is very limited scope for improvement in these traits.

Cluster Analysis

It is based on Euclidean dissimilarity distance using Ward's method divided the accessions in six clusters (Table 4). Cluster 1 consists of eight accessions and 2 consists of nine accessions, cluster 3 & 6 each comprised seven accessions, cluster 4 consists of five accessions and cluster 5 consists of 29 accessions (Table 5). Cluster 1 consists of highest number of grains spike^{-1}, 1000-grain weight and grain yield plant^{-1} and selection for these traits can be made more effectively. Cluster 2 consists of highest number of spikelets spike^{-1}. Cluster 3 consists of maximum flag leaf area, chlorophyll concentration index and grain yield plant^{-1}. Maximum plant height was found in cluster 4. Cluster 6 consists of earliest maturing accessions. Minimum days to heading and physiological maturity was found in cluster 6 and selection for early maturity can be made more effectively from cluster 6.

Table 5. Cluster classification of 65 bread wheat accessions evaluated during winter 2010-2011

Cluster							
1	2	3	4	5			6
Gomal 08	10718	10724	10739	10726	10777	10781	Hashim 088
Zam 04	10730	10752	10786	10728	10778	10782	Dera 98
10737	10754	10780	10791	10731	10779	10800	10743
10741	10804	10785	10796	10738	10783	10802	10775
10750	10805	10797	10803	10740	10787	10809	10790
10784	10806	10799		10744	10788	11864	10801
10807	11809	11866		10748	10789	11865	11861
11862	11860			10749	10792	11867	
				10751	10795	11868	
				10753	10798		

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