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GENTETIC VARIABILITY, CORRELATION AND DIVERSITY STUDIES IN BREAD WHEAT (*Triticum aestivum* L.) GERMPLASM

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ABSTRACT

Forty one bread wheat genotypes grown in Peshawar, Pakistan during winter 2009-2010 were evaluated for variability parameters and correlation for number of grains/spike, number of tillers per plant, 1000-grain weight, flag leaf area, grain yield per plant and spike density. Significant genotypic differences were observed for all the traits studied indicating considerable amount of variation among genotypes for each character. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield per plant, flag leaf area and number of tillers per plant. The remaining traits exhibit moderate to low PCV and GCV estimates. High heritability estimates were recorded for all the traits studied. These traits also indicate high expected genetic advance except spike density and number of tillers per plant. Grain yield per plant showed highly significant positive correlation with number of tillers per plant and number of grains/spike and significant positive correlation with 1000-grain weight. Based on Euclidian dissimilarity distance, the cluster analysis separated the 41 wheat genotypes into eight different clusters.

Key words: Genetic variability, bread wheat germplasm, correlation.

INTRODUCTION

Wheat is the staple food for a large part of the world population including Pakistan. Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations. In plant breeding programme, direct selection for yield as such could be misleading. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. Kumar *et al.* (2003) reported high heritability coupled with high genetic advance for plant height, number of spikelet per spike and 1000-grain weight in wheat. The grain yield was significantly and positively correlated with 1000-kernel weight and the number of spikes per square meter (Korkut *et al.*, 2001).

In this investigation, the study of different genotypes were made with an attempt to generate information on inheritance, relationship of yield and its components and their implication in selection of better genotypes of wheat for the development or improvement of cultivars and germplasm.

MATERIALS AND METHODS

The wheat germplasm consisted of 41 genotypes were collected from different National Agricultural Research Institutes as presented in Table 1. The experiment was conducted at Nuclear Institute for Food and Agriculture (NIFA), Peshawar, during winter 2009-2010. Each plot consisted of two rows, each 3.0 m long with 30 cm and 15 cm spacing between and within rows, respectively. All the cultural practices were performed as usual. At maturity five guarded plants from each plot were selected at random for recording data on number of grains per spike, number of tillers per plant, 1000-grain weight, flag leaf area, spike density and grain yield per plant. The mean data were subjected to analysis of variance to test the level of significance among the genotypes for different characters according to Steel *et al.* (1997).

Genotypic and phenotypic variances, genotypic and phenotypic coefficient of variability, broad sense heritability and genotypic and phenotypic correlation 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: Mean squares of grains per spike, number of tillers per plant, 1000-grain weight, flag leaf area, spike density and grain yield per plant showed highly significant differences between genotypes (Table 2). Genotypic and phenotypic variance, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability and expected genetic advance expressed as percentage of mean for six characters are presented in Table 3. The estimates of GCV were high for grain yield per plant (33.32), flag leaf area (22.49) and number of tillers per plant (21.05). The remaining traits recorded moderate to low GCV estimates. High heritability estimates and expected genetic advance were recorded for all the traits studied. Such considerable range of variations provides a good opportunity for yield improvement. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of all the traits. Khan *et al* (2010 a) and Salem *et al* (2008) also recorded high heritability estimates for grain yield per plant, number of tillers per plant which supports these findings. Heritability and expected genetic advance are 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 in case of number of grains per spike, grain yield per plant, flag leaf area and 1000-grain weight indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Similar findings have been reported by Munir *et al* (2007). High heritability for number of tillers per plant and spike density coupled with low expected genetic advance indicates non-additive gene effects. Therefore, there seems a limited scope for improvement in this trait.

Correlation coefficient analysis: The phenotypic and genotypic correlations for morphological traits are presented in table 4. Grain yield per plant had highly significant and positive genotypic and phenotypic correlations with number of tillers per plant and number of grains per spike and significant positive correlation with 1000-grain weight. Spike density and flag leaf area showed positive but non significant genotypic and phenotypic correlations with grain yield per plant.

The yield components exhibited varying trends of association among themselves. Number of tillers showed negative and highly significant and negative non significant phenotypic and genotypic correlation with flag leaf area. Grains per spike showed positive non significant correlation with number of tillers per plant and negative non significant correlation with 1000-grain weight. Similarly grains per spike have highly significant positive genotypic correlation with spike density and positive non significant correlation with spike density. 1000-grain weight has significant positive genotypic and phenotypic correlation with spike density. Similar findings were also found by Khan *et al* (2010 a, b).

Cluster analysis: The analysis of genetic diversity through the cluster analysis based on Euclidean dissimilarity distance using Ward's method categorized the germplasm into eight different clusters (Table 5). Cluster I and II consisted of seven genotypes, cluster III and VIII consists of three genotypes each. Cluster IV consists of five and each of cluster V and cluster VI consists of six genotypes.

Table 1. Description of Forty one wheat genotypes grown during winter 2009-2010.

S. No	Genotype	Source	S. No	Genotype	Source
1	Bakhtawar-92	NIFA, Pesh	22	E-253	NIFA, Pesh
2	Frontana	-do-	23	E-238	-do-
3	Saleem-2000	-do-	24	E-202	-do
4	Tatara	-do-	25	E-107	-do-
5	Inqilab-91	NARC, Isl	26	E-186	-do-
6	Fakhar-e-sarhad	NIFA, Pesh	27	E-187	-do-
7	Karwan	-do-	28	E-246	-do-
8	Blue silver	-do-	29	Sehar	NARC, Isl
9	Lu-26	NARC, Isl	30	Shafaq	NIFA, Pesh
10	WS-10	NIFA, Pesh	31	QS-1	-do-
11	TD-1	-do-	32	Maria	-do-
12	D-97603	-do-	33	Farid-06	NARC, Isl
13	Iqbal-2000	-do-	34	Chakwal-86	-do-
14	Era	-do-	35	Chakwal-58	-do-
15	Parula	-do-	36	GA-2000	-do-
16	HD-2169	-do-	37	AS-2002	-do-
17	E-4	-do-	38	Bathoor-08	NIFA, Pesh
18	E-6	-do-	39	Hashim-08	ARI, Ratta Kulach, D.I.K
19	E-104	-do-	40	Zam-04	-do-
20	E-110	-do-	41	Gomal-08	-do-
21	Watan x era	-do-			

Table 2. Range, mean, mean squares and standard error of means for six quantitative characters of forty one wheat genotypes.

Character	Range	Mean	Mean square	SE of mean
Grains/spike	43.10	53.45	186.50**	1.48
No of tillers	8.86	9.72	8.95**	0.33
1000-grain weight	35.23	39.25	84.65**	1.02
Flag leaf area	54.44	37.06	145.74**	1.34
Grain yield/plant	27.32	19.86	88.06**	1.03
Spike density	0.85	1.70	0.06*	0.0278

* and ** significant at 5% and 1% level of significance respectively.

Table 3. Genetic parameters of various yield components of wheat.

Character	GV	PV	GCV	PCV	H (%)	Exp. Genetic advance
Grains/spike	91.99	94.50	17.98	18.22	97.34	19.49
Number of tillers	4.19	4.76	21.05	22.45	88.12	3.95
1000-grain weight	41.92	42.73	16.49	16.65	98.11	13.43
Flag leaf area	69.71	76.03	22.49	23.53	91.69	16.48
Grain yield/plant	43.79	44.26	33.32	33.49	98.93	14.02
Spike density	0.02	0.03	9.48	11.16	72.47	0.28

Table 4. Genotypic and phenotypic correlations among different quantitative characters in wheat.

	Correlation	Grains/spike	No of tillers	1000-grain weight	Flag leaf area	Spike density
Grains/spike						
No of tillers	G	0.060				
	P	0.049				
1000-grain weight	G	-0.080	-0.064			
	P	-0.069	-0.063			
Flag leaf area	G	0.353*	-0.194	0.334*		
	P	0.318*	-0.471**	0.320*		
Spike density	G	0.585**	0.314*	-0.327*	-0.130	
	P	0.144	0.272	-0.274	-0.167	
Grain yield/plant	G	0.502**	0.775**	0.344*	0.105	0.238
	P	0.510**	0.713**	0.343*	0.090	0.189

* and ** significant at 5% and 1% level of significance respectively. G: genotypic correlation, P: phenotypic correlation.

Table 5. Grouping based on different clusters for 41 bread wheat accessions evaluated during Winter 2009-10

Character	cluster 1	cluster 2	cluster 3	cluster 4	cluster 5	cluster 6	cluster 7	cluster 8
grains/spike	54.07±4.86	56.92±3.25	53.27±5.57	48.14±4.7	47.97±5.36	44.75±3.87	58.86±15.26	74.01±6.29
No. tillers	10.99±2.6	8.99±1.41	9.88±1.25	10.46±2.37	9.11±1.67	7.99±1.3	10.86±1.03	10.16±3.91
1000-grn wet	40.71±4.24	38.18±4.85	33.6±2.44	37.51±3.89	36.83±5.34	37.18±3.53	49.87±11.82	41.69±6.42
Flag leaf area	37.48±5.14	36.23±4.48	32.57±5.12	36.15±1.12	36.65±5.78	31.35±3.74	39.25±6.97	53.34±23.86
Grn yld/plnt	23.75±5.48	18.54±3.12	17.39±4.18	18.22±3.37	15.6±3.15	12.85±2.6	30.04±3.99	28.13±8.24
Spk dnsty	1.72±0.17	1.75±0.21	1.93±0.105	1.67±0.17	1.63±0.45	1.62±0.17	1.69±0.14	1.66±0.19

Genotypes of cluster-I have highest number of tillers per plant. Similarly Cluster III consists of high spike density. Highest number of grains per spike and flag leaf area was observed in cluster VIII, fallowed by cluster VII. 1000-grain weight was maximum in cluster VII fallowed by cluster VIII. Maximum grain yield per plant was observed in cluster VII fallowed by cluster VIII.

Selection from cluster I can be made for higher number of tillers/plant and 1000-grain weight. Similarly selection for highest number of grains/spike and flag leaf area can be made from cluster VIII. Highest grain yield/plant and 1000-grain weight was observed in cluster

VII and selection for these traits will be very effective from cluster VII.

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