VARIABILITY, HERITABILITY AND GENETIC PROGRESS FOR SOME YIELD COMPONENTS IN COMMON WINTER WHEAT GENOTYPES (*TRITICUM AESTIVUM* L.)

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Summary: Sixteen common winter wheat genotypes grown in IPGR-Sadovo, Bulgaria during 2011-2013 were evaluated for variability, heritability and genetic progress in a randomized block design. Significant genotypic differences were observed for all traits studied indicating considerable variations among genotypes for each character. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), which indicates a slight effect of environment on the expression of the characters studied. High PCV and moderate GCV were observed in traits spike length (PCV=20.40%, GCV=19.55%), number of grain per spike (PCV=23.65%, GCV=19.42%), grain weight per spike (PCV=21.60%, GCV=15.54%) and grain yield per plant (PCV=28.24%, GCV=18.12%). Heritability revealed that characters like plant height (95.26%) exhibited the highest heritability followed by spike length (91.78%) and number of grain per spike (67.40%). Genetic progress revealed that it was high for spike length, number of grain per spike, plant height, grain weight per spike and grain yield per plant, whereas low genetic progress was observed for number of productive tillers per plant and number of spikelets per spike. Characteristics like plant height, spike length and number of grain per spike showed high heritability coupled with high genetic progress. Therefore, these characters should be given top priority during selection breeding in wheat. The cluster analysis based on Euclidean dissimilarity using the Between-groups linkage method categorized the germplasm into three clusters. Genotypes 81BM039, 7450, A1BM0309, 81BM052 and 81BM003 are suitable for breeding programs aimed at improving yield in hybridization programs to develop high yielding wheat varieties.

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INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important food crop in the world including Bulgaria. Grain yield is a complex trait that is highly influenced by many genetic factors and environmental fluctuations. The success of a crop improvement program depends upon the amount of genetic variability existing in the germplasm. To bring the heritable improvements in economic characters through selection and breeding, estimation of genetic parameters must be made before starting a program. There are different techniques available to compute the genetic parameters and the index of transmissibility of characters (Waqar-Ul-Haq et al., 2012). The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding program (Bisne, 2009). Heritability estimates provide information about the extent to which a particular character can be transmitted to the successive generations. Knowledge of heritability of a trait thus guides a plant breeder to predict the behavior of succeeding generations and helps to predict the response to selection. High genetic progress coupled with high heritability estimates offer the most suitable condition for selection (Larik et al., 1989). Therefore, availability of good knowledge of heritability and genetic progress existing in different yield parameters is a prerequisite for effective plant improvement exercise. A number of researchers in their studies have reported the presence of high heritability and genetic progress in different yield related attributes in wheat (Afiah et al., 2000;

Ashraf et al., 2002; Arshad and Chowdhry, 2003; Baloch et al., 2003; Kamal et al., 2003; Khalil and Afridi, 2004; Ansari et al., 2004, 2005; Inamullah et al., 2006; Shabana et al., 2007; Khan et al., 2012; Kumar et al., 2014).

The present study was carried out to estimate genetic variability, heritability and genetic progress in the available germplasm of common winter wheat (*Triticum aestivum* L.).

MATERIALS AND METHODS

The present study was conducted in the experimental field of the Konstantin Malkov Institute of Plant Genetic Resources-Sadovo, Bulgaria during 2010-2011, 2011-2012 and 2012-2013 growing seasons. Sixteen common winter wheat accessions maintained in the *ex-situ* field collection were examined (Table 1). The experiment was conducted in a randomized block design in four replications on a 10 m^2 plot size. Normal agronomic and cultural practices were applied to the experiment throughout the growing seasons. The agronomic characters were estimated after harvesting the plants. From each accession, 10 plants were collected for biometrical measurements. Data were recorded for plant height, number of productive tiller per plant, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike 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 and Torrie (1980). Genotypic and phenotypic variances, genotypic and phenotypic coefficients of variability, broad sense

Table 1. List of accessions included in the study.

№	Number of accessions	Name of varieties	Genus	Spesies	Subspecies
1	A1BM0309	Charodeyka	Triticum	aestivum	lutescens
2	81BM052	Prespa	Triticum	aestivum	lutescens
3	81BM053	Katja	Triticum	aestivum	lutescens
4	56739	№301	Triticum	aestivum	erythrospermum
5	81BM003	Rekviem	Triticum	aestivum	lutescens
6	7911682	Bezhostaja 1	Triticum	aestivum	lutescens
7	A1BM0301	Dobrudzha 1	Triticum	aestivum	milturum
8	A1BM0293	Jubileina 2	Triticum	aestivum	erythrospermum
9	644065	Jubileina 3	Triticum	aestivum	erythrospermum
10	7810926	№14	Triticum	aestivum	ferrugineum
11	A1BM0314	Momchil	Triticum	aestivum	lutescens
12	81BM039	Ogosta	Triticum	aestivum	lutescens
13	85BM106	Kaliakra	Triticum	aestivum	erythrospermum
14	7911257	Hebros	Triticum	aestivum	lutescens
15	7450	Vraca	Triticum	aestivum	lutescens
16	7911745	Toshevka	Triticum	aestivum	lutescens

heritability were computed according to the method suggested by Singh and Chaudhary (1985). Genetic progress in terms of percentage of means was estimated as described by Brim et al. (1959). A cluster analysis based on the Between-groups linkage method using Euclidian distance was performed by using the SPSS 13 software.

RESULTS

Analysis of variance

Mean squares of plant height, number of productive tiller per plant, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike and grain yield per plant showed highly significant differences between genotypes (Table 2).

Phenotypic, genotypic and environmental variance

Phenotypic variance ranged from 0.12 (grain weight per spike) to 237.07 (plant height). The values for genotypic variances ranged between 0.05 (number of productive tiller per plant) and 225.82 (plant height). Environmental variances ranged from 0.06 (grain weight per spike) to 24.63 (number of grain per spike) (Table 3).

Genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV)

GCV ranged from 6.22% for the number of spikelets per spike to 19.55% for spike length, whereas PCV ranged from 8.38 % for the number of spikelets per spike to 28.24% for grain yield per plant (Table 3).

Table 2. Mean squares of grain and yield related components for sixteen winter wheat genotypes.

Source of variance	df	Plant height	Number of productive tillers per plant	Spike length	Spikelets per spike	Number of grains per spike	Grain weight per spike	Grain yield per plant
Genotype (G)	15	6808.43*	2.12*	164.42*	42.32*	1601.54*	1.95*	18.89*
Environment (E)	2	2122.41*	21.41*	142.99*	30.44*	3193.73*	9.47*	133.91*
G x E	30	464.06*	1.36*	7.58*	11.40*	182.08*	0.33*	5.02*
Error	430	35.03	0.79	1.87	3.09	68.19	0.16	2.46
CV [%]		15.27	8.19	19.63	6.47	19.88	16.24	19.37

* – Significance at p< 0.001 level. CV – Coefficient of variability.

Table 3. Genetic parameters of various yield components for 16 winter wheat genotypes.

Characters	Genotypic variance	Phenotypic variance	Environmental variance	Genotypic coefficient of variability [%]	Phenotypic coefficient of variability [%]	Heritability [%]	Genetic progress [% of means]
Plant height	225.82	237.07	2.36	15.23	15.61	95.26	30.62
Number of productive tillers per plant	0.05	0.29	0.24	6.65	16.53	16.20	5.51
Spike length	5.43	5.92	0.49	19.55	20.4	91.78	38.57
Number of spikelets per spike	1.3	2.36	1.06	6.22	8.38	55.21	9.53
Number of grains per spike	50.92	75.55	24.63	19.42	23.65	67.4	32.84
Grain weight per spike	0.06	0.12	0.06	15.54	21.60	51.74	23.02
Grain yield per plant	0.55	1.34	0.79	18.12	28.24	41.16	23.94

Heritability and genetic progress expressed as percentage of mean

In the present study, heritability estimated ranged from 16.20% to 95.26 % (Table 3). High estimates of heritability (above 60%) in broad sense were recorded for three characters studied (plant height-95.26%, spike length-91.78% and number of grain per spike-67.40%). The expected genetic progress expressed as a percentage of the mean varied between 5.51% for number of productive tiller per plant and 38.58% for spike length (Table 3). Genetic progress as a percentage of the mean was high for spike length (38.57%) followed by number of grain per spike (32.84%) and plant height (30.62%). Genetic progress was low for number of productive tiller per plant (5.51%) and number of spikelets per spike (9.53%).

Cluster analysis

The analysis of genetic diversity through the cluster analysis is shown in Fig. 1. The cluster diagram based on Euclidean dissimilarity using the Between-groups linkage method categorized the germplasm into three clusters at a 15% linkage distance. The average of characters for each cluster and the difference between each cluster with the total mean (Diff) are presented in Table 4.

First cluster

56739, 7810926, A1BM0293 and 644065 accessions were classified in the first cluster, including 25% of total genotypes. The average values of traits in this group except spike length and plant height were less than total means of all genotypes (Table 4).
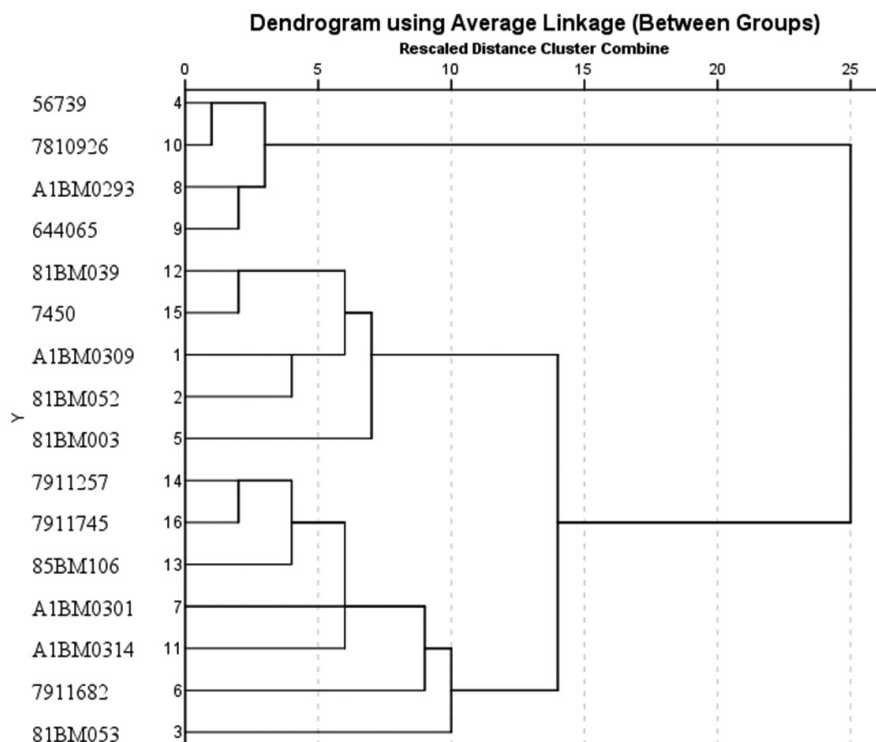

Figure 1. Tree diagram of 16 genotypes for 7 studied variables using hierarchical cluster analysis (Between-group linkage method and Euclidean distance).

Table 4. The average of characters for each cluster and difference between each cluster and the total mean (Diff).

Clusters		Spike length	Number of spikelets per spike	Number of grains per spike	Grain weight per spike	Grain yield per plant	Plant height	Number of productive tillers per plant
I	Mean	15.25	17.44	28.84	1.29	3.17	120.88	3.10
	Diff	2.98	-0.90	-7.52	-0.27	-0.86	20.49	-0.12
II	Mean	10.54	19.57	44.56	1.87	4.77	83.42	3.19
	Diff	-1.73	1.23	8.20	0.31	0.74	-16.96	-0.03
III	Mean	11.01	18.00	35.69	1.52	4.15	96.85	3.37
	Diff	-1.25	-0.33	-0.67	-0.04	0.12	-3.53	0.15
Total mean		12.27	18.34	36.36	1.56	4.03	100.38	3.22

Second cluster

The second group comprises 5 accessions –81BM039, 7450, A1BM0309, 81BM052 and 81BM003 including 31.25% of total genotypes. The genotypes in this group were in the highest rate with respect to number of spikelets per spike (19.57), number of grains per spike (44.56), grain weight per spike (1.87) and grain yield per plant (4.77). The varieties in this cluster had the lowest values for plant height (Table 4).

Third cluster

In the third group, 7 genotypes (7911257, 7911745, 85BM106, A1BM0301, A1BM0314, 7911682 and 81BM053) were classified including 43.75% of total accessions. The values for the number of productive tillers per plant in this cluster were highest compared with the total means of all genotypes (Table 4).

DISCUSSION

In the present study, 16 genotypes of common winter wheat were studied to assess their genetic potential. The analysis of variance showed that the mean squares for genotypes were significant (p<0.001) for all traits studied. This indicated the existence of a high degree of genetic variability in the material to be exploited in a breeding program, and also reflected the broad ranges observed for each trait (Yousaf et al., 2008; Kalimullah et al., 2012; Kumar et al., 2014).

Relatively higher phenotypic variance values of 237.07 for plant height and 75.55 for number of grains per spike were recorded in the study. Likewise, the genotypic variances for these traits were also high, indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance of these traits (Degewione et al., 2013). The result of the present study concurs with that reported by Cheema et al. (2006), Yousaf et al. (2008), Kalimullah et al. (2012) and Kumar et al. (2014).

Deshmukh et al. (1986) classified PCV and GCV values as high (>20%), moderate (10-20%) and low (<10%). In our study, high PCV and moderate

GCV were observed in the following traits: spike length (PCV=20.40%, GCV=19.55%), number of grain per spike (PCV=23.65%, GCV=19.42%), grain weight per spike (PCV=21.60%, GCV=15.54%) and grain yield per plant (PCV=28.24%, GCV=18.12%). Moderate PCV and GCV were found for plant height (PCV =15.61% and GCV=15.23%). Similar observations for plant height were also reported by Basheeruddin and Sahib (2004), Shashikala (2006), Yousaf et al. (2008) and Kumar et al. (2014). On the other hand, the number of spikelets per spike showed low GCV and PCV (6.22% and 8.38%, respectively), indicating a less scope of selection as it is under the influence of environment. Large differences between the PCV and GCV values were observed for the number of productive tiller per plant and grain yield per plant indicating the high contribution of environmental variance to phenotypic variance. The phenotypic coefficients of variation were generally higher than the genotypic coefficients of variation for all traits studied, indicating the influence of growing environments (Table 2). These findings were in agreement with those reported by Panwar and Singh (2000), Bergale et al., (2001), Pawar et al. (2002), Dwivedi et al. (2004) and Kumar et al. (2014).

Heritability in broad sense is the ratio of genotypic variance to the total variance. In the present study, high estimates of heritability (above 60%) in broad sense were recorded for three characters studied (plant height-95.26%, spike length- 91.78% and number of grain per spike-67.40%). According to Panwar and Singh (2000), Jedynski (2001), Kashif et al. (2004), Asif et al., (2004), Rasal et al.,

(2008) and Kumar et al. (2014) the highest heritability values indicate that heritability may be due to the higher contribution of the genotypic component. The high value for heritability in broad sense indicates that the character is least influenced by environmental effects. Heritability combined with genetic advance is a more reliable index for selections of traits (Anshuman et al., 2013). High heritability accompanied with high expected genetic progress in the case of plant height, spike length and number of grains per spike indicated that most likely the heritability was due to additive gene effects and selection may be effective in early generations for these traits. Gupta and Verma (2000) also reported high values for heritability and high genetic progress for the number of grain per spike. The number of spikelets per plant moderate heritability coupled with low expected genetic progress indicated non-additive gene effects. Moderate heritability with low genetic progress indicated slight chances of improvement of this trait in subsequent generations as discussed by Kalimullah et al. (2012).

Quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in a proper choice of parents for realizing higher heterosis and obtaining useful recombinants (Ali et al., 2008; Rahim et al., 2010; Khodadadi et al., 2011). In the present investigation, cluster analysis based on Euclidean dissimilarity using the Between-groups linkage method categorized the germplasm into three clusters at a 15% linkage distance. Genotypes in the first cluster- 56739, 7810926, A1BM0293 and 644065 had greatest values for plant height and spike

length. They can be used to increase spike length in the breeding program. Genotypes in the second group were in the highest rate with respect to number of spikelets per spike, number of grains per spike, grain weight per spike and grain yield per plant and in the least rate with respect to plant height. The members of this group (81BM039, 7450, A1BM0309, 81BM052 and 81BM003) are suitable for breeding programs aimed at improving the yield in hybridization programs to develop high yielding wheat varieties. Crossing among the existing genotypes in the first and second groups provides more possibilities to achieve higher genetic variance and optimal genotypes with respect to yield performance. Genotypes in the third cluster (7911257, 7911745, 85BM106, A1BM0301, A1BM0314, 7911682 and 81BM053) were in the highest rate with respect to number of productive tillers per plant and may be used to increase the number of productive tiller per plan in breeding programs.

CONCLUSION

Analysis of variance revealed highly significant differences among the accessions for all parameters. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all traits studied, indicating the influence of growing environment. The characters plant height, spike length and number of grains per spike, exhibited high heritability coupled with high genetic progress indicating that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Evaluation of genetic diversity with cluster analysis on

Euclidean dissimilarity using the Between-groups linkage method categorized the germplasm into three clusters. Genotypes 81BM039, 7450, A1BM0309, 81BM052 and 81BM003 are suitable for breeding programs aimed at improving the yield in hybridization programs to develop high yielding wheat varieties. Genotypes 56739, 7810926, A1BM0293 and 644065 can be used to increase spike length, while genotypes 7911257, 7911745, 85BM106, A1BM0301, A1BM0314, 7911682 may be used to increase the number of productive tiller per plan in breeding programs.

REFERENCES

Afiah S, N Mohammad, M Saleem, 2000. Statistical genetic parameters, heritability and graphical analysis in 8 x 8 wheat diallel crosses under saline condition. Annals J Agric Sci, 4: 257–280.

Ali, Y., B. M. Atta, J. Akhter, P. Monneveux, Z. Lateef. 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. Pak J Bot, 40: 2087–2097.

Ansari K, B Ansari, A Khund, 2004. Extent of heterosis and heritability in some quantitative characters of bread wheat. Indus. J Pl Sci, 3: 189–192.

Ansari K, Z Soomro, B Ansari, M Leghari, 2005. Genetic variability and heritability studied for some quantitative traits in bread wheat (*Triticum aestivum* L.). Pak J Agric Agril Eng Vet Sci, 21(1): 18–24.

Anshuman V, N Dixit, Dipika, S Sharma, S Marker, 2013. Studies on heritability and genetic advance estimates in Maize genotypes. Bioscience

Discovery, 4(2): 165–168.

Arshad M, M Chowdhry, 2003. Genetic behavior of wheat under irrigated and drought stress environment. Asian J Plant Sci, 2 (1): 58–64.

Ashraf M, A Ghafoor, N Khan, M Yousaf, 2002. Path coefficient in wheat under rainfed conditions. Pak J Agric Res, 17(1): 1–6.

Asif M, Mujahid MY, Kisana MS, Mustafa SZ and Ahmad I, 2004**.** Heritability, genetic variability and path analysis of traits of spring wheat. Sarhad J Agric, 20(1):87–91.

Baloch MZ, BA Ansari, N Memon, 2003. Performance and selection of intra-specific hybrids of spring wheat (*Triticum aestivum* L.). Pak J Agric Vet Sci, 19: 28–31.

Basheeruddin M, H Sahib, 2004. Genetic variability andcorrelation studies in foxtail millet (*Setaria italica*). Crop Res, 28(1, 2 & 3): 94–97.

Bergale S, Billore M, Halkar AS, Ruwali KN, Prasad SVS and Mridulla B, 2001. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat. Madras Agric J, 88 (7-9): 457–461.

Bisne R, AK Sarawgi, SB Verulkar, 2009. Study of heritability, genetic advance and variability for yield contributing characters in rice. Bangladesh J Agric Res, 34(2): 175–179.

Brim CA, HW Johnson, CC Cockerham, 1959. Multiple selection criteria in soybean. Crop Sci, 1: 187–190.

Cheema NM, MA Mian, M Ihsan, G Rabbani, A Mahmood, 2006. Studies on variability and some genetic parameters in spring wheat. Pak J Agric Sci, 43(1-2): 32–35.

Degewione A, T Dejene, M Sharif, 2013. Genetic variability and traits association in bread wheat (Triticum aestivum l.) genotypes. Int Res J Agric Sci, 1(2): 19–29.

Deshmukh SNN, MS Basu, PS Reddy, 1986. Genetic variability, character association and path coefficient analysis of quantitative traits in Viginia bunch varieties of groundnut. Indian J Agric Sci, 56: 516–521.

Dwivedi AN, Pawar IS, S Madan, 2004. Studies on variability parameters and characters association among yield and quality attributing traits in wheat. J Crop Res, 32: 77–80.

Gupta SK, SR Verma, 2000. Variability, heritability and genetic advance under normal and rainfed conditions in durum wheat (*Triticum durum* Desf.). Ind J Agric Res, 34 (2): 122–125.

Inamullah H, Ahmad, F Mohammad, SU Din, G Hassan, R Gul, 2006. Evaluation of the heterotic and heterobeltiotic potential of wheat genotypes for improved yield. Pak J Bot, 38(4): 1159–1167.

Jedynski S, 2001. Heritability and path coefficient analysis of yield components in spring wheat. Grupy Problemowej hoodowli Pszenicy. Proceeding of Symposium, pp. 30–31.

Kalimullah S, J Khan, M Irfaq, HU Rahman, 2012. Gentetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. The J Anim & Plant Sci, 22(2): 330–333.

Kamal AMA, MR Islam, BLD Chowdhry, MAM Talukdar, 2003. Yield performance and grain quality of wheat varieties grown under rainfed and irrigated conditions. Asian J Plant Sci, 2 (3): 358–360.

Kashif M, I. Khaliq, 2004. Heritability, correlation and path coefficient analysis for some metric traits in wheat. Int J Agric & Biol, 06 (1), 138–142.

Khalil IH, N Afridi, 2004. Heritabilities and selection responses for yield and yield associated traits in spring wheat. Sarhad J Agric, 20(3): 401–404.

Khan N, MA Bajwa, 1993. Variability and correlation between metric traits in wheat. J Agric Res, 31 (2): 131–137.

Khodadadi, M., M. H. Fotokian, M. Miransari. 2011. Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. AJCS, 5, 17–24.

Kumar N, Sh Markar, V Kumar, 2014. Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). Bioscience Discovery, 5(1): 64–69.

Larik AS, HMI Hafiz, AM Khushk, 1989. Estimation of genetic parameters in wheat populations derived from intercultivaral hybridization. Pakphyton, 1: 51–56.

Panwar D, I Singh, 2000. Genetic variability and character association of some yield components in winter x spring nursery of wheat. Adv Plant Sci, 8(1): 95–99.

Pawar SV, SC Patil, Naik, VM Jambhale, 2002. Genetic variability and heritability in wheat. J Maharashtra Agric, 27(3): 324–325.

Rahim, M. A., A. A. Mia, F. Mahmud, N. Zeba, K. Afrin. 2010. Genetic variability, character association and genetic divergence in Mungbean (*Vigna radiate* L. Wilczek). Plant Omic, 3: 1–6.

Rasal PN, KD Bhoite, DA Godekar, 2008. Genetic variability heritability and genetic advance in durum wheat. J Maharashtra Agric, 33(1): 102–103.

Shabana M, MUD Qureshi, BA Ansari, MA Sial, 2007. Genetic heritability for grain yield and its related characters in spring wheat (*Triticum aestivum* L.). Pak J Bot, 39(5): 1503–1509.

Shashikala SK, 2006. Analysis of genetic diversity in wheat. Thesis. University of Agricultural Sciences, Dharwad.

Singh RK, BD Chaudhary, 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publ., New Delhi.

Steel RGD, JS Torrie, 1980. Principles and Procedures of Statistics. A biological approach. Second Edition. McGraw Hill Book Company Inc., New York, USA.

Waqar-Ul-Haq, MF Malik, M Rashid, M Munir, Z Akram, 2008. Evaluation and estimation of heritability and genetic advancement for yield related attributes in wheat lines. Pak J Bot, 40(4): 1699–1702.

Yousaf A, BM Atta, J Akhter, Ph Monneveux, Z Lateef, 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) Germplasm. Pak J Bot, 40(5): 2087–2097.