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REGULAR ARTICLE

Genetic diversity assessment of common winter wheat (*Triticum aestivum* L.) genotypes

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Abstract

The knowledge about of genetic diversity of common winter wheat (*Triticum aestivum* L.) genotypes is useful for production of more efficient crops adapted to diverse conditions. A set of 32 common winter wheat varieties was used to estimate and then utilize the genetic diversity between common winter wheat genotypes by using cluster analysis and factor analysis and to identify effective factors on genetic improvement. Eight agronomic traits were included in the study. The GCV values were lower than PCV values for all the traits. High genetic advance combined with high heritability showed characters: plant height and spike length. Cluster analysis based on ward's method using Euclidian distance, grouped the cultivars into four clusters. Genotypes in the second group were in the highest rate with respect to number of productive tillers per plant, number of spikelets per spike, number of grains per spike, grain weight per spike and yield per plant. Principal Component analysis was applied to group accessions according to similarity on the basis of eight traits in tree components in the factor plane. The first three components explained 82.63% of total variation in the experiment. Cluster analysis based on the three factors grouped the varieties into four clusters. Genotypes of the first cluster can be used for increase in number of productive tillers per plant in breeding programs. Genotypes of the second cluster can be used for increase in thousand grain weight. Genotypes in the fourth cluster had highest mean with respect to first factor and can be used for increase in number of grain per spike.

Key words: Agronomic traits, Cluster analysis, Common winter wheat, Factor analysis, Genetic diversity

Introduction

The knowledge of genetic diversity and relatedness in the germplasm is a pre-requisite for crop improvement programmes. Decreases of genetic variation within cultivars as result of conventional breeding practices affect the success for productivity and adaptability improvement of crops - particularly bread and durum wheat. Because approaching to the limits of biological productivity as result of global climate change the need of new genetic pools is essential (Stoeva et al., 2009). Breeding for developing of accessions with high yield and grain quality is a long and complex process, the success of which is by no means guaranteed (Tsenov et al., 2009). So precise information on the nature and degree of genetic diversity present in wheat collections from its principal areas of cultivation would help to select parents for evolving superior varieties (Islam, 2004; Khodadadi et al., 2011; Aharizad et al., 2012). For the genetic amelioration of this crop, diverse genotypes from the existing germplasm should be selected and used in further breeding programme (Shashikala, 2006). There are various analyses and statistical approaches for genetic diversity identification - cluster analysis, PCA and factor analysis (Bhatt, 1970; Carves et al., 1987; Mohammadi and Prasanna, 2003; Eivazi et al., 2007; Khodadadi et al., 2011). Hierarchical cluster analysis can be used to estimate genetic dissimilarity and similarity in collections. According to Peeters and Martinelli (1989) the analysis could have applications for the selection of parental lines for which varying degrees of segregation are sought. Grouping genotypes at the basis of studied characteristics is one of the suitable methods for determining nearness, distance and closeness of them. Factor analysis has been used by many researchers to determine the factors with contributed to the variation of quantitative traits in common winter wheat.

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The aim of this study was to estimate and then utilize the potential genetic diversity between common winter wheat genotypes and to identify effective factors on genetic improvement.

Materials and Methods

The study is carried out in the experimental field of Institute of Plant Genetic Resources “Konstantin Malkov”-Sadovo, Bulgaria during 2011-2013 growing seasons. Thirty two common winter wheat varieties from different countries (Rumania, Serbia, Hungary and China) were examined (Table 1). The cultivars were sown in harvest plots each of 10 m2 in three replications, in the randomized block design. Normal agronomic and cultural practices were applied to the experiment throughout the growing seasons. The agronomic characters were taken after harvesting the plants. From each variety, 20 plants were collected for biometrical measurements. Data were registered for number of productive tillers per plant, plant height, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, thousand grain weight and grain yield per plant. The mean data from all eight characters were used to analysis of variance according to Lidansky (1988). Genotypic and phenotypic variances, genotypic and phenotypic coefficient of variability, broad sense heritability were calculated according to Singh & Chaudhary (1985). Genetic advance in terms of percentage of means was assessed by Brim et al. (1959). Hierarchical cluster analysis (Ward's method) using Euclidian distance was performed by using the STATISTICA software. PC-analysis was applied to group accessions according to similarity on the basis of eight traits (number of productive tillers per plant, plant height, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, thousand grain weight and grain yield per plant) in three components in the factor plane by using SPSS 13 software and the related clusters were plotted based on the main components.

Results

Analysis of variance

The results of analysis of variance are shown in Table 2. The values of mean squares for all eight characters indicated highly significant differences between common winter wheat accessions (Table 2).

Phenotypic variance ranged from 0.42 (grain weight per spike) to 201.09 (plant height). Values of genotypic variances ranged between 0.08 (grain weight per spike) and 166.95 (plant height) (Table 3). Higher phenotypic and genotypic variance values of 201.09 and 166.95 for plant height and 142.35 and 40.39 for number of grains per spike were recorded in the study.

Table 1. List of accessions included in the investigation.

No.	Genotype	Country of origin	No.	Genotype	Country of origin
1	Gruia	Romania	17	Evropa 90	Serbia
2	Faur	Romania	18	Renesansa	Serbia
3	Litera	Romania	19	Gora	Serbia
4	Boema	Romania	20	Rapsodia	Serbia
5	Golosa	Romania	21	Lillyana	Serbia
6	Delabrad	Romania	22	Xu zhou 2962	China
7	Izvor	Romania	23	Feng kang 8	China
8	MV-Kikelet	Hungary	24	Da mai zi	China
9	MV-Lepeny	Hungary	25	Long chun 8	China
10	MV-Aprod	Hungary	26	Long chun 5	China
11	MV-Taller	Hungary	27	Karma	Ukraine
12	Gordana	Serbia	28	Fermerka	Ukraine
13	Dragana	Serbia	29	Statna	Ukraine
14	Zvezdana	Serbia	30	Zapashna	Ukraine
15	Pobeda	Serbia	31	Harkivska 81	Ukraine
16	Rusiya	Serbia	32	Lyutizha	Ukraine

Table 2. Minimum, maximum, means, mean squares and standard error of means for eight quantitative characters of thirty two genotypes (*Triticum aestivum* L.).

Characters	Minimum	Maximum	Means	Mean squares	Standard error of means
Number of productive tillers per plant	3.20	7.40	5.11	5.87***	0.19
Plant height	66.00	117.00	91.97	868.86***	2.33
Spike length	9.20	17.60	13.06	29.66***	0.43
Spikelets per spike	17.60	22.80	20.01	7.40***	0.22
Number of grains per spike	40.00	70.20	53.92	303.90***	1.38
Grain weight per spike	1.58	2.82	2.17	0.74***	0.07
Thousand grain weight	28.35	48.86	40.10	103.39***	0.80
Grain yield per plant	3.20	11.42	6.87	26.69***	0.41

*p<0.05, **p<0.01, *** p<0.001

Table 3. Genetic parameters of various yield components of 32 common winter wheat genotypes.

Characters	Genotypic variance	Phenotypic variance	Genotypic coefficient of variability, %	Phenotypic coefficient of variability, %	Heritability, %	Genetic advance, % of means
Number of productive tillers per plant	0.96	2.02	19.18	27.83	47.51	27.23
Plant height	166.95	201.09	14.05	15.42	83.02	26.37
Spike length	5.70	6.88	18.28	20.08	82.87	34.28
Number of spikelets per spike	1.10	3.02	5.23	8.69	36.28	6.49
Number of grains per spike	40.39	142.35	11.79	22.13	28.37	12.93
Grain weight per spike	0.08	0.42	13.14	29.92	19.30	11.90
Thousand grain weight	13.14	50.83	9.04	17.78	25.85	9.47
Grain yield per plant	3.61	12.27	27.66	51.00	29.42	30.90

The Genotypic coefficient of variability (GCV) ranged from 5.23% for number of spikelets per spike to 27.66% for grain yield per plant, whereas, phenotypic coefficient of variability (PCV) ranged from 8.69% for number of spikelets per spike to 51.00% for grain yield per plant (Table 3). The recorded of GCV were high for grain yield per plant (27.66%), moderate for number of productive tillers per plant (19.18%), spike length (18.28%), plant height (14.05%), grain weight per spike (13.14%) and number of grains per spike (11.79%). The characters: number of spikelets per spike and thousand grain weight recorded low GCV estimates. The recorded of PCV were high for grain yield per plant (51.00%), grain weight per spike (29.92%), number of productive tillers per plant (27.83%), number of grains per spike (22.13%) and spike length (20.08%), moderate for thousand grain weight (17.78%) and plant height (15.42%).

Estimation of broad sense heritability and genetic advance

Moderate heritability was recorded for number of productive tillers per plant (47.51%) and number of spikelets per spike (36.28%). High heritability estimates were observed for plant height (83.02 %) and spike length (82.87%). Genetic advance expressed as percentage of mean was high for spike length (34.28%), grain weight per spike (30.90%), number of productive tillers per plant (27.28%) and plant height (26.37%).

Clustering of genotypes

Hierarchical cluster analysis based on Euclidean dissimilarity using Ward's method classified the tested wheat cultivars into four significant different clusters at 50% linkage distance (Figure 1). The first cluster included six genotypes, the second cluster seven, the third cluster six and the forth cluster thirteen genotypes. Analysis of mean and standard deviation were made for all four clusters (Table 4). Feng kang 8, Da mai zi, Long chun 8, Long chun 5, Zapashna and Harkivska 81 were grouped in the first cluster including 18.75% of total genotypes. The average values of genotypes in this cluster for number of productive tillers per plant, plant height, grain weight per spike, thousand grain weight and grain yield per plant were higher than the total means of all genotypes (Table 4). Standard deviations of traits in this group except number of productive tillers per plant, number of grains per spike and grain weight per spike were less than the total standard deviations. Genotypes in this cluster had greatest values for plant height (110.00) and 1000 grain weight (48.55). Rusiya, Lillyana, Renesansa, Gora, Evropa 90, Pobeda and Lyutizha genotypes were classified in second cluster including 21.87% of total genotypes. Genotypes in this group were in the highest rate with respect to number of productive tillers per plant (6.26), number of spikelets per spike (20.86), number of grains per spike (58.17), grain weight per spike (2.37) and yield per plant (9.73). Karma, Izvor, Dragana, Rapsodia, Golosa and MV-Lepeny genotypes were classified in third cluster including 18.75% of total genotypes. The average values of traits in this group except plant height were less than total means of all genotypes. In the fourth cluster 13 genotypes were classified including 40.62% of total varieties. Values of number of productive tillers per plant, plant height, thousand grain weight and grain yield per plant in this cluster were less than the total means of all genotypes. Genotypes in this cluster were in the highest rate with respect to spike length (14.69) and in the least rate with respect to plant height.

Principal component analysis (PC-analysis)

PC-analysis was applied to arrange accessions by their similarity. The values of the three components to each of the studied parameters were calculated empirically. The first three factors explained 82.63% of total variation (Table 5). First factor determining 36.72% of the variation has an important role to justify alteration of spike length, number of spikelets per spike, number of grains per spike and grain weight per spike (Table 5). Second factor had justified 29.91% of total variance. The factorial coefficients of number of productive tillers per plant and grain yield per plant were high and positive. In the third factor that had explained 16.00% of alteration, thousand grain weight had the greatest effect.

Cluster analysis based on the three factors grouped the varieties into four groups (Fig. 2). Average of factors for each cluster is shown in table 6. In the first cluster, five accessions were classified including 15.62% of total genotypes. Varieties in this cluster were in the highest rate with respect to second factors. Second group comprises 9 varieties including 28.13% of total genotypes. The varieties in this cluster had greatest values for third factor. Therefore, these genotypes were superior with respect to 1000 grain weight. In the third group, 11 genotypes were classified including 34.38% of total accessions. In the fourth group, 7 varieties were classified 21.87% of total genotypes. Genotypes in this cluster had highest mean with respect to first factor.

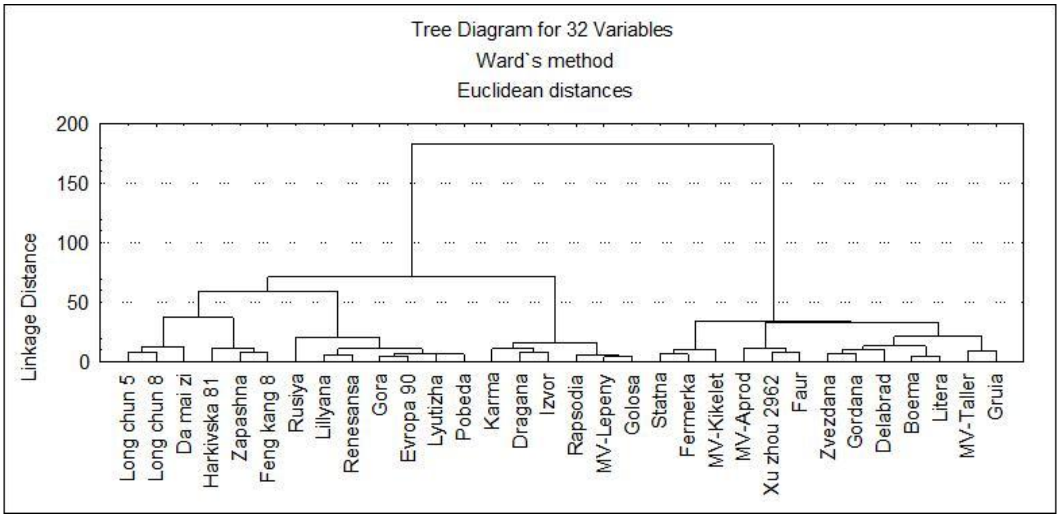

Figure 1. Tree diagram of 32 genotypes for 8 studied variables using hierarchical cluster analysis (Ward’s method and Euclidean distance).

Table 5. Factor analysis of traits using principal components analysis in 32 wheat genotypes.

Rotated Component Matrix Characters	Factor 1	Factor 2	Factor 3
Number of productive tillers per plant	0.033	0.961	-0.009
Plant height	-0.396	0.228	0.685
Spike length	0.601	-0.409	-0.332
Spikelets per spike	0.795	0.209	-0.084
Number of grains per spike	0.931	0.117	-0.074
Grain weight per spike	0.827	0.121	0.527
Thousand grain weight	0.118	0.043	0.939
Grain yield per plant	0.256	0.886	0.273
Eigen values	2.937	2.392	1.281
Proportional variance,%	36.719	29.905	16.006
Cumulative variance, %	36.719	66.624	82.630

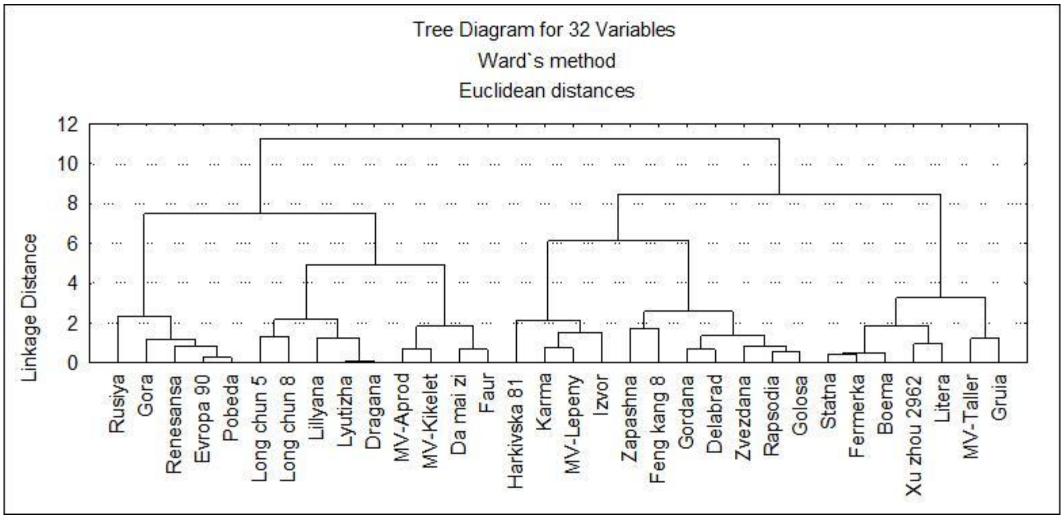

Figure 2. Tree diagram of 32 genotypes for 3 extracted factors using hierarchical cluster analysis (Ward's method and Euclidean distance).

Table 6. The average of traits for achieved groups from cluster analysis based on factor analysis in 32 wheat genotypes.

	Factor 1	Factor 2	Factor 3
Cluster 1	0.451	1.664	0.121
Cluster 2	0.619	-0.125	0.857
Cluster 3	-1.071	-0.326	-0.085
Cluster 4	0.564	-0.513	-1.055

Discussion

In present study, 32 genotypes of common winter wheat varieties were studied to assess their genetic potential. The analysis of variance showed the presence of significant differences between common winter wheat accessions for all traits analyzed with probability F< p 0.001. According to many researcher as Kamat (1996), Kamboj et al.(2000), Shashikala (2006), Yousaf et al. (2008), Kalimullah et al. (2012) and Kumar et al. (2014) this means the existence of a high degree of genetic variability in the material to be exploited in breeding program.

The assessment of heritable and non-heritable factors in the total variability observed is indispensable in adapting suitable breeding procedure. The heritable portion of the overall observed variation can be ascertained by studying the components of variation such as GCV, PCV, heritability and predicted genetic advance

(Shashikala, 2006). In the study GCV was high for grain yield per plant, moderate for number of productive tillers per plant, spike length, plant height, grain weight per spike and number of grains per spike. The GCV values were lower than PCV values for all the traits which reflect the influence of environment on the expression of traits. These findings were in agreement with those of 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 that portion of total variability or phenotypic variability which is heritable and due to the genotype. It is a measure of the extent of phenotypic variation caused by the action of genes. According to Kumar et al. (2014) heritability in broad sense plays an important role in deciding the suitability and strategy for selection of a character. In our investigation high estimates of heritability (above 60%) in broad sense were recorded for two characters studied (plant height- 83.02% and spike length- 82.87%). The highest heritability values indicate that heritability may be due to higher contribution of genotypic component. Similar results were reported by Panwar and Singh (2000), Jedynski (2001), Kashif et al. (2004), Asif et al. (2004) and Rasal et al. (2008). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson et al., 1955; Athwal and Gain Singh 1966, Anshuman et al., 2013). The high genetic advance accompanied with high estimate of heritability observed for plant height and spike length indicates that heritability is mainly due to additive gene effect and selection may be effective to improve the traits. Similar results also reported by Thakur et al. (1999), Dwivedi et al. (2002) and Sharma and Garg (2002).

Quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. In the present investigation hierarchical cluster analysis based on Euclidean dissimilarity using Ward's method grouped the tested common winter wheat cultivars into four significant different clusters. Genotypes in the first cluster had greatest values for plant height and 1000 grain weight. Genotypes in the second group were in the highest rate with respect to number of productive tillers per plant, number of spikelets per spike, number of grains per spike, grain weight per spike and yield per plant. Crossing among existing genotypes in first and second groups provided more possibility to having more genetic variance and optimal genotypes with respect to yield performance. Genotypes in the fourth cluster were in the highest rate with respect to spike length and in the least rate with respect to plant height. The highest genetic distance was observed between Long chun 5 and Gruia. According to Khodadadi et al. (2012), Rahim et al. (2010) and Ali et al. (2008) the cross between genotypes with maximum genetic distance can be used in breeding programs to achieve maximum heterosis. In our investigation Long chun 5 and Gruia showed the highest genetic distance.

Principal Component Analysis arranges accessions by their similarity. The first three components explained 82.63% of total variation. First factor determining 36.72% of the variation has an important role to justify alteration of spike length, number of spikelets per spike, number of grains per spike and grain weight per spike. If the selection had complemented on the basis of first factor, this selection will has the most effectiveness in the grain yield. Cluster analysis based on the three factors grouped the varieties into four groups. Genotypes of the first cluster can be used for increase in number of productive tillers per plant in breeding programs. Genotypes of the second cluster can be used for increase in thousand grain weight. Genotypes in the fourth cluster had highest mean with respect to first factor. Members of this group can use for increase in number of grain per spike, in breeding programs.

Conclusion

Analysis of variance showed highly significant differences among the accessions for all characters included in the study. The recorded of GCV, were high for grain yield per plant (27.66%). GCV values were lower than PCV values for all the traits which reflect the influence of environment on the expression of traits. High heritability estimates were recorded for plant height (83.02 %) and spike length (82.87%). Genetic advance expressed as percentage of mean was high for spike length (34.28%), grain weight per spike (30.90%), number of productive tillers per plant (27.28%) and plant height (26.37%). The high genetic advance accompanied with high estimate of heritability observed for plant height and spike length indicates that heritability is mainly due to additive gene effect and selection may be effective to improve the traits. Parents may be selected from those clusters which had significant genetic distance for crossing in order to obtain genetic recombination and transgressive segregation in the subsequent generations.

Author contributions

G. D. designed and conducted most of the experiments, analyzing the results and preparing the manuscript and B. K. assisted field activities and data collections.

References

Aharizad S., S. Mohsen, M. S. Abolghasem and E. Khodadadi. 2012. Multivariate analysis of genetic diversity in wheat (*Triticum aestivum* L.) recombinant inbred lines using agronomic traits. Annals of Biol. Res. 3(5):2118-2126.

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.

Anshuman, V., N. Dixit, Dipika, S. Sharma, S. Marker. 2013. Studies on heritability and genetic advance estimates in Maize genotypes. Biosci. Disc. 4(2):165-168.

Asif, M., M. Y. Mujahid, M. S. Kisana, S. Z. Mustafa and I. Ahmad. 2004. Heritability, genetic variability and path analysis of traits of spring wheat. Sarhad J. Agric. 20(1):87-91.

Athwal, D. S. and G. Singh. 1966. Variability in Kagni-1. Adaptation and genotypic and phenotypic variability in four environments. Indian J. Genet. Plant Breed. 26:153-161.

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

Bhatt, G. M. 1970. Multivariate analysis approach to selection of parents for hybridization aiming at yield component in self pollination crops. Aus. J. Agric. Res. 21:1-7.

Brim, C. A., H. W. Johnson and C. C. Cockerham. 1959. Multiple selection criteria in soybean. Crop Sci. 1:187-190.

Carves, B. F., E. L. Smith, H. O. England. 1987. Regression and cluster analysis of environmental responses of hybrid and pure line winter wheat cultivars. Crop Sci. 27:659-664.

Dwivedi, A. N., I. S. Pawar, M. Shashi and S. Madan. 2002. Studies on variability parameters and character association among yield and quality attributing traits in wheat. Haryana Agric. Univ. J. Res. 32(2):77-80.

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

Eivazi, A. R., M. R. Naghavi, M. Hajheidari, S. M. Pirseyedi, M. R. Ghaffari, S. A. Mohammadi, I. Majidi, G. H. Salekdeh and M. Mardi. 2007. Assessing wheat (*Triticum aestivum* L.) genetic diversity using quality traits, amplified fragment length polymorphisms, simple sequence repeats and proteome analysis. Ann. App. Biol. 152:81-91.

Islam, M. R. 2004. Genetic diversity in irrigated rice. Pak. J. Biol. Sci. 2:226-229.

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

Johnson, H. W., H. F. Robinson and R. E. Comstock. 1955. Estimates of genetic and environmental variability in soybeans. Agron. J. 47(7):314-318.

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

Kamat, R. T. 1996. Genetic analysis of heat tolerance in tetraploid wheat. Ph.D. Thesis, University of Agricultural Sciences, Dharwad.

Kamboj, M. C., Naveen, C. Subhandra, R. K. Yadav and N. Chaundra. 2000. Genetic analysis of yield and its components in bread wheat (*Triticum aestivum* L.). Atlas Agri-Bio. Res. 5(1):41-43.

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

Khodadadi, M., M. H. Fotokian and 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 and V. Kumar. 2014. Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). Biosci. Disc. 5(1):64-69.

Lydansky, T. 1988. Statistical methods in biology and agriculture. Zemizdat. Sofia.

Mohammadi, S. A. and B. M. Prasanna. 2003. Analysis of genetic diversity in crop plants: salient statistical tools and considerations. Crop Sci. 43:1235-1248.

Panwar, D. and 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, S. V., S. C. Patil, Naik and V. M. Jambhale. 2002. Genetic variability and heritability in wheat. J. Maharashtra Agric. 27(3):324-325.

Peeters, J. P. and J. A. Martinelli. 1989. Hierarchical cluster analysis as a tool to manage variation in germplasm collection. Teor. Appl. Genet. 78:42-48.

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

Rasal, P. N., K. D. Bhoite and D. A. Godekar. 2008. Genetic variability heritability and genetic advance in durum wheat. J. Maharashtra Agric. 33(1):102-103.

Sharma, A. K. and D. K. Garg. 2002. Genetic variability in wheat (*Triticum aestivum* L.) crosses under different normal and saline environments. Ann. Agric. Res. 23(3):497-499.

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

Singh, R. K. and B. D. Chaudhary. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publ., New Delhi.

Stoeva I., P. Chamurliysky and N. Tsenov. 2009. Investigation on Bulgarian and foreign common winter wheat varieties and lines with a view of their using in breeding for productivity and quality. Field Crops Studies 5(2):253-260.

Thakur, S. K., R. L. Pandey and U. S. Kandarlkar. 1999. Genetic association and variability of grain yield and other quantitative characters in F2 population of wheat crosses. Adv. Plant Sci. 12:237-239.

Tsenov, N., K. Kostov, I. Todorov, I. Panayotov, I. Stoeva, D. Atanassova, I. Mankovsky and P. Chamurliysky. 2009. Problems, achievements and prospects in breeding for grain productivity of winter wheat. Field Crop Studies 5(2):261-273.

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