Food Science and Quality Management
ISSN 2224-6088 (Paper) ISSN 2225-0557 (Online)
Vol.47, 2016

Multivariate Analysis of Some Metric Traits in Durum Wheat (Triticum durum L.) Accessions

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Abstract

Ethiopia is considered as one of the center of genetic diversity of durum wheat, with important sources of rust and drought resistance, water logging tolerance and early ripening. Up to now, slight works made on genetic diversity study in durum wheat accessions in Ethiopia. Therefore, diversity study in durum wheat accessions is helpful for genetic improvement. The experimental material consisted of sixty eight durum wheat accessions tested in an augmented block design at Kulumsa. The overall objective was to assess the genetic diversity of durum wheat accessions by cluster and principal component analysis. Analysis of variance revealed highly significant differences among accessions for all traits. Cluster analysis revealed that the 64 genotypes and 4 checks were grouped into five clusters. The inter cluster distance revealed high significant differences among clusters which enhance to develop potential hetrotic groups up on crossing. Four principal components (PC1-PC4) exhibited eigen value greater than one and accounted 75.9% of the total variation. This exhibited significant variation for the characters studied suggesting that many opportunities exist for genetic improvement through selection.

Keywords: Accessions, Cluster, Hetrotic group, Principal component, genetic diversity

Introduction

Durum wheat (*Triticum durum L.*) is a monocotyledonous plant of the *Gramineae* family. It is the major food crop in the world, grows in most countries except in the hot, humid tropical regions. Durum wheat is thought to have originated in present day Turkey, Syria, Iraq, and Iran

(Feldman, 2001). Durum wheat is an allotetraploid (two genomes: AABB) with a total of 28 chromosomes (2n=4x=28), containing the full diploid complement of chromosomes from each of its progenitor species. Based on cytological and molecular analysis, T. turgidum subspecies are believed to have originated from the natural hybridization of Triticum monococcum L. subsp. boeoticum (Boiss.) (Synonym: Triticum urartu, AA) and an unknown diploid wheat species containing the B genome (Feldman, 1976). Kimber and Sears (1987) suggested that one or more of five diploid species in section Sitopsis of Triticum may have donated the B genome to the polyploid wheats. Molecular evidence suggests that the genome from T. speltoides is most related to the durum and common wheat B genome (Talbert *et al.,* 1995; Khlestkina and Salina 2001). Unlike common wheat, there is one predominant class of durum wheat (Abaye *et al*., 1997).

Ethiopia is considered as one of the center of genetic diversity of durum wheat, with important sources of rust and drought resistance, water logging tolerance and early ripening (Payne *et al*., 2001). Ethiopia is the second largest producer of wheat in Sub-Saharan Africa. The current total area and production of both durum (Triticum durum Desf.) and bread wheat (Triticum aestivum) is estimated to be 17.46 q/ha, which is lower than the average world productivity (25q/ha) (CSA, 2011).

As Ethiopia is a center of diversity for tetraploid wheat, generating fertile genetic diversity information among durum wheat genotypes is very important tools because, the information will help the wheat breeders to bread for many characters (earliness, yield increase, drought tolerance, etc. Within the investigated material and this new material will serve as a new stock for improvement wheat breeding program for traits of interest. Therefore, the objective of this study was to assess the genetic diversity of durum wheat accessions by cluster and principal component.

Materials and Methods

Description of the Study Area

The experiment was conducted at Kulumsa Agricultural Research Center in the 2013/2014 main cropping season. It is located 160 km southeast of Addis Ababa at 8' degree to 8' degree 02 northern latitude and 39' degree 07 to 39' degree'10' eastern longitude. The altitude of the center is 2200m.a.s.l with annual average rainfall of 832 mm. The annual average temperature of the study area is 16.65$^{o}{}_{C}$ with maximum and minimum temperature of 22.8$^{o}{}_{C}$ and 10.5$^{o}{}_{C}$ respectively. With the soil type classified as clay loam soil with a pH of 6.

Experimental materials

The experimental materials consisted of 64 accessions of durum wheat (*T. durum L.*) obtained from the Institute of Biodiversity Conservation (IBC) including 4-four standard checks (Hitosa, Mangudo, Tate and Denbi)

Experimental Design and Trial Management

The experiment was carried out in an Augmented Block Design comprising of 4 blocks, where each block contains 16 test entries and 4 checks (randomly allocated) with the total of 20 accessions in each blocks. The accessions were grown under rain fed conditions. Each accession was sown in 2 rows of 1.25 meter long and 20 cm apart with seed rate of 7.5g. Weeds were controlled manually. Planting was done by hand drilling in July 05, 2013. Recommended fertilizer rate of 100/100 kg/ha N/P_2O_5 in the forms of Urea and DAP was applied to each plot in the shallow furrow depths and mixed with soil at the same time during sowing.

Statistical Analysis

The data were subjected to analysis of variance according to (Weber *et al.,* 1988),using the SPAD software developed by IASRI New Delhi, India (Federer, 1956), cluster analysis and principal component analysis Version 9.2 (SAS Institute, 2008).

Analysis of variance (ANOVA)

The quantitative data collected from the locations for all the parameters will be subjected to analysis of variance (ANOVA) using SPAD (Statistical Package for Augmented Design) based on augmented design. Least Significant Difference (LSD at P = 0.05) will be employed to identify accessions that are significantly different from each other. The analysis will be carried out according to the following model (Federer, 1956).

$$Y_{ij} = \mu + gi + cj + \beta j + \varepsilon ij$$

Where: Y_{ij} is the observation of treatment i in jth block μ is the general mean, g_i is the effect of test treatment, c_j is the effect of control treatments in jth block, βj is the block effects, (ε) is the error term

Cluster Analysis

Clustering of genotypes was performed by canonical roots method using procedures of SAS (SAS Institute, 2008) version 9.2. The numbers of clusters were determined by following the approach suggested by Copper and Miligan (1988) by looking into three stastics namely Pseudo F, Pseudo t^2 and cubic clustering criteria. That is, local peaks of the CCC and pseudo F statistics combined with a small value of the pseudo t2 statistic and a larger pseudo t^2 for the next cluster fusion.

Principal Component Analysis (PCA)

The principal component analysis was carried out using Statistical Analysis System Version 9.2 (SAS Institute, 2008).

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance for the 12 characteristics is presented in Table 1. It revealed that significant ($P<0.1$) differences were observed among treatments for all characters studied. This gives an ample opportunity to plant breeders for improvement of these characters through selection. Similarly, the research finding of Abinasa *et al* (2011) reported highly significant differences among durum wheat genotypes for days to heading, days to maturity, number of productive tillers per plant, plant height, spike length, spikilets per spike, thousand grain weight, biomass yield, grain yield and harvest index. Alam *et al*. (2013) reported significant differences for grains per spike, 1000 grain weight, plant height and grain yield among fifteen durum wheat genotypes.

Table1 Analysis of variance (Mean squares) for the 12characters of 68 durum wheat accessions

Character	Block(adj) (df=3)	Error (df=9)	Trt(adj) (df=67)	Among-controls (df=3)	Among-test (df=63)	Test-v-Control (df=1)	CV (%)
Days to heading(days	1.22	4.95	38.23**	118.22**	32.48**	161.02**	3.37
Days to maturity(days)	5.16	2.83	52.64**	36.66**	47.88**	400.51**	1.51
Grain filling period(days)	4.22	12.11	57.15**	273.22**	30.79*	1069.45**	7.67
Plant height(cm)	1.66	1.13	304.07**	57.01**	61.35**	16336.32**	0.92
No. of productive tillers plant^{-}	0.68	0.62	2.12*	0.50^{ns}	1.64*	37.46**	16.55
Spike length(cm)	0.68	0.50	3.01**	0.85^{ns}	1.33*	115.80**	8.25
Number of spikelets spike^{-1}	2.64	1.15	5.1*	3.18^{ns}	4.14*	71.25**	5.23
Number of kernels spike^{-1}	4.72	4.11	118.43**	283.22**	46.75**	4140**	5.53
Thousand kernels weight(g)	8.05	3.30	142.99**	300.60**	38.28**	6267.21**	7.43
Grain yield plot^{-1}(g)	4.91	9.75	295.13**	128.41**	146.51**	10158.77**	10.12
Biomass yield plot^{-1}(g)	6.22	11.17	1336.67**	1050.89**	1264.31**	6752.81**	2.07
Harvest index (%)	3.08	3.744	89.02**	2.74^{ns}	58.16**	2292.15**	10.16

df=Degrees of freedom *=significant at 5% probability level and **=highly significant at 1% probability level, CV= Coefficient of Variation

Clustering of Durum Wheat Accessions

Based on cluster analysis, the 64 durum wheat accessions and four check varieties were grouped into five clusters (Table 3). The accessions were clustered in such a way that four accessions (5.9%) were grouped into cluster I, two accessions (2.9%) were grouped into cluster II, twenty accessions (29.4%) were grouped into cluster III. Thirty eight accessions (55.9%) grouped into clusters IV this cluster consisted the largest group of accessions. The checks (5.9%) were separately grouped into cluster V. This indicates that crossing between superior accessions of above diverse cluster pair's might provide desirable recombinants for developing high yielding durum wheat varieties. Similar works were presented by Verma *et al.* (2013) who grouped 108 genotypes of wheat into 11 clusters, Mostafa *et al.* (2011) grouped 36 genotypes of wheat into seven clusters, Tsegaye *et al.* (2012) grouped 21 exotic and two standard check varieties of durum wheat into six clusters

Table 3 Distribution of 64 durum wheat Accessions and 4 checks in to five clusters based on D^2 analysis

Number of cluster	Number of observation	Cluster groups
I	**4**	**5454, 208253, 210805, 238878**
II	**2**	**7073, 208783**
III	**20**	**7345, 204470, 204483, 208240, 208243, 208321, 208331, 208780, 226094, 226914, 226922, 226951, 226954, 236274, 236276, 236286, 236287, 238116, 238126 , 238133**
VI	**38**	**8436, 204349, 204392, 204411, 204417, 204464, 204482, 208241, 208267, 208322, 208746, 208873, 208931, 210795, 222426, 222795, 226327, 226345, 226839, 226844, 226888, 226913, 227058, 231569, 231592, 236288, 236290, 236291, 238113, 238115, 238117, 238124, 238135, 238137, 238871, 238873, 238880, 238891,**
V	**4**	**Hitosa, Mangudo, Tate, Denbi**

Genetic Divergence

D-square statistics (D^2) developed by Mahalanobis (1936), has been used to classify the divergent genotypes into different groups. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization. The more divergent the two genotypes are the more will be the probability of improving through selection and hybridization.

Average Intra and Inter Cluster Distance (D^2)

The intra-cluster distance varied from 25.81 to 13.12, with the maximum distance in cluster-VI (25.81) followed by cluster III (21.86). The range of inter cluster distance of the studied accessions ranged from 115.606 to 37.66. The maximum inter cluster distance was between cluster I and cluster II (115.6) followed by I and III (115.2). This indicated crossing among these clusters provides high and potential heterotic groups. The minimum inter cluster distance was noticed between clusters II and III (37.66). Thus, crossing of accessions from these two clusters may not produce a high amount of heterotic expression in the F1's and broad-spectrum of variability in segregating (F^2) populations. The chi-square test for the clusters indicated that there was a statistically significant difference in all characters (Table 4). Generally, the accessions of durum wheat in this study exhibited moderately divergent. Similarly the study of Singh *et al.* (2013) reported maximum inter cluster distance exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme. According to Rahim *et al.* (2010) who pointed out that the hybrids of genotypes with maximum distance resulted in high yield, the cross between these genotypes can be used in breeding programs to achieve maximum heterosis.

Table 4. Average intra (bold) and inter cluster (off diagonal) D^2 values among five clusters in durum wheat Accessions

	I	II	III	IV	V
I	**13.5174**	115.606 **	115.209**	56.8459 **	62.2261**
II		**13.1240**	37.657**	70.9600**	81.8622**
III			**21.8624**	60.8614**	89.7850**
IV				**25.8101**	57.7764**
V					**19.6816**

X^2=19.61 at 5% probability level and x^2=24.72 at 1% probability level

Principal Component Analysis

In the present investigation only the first four principal components showed eigen values greater than one and cumulatively they explained 75.9% variability (Table 5). So these four components given due to their importance for further explanation. The PC1 had 34.8%, PC2 showed 20.5%, PC3 exhibited 11.8% and PC4 showed 8.8% variability among the accessions for the characters under study. The first two principal components PC1 and PC2 values of contributed more to the total variation. Leilah and Khateeb (2005) reported the first principal component accounts for maximum variability in the data with respect to succeeding components.

Table 5. Eigen values and Eigenvectors of the first four principal components (PCs) for 12 characters of durum wheat accessions

Characters	PC1	PC2	PC3	PC4
Days to heading(days)	0.134	-0.460	-0.260	-0.450
Days to maturity(days)	0.148	-0.517	0.199	-0.056
Grain filling period(days)	0.285	-0.131	0.458	0.360
Plant height(cm)	-0.240	-0.170	0.163	0.377
No. of productive tillers plant^{-1}	0.197	-0.142	-0.525	0.208
Spike length(cm)	-0.215	-0.359	-0.005	0.405
Number of spikelets spike^{-1}	-0.097	-0.534	-0.130	0.058
Number of grains spike^{-1}	0.390	-0.122	-0.104	-0.177
Thousand grain weight(g)	0.429	-0.015	-0.143	-0.157
Grain yield kgha^{-1}	0.449	-0.044	0.065	0.091
Biomass yield kgha^{-1}	0.157	-0.153	0.539	-0.359
Harvest index (%)	0.405	0.019	-0.192	0.344
Eigen value	4.1780	2.4610	1.4140	1.0529
Proportion	0.348	0.205	0.118	0.088
Cumulative	0.348	0.553	0.671	0.759

Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. Differentiation of the accessions into different cluster provides cumulative effect of a number of characters rather than the contribution of specific few characters. The first principal component (PC1) is mostly affected by grain yield per plot, harvest index and thousand kernel weight and number of grains per spike. The most effective character in the second principal component (PC2) was days to 50% heading, days to maturity, spike length and number of spikelets spike^{-1}. The third principal component (PC3) exhibited high contribution to the total variation with grain filling period, number of productive tillers per plant and biomass yield. The fourth principal component (PC4) mostly affected by days to heading, spike length and plant height. The present study showed that durum wheat accession had significant variations for the characters studied and it suggested that many opportunities exist for genetic improvement through selection and conservation of the accessions for future utilization. Similar works have been reported by Tsegaye *et al.* (2012), Saif *et al.* (2013), Ashraf *et al.* (2012) and Dargicho *et al* (2015) by grouping wheat genotypes based on principal component analysis.

Conclusion

The present study comprised 64 durum wheat accessions along with four standard checks that were evaluated at Kulumsa with the objective of assessing the genetic variability in yield and yield related traits among 12 characters. The analysis of variance showed the accessions were significantly (p< 1%) different for all the characters studied. The ranges of mean values for most of the characters were large showing the existence of variation among the tested accessions.

The cluster analysis based on D^2 analysis classified the 68 accessions into 5 clusters, which makes them to be moderately divergent. There was statistically approved difference between all of the clusters. Principal component analysis showed that the first four principal components exhibited eigen values greater than one and cumulatively they explained 75.9% variability. This illustrated the existence of wide ranges of variations for most of the traits among durum wheat accessions. However, the present result is only an indication and we cannot reach a definite conclusion. Therefore, it is advisable to conduct a follow up study over different years and locations.

Acknowlements

The authors would like to thank Jimma University College of Agriculture and Veterinary Medicine (JUCAVM) and Kulumsa Agricultural Research Center (KARC) for their financial support.

References

Abaye, A.O., Brann, D.E., Alley, M.M. and Griffey, C.A. (1997) Winter durum wheat: Do we have all the answers? Knowledge for the Common Wealth, Virginia State University, Publication No. 424-802.

Abinasa, M., Ayana, A. and Bultosa, G. 2011. Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. *durum*) genotypes. African Journal of Agricultural Research. 6 (17): 3972 - 3979.

Ashraf A. Abd El- Mohsen, Samir R. Abo Hegazy and Moemen H. Taha, 2012.Genotypic and phenotypic interrelationships among yield and yield componentsin Egyptian bread wheat genotypes, Cairo University, Giza, Egypt.

Bhuri Singh and P.K. Upadhyay (2013) Genetic Variability, Correlation and Path Analysis in Wheat (Triticum aestivum L.) Indian Res. J. Genet. & Biotech. 5(3) : 197-202.

Copper MC, Milligan GW (1988). The effect of error on determining the number of clusters. Proceeding of International Workshop on Data Analysis, Decision Support and Expert Knowledge Representation in Marketing and Related Areas of Research pp: 319-328.

Dargicho Dutamo, Sentayehu Alamerew, Firdisa Eticha, Ermias Assefa (2015). Genetic variability in Bread Wheat (Triticum aestivum L.) Germplasm for Yield and Yield Component Traits.Journal of Biology, Agriculture and Healthcare, 5, (17): 140-147.

Dawit Tsegaye, Tadesse Dessalegn, Yigzaw Dessalegn and Getnet Share, 2012. Genetic variability, correlation and path analysis in durum wheat germplasm (Triticum durum Desf), African Journal of Biotechnology Vol. 11(40), pp. 9606-9611.

Feldman M. 1976. Taxonomic Classification and Names of Wild, Primitive, Cultivated, and Modern Cultivated Wheats. Wheats. In: Simmonds, N.W. (ed). Evolution of Crop Plants. Longman, London. pp 120-128.

Feldman M. 2001. Origin of Cultivated Wheat. In Bonjean AP and Angus WJ (eds) The World Wheat Book: a history of wheat breeding. Intercept Limited, Andover, England, pp 3-58.

Jagadev PN, Shamal KM, Lenka L (1991). Genetic divergence in rape mustard. Indian J. Genet. Plant Breed. 51:465-466.

Khlestkina EK, EA Salina. 2001. Genome-specific markers of tetraploid wheats and their putative diploid progenitor species. Plant Breeding, 120: 227-232.

Kimber G, ER Sears. 1987. Evolution in the Genus Triticum and the Origin of Cultivated Wheat. In: Heyne, E.G. (ed). Wheat and Wheat Improvement. American Society of Agronomy, Madison, WI. pp.-31.

Leilah, A.A. and S.A. Al-Khateeb.2005. Statistical analysis of wheat yield under drought conditions. Elsevier, 61: 483-496.

Mahalanobis, P.C., 1936. On the generalized distance in statistics. Proc. Nat. Inst. Sci., 2: 49-55.

M. A. Alam, A. A. Khan, M. K. Alam , Z. I. Sarker and M. M. Rahman (2013) variability and diversity studies in durum wheat (triticum durum) Journal of Science and Technology: 1-5.

Mostafa *Khodadadi*, Mohammad Hossein Fotokian, Mohammad Miransari (2011) Genetic diversity of wheat (Triticum aestivumL.) genotypes based on cluster and principal component analyses for breeding strategies. AJCS 5(1):17-24.

Payne, T.S, Wanjama, J.K. and Girma, B. 2001. Eastern African wheat pool. In: Bonjean, A.P. and Angus, W.J. (Eds.). The wheat world book: A history of wheat breeding. Lavoisier publishing, France.

Rahim, M.A., Mia, A.A, Mahmud, F., Zeba, N. and Afrin, K. 2010. Genetic variability, character association and genetic divergence in murgbean platn Omic 3:1-6.

Saif Ullah Ajmal, Nasir Mahmood Minhas, Anber Hamdani, Ammara Shakir, Muhammad Zubair And Zaheer Ahmad (2013) multivariate analysis of genetic divergence in wheat (triticum aestivum) germplasm. Pak. J. Bot., 45(5): 1643-164.

SAS, 2008. Statistical Analysis System. Version 9.2, SAS Institute Inc., Cary, NC., USA.

Talbert LE, NK Blake, EW Storlie, M Lavin. 1995. Variability in wheat based on low-copy DNA sequence comparisons. Genome, 38: 951-957.

Verma P N, B N Singh, R K Yadav (2013) Genetic variability and divergence analysis of yield and its contributing traits under sodic soil condition in wheat (T. aestivum L.).