



VARIABILITY AND DIVERSITY STUDIES IN DURUM WHEAT (*Triticum durum*)

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Received 01 January 2012, revised 25 June 2012, accepted 08 November 2012

ABSTRACT

The present investigation was carried out to study genetic variability and diversity in 13 advanced durum wheat genotypes along with the two local checks namely WRF-7 and Prodip. Statistical analysis revealed significant differences for all the characters studied, indicating presence of considerable amount of variations among genotypes for each character. The high genotypic and phenotypic coefficient of variation were obtained for grains/spike and spikes/m². Moderate to high heritability with moderate genetic advances in percent of means were estimated against plant height, spikes/m² and 1000-grain weight and these characters could be efficiently exploited through selection. Fifteen genotypes were grouped into five clusters based on D²-statistics. Genotypes in cluster III showed maximum intra-cluster distance (0.3193) and the clusters IV and V exhibited the highest genetic distance (24.774). Therefore, parental selection from these two clusters would be effective for improvement. Maturity days was the greatest contributor to genetic divergence. Genotypes in cluster IV showed maximum diversity and can be used as parents in hybridization programs to develop high-yielding varieties. The genotypes in cluster IV may be included in crossing programme for the improvement of yield potential in durum wheat.

Key words: D²-statistics, diversity, durum wheat, PCA, variability

INTRODUCTION

Durum wheat (*Triticum durum* Desf.) is one of the most important widely grown cereal crops in the world, and mainly (>90%) cultivated in Mediterranean basin, Europe and India (Abaye *et al.* 1997 and Nachit *et al.* 1998). Durum wheat is consumed as flat, unleavened bread, couscous and bulgur in North Africa and Middle East and as Chapati in India. The major breeding objective in durum wheat is to improve genetic background with features that contribute to higher yield potential, more yield stability and improved product quality (Poehlman and Sleeper 1995). Variability study is limited in durum wheat. Variability particularly decides the effectiveness of selection (Subhashchandra *et al.* 2009). It is fact that the higher the variability among the genotypes betters the chances for further improvement in the crop (Subhashchandra *et al.* 2009). The grain yield of crop plants is influenced by the number of component characters, but their influence highly fluctuates both in direction and magnitude.

With the development of multivariate analysis (Rao, 1952) based on Mahalanobis's D²-statistics (1936) and principal component analysis (PCA) it has become possible to quantify the magnitude of diversity among the genotypes. Both the analyses are important for assessment of genetic divergence among the parents and the relative contribution of different characters to the total divergence (Golakia and Makne 1992; Nataranjan *et al.* 1988; Das and Gupta 1984 and Sindhu *et al.* 1989). Genetically distant parents usually able to produce higher heterosis (Falconar 1960; Moll *et al.* 1962 and Mian and Bhal 1989). Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production (Khodadadi *et al.* 2011). The objective of the investigation was to study genetic variability and diversity among durum wheat genotypes and also to assess their potential as parents for improvement.

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MATERIALS AND METHODS

The study was carried out with 15 genotypes in Randomized Complete Block Design with three replications at the Regional Agricultural Research Station of Bangladesh Agricultural Research Institute, Ishurdi, Pabna, during the winter season of 2008-09. The unit plot size was 5×1.2 m following 20 cm row spacing. Standard package of practices were followed for raising the crop. The studied characters were head days, maturity days, plant height (cm), spikes m⁻², grains spike⁻¹, 1000-grain weight (g) and grain yield (kg ha⁻¹).

Table 1. Genotypes used in the study

Genotype	Description	Source of collection
D-001, D-002, D-003, D-004, D-005, D-006, D-007, D-008, D-009, D-010, D-011, D-012, and D-013	Advanced durum wheat lines	WRC, BARI, Bangladesh
WRF-7	Local durum wheat cultivar	WRC, BARI, Bangladesh
Prodip	Local bread wheat cultivar	WRC, BARI, Bangladesh

The analyses of variances for different characters were measured according to Steel and Torrie (1960). The mean squares were used to estimate genotypic and phenotypic variances according to Johnson *et al.* (1955). The genotypic and phenotypic coefficient of variations and heritability values were calculated as suggested by Singh and Chaudhary (1985). Mahalanobis's D²-statistics was used for estimating genetic divergence among the genotypes. The genotypes were grouped into clusters following Tocher's method given by Rao (1952).

RESULTS AND DISCUSSION

Highly significant differences and wide ranges of variation for grain yield and other yield contributing characters indicated the presence of sufficient variability among the genotypes (Table 2).

The genotypic and phenotypic coefficient of variations and heritability estimates were presented in Table 3. The highest GCV was obtained from spikes/m² (8.71) followed by grains/spike (8.41) and 1000-grain weight (8.19). The highest PCV was obtained from grains spike⁻¹ (12.47) followed by the spike m² (11.44). The differences between GCV & PCV were relatively very small which indicated that the major amount of variation was contributed by genetic component and less by environment which

also supported the findings of Jagashoran and Mishra (2005). Moderate to high heritability along with moderate genetic advances in percent of means were obtained from plant height, spikes/m² and 1000-grain weight indicated that predominance of additive gene effects (Jalal and Ahmad, 2012) and therefore, these characters can be exploited through selection. Sachan and Singh (2003) reported high heritability estimates for plant height and 100-seed weight. Comparatively low heritability was obtained for yield which is similar to the findings of Maniee *et al.* (2009). Johnson *et al.* (1955) impressed that heritability along with genetic advance in percentage of mean was more useful than heritability alone in predicting the benefit from selection.

The variation among the durum genotypes and check varieties were studied by multivariate scale using Mahalanobis's D² -statistics. On the basis of D² values it appeared that there were significant variations among the entries. Fifteen genotypes were grouped into five clusters presented in Table 4. The cluster I was the largest containing six genotypes followed by cluster II having three genotypes. The rest three clusters i.e., III, IV and V included two genotypes in each. Elias and Shamsuddin (2000) studied genetic divergence in bread wheat and grouped 10 genotypes into six distinct clusters.

The average intra and inter cluster distances of five clusters were presented in Table 5. The inter cluster distances were large than the intra cluster distances, indicating wider diversity among the genotypes of different clusters (Dawit *et al.*, 2012). The magnitude of intra-cluster distance indicated the extent of genetic diversity among the genotypes in the same cluster. The highest inter cluster distance was measured between cluster IV and cluster V (24.774) followed by the distance between cluster III and V and II and V denoting that the genotypes of these clusters were more diversified. It was general observations that cluster V had higher distances from the other clusters indicated that the genotypes in cluster V were distinctly different from the others. The lowest distance was found between cluster II and cluster III followed by the distance between cluster III and cluster IV. It indicated that the genotypes under these clusters were genetically closely related. Thus, crossing of genotypes from these four clusters may not produce a high heterotic expression in the F₁'s and broad-spectrum of variability in segregating (F₂) generation. It was reported that clusters with lower magnitude of divergence showed instability, while widely divergent clusters remained distinct in different environments (Somayajulu *et al.* 1970; Raut *et al.* 1985 and Singh *et al.* 1980).

In the PCA the first two components contributed 99.86% of the total variation. The scores obtained from these two components were plotted against two

main axes and then superimposed with clustering (Figure 1). This clustering pattern confirmed the results obtained by D^2 analysis.

The coefficient pertaining to the different characters in the first two canonical roots were presented in

Table 6. The table exhibited that head days, maturity days and grains/spike proclaimed the positive absolute values of the two vectors; revealed these characters had the greatest contribution towards genetic divergence.

Table 2. General statistics of seven characters studied in 15 wheat genotypes

Sl. No.	Characters	Mean range	Mean± SE	Mean square	CV%
1	Head Days	63.00-76.33	70.53±0.57	39.70**	2.20
2	Maturity Days	106.00-118.67	111.56±0.50	33.03**	0.82
3	Plant Height	70.00-98.93	83.71±1.15	150.89**	5.54
4	Spikes/ m ²	253.33-353.33	306.44±5.87	2654.60**	7.42
5	Grains/ spike	38.00-54.00	45.64±0.87	61.88**	9.20
6	1000-grain wt	43.28-61.48	54.78±0.78	68.11**	5.08
7	Grain Yield	3270.67-4083.33	3709.02±49.28	165051.21**	6.42

** Significant at 1% level of probability

Table 3. Genotypic and phenotypic coefficient of variations and heritability estimates of seven characters studied in 15 wheat genotypes

Sl. No.	Characters	GCV (%)	PCV (%)	Heritability (%)	GA (%)	GA % of mean
1	Head Days	5.00	5.46	83.82	5.68	8.06
2	Maturity Days	2.94	3.09	90.46	5.48	4.92
3	Plant Height	7.48	9.61	66.69	9.44	11.28
4	Spikes/ m ²	8.71	11.44	57.97	35.77	11.67
5	Grains/ spike	8.41	12.47	45.55	4.56	9.99
6	1000-grain wt.	8.19	9.64	72.25	6.71	12.25
7	Grain Yield	5.12	8.21	38.92	208.69	5.63

Table 4. Distribution of 15 wheat genotypes in 5 clusters

Cluster	No. of genotypes	Genotypes
I	6	WRF-7, D-002, D-006, D-008, D-010, D-012
II	3	D-003, D-004, D-005
III	2	D-007, D-009
IV	2	D-001, D-013
V	2	Prodip, D-011

Table 5. Average intra and inter cluster distances (D^2) in wheat

Clusters	I	II	III	IV	V
I	0.24932	6.609	9.475	12.020	13.764
II		0.19253	3.231	6.755	20.348
III			0.3193	3.828	22.997
IV				0.1779	24.774
V					0.1884

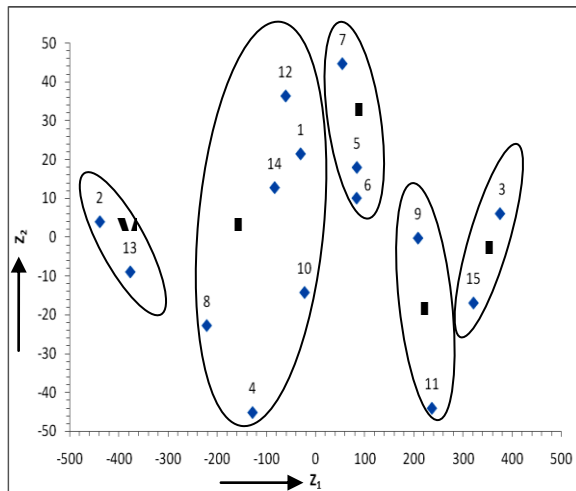
The values on the diagonals (**bold**) are the intra-cluster and those off-diagonals are the inter cluster distance.

Table 6. Latent vectors for seven characters

Characters	Vector I	Vector II
Head Days	+0.384	+0.332
Maturity Days	+0.401	+0.401
Plant Height	-0.267	+0.537
Spikes/ m ²	+0.276	-0.541
Grains/ spike	+0.339	+0.331
1000-grain wt	-0.473	+0.049
Grain Yield	+0.453	-0.186

Table 7. Cluster mean values of seven characters

Cluster	Head Days	Maturity Days	Plant Height (cm)	Spikes/ m ² (no.)	Grains/ spike (no.)	1000-grain wt. (g)	Grain Yield (kg/ha)
I	71.4	112.4	83.6	298.6	44.8	56.3	3618.1
II	69.9	110.3	79.3	335.0	46.2	52.1	3781.2
III	73.3	114.0	80.8	298.3	50.8	48.1	3932.5
IV	70.8	111.7	83.0	323.3	47.2	55.4	4057.2
V	65.7	108.3	94.3	278.3	40.5	60.2	3302.0

**Figure 1.** Scatter distribution of 15 wheat genotypes based on their principal components scores superimposed with clusterings

The positive values of vector-I and negative values of vector-II for spikes/m² and grain yield indicated the responsibility of primary differentiation of genetic distance (Rahman *et al.* 2007). On the contrary, the negative absolute values of vector-I and positive absolute values of vector-II for plant height and 1000-grain weight indicated the responsibility of secondary differentiation. Rahman *et al.* (2007) noticed similar results for 1000-grain weight. Jatrasa (1980) found plant height as the most important contributing character towards genetic divergence.

Mean values of different clusters for yield and its different contributing characters were presented in Table 6. From the table it was appeared that cluster V included the early heading and early maturing genotypes whereas cluster II included intermediate types for both of these characters. Both the clusters II and III included dwarf type genotypes while cluster V contained tall genotypes. The maximum no. of spikes/m² was found from the cluster II (335.0) followed by cluster IV (323.3) and the rests were produced moderate no. of spikes m⁻². There were little differences among the cluster means of grains/spike and 1000-grain weight for genotypes of clusters I, II and IV. The highest grain yield was obtained from the genotypes of cluster IV (4057.2 kg ha⁻¹). The genotypes in this cluster had intermediate maturing duration, intermediate plant

height, high spikes/m², moderate grains/spike and higher 1000-grain weight. Considering all the characters it was appeared that the genotypes in cluster IV appeared as outstanding for the improvement of wheat particularly durum.

Endang *et al.* (1971) stated that the clustering pattern could be utilized in choosing parents for cross combinations which likely to generate the highest possible variability for effective selection of various economic characters in rice. Keeping this in view, the findings from the present study indicated that the cluster II and V, III and V; IV and V showed higher distance between them. Parental material selection from these clusters would give high manifestation of heterosis as well as wide spectrum of variation in segregating generations.

REFERENCES

- Abaye AO, Brann DE, Alley MM and Griffy CA. 1997. Winter Durum Wheat: Do We Have All the Answer? 1st Edn. Virginia Tech Publication. USA. pp: 424-802.
- Das PK and Gupta TD. 1984. Multivariate analysis in blackgram. Indian. J. Genet. 44(2): 243-247.
- Dawit Tsegaye, Tadesse Dessalegn, Yigzaw Dessalegn and Getnet Share. 2012. Analysis of genetic diversity in some durum wheat (*Triticum durum* Desf) genotypes grown in Ethiopia. African. J. Biot. 11(40): 9606-9611.
- Elias MA and Shamsuddin AKM. 2000. Genetic divergence in bread wheat (*Triticum aestivum* L.) for source sink characters. Bangladesh J. Pl. Breed. Genet. 13(2): 19-24.
- Endang S, Andani S and Nasoetion H. 1971. Multivariate classification of some rice (*Oryza sativa* L.) varieties and strain on yield components. Int. Rice comm. Newst. 20: 26-34.
- Falconar DS. 1960. Introduction to Quantitative Genetics. Oliver and Bond. London. p. 304.

- Golakia PR and Makne VG. 1992. D^2 analysis in virginal runner groundnut genotypes. *Indian J. Genet.* 55(3): 252-256.
- Jagashoran and Mishra B. 2005. Progress Report of Project Director of Directorate of Wheat Research, Karnal. pp. 1-5.
- Jalal A Al-Tabbal and Ahmad H Al-Fraihat. 2012. Heritability studies of yield and yield associated traits in wheat genotypes. *J. Agril. Sci.* 4(4): 11-22.
- Jatasra DS. 1980. Genetic divergence in bread wheat. *Haryana Agril. Univ. Res.* 10(1): 18-25.
- Johnson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in Soybeans. *Agron. J.* 47: 314-318.
- Khodadadi M, Mohammad HF and Mohammad M. 2011. Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. *Aus. J. Crop. Sci.*
- Mahalanobis PC. 1936. The generalized distance in statistics. *Pro. India Nat. Inst. Sci.* 2: 49-55.
- Maniee M, Kahrizi D and Mohammadi R. 2009. Genetic variability of some morpho-physiological traits in durum wheat (*Triticum turgidum* var. durum). *J. Appl. Sci.* 9(7): 1383-1387.
- Mian MAK and Bhal PN. 1989. Genetic divergence and hybrid performance in chickpea. *Indian J. Genet.* 49(1): 119-129.
- Moll RH, Salhwana WS and Robinson HR. 1962. Heterosis and genetic diversity in variety crosses in crop maize. *Crop Sci.* 2: 197-198.
- Nachit MM, Baum M, Poreciddu E, Monneveux P and Picard E. 1998. SEWANA (South Europe, West Asia and North Africa) durum research network. Proceeding of the SEWANA Durum Network Workshop, Mar. 20-23, ICARDA, Aleppo, Syria. pp: 361-361.
- Nataranjan C, Thiyagarajan K and Rathanaswamy R. 1988. Association and genetic performance in mungbean. *Theor. Appl. Genet.* 44(5): 211-214.
- Poehlman JM and Sleeper DA. 1995. *Breeding Field Crops* (4th edition). Iowa State Univ. Press. Iowa. pp. 259-261.
- Rahman MM, Shamsuddin AKM, Asad U and Islam SMN. 2007. Genetic divergence in doubled haploid lines of lines of spring wheat (*Triticum aestivum* L.). *Bangladesh J. Genet. Pl. Breed.* 20(2): 37-41.
- Rao CR. 1952. *Advanced Statistical Method in Biometric Research*. Ednl. John Wiley and Sons, New York.
- Raut VM, Rao VSP, Patel VP and Deodikar GB. 1985. Genetic divergence in *triticum durum*. *Indian J. Genet.* 45: 141-151.
- Sachan MS and Singh SP. 2003. Genetics of yield and its components in durum wheat (*Triticum durum* Desf.). *J. Interacademia.* 7(2): 140-143.
- Sindhu JS, Ahmed M, Singh M and Singh KP. 1989. Multivariate analysis in blackgram. *Legume Res.* 12(1): 35-37.
- Singh D, Kumar P and Chandan BPS. 1980. Genetic diversity for some quantitative characters in barley. *Indian J. Genet.* 40(2): 391-395.
- Singh RK and Chaudhary BD. 1985. *Biometrical methods in quantitative genetic analysis*. Kalyani Publ., New Delhi.
- Somayajulu PLN, Joshi AB and Murty BR. 1970. Genetic divergence in wheat. *Indian J. Genet.* 30(1): 47-58.
- Subhashchandra B, Lohithaswa HC, Desai SA, Hanchinal RR, Kalapranavar IK, Math KK and Salimath PM. 2009. Assessment of genetic variability and relationship between genetic diversity and transgressive segregation in tetraploid wheat. *Karnataka J. Agric. Sci.* 22(1): 36-38.
- Steel RGD and Torrie JH. 1960. *Principles and Procedures of Statistics*. 1st Edn., McGraw Hill, Tokyo, Japan.