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Analysis of genetic diversity in some durum wheat (*Triticum durum* Desf) genotypes grown in Ethiopia

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An experiment was conducted to examine the magnitude of genetic diversity and characters contributing to genetic diversity among 23 durum wheat genotypes grown at Adet, northwest Ethiopia, in 2010 main cropping season. Genetic divergence was carried out according to Mahalanobis D^2 statistics. Genetic distance analysis revealed that the Euclidean genetic distance values ranged from 2.69 (between D-1 and D-11) to 9.68 (between D-13 and D-21) and 82.2% of the pair comparisons had values between 3.76 and 7.50. Cluster analysis grouped genotypes into six genetically distinct clusters. The highest inter-cluster distance was 8.30 (between clusters III and VI) followed by 7.99 (between clusters V and VI), indicating the wide genetic diversity among these clusters. The highest intra-cluster distance was observed in cluster I (4.91) and the lowest in cluster III (2.36). The average inter-cluster distances were higher than the average intra-cluster distances, which showed the presence of wide genetic diversity among the genotypes of different clusters than those of the same cluster. The first four principal components whose Eigen values are greater than one, accounted for 80.46% of the total variation of the original variables. The information obtained from the study is useful in planning further crossing programme for durum wheat crop improvement.

Key words: Cluster analysis, genetic distance, principal component analysis.

INTRODUCTION

Durum wheat (*Triticum durum* Desf.) is one of the important cereal crops in many countries in the world (Maniee et al., 2009; Kahrizi et al., 2010a, b; Mohammadi et al., 2010). Also, this crop plant is the most important *Triticum* species constituting 10 to 11% of the world wheat crop and accounting for 8% of the total wheat production in the world, and grows in most countries except in the hot and humid tropical regions (Peña et al., 2002; Ganeva et al., 2011). It has various traits of interest such as resistance to yellow rust (Beharav et al., 1997), environmental stability and high quality of its end products (Almansouri et al., 2001). The crop is widely grown in the Middle East, North Africa, the Indian subcontinent and Mediterranean Europe and part of

Ethiopia, Argentina, Chile, Mexico, the United States and Canada (Abdalla et al., 1992). According to Central Statistics Authority (CSA, 2008), the average productivity of durum wheat in Ethiopia is estimated to be 17.46 q/ha, which is lower than the average world productivity (25 q/ha).

The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful durum wheat breeding programme. Developing durum wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (Maniee et al., 2009; Kahrizi et al., 2010a, b). The more the genetic diverse parents, the greater the chances of obtaining higher heterotic expression in F_1 s and broad spectrum of variability in segregating population (Shekhawat et al., 2001). Generally, parents with a long genetic distance can produce a hybrid with better yield performance (Diers et al., 1996). Clear information on the nature, pattern and

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degree of genetic diversity helps breeders in choosing the diverse parents for purpose of hybridization and crossing programme. Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Shekhawat et al., 2001; Arega et al., 2007; Haydar et al., 2007; Ahmadzadeh et al., 2011; Daniel et al., 2011). The present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among durum wheat genotypes.

MATERIALS AND METHODS

Experimental procedures

The field experiment was conducted in 2010 main cropping season at Adet Agricultural Research Center (AARC) which is located at longitude 37°29'E and latitude 11°16'N with an average altitude of 2,240 m above sea level in the northwest of Ethiopia. The mean annual rainfall of the study area is 1,230 mm and the average annual maximum and minimum temperature are 25.5 and 9.8°C, respectively. The soil type is vertisol with pH value of 6.0.

The experiment consisted of 21 exotic durum wheat genotypes received from International Maize and Wheat Improvement Centre: CDSS02Y00201S-0Y-0M-15Y-0Y (D-1), CDSS 02Y00331S-0Y-0M-22Y-0Y (D-2), CDSS02Y00267S-0Y-0M-2Y-0Y (D-3), CDSS02Y0123 3T-0TOPB-0Y-0M-32Y-0Y (D-4), CDSS01Y01040T-0TOPB-84Y-0M-0M-0M-0Y (D-5), CDSS02Y00276S-0Y-0M-20Y-0Y (D-6), CDSS02Y00024S-0Y-0M-24Y-0Y (D-7), CDSS0 1B00420S-0Y-0M-27Y-0Y (D-8), CDSS02Y001160S-0Y-0M-5Y-0Y (D-9), CDSS02Y003 68S-0Y-0M-17Y-0Y (D-10), CDSS02Y00221S-0Y-0M-22Y-0Y (D-11), CDSS02Y00270S-0Y-0M-11Y-0Y (D-12), CDSS02Y00233S-0Y-0M-9Y-0Y (D-13), CDSS01B00073S-0Y-0 M-14Y-0Y (D-14), CDSS02Y00524S-0Y-0M-6Y-0Y (D-15), CDSS01B00094S-7M-0M-0Y-0Y (D-16), CDSS02Y00198S-0Y-0M-32Y-0Y (D-17), CDSS02Y00062S-0Y-0M-11Y-0Y (D-18), CDSS01B00472S-3M-0M-0Y-0Y (D-19), CDSS96B0054540S...-1Y...-4Y (D-20), ICD97-0396-T...14AP (D-21) along with two released varieties: DZ-1666-2 (D-22) and DZ-2212 (D-23) as standard checks which were released by AARC for northwest part of the country. The trial was laid down in randomized complete block design with three replications. Each genotype was planted in six rows of 2.5 m row length by 0.2 m spacing between rows. The distance between replications and plots was 1.5 and 0.2 m, respectively. Urea and DAP fertilizers were applied at the recommended rate of 161 and 100 kg/ha, respectively (AARC, 2009). The whole DAP was applied at sowing, while urea was applied in splits with the first half at sowing and the second top-dressed at full tillering stage. Sowing was done by hand drilling at a seed rate of 150 kg/ha.

Data collection

Data on different morphological and quality characters was done on plant and plot basis. Number of spikelets per spike, number of kernels per spike, plant height (cm), number of effective tillers per plant, spike length (cm), stem dry weight (g), leaf dry weight (g) and flag leaf length (cm) were recorded on plant basis; whereas, days to heading, days to maturity, thousand grain weight (g), biological yield per plot (g), harvest index per plot (%), grain yield per plot (g), grain moisture content (%), vitreousness (%), ash content (%) and

Table 1. Euclidean genetic distance ranges of durum wheat genotypes.

Genetic distance	Frequency	Frequency (%)
<3.00	1	0.40
3.01-3.75	8	3.16
3.76-4.50	22	8.70
4.51-5.25	47	18.58
5.26-6.00	54	21.34
6.01-6.75	44	17.39
6.76-7.50	41	16.21
>7.50	36	14.23
Total	253	100

flour protein content (%) were estimated on plot basis. Grain moisture content of the sample seed was measured by moisture analyzer. 10 g sample was heated for 1 h in a semi-automatic Brabender oven at 130°C to measure the grain moisture content. The percentage of vitreous kernels was determined by examining the cross section of the kernels, which was actually measured by using near-infrared spectroscopy. Ash content was determined by standard method 08-12 on milled grain at Amhara Regional Agricultural Research Institute's grain quality laboratory. Samples were incinerated overnight in a muffle furnace at 600°C. Flour protein content of the composite samples was determined by combustion nitrogen analysis and calculated from total nitrogen as determined on a LECO Model FP-528 CNA analyzer calibrated with EDTA and reported on a constant moisture basis.

Data analysis

Genetic diversity analysis was computed based on multivariate analysis using Mahalanobis's D^2 statistics. The genotypes were grouped into clusters using Tocher method as described by Singh and Chaudhary (1979). Principal component analysis and cluster mean analysis were carried out using Statistical Analysis System Version 8 (SAS Institute, 2000). The cluster mean of a particular character was calculated by the summation of mean value of genotypes included in a cluster, divided by number of genotypes in the same cluster.

RESULTS AND DISCUSSION

Genetic distance analysis

The data matrix of the tested characters formed the basis of Euclidean genetic distance calculations. Genetic distance values for all 253 pairs wise comparisons of the 23 durum wheat genotypes is presented in Table 1. The estimated genetic distance values ranged from 2.69 (between D-1 and D-11) to 9.68 (between D-13 and D-21) with mean value of 6.02. The frequency distribution of genetic distance values indicates that 82.2% of the pair comparisons had values between 3.76 and 7.50; more than 14% had value larger than 7.50 and only a single pair (between D-1 and D-11) had value lower than 3.0. The wide range of genetic distance among the genotypes showed the presence of wide range of genetic variations

Table 2. Distribution of 23 durum wheat genotypes among the six clusters.

Cluster	Number of genotype	Genotype
I	12	D-1, D-2, D-6, D-8, D-9, D-10, D-11, D-12, D-14, D-15, D-16, D-19
II	5	D-3, D-4, D-17, D-18, D-20
III	2	D-22, D-23
IV	1	D-7
V	2	D-5, D-13
VI	1	D-21
Total	23	23

Table 3. Intra-cluster (diagonal) and inter-cluster distance D^2 values among the six clusters.

Cluster	I	II	III	IV	V	VI
I	4.91	4.09	5.48	4.77	4.80	5.48
II		4.80	5.27	5.89	6.92	5.21
III			2.36	6.61	6.26	8.30
IV				0.00	6.48	7.24
V					2.39	7.99
VI						0.00

among them and an opportunity to improve the genetic basis of durum wheat by implementing crossing.

Cluster analysis

The results of the cluster analysis were presented in groups of genotypes to infer relationships among genotypes (Table 2). The genotypes were grouped into six genetically distinct clusters at a cut off value of 1.0. Four of them are real clusters (I, II, III and V) and the remaining two are singletons (IV and VI). The number of genotypes per cluster varied from 1 to 12. Clusters I and II contained 12 and 5 genotypes, respectively, cluster III and V had 2 genotypes and clusters IV and VI had only 1 genotype. The two standard checks, varieties developed at local level, were separately categorized in cluster III. This wider genetic variability may be due to the adaptation of these genotypes to specific environmental conditions. Similar results were presented by Arega et al. (2007) on exotic and indigenous durum wheat genotypes in the northeast Ethiopia. Previous results also reveal that there were relationships between genetic divergence and geographic distance among countries of origin and environmental differences among sites of selection (Adary, 1978; Martha, 2007).

Intra-and inter-cluster D^2 values

Genotypes grouped in the same cluster (intra-cluster) are expected to be genetically more similar than genotypes grouped in different clusters (inter-clusters). The average

intra- and inter-cluster distances are presented in Table 3. The highest inter-cluster distance was observed between clusters III and VI (8.30), followed by clusters V and VI (7.99) indicating the presence of wider genetic divergence between these clusters. Crossing genotypes from genetically distant clustered population may result in the expression of more heterosis in F_1 generation and wider genetic variability in the segregating generations. Parents for hybridization could be selected on the basis of large inter-clusters distance for isolating useful recombinants in the segregating generations (Ghaderi et al., 1984; Diers et al., 1996). Thus, diverse lines from different clusters should be chosen for crossing in durum wheat breeding programme. The lowest inter-cluster distance was recorded between clusters I and II (4.09) showing narrow genetic divergence between these clusters. The lines belonging to these clusters were relatively closer to each other, in comparison to lines grouped in other clusters. The highest intra-cluster distance was observed for cluster I (4.91) and the lowest for cluster III (2.36). Clusters IV and V were singletons and unique in one or more characters, which made them so divergent from the rest of the genotypes. The average inter-cluster distances were higher than the average intra-cluster distances, which indicates the presence of wide genetic diversity among the genotypes of different clusters than those of the same cluster.

Cluster mean analysis

Mean values of the traits for each cluster are presented in Table 4. Cluster I had relatively higher grain yield,

Table 4. Mean values of 18 characters in the six clusters.

Character	Cluster					
	I	II	III	IV	V	VI
Days to heading	64.17	65.40	64.50	65.30	69.35	63.30
Days to maturity	103.62	104.08	102.35	103.30	106.85	103.00
Number of spikelets/spike	14.97	14.94	16.00	16.30	18.35	12.70
Number of kernels/spike	36.81	35.40	38.00	40.70	44.65	29.00
Plant height	76.72	66.24	81.75	82.90	80.15	71.10
Number of tillers/plant	2.98	2.40	2.50	3.30	2.65	3.00
Spike length	5.26	5.52	5.70	4.60	6.70	4.40
Thousand grain weight	29.08	27.44	33.20	30.50	28.50	27.00
Biological yield	1382.52	1237.88	1515.65	1311.10	1268.95	1041.10
Harvest index	29.69	25.80	26.05	37.30	27.30	22.90
Stem dry weight	0.96	0.93	1.72	1.13	1.14	0.77
Leaf dry weight	0.09	0.10	0.12	0.09	0.09	0.11
Flag leaf length	21.08	20.64	21.25	19.60	19.75	20.30
Grain yield	13.81	11.12	13.26	15.02	11.54	9.62
Moisture content	10.96	11.05	10.75	11.07	11.02	10.70
Ash content	1.31	1.30	1.29	1.24	1.31	1.29
Vitreousness	45.33	50.00	36.67	27.33	28.00	58.00
Flour protein content	10.34	10.57	10.37	9.83	10.27	11.30

acceptable level of flour protein content and intermediate values for most of the traits. Low plant height and small number of tillers per plant were characteristics of cluster II. Two standard varieties are grouped in cluster III which can be characterized by short days to maturity, high thousand grain weight, high biological yield and large number of spikelets per spike. Cluster IV had only one genotype with a characteristic feature of high plant height, high number of spikelets per spike and high grain yield.

Cluster VI had the lowest mean value for number of spikelets per spike, number of kernels per spike, spike length, thousand grain weight, biological yield, harvest index and grain yield, though it had maximum values of vitreousness and flour protein content.

Principal component analysis

Six principal components (PCs) whose Eigen values were greater than one accounted for 80.46% of the total variation of the original variables. The first PC explained about 23.45%, the second 20.14%, the third 13.25%, the fourth 9.59%, the fifth 7.13% and the sixth 6.9% of the total variation (Table 5).

Chahal and Gosal (2002) reported that characters having the highest absolute values closer to one within the given PC can influence the clustering more than

variables having lower absolute value closer to zero. In the first PC, biological yield, thousand grain weight and grain yield showed positive loadings but negative with flour protein content and vitreousness. Similarly, days to heading, days to maturity, number of spikelet per spike, spike length, number of tillers per plant, harvest index and grain yield showed greater loadings in the second PC.

The third PC had high positive component loadings with thousand grain weight, stem dry weight, leaf dry weight and flag leaf length; and negative with number of tillers per plant and harvest index. Ash content and flag leaf length are important characters in the fourth PC. The greater loadings were also observed in fifth PC with days to maturity, number of tillers per plant and thousand grain weight; while greater loadings were observed in the sixth PC with leaf dry weight and flag leaf length.

Conclusion

The results of the present study indicate the presence of genetic diversity among the tested durum wheat genotypes. Parents from divergent clusters can be used for hybridization in order to isolate useful recombinants in the segregating generations. This information might be used in the genetics and breeding programmes for improvement of durum wheat.

Table 5. Vector loadings and percentage shown by variation of the first six PCs.

Character	Eigen vector					
	PC1	PC2	PC3	PC4	PC5	PC6
Days to heading	0.11	0.44	-0.11	-0.13	0.19	-0.10
Days to maturity	0.14	0.34	-0.18	0.14	0.50	-0.07
Number of spikelets/spike	0.32	0.32	-0.02	0.11	-0.15	0.06
Number of kernels/spike	0.29	0.19	0.01	0.28	-0.33	0.26
Plant height	0.20	-0.08	0.11	-0.02	0.11	-0.07
Number of tillers/plant	0.07	-0.32	-0.25	-0.12	0.44	0.10
Spike length	0.23	0.38	0.16	0.17	0.09	-0.07
Thousand grain weight	0.30	-0.17	0.23	-0.20	0.34	-0.09
Biological yield	0.36	-0.21	0.13	0.06	-0.21	-0.15
Harvest index	0.27	-0.27	-0.28	0.23	0.03	0.19
Stem dry weight	0.30	0.03	0.39	-0.26	-0.18	0.14
Leaf dry weight	-0.08	0.06	0.43	0.04	0.26	0.46
Flag leaf length	-0.01	-0.14	0.32	0.44	0.28	0.30
Grain yield	0.33	-0.33	-0.09	0.19	-0.08	-0.05
Moisture content	-0.07	0.07	-0.42	0.27	-0.04	0.40
Ash content	-0.05	0.01	0.11	0.50	0.08	-0.53
Vitreousness	-0.21	-0.13	0.20	0.31	-0.01	-0.23
Flour protein content	-0.38	0.05	0.19	0.10	-0.12	0.13
Eigenvalue	4.22	3.63	2.39	1.73	1.28	1.24
Individual percentage	23.45	20.14	13.25	9.59	7.13	6.90
Cumulative percentage	23.45	43.59	56.84	66.43	73.56	80.46

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