

RESEARCH ARTICLE

(Open Access)**Morphological characterization of durum wheat (*T. durum* Desf.) germplasm stored in Albanian genebank**VALBONA HOBDARI^{1*}, DORIANA BODE¹, BELUL GIXHARI¹, FETAH ELEZI¹, ADRIAN DOKO²¹Institute of Plant Genetic Resources, Agricultural University of Tirana, Tirana, Albania²Department of Environment, Agricultural University of Tirana, Tirana, AlbaniaCorresponding author e-mail: vhobdari@ubt.edu.al**Abstract**

Study for characterization of genetic diversity present in the durum wheat (*Triticum durum* Desf.) germplasm stored in genebank was carried out in the Experimental Field of Agriculture University of Tirana during the growing 2015-2016 season. The study analyzed 99 durum wheat accessions genotypes of local origin for 15 quantitative morphological characters and had the objective to characterize and select those with favorable characteristics for use in breeding programs and for accomplishment of farmer requests. Variance analysis, and correlation and cluster analysis reveal presence of significant variability between and the association among different traits. Most of the quantitative morphological characters (11 traits) showed significant differences for the important agronomic traits. Cluster analysis for morphological data divide the whole-wheat genotypes into six cluster groups in respect of genetic diversity and similarity among durum wheat accessions. Higher number of the wheat accessions was included into the fifth and the sixth cluster groups (21 and 24 accessions respectively). The study identifies traits with agronomic interest that account for genetic diversity and which will facilitate the maintenance and agronomic evaluation of the wheat collections.

Keywords: Clusters analysis, diversity, germplasm, quantitative characters.

Introduction

Durum wheat (*Triticum turgidum* var. *durum* Desf.) is a minor cereal crop. It represents just the 5% of the total wheat crop, which in the last three years has overcome the 700 million metric tons durum wheat crop. In 2014/2015 period grain production was 33 million metric tons [18]. The total production, under winter cycle, in the Mediterranean Basin varies significantly because the whole crop relies on rain. Among all the countries that appear on the Mediterranean Sea, Italy is the major durum wheat producer with almost 4.0 MMT in average. Durum wheat is cultivated in many other countries; mostly as new crop, farmers are trying to cultivate it because of the price (generally 20% higher than the price of common wheat) and because of the need to rotate [18]. Even though many studies demonstrated the worth of the genetic diversity held in gene banks in the whole *Turgidum* subsp, especially in the wild and cultivated emmers, the use of this valuable diversity is

not easy and may not be really successful if one expects the use of valuable alleles at some major genes, such as disease resistance [4]. In Albania in 1950, about 60 names of wheat of different origins were planted [19]. Some cultivars of traditional durum wheat are cultivated in the mountainous areas of which were distinguished for tolerance to cold [6]. Differences among lines in terms of phenological extension are minor and major, in maintenance for plant and spike characteristics are major [11]. Albania has very good condition for cultivation of durum wheat (*Triticum durum* Desf.). The area planted with durum wheat before the year 90s was 6-8 thousand ha per year [15]. Albanian Gene Bank has rich collection of durum wheat. The study of the Albanian base collection showed that there is a high genetic diversity of wheat cultivars [7]. Study results suggest possible parental lines among the bread wheat accessions analyzed can be selected and utilised for sustainable field bread wheat breeding programs [2, 21, 1, 24, 9, 10, 17, 22]. The maximum information for analysis of

the relationships among bread wheat accession and morphological traits was received using ordination methods (principal coordinate's analysis) in combination with cluster analyses [13]. From the study result that characters: plant height, vegetative period and average spike weight have the direct influence in the grain yield [12]. The principal variables selected for evaluation of ex situ collections in genebank [3]

Materials and methods

Plant Materials: In this study, we used durum wheat (*Triticum durum* L.), 100 accessions by base collection of Albanian Gene Bank, conserved during 2001-2003.

Experimental site: The study was conducted in Agriculture University of Tirana, in Experimental Station of Institute of Plant Genetic Resources in Valias. It lies at an altitude of 40 m above sea level and at Latitude 41°24'6.14"N and Longitude 19°44'9.93"E.

Methods (Experimental Design): Experiment carried one replication during the autumn season of 2015/2016. Each accession was planted in 1 m long plot with a between-row spacing of 25 cm and within-row spacing 10 cm. Fertilizer was broadcast on the plots at the rate of 400 kg ha⁻¹, N.P.K. 8:16:20. At physiological maturity, seeds were harvested and after they were cleaned for analysis.

The traits: sowing-germination, growth class (seasonality), spikelet time, days to flower, falling of plants tillering capacity were investigated. Grain yield components, plant height (cm), 1000-seed weight (g), hectolitre weight (kg) were analyzed. Biochemical traits, seed humidity (%), protein content (%), gluten (%) and sediment (%) were analyzed.

Data analysis

Descriptive statistics and Analysis of variance of quantitative agronomical traits. The mean values, standard deviation, cluster, error of different accessions were subjected to of the observed means was found as significant level. (*) equal to the 0.05 and (**) equal to the 0.01 of probability. Cluster analysis

identified the most number of durum wheat accessions. Principal components analysis (PCA) on correlations of quantitative morphological and agronomical traits identified the variances of the principal components (PC) and the proportion of the total variance accounted for by each factor. Eigen values matrix of principal components analyzed of quantitative agronomical characters. Eigen vector values for three principal components of quantitative traits.

Results and Discussions

ANOVA and cluster analysis showed the presence of variability among the durum wheat (*T. durum* Desf.) accessions and between quantitative morphological and agronomical traits analysed. Highly significant variation was found in all quantitative traits, except for TC, SpL, NSeSpk and SG not significant at the probability $P_{0.05}$. Highly significant variances among agronomical traits as PH, SD, NSpkSp and NSeSp were found. The high amount of variability found in the present study suggests the Albanian durum wheat (*T. durum* Desf.) germplasm has considerable level of variance available to the breeders and it must be considered sufficient for the creation of new favourable gene combinations. Study results (Table 1) in concordance with [2, 21, 1, 24, 9, 10, 17, 22] suggest that possible parental lines among the durum wheat accessions analyzed can be selected and utilised for sustainable field durum wheat breeding programs.

Relationships between durum wheat accessions assessed by morphological data and genetic similarity/distances revealed by cluster analyses (Euclidean distances) ranged durum wheat accessions into the four different cluster groups. Analysing the number of cases in each cluster group, results that the first cluster group include 44 durum wheat accessions, the second and the third cluster groups includes each respectively 22 durum wheat accessions and the fourth cluster group cluster group includes only 12 durum wheat accessions. Cluster

analysis identified the most number of durum wheat accessions (44 accessions) with similarity between them were included in the first cluster group. The contribution of all these durum wheat accessions on the total variance was found less in comparison with the contribution of durum wheat accessions of the other groups.

Similarity among some of the durum wheat accessions found in each cluster group could be explained by common parent origin in their pedigree [16, 10]. The higher estimated genetic distance found

especially among durum wheat accessions included in the first and the second cluster groups (distance = **13.87055825**, AGB0122 leader and AGB0162 joiner), could be ascribed to differences between durum wheat accessions of different genotypes that can be utilized for genetic improvement without losing genetic diversity in durum wheat germplasm. Clusters were differentiated especially by PH, NSpkSp, NSeSp, GSpk, SpkF and FM agronomical traits significant at the probability $F < P_{0.01}$.

Table1: ANOVA analysis of 15 quantitative agro-morphological traits of durum wheat germplasm stored in Albanian genebank

Traits	Descriptive Statistics		Cluster		Error		F	Sig.
	Mean	Std. Deviation	Mean Square	df	Mean Square	df		
TC	2.5793	.68549	.649	5	.460	93	1.411	.228
PH	98.2232**	8.43703	608.749	5	42.282	93	14.397	.000
SpL	7.1686	1.34925	3.456	5	1.733	93	1.995	.087
SD	20.6152**	2.35958	27.805	5	4.372	93	6.360	.000
NSpkSp	20.5838**	2.35392	29.789	5	4.237	93	7.030	.000
NSeSpk	3.0747	.32618	.216	5	.101	93	2.145	.067
NSeSp	47.2596**	10.12827	1392.228	5	33.246	93	41.877	.000
SeS	6.3679*	1.35095	4.291	5	1.693	93	2.535	.034
WSeSp	2.3620**	1.61979	7.799	5	2.345	93	3.325	.008
SG	19.5152	1.31214	2.686	5	1.670	93	1.608	.166
GSpk	145.0606**	7.27425	742.789	5	15.825	93	46.939	.000
SpkF	4.6566**	1.15318	6.204	5	1.068	93	5.811	.000
FM	47.3333**	7.15855	592.048	5	22.169	93	26.706	.000
GM	197.3131**	4.31099	160.081	5	10.977	93	14.583	.000
DM	216.8283**	4.54016	164.677	5	12.868	93	12.798	.000

F – F-ratio; Sig.- significance level (*) equal to the 0.05 and (**) equal to the 0.01 of probability. df- degree of freedom.

Principal components analysis (PCA) on correlations of quantitative morphological and agronomical traits identified the variances of the principal components (PC) and the proportion of the total variance accounted for by each factor. Comparing the eigenvalues for each factor using the minimum eigenvalue criterion [14], five PC with eigenvalues > 1.00 were maintained for further analysis. The sixth PC component that account for 6.2% on the total variance, is not retained in analysis (**Table 2**).

The maximum information for analysis of the relationships among durum wheat accession and

morphological traits was received using ordination methods (principal coordinate's analysis) in combination with cluster analyses [13] (PCA on correlations identified the total variance of the principal components (PC) and the proportion of the

variances explained by each factor. All quantitative variables contribute to 100% of total variation. The first five PCs explain 67.61% > 65.0% and about equal to 70% of the total variation, acceptable for evaluation and characterization of ex situ collections in genebank [3, 13]

Table 2. Eigenvalues matrix of principal components analysed (100 durum wheat accessions and 15 quantitative morphological and agronomical characters).

Principal Components/factor analysis						
PC No.	Eigenvalue	Percent variance	Cumulative Percent	²	DF	Prob. > ²
1	3.4806	23.204	23.204	684.051	104.243	<.0001**
2	2.4445	16.297	39.501	541.962	95.700	<.0001**
3	1.6557	11.038	50.539	441.767	85.721	<.0001**
4	1.3350	8.900	59.439	384.489	74.884	<.0001**
5	1.2256	8.171	67.610	340.479	64.264	<.0001**
6	0.9293	6.195	73.805	292.985	54.292	<.0001**

² – Chi Square, DF – degree of freedom; Prob. – probability; **significance level 0.01 of probability

Factorial analysis indicates that the contribution of each durum wheat accession and of each quantitative agronomical trait on the total of variation is not equal. Dimensional scaling of relationships (accession x quantitative traits) that accounts for the larger proportion of the total variance in PC1, PC2, PC3, PC4 and PC5 revealed by PCA identified highest weighting (PC1 = 23.2%) of total variation was explained by 22 durum wheat accessions (**Figure 1**).

The higher level of variation showed by durum wheat accessions (Cluster II, III and IV), can

be explained by the low breeding works used in these accessions groups. Some of these durum wheat genotypes could have interest as possible reserve of desirable traits (genes) for breeding schemes. The lowest weighting of total variation was showed by durum wheat accessions included in the first cluster groups (44 durum wheat accessions). These accessions showing low level of genetic diversity were more uniform. Uniformity of these accession could be ascribed to possible their inclusion in modern breeding programs that usually result in low level of genetic diversity.

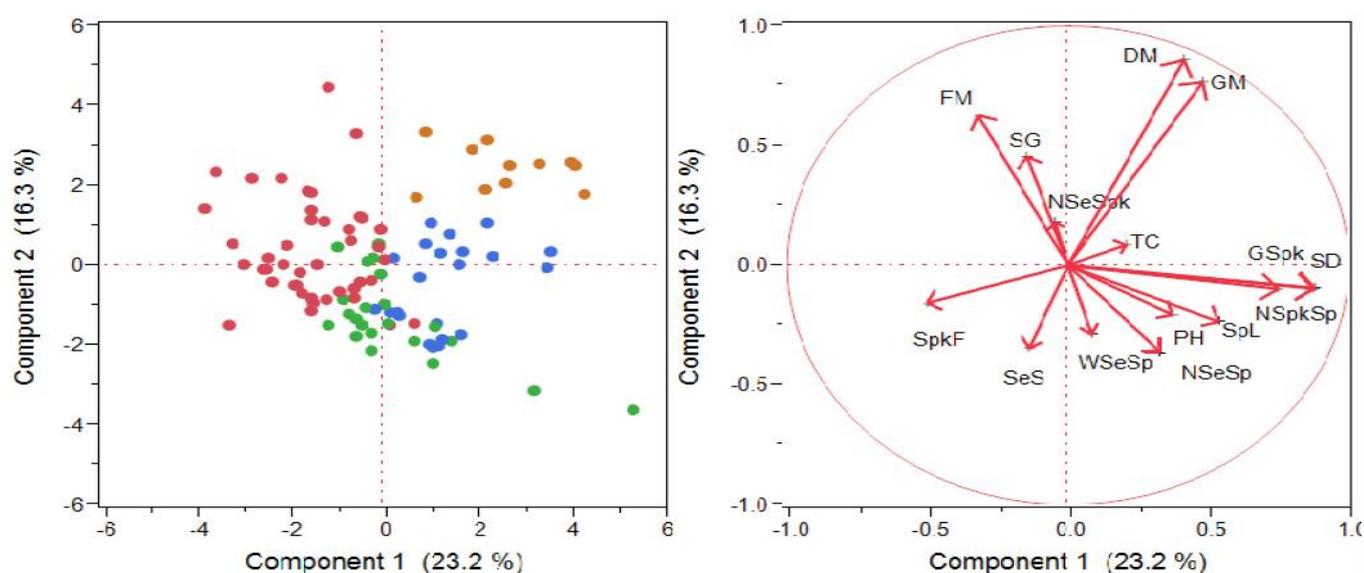


Figure 1. Relationships among the 100 durum wheat accessions based on quantitative agronomical traits revealed by principal component analyses

Factorial analysis and dimensional scaling for relationships among the quantitative agronomical

characters, showed the first component (PC1) explained 23.2% of the variation and was positively

related to the **six quantitative** agronomical traits (PH, SpL, SD, NSpkSp, GSpk and GM) with eigenvalues more than 0.25 and a coefficient of correlation (r) that range from 0.308 to 0.521. Four variables (PH, SD, NSpkSp and GSpk) positively correlated (coefficient of correlation (r) range from 0.480 to 0.932) with nearly the same value of eigenvectors, were the same important to the PC1.

The second component (PC2) explained 16.3% of the variation and was positively related to SG, FM, GM and DM traits. The correlations among these traits range from 0.277 to 0.96. Variables as FM,

GM and DM were the same important to the PC2. In this study trait GM of PC2 account for the rest amount of variance on PC1. The third component (PC3) was positively related to SpL, SeS, WSeSp, SpkF and FM traits (**Table 3, Figure 1**). The fourth and the fifth components (PC4 and PC5) contribute nearly the same variance to the total of variance (respectively 8.9% and 8.2%). There were four quantitative traits that contribute on the variance of the PC4 (TC, NSeSp, WSeSp and SG), and only one trait NSeSpk was the most important for the variance of PC5.

Table 3. Eigenvector values for three principal components of 10 quantitative traits in durum wheat.

Morphological Characters	Eigenvectors				
	PC1	PC2	PC3	PC4	PC5
TC	0.10960	0.05400	0.14562	0.30270	-0.46081
PH	0.39906	-0.13205	0.25901	-0.36927	-0.35205
SpL	0.28785	-0.15110	0.34454	-0.10185	0.20319
SD	0.46926	-0.06206	0.07573	0.01773	0.18313
NSpkSp	0.47127	-0.06092	0.07603	0.02378	0.19938
NSeSpk	-0.02474	0.11414	-0.02286	0.23942	0.68100
NSeSp	0.17612	-0.23250	0.07397	0.54829	-0.09152
SeS	-0.07405	-0.22296	0.40494	-0.03731	0.09075
WSeSp	0.04536	-0.18514	0.31663	0.42614	-0.13999
SG	-0.07839	0.28929	-0.18187	0.35367	-0.14969
GSpk	0.40077	-0.06293	-0.38512	-0.12231	-0.08610
SpkF	-0.26901	-0.10087	0.28666	-0.23921	0.00171
FM	-0.17219	0.40123	0.46326	0.07753	0.09543
GM	0.25722	0.48902	0.15522	-0.12729	-0.04816
DM	0.22158	0.54794	0.09482	-0.01865	-0.08899

(In bold eigenvectors > 0.25).

Good understanding of the most important quantitative agronomical traits in durum wheat can facilitate identification of any individual accession and selection of desirable traits (genes), increasing the information and the representativeness of the wheat germplasm¹⁵ in genebank. The traits with more significant weighting on respective PC variance can be utilised successfully as quantitative markers for evaluation, characterization and classification of the wheat germplasm [21, 17, 10] stored in genebank, and in plant breeding programs [24, 23, 8]. Assessment of the genetic diversity, identification of differences/distances among durum wheat genotypes (where some possible genotypes can be selected as

parental lines) and characteristics with potential for future genetic programs within the Albanian genebank durum wheat collection, can be considered as a useful step for sustainable wheat breeding in Albania.

Conclusions

- The field trials accomplished in this study permitted the assessment of the most important agronomical traits and determined the patterns of variation of Albanian durum wheat germplasm with potential for sustainable their future breeding programs.
- PCA results showed the first five PCs account for a substantial proportion of total variation, 67.61%.

The percentages of total variation accounted for by each of the first three PCs were 23.2%, 16.3% and 11.04%, respectively. Cluster analysis clearly ranged durum wheat accessions with similarity between them into the four different cluster groups, and allowed the identification of wheat accessions with large variability.

- The study identified the agronomical traits with more significant weighting on PC variance (PH, SpL, SD, NSpkSp, GSpk and GM) significant at the probability $F < P_{0.01}$.
- The significant differences found in the present study show the existence of a high genetic variability among the durum wheat genotypes and quantitative traits analysed, sufficient for selection of desirable traits, and creation of new favourable gene combinations. Possible parental lines among these durum wheat genotypes could be selected and utilised for sustainable field grass pea breeding programs

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