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Diversity of Durum Wheat Genotypes of Albanian Gene Bank Collection

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Abstract

Wheat is a major cereal and is grown under a wide range of environmental conditions in the world. Currently, the Genetic Bank has 300 over wheat accessions. There is also missing the data of characterization and evaluation of accessions of wheat which are necessary for base collection or long-term storage. Our study is based on the characterization of the diversity of durum wheat (*Triticum durum* Desf.). The plant material is characterized by a survey field trial and laboratory. Analysis of variance (ANOVA) was performed to calculate the variance among the wheat accessions at a level of significance $p \leq 0.05$.The purpose of this work was to study the genetic variability durum wheat lines by analyzing 15 agronomic quantitative traits. Significant differences were found among the morphological traits. The ANOVA analysis showed significant differences at $p \leq 0.05$ and the PCA revealed which of this traits. The variability found in this durum wheat could be used to select preferable traits for crosses in the improvement genetic programs. Especially the genotypes from cluster I in HCA analysis: AGB0314, AGB0317, AGB0318 and AGB0319 might have a very interesting genetic pool.

Key-words: genetic variability, characterization, quantitative traits

1. Introduction

Durum wheat (*Triticum durum* Desf.) is an important food crop of the world, with an estimated 36 million of annual global production [2]. A very large amount of genetic diversity exists for this crop and that diversity also extends to the many traditional ways of consuming it, including several unique dishes that represent with pride the national identities: pasta, couscous, bulgur, freekeh, gofio and unleavened breads, just to name a few [5]. Wheat grain is a staple food used to make flour for leavened, flat and steamed breads, biscuits, cookies, breakfast cereal, pasta, noodles, and bio-fuel [20]. It only has minor importance on the global wheat market (about 5%) compared to bread wheat [7]. Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance, genetic and environmental factors that influence their expression [13, 16].

Morphological and agronomic characters of wheat have a special role in determining the importance of each trait in increasing yield, so these traits are used in breeding programs, which at least lead to improving yield and introducing commercial varieties [14].

The Food and Agriculture Organization estimates that until the year 2050 the world's population reaches 9.1 billion. In order to feed this more urban population, food production must increase by 70% [6]. The Food and Agriculture Organization estimates that until the year 2050 the world's population reaches 9.1 billion. In order to feed this more urban population, food production must increase by 70% [6]. Durum wheat is the main cereal crop in the Mediterranean regions and it is mainly used in pasta production. The color of pasta products is the result of the natural carotenoid pigments present in the semolina, of their residual content after storage and milling [18,12]. Several studies [17,10,13] have shown that environmental conditions have a significant influence on the quality of wheat, particularly the protein content and gluten

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index. The study of the variation presence in the collections of durum wheat cultivars is carried out using morphologic characterization [3, 8]. The investigation of morphological traits is very significant to evaluate different components, production elements, extension of the vegetative period of durum wheat germplasm [19]. In Albania in 1950, about 60 names of wheat of different origins were planted [15]. Some cultivars of traditional durum wheat are cultivated in the mountainous are soft which were distinguished for tolerance to cold [4]. Differences among lines in terms of phonological extension are minor and major, in meantime for plant and spike characteristics are major[9]. Albania has very good condition for cultivation of durum wheat (*Triticum durum* Desf.). The characterization and the evaluation of crop varieties allow us to protect and restore this genetic heritage to be used at the end in breeding programs [1]. The Knowledge of any existent link between the grain yield and its component can be useful to identify interesting traits for selection. This information is used to guide the selection process to promote the features able of generating improved performance [11].

In this context our study aimed to evaluate thirty of durum wheat lines, based on agro- morphological characters to identify the most relevant characteristics for choosing the more efficient and adapted genotypes.

2. Materials and methods

Plant material used for our study consists of 30 durum wheat accessions genotypes of local origin conserved at Gene Bank (*Triticum durum*. Desf) (Tab.1). The assay was conducted during the 2016-2017 season in Agriculture University of Tirana, in Experimental Station of Institute of Plant Genetic Resources, located at an altitude of 40 m above sea level and at Latitude 41°24'6.14"N and Longitude 19°44'9.93"E.

Our study is based on the characterization of the diversity of durum wheat (*Triticum durum*.Desf). The plant material is characterized by a survey field trial and testing. Each accession was planted in 1 m long plot with a between-row spacing of 25 cm and with in a row spacing 10 cm.

Measured parameters

Phonological observations were held throughout the vegetative cycle of the wheat (seedling to maturity) for 15 morphological traits. The traits studied were: Tillring Capacity (TC), Plant Height (PH), Spike Length (SL),Density of Spike (DS), Needles (N), Glume Color (GC), Glume hairiness (GH), Number of spikelet per spike (NSpkSp), Number of seed per spike (NSeSp), Seed Color (SeC), Seed Size (SeS), Crystallinity, Weight of seeds per spike (WSeSp),1000 Seeds Weight (1000W), Number of seeds per spike (No.SeSp). Frequency distributions for all the morphological traits were computed for drawing necessary conclusions.

Statistical analyses

Statistical analysis was carried out using the Statistical Package for the Social Sciences (SPSS). Analysis of variance (ANOVA) was performed to calculate the variance among the wheat accessions at a level of significance $p \leq 0.05$. Hierarchical cluster analysis (HCA) was used to group the accessions based on the similarities showed by the quantitative traits. Principal components analysis (PCA) as well as K-mean cluster was carried out to see how the data correlate.

Table.1 The list of durum wheat accessions

Nr	*Code of AGB*	*Species*	*Nr*	*Code of AGB*	*Species*	*Nr*	*Code of AGB*	*Species*
1	AGB0314	T. durum	11	AGB0479	T. durum	21	AGB0489	T. durum
2	AGB0315	T. durum	12	AGB0480	T. durum	22	AGB0490	T. durum
3	AGB0316	T. durum	13	AGB0481	T. durum	23	AGB0491	T. durum
4	AGB0317	T. durum	14	AGB0482	T. durum	24	AGB0492	T. durum
5	AGB0318	T. durum	15	AGB0483	T. durum	25	AGB0493	T. durum
6	AGB0319	T. durum	16	AGB0484	T. durum	26	AGB0494	T. durum
7	AGB0320	T. durum	17	AGB0485	T. durum	27	AGB0495	T. durum
8	AGB0476	T. durum	18	AGB0486	T. durum	28	AGB0496	T. durum
9	AGB0477	T. durum	19	AGB0487	T. durum	29	AGB0497	T. durum
10	AGB0478	T. durum	20	AGB0488	T. durum	30	AGB0498	T. durum

AGB = Albanian Gene Bank

3. Results and Discussions

The quantitative traits measured for each one of the durum lines were statistically evaluated and the results are shown by the descriptive statistics in **Tab.2**. Correlation coefficient matrix has also been generated in order to identify the interrelationships between the parameters **(Tab.3).** Strong positive correlation are observed (r=0.72) between the number of seeds per spike (No.SeSp) and the Weight of seeds per spike (WSeSp). Positive high correlation are also observed between Spike Length (SL) and plant height (PH) (r=0.6), spike length (SL) and tillring capacity (TC) (r=0.7) and glume color (GC) and plant height (PH) with an r coefficient of 0.62.

Descriptive Statistics

Table 2 Descriptive statistics of the quantitative agronomical traits

	N	*Minimum*	*Maximum*	*Mean*	*Std. Deviation*
TC	30	2,00	3,50	2,5967	,40555
PH	30	82,00	159,00	111,6200	25,09735
SL	30	5,50	12,40	8,1133	1,82219
DS	30	13,80	23,80	19,2533	2,41028
N	30	1,00	9,00	7,4667	2,81294
GC	30	1,00	3,00	1,8000	,99655
GH	30	,00	5,00	3,3333	1,26854
NSpkSp	30	13,80	23,80	19,2533	2,41028
NSeSp	30	2,00	4,00	2,9300	,70718
SeC	30	1,00	5,00	1,8667	1,04166
SeS	30	3,66	6,55	5,3523	,99707
Qelquriteti	30	3,00	7,00	5,1217	1,63761
WSeSp	30	,98	4,14	2,5427	,77007
SW	30	34,60	71,50	57,3067	10,25004
No.SeSp	30	17,00	60,40	41,2900	8,81153
Valid N (listwise)	30				

Table 3. Correlation matrix between the variables

	Correlation														
	TC	PH	SL	DS	N	GC	GH	NSpkSp	NSeSp	SeC	SeS	Qelquriteti	WSeSp	SW	No.SeSp
TC	1,000	0,512	0,698	0,369	0,231	0,280	0,418	0,369	-0,446	0,015	0,190	-0,184	0,269	-0,009	0,139
PH	0,512	1,000	0,604	0,371	0,220	0,619	0,437	0,371	-0,435	0,244	-0,047	-0,014	-0,066	-0,172	-0,228
SL	0,698	0,604	1,000	0,565	-0,086	0,212	0,203	0,565	-0,294	0,012	0,056	-0,208	0,041	-0,252	-0,030
DS	0,369	0,371	0,565	1,000	0,230	0,292	0,183	1,000	-0,218	0,272	0,292	0,130	0,323	0,110	0,255
N	0,231	0,220	-0,086	0,230	1,000	0,207	0,341	0,230	0,017	0,116	0,355	0,590	0,255	0,591	0,402
GC	0,280	0,619	0,212	0,292	0,207	1,000	0,546	0,292	-0,280	0,173	0,000	0,065	-0,100	-0,093	-0,141
GH	0,418	0,437	0,203	0,183	0,341	0,546	1,000	0,183	-0,104	0,296	0,120	0,124	-0,055	0,108	0,154
NSpkSp	0,369	0,371	0,565	1,000	0,230	0,292	0,183	1,000	-0,218	0,272	0,292	0,130	0,323	0,110	0,255
NSeSp	-0,446	-0,435	-0,294	-0,218	0,017	-0,280	-0,104	-0,218	1,000	-0,308	0,303	0,393	-0,067	0,258	0,205
SeC	0,015	0,244	0,012	0,272	0,116	0,173	0,296	0,272	-0,308	1,000	-0,237	-0,140	0,125	-0,042	0,146
SeS	0,190	-0,047	0,056	0,292	0,355	0,000	0,120	0,292	0,303	-0,237	1,000	0,334	0,276	0,486	0,321
Qelquriteti	-0,184	-0,014	-0,208	0,130	0,590	0,065	0,124	0,130	0,393	-0,140	0,334	1,000	0,072	0,627	0,260
WSeSp	0,269	-0,066	0,041	0,323	0,255	-0,100	-0,055	0,323	-0,067	0,125	0,276	0,072	1,000	0,515	0,715
SW	-0,009	-0,172	-0,252	0,110	0,591	-0,093	0,108	0,110	0,258	-0,042	0,486	0,627	0,515	1,000	0,453
No.SeSp	0,139	-0,228	-0,030	0,255	0,402	-0,141	0,154	0,255	0,205	0,146	0,321	0,260	0,715	0,453	1,000

Hiarerchical Cluster Analysis (HCA) was performed on the selected 15 measured quantitative traits, to determine the genetic similarities and variability among the genotypes. Elements belonging to the same cluster are likely to have originated from a common genetic source. HCA retains three main clusters for the analyzed parameters. The genotypes which are grouped in a particular cluster share similar characteristics in relation to the investigated traits. The dendrogram in **Fig.1** shows all the durum genotypes grouped in three statistically significant main clusters. Cluster I which group together the genotypes: AGB0314, AGB0317, AGB0318 and AGB0319 are very different from the rest **(Fig.1)**. These lines are very similar to each other indicating probably a common genetic ancestor. These lines also differ a lot from the other lines grouped in cluster II and cluster III. This difference is very interesting meaning that these lines might have a unique genetic pool which can be used in the breeding programs to obtain new line with new important characteristics. Cluster II and cluster III are also significantly different from each other**.**

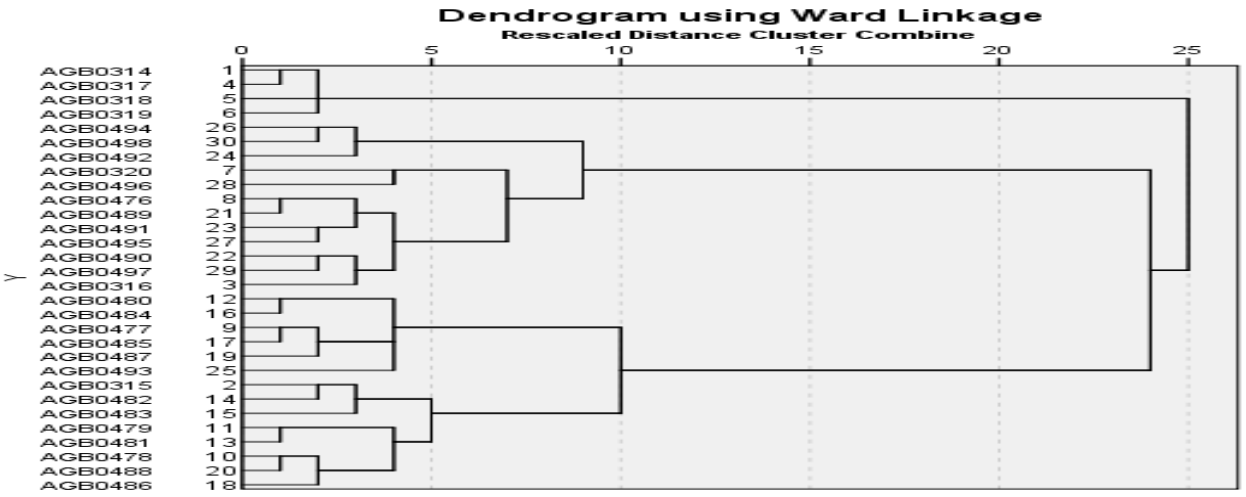

Fig.1. Dendrogram of the 30 T. durum lines

The 15 parameters chosen to be measured and to be analyzed are directly correlated with the grain yield and the information gathered from this study can help to select high yielding genotypes. The analysis of variance ANOVA **(**Tab.4**)** shows a high significant variability among all the variables except for glume hairness (GH) and for seed color (SeC)

Table 4 ANOVA analysis of the variables

	Cluster		*Error*		*F*	*Sig.*
	Mean Square	df	Mean Square	df		
TC	4,815	2	,717	27	6,711	,004
PH	3,326	2	,828	27	4,019	,030
SL	5,292	2	,682	27	7,759	,002
DS	8,554	2	,440	27	19,422	,000
N	6,687	2	,579	27	11,556	,000
GC	3,057	2	,848	27	3,607	,041
GH	1,506	2	,962	27	1,565	,227
NSpkSp	8,554	2	,440	27	19,422	,000
NSeSp	4,814	2	,717	27	6,710	,004
SeC	,859	2	1,010	27	,850	,438
SeS	6,559	2	,588	27	11,151	,000
Qelquriteti	5,425	2	,672	27	8,070	,002
WSeSp	4,904	2	,711	27	6,899	,004
SW	10,127	2	,324	27	31,266	,000
No.SeSp	3,340	2	,827	27	4,041	,029

Principal Component Analysis (PCA) has also been used to determine the interdependence of each trait and to estimate the amount of variation in each parameter explained by the components. Components with eigenvalue > 1 explains more total variation in the data than individual parameter, and components with eigenvalue < 1 explains less total variation. Therefore only components with eigenvalue >1 are retained for the interpretation and the retained factors are subjected to varimax rotation which is an orthogonal rotation method that minimizes the number of variables, retaining only the variables that have high loading on the components. The loading values between 0.50 and 0.75 are considered to be strong and show a high proportion of variance explained by the component. The loading values 0.30 - 0.50 are considered to be weak indicating that most of variance remains unexplained and it is less important. The scree plot **(Fig.2)** has been utilized to distinguish the number of principal components (PC) to be employed to understand and explain the variance between the parameters. The percentage of variance explained the cumulative percentage of variance and the eigenvalues are listed in **Tab.5** As they shows in there are 5 component that have an eigenvalue > 1 and these components explain 78.6 % of the total variance. Anyway, looking at the eigenvalues and the scree plot **(Fig. 2)** we decide to retain only the first two components and these are the principal component 1 (PC1) and the principal component 2 (PC2) **(Tab.5)**. These two components explain a total variance of 50 % which is less but it is easy to read the data due to a higher dimension reduction. In **Tab. 6** are also show the loading scores of each factor. After Varimax rotation only the loadings higher than 0.3 are shown and we can see that the factors PH, SL, TC, DS, NSpkSp have high loading scores on the first component (PC1) which means that these are the factors that better explain the variance among the genotypes for the first component. The factors SW, No.SeSp and N have instead high loading scores on the second principal component (PC2). The loadings of each factor to the two components (PC1) and PC2) are also shown by the scatter plot in **Fig. 3** and we can see how traits like: PH, SL, TC, DS, NSpkSp group together and contribute more to PC1 , instead traits like SW, No.SeSp and N group together and contribute more to the second component PC2.

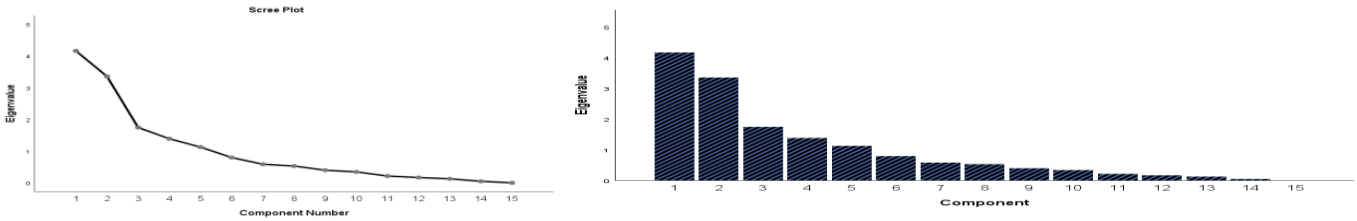

Figure 2. Scree plot

Table 5 Principal Component analysis and Total variance explained

	Eigenvalue	*% of Variance*	*Cumulative %*
1	4,166	27,774	27,774
2	3,357	22,381	50,156
3	1,745	11,633	61,789
4	1,391	9,272	71,061
5	1,128	7,520	78,581
6	,798	5,318	83,898
7	,586	3,907	87,806
8	,530	3,534	91,340
9	,398	2,651	93,991
10	,345	2,301	96,292
11	,215	1,434	97,726
12	,167	1,111	98,837
13	,126	,843	99,680
14	,048	,320	100,000
15	-1,665E-16	-1,110E-15	100,000

Table 6 Factor loadings on the two principal components retained

	Component	
	PC1	PC2
PH	,800	
SL	,766	
TC	,736	
DS	,721	,373
NSpkSp	,721	,373
GC	,607	
NSeSp	-,578	,348
GH	,515	
SeC	,366	
SW		,844
No.SeSp		,733
N		,701
Qelquriteti		,682
SeS		,657
WSeSp		,625

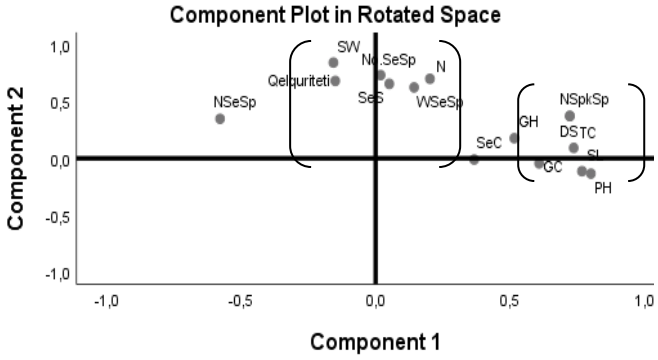

Figure 3 Diagram plots of PC1 and PC2

4. Conclusions

- Study the genetic variability among durum wheat lines by agronomic analyzing quantitative showed significant differences were found among the morphological traits that show a considerable genetic variability.
- The hierarchical cluster analysis grouped the genotypes in three main different clusters. The ANOVA analysis showed significant differences at $p \leq 0.05$ and the PCA revealed.
- The variability found in these Triticum durum, could be used to select preferable traits for crosses in the genetic improvement programs. Especially the genotypes: AGB0314, AGB0317, AGB0318 and AGB0319 might have a very interesting genetic pool.

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