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ESTIMATION OF GENETIC VARIABILITY OF AUTOCHTHONOUS WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES USING MULTIVARIATE ANALYSIS

SUMMARY

This study was conduct to evaluate the morphological variability of 23 autochthonous wheat genotypes (*Triticum aestivum* L.) part of the base collection of the Gene Bank (Agricultural University of Tirana). Crop production is strongly related with genetic diversity within germplasm and its improvement. Various statistical techniques have been used to study diversity among different genotypes. Among these techniques multivariate is most frequently used one for the genetic association of genotypes. Principal components and cluster analysis were carried out involving quantitative traits, such as tiller capacity, plant height, spike length, number of spikelet per spike, number of seeds per spikelet, seed size, weight of seeds per spike and seed yield. According to PCA, three components exhibited about 67.15% of the variability within 23 wheat genotypes. Accessions were grouped into three major clusters based on Euclidean distance, suggesting a variance of 41.72% within classes and 58.28% between classes. Accessions with major level of dissimilarity between them were AGB 3071 (Univers 6) and AGB 3064 (IKBA_05). The results suggested that plant height, spike length, number of spikelet per spike and weight of seeds per spike were the most important characters in differentiating the genotypes. The use of principal component and correlation coefficient analysis in the wheat germplasm, simplify dependable classification of genotypes, the identification of the superior genotypes and their relation with morphological traits with possibility expenditure in breeding programs.

Keywords: cluster, PC, genotypes, morphological, traits, variability

INTRODUCTION

Agriculture in Albania is still a significant sector of the economy which contributes to 22.5% of the country's GDP providing the income base for most of the population and serves as an employment safety net. Wheat and especially

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bread wheat (*Triticum aestivum* L.) is one of the most important cultivated food crops in Albania, with 70 000 ha of cultivated area.

The priority of wheat improving program is to increase grain yield. Any improvement program for increasing yield requires sufficient information on their parental materials in respect of variation for yield and yield contributing characters.

The evaluation of genetic variability based on morphological characters especially those of economic interest might be used to select appropriate materials in breeding programs for crop improvement (Dos Santos *et al.* 2009). Various statistical techniques have been used to study diversity among different genotypes. Among these techniques multivariate is most frequently used one for the genetic association of genotypes (Ali *et al.* 2021).

Quantitative traits are often used to assess and describe the wheat characters due to their role in the estimation of genetic diversity and discrimination of closely related types (Al Khanjari *et al.* 2008). The correlation coefficient analysis is useful in the identification of characters that are positively correlated with yield (Maqbool *et al.* 2010). This analysis is a reliable statistical method, which provides tool to quantify the associations among different traits and indicate whether the influence is reflected in the yield (Sabaghina *et al.* 2014).

The Institute of Plant Genetic Resources (former Albanian Gene Bank) has a total of 270 accessions of bread wheat genotypes (*Triticum aestivum* L.) in long-term storage (https://www.eurisco.ipk-gatersleben.de/apex/). This gene bank has the aim not only to preserve the germplasm but also to make available the plant resources into breeding programs, to improve cultivars or to develop new ones.

Therefore, the characterization of plant germplasm (accessions) maintained in active or base collections in such institutions, and the examination of the genetic relationship between them, is an important tool for the sustainable conservation and certainly to increase use of crop genetic resources. This study seeks to be attached to previous studies conducted by this institution (Bode *et al*. 2012; 2013; 2015; Cakalli *et al.* 2017; Xhulaj *et al.* 2018), on the evaluation and characterization of different plant genetic resources held in conservation, in order to enrich the database (passport data) with additional biological information, essential for sustainable collection management but also for direct use in agriculture.

The object of this study was the assessment of diversity, the evaluation of possible interrelationships among yield contributing traits through characterization of 23 accessions of bread wheat (*Triticum aestivum* L.), will help in selecting the desirable characters and serves as a valuable source for creation of new gene combinations to sustain common wheat future breeding programs.

MATERIAL AND METHODS

The study is based on the characterization of the diversity of bread wheat (*Triticum aestivum* L) germplasm. The plant material is characterized by a survey on land and laboratory, in the experimental field of the Agricultural University of Tirana.

Plant Material: Object of the study, 23 genotypes of bread wheat (*Triticum aestivum* L.), part of the base collection (Table 1, https://www.eurisco.ipk-gatersleben.de/apex/).

Experimental site: The study was conducted at the Experimental Station of Institute of Plant Genetic Resources Valias, Tiranë (altitude of 40 m above sea level and at Latitude 41°24'6.14"N and Longitude 19°44'9.93"E).

Table 1. List of the 23 wheat (*Triticum aestivum* L.) accessions object of the study

Accession code	Accession name	Origin	Acquire date
AGB 0330	-	Albania	2003/01/08
AGB 0331	-	Albania	2003/01/08
AGB 0332	-	Albania	2003/01/08
AGB 0333	-	Albania	2003/01/08
AGB 0334	-	Albania	2003/01/08
AGB 0335	-	Albania	2003/01/08
AGB 0336	-	Albania	2003/01/08
AGB 0337	-	Albania	2003/01/08
AGB 0338	-	Albania	2003/01/08
AGB 0339	-	Albania	2003/01/08
AGB 0340	-	Albania	2003/01/08
AGB 3066	Univers 1	Albania	2010/11/25
AGB 3067	Univers 2	Albania	2010/11/25
AGB 3068	Univers 3	Albania	2010/11/25
AGB 3069	Univers 4	Albania	2010/11/25
AGB 3070	Univers 5	Albania	2010/11/25
AGB 3071	Univers 6	Albania	2010/11/25
AGB 2837	Golia	Albania	2001/06/26
AGB 2838	Agimi	Albania	2001/06/26
AGB 2840		Albania	2001/06/26
AGB 2842		Albania	2001/06/26
AGB 3064	IKBA_05	Albania	2010/11/25
AGB 3065	IKBA_06	Albania	2010/11/25

Methods (Experimental Design): Experiment carried two replication during the autumn season 2017-2018. During the crop year, the accessions were evaluated for different characters of quantitative type as: tiller capacity (TC), plant height/cm (PH), spike length/cm (SL), number of spikelet per spike (NSpkSp), number of seeds per spikelet (NSSpk), number of seeds per spike (NSSp), weight of seeds per spike/g (WSSp), weight of 1000 seeds (W1000S) and seed yield/g (SY). The wheat accessions were also evaluated for qualitative traits as: awnedness, glumes color, glumes hairiness, seed color and seed

virtuousness. Morphological characterization of the accessions was conducted according to international standards (IPGRI, 1985).

Statistical analyses: Statistical tests were carried out by the Statistical Package for Social Sciences (version 21).

RESULTS AND DISCUSSION

The genetic variability among 23 autochthonous wheat genotypes stored in the Gene Bank is assessed using different agronomic traits, especially those related to yield component as plant height, spike length, number of spikes per spike and grain weight. Basic statistic for qualitative traits (Table 2) and quantitative traits (Table 3) were used and the estimated variation coefficient was high for agronomic traits as number of seeds per spike, spike length, weight of seeds per spike and weight of 1000 seeds, similar with others authors (Ali *et al*. 2008; Sabaghina *et al.* 2014). Regarding qualitative traits 47.82% of the bread wheat genotypes presented conspicuous awns (awned), while 26.08% short awns and AGB 3069, AGB 2837, AGB 2838, AGB 3064 and AGB 3065 with no awns. Major part of wheat genotypes 65.21% after transversely section appear partly vitreous while 34.78% of wheat accessions non vitreous (Table 2).

Table 2. Data of qualitative morphological traits of 23 *Triticum aestivum* L. genotypes

Accession code AGB	Awnedness	Glumes color	Glumes hairiness	Seed color	Seed Size	Vitreousness
0330	awned	red to brown	absent	purple	large	partly vitreous
0331	awned	red to brown	absent	red	large	partly vitreous
0332	awned	red to brown	low	red	intermediate	partly vitreous
0333	awned	red to brown	low	red	large	partly vitreous
0334	awned	red to brown	absent	red	large	partly vitreous
0335	awned	white	low	red	large	partly vitreous
0336	awned	white	absent	white	large	partly vitreous
0337	awned	purple to black	high	red	large	non vitreous
0338	awned	red to brown	absent	red	small	partly vitreous
0339	awned	white	absent	red	small	partly vitreous
0340	awned	red to brown	high	red	large	partly vitreous
3066	awn less	red to brown	low	purple	small	non vitreous
3067	awnletted	red to brown	low	purple	small	partly vitreous
3068	awnletted	red to brown	absent	red	intermediate	partly vitreous
3069	awn less	red to brown	absent	red	small	non vitreous
3070	awnletted	red to brown	absent	white	small	partly vitreous
3071	awnletted	red to brown	high	red	intermediate	partly vitreous
2837	awn less	red to brown	absent	red	small	non vitreous
2838	awn less	red to brown	absent	white	small	non vitreous
2840	awnletted	red to brown	low	purple	large	partly vitreous
2842	awnletted	red to brown	low	purple	intermediate	non vitreous
3064	awn less	white	absent	purple	intermediate	non vitreous
3065	awn less	purple to black	low	purple	intermediate	non vitreous

Variability is observed for seed size trait, 34.78% of the genotypes presented small size, 26.08% intermediate size and 39.13% of the wheat genotypes presented large seed size. Wheat grain yield is the result of some important physiological traits occurring in the growth and mostly is determined by the number of spikes, the number of grains and grain weight (Zecevic *et al*. 2010; Sabaghina *et al*. 2014). Results for tiller capacity trait reveal two accessions AGB 0332 and AGB 0334 with the highest value (2.6) while 9 from 23 wheat genotypes presented the same lowest value. AGB 3068 recorded the lowest value for four quantitative traits as tiller capacity, plant height, spike length and number of seeds per spikelet while AGB 2840 the highest value for two traits as, plant height and spike length (14, 72 cm). Results presented for spike length are higher from those reported from other authors (Peltonen *et al*. 2007; Xhulaj *et al*. 2017). Genotype AGB 2838 presented the highest values for number of seeds per spikelet and number of seeds per spike. As previously reported (Sabaghina *et al.* 2014; Xhulaj *et al.* 2020) grain yield is influenced by spike properties and the spikelet number plays a very important role in the wheat grain yield. AGB 0338 recorded the highest value (25.8) and the lowest one at AGB 3064 (16.2).

Table 3. Descriptive statistics of quantitative traits in 23 genotypes of bread wheat (*Triticum aestivum* L.)

Code AGB	TC	PH	SL	NSpkSp	NSSpk	WSSp	W1000S	NSSp
0330	2.3±0.2	93.5±1.7	8.4±0.2	23.8±0.3	3.0±0.1	1.92±0.1	40.0±0.1	54.0±0.5
0331	2.5±0.2	91.7±0.6	8.1±0.1	20.2±0.3	3.0±0.1	2.4±0.1	48.0±0.1	59.8±1.2
0332	2.6±0.1	91.7±0.9	8.4±0.1	19.4±0.4	3.0±0.1	2.66±0.2	50.1±0.5	62.0±1.9
0333	2.0±0.1	97.6±0.7	8.2±0.1	20.8±0.2	3.0±0.1	2.42±0.1	51.0±0.1	48.0±2.3
0334	2.6±0.1	99.8±0.9	9.1±0.2	21.6±0.4	3.0±0.1	2.38±0.1	41.7±0.1	57.0±0.5
0335	2.0±0.1	101.8±0.6	8.3±0.1	23.0±0.1	3.0±0.1	2.62±0.1	57.0±0.1	46.0±0.4
0336	2.5±0.2	99.8±1.4	7.8±0.1	23.6±0.3	3.0±0.2	1.64±0.1	39.6±0.5	41.6±1.0
0337	2.0±0.3	97.5±0.8	8.2±0.2	21.6±0.3	3.0±0.1	2.34±0.5	50.1±0.7	56.0±1.3
0338	2.3±0.2	105.1±1.3	9.4±0.2	25.8±0.3	3.0±0.1	1.44±0.2	39.2±0.1	54.8±1.2
0339	2.2±0.2	99.3±1.2	8.2±0.1	24.6±0.3	3.0±0.2	2.1±0.3	54±0.1	52.8±1.4
0340	2.4±0.2	96.6±1.3	7.8±0.2	21.6±0.3	3.0±0.1	2.74±0.2	50.2±0.3	58.9±1.4
3066	2.0±0.1	101.7±0.6	13.7±0.1	23.4±0.3	2.0±0.1	1.42±0.2	30.1±0.1	38.0±0.8
3067	2.0±0.7	73.5±1.1	11.3±0.2	22.6±0.4	3.0±0.2	1.44±0.1	35.2±0.5	50.0±1.8
3068	2.0±0.1	71.7±0.6	7.1±0.1	20.4±0.3	2.0±0.2	1.96±0.2	34±0.7	55.8±0.1
3069	2.0±0.5	93.5±1.0	9.5±0.1	19.8±0.3	2.0±0.1	1.46±0.1	31.1±0.1	18.6±0.2
3070	2.2±0.2	83.3±0.8	10.9±0.2	22.6±0.5	3.0±0.1	1.84±0.2	41.3±0.7	56.4±1.2
3071	2.0±0.2	73.5±0.8	12.2±0.1	23.2±0.5	3.0±0.1	1.88±0.1	39.1±0.7	69.0±1.5
2837	2.0±0.3	72.5±0.8	8.5±0.2	21.4±0.3	3.0±0.2	2.26±0.2	34±0.5	57.8±1.1
2838	2.4±0.2	88.0±0.8	11.4±0.2	22.2±0.3	4.0±0.4	2.72±0.2	39±1.2	72.4±0.4
2840	2.0±0.8	136.2±2.1	14.7±0.5	18.2±0.3	3.0±0.1	2.0±0.1	45±1.5	48.4±1.2
2842	2.1±0.1	129.3±1.5	12.2±0.4	19.8±0.3	3.0±0.1	2.32±0.3	42.3±0.3	28.4±0.2
3064	2.4±0.2	102.3±0.8	10.2±0.2	16.2±0.3	4.0±0.2	2.61±0.3	47±1.2	66.4±1.8
3065	2.5±0.2	83.5±1.1	10.1±0.2	19.4±0.6	3.0±0.2	2.1±0.2	32±1.3	65.6±1.5
Min.	2.01	71.70	7.10	16.20	2.00	1.42	30.10	18.60
Max.	2.60	136.2	14.72	25.80	4.00	2.74	57.00	72.40
Mean	2.21	94.93	9.73	21.53	2.95	2.11	42.21	52.94
St.deviation	0.22	15.49	1.99	2.151	0.46	0.42	7.482	12.25
CV	0.10	0.16	0.20	0.10	0.15	0.20	0.17	0.23

Three wheat genotypes presented the lowest values measured for number of seeds per spikelet trait (AGB 3066, AGB 3068 and AGB 3069) while two other accessions are similar for the same trait with 4 numbers of seeds per spikelet (AGB 2838 and AGB 3064). High variation is observed between wheat germplasm for weight of seeds per spike from 1.42 at AGB 3066 to 2.74 (AGB 0340). Seed weight parameter also is important in wheat increasing seed germination percent, seedling emergence, tiller capacity, spike density and yield (Bellatreche *et al.* 2017). AGB 3070 recorded the highest value for weight of 1000 seeds (57g). According to Okamoto *et al.* (2013) the grain number and weight as two main components in wheat grain yield are determined at different times of the growing season. This author suggested that seed weight best-explained genotype by environmental interaction for wheat grain yield.

Regarding plant height trait was observed a high variation among 23 wheat germplasm, whereas AGB 3068 recorded the lowest value (71.1cm) and AGB 2840 the highest value (136.2cm). The results are higher from those reported by other authors (Sabaghina *et al.* 2014) for the same trait (54.9 cm to 109.53 cm), whereas Mahmood *et al.* (2006) obtained results ranging from 62 cm to 110 cm, while Aliu *et al.* (2010) reported a range from 71 to 79 cm in different bread wheat genotypes.

Correlation Coefficient Analysis:

To measure the interdependence between a pair of characters, correlation of quantitative morphological traits was calculated by studying the data of 23 bread wheat germplasm (Table 4).

Table 4. Correlation matrix among the morphological traits (Pearson (n))

Variables	TC	PH	SL	NSpkSp	NSSpk	WSSp	W1000S	NSSp	SY
TC	1	0.019	-0.295	-0.105	0.429	0.354	0.139	0.425	0.339
PH	0.019	1	0.368	-0.208	0.111	0.110	0.357	-0.429	0.060
SL	-0.295	0.368	1	-0.144	0.043	-0.304	-0.343	-0.130	-0.293
NSpkSp	-0.105	-0.208	-0.144	1	-0.160	-0.422	-0.047	-0.034	-0.053
NSSpk	0.429	0.111	0.043	-0.160	1	0.573	0.413	0.607	0.319
WSSp	0.354	0.110	-0.304	-0.422	0.573	1	0.656	0.462	0.250
W1000S	0.139	0.357	-0.343	-0.047	0.413	0.656	1	0.180	0.247
NSSp	0.425	-0.429	-0.130	-0.034	0.607	0.462	0.180	1	0.241
SY	0.339	0.060	-0.293	-0.053	0.319	0.250	0.247	0.241	1

Knowledge of correlation is required to obtain the expected response of other traits when selection is applied to the trait of interest in a breeding program (Maqbool *et al.* 2010). Tiller capacity trait exhibited positive significant correlation with number of seeds per spikelet (r=0.429), number of seeds per

spike (r=0.425) and weight of seeds per spike (r=0.354). It presented negative relations with spike length and number of spikelets per spike.

Positive relationship is observed between plant height and traits as spike length (r= 0.368) and weight of 1000 seeds (r=0.357) (Zecevic *et al*. 2004; Bilgin *et al*. 2011). Strong negative correlation is observed among plant height and number of seeds per spike (r=-0.429). Spike length exhibited negative correlation with most of the traits especially with weight of 1000 seeds (r=-0.368). Number of spikelet per spike it is negatively correlated with all of the traits.

At genotypic level number of seed per spikelet possessed positive significant correlation with yield contributing traits as the number of seeds per spike (r=0.607) and weight of seed per spikelet (r=0.573). Strong positive correlation is observed among weight of 1000 seeds and weight of seeds per spike (r=0.656). This trait exhibited negative correlation with spike length (r=-0.343). Number of seeds (grains) per spike is positive related with weight of seeds per spike (r=0.462) but strongly negative related to plant height. Positive relationship is observed among seed yield and two other traits as tiller capacity (r=0.339) and number of seeds per spikelet (r=0.319). Similar results for positive correlations between yield components such as tiller capacity and number of seeds per spikelet's with grain yield are reported from different authors (Desheva *et al*. 2016; Okuyama *et al.* 2004; Zecevic *et al*. 2004; Xhulaj *et al.* 2019).

Principal Component analysis:

Results of PCA suggest that 77.50% of the variability is exhibited among 23 common wheat genotypes by four components (Table 5) where the two first components influenced mostly the variability (F1 34.54% and F2 18.89% Figure 1).

Table 5. Eigen values and % total variance for PCA in 23 accessions of wheat

PCA	F1	F2	F3	F4	F5	F6	F7	F8	F9
Eigen value	3.109	1.700	1.235	0.932	0.884	0.633	0.242	0.165	0.099
Variability (%)	34.54	18.88	13.72	10.35	9.826	7.033	2.694	1.838	1.104
Cumulative %	34.54	53.43	67.15	77.50	87.33	94.36	97.05	98.89	100.00
Eigenvectors									
TC	0.359	-0.137	0.098	0.346	-0.360	0.708	-0.128	-0.023	-0.274
PH	0.022	0.683	-0.185	0.332	0.015	0.193	-0.130	0.012	0.578
SL	-0.222	0.401	0.578	0.259	0.214	-0.135	-0.304	0.144	-0.460
NSpkSp	-0.156	-0.380	-0.310	0.469	0.604	0.132	-0.050	0.362	0.007
NSSpk	0.440	0.096	0.315	0.213	0.305	-0.057	0.738	-0.103	0.027
WSSp	0.479	0.162	-0.034	-0.390	0.047	0.003	-0.091	0.762	-0.034
W1000S	0.370	0.248	-0.454	-0.142	0.389	-0.025	-0.228	-0.448	-0.414
NSSp	0.382	-0.329	0.417	-0.029	0.237	-0.107	-0.507	-0.221	0.445
SY	0.303	-0.072	-0.214	0.514	-0.396	-0.641	-0.098	0.089	-0.090

The variability presence within the first component was related with number of seed per spikelet and weight of seeds per spike traits at the level of 42.26% but poor in plant height. This last trait strongly contributes at the level of 46.61% of the genotypes variability in the second component, but was very poor in number of seeds per spikelet (0.92%). The third principal component exhibited positive effects for spike length trait (33.44%) and number of seeds per spike (17.4%). The seed yield trait was responsible for the variability at the fourth principal component at the level of 26.38%. According to this analyze, the variables that effect most the variability within the forth components are plant height and number of seeds per spikelet.

In addition to cluster analysis, the biplot (genotype by trait) has been applied to study the relation among studied traits in a set of genotypes (Aghaee *et al*. 2010; Peterson *et al*. 2005).
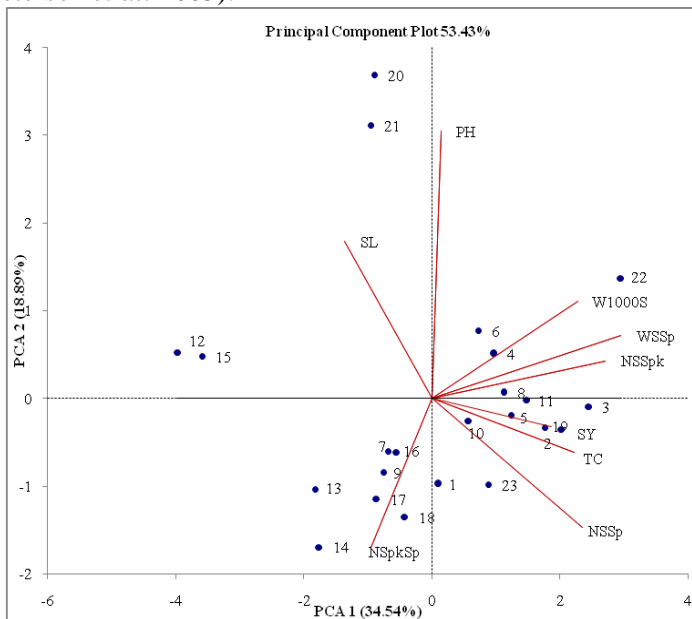

Figure 1. Principal component biplot of 23 wheat (*Triticum aestivum* L.) accessions

The biplot (Figure 1) suggest that the best or the incompatible wheat genotypes in most of the traits, since they had the longest distance from the origin for the two principal components were AGB 2840 (20), AGB 2842 (21), AGB 3064 (22), AGB 0332 (3) and AGB 2838 (19). Therefore it seems that for the first PC wheat genotypes (numbered at Figure 1) AGB 3064 (22), AGB 2838 (19) and AGB 0340 (11) have the highest values mostly for number of seeds per spikelet's, number of seeds per spike and weight of seeds per spike traits, while genotypes as AGB 0332 (3) and AGB 0334 (5), resulted with the highest values basically for tiller capacity trait.

The genotypes that presented not suitable performance for the measured traits within the first component, with lower distance from the origin of the biplot

were AGB 3066 (12), AGB 3069 (15), and AGB 3067 (13). According to the PC analyze the wheat genotypes that presented the highest variability for the traits in the second component were AGB 2840 (20), AGB 2842 (21), AGB 0335 (6) and AGB 0333 (4) basically for plant height and spike length, and the other related cultivars which fall in its sector were suitable for the same traits too. Within this component the group of genotypes AGB 3068 (14), AGB 3071 (17), AGB 2837 (18) and AGB 3065 (23) resulted with the lowest performance for the measured traits (Figure 1).

The vector view of the biplot suggest a strong positive correlation among traits, as indicated by the small obtuse angles between their vectors, especially between tiller capacity of the genotypes and seed yield, number of seeds per spike. Also this positive relation (r=cos 0= +1) is observed through weight of seeds per spike and thousand-seed weight and number of seeds per spikelet. The correlation between traits, plant height and tiller capacity, weight of seeds per spike, seed yield and finally number of seeds per spikelet's, was near zero (r=cos 90= 0) as indicated by the near perpendicular vectors. The existence of a strong negative correlation of the vectors, indicated by the near angle of approximately 180 degrees is observed between NSSP and PH, SL; also among WSSP and NSpkSp. Comparing the Eigen values for each factor using the minimum Eigen value criterion, there are 3 main PC with Eigen values > 1.00 (Table 5 and Figure 1) that influence the genetic variability among 23 wheat genotypes.

The first principal component showed 34.54 % of variability with Eigen value 3.109 in germplasm which then reduced gradually. After the fourth component little variance was observed and it ended at 1.1 % (Eigen value 0.09). From the graph (Figure 1) the maximum variation was present in the first component so the selection of genotypes with desirable traits from this principal component will be useful for further breeding programs.

Cluster analysis:

Genetic diversity among autochthons wheat germplasm was calculated after Agglomerative hierarchical clustering (AHC, Wards method). The tree (Figure 2.) was divided in three major clusters. The first cluster include 11 wheat accessions with AGB 0337 as central observation, basically grouped for similarity in traits as tiller capacity, number of seeds per spikelet, weight of 1000 seeds and plant height but different in number of seeds per spike and weight of seeds per spike. Two most closely wheat genotypes within this cluster are AGB 0337 (observation 8) and AGB 0340 (observation 11 with 3.13 Euclidean distance), fully similar for traits as number of spikelet per spike, number of seeds per spikelet. These two accessions were joined from another sub-cluster formed by AGB 0331 (observation 2) and AGB 0332 (observation 3). The second cluster grouped five accessions with its central observation AGB 3066. These wheat genotypes presented similarity in traits as tiller capacity, weight of seeds per spike and weight of 1000 seeds, but were different in plant height, spike length and number of seeds per spike.
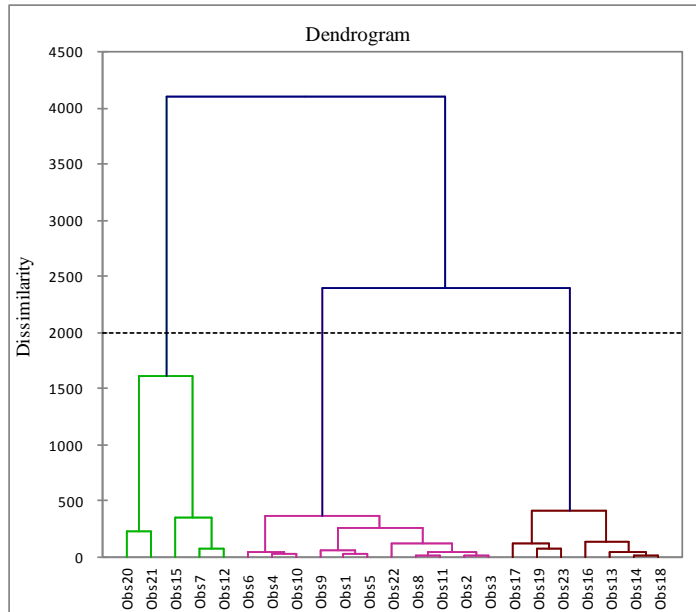
Figure 2. Dendrogram from cluster analysis of 23 bread wheat accessions based on quantitative traits

The third cluster included 7 wheat germplasm that presented similarity for the major part of the quantitative traits but very different for number of seeds per spike. Sub cluster at this group are AGB 2837 (observation 18) and AGB 3068 (observation 14) with the lowest dissimilarity level presented not only in this cluster but among the 23 wheat genotypes. These accessions were mostly similar for traits as tiller capacity, plant weight and weight of 1000 seeds. High dissimilarity level is observed among wheat genotypes part of the second cluster and the third one. The two most different wheat genotypes, with the highest dissimilarity level measured between them are AGB 2842 (observation 21) and AGB 3071 (observation 17). Genetic dissimilarity values of these two accessions basically consists for traits as plant height, number of spikelet per spike, weight of seeds per spike, weight of 1000 seeds and number of seeds per spike. Other pairs of wheat genotypes with high dissimilarity level between them are AGB 2842 (observation 20) with AGB 3071 (observation 17) and with observation 14 (AGB 3068), basically for traits as plant height, spike length, number of spikelet per spike, weight of 1000 seeds and number of seeds per spike. These traits are also responsible for the level of dissimilarity that exist between observation 21 (AGB 2842) of the second cluster and observation 18 (AGB 2837) of the third cluster. The results reveal that the genetic distance that exist between these wheat genotypes is based in yield contributing characters as tiller capacity, weight of 1000 seeds and number of seeds per spike. According to Singh *et al*. (2018) the knowledge of genetic variability for yield contributing components helps in the improvement of grain yield and planning of effective breeding program.

CONCLUSIONS

Results of this study succeed in obtaining important scientific information on autochthonous wheat germplasm stored in the Institute of Plant Genetic Resources, and for further wheat breeding programs. The significant differences found in the present study show the existence of a high genetic variability among the 23 bread wheat genotypes and quantitative traits analyzed, adequate for selection of desirable traits, and creation of new favorable gene combinations. Results for tiller capacity trait reveal two accessions AGB 0332 and AGB 0334 with the highest value. AGB 3068 recorded the lowest value for four quantitave traits as tiller capacity, plant height, spike length and number of seeds per spikelet while AGB 2840 the highest value for two traits plant height and spike length. AGB 2838 presented the highest values for number of seeds per spikelet and number of seeds per spike.

The two most different wheat genotypes, with the highest dissimilarity level measured between them are AGB 2842 (observation 21) and AGB 3071 (observation 17). Genetic dissimilarity values of these two accessions basically consists for traits as plant height, number of spikelet per spike, weight of seeds per spike, weight of 1000 seeds and number of seeds per spike. The results reveal that the genetic distance that exist between these wheat genotypes is based in yield contributing characters as plant height, tiller capacity, thousand-seeds weight and number of seeds per spike.

At genotypic level number of seed per spikelet possessed positive significant correlation with yield contributing traits as the number of seeds per spike (r=0.607) and weight of seed per spikelet (r=0.573). Plant height showed positive significant correlation with traits as spike length (r=0.368) weight of 1000 seeds (r=0.357). Three principal components exhibited about 67.15% of variability where two PCs components influenced mostly the variability (PC1 with 34.54 % and PC2 with 18.88 %). The results suggested that plant height, spike length, number of spikelet per spike were the most important characters in differentiating the genotypes. The use of principal component analysis (showing the largest contributor to the total variance) and correlation coefficient analysis in the wheat germplasm, simplify dependable classification of genotypes, the identification of the superior genotypes (considering the evaluation of mean values) and their relation with morphological traits with possibility expenditure in breeding programs. The traits with more significant weighting on respective PC variance can be utilized successfully as quantitative markers for evaluation, characterization of the wheat germplasm stored in the gene bank.

This paper has been a contribution to increase the knowledge about the wheat germplasm collection maintained in conservation at the Gene Bank (Agriculture University of Tirana). This better understanding should allow a better conservation and use of the collection in future breeding programs. The research will also assist in the conservation of valuable germplasm, as is the case of local varieties, which are widespread use by farmers throughout the entire country.

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