DIVERSITY OF SOME SORGHUM GENOTYPES EVALUATED BY AGRO-BIO-MORPHOLOGICAL TRAITS

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ABSTRACT

The sorghum germplasm stored in Gene Bank has more than 20 genotypes of known or unknown origin and the Sorghum species are a modest valuable group of species used especially for animal production purposes. However, little is known about the extent and nature of the variability of these species. Eight genotypes local forms or cultivars, evaluating 13 quantitative agro-bio-morphological traits, were used for the assessment of genetic diversity of Sorghum genotypes. The study was carried out at the experimental field of Agricultural University of Tirana, Albania and aimed at evaluating the major agro-bio-morphological traits, characterizing the sorghum genotypes, and defining patterns of potential Sorghum forage species using PCA, correlation and cluster methods. Principal Components Analysis (PCA) and cluster analysis identified the variances of the first two principal components (78.9%) and the proportion of the total variance each factor accounts for and range Sorghum genotypes into three different cluster groups. Study analysis identifying quantitative morphological characters with most agronomic interest which account for genetic diversity will facilitate the maintenance and agronomic evaluation of the Sorghum germplasm.

***Keywords**: Sorghum genotypes, principal components, cluster analysis*

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1. INTRODUCTION

Sorghum (*Sorghum ssp.* (L.) Moench.) belongs to the Poaceae family and it is one of the most important cereal crops in the world. There are about 30 *Sorghum* species; *S. bicolor* is cultivated for grain and forage, while *S. halepense* (L.) Pers. (Johnson grass) and *S. propinquum* (Kunth) Hitchc., are cultivated only for forage. Most species are annuals although some are perennial. Sorghum stems may reach over 4 m height, the inflorescence, with small grains of 3–4 mm diameter, varies greatly in size and shape (IBPGR and ICRISAT 1993).

Sorghum is extensively grown in arid and semi-arid tropical and subtropical regions of the world (Doggett, 1988). FAO (2012) stated that the Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth most important cereal crop in the world. Sorghum crop ranks fifth in production after wheat, maize, rice, and barley and has a predominant contribution towards food and fodder security in the arid and semi-arid regions of the world (Chittapur *et. al*., 2015).

Sorghum, considered as an important part of the diet for many of the world's population, is also used as a forage crop (Bioversity 2010) and for industrial purpose (sweet sorghum) to produce sorghum syrup. Cultivated sorghum [*Sorghum bicolor* (L.) Moench] is an annual C4 photosynthetic monocotyledonous plant (Mutegi *et. al.*, 2010), and it will remain a basic staple food for many rural communities.

Sorghum, widely cultivated especially on shallow and heavy clay soils, is extremely drought-tolerant, making it an excellent choice for semi-arid and dry areas. In recent years, there has been a shift in sorghum production from the drier production areas to the wetter areas. This change has resulted in the identification and development of genotypes which are more tolerant to lower temperatures (Bernardo 2010; Alina *et. al*., 2017).

Sorghum yield increase (grain and forage) is of primary interest in food security for an increasing world population, and especially for millions of rural families in the arid and semi-arid areas of the world. Yield depends largely on the ability of plant breeders to increase sorghum grain yield and forage, which depends on several yield components (Gerrano *et al.*, 2014).

Sorghum yield improvement involves the identification and dissection of the most important agronomic yield components (Gixhari, *et. al*., 2014). Akatwijuka *et. al*., (2016) and Ramya *et. al*., (2017) reported that sorghum grain yield has low heritability, so, improvement of yield remains one of the major breeding objectives of many cereal improvement programs. Traditionally, germplasm diversity is evaluated by morphological descriptors (Gixhari *et. al.*, 2013; Gixhari *et. al.*, 2014), which remain the only legitimate

marker types accepted by the International Union for the Protection of New Varieties of Plants (UPOV 2012).
The Albanian germplasm of the sorghum collection is a modest valuable group of forage species for animal production. Despite its economic importance, however, sorghum has not been characterized very well genetically, and little is known about the extent and nature of the variability of these species. Therefore, the information about extent of uses of various gene pools are extremely valuable for the rational planning of the use of germplasm in breeding programs (Gixhari *et. al.*, 2016).
The present study analyses the genetic diversity among sorghum genotypes and investigates the association among the most important morphological characters, to aid in the selection and more efficient use of sorghum germplasm in breeding programs.

2. MATERIALS AND METHODS

Plant material and cultural practices: Eight sorghum genotypes: AGB2642, AGB2647, AGB2650, AGB3077, AGB3078, AGB3097, and two collected genotypes AGB-1 and AGB-2 were investigated.
Cultural practices: Sowing date and growing conditions as the distance between plants in a row and between rows, fertilizer application, number of plants established, plant protection, harvest date etc. were the same for each genotype and consistent with established farming practices of the area and with the variety used.
Agro-morphological characters: Plant height (PH) (cm), Number of internodes (NI), number of leafs (NL), leaf length (LL), leaf width (LW) (cm), panicle (inflorescence) length (PL) (cm), number of plants (NP), field germination (FG) (percentage), days to germination (DG), days to flowering (DF), panicle flowering duration days (PFD), days to maturity (DM), days to harvesting (DH).
The experimental site and field observations: The study for the assessment of sorghum diversity was carried out at the experimental field of Agriculture University of Tirana (latitude: 402405N; longitude: 0194108E; elevation: 40 m) during two growing seasons (2017, 2018).
Field observations: The descriptors used for evaluation of sorghum species include quantitative and qualitative (or coded) plant characters or descriptors) (IBPGR and ICRISAT. 1993). Field observations and evaluation of qualitative traits were realized on 25 plants of each plot.
Statistical Analysis: The differences between sorghum genotypes for the mean values of the bio-morphological quantitative characters observed and evaluated were carried out using ANOVA analysis. Identification of sorghum genotypes of relatively similar characteristics or genetic distances and identification of the most important agro bio-morphological characters that influence highly on the total variation, was realized using Principal Components Analysis (PCA) on correlation and cluster analysis methods. All statistics data for bio-morphological characters were calculated employing the SAS JMP Statistical Discovery (2012), and a dendrogram (ward method) and two-dimensional relationship diagram (sorghum genotypes x morphological characters) were carried out.

3. RESULTS AND DISCUSSIONS

Analysis of morphological quantitative characters: ANOVA analysis found the presence of significant differences between sorghum genotypes for the most of bio-morphological characters at the probability $P_{0.05}$. High degree of variation was observed for DM, DH, PF, DF, LW, DG, NP and FG characters. Moderate differences were found for LL and PH characters, and no significant differences, at the probability $P_{0.05}$, for NL, NI and PL characters.
Principal Components Analysis: Principal Components Analysis on Correlations identified the variances of the principal components and the proportion of the total variance each factor accounts for. Eigenvalues and percent of variances each factor accounts for are in table 1 reported. Based on the mineigen criterion (Kaiser 1960) three principal components that account for 93.38% of the total variation are retained for further analysis. PCA results show that the major sources of variation in the measurements are given by the first two PCs. All quantitative variables contribute to 100% of total variation.
The percentages of total variation accounted for by each of the first three PCs are 49.2%; 29.7% and 14.4% respectively (Table 1). The first three PCs explain 93.38% of the original variation, and the

variation > 80.0% is acceptable for characterization and evaluation of plant collections in a Gene Bank (Jolliffe 2002).

Table 1. Eigenvalues matrix of principal components (8 sorghum genotypes x 13 agro-morphological characters)

Principal Components/factor analysis						
PC No.	Eigenvalue	Percent variance	Cumulative Percent	χ^2	df	Prob. > χ^2
1	6.4025	**49.2**	**49.2**	319.781	76.698	<.0001*
2	3.8647	**29.7**	**78.9**	233.008	75.169	<.0001*
3	1.8723	14.4	**93.381**	151.131	69.270	<.0001*
4	0.3998	3.076	96.457	76.809	60.179	0.0729

χ^2 – Chi Square, df – degree of freedom; Prob. – probability; *significance level equal to the 0.05 of probability

The maximum information from agro-morphological data was received using ordination methods in combination with cluster analyses (Jolliffe 2002). Dimensional scaling of relationships (sorghum genotypes x bio-morphological characters) that accounts for the larger proportion of the total variance in PC1, PC2 and PC3 revealed by PCA indicate that the contribution of each sorghum genotypes and of each quantitative agro-morphological character on the total of variation was found inequal.

There were five sorghum genotypes included in PC1 and PC2 (AGB2647, AGB2650, AGB3097, AGB-1 and AGB-2) that account for 78.9% of total variation, and three sorghum genotypes in PC3 (AGB2642, AGB3077 and AGB3078) which contribute with only 14.4% on the total variation (Table 1; Figure 1).

For PC1 (with 49.2% contribute on the total variation) characters as DM, DH, PF, DF, LW and DG were the most important source for the variation of PC1 (Figure 1). Four agro-morphological characters (PF, DF, LW and DG) with nearly the same value of eigenvectors are the same important to the PC1 (Table 2, Figure 1). The characters as FG, NP and PH showed important negative influence on the PC1 variance (Figure 1).

Variation in Component two (PC2 = 29.7% of total variation) was mainly result of differences in LL, NI and NL bio-morphological characters. Characters as DG, DF, DH and PH account for nearly the same amount of variance on PC2. The characters PL showed important negative influence on the PC2 variance (Table 2, Figure 1).

For PC3 (with only 14.4% contribute on the total variation) characters as DH, NL and NI were the most important source for the variation on the PC3 variance. The characters as PF and PH showed important negative influence on the PC3 variance (Table 2, Figure 1).

Table 2. Matrix of vectors of three PC for 8 sorghum genotypes x 13 agro-morphological characters

No	Agro bio-morphological characters		PC1	PC2	PC3
1	Plant height	PH	-0.27410	0.28535	0.27098
2	Number of internodes	NI	-0.16944	**0.34332**	**0.39076**
3	Number of leafs	NL	-0.17050	**0.34154**	**0.39322**
4	Leaf length	LL	-0.23570	**0.35050**	0.11193
5	Leaf width	LW	**0.31499**	-0.19995	0.24819
6	Panicle length	PL	0.05646	-0.28717	**0.53684**
7	Number of plants	NP	**-0.30998**	0.14928	**-0.34085**
8	Field germination	FG	**-0.31023**	0.14923	**-0.34023**
9	Days to germination	DG	**0.31106**	0.29887	-0.13057
10	Days to flowering	DF	**0.31866**	0.29410	-0.06771
11	Panicle flowering duration	PF	**0.31909**	0.28446	-0.01294
12	Days to maturity	DM	**0.33368**	0.23586	-0.00349
13	Days to harvesting	DH	**0.32454**	0.28607	-0.05638

In bold all eigenvectors > 0.30

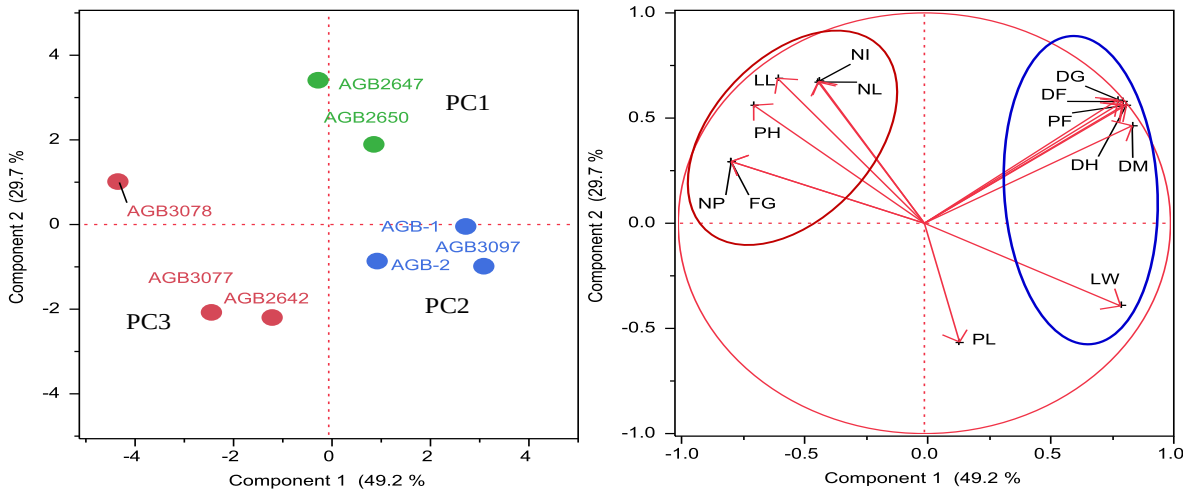


Fig. 1: Relationships among 8 sorghum genotypes based on agro-morphological characters revealed by PCA.

Cluster analysis: Relationships between 8 sorghum genotypes assessed by agro-morphological characters and genetic similarity/distances coefficients revealed by cluster analyses categorized all sorghum genotypes into three clusters (Figure 2).

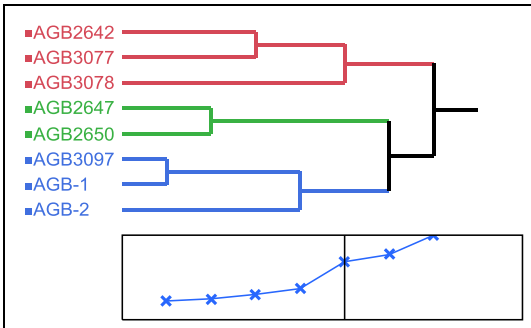
All three clusters were differentiated especially by eight bio-morphological characters of PC1, and three characters of PC2.

The first cluster consists of two sorghum genotypes (AGB2647, AGB2650) and was differentiated by DM, DH, PF, DF, LW and DG agro-bio-morphological characters of PC1. Correlation analysis found strong positive correlation between these characters (r ranges from 0.70 to 0.94). Elangovan *et. al*., (2013) and Verma *et. al*., (2017) reported similar results for the most of these traits.

Only LW character showed negative correlation with all other characters (r ranges from -0.41 to -0.72).

The second cluster includes three sorghum genotypes (AGB3097, AGB-1 and AGB-2) and were differentiated by LL, NI and NL quantitative morphological characters of PC2. These three characters showed strong positive correlation between them (r range from 0.71 to 0.98). Durrishahwar *et. al*., (2012) found low and negative correlation among these traits.

The third cluster includes three sorghum genotypes (AGB2642, AGB3077 and AGB3078) and were differentiated by DH, NL and NI bio-morphological characters of PC3 (Figure 2).



Clustering History			
Clusters	**Distance**	**Leader**	**Joiner**
7	1.367070341	AGB3097	AGB-1
6	1.525840283	AGB2647	AGB2650
5	1.846136138	AGB2642	AGB3077
4	2.265843250	AGB3097	AGB-2
3	4.226051924	AGB2642	AGB3078
2	4.741174084	AGB2647	AGB3097
1	6.158118161	AGB2642	AGB2647

Fig. 2: Dendrogram of relationships among sorghum genotypes and bio-morphological characters.

Highest distance was found between AGB2642 (leader) and AGB2647 (joiner) sorghum genotypes, and low distance (higher similarity) was found among sorghum genotypes as AGB3097 (leader) and AGB-1 (joiner) (Figure 2).

The data about genetic similarity and distances provides a better information on germplasm sampling. Separation of sorghum genotypes into three clusters helps select the parents for crosses and gene introgression from distantly related germplasm. The presence of some interrelationships among quantitative morphological characters of different sorghum genotypes suggests the biological status origin of these sorghum genotypes is their breeding pedigree (Gixhari *et. al*., 2014) or research materials status. No one of these sorghum genotypes fulfil the characteristics of an advanced or improved cultivar.
Study identified the agro bio-morphological characters with more significant weighting on respective PC1 and PC2 variances (DM, DH, PF, DF, LW, DG, LL, NI and NL characters), which can be used successfully as morphological quantitative markers for evaluation and characterization of the sorghum germplasm.
The amount of genetic variability found in the present study, available to the breeders, is sufficiently helpful for the selection of desirable characters. This variability serves as a possible reserve of desirable traits (genes), and it is a valuable source for creation of new favourable gene combinations to sustain field sorghum breeding programs.

4. CONCLUSION

The field evaluation test in the present study addresses the first characterization of sorghum genotypes and the identification of the most important agro-morphological diversity and determination of the patterns of sorghum genotypes with high forage value.
PCA results showed that the first three PCs account for a substantial proportion of total variation, 93.4%. The percentages of total variation accounted for by each of the first three PCs were 49.2%, 29.7% and 14.4%, respectively.
PCA and cluster analysis identified the agro bio-morphological characters with more significant weighting on respective PC1 and PC2 variances (DM, DH, PF, DF, LW, DG, LL, NI and NL characters), which can be used successfully as morphological quantitative markers for evaluation and characterization of the sorghum germplasm.
The amount of genetic variability found in the present study helps sufficiently select the desirable characters and serves as a valuable source for creation of new gene combinations to sustain field sorghum breeding programs.

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