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Genetic diversity of aerial yam /*dioscorea bulbifera* (l.)/ accessions in Ethiopia based on agronomic traits

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Abstract: The experiment was conducted at Jimma Agricultural Research Centre during 2007 cropping season. The objectives of the study were to evaluate the genetic diversity of aerial yam using agronomic traits so as to characterize and cluster with in collected aerial yam genotypes. Forty-seven aerial yam genotypes were sampled from the collection. Relatively high broad sense heritability was observed for Vine dry weight (53.14), tuber diameter (42.54), tuber length (42.04) and vine length (39.69) indicating the existence of possibility for selection of genotypes for high fresh tuber yield. The clustering of genotypes based on 11 quantitative traits revealed the existence of five distinct groups. The maximum inter cluster distance was observed between genotypes under cluster II and V and I (D^2=1844) IV and V (D^2=1702) hence, the genotypes grouped in these clusters could be used for crossing if high fresh tuber yield genotypes are planned in breeding program.

Keywords: Aerial Yam, Dioscorea bulbifera, Genetic Diversity

1. Introduction

Yam is a multi species crop that belongs to the genus Dioscorea and family Dioscoreaceae. It is found in Africa, India, Southeast Asia, Australia and tropical America with about 600 described species [1,2 and 3]. Food yams, which contain about eight species, are cultivated as staples throughout the tropics [1and4].

Dioscorea bulbifera is distinguished from all other species by having specialized aerial bulbils on the base of petioles [5]. To such an extent that tuberization is solely aerial [6].The bulbelates of D. bulbifera have very high dry matter content; the flesh being very firm after cooking. D. bulbifera produces bulbilates 4-6 months after planting [7].In south and south-western parts, there are huge amounts aerial yam genotypes are distributed across diverse agro-geographical areas and that have not been properly evaluated before [8] and their attribute remains unknown by breeders [9]. So, detailed descriptions of genotypes based on agronomical characters have tremendous impact on the conservation, diversity analysis and genetic improvements of the crop [10]. The present study, therefore, intended to evaluate the genetic diversity of aerial yam using agronomic traits so as to characterize and cluster with in collected genotypes for further breeding works.

2. Materials and Methods

2.1. Description of the Study Area

The experiment was conducted at Jimma Agricultural Research Center located at 366 km south west of Addis Ababa. The site is situated at latitude 7o 46' N and longitude 36o E with an altitude of 1753 m.a.s.l.The soil of the study area is Eutric Nitosole with a pH of 5.3. The area receives mean annual rainfall of 1432 mm with maximum and minimum temperature of 29.2 0 C and of 8.90 0 C, respectively. These environmental conditions are conducive for production of Dioscorea bulbifera.

2.2. The Accessions Evaluated

A total of 47 D. bulbifera accessions were considered in this study. The accessions were collected from south and southwestern parts of Ethiopia, during the period 2004-2006 by Jimma and Areka Agricultural Research Centers. The collections covered diverse agro-ecologies with an altitude range of 1375-2500 m.a.s.l, representing one of the major yam production areas in the country.

2.3. Experimental Design and Management

The experiment was laid out in randomized complete block design with three replications, and planting was carried out at the beginning of the rainy season on flat ground.Single row plots, with each row 6m long were used in the experiment. A spacing of 1.5m between rows and 1m between plants within a row was used. The middle four plants of the row were used for data collection and for harvesting. Plants were supported by individual stake of eucalyptus about 3.5-4.00 m above ground to induce good canopy development. One month after planting, after the crop was well established, the plants were earthed up. Cultivation and weeding were carried out when necessary.

2.4. Data Collection

Data were collected on individual and plot bases. Leaf length (cm), leaf width (cm), petiole length (cm), bulbils length (cm), bulbils diameter (cm), vine length (cm), tuber length (cm), tuber diameter (cm) were assessed. Number of bulbils plot, Bulbils fresh weight (t/ha), Bulbils dry weight (t/ha), vine fresh weight (kg), vine dry weight (kg), tuber fresh weight (t/ha) and tuber dry weight (t/ha) were recorded for each plot.

2.5. Statistical Analysis

Heritability in broad sense (h^2B) and genetic advance as percent of means were calculated for all characters according to the method described by [11]. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated according to [12] while the Mahalanobi's generalized distance (D^2) statistics [13] was used for clustering of genotypes by assessing the divergence between genotypes for the traits measured by using SAS software statistical package [14].

Genotypic variance component

$$t^2_g = MS_g - MS_e)/r \quad (1)$$

Where MS_g is genotypic mean square, MS_e is error mean square and r is replication

Environmental variance component (On genotypic mean basis)

$$^2_e = MS_{e/r} \quad (2)$$

Phenotypic variance component

$$^2_p = ^2_g + ^2_e \quad (3)$$

Genotypic and phenotypic coefficients of variation were calculated according to the method suggested [15] as: Genotypic coefficients of variation (GCV)

$$GCV = \frac{\sqrt{^2_g} * 100}{X^-} \quad (4)$$

Phenotypic coefficients of variation (PCV)

$$PCV = \frac{\sqrt{^2_p} * 100}{X^-} \quad (5)$$

Where X^- is the grand mean value of the trait

Broad sense heritability (h^2B) in percents in estimated was estimated in each character using variance components as described by [16].

$$h^2B = \frac{\sigma^2_g}{\sigma^2_p} x\ 100 \quad (6)$$

The expected gain or genetic advance with one cycle of selection, assuming the selection intensity of 5%, was predicted as suggested by [11].

$$G_A = (k)\ (_p)\ (h^2) \quad (7)$$

Genetic advance in percent of the mean (GAM) was calculated to compare the extent of predicted genetic advance of different traits under selection, using the following formula:

$$GAM = (GA / X^{-)}\ x100 \quad (8)$$

Genetic distance between clusters was calculated using the generalized Mahalanobis's D^2 statistics. The D^2 value obtained for pairs of clusters was considered as the calculated value of Chi-squire (χ^2) and was tested for significance at the required level of probability against the tabulated values of χ^2 for p degrees of freedom, where p is the number of characters considered [17and13].SAS software was employed for the analysis.

The D^2 is defined as

$$D^2_{ij} = (X_i - X_j)\ ^1\ S^{-1}\ (X_i - X_j) \quad (9)$$

Where, D^2_{ij}=is the distance between two groups i and j; X_i and X_j are the two vector mean of the traits for i^{th} and j^{th} groups respectively, and S^{-1} is the inverse of the pooled covariance.

3. Results and Discussion

3.1. Genetic Variance

The estimates of genotypic variance, phenotypic variance, broad sense heritability, genetic advance, genetic advance in percent of means, and phenotypic and genotypic coefficients of variations are presented in Table 1. The magnitude of phenotypic variance was higher than genotypic variance as the latter is a component of the former. The phenotypic variance (^2_p) is the sum of environmental variance (^2_e), genetic variance(^2_g) and their interaction ($^2_{ge}$). However, the phenotypic and genotypic variance values can not be used for comparing degrees of variability since different traits have different means across environments. For this reason, the genotypic and phenotypic coefficients of variations were used.

Table 1. *Estimation of means, ranges, variance components, PCV, GCV, broad sense heritability (%) (h^2), genetic advance (GA), and genetic advance as percent of the mean (GA) for 11 traits of 47 aerial yam accessions grown at Jimma, 2008.*

Traits	Mean ± SE	Range	σ2g	σ2p	PCV	GCV	Heritability (%)	Genetic advance	GAM (%)
VL	3.2 ± 0.5	2.3 – 4.2	0.0950	0.244	15.46	9.66	39.69	0.3969	12.42
LL	11.9 ± 1.0	9.5 – 14.0	0.3740	1.1620	9.08	5.15	32.17	0.7145	6.01
LW	10.5 ± 1.6	9.2 – 12.9	0.1900	0.7840	8.30	4.08	24.24	0.4422	4.15
VFW	0.2 ± 0.05	0.1 – 0.3	0.0003	0.0020	26.07	11.18	18.38	0.0193	9.87
VDW	0.12 ± 0.1	0.06 – 0.4	0.0001	0.0020	53.96	12.44	53.14	0.0482	5.90
NoBe	60.5 ± 11.3	43.6 – 99	25.040	128.02	18.69	8.26	19.56	4.560	7.53
BFW	9.5 ± 2.4	4.4 – 14.5	0.0130	0.1280	25.12	8.09	10.36	0.0763	5.36
BL	7.1 ± 0.8	5.3 – 9.0	0.1100	0.3400	7.78	4.43	32.45	0.3900	5.20
TDW	1.5 ± 0.8	0.6 – 4.8	0.0020	0.0090	44.99	22.81	25.70	0.0508	23.83
TL	6.2 ± 0.68	4.6 – 7.9	0.1930	0.4600	10.92	7.08	42.04	0.5875	9.45
TDi	7.2 ± 0.77	5.6 – 9.1	0.2550	0.6000	10.80	7.04	42.54	0.6791	9.46

Comparatively wider differences between genotypic and phenotypic coefficients of variations were observed for traits vine length(m), vine fresh weight(kg/plot), vine dry weight (kg/plot), bulbils fresh weight(t/ha) andtuber dry weight (t/ha)while relatively narrow differences were observed for traits bulbils length (cm), tuber diameter (cm) and tuber length (cm). This implies that, traits showed narrow differences between genotypic coefficients of variation and respective phenotypic coefficients of variations had somewhat low sensitivity to the environmental effects while those with wider differences were affected by environmental factors.

VL= vine length (m); LL=Leaf length(cm); LW= leaf width(cm); VFW= Vine fresh weight (kg/plot); VDW=Vine dry weight(kg/plot); NoBe=number of bulbils per plot; BFW= Bulbils fresh weight(t/ha); BL= Bulbils length(cm); TDW=Tuber dry weight(t/ha); TL=Tuber length(cm) and TDi=Tuber diameter (cm).

3.2. Heritability

Heritability estimates ranged from 10.36% for bulbils fresh weight to 53.14% for vine dry weight (Table 1). Maximum heritability was obtained from vine dry weight per plot followed by tuber diameter and tuber length. Although yield is a complex character liable to have more environmental influence, heritability of vine dry weight kg per plot had maximum in this study. On the other hand, bulbils fresh weight, vine fresh weight and number of bulbils per plot have relatively low heritability estimates (Table 1). On the same analogy, [18] found heritability of 18.22% for tuber yield per plant in potato, which is very low as compared to the heritability obtained in this study even if the crop is different. Genetic advance indicates the degree of gain in a character obtained under a particular selection and helps the breeder to predict the extent of improvement that can be achieved in different characters. High heritability coupled with high genetic advance is an important instrument for ensuing selection of the best individuals and for successful genetic improvement.

Estimates of genetic advance varied from 0.0193 for vine fresh weight (kg/plot) to 0.71 for leaf length (cm) (Table 1). The value of genetic advance as percent of mean varied from 4.15% for leaf width to 23.83% for tuber dry weight. It was observed that fresh bulbils yield with the high heritability (19.56%) had the highest genetic advance (4.56 t/ha) tuber length and diameter showed similar trend in heritability and genetic advance. The genetic advance as percent of mean was also relatively higher for tuber length (9.45%) and diameter (9.46%), and this in line with their respective heritability (Table 1). This is indicated that selection for the traits like for tuber length and diameter is easier than selection for other characters.

High GCV along with high heritability and high genetic advance will provide better information than single parameters alone [19 and 20]. Hence, in this study, tuber dry weight (22.81), vine length (9.66) and vine fresh weight (11.18) exhibited high genotypic coefficients of variation, high heritability together with high genetic advance as percent of means. This indicates that these characters would be very useful as a base for selection in Dioscorea bulbifera improvement.

3.3. Genotype Clustering

In this study, genotypes were grouped into five distinct clusters with different sizes. The clustering patterns of the genotypes based on quantitative characters are presented in Table 2. Cluster means of 11 quantitative traits used for clustering are presented in Table 3. A dendrogram summarizing similarity among 47 genotypes of Dioscorea bulbifera is given in Figure 1.

Table 2. *Distribution of 47 Dioscorea bulbifera accessions into five clusters.*

Clusters	Number of accessions in each cluster	Serial number	Name of accession in each cluster
I	10	44,46,39,2,19,1,15,25,40 ,3	0013/2005, 0015/2005, 008/2005, 036, 103, 016, 030,019, 009/2005 and 12.
II	12	13,18,9,17,16,5,14,47,12,29,43, 30.	078,023,005,040,051,081, 043, 0016/2005, 114, 037, 0012/2005 and 056.

III	19	11,26, 6,21,23,45,8,27,7,31, ,20,36,32,35,4,22 28,24,10	013,047,014,042,049, 0014/2005,069,029,110, 060,034,005/2005, 075, 004/2005, 026, 011, 050,031 and 074.
IV	5	37, 42, 34, 38, 41.	006/2005,0011/2005, 136, 007/2005 and 0010/2005.
V	1	33	077

Table 3. *Cluster means for 11 quantitative traits of Dioscorea bulbifera accessions.*

Clusters	VL	LL	LW	VFW	VDW	NoBe	BFW	BL	TL	TDi	TDW
I	3.23	11.93	10.490.18	0.074	66.55	1.53	4.40	8.80	6.84	0.17	
II	3.06	11.55	10.220.19	0.076	47.33	1.06	4.43	6.44	7.15	0.21	
III	3.18	11.88	10.850.19	0.072	56.88	1.42	3.95	6.31	7.23	0.24	
IV	3.27	12.21	11.060.24	0.089	78.73	1.73	4.53	6.38	7.32	0.21	
V	4.19	12.67	11.600.22	0.35	98.67	2.18	4.55	6.20	7.53	0.26	

VL= Vine length (m); LL=Leaf length (cm); LW= Leaf width (cm); VFW= Vine fresh weight (kg/plot); VDW=Vine dry weight (kg/plot); NoBe=Number of bulbils per plot; BFW= Bulbils fresh weight (t/ha); BL= Bulbils length (cm); TL=Tuber length (cm); TDi=Tuber diameter (cm); TDW=Tuber dry weight (t/ha).

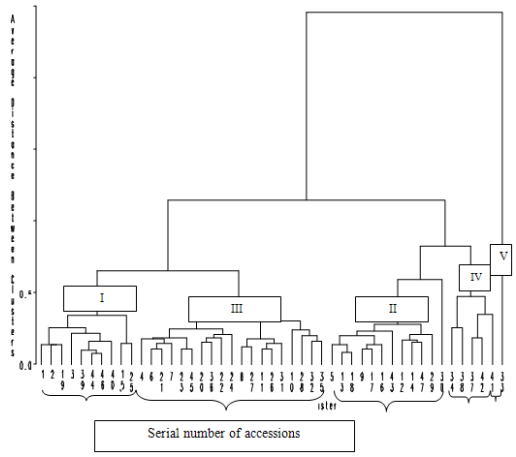

Figure 1. *Dendrogram showing hierarchical clusters of 47 D. bulbifera accessions (UPGMA) based on quantitative characters.*

The clustering pattern indicated that the number of accessions in each cluster varied from one in cluster V to 19 in cluster III. Cluster I, which comprised ten accessions (21.27%) four from Jimma, two accessions each from Gamo-Gofa and Dawro, one accession each from Kefa and Bench-maji zones. Accessions in this cluster were predominantly longer leaf, vine and tuber (Table 3).

Cluster II includes 12 accessions (25.53%), five were from Jimma collection, four from Kefa, two from Gamo-Gofa and one from Illubabor zones. Accessions in this cluster are relatively longer bulbils and higher vine dry weight (Table 3). Cluster V had only one accession (2.13%) originally from Jimma; it was superior in almost all parameters of quantitative traits to other clusters. For example, it has an average of 99 bulbils per plot whereas the cluster with the highest mean next to it has only 78 bulbils in cluster IV. All other clusters have much less number of bulbils (Table 3). Cluster III consisted of maximum number of accessions, accounting for about 40.42% of the total accessions; from this, eleven were from Jimma collection, two accessions each from Bench-maji, Kefa, and Gamo-Gofa respectively, one accession each from Wolaita and Illubabor zones. Accessions in this cluster have maximum tuber dry weight per plot next to cluster V. Similarly, cluster IV includes five members (10.64%) two from Gamo-Gofa, one accession each from Dawro, Bench-maji and Wolaita zones. Accessions falling in this cluster showed higher performance for the majority of the characters of interest (Table 3).

The cluster mean of all characters is presented in (Table 3) showed that genotypes falling in cluster IV and V showed the highest mean performance for most of characters of interest. For example, as tuber fresh weight, tuber diameter, bulbils length, bulbils fresh weight, number of bulbils per plot, vine fresh and dry weight, vine length, leaf length and diameter. In line with this, cluster II, which consisted of 12 genotypes was the higher mean performance of some quantitative characters studied (Table 3). For example, the genotypes grouped under this cluster gave the higher leaf length and width, vine fresh weight and bulbils length. This indicated that different clusters have different breeding values that enable breeders to improve different traits and parental selection should be made based on the relative merits of each cluster for each trait depending on the objective of the breeding program. [21] quoted by [22 and 23] further showed that while selecting genotypes from a particular cluster, the inter cluster distance and cluster mean performance should be taken into consideration.

The pair wise generalized square distances (D2) between the clusters (Table 4) showed that the distance between most of the clusters were highly significant ($P < 0.01$) suggesting diversity among Genotypes in different clusters. The maximum inter-cluster distance (D2 = 1854) was noticed between cluster II and V followed by III and V (D2 = 1702) and I and V (D2 = 1520) suggesting diversity between these groups (Table 4).

Table 4. *Pair wise generalized squared distances between five clusters of D. bulbifera.*

Cluster	I	II	III	IV	V
I	-	68.05**	19.39*	28.83**	1520**
II			17.75	182.82**	1854**
III				92.71**	1702**
IV					1404**
V					

= Significant at 0.05 probability level ($x^2_{10} = 18.31$)= Highly significant at 0.01 probability level ($x^2_{10} = 23.21$).*

Crossing of accessions that have high inter cluster distance is expected to produce more genetic variability and desirable recombinants than those with smaller inter cluster distance. Therefore, crossing of accessions, for

example, crossing accessions from cluster II with that of cluster V, III with V, and II with IV may produce desirable recombinants for high total (bulbils and tuber) fresh yield. On the other hand, crossings between accessions of II with III may not produce desirable recombinants this might be due to low inter cluster distance. Intensive selection for agronomically important characters and similarity in parentage might be the cause of narrow genetic diversity and uniformity between these clusters.

4. Conclusion

In this study there was no clear grouping of the accessions according to regions of collection. Accessions of one region were classified into different clusters although some of them also belonged to the same cluster. Accessions collected from different regions were also grouped into the same cluster.Therefore, it may be of considerable importance to enlarge the genetic base of Dioscorea bulbifera by sustainable and continual collection of accessions throughout the growing areas of the country, conduct genetic improvement work to exploit desirable traits of the accessions.

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