Genetic variability and association among yield and yield related traits in Aerial Yam /*Dioscorea bulbifera* (L.)/ Accessions at South-western Ethiopia

[1]Tewodros Mulualem,
Jimma Agricultural Research Center
P.O. Box 192, Jimma, Ethiopia

Tel: +251-9-11748530 E-mail: tewodros74@yahoo.com

[2] Hussien Mohammed,
[2]Hawassa University, College of Agriculture,
Po. Box 05, Hawassa

Abstract
Genetic variability and heritability analysis of different yield and yield related traits were studied in 47 accessions of Dioscorea bulbifera. The objectives of the study were to estimate the genetic variability and association among yield and yield related traits based on key morphological descriptors. Variance analysis of characters revealed significant differences among the accessions. Genotypic coefficient of variation (GCV %) was found lower than phenotypic coefficient of variation (PCV %) for all characters studied. High genetic advance coupled with heritability was observed in the characters namely; vine length and tuber dry weight per plot. Significant and strong positive correlations to bulbils fresh weight /plot were observed for the characters vine length (r=1.000), leaf length(r=1.000), Leaf width (r=1.000), vine fresh weight (r=1.000) vine dry weight (r=1.000), bulbils length (r=1.000) and bulbils number (r=0.88). Bulbils fresh weight is important agronomic trait induced by many associated traits and thus characters like vine length, leaf length, Leaf width and vine fresh weight should be considered essential parameters for selection aerial yam for further breeding programme.
Key words: Aerial yam, variability, heritability, association.

1. INTRODUCTION

Dioscorea bulbifera (Aerial yam) is a monocotyledonous bulbilate and tuber crop of the *Dioscoreaceae* family and is native to two continents, Africa and Asia including Ethiopia (Miege and Demessew, 1997). Its tuber and bulbils have high nutritional value and were probably the main source of sustenance for the people of Africa and Asia for several decades (Burkill, 1966; Martin, 1976). Today, it is recognized as an important food crop in many parts of the tropical and sub-tropical regions of the world (Purse glove, 1983).

Dioscorea bulbifera (Air potato*)* is the most polymorphic species in the genus *Dioscorea* (Martin and Delpin, 1978). Typically, it is distinguished from all other species in the genus *Dioscorea* by its specialized aerial bulbils on the base of petioles (Marthin, 1974). To such an extent that tuberization is solely aerial. However, much confusion exists among the cultivated varieties (cultivars) of the species (Coursey, D.G. 1967; Onwueme and Ganga, 1996), perhaps due to the presence of hundreds of variants carrying numerous complex characteristics that overlap. Determining the level of variation and identifying the variants within the species is invaluable for genetic improvement and conservation of the crop (Okoli, 1988).

Such information with respect to aerial yam is very scarce and in the present study an attempt was made to estimate the magnitude of genotypic variation, heritability, genetic advance and correlation of yield contributing traits among the collected accessions of yam.

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 7° 46' N and longitude 36° E with an altitude of 1753 m.a.s.l. The soil of the area 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 Plant material

A total of 47 *D. bulbifera* accessions were considered in this study. The accessions were collected from south and south-western parts of Ethiopia. The collection was made in 2006-2008 during the growing season (October to December). 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. The accessions name and area of collections are presented in (Table 1).

Table 3. Accessions of *D.bulbifera* and their areas of collection

Serial number	Name of accession	Area of collection		
		Zone	Wereda	Altitude
1	016	Bench-maji	Bench	1700
2	036	Jimma	Limukosa	1709
3	012	Jimma	Kersa	1460
4	026	Jimma	Seka	1877
5	081	Jimma	Kersa	1700
6	014	Jimma	Seka	1820
7	110	Jimma	Dedo	1957
8	069	Jimma	Setema	2040
9	005	Jimma	Dedo	2147
10	074	Jimma	Sekoru	1880
11	013	Jimma	Kersa	1460
12	114	Kefa	Gimbo	1600
13	078	Jimma	Asendabo	1900
14	043	Jimma	Agaro	1640
15	030	Jimma	Seka	1789
16	051	Kefa	Chena	1910
17	040	Kefa	Gera	1940
18	023	Jimma	Seka	1894
19	103	Kefa	Gimbo	1860
20	034	Jimma	Limukosa	1692
21	042	Kefa	Gimbo	1700
22	011	Bench-maji	Sheko	1460
23	049	Jimma	Seka	1789
24	031	Jimma	Sekacherkosa	1911
25	019	Jimma	Sekacherkosa	1837
26	047	Jimma	Deado	1940
27	029	Bench-maji	Bench	1380
28	050	Kefa	Chena	1920
29	037	Kefa	Decha	1840
30	056	Illubabor	Bedele	1880
31	060	Illubabor	Bedele	1960
32	075	Jimma	Limu	1799
33	077	Jimma	Sekoru	1720

34	136	Bench-maji	Bench	1460
35	004/2005	Wolaita	Humbo	1650
36	005/2005	Gamo-Gofa	Kucha	1860
37	006/2005	Gamo-Gofa	Kucha	1960
38	007/2005	Gamo-Gofa	Kucha	1750
39	008/2005	Dawro	Mareke	1750
40	009/2005	Dawro	Mareke	2500
41	0010/2005	Dawro	Gesachare	1680
42	0011/2005	Wolaita	Humbo	1750
43	0012/2005	Gamo-Gofa	Chancha	1375
44	0013/2005	Gamo-Gofa	Gopzunic	1375
45	0014/2005	Gamo-Gofa	Gopzunic	1400
46	0015/2005	Gamo-Gofa	Gopzunic	1375
47	0016/2005	Gamo-Gofa	Gopzunic	1375

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 Morphological data recording

The morphological data were recorded on the living plants under field conditions by using 11 agro-morphological traits (Table 2). The characters used and methods of data recording were according to the International Plant Genetic Resources Institute's (IPGRI) descriptors for yam (*Dioscorea spp.*) with some modification (IPGRI, 1997). Only those that discriminated between our samples were used for the present analysis. The characters were measured on at least four different healthy plants and the data were then averaged for analysis. All data were standardized and subjected to analysis of variance for all the characters according to Federer (1977). Phenotypic and genotypic coefficients of variation were computed by Burton and Dewane (1953) considering genotypes as random effects using SAS statistical packages (SAS 1999).

Genotypic variance component
$$\sigma^2_g = MS_g - MS_e)/r$$
Where MS_g is genotypic mean square, MS_e is error mean square and r is replication

Environmental variance component (On genotypic mean basis)
$$\sigma^2_e = MS_{e/r}$$

Phenotypic variance component
$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Genotypic and phenotypic coefficients of variation were calculated according to the method suggested Burton and Dewane (1953) as: Genotypic coefficients of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} * 100$$

Phenotypic coefficients of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} * 100$$

Where $\bar{X}$ is the grand mean value of the trait

Broad sense heritability (h^2) in percents in estimated was estimated in each character using variance components as described by Allard (1960).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \text{ x } 100$$

The expected gain or genetic advance with one cycle of selection, assuming the selection intensity of 5%, was predicted as suggested by Johnson *et al.,* (1955a).

$$G_A = (k) \, (\sigma_p) \, (h^2)$$

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:

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

Covariance analysis was carried out in the same way in that of analysis of variance, and the mean cross produce was equated with the expected mean square product. Calculate the covariance component used to compute correlation coefficients.

Genotypic covariance of traits
$$\sigma^2_{g\,xy} = \frac{MSCP_{gxy} - MSCP_{exy}}{r}$$
Where, $MSCP_{gxy}$ is genotypic mean cross product of traits x and y. $MSCP_{exy}$, is error mean cross product of traits x and y.

Phenotypic covariance

$$\sigma^2_{p\,xy} = \sigma^2_{g\,xy} + \frac{\sigma^2_{gexy}}{r}$$

Genotypic and phenotypic correlation coefficients of fresh bulbils yield and its components were estimated calculating the variance and covariance at phenotypic and genotypic level by using the formula suggested by Singh and Chaudhury (1985).

Phenotypic correlation, the observable correlation between two variables, which includes both genotype and environmental components between two variables, was estimated using the formula suggested by Miller *et.al.* (1958)

$$r_{p\,xy} = \frac{\sigma_{p\,xy}}{\sqrt{(\sigma^2_{px\,)(}} \sqrt{(\sigma^2_{py)}}}$$

Genotypic correlation between traits x and y was computed as

$$r_{gxy} = \frac{\sigma_{p\,xy}}{\sqrt{(\sigma^2_{gx\,)(}} \sqrt{(\sigma^2_{gy)}}}$$

Where, σ^2_{gx} and σ^2_{px} are genotypic and phenotypic variance components of trait x. The coefficient correlation at phenotypic level were tested for their significance using the t-test as:

$$t = r_{pxy}\sqrt{g-2} \, / \sqrt{(1 - r^2_{pxy})}$$

The calculated 't' value was compared with tabulated 't' at g-2 degree of freedom, where g is the number of genotypes. The correlation coefficients at genotypic level were tested with the following formula suggested by Robertson (1959).

$$t = r_{gxy} / SEr_{gxy}$$

Where, r_{gxy} is the genotypic correlation coefficient, SEr_{gxy} is the standard error of genotypic correlation coefficient and

$$SEr_{gxy} = \sqrt{\frac{(1-r2\_gxy)2}{2h2\ xh2y}}$$

3. RESULTS AND DISCUSSION

Genetic variability in any crop is a pre-requisite to initiate the breeding programme for the selection of superior entries over the existing cultivars (keshava 2010). Variance analysis for characters revealed significant differences among the accessions studied and are presented in table 2 and table 3. Analyzed data indicated the presence of variability in the collected plant material thus providing the scope for selection of accessions to manage the breeding agenda.

Wide range of variation was observed for the character, number of bulbils/plot followed by Leaf length (cm) and tuber dry weight (t/ha). Phenotypic and genotypic variances, heritability, genetic advance and genetic advance of mean of the characters studied are presented in table 2. Higher values of most of the characters show the high environmental effect. Higher variance was observed for the characters, number of bulbils/plot, Leaf length (cm) and leaf width (cm). Root and bulbils yields are being quantitative characters and are influenced by many genes and are highly controlled by a biotic factor. Observed variability is the sum total of hereditary effects from concerned genes as well as the environment. Therefore, the variability is partitioned into heritable and non-heritable components with suitable genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA). These genetic parameters aid the breeders in selection of accessions and for further crop improvement programme.

Phenotypic coefficient of variation (PCV %) was found higher than the genotypic coefficient of variation (GCV %) for all the characters studied. High GCV along with high heritability and high genetic advance will provide better information than single parameters alone (Baye, B., Ravishankar, R., and Singh, H. 2005; Saha *et al.,* 1990). 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 suggests the prevalence of additive gene action with low environmental influence for the determination of these characters and could be effective in phenotypic selection in *Dioscorea bulbifera* improvement.

Heritability estimates ranged from 10.36% for bulbils fresh weight to 53.14% for vine dry weight (Table 2). The higest heritability was obtained from vine dry weight / plot followed by tuber diameter and tuber length. It was observed that the maximum genotypic coefficients of variation were supported by high estimates of heritability. On the other hand, bulbils fresh weight, vine fresh weight and number of bulbils/ plot have relatively low heritability estimates (Table 2). Genetic advance indicates the degree of gain in a character obtained under a particular selection and helps the breeder to forecast 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 2). The value of genetic advance as percent of mean varied from 4.15% for leaf width to 23.83% for tuber dry weight (t/ha). 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 2). This is indicated that selection for the traits like for tuber length and diameter is easier than selection for other characters. Moderate genetic advance coupled with high heritability noticed for the characters vine length and vine dry weights indicated the presence of intra and inter allelic interactions in the expression of these characters.

Correlation among the characters studied revealed considerable differences between phenotypic and corresponding genotypic correlations in all pairs of characters. The magnitude of genotypic correlations was always higher than their corresponding phenotypic correlations. Significant and strong positive correlations to bulbils fresh /plot were observed for the characters, vine length, leaf length, leaf width, vine dry weight, number of bulbils/plot and bulbils

length (Table 3). Vine fresh weigh, tuber dry weight, tuber length and tuber diameter showed non-significant and positive correlation with bulbils fresh weight. Based on the correlations between characters at genotypic level, accessions with high vine length, leaf length, leaf width, vine dry weight, number of bulbils/ plot and bulbils length will maximize yield and may need high consideration in efforts towards bulbils yield improvement.

Tuber dry weight, showed a non-significant genotypic correlation for most of the foliar characters such as vine length, leaf width, vine fresh weight, bulbils number/ plot and bulbils length. Number of bulbils/ plot, vine length and tuber dry weight showed non-significant and negative correlation with that of tuber length. Bulbils number per/plot showed strong and positive correlation with most of the characters for example, with leaf length, leaf width and vine dry weight. Moreover, except tuber length, vine dry weight showed strong and positive genotypic correlations with all of the characters that considered.

4. CONCLUSION

The range and mean performance showed the presence of considerable amount of variability among the accessions. For instance, bulbils fresh yield varied from 4.39 to 14.57 tones/ha, tuber yield varied from 2.0 to 8.22 tones/ha, number of bulbils varied from 43.66 to 98.67/plot, bulbils length varied from 5.33 to 9.0 cm and tuber diameter varied from 5.64 to 9.15 cm. The estimate of heritability ranged from 10.36% for bulbils fresh weight to 53.14% for vine dry weight. Values of genetic advance expected from selection of the superior 5% of the accessions and expressed relative to the means ranged from 4.15 for leaf width to 23.83 for tuber dry weight. In general, it can be conclude that the variability with in *D. bulbifera* accessions collected from southern and south-western parts of Ethiopia is low and the scope of its improvement narrow.

PCV ranged from 7.78 for bulbils length to 53.96 percent for vine dry weight whereas GCV ranged from 4.08 for leaf width to 22.81 percent for tuber dry weight. Among the various quantitative characters, relatively higher PCV and GCV were observed for vine dry weight (53.96 and 12.44), tuber dry weight (44.99 and 22.81) and vine fresh weight (26.07 and 11.18). It may therefore be given due attention for an effective selection in yield improvement of *D. bulbifera*. Bulbils fresh weight was significantly and positively correlated with vine length, leaf length, leaf width, vine dry weight, number of bulbils per plot and bulbils length at genotypic level. On the other hand, at phenotypic level, most of the correlation between characters showed significant.

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Table 2. 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.

Table 2. 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.

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).

Traits	Mean ± SE	Range	σ^2_g	σ^2_p	PCV	GCV	Heritability (%)	Genetic advance	GAM (%)
VL	3.2 ± 0.5	2.3 – 4.2	0.095	0.244	15.46	9.66	39.69	0.3969	12.42
LL	11.9 ± 1.0	9.5 – 14.0	0.374	1.162	9.08	5.15	32.17	0.7145	6.01
LW	10.5 ± 1.6	9.2 – 12.9	0.190	0.784	8.30	4.08	24.24	0.4422	4.15
VFW	0.2 ± 0.05	0.1 – 0.3	0.0003	0.002	26.07	11.18	18.38	0.0193	9.87
VDW	0.12 ± 0.1	0.06 – 0.4	0.0001	0.002	53.96	12.44	53.14	0.0482	5.90
NoBe	60.5 ± 11.3	43.6 – 99	25.04	128.02	18.69	8.26	19.56	4.560	7.53
BFW	9.5 ± 2.4	4.4 –14.5	0.013	0.128	25.12	8.09	10.36	0.0763	5.36
BL	7.1 ± 0.8	5.3 – 9.0	0.110	0.340	7.78	4.43	32.45	0.3900	5.20
TDW	1.5 ± 0.8	0.6 – 4.8	0.002	0.009	44.99	22.81	25.70	0.0508	23.83
TL	6.2 ± 0.68	4.6 – 7.9	0.193	0.460	10.92	7.08	42.04	0.5875	9.45
TDi	7.2 ± 0.77	5.6 – 9.1	0.255	0.600	10.80	7.04	42.54	0.6791	9.46

Table 3. Genotypic (above diagonal) and Phenotype (below diagonal) Correlation coefficient among 11 traits in 47 *Dioscorea bulbifera* accessions grown at Jimma.

Traits	BFW	VL	LL	LW	VFW	VDW	NoBe	BL	TDW	TL	TDi
BFW		1.00**	1.00**	1.00**	0.06	1.00**	0.88 **	1.00**	0.27	0.23	0.81
VL	0.34**		0.08	0.19	0.10	1.00**	0.72	0.54	0.23	-0.42	0.33
LL	0.40**	0.22*		1.00**	0.41	1.00**	0.94**	0.62	-0.01	0.24	0.91**
LW	0.38**	0.22 *	0.83**		1.00**	1.00**	1.00**	0.33	0.30	0.73	0.87**
VFW	0.07	0.36**	0.31**	0.39**		0.95**	0.79	0.73	0.32	0.54	1.00**
VDW	0.32**	0.35**	0.20*	0.25*	0.39**		1.00**	1.00**	1.00**	0.54	1.00**
NoBe	0.64**	0.29**	0.16*	0.18*	0.18*	0.52 **		0.93**	0.21	-0.66	0.16
BL	0.39**	0.41**	0.16*	0.218*	0.38**	0.34**	0.34**		0.55	0.03	0.88**
TDW	-0.06	0.20*	0.07	0.13*	0.31**	0.17*	0.00	0.20*		-0.06	0.55
TL	-0.01	-0.04	0.14*	0.27**	0.20*	0.06	-0.16	0.05	0.24 *		0.42
TDi	0.13*	0.25*	0.38**	0.39**	0.43**	0.21*	0.069	0.41**	0.37**	0.56**	

* Significant 0.05 probability level; **= Highly significant at 0.01 level of probability level.

BFW= Bulbils fresh weight(t/ha); 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; BL= Bulbils length(cm); TDW=Tuber dry weight(t/ha); TL=Tuber length(cm) and TDi=Tuber diameter (cm).