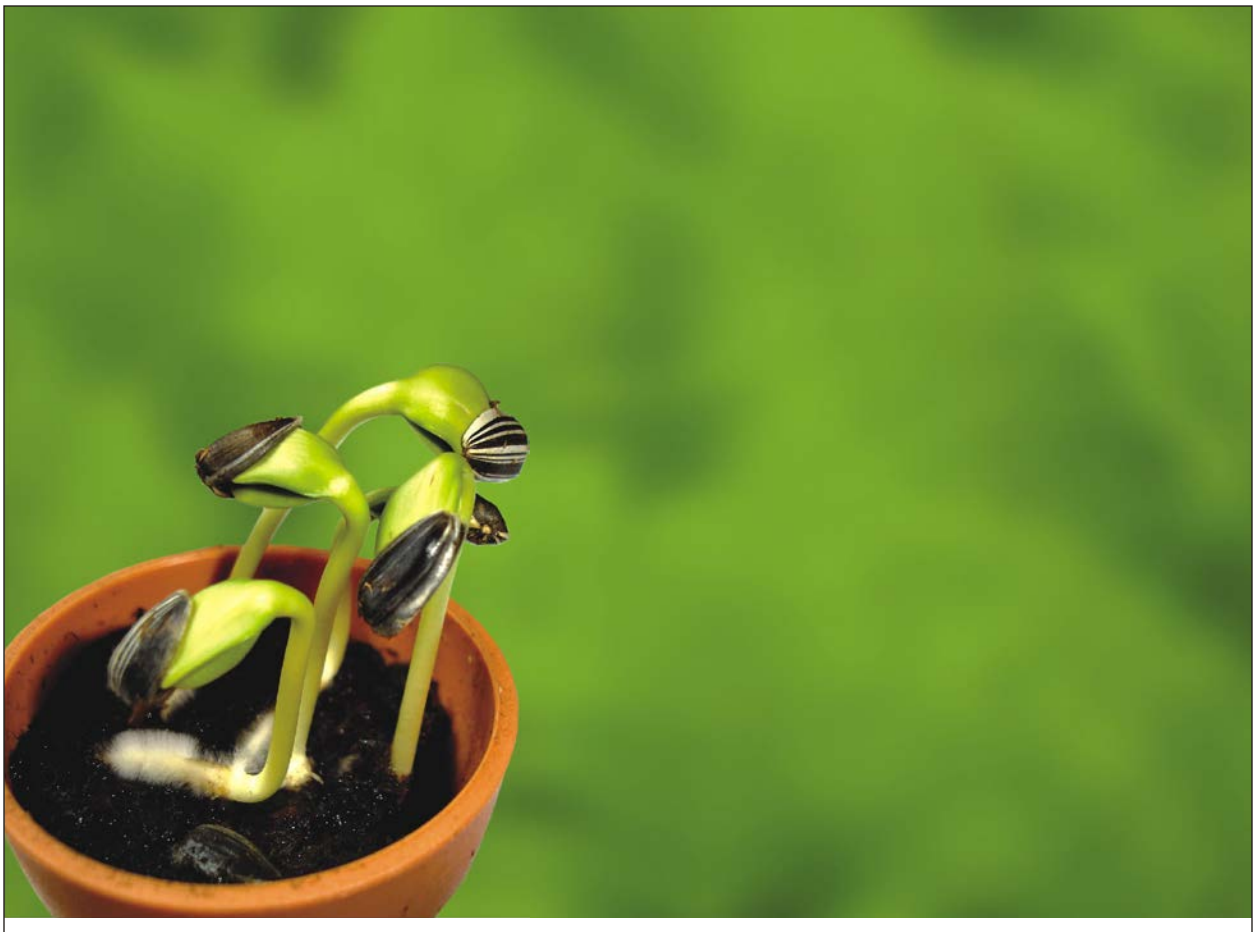

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Genetic Diversity of Tannia (*Xanthosoma sagittifolium* (L.) Schott) Genotypes Using Multivariate Analysis at Jimma, Southwest Ethiopia

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ABSTRACT

A total of sixty four tannia genotypes were characterized and evaluated based on 16 quantitative characters at Jimma Agricultural Research Center during the 2013/14 cropping season. Sixty two of the genotypes were collected from South, South western and western parts of Ethiopia and two were introduced from Cuba, laid out in 8×8 simple lattice design. The objectives of the present study were to classify genotypes in to smaller groups and to identify the traits accounted for gross diversity of the population. The data was subjected to cluster analysis and genetic divergence analysis. The genotypes were grouped into five clusters according to their similarity level which had significant genetic distance, suggesting the possibility to develop better performing varieties by selecting parents having high mean values for the characters of interest. The principal component analysis further reduced this dataset to four principal components which explained 70.5% of the variation present among the genotypes. The first principal component analysis accounted for 40.3% of the total variation and contributed by discriminating traits of plant height, petiole length, total yield per plant, number of sucker per plant, lamina length, lamina width, number of cormel per plant, plant canopy diameter, corm weight, cormel fresh weight, cormel length, corm length and corm diameter. In general, this study reveals the presence of diversity among the tannia genotypes which can give opportunity for genetic improvement for desirable character. Further, multi location and season evaluation is suggested for future study.

Key words: Cluster analysis, genetic distance, principal component, genotype biplot

INTRODUCTION

Tannia (*Xanthosoma sagittifolium* (L.) Schott) is the sixth most important root and tuber crops of the world next to cassava, potato, sweet potato, yam and taro in planted area and production (Perez, 2009). It is a herbaceous perennial plant but for production purposes, it is harvested after 9-12 months of growth (Lebot, 2009). Tannia belongs to the family Araceae and originally came from tropical America (Ramesh *et al*., 2007). Tannia was introduced to West Africa between the 16th and 17th centuries and was spread by traders, missionaries and other travelers (George, 2011).

In Ethiopia, root and tuber crops are part of the traditional food systems of the people especially in the southern, southwestern and western part of the country. Among the root and tuber crops, taro (*Colocasia esculenta* (L.) Schott) and tannia (*Xanthosoma sagitiffolium* (L.) Schott), locally known as 'Godare', are tuberous tropical food crops that supply high-energy food. Simone (1992) reported that godare has been grown in Ethiopia since time immemorial but how and when it was introduced to Ethiopia remains unclear Asfaw (2005). However, Amsalu *et al.* (2008) reported that 120 taro and 87 tannia collections were introduced to Ethiopia in 1978 from Cuba. There is enormous possibility for millions of poor farmers to boost productivity and their livelihood using root and tuber crops. During 2011/2012 production year, taro and tannia production area in Ethiopia reached 39,696 ha (CSA, 2012a) with total production of 315,242 t of which 81.2% is used for human consumption and 11.5% reserved for planting material. From the total national production, SNNP accounted for 84.5% (266,293.5 tons), Oromia region for 15.2% (48,015.1 tons), Benshangul-Gumuz for 0.05% (154.6 tons) and Gambela Region for 0.25% (779 tons) (CSA, 2012b).

Even though, tannia has many roles as strategic crop for the Ethiopian economy, perhaps it is highly neglected (Amsalu *et al.*, 2008). So far, there is no previous study on genetic diversity of tannia germplasm in Ethiopia. Hence, there is paucity of information about its diversity. In addition, there is no responsible agent for its improvement. However, in recent time, some germplasm collection and conservation works have been started by agricultural research centers (Amsalu *et al.*, 2008).

The knowledge of genetic diversity is very important for conserving, evaluating and utilizing genetic resources in breeding programs such as breeding for required quality, increasing yield, disease and pest resistance. Multivariate methods are useful for characterization, evaluation and classification of plant genetic resources based on morphological and agronomic traits when a large number of germplasms are to be assessed for several characters (Peeters and Martinelli, 1989). This procedure permit to establish the relationship among the variables and to determine how the plants vary in terms of all variables considered together. Cluster analysis and principal component analysis can be jointly used to explain the variations in breeding materials and are most frequent genetic diversity assessing methods (Aremu, 2012; Ravishanker *et al.*, 2013). Genetic distances are measures of the average genetic divergence between species or between populations within a species (Aremu, 2011, 2012). Therefore, the objectives of the present study were to classify genotypes in to smaller groups and to identify the traits accounted for gross diversity of the population through multivariate analysis.

MATERIALS AND METHODS

The experiment was conducted at Jimma Agricultural Research Center (JARC) located at 366 km South West of Addis Ababa. The site is situated at a latitude 7°46' N and longitude 36°E with an altitude of 1753 m.a.s.l. The soil of the study area is Eutric Nitisol with a pH of 5.3. The area receives mean annual rainfall of 1432 mm with maximum and minimum temperature of 29.2°C and of 8.9°C, respectively.

A total of 64 tannia genotypes having same cormel size, 62 genotypes collected from South, South western and western parts of Ethiopia and 2 introductions from Cuba (Table 1), laid out in 8×8 simple lattice design using single row plots of each 8.25 meter long, spaced 1 m apart between rows and 0.75 m between plants. There were 11 plants per row and the middle 5 plants were used for data collection.

Table 1: List of genotypes of tannia studied at Jimma during 2013/14

Genotype	District	Kebele/village	Altitude	Genotype	District	Kebele/village	Altitude
AAGT003	Chena	Bobakrcha	2100	AAGT109	Gesha	Hinigdo	1640
AAGT008	Bench	Kochi	1380	AAGT112	Gimbo	Kaikelo	1600
AAGT020	Bench	Wachamaji		AAGT116	Gimbo	Kembo	1820
AAGT022	Bench	Aman Gonji	1380	AAGT120	Chena	Kutasheorai	1820
AAGT030	Bench	Mizan		AAGT121	Chena	Agaro	1980
AAGT031	Bench	Koda	2040	AAGT127	Chena	Culish	
AAGT034	Chena	Ralakocho Bacha	1960	AAGT132	Bench	Aman	
AAGT035	Decha	Chalta	1620	AAGT135	Bench	Gerika	1460
AAGT036	Decha	Shapa	1840	AAGT138	Sheka	Bukita	1460
AAGT043	Decha	Deha	1880	AAGT144	Sheka	Selale	1640
AAGT045	Decha	Chiri		AAGT148	Sheka	Wesheka	1660
AAGT046	Decha	Chiri		AAGT152	Sheka	Shimi	1320
AAGT051	Gimbo	Kaiketa	1860	AAGT155	Sheka	Gizm	
AAGT052	Gimbo	Beyamo	1680	AAGT159	Yeki	Korech	1140
AAGT054	Gimbo	Aman	1700	AAGT163	Yeki	Korech	1380
AAGT058	Gimbo	Getoacho	1640	AAGT171	Mesha	Tugri	1840
AAGT061	Gimbo	Shamba	1500	AAGT176	Mesha	Toba	2220
AAGT065	Decha	Erma	1860	AAGT177	Mesha	Keja	2140
AAGT069	Decha	Adaiminja	1860	AAGT178	Mesha	Chewaka	1840
AAGT077	Decha	Muga	1900	AAGT180	Gesha	Asho	2160
AAGT080	Decha	Gedam	1680	AAGT183	Gesha	Yershiniti	2180
AAGT083	Telo	Tura	2020	AAGT186	Mesha	Gecha	
AAGT085	Telo	Shadie	1640	AAGT188	Yeki	Chati	1820
AAGT088	Telo	Felegeselam	2060	AAGT193	Yeki	Gendekore	1260
AAGT092	Gimbo	Beymo	1660	AAGT195	Yeki	Sbosha	1220
AAGT093	Gimbo	Kicho	1720	AAGT199	Yeki	Bechi	1180
AAGT094	Gimbo	Kuti	1760	AAGT202	Yeki	Kura Alamo	1220
AAGT097	Gimbo	Emicho	1820	AAGT205	Yeki	Alamo	1380
AAGT099	Gimbo	Saja	2060	AAGT208	Chena	Tofa	1820
AAGT100	Gimbo	Medaobo	1600	0002/07			
AAGT102	Gimbo	Medaobo	1560	0003/07			
AAGT106	Gimbo	Konda		AAGT174	Mesha	Gtimo	2250

Data on 16 quantitative traits were recorded on plant basis following descriptor of tannia developed by International Board for Plant Genetic Resources (IBPGR, 1989). Measurements of above ground morphological characters were carried out from middle five plants in each plot at 5th to 6th months after planting, when the plants have reached their peak above ground vegetative growth while subterranean traits were evaluated at harvest (nine and half months after planting). The data was collected on lamina length (cm), lamina width (cm), number of suckers per plant, petiole length (cm), plant height (cm), plant canopy diameter (cm), corm length (cm), corm diameter (cm), corm fresh weight per plant (kg), cormel length (cm), cormel diameter (cm), cormel fresh weight per plant (kg), total root yield per plant (kg), number of cormels per plant, corm dry matter content (%) and cormel dry matter (%).

Statistical analysis: Clustering procedure was performed using the proc cluster procedure of SAS version 9.2 (SAS, 2008) by employing the method of average linkage clustering strategy of the observations and information summarized by constructing dendrograms by Minitab version 16

(Minitab, 2010) statistical soft ware. The number of cluster was determined by looking Cubic Clustering Criterion (CCC), pseudo F (PSF) and pseudo t^2 (PST^2) statistics. The genetic divergence between clusters was estimated by Mahalanobis's D^2 statistics using SAS 9.2 (SAS, 2008). The test was done against the tabulated values of χ^2 for p degrees of freedom, where p is the number of characters considered (Singh and Chaudhury, 1987).

Principal component analysis was performed using Proc FACTOR procedure in SAS 9.2 (SAS, 2008) and PAST Statistical Software (Hammer *et al*., 2001) to draw genotype by trait bi-plot diagram. PCAs that had had eigen values >1.0 were selected and loading coefficient values >0.40 (ignoring the sign) were considered as relevant scores for the PCAs (Costello and Osborne, 2005; Biabani and Pakniyat, 2008).

RESULTS AND DISCUSSION

Cluster analysis based on the mean values of the 16 studied characters resulted in the grouping of the 64 tannia genotypes in to five major clusters as shown in Fig. 1. Cluster (C-I) was the second larger as well as tight clustered which comprised 26 genotypes accounted 40.63% of the total genotypes, collected from nine different districts, Chena (4), Bench (2), Gimbo (6), Decha (1), Sheka (4), Yeki (4), Mesha (3), Telo (1) and Gesha (1). This cluster was subdivided into different sub clusters based on their similarity level which ranges from the 64.34 up to 87.92%. Cluster (C-II) was the broadest group which accounts 43.75% of all and consists of 28 genotypes which were collected from Bench (5), Decha (5), Gimbo (6), Telo (2), Gesha (2), Chena (2), Yeki (4) and Mesha (2) district, their similarity level ranged from 72.35-90.5%. Cluster (C-II) was subdivided

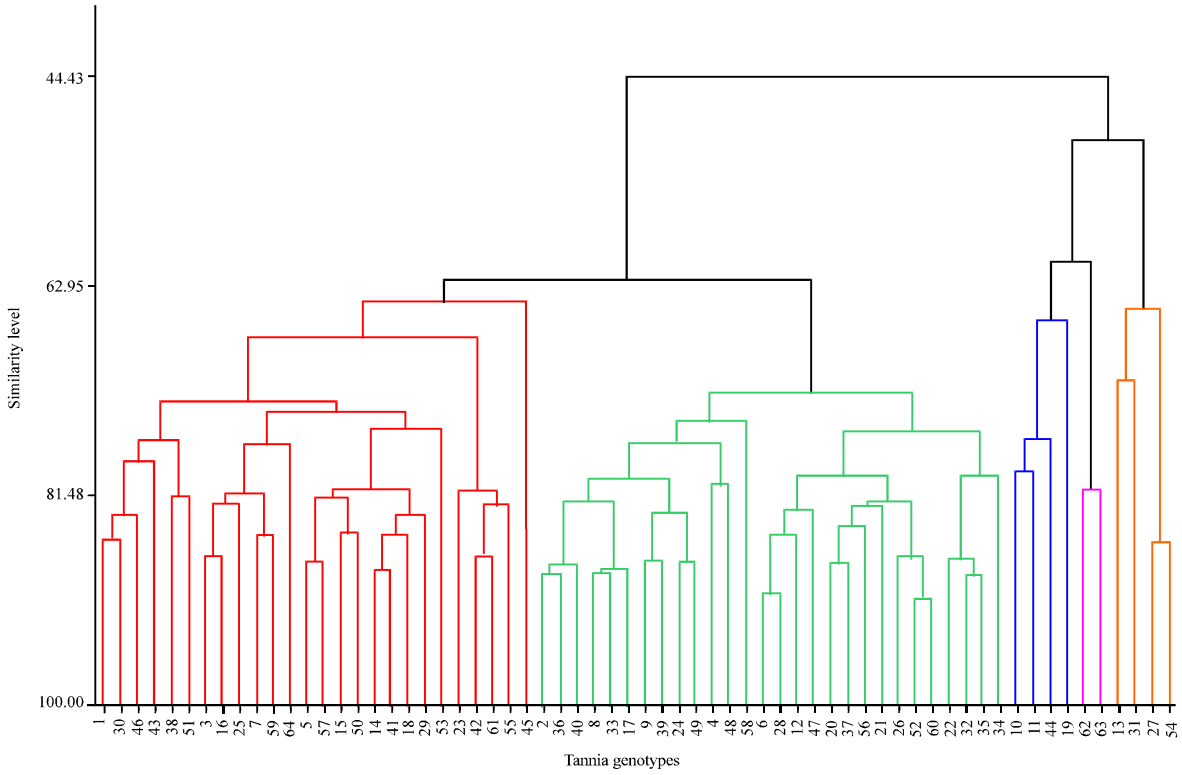

Fig. 1: Dendnogram of 64 tannia genotypes studied at Jimma during 2013/14

into different sub clusters having range of similarity from 72.35 up to 90.5%. Likewise, cluster III, IV and V have 3, 3 and 2 genotypes, respectively.

In the present study, most of the genotypes collected from different districts and different kebele clustered together. The probable cause for this is, those genotypes might have originated in localities different from those assigned based on their collection points. This suggests that tannia genotypes may have been transported between localities at random for suiting their local needs and the genetic drift as vigorous plants are invariably saved by the farmers as seed for the next planting. This may have been enhanced by the closeness of the districts to each other.

However, morphological variation is more important than geographical variation. In line with this finding, Offei *et al.* (2004) in Ghana reported that 70 tannia accessions collected from different geographical regions were clustered together in different cluster group. Similarly, Opoku-Agyeman *et al.* (2004) clustered 78 tannia accessions collected from seven regions of Ghana into eight different groups based on some morphological characters. Wondimu *et al.* (2014) in Ethiopia clustered 49 Anchote (*Coccinia abyssinica*) accessions in to 5 major clusters. Mondal *et al.* (2007) clustered 31 potato genotypes to five major clusters in Bangladesh.

The cluster means of different characters were noted to have variability in 16 quantitative characteristics (Table 2). Genotypes in cluster I were characterized by the highest mean value for corm dry matter (28.1%) and minimum for cormel diameter (5.04 cm). Cluster II was unique of all in the mean of genotypes, in this cluster no high value even for a single character. Cluster III was characterized by highest mean value of lamina width (26.25), cormel length (11.67 cm), cormel diameter (5.59 cm) and corm weight (0.35 kg plant^{-1}). Likewise, cluster IV was characterized

Table 2: Cluster means for 16 quantitative characters of tannia genotypes studied at Jimma during 2013/14

	Cluster				
Character	I	II	III	IV	V
SU	2.34	2.16*	2.53	3.31	3.40**
LL	24.76	22.83*	27.54	26.43	27.75**
LW	23.22	21.31*	26.23**	24.57	23.05
PLC	67.60	61.45*	68.28	78.87**	72.74
PTLg	47.05	41.56*	54.92	48.04	55.63**
PH	58.30	51.57*	66.87	59.22	70.51**
COL	10.38	10.14*	11.67**	10.83	10.21
CLD	5.04*	5.27	5.59**	5.37	5.22
NCL	12.31	10.68	12.40	16.22**	9.26*
CML	8.09	7.62*	8.78	7.93	8.89**
CMD	8.34	7.98*	8.85	9.04	9.10**
COW	0.44	0.41*	0.63	0.53	0.71**
CMW	0.23	0.21*	0.35**	0.28	0.34
CMDM	27.98	28.14	28.38	29.13**	21.50*
CODM	28.1**	27.82	27.75	26.63	20.25*
Tot. Yi	0.67	0.62*	0.98	0.81	1.06**

SU: No. of suckers per plant, LL: Lamina length (cm), LW: Lamina width (cm), PLC: Plant canopy diameter (cm), PTLg: Petiole length (cm), Ph: Plant height (cm), COL: Cormel length (cm), CLD: Cormel diameter (cm), NCL: No. of cormels per plant, CML: Corm length (cm), CMD: Corm diameter (cm), COW: Cormel fresh weight per plant (kg), CMW: Corm fresh weight per plant (kg), CMDM: Corm dry matter content (%), CODM: Cormel dry matter content (%), Tot. Yi: Total root yield per plant (kg). *, **Minimum and maximum cluster mean value for a character, respectively

Table 3: Inter (above diagonal) and intra (bold and diagonals) cluster distances among 5 major clusters

Clusters	I	II	III	IV	V
I	1.80ns	16.06ns	31.33**	28.35*	115.82**
II		1.65ns	67.14**	53.37**	155.04**
III			5.55ns	44.62**	68.84**
IV				5.55ns	108.63**
V					6.93ns

**Highly significant at p<0.01, *Significant at p<0.05, ns: Non significant at 5%

with the highest mean value of corm dry matter content (29.13%), number of cormel per plant (16.22) and plant canopy diameter (78.87 cm). Finally, cluster V characterized by highest mean value for total yield (1.06 kg plant^{-1}), cormel fresh weight (0.71 kg plant^{-1}), corm length (8.89 cm), corm diameter (9.01 cm), plant height (70.51 cm), petiole length (55.63 cm), lamina length (27.75 cm) but had lowest mean value for characters of number of cormel per plant (9.26 cm), cormel dry matter content (20.25%) and corm dry matter content (21.5%).

Divergence analysis is usually performed to classify the diverse genotypes by using Mahalanobis (1936) generalized distance D-square techniques which has been one of the important statistical tools to provide a rational basis for selection of parents in breeding program since the genetic improvement through hybridization and selection depends upon the extent of genetic diversity between parents. The more divergent the two genotypes are, the more will be the probability of improving through selection and hybridization.

Mahalanobis inter and intra cluster genetic distance (D^2) values among the five clusters for the 64 tannia genotypes based on 16 quantitative characteristics is presented in Table 3. The maximum and highly significant (p<0.01) genetic distance was between cluster II and V (D^2 = 155.04) while, the minimum and non-significant distance was between cluster I and II (D^2 = 16.06). Intra cluster distance was being much lower than the inter cluster suggested heterogeneous and homogeneous nature between and within groups, respectively. The distance between cluster IV and V (D^2 = 108.62), cluster I and cluster V (D^2 = 115.82), cluster III and V (D^2 =68.84), cluster II and IV (D^2 = 53.37), cluster II and III (D^2 = 67.14), clusters III and IV (D^2 = 44.62) and clusters I and III (D^2 = 31.33) was highly significant. The differences between I and IV (D^2 = 28.35) was significant (p<0.05). In similar way, significant distance were reported previously for other root crops such as Wondimu *et al.* (2014), who reported that highly significant inter-cluster distance among 49 Anchote accessions in Ethiopia. Also, Asfaw (2005) found highly significant divergence among taro 70 accessions in Ethiopia.

According to Mondal *et al.* (2007), crossing of genotypes that have high inter cluster distance is expected to produce maximum heterosis and generate wide variability in genetic architecture than those with smaller inter cluster distances. Genotypes grouped together are less divergent than genotypes that fall into different clusters (Yadav *et al.*, 2007), particularly clusters separated by largest statistical distance (such as, between cluster I and V, cluster II and V, cluster IV and V) showed the maximum distance. Also, the cluster mean (Table 2) reveals that cluster I was characterized by maximum cluster mean of cormel dry matter content while, cluster V had the lowest cluster mean for the character. Similarly, for most character, cluster II had the lowest cluster means (total yield per plant, cormel weight, corm length and width, plant height, petiole length, lamina width and length) while that of cluster V had the maximum cluster mean values. Also, cluster IV had the maximum cluster mean values for plant canopy diameter while cluster II had the minimum cluster mean. On the other hand, crossing between genotypes of cluster I with II and cluster I with IV may not produce desirable recombinants since they had low inter cluster distance, indicating the close relationship and having recent common ancestors between them.

Table 4: Principal components and their loading values, eigen values and percentage of total variances for 16 quantitative characters studied at Jimma during 2013/14

	PCA			
Character	1	2	3	4
SU	0.474*	0.254	-0.392	0.394
LL	0.783*	-0.445*	0.124	0.180
LW	0.714*	-0.370	0.344	0.187
PLC	0.653*	0.004	-0.288	0.401*
PTLg	0.841*	-0.287	0.025	0.065
PH	0.862*	-0.335	-0.015	-0.012
COL	0.467*	0.457*	0.293	-0.173
CLD	0.303	0.418*	0.262	-0.387
NCL	0.433*	0.566*	-0.205	0.465*
CML	0.597*	-0.142	0.307	-0.208
CMD	0.647*	-0.208	0.426*	0.016
COW	0.745*	0.342	-0.225	-0.403*
CMW	0.813*	0.276	-0.102	-0.029
CMDM	-0.134	0.374	0.512*	0.296
CODM	-0.137	0.478*	0.571*	0.318
Tot. Yi	0.838*	0.347	-0.198	-0.299
Eigen value	6.442	2.045	1.530	1.271
Vriance (%)	40.300	12.800	9.600	7.900
Cmulative variance (%)	40.300	53.000	62.600	70.500

SU: No. of suckers per plant, LL: Lamina length (cm), LW: Lamina width (cm), PLC: Plant canopy diameter (cm), PTLg: Petiole length (cm), Ph: Plant height (cm), COL: Cormel length (cm), CLD: Cormel diameter (cm), NCL: No. of cormels per plant, CML: Corm length (cm), CMD: Corm diameter (cm), COW: Cormel fresh weight per plant (kg), CMW: Corm fresh weight per plant (kg), CMDM: Corm dry matter content (%), CODM: Cormel dry matter content (%), Tot. Yi: Total root yield per plant (kg)

The PCA resulted that only the first four principal component axes had eigen values up to 1.0 which explained 70.5% of the variation present among genotypes (Table 4). This indicates that the identified characters within these components exhibited great influence on the phenotype of the genotypes and could effectively be used for selection among them. Plant height (0.86) had the maximum loading value followed by petiole length (0.84) and total yield per plant (0.838) while plant canopy diameter (0.004) showed the minimum loading value.

The first principal component accounted for 40.3% of the total variation among genotypes. Plant height (0.86), petiole length (0.84), total yield per plant (0.84), number of sucker per plant (0.47), lamina length (0.78), lamina width (0.71), number of cormel per plant (0.43), plant canopy diameter (0.65), corm weight (0.81), cormel fresh weight (0.74), cormel length (0.47), corm length (0.60) and corm diameter (0.64) contributed positive loading effect and were the discriminatory characters for this principal component. As Tabachnick and Fidell (2001) and Costello and Osborne (2005), it is possible to take PCA1 as representative component since it had more than 5 strongly loading items, accounted for maximum proportion of total variability in the set of all variables and also had higher eigen values of all components.

PCA 2 accounted 12.8% of the total variation and had strong positive loading of cormel length (0.46), cormel diameter (0.42), number of cormel per plant (0.57) and percentage of cormel dry matter content (0.49) while strong negative loading value of lamina length (-0.45). The third principal component explained 9.6% of total variability among genotypes. It was strongly loaded by corm diameter (0.43), corm dry matter content (0.51) and cormel dry matter content (0.57).

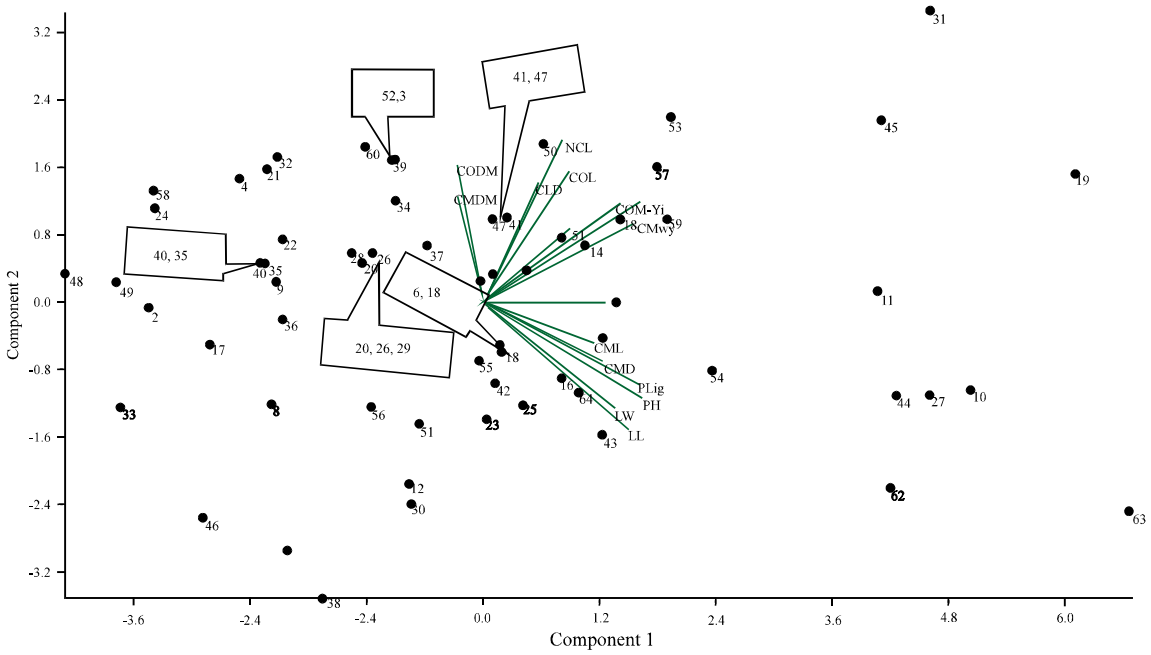

Fig. 2: Principal components genotype by traits bi-plot diagram of PCA 1 and PCA 2

Similarly, traits like plant canopy diameter (0.4), number of cormel per plant (0.46) and cormel weight (0.4) contributed more to the variation of principal component four (7.9%).

In line with this result, many authors performed PCA to identify genetic variability of different plant genotypes. For instance, Okpul *et al.* (2004) reported 6 principal components for 276 taro accessions based on their eigen values, loading effect and cumulative variations in New Guinea. Similarly, Afuape *et al.* (2011) obtained 3 principal components which had eigen values up to 1.0 and explained 76% cumulative variation in 21 sweet potato genotypes in Nigeria. Also, Ahmadizadeh and Felenji (2011) reported three principal components which had eigen value up to 1.0 and explained cumulative variance of 80.1% among 22 potato cultivars in Iran.

After PCA was performed, bi-plot of first (horizontal axis) and second (vertical axis) components was drawn to study the relationships between characters and diversity among the genotypes (Fig. 2). According to Ahmadizadeh and Felenji (2011) and Ghaffari *et al.* (2011), if the angle between vectors or lines are closer to each other, i.e., the angle between them is less than 90°, this represents a positive correlation; the more acute the angle, the greater positive correlation among related traits and vice versa and if the angle between the lines is more than 90°, this indicates the correlation is negative, also if the angle is equal or nearest to 90° it shows independency of traits.

Therefore, some vectors of traits had angle lower than 90° with each other such as total yield per plant, cormel fresh weight and corm weight, cormel fresh weight, corm yield and total yield per plant with number of cormel per plant, corm length, cormel diameter, plant canopy diameter, corm length and diameter, plant height, number of sucker per plant and petiole length. Also, plant height had smaller angle with petiole length, corm length and diameter, plant canopy diameter, lamina length and lamina width. This indicates that they had positive correlations. But larger angle (>90°) between plant height, plant canopy diameter, lamina length, lamina width, petiole

length and that of cormel and corm dry matter content indicates their negative correlation. Similarly, the dry matter content for corm and cormel had wider angle near to 90° with total yield per plant, cormel fresh weight and corm weight which showed their weak correlation.

Genotypes scattered around the vectors in the bi-plot diagram indicates comprising of distinct groups of genotypes for the nearby vectors and selection for one of these traits should be accompanied by the associated traits (Ghaffari *et al*., 2011). Therefore, this association of traits would provide the opportunity to exert multi-traits selection in tannia breeding programs. For example, genotype numbers 57, 53, 59, 31, 45, 19, 50 and 15 scattered around the cormel weight, corm weight and total yield. Similarly, genotypes numbers 64, 16, 43, 44, 54, 27, 10, 62 and 63 scattered around the plant height, lamina length and width, corm length and diameter. Also, genotypes 60, 52, 39, 34, 50, 47 and 41 were scattered around corm and cormel dry matter content.

PCA bi-plots ordination generates ways to identify traits that could be used for efficient selection (Ghaffari *et al*., 2011). For example, if one wants to select higher yielder and higher dry matter content, genotype 31 as well as 53, 57, 45 and 50 would be a suitable selection. Therefore, it is possible to say genotype number 31 is good since it had coupled good yield with dry matter content and good cormel size. Even if genotype 63 had very large plant size, (taller in height, wider and longer lamina) and the highest in yield among all, lowest in corm and cormel dry matter and lower in number of cormels. On the other hand, genotype 39 had highest dry matter content and good in number of cormel per plant but lower yield and lower cormel size smaller plant size. According to the bi-plot diagram, two genotypes (63 and 39) were found in opposite direction (nearly 180°). Therefore, it is possible to ascertain that they had distinct variability between them and crossing of these genotypes may advance to improve yield and dry matter content.

Regardless of the geographic sources, closeness of genotypes like 39 and 52, 47 and 41, 20, 26 and 29, 6 and 18, 40 and 35 showed strong similarities between them indicating that genotypes with different names could be shared the same parental background. So, further study employing molecular tools may be needed to arrive at a good conclusion about their relatedness. On the other hand, weak similarities between genotypes 44, 27 and 10, 64, 43, 16, 7, 25, 42, 23 and 42, 53, 57, 59, 14, 13, 50 and 15; 4, 21, 32, 58 and 24; 48, 2 and 49 are depicted by the relative distance among the genotypes, is a measure of the existence of exploitable variability existing among the genotypes. Genotypes such as 31, 45, 19, 11, 63, 62, 54, 46, 1, 38, 33 and 8 are completely distinct from others. Such a wide variability gives good opportunity for the exploitation of the benefits of heterosis after good parent selection. Hence, the bi-plot showed wide diversity between most of the genotypes, though few genotypes exhibited strong similarities.

In general, the study reveals the presence of trait diversity among the tannia genotypes, suggests that there is opportunity for genetic improvement though selection directly from the genotypes and selection of diverse parents for hybridization program and conservation of germplasm for future utilization.

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REFERENCES

Afuape, S.O., P.I. Okocha and D. Njoku, 2011. Multivariate assessment of the agromorphological variability and yield components among sweet potato (*Ipomoea batatas* L. Lam) landraces. Afr. J. Plant Sci., 5: 123-132.

Ahmadizadeh, M. and H. Felenji, 2011. Evaluating diversity among potato cultivars using agro-morphological and yield components in fall cultivation of Jiroft area. Am. Eurasian J. Agric. Environ. Sci., 11: 655-662.

Amsalu, N., G. Weyessa, T. Asefa, A. Wubshet, K. Asfaw and E. Edossa, 2008. Variety Development for other Root and Tuber Crops (Taro, Cassava and Yam). In: Root and Tuber Crops: The Untapped Resources, Gebremedihin, W., G. Endale and L. Berga (Eds.). Ethiopian Institute of Agriculture Research, Addis Ababa, Ethiopia, pp: 303-316.

Aremu, C.O., 2011. Genetic diversity: A review for need and measurements for intraspecie crop improvement. J. Microbiol. Biotechnol. Res., 1: 80-85.

Aremu, C.O., 2012. Exploring Statistical Tools in Measuring Genetic Diversity for Crop Improvement. In: Genetic Diversity in Plants, Caliskan, M. (ed.). Chapter 17, InTech Publisher, Rijeka, Croatia, ISBN: 978-953-51-0185-7, pp: 339-348.

Asfaw, K., 2005. Characterization and divergence analysis of some Ethiopian Taro (*Colocasia esculenta* (L.) Schott.). M.Sc. Thesis, Haramaya University, Ethiopia.

Biabani, A.R. and H. Pakniyat, 2008. Evaluation of seed yield-related characters in sesame (*Sesamum indicum* L.) using factor and path analysis. Pak. J. Biol. Sci., 11: 1157-1160.

CSA, 2012a. Agricultural sample survey 2011/2012 (2004 E.C.) (September-December, 2011), Volume IV, Report on land utilization (private peasant holdings, meher season). Statistical Bulletin 532, May 2012, Central Statistical Agency, Addis Ababa, Ethiopia, pp: 92-169.

CSA, 2012b. Agricultural sample survey 2011/2012 (2004 E.C.) (September-January 2011/2012), Volume VII, Report on crop and livestock product utilization (private peasant holdings, meher season). Statistical Bulletin 532, August, 2012, Central Statistical Agency (CSA), Addis Ababa, Ethiopia, pp: 11-97.

Costello, A.B. and J.W. Osborne, 2005. Best practices in exploratory factor analysis: Four recommendations for getting the most from your analysis. Practical Assess. Res. Eval., 10: 1-9.

George, R.A.T., 2011. Tropical Vegetable Production. CAB International, UK., pp: 162-175.

Ghaffari, M., I. Farokhi and M. Mirzapour, 2011. Combining ability and gene action for agronomic traits and oil content in sunflower (*Helianthus annuus* L.) using F1 hybrids. Crop Breed. J., 1: 75-87.

Hammer, O., D.A.T. Harper and P.D. Ryan, 2001. PAST: Paleontological statistics software package for education and data analysis. Palaeontol. Electronica, Vol. 4.

IBPGR, 1989. Descriptors for *Xanthosoma*. Bioversity International, Rome, Italy, ISBN: 9789290431329, Pages: 30.

Lebot, V., 2009. Aroids. In: Tropical Root and Tuber Crops: Cassava, Sweet Potato, Yams and Aroids, Lebot, V. (Ed.). CAB International, UK., ISBN: 9781845934248, pp: 279-355.

Mahalanobis, P.C., 1936. On the generalised distance in statistics. Proc. Nat. Inst. Sci. India, 2: 49-55.

Minitab, 2010. Minitab Statistical Software. Version 16, Minitab Inc., USA.

Mondal, M.A.A., M.M. Hossain, M.G. Rasul and M.S. Uddin, 2007. Genetic diversity in potato (*Solanum tuberosum* L.). Bangladesh J. Bot., 36: 121-125.

Offei, S.K., I.K. Asante and E.Y. Danquah, 2004. Genetic structure of seventy cocoyam (*Xanthosoma sagittifolium*, Linn, Schott) accessions in Ghana based on RAPD. Hereditas, 140: 123-128.

Okpul, T., T. Gunua and M.E. Wagih, 2004. Assessment of diversity using agro-morphological traits for selecting a core sample of Papua New Guinea taro (*Colocasia esculenta* L.) Schott) collection. Genet. Resour. Crop Evol., 51: 671-678.

Opoku-Agyeman, M.O., S.O. Bennett-Lartey and C. Markwei, 2004. Agro-morpho-logical and sensory characterization of cocoyam (*Xanthosoma sagittifolium* (L.) (Schott) germplasm in Ghana. Ghana J. Agric. Sci., 37: 23-31.

Peeters, J.P. and J.A. Martinelli, 1989. Hierarchical cluster analysis as a tool to manage variation in germplasm collections. Theor. Applied Genet., 78: 42-48.

Perez, P.J., 2009. Cocoyam. In: Quality Declared Planting Material: Protocols and Standards for Vegetatively Propagated Crops, Fajardo, J. (Ed.). Food and Agriculture Organization of the United Nations, Rome, Italy, pp: 41-48.

Ramesh, V., K.S. John, C.S. Ravindran and S. Edison, 2007. Agro-techniques and plant nutrition of tannia (*Xanthosoma* sp.): An overview. J. Root Crops, 33: 1-11.

Ravishanker, S. Kumar, D.K. Baranwal, A. Chatterjee and S.S. Solankey, 2013. Genetic diversity based on cluster and principal component analyses for yield and quality attributes in ginger (*Zingiber officinale* Roscoe). Int. J. Plant Breed. Genet., 7: 159-168.

SAS, 2008. Statistical Analysis System Software. Version 9.2, SAS Institute INC., Cary, NC., USA.

Simone, A., 1992. Taro root in North Omo. FPR Technical Pamphlet No. 2, Addis Ababa, Ethiopia.

Singh, R.K. and B.D. Chaudhury, 1987. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, Pages: 318.

Tabachnick, B.G. and L.S. Fidell, 2001. Using Multivariate Statistics. 4th Edn., Allyn and Bacon, Boston, MA., USA., ISBN-13: 9780321056771, Pages: 966.

Wondimu, T., S. Alamerew, A. Ayana and W. Garedew, 2014. Genetic diversity analysis among Anchote (*Coccinia abyssinica*) accessions in Western Ethiopia. Int. J. Agric. Res., 9: 145-157.

Yadav, R.K., N. Rai, D.S. Yadav and S.K. Sanwal, 2007. Correlation, Path coefficient and genetic diversity pattern in colocasia (*Colocasia esculenta*) genotypes. Vegetable Sci., 34: 153-156.