International Scholars Journals

African Journal of Agriculture ISSN 2375-1134 Vol. 2 (6), pp. 099-106, June, 2015. Available online at www.internationalscholarsjournals.org © International Scholars Journals

Full Length Research Paper

Agronomic evaluation and germplasm characterization of Tannia (*Xanthosoma sagittifolium* (L.) variety development in Ethiopia

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Accepted 26 May, 2015

Tannia is one of the most important root and tuber crops for food, feed and industrial applications worldwide. However, the progress to variety development in Ethiopia is so slow due to lack of adequate germplasm characterization and agronomic evaluation for yield and quality. Therefore, a total of 64 tannia genotypes were studied to determine the extent of genetic variability among genotypes at Jimma agriculture research center during 2013/2014 cropping season. 62 of the genotypes were collected from south, south western and western parts of Ethiopia and the rest two were introduced from Cuba, laid out in 8 × 8 simple lattice design. Analysis of variance revealed significant (P 0.01) differences for most of the characters, indicating the existence of variability among the studied genotypes. High phenotypic coefficient of variation (PCV) along with moderate to high genotypic coefficient of variation (GCV) as well as high heritability coupled with high genetic advance as percent of the mean were obtained for number of suckers per plant, number of cormel per plant, total yield per plant, corm and cormel fresh weight per plant. This indicates that there is an opportunity and potential for further utilization of its genetic improvement through selection and hybridization. However, the presence of morphological variation between genotypes is not a guarantee for high genetic variation. Hence, there is a need to confirm genotype-environment interactions and use biotechnological approaches as a complementary to this study.

Key words: Genetic advance, genetic variability, genotypic coefficient of variation, heritability.

INTRODUCTION

Tannia is an herbaceous, monocotyledonous, perennial stem tuber crop that is widely cultivated in tropical and subtropical regions of the world. Tannia belongs to the family Araceae and originally came from tropical America (Ramesh et al., 2007). Tannia ranked sixth in planted area area and production after cassava, potato, sweet potato, yam and taro in the world (Perez, 2010).

Root and tuber crops including tannia can play multi-purpose roles in the global food system to address the ever increasing demand for food and feed millions of people

people (Ceballos, 2009; Lebot, 2009; Ndabikunze et al., 2011). According to FAOSTAT (2012), world production for taro and tannia in 2011 was 10.37 million tonnes. Africa as a continent produces more than 71% of world production. Globally, tannia is an important food for about 400 million people (Lebot, 2009) and in Ethiopia a total of 1.5 million farmers mainly in Southern Nations Nationalities and Peoples (SNNP) region (0.96 million) and in Oromia region (0.5 million) are dependent on taro and tannia as their food source (CSA, 2012b). During 2011/2012 production year, taro and tannia production area in Ethiopia reached 39,696 hectares (CSA, 2012b) with total production of 315,242 tonnes of which 81.2% is used for human consumption and 11.5% reserved for planting material (CSA, 2012a). Even though tannia has many roles, it is unexploited and neglected crop. Lack of improved varieties and need of large planting material (Onokpise et al., 1999), rare natural flowering and seed setting (Mbouobda et al., 2007), transmission of pathogens specially dasheen mosaic virus (DsMV) via vegetative propagation which can cause yield losses up to 90% (Onokpise et al., 1999; Reyes et al., 2006; Mbouobda et al., 2007) are major constraints of tannia production.

To overcome these constraints and improve production and productiveness of tannia, research has been conducted in different countries. In Costa Rica, genetic variability is generated by induction mutation (Saborio et al., 2004), in Ghana, Blay et al. (2004) irradiated tannia shoot tips with gamma rays to generate variability, In Bangladesh, protocol establishment for micro propagation and vitro callus regeneration were performed (Paul and Bari, 2007). Also, Onokpise et al. (1992) sprayed Gibberellic acid (GA_3) to induce flowering and seed setting.

But tannia in Ethiopia is still neglected, so far no improved varieties are available and no characterization and other works have been undertaken. Even though, the national average yield level of tannia in Ethiopia is greater than the global average yield of 7.4 tonnes/ hectar (FAOSTAT, 2012), its productivity is far below the crop's potential which is 30 to 60 tonnes/hectare (Lebot, 2009; Mwenye et al., 2010). For crop improvement program genetic variability is an essential prerequisite for obtaining high yielding, quality, pest and disease resistant varieties (Paul and Bari, 2012).

As Amsalu and Tesfaye (2006) and Tewodros (2008) state, tannia has a large gene pool in south and southwest Ethiopia in farmers' field and homesteads. Recently some germplasm collection and conservation works have been started by agricultural research centers (Amsalu et al., 2008). Nevertheless, the collected genotypes have never been characterized or evaluated for desirable characteristics. So, there is paucity of information in respect to their genetic variability and agronomic performance. Therefore, the present study was conducted with the objective of determining the extent extent of genetic variability based on quantitative characters.

MATERIALS AND METHODS

Study area

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 and of 8.9°C, respectively.

Expermental design

A total of 64 tannia genotypes having same cormel size, 62 genotypes collected from south, south western and western parts of Ethiopia and two introductions from Cuba (Table 1), laid out in 8 × 8 simple lattice design using single row plots of 8.25 meter long, each spaced 1 m apart between rows and 0.75 m between plants. There were 11 plants row^{-1} and the middle five plants were randomly selected and used for data collection. After the crop established well, earthing up and weeding were carried out when necessary.

Data collection

Descriptor of tannia developed by International board for Plant Genetic Resources (IBPGR, 1989) was followed for data collection. 16 quantitative data were used, most of which were distinguished as highly heritable traits. Measurements of above ground morphological characters were carried out from those selected middle five plants in each plot at 5^{th} to 6^{th} 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). Data were collected on traits: 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), cormel length (cm), cormel diameter (cm), corm fresh weight per plant (kg), 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

Collected data were subjected to ANOVA based on simple lattice design using SAS version 9.2 (SAS, 2008). Then the differences between genotypes mean were compared using LSD (Least significance difference) at 5% probability level. The ANOVA model for simple lattice design is:

$$Y_{ijklm} \quad t_{i} \quad (k) \quad y_{l} \quad m \quad o_{ijklm}$$

Where: Y_{ijklm} = response of Y trait from the i^{th} genotypes, j^{th} replication, μ = Overall mean effects, t_i = Effects of i^{th} level of treatments, β = Effects of j^{th} level of replication, χ_k = Effects of K^{th} level of blocks within replications (adjusted for treatments), y_l = Effects of l^{th} level of intra block error, π_m = Effects of the m^{th} randomized complete block error and O_{ijklm} = is a random error component.

Table 1. List of genotypes of tannia studied studied at Jimma, 2013/2014.

Genotype	Destrict	Kebele/Village	Altitude (masl)	Genotype	Destrict	Kebele/Village	Altitude (masl)
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

Genotypic (^{2}g), environmental (^{2}e) and phenotypic (^{2}p) variance component were computed as (Singh, 2001) as follow:

$$^2 g \quad \frac{MSg - MSe}{r}, \quad ^2 p \quad ^2 ge \quad \text{and} \quad ^2 e \quad MS$$

Where: MSg is genotypic mean square, MSe is error mean square and r is replication.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated according to the method suggested by Burton and De Vane (1953), as:

$$PCV = \frac{\sqrt{^2 p}}{100 x}$$

$$GCV = \frac{\sqrt{^2 g}}{100 x}$$

Where: is the grand mean value of the trait.

Heritability in Broad Sense (h^2B) estimated as described by Allard (1960) as follow:

$$h^2 B \quad \frac{^2 g}{^2 p} 100$$

Expected Genetic Advance (GA) and Expected genetic advance as percent of the mean (GAM) were predicted as suggested by Johnson et al. (1955):

$$GA \quad (K).(p).(h^2 B)$$

$$GAM \frac{GA}{100} *$$

Where: K = selection differential which varied with selection intensity (5% intensity was used at which K = 2.06), σp = phenotypic standard deviation, h2B = heritability and $\bar{x}$ = population mean.

Table 2. Mean squares of tannia genotypes for 16 quantitative characters studied at Jimma, 2013/14**.**

Character	Mean square		CV (%)	R^2
	Treatment	Error		
SU	0.76**	0.15	16.73	88.4
LL	6.32**	1.4	4.87	91.89
LW	6.18**	1.5	5.42	89.11
PLC	61.01**	14.04	5.69	87.75
PTLg	35.87**	8.88	6.54	89.61
Ph	57.96**	15.91	7.08	88.78
COL	2.48*	1.43	11.52	77.89
CLD	0.44**	0.17	7.9	80.41
NCL	14.48**	4.9	18.84	83.98
CML	0.95** $^{ad.}$	0.48	8.04	81.79
CMD	0.93*	0.59	9.27	75.5
COW	0.0226**	0.008	19.7	84.5
CMW	0.0064**	0.0014	16.09	91.62
CMDM	10.41**	4.09	7.24	81.78
CODM	11.23**	4.46	7.65	78.7
Tot Yi.	0.043**	0.0137	17.01	87.55

**, * significance at 0.01 and at 0.05 probability level; ^{ad} = adjusted treatment mean. SU = number 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 = number 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 (%), TotYi = total root yield per plant (kg).

Where: K = selection differential which varied with selection intensity (5% intensity was used at which K = 2.06), σ p = phenotypic standard deviation, h^2B = heritability and = population mean.

RESULTS AND DISCUSSION

The analysis of variance showed presence of significant variations (P ≤ 0.05) among genotypes for the studied characters (Table 2). This significant variation among tested genotypes for the characters is the result of combinations of genotypic and phenotypic effect (Acquaah, 2012). Such a significant variation was reported previously such as: Paul and Bari (2012) were reported a significant difference among tannia genotypes for characters like plant height, petiole length, cormel breadth, corm breadth, cormel weight, corm weight and yield per plant. Similarly, Tewodros (2013) reported that petiole length and plant canopy diameter showed highly significant variation; but he reported that non-significant variation of lamina length, lamina width, number of sucker per plant, plant height and tuber fresh weight among taro genotypes in Ethiopia.

The range and mean of genotypes for the studied characters also showed wide ranges of variation (Table 3) like number of sucker per plant (1.19 to 4.42), lamina length (20.81 to 29.61 cm), lamina width (18.44 to 27.94 cm), plant canopy diameter (56.33 to 82.03 cm), petiole length (37.72 to 57.52 cm), plant$\bar{x}$ height (44.68 to 72.72 cm), cormel length (7.83 to 13.13), number of cormels per plant (7.38 to 13.57), cormel weight (0.27 to 0.74 kg/plant), corm weight (0.13 to 0.43 kg/plant), corm dry matter content (21.5 to 32.5%), cormel dry matter content (20 to 32.5%) and total yield per plant (0.44 to 1.10 kg/plant). Moreover, the difference between the minimum and the maximum mean values were high, indicating the availability of variation for improvement through selection. Such a wide range of variation in plant height, plant canopy diameter, lamina width and lamina length gives good opportunity for selection to have desired plant characters by selection or hybridization with respect to spacing (plant population per hectare), leaf area with respect to other physiological characters like transpiration and photosynthesis (light harvesting structure) and availability of moisture to improve productivity per hectare base.

Based on the mean values, the average value was almost twice that of the minimum mean values for character cormel fresh weight and corm weight indicating that their maximum contribution to the total variability observed among the genotypes was high. More than half of the tested genotypes had mean corm and cormel dry

Table 3. The range and the mean values of Tannia genotypes for 16 characters studied at Jimma, 2013/14.

Character	Maximum mean		Minimum mean		Grand mean
	Value	Acc.	Value	Acc.	
SU	4.42	AAGT102	1.19	AAGT127	2.36
LL	29.61	AAGT152	20.81	AAGT199	24.29
LW	27.94	AAGT152	18.44	AAGT199	22.65
PLC	82.03	AAGT102	56.33	AAGT135	65.51
PTLg	57.52	AAGT069	37.72	AAGT199	45.59
Ph	72.72	0003/07	44.68	AAGT171	56.33
COL	13.13	AAGT152	7.83	AAGT003	10.38
CLD	5.98	AAGT163	3.33	AAGT159	5.19
NCL	13.57	AAGT106	7.38	AAGT003	11.67
CML	9.64	0003/07	6.43	AAGT171	7.94
CMD	10.15	AAGT094	6.59	AAGT159	8.28
COW	0.74	AAGT183, 0003/07	0.27	AAGT171	0.454
CMW	0.43	AAGT069	0.13	AAGT199, AAGT176, AAGT109	0.24
CMDM	32.50	AAGT132	21.50	0002/07	27.94
CODM	32.50	AAGT202	20.00	0002/07	27.61
Tot. Yi	1.10	0003/07	0.44	AAGT127, AAGT159	0.69

SU = number 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 = number 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 (%), TotYi = total root yield per plant (kg).

matter content of above the overall mean of the genotypes (27.94 and 27.61% respectively). Similarly, 25, 42 and 36% of the genotypes showed higher weight of cormel, corm and total yield than the grand mean yield 0.454, 0.24, 0.69 kg/plant respectively. Hence, there is an opportunity to find genotypes among the tested entries that give better yield of cormel and corm as well as genotypes which have higher dry matter content of corm and cormel. Such a wide variation were observed before and the results were in agreement with the findings of Opoku-Agyeman et al. (2004) who reported a wide ranges of variation of 78 tannia genotypes for characters like petiole length, plant height, number of cormel per plant and cormel fresh weight in Ghana. Similarly, ReyesCastro et al. (2005) reported variation between tannia genotypes for traits of plant height, number of suckers, number of cormels per plant, cormel length, cormel weight and total yield.

The maximum phenotypic variances were obtained for plant canopy (37.52) followed by plant height (36.94) and petiole length (22.37). As in Table 4 the genotypic variances for these characters were also high for plant canopy (23.49) followed by plant height (21.03) and petiole length (13.5), indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on phenotypic performances of these characters. Relatively lower variances were observed for number of suckers per plant, cormel diameter, cormel length, corm diameter, corm length, corm fresh weight, cormel fresh weight and total root yield per plant.

On the other hand, PCV ranged from 8.09 for lamina length to 28.64 for number of sucker per plant and GCV ranged from 4.98 for cormel diameter to 23.48 for number of sucker per plant. According to Deshmukh et al. (1986) PCV and GCV values of more than 20% are considered as high, values less than 10% as low and values between 10 and 20 as moderate. Hence, number of sucker per plant (GCV = 23.48; PCV = 28.64), number of cormels per plant (GCV = 18.64; PCV = 26.49), cormel fresh weight (GCV = 18.81; PCV = 27.24), corm fresh weight (GCV = 21.13; PCV = 26.42) and total yield per plant (GCV = 17.54; PCV = 24.40) showed moderate to high GCV along with higher PCV. While the rest showed lower PCV and GCV.

In the present study, almost all characters exhibited higher PCV than their corresponding GCV (Table 4), indicating the apparent variations in the genotypes were not only due to genotypic effect but also due to environmental influences, since phenotypic variances were contributed by the effect of interaction of genotypes and environment (Acquaah, 2012). However, the difference between PCV and GCV were relatively narrow, shows that the observed variations for the trait were mostly due to genetic factors so, selection could be advanced here. The PCV and GCV gap between number of cormel per plant, corm diameter and cormel length was wider indicating the greater contribution of environment on these traits. This is in support of Bisne et al. (2009) who stated that high phenotypic variations composed of high genotypic variations and less of environmental variations

Table 4. Estimates of phenotypic (σ^2p), environmental (σ^2e) and genotypic (σ^2g) variances, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad sense (h^2B), genetic advance (GA) and genetic advance as percent of mean for characters studied at Jimma, 2013/14.

Character	σ^2g	σ^2e	σ^2p	PCV	GCV	h^2B	GA	GAM
SU	0.307	0.15	0.457	28.64	23.48	67.18	0.94	39.64
LL	2.46	1.4	3.86	8.09	6.46	63.73	2.58	10.62
LW	2.34	1.5	3.84	8.65	6.75	60.94	2.46	10.86
PLC	23.49	14.04	37.52	9.31	7.36	62.58	7.90	12.00
PLlg	13.5	8.88	22.37	10.38	8.06	60.31	5.88	12.89
PH	21.03	15.91	36.94	10.79	8.14	56.92	7.13	12.65
COL	0.525	1.43	1.955	13.47	6.98	26.85	0.77	7.45
CLD	0.135	0.17	0.305	10.64	7.08	44.26	0.50	9.70
NCL	4.79	4.9	9.69	26.49	18.64	49.43	3.17	26.98
CML	0.235	0.48	0.715	10.65	6.11	32.87	0.57	7.21
CMD	0.17	0.59	0.76	10.53	4.98	22.37	0.40	4.85
COW	0.0073	0.008	0.0153	27.24	18.81	47.68	0.12	26.75
CMW	0.0025	0.0014	0.0035	26.42	21.13	63.96	0.08	34.82
CMDM	3.16	4.09	7.25	9.64	6.36	43.59	2.42	8.65
CODM	3.385	4.46	7.845	10.14	6.66	43.15	2.49	9.02
Tot. Yi	0.0146	0.0137	0.0284	24.40	17.54	51.68	0.18	25.98

SU = number 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 = number 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 (%), TotYi = total root yield per plant (kg)

indicate the presence of high genetic variability for different traits and less influence of environment.

The result is in agreement with Choudhary et al. (2013) which reported high value of phenotypic coefficient of variation along with genotypic coefficient of variation for number of suckers per plant and cormel yield on taro genotypes. Paul and Bari (2012) reported high PCV along with high GCV for cormel weight, corm weight, number of cormels per plant and total fresh weight per plant for tannia genotypes. Similarly, Cheema et al. (2006) reported high PCV and GCV for number of cormels per plant, total yield per plant and corm fresh weight on taro genotypes.

The estimate of broad sense heritability values ranged from 22.37 to 67.18% (Table 4). According to Verma and Agarawal (1982) heritability values greater than 50% are considered as high, values between 20 to 50% as medium and values less than 20 are as low heritable. Based on this, lamina length (63.73%), lamina width (60.94%), number of suckers per plant (67.18%), plant canopy diameter (62.58%), petiole length (60.31%), plant height (56.92%), corm weight (63.96%) and total yield per plant (51.68%) exhibited high heritability estimates, suggesting that, greater effectiveness of selection and improvement to be expected from these characters in future breeding program.

This is in support of Sedeek et al. (2009) who stated that selection would be effective when major portion of variability for different traits in the source population is heritable. This is because there would be a close correspondence between the genotype and phenotype due to relatively small contribution of the environment to the phenotype. Also moderate heritability estimate of cormel diameter (44.26%), cormel fresh weight (47.68%), number of cormels per plant (49.43%), corm dry matter (43.59%), cormel dry matter (43.15%), cormel length (26.85%), corm diameter (22.37%) and corm length (32.87%) exhibited, which indicates the presence of more environmental effect, because of this selection may be difficult due to the masking effect of the environment on germplasm.

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Bisne et al., 2009). The expected genetic advance expressed as a percentage of the mean (GAM) ranged from 4.85% for corm diameter to 39.64% for number of suckers per plant (Table 4). This indicated that selecting the top 5% of the base population could result in an advance of 4.85 to 39.64% over the population mean.

According to Johnson et al. (1955) genetic advance as percent of mean could be considered as low if it ranges between 0 and 10%, as moderate 10 and 20% and high if it becomes above 20%. Consequently, number of sucker per plant, number of cormel per plant, cormel weight, corm weight and total yield per plant had high genetic advance along with high heritability. Lamina length, lamina width, plant canopy diameter, petiole length and

plant height showed moderate genetic advance along with high heritability. The presence of high heritability coupled with moderate to high genetic advance indicates that these are more inherited traits and most likely the heritability was due to additive gene effects of these characters. Hence, selection for these characters is likely to be more effective and have a greater scope of improvement. This is in support of Johnson et al. (1955) who stated that high heritability along with high genetic advance is more reliable than heritability alone in predicting the results of selection.

Low values of genetic advance were recorded for corm diameter (4.85%), corm length (7.21%), cormel diameter (9.70%) corm dry matter content (8.65%), cormel dry matter content (9.02%) and cormel length (7.45%). These low genetic advances arise from moderate heritability and low estimate of genotypic variances. Therefore, it is imperative that selection of genotypes based on phenotypic performance for these characters would not be effective for improvement. Low genetic advance as part of mean with moderate heritability suggested the role of non-additive gene action (dominance and epistasis) for the control of these characters and most of the variation for these traits were environmental.

This finding is in harmony with that of Singh et al. (2003) who reported high heritability estimates along with high genetic advance for weight of corm per plant, number of cormels per plant and cormels fresh weight per plant among taro germplasms. Similarly, Yadav et al. (2007) and Cheema et al. (2006) reported high heritability along with high genetic advance for number of cormels per plant, corm weight per plant, cormel fresh weight per plant and total yield in taro genotypes. Also Paul and Bari (2012) reported high genetic advance as a percent of mean along with high to moderate heritability for number of cormels per plant, lamina length, lamina width, petiole length, plant height, cormel fresh weight, corm weight and total yield per plant; and also low genetic advance for corm length of tannia germplasm.

In general, the study has shown that there is a wide genetic variability between genotypes of tannia for further utilization in tannia improvement program. However, the result of the present investigation may vary with location and season since this study was conducted in single environment for one season. That means, the available genotypes should be further studied with due emphasis on quantitative characters required to determine further variations and observe the presence and magnitude of genotype-environment interaction. Furthermore, the presence of morphological variation between genotypes is not a guarantee for high genetic variation. Hence, molecular or biochemical studies need to be considered as complementary to this study. Since simple selection of superior types among the existing genotypes could result in identification of promising lines, tannia accessions from other growing areas of Ethiopia need to be collected, so as to broaden the base of existing breeding program. In addition way of inducing flowering and seed propagation, Calcium oxalate content of corm and cormel, effect of time of planting and harvesting, also effect of type of planting material on yield and dry matter content should be considered as future line of work.

Conflict of Interest

The authors have not declared any conflict of interest.

ACKNOWLEDGMENTS

The author is grateful to the Agriculture Faculty of Arba Minch University for their unwavering support they gave to make the research work a success

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