Sky Journal of Agricultural Research Vol. 2(11), pp. 154 - 158, December, 2013
Available online http://www.skyjournals.org/SJAR
ISSN 2315-8751 ©2013 Sky Journals

Full Length Research Paper

Study on genotypic variability estimates and interrelation-ship of agronomic traits for selection of taro (*Colocasia esculenta* (L.) Schott) in Ethiopia

Tewodros Mulualem* and Getachew WeldeMichael

Root, Fruit and Vegetable Crops Research, Jimma Agricultural Research Centre, Jimma, P.O. Box 192, Ethiopia.

Accepted 21 October, 2013

The study was carried out with the objective to estimate the genotypic variability and other yield related traits of taro in Ethiopia. A total of 100 accessions of taro were considered to this study. Analysis of variance was computed to contrast the variability within the collected accessions based on yield and other yield related traits. The results revealed significant differences among the accessions. Genotypic coefficient of variation (GCV %) was lower than phenotypic coefficient of variation (PCV %) for all the traits studied. High genetic advance with heritability was observed in the following characters petiole length, number of active leaves/plant and average leaf length per plant. At genotypic level, merely tuber dry weight (r = -1.00) showed significant and strong negative correlations to tuber fresh weight. Therefore, it can be safely concluded that the variability with in taro accessions collected from southern and south-western parts of Ethiopia is low and the extent of its improvement is narrow.

Key words: Association, heritability, taro, variability.

INTRODUCTION

Taro (*Colocasia esculenta* (L.) Schott) is a herbaceous, monocotyledonous, perennial stem root crop that is widely cultivated in tropical and subtropical regions of the world. It is a globally important crop, ranked fifth in area and production after cassava, potato, sweet potato and yam (FAO, 2010).

In Ethiopia, although reliable statistical information on the distribution and production of taro is lacking, the crop has been cultivated widely in many areas of the country with low amount of yield (Norman et al., 1985). This might be due to the fact that taro has been widely neglected by research and development programs (Jianchu et al., 2001) and the taro genetic resources are being eroded by physical and bio-physical factors (Edossa, 1996). As a result, the country frequently faces a considerable amount of food shortage for the last decades. Therefore, collection and introduction of taro genotypes is the best means of obtaining genetic variability for further improvement of this crop (Asfaw, 2006; Schott, 2000). Genetic variability is found to be the principal raw materials of any breeding programme (Yared, 2007). Determining the level of variation and identifying the variants within the collected species is invaluable for genetic improvement and conservation of the crop (Amsalu, 2003; IPGRI/IITA, 1997). However in Ethiopia, where taro is becoming an important food security crop, previous there has been no any effort so far done with regard to the estimation of the magnitude of genotypic variation, heritability, genetic advance and correlation of yield contributing traits among the collected accessions of this crop. The present study, therefore, intended to assess the nature and extent of genetic variability of taro in Ethiopia.

*Corresponding author: E-mail: tewodros 74@yahoo.com

MATERIALS AND METHODS

Description of the study area

The experiment was conducted at Jimma Agricultural Research Center, the center is located at a latitude of 7^{o} 46' N and longitude 36^{o}E at an altitude of 1753 m.a.s.l. The area receives mean annual rainfall of 1432 mm with maximum and minimum temperature of 29.2 and of

8.90°C, respectively. The soil is Eutric Nitosole (reddish brown) with pH of 5.3. A total of 100 *Colocasia esculenta* accessions were considered in this study. The accessions were collected from south and south-western parts of Ethiopia, during March - April 2000. The collections covered diverse agro-ecologies with an altitude range of 1130 - 2340 m.a.s.l, representing one of the major taro production areas in the country.

The study was laid as 10 X10 simple lattice design using 10 m x 10 m plots with two replications. Single row plot, with each row 10 m long and spacing 0.75 m between rows and 0.5 m between plants within a row was used. Corms of the same size were used as planting materials on a ridge during the onset of rainy season (early April). The middle six plants of the row were used for data collection and harvesting.

Data collection

Descriptors for taro (*C. esculenta*) (Federer, 1997) developed by International Plant Genetic Resources Institute was used with some modifications for this study. Thirteen different quantitative data were recorded on the plants under field conditions to evaluate the genotypes. All data were standardized and subjected to analysis of variance for all the characters according to Burton and Dewane (1953).

Statistical analysis

The phenotypic and genotypic coefficients of variation were computed by SAS (1999) considering genotypes as random effects using SAS statistical packages (Allard, 1960).

Genotypic variance component

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

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

Environmental variance component (On genotypic mean basis)

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

Phenotypic variance component

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

Genotypic and phenotypic coefficients of variation were calculated according to the method suggested [13]. as: Genotypic coefficients of variation (GCV)

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

Phenotypic coefficients of variation (PCV)

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

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

Broad sense heritability (h^2) in percents in estimated was estimated in for each character using variance components as described by Johanson (1955a).

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

The expected gain or genetic advance with one cycle of selection, assuming the selection intensity of 5%, was predicted as suggested by Singh (1985).

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

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:

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

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

Genotypic covariance of traits

$$\sigma^2_{g\,xy} = \frac{MSCP_{gxy} - MSCP_{exy}}{r} \quad (9)$$

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

$$\sigma^2_{p\,xy} = \sigma^2_{g\,xy} + \frac{\sigma^2_{gexy}}{r} \quad (10)$$

Genotypic and phenotypic correlation coefficients of fresh tuber yield and its components were estimated calculating the variance and covariance at phenotypic and genotypic level by using the formula suggested by

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 (GAM) for 13 traits of *Collocasia esculenta* Grown at Jimma in 2011.

Traits	Mean ± SE	Range	σ^2_g	σ^2_p	PCV	GCV	Heritability (%)	Genetic advance	GAM (%)
LL	40.5 ± 2.65	20.0 –29.0	5.398	42.599	15.843	5.639	12.67	1.70	4.135
LW	25.8 ± 2.40	19.0 –26.2	0.806	22.865	17.461	3.277	3.52	0.34	1.267
NAL	15.7 ± 2.46	7.0 – 14.2	6.235	25.979	33.510	16.417	24.00	2.52	16.56
PL	52.4 ± 3.13	29.0 –48.0	29.669	97.139	18.809	10.394	30.54	6.20	11.83
BaRL	57.9 ± 3.38	35.0 –50.0	4.453	130.741	19.751	3.645	3.41	0.80	1.385
MHD	0.96 ± 0.43	0.65 –0.85	0.003	0.029	17.986	5.460	9.22	0.03	3.414
PH	0.98 ± 0.50	0.60 –0.90	0.005	0.078	28.366	7.008	6.10	0.03	3.566
NSu	6.28 ± 1.57	1.0 – 4.0	0.109	5.274	34.839	5.009	2.07	0.09	1.483
NT/hil	7.59 ± 1.59	3.0 – 5.0	0.456	6.210	32.425	8.782	7.34	0.37	4.900
TL	11.64 ± 1.20	8.0 – 11.0	0.010	2.144	12.574	0.854	0.46	0.13	0.119
TDi	62.66 ± 3.07	31.9 –56.3	4.319	89.463	15.119	3.321	4.83	0.94	1.503
TFW	0.80 ± 0.52	0.2- 0.60	0.004	0.082	35.656	8.266	5.37	0.03	3.947
TDW	28.5 ± 2.04	18.3- 25.3	0.041	17.263	14.614	0.715	0.24	0.20	0.072

LL=Leaf length(cm); LW= leaf width(cm); NAL = Number of active leaves, Pl= Petiole length(cm), BaRL = Basal ring length(cm), MHD= Maximum horizontal distance(m), PH= Plant height(m), Nsu= Number of sucker/plant, NT/hil= Number of tuber/hill, TL=Tuber length(cm), TDi=Tuber diameter(cm), TFW=Tuber fresh weight(kg/plot) and TDW=Tuber dry weight.(kg/plot).

Miller et al. (1958).

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 Robertson (1959).

$$r_{p\,xy} = \frac{\sigma_{p\,xy}}{\sqrt{(\sigma^2_{px})(\sqrt{(\sigma^2_{py})}} \quad 11$$

Genotypic correlation between traits x and y was computed as

$$r_{gxy} = \frac{\sigma_{p\,xy}}{\sqrt{(\sigma^2_{gx})(\sqrt{(\sigma^2_{gy})}} \quad 12$$

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:

$$t = r_{pxy}\sqrt{g-2} \,/\sqrt{(1-r^2_{pxy})} \quad 13$$

The calculated 't' value was compared with tabulated 't' at n-2 degree of freedom, where n is the number of characters. The correlation coefficients at genotypic level were tested with the following formula suggested by Baye et al. (2005).

$$t = r_{gxy} / SEr_{gxy} \quad 14$$

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

$$SEr_{gxy} = \sqrt{\frac{(1-r2\_gxy)2}{2h2\ xh2y}} \quad 15$$

RESULTS AND DISCUSSION

The analysis of variance for characters showed significant differences between the genotypes (Tables 1 and 2). Analyzed data indicated the existence of variability in the collected genotypes. This provides for selection from collected genotypes and genetic improvement.

Ample amount of variation was observed for petiole length (cm), plant height (m) and tuber diameter (cm). Phenotypic and genotypic variances, heritability, genetic advance and genetic advance of mean of the characters is shown in Table 2. Higher variance was observed in the traits, petiole length (cm), basal ring length / plant (cm), tuber diameter (cm), leaf length (cm) and leaf width (cm). Tuber fresh yields being a quantitative trait is influenced by many genes and are highly controlled by a biotic factors. Variability is the addition of total hereditary effects from alarmed genes as well as the environment. Therefore, the variability is grouped into heritable and non-heritable components with suitable genetic parameters such as genotypic coefficient of variation

Table 2. Genotypic (above diagonal) and Phenotype (below diagonal) Correlation Coefficient among 13 Traits in 100 *Taro* Accessions Grown at Jimma.

Traits	TFW	LL	LW	NAL	PL	BaRL	MHD	PH	NSu	NT/hil	TL	TDi	TDW
TFW		0.17	0.01	0.16	-0.02	0.12	0.02	0.08	0.06	0.15	-0.08	0.05	-1.00**
LL	0.47		-1.00**	0.67*	0.30	-1.00**	1.00**	0.24	1.00**	1.00**	-1.00**	-1.00**	-1.00**
LW	-0.78**	0.41		1.00**	-0.60*	-1.00**	1.00**	-0.72**	1.00**	1.00**	-10.0**	-1.00**	-1.00**
NAL	0.34	0.04	-0.03		-0.38	0.41	0.05	0.10	1.00**	0.08	-0.74**	-0.38	0.50
PL	0.54*	0.09	-0.06	-0.03		1.00**	1.00**	0.89**	1.00**	0.20	-0.39	1.00**	-0.23
BaRL	1.00**	0.41	0.22	0.12	0.34		1.00**	-0.58*	1.00**	-1.00**	-1.00**	-1.00**	-1.00**
MHD	-0.18	0.16	0.07	0.01	0.04	0.09		1.00**	0.83**	0.14	1.00**	1.00**	-1.00**
PH	1.00**	0.31	0.12	-0.01	0.23	0.44	0.15		0.45	-0.92**	1.00**	0.45	-1.00**
NSu	1.00**	-0.04	-0.14	0.35	0.11	0.05	0.09	0.02		0.19	1.00**	1.00**	-1.00**
NT/hil	1.00**	0.05	-0.05	0.07	0.03	0.06	0.04	0.23	0.09		0.61*	-0.76**	0.65*
TL	-1.00**	0.15	0.12	-0.12	0.01	0.16	-0.06	0.07	-0.09	-0.17		-1.00**	-1.00**
TDi	-0.97**	0.28	0.16	-0.06	0.10	0.37	0.18	0.32	-0.12	-0.01	0.29		-1.00**
TDW	-0.08	-0.12	-0.08	-0.18	-0.03	-0.06	-0.08	-0.14	-0.16	-0.05	0.04	-0.06	

LL=Leaf length(cm); LW= leaf width(cm); NAL = Number of active leaves, Pl= Petiole length(cm), BaRL = Basal ring length(cm), MHD= Maximum horizontal distance(m), PH= Plant height(m), Nsu= Number of sucker/plant, NT/hil= Number of tuber/hill, TL=Tuber length(cm), TDi=Tuber diameter(cm), TFW=Tuber fresh weight(kg/plot) and TDW=Tuber dry weight.(kg/plot)

(GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA). These genetic parameters help the breeders in selection of the genotypes and for genetic improvement of this crop.

Phenotypic coefficient of variation (PCV %) was found superior than the genotypic coefficient of variation (GCV %) for all the characters. High GCV together with high heritability and high genetic advance will give good information than each parameter alone (Saha,1990). Thus, in this study, number of leaves (16.41), petiole length (10.39) and number of tuber/hill (8.78) showed high genotypic coefficients of variation, high heritability together with high genetic advance as percent of means. This suggests that occurrence of additive gene action with low environmental influence for the determination of these traits and could be valuable in phenotypic selection of taro.

Heritability estimates varied from 0.24% for tuber dry weight to 30.54% for petiole length/ plant (Table 1). The maximum heritability was obtained from petiole length/plant, number of active leaves/plant and average leaf length per plant. It was observed that the maximum genotypic coefficients of variation were supported by high estimates of heritability. Moreover, tuber dry weight, tuber length, vine fresh weight and average basal root length/plant have comparatively low heritability estimates (Table 1). Genetic advance indicates the degree of gain in a character obtained under a particular selection and helps the breeder to predict the degree of improvement that can be achieved in different characters.

High heritability together with high genetic advance is a vital tool for selection of the best individuals and for successful genetic improvement. Estimates of genetic advance ranged from 0.03 for tuber fresh weight (kg/plant) to 6.20 for petiole length (m) (Table 1). The value of genetic advance as percent of mean varied from 0.072% for tuber dry weight (kg/plant) to 16.56% for number of active leaf per plant. It was indicated that petiole length per plant with the high heritability (30.54%) had the highest genetic advance (6.20), number of active leaves and average leaf length/plants showed similar tendency in heritability and genetic advance. The genetic advance as percent of mean was also moderately higher for number of active leaves/ plant (16.56%) and petiole length/ plant (11.83%), and this in line with their respective heritability (Table 1). This indicates that selection for the traits like for number of active leaves/plant and petiole length/plant is easier than selection for other characters. Moderate genetic advance together with high heritability observed for leaf length indicated the presence of intra and inter allelic interactions in the appearance of these characters.

Correlation among the characters studied revealed significant differences between phenotypic and genotypic correlations in all pairs of traits. The amount of genotypic correlations was always higher than phenotypic correlations. In this study, there was no character that showed significant and strong positive genotypic correlations to tuber fresh/plant (Table 2). Almost all characters showed non-significant and positive correlation with tuber fresh weight/plant. Based on the correlations between characters at genotypic level, accessions with high fresh weight, leaf length, number of active leaves /plant, petiole length, basal ring length and diameter will not maximize tuber yield, for this reason, it does not need high consideration in efforts towards tuber yield improvement.

Tuber dry weight, showed very high significant negative

genotypic correlation for most of the foliar and subterranean traits as leaf length, leaf width, basal ring length, maximum horizontal distance, plant height, number of suckers/plant, tuber length and tuber diameter. Number of suckers/ plant showed strong and positive correlation with most of the characters for example, with leaf length, leaf width, number of active leaf/plant, petiole length, basal ring length/ plant; and maximum horizontal distance.

Conclusions

The range and mean performance of the character showed substantial amount of variability among the genotypes. For instance, tuber fresh yield ranged from 0.2 to 0.60 ton/plot, leaf length varied from 20.0 to 29.0 cm, leaf width varied from 19.0 to 26.2 cm and tuber diameter varied from 31.9 to 56.3 cm. The estimate of heritability ranged from 0.24% for tuber dry weight to 30.54% for petiole length. Values of genetic advance expected from selection of the superior 5% of the accessions and expressed relative to the means ranged from 0.03 for tuber fresh weight, plant height and maximum horizontal distance to 6.20 for petiole length. PCV ranged from 12.54 for tuber length to 34.839% for number of sucker/plant whereas GCV ranged from 0.715 for tuber dry weight to 16.417% for number of active leaves/plant. Among the various quantitative characters, relatively higher PCV and GCV were observed for number of active leaves/plant (33.51 and 16.41, petiole length (18.80 and 10.39), tuber fresh weight (35.65 and 8.26) and number of tuber/hill (32.42 - 8.78). It may therefore be given due attention for an effective selection in yield improvement of *C. esculenta.* Tuber fresh weight was significantly and positively correlated with petiole length, basal ring length, plant height, number of sucker/hill and number of tuber/hill at phenotypic level. On the other hand, at genotypic level, most of the correlation between characters showed non-significant. In general, it can be concluded that the variability with in *C. esculenta* accessions collected from southern and south-western parts of Ethiopia is low and the scope of its improvement is narrow.

Acknowledgments

The authors we like to acknowledge Jimma Agricultural Research Centre for the financial support.

REFERENCES

FAO (2010). Quality declared planting material Protocols and standards for vegetative propagated crops, ISBN 978-92-5-106425-2 Rome, Italy, pp. 41–48.

Norman MJT, Pearson CJ and Searle PGE (1985). The ecology of tropical foods crops, Cambridge University Press 2: 305-327.

Jianchu X, Yang Y, Yingdong PW, Ayad G, Eyzagůirre PB (2001). The genetic diversity in taro (*Colocasia esculenta* Schott-*Araceae*) in China: An Ethno botanical and genetic approach Economic Botany. 55 (1): 14-31.

Edossa Etissa (1996). Root and Tuber Crops:" Potential as food crops in the humid areas of Ethiopia". Institute of Agricultural Research, pp. 2-4.

Asfaw K (2006). Characterization and divergence analysis of some Ethiopian taro (*Collocasia esculenta* (L.) Accessions M.Sc thesis, Alemaya University, Ethiopia, pp.45-56.

Schott GA (2000). Best and R. Bokanga,. Roots and tubers in the global food system: A vision statement to the year 2020. Lima, Peru, A co publisher of CIP, CIAT, IFPRI, IITA, IPGRI. Printed in: international potato center.

Yared D (2007). Studies on indigenous production and evaluation of landrace taro clones (*Colocasia esculenta* L. (Schott) at Dalbo watershed, Wolaita, South Ethiopia. M.Sc. thesis, Hawassa University, Awassa, pp. 67-72.

Amsalu N (2003). Characterization and divergence analysis in cassava (*Manihot esculenta* Cranz) Genotypes at Jimma. MSc thesis, Alemaya University, Ethiopia, pp. 7 - 9.

IPGRI/IITA (1997). International Plant Genetic Resources Institute/International Institute for Tropical Agriculture, Descriptors for taro (*Collocasia spp*), Ibadan, Nigeria, Rome, Italy.

Federer WT (1997). Experimental Design: Theory and Application. New York: Mc Millan.

Burton GW, Dewane EM (1953). Estimating heritability in tall Fesue (Fistula arundanaceae) from replicated clonal material. Agron J., 48: 478-481.

SAS (1999). Statistical Analytical Systems SAS / STAT user's guide version 8(2) cary NC :SAS institute inc.

Allard RW (1960). Principles of Plant Breeding. John Wiley and Sons Inc. New York.

Johanson HW (1955a). Robinson and R.E. Comostock. Estimates of genetics and environmental variability in soybeans. Agron. J., 47: 314-318.

Singh RK, Chaudhury BD (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, p. 318.

Miller PA, Williams JC, Robinson HF, Comstock RF (1958) Estimation of genetic and environmental variances and their implications in selections. Agron. J., 50: 126-131.

Robertson GR (1959). The sampling variances of the genetic correlation coefficients. Biometrics, 15: 469-485.

Baye B, Ravishankar R, Singh H (2005). Variability and Association of Corm Yield and Yield Related Traits in Potato, Eth. J. Agric. Sci., 18(1): 103-121.

Saha SC, Mishira SN, Mishira RS (1990). Genetic variation in F_2 generation of chilli Capsicum News Letter, 8: 29-30.