Genetic Variability among Six Traits in Twelve Cassava (Manihot esculenta Crantz) Genotypes in Southern Tanzania

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Abstract
Twelve cassava genotypes were evaluated to assess genetic variability for root yield and its components at three locations (Naliendele, Mtopwa and Nachingwea) in Southern Tanzania during 2011/2012 cropping season. Data exploited for this purpose were, number of branches per plant, plant height, root number, root weight, shoot weight and root dry matter. Genotype x location interaction was significant for all the characters studied indicating considerable influence of the environment on the expression of the traits. High heritability and relatively high genetic gain were observed in plant height (72.90% and 36.67%), stem girth (69.41% and 33.63%) and roots per plant (44.88 and 37.05%) respectively, suggesting that the traits are primarily under genetic control and that reliable selection with simple recurrent phenotypic selection would be rewarding. Most of genotypic correlations were significant and positive. Though genotypes differed significantly at ($p > 0.05$) for all the traits studied, two genotypes (NDL 2006/487 and NDL 2006/438) and two varieties (Kiroba and Naliendele), were found to constitute a pool of germplasm with adequate genetic variability from which selection will bring about significant progress in cassava improvement programs.

Keywords: Cassava genotypes, Root yield, Genetic variability, Heritability, Genetic gain, Genetic correlations.

1.0 Introduction

Cassava (*ManihotesculentaCrantz*) is from the family *Euphobeaceae*. It is among the most important root crops worldwide and provides food for one billion people (Bokanga, 2001; Nuwamanya *et al.,* 2009). It is an important food crop in developing countries, and it is the fourth source of calories, after rice, sugar cane and maize worldwide (Akinwale *et al.,* 2010). The edible roots supply energy for more than 500 million people worldwide (Ceballos *et al.,* 2006). It is a perennial crop, native to America and grown in agro ecologies which differ in rainfall, temperature regimes and soil types (Olsen and Schaal, 2001). Cassava constitutes an essential part of the diet of most tropical countries of the world (Calle *et al.,* 2005). In Africa the crop is the most important staple food grown and plays a major role in the effort to alleviate food crisis (Hann and Keyer, 1985). In Nigeria cassava is grown extensively in the humid and sub humid areas and it has moved from being a subsistence crop to a full commercial crop for its income generating capacity (Akinwale, *et al*., 2010). The crop is now widely cultivated for vast industrial potentials. The potential for genetic improvement of cassava has been made in increasing its yield potential. Breeding efforts are focusing on the improvement of the yield potentials and quality traits through development of new cassava genotypes with a view to further broadening the genetic base of cassava. A cassava grows and yields in different environments but shows different growth behaviors in different locations as a result of variation in climatic and soil conditions. There new genotypes are developed, there is a need to evaluate their performance in different agro ecologies in order to identify those that are suitable for each agro ecology as well as those that are stable across varying environments. Many of the economic characters of cassava are quantitatively inherited are highly influenced by environmental conditions. Breeding progress is primarily determined by the magnitude, nature and inter-relations of genotypic and phenotypic variations in the various characters. This necessitates partitioning of the overall variability into its heritable and non-heritable components with the use of suitable genetic parameters, such as genetic coefficient of variation, heritability estimates, genetic advance and correlations. Heritability estimates in the broad sense quantifies the relative magnitudes of genotypic and phenotypic variances for traits and serves as a predictive role in selection procedures (Allard, 1960). This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation (Mba and Dixon, 1995). Knowledge of variability and heritability of various characters contributing to yield and to develop optimal breeding procedure is needed by cassava breeders. Yield is a complex character controlled by many quantitative genes. Its expression is therefore highly variable and it is improved by selecting for the components to yield (Akinyele and Osekita, 2006; Odeleye *et al.,* 2007; Osekita and Akinyele, 2008). Selection of one of the components may however fail to result in yield increase because of negative association among components (Makame, 1995). The degree of those correlations is not only of interest from a theoretical point of quantitative inheritance of characters, but also of practical value of selecting for two or more traits to estimate genetic parameters of some important quantitative characters and their implications in selection.

2.0 Materials and Methods

2.1 Description of the study area

The study was conducted in three locations of Southern Tanzania at Naliendele (Coastal low land plains), Mtopwa(Makonde plateau) and Nachingwea(Masasi-Nachinwea plains), during the 2011 – 2012 cropping season under rain fed conditions.Naliendele is located at 10° 22'S and 40° 10'E, 120m above sea level and receives mean annual rainfall of 950mm with monthly mean temperature of 27°C and average relative humidity of 86%. Nachingwea is located at 10° 20'S and 38°46'E, 465 m above sea level has a mean annual rainfall of 850mm, mean monthly temperature of 25°C and annual mean relative humidity of 78%. Mtopwa is located at 10° 41'S and 39° 23'E, 760m above sea level receives a mean annual rainfall of 1133mm with monthly mean temperature of 23°C and mean relative humidity of 75%. All the three sites experience a mono-modal type of rainfall.

2.2 Experimental materials and design

Twelve cassava genotypes obtained from Naliendele Agricultural Research Institute, Mtwara, Tanzania were evaluated in Southern Zone of Tanzania during 2011/2012 cropping season to determine the genetic variability for root yield and its components. The locations were: Naliendele, Mtopwa and Nachingwea. A Randomized Complete Block Design (RCBD) with three replications was used at each location. Plants were established at 1m x 1m spacing in 28m^2 plots. Neither fertilizer nor herbicide was applied to the plants. Weeding was done when necessary. Eight quantitative traits were evaluated at various stages of the crop growth. The traits evaluated were: plant height, number of roots per plant, number of branches per plant, root size, root dry matter, and stem girth.

2.3 Statistical analysis

Analysis of variance (ANOVA) was done to assess the genotype effects and their interaction using General Linear Model (GLM) procedure for randomized complete block design in Genstat version 14/IndostatWindostat version 8.5 programs from which estimates of variance components were generated. Broad sense heritability (h^2) was calculated as the ratio of the genotypic variance using the formula: $h^2 = \sigma^2_g / \sigma^2_{ph} \times 100$ (Allard, 1960) where h^2 = broad sense heritability (%), σ^2_g = genotypic variance and σ^2_{ph} = phenotypic variance. Phenotypic and genotypic coefficients of variations were computed following the methods outlined by Singh and Chaudhary (1979):

Phenotypic coefficient of variation (PCV) = $\sqrt{\delta^2 \text{ ph}/\bar{x}}$

Genotypic coefficient of variance (GCV) = $\sqrt{\delta^2 \text{ g}/\bar{x}}$

Where: σ^2_{ph}=Phenotypic variance; $\sigma^2 g$= Genotypic variance and $\bar{x}$= Mean of the population.

Also expected genetic gain (5%) as a percentage mean was estimated according to Singh and Chaudhary (1985) as follows:

$G.A = IH_b\sigma_p$

Where: I = standardized selection differential at 5% (2.06), H_b = broad sense heritability,

σ_p = phenotypic standard deviation, $\sigma^2_{ph.}$ = Genotypic correlations between pairs of traits were calculated from the components of variance and covariance estimate. Covariance for each trait, and genetic correlation were calculated using the formulae of Falconer and Maekey, 1996. Genetic correlation was considered significant at level of probability when its value is more than twice the standard error value.

$$\text{rg}_{xy} = \frac{\text{Covg}_{xy}}{\sqrt{\text{Varg}_x \times \text{Varg}_y}}$$

Where: rg_{xy} = Genotypic Correlation between trait X and Y,
Covg_{xy} = Genotypic covariance of trait pair,
Varg_x= Genotypic variance of X.
Varg_y = Genotypic variance of Y.

Phenotypic correlation was calculated using Pearson's linear correlation.

$$r_{12} = \frac{\sum x_1 x_2}{\sqrt{\sum x_1^2 \sum x_2^2}} \text{ (Steel and Torrie, 1984)}$$

Where: r_{12} = Correlation coefficient between character x_1 and x_2
$\sum x_1 x_2$= Correlation sum of cross products of characterx_1 and x_2
$\sum x_1^2$= Correlation sum of squares of traitx_1
$\sum x_2^2$= Correlation sum of squares of traitx_2

3.0 Results and Discussion

3.1 Performance of the Evaluated Cassava Clones

Results from combined analysis of genotypes differed significantly at ($p > 0.001$) (Table1). The highest root yield was found from the variety Kriroba (21.72 t ha^{-1}), while the lowest yielder was Albert with a root yield of 7.32 t ha^{-1}. Mean plant height ranged between 112cm (NDL 2006/741) and 143cm which was found from the genotype 2006/850. Number of roots per plant was between 3.33 from NDL 2006/030 and 7.03 from Kiroba. The genotype with the lowest mean for number of branches per plant was NDL 2006/487 (1.22), while Kiroba had the highest mean for number of branches per plant (3.71). Genotype NDL 2006/487 had the lowest harvest index of 0.60, while the highest harvest index of 0.74, was obtained from the genotype NDL 2006/738. The average root size ranged from 0.19 kg and 0.38 kg from genotypes NDL 2006/104 and NDL 2006/738 respectively. Two genotypes (NDL 2006/487 and NDL 2006/438) and two varieties (Kiroba and Naliendele), were found to constitute a pool of germplasm with adequate genetic variability from which selection will bring about significant progress in cassava improvement programs (Kundy *et al.,* 2014).

Table 1: Means for yield and growth parameters in tested cassava genotypes in combined analysis

Genotype	PHT	BRP	STG	RTP	RTS	DM%	HI	RTY
ALBERT	134.20^{bc}	2.93^{bcd}	4.12^{ef}	3.64^{fgh}	0.24^{bcd}	36.81^{cdef}	0.67^{bc}	7.32^{g}
KIROBA	116.90^{ef}	3.71^{a}	4.85^{a}	7.03^{a}	0.28^{bcd}	38.10^{bcd}	0.73^{ab}	21.72^{a}
NALIENDELE	123.40^{de}	2.86^{cd}	4.27^{def}	5.24^{c}	0.20^{d}	37.39^{cde}	0.67^{bc}	11.40^{e}
NDL 2006/030	126.30^{d}	2.80^{cde}	4.07^{f}	3.33^{h}	0.22^{cd}	35.57^{ef}	0.68^{abc}	8.95^{f}
NDL 2006/104	130.20^{cd}	2.97^{bc}	4.59^{bc}	3.52^{gh}	0.19^{d}	38.68^{abc}	0.67^{abc}	8.71^{f}
NDL 2006/283	137.80^{ab}	2.48^{efg}	4.37^{cde}	4.17^{de}	0.25^{bcd}	38.49^{abcd}	0.69^{abc}	10.88^{e}
NDL 2006/438	143.40^{a}	2.51^{efg}	4.32^{def}	5.83^{b}	0.22^{cd}	38.19^{bcd}	0.71^{abc}	18.61^{c}
NDL 2006/487	138.80^{ab}	1.22^{h}	4.71^{ab}	4.37^{d}	0.22^{cd}	40.52^{a}	0.60^{d}	19.50^{b}
NDL 2006/738	129.20^{cd}	2.59^{def}	4.43^{cd}	3.89^{efg}	0.38^{a}	36.53^{cdef}	0.74^{a}	13.47^{d}
NDL 2006/741	112.60^{f}	3.24^{b}	4.35^{cde}	3.81^{efg}	0.23^{cd}	39.88^{ab}	0.66^{c}	8.93^{f}
NDL 2006/840	126.40^{d}	2.21^{g}	4.28^{def}	3.77^{efg}	0.33^{ab}	36.39^{def}	0.68^{abc}	7.94^{fg}
NDL 2006/850	144.90^{a}	2.28^{fg}	4.87^{a}	4.07^{def}	0.30^{abc}	35.02^{f}	0.71^{abc}	14.17^{d}
Overall mean	**130.32**	**2.65**	**4.44**	**4.39**	**0.25**	**37.63**	**0.68**	**12.63**
s.e	10.36	0.48	0.36	0.59	0.13	2.91	0.08	1.49
c.v. (%)	8	18.1	8.1	13.4	12.1	7.7	11.9	11.8

Means with the same superscript letter(s) in the same column are not significantly different ($P \leq 0.05$) following separation by Duncan's Multiple Range Test.

Key: PHT = Plant height (cm), BRP = Number of branches per plant, STG = Stem girth (cm), RTP = Number of roots per plant, RTS = Root size (kg) HI = Harvest index and RYD = Root yield (t ha^{-1}).

3.2 Estimates of Parameters of Variability for Yield and Yield Components for Cassava in the Trial Sites

The results of this study revealed that, phenotypic estimates were higher than genotypic estimates an indication that, the apparent variations in the genotypes were not only genotypic but also due to environmental influence (Table 2). This observation agrees with the earlier findings by CIAT, (1984), Cock, (1985) and IITA, (1990). The extent of the environmental influence on any character is indicated by the magnitude of the difference between phenotypic coefficient of variation and genotypic coefficient of variation. Large differences reflect high environmental influence, while small difference reveals high genetic influence.

The magnitude of phenotypic coefficient of variation was consistently higher than the genotypic coefficient of variation in all the characters studied. The phenotypic coefficient of variation ranged between 8.48% to 63.55%, cassava root yield showing the highest magnitude followed by root size (61.91%), while the lowest (8.48%) was observed on dry matter. Also the highest genotypic coefficient of variation (45.02%) was observed on root yield and the lowest (1.94%) in dry matter. Broad sense heritability (h^2_b) and genetic gain for different characters varied considerably. Heritability obtained over locations ranged between 5% and 72.9%. Plant height had the highest h^2_b of 72.9% while root dry matter had the lowest h^2_b of 5%. Stem girth, roots per plant, branches per plant, and root size recorded broad sense heritability of 69.4%, 50.19%, 28.52, and 11.47% respectively. The expected genetic gain values were moderate ranging between 0.91% to 37.05%, number of roots per plant recording the highest while the lowest expected genetic gain was recorded for root dry matter. Roots per plant, plant height, stem girth, branches per plant and root size recorded expected genetic gains of 37.05%, 36.67%, 33.63, 17.60 and 14.63 respectively.

Plant height, stem girth and roots per plant had high to medium broad sense heritability of 72.9, 69.4 and 44.9 respectively. The high heritability in the broad sense observed for plant height and stem girth suggests the presence of large components of cassava heritable portion of variation, which is the selection portion exploited by plant breeders (Aina *et al*., 2009). This has also been observed from the findings by Naskar *et al.,* (1991). Furthermore, the high broad sense heritability and expected genetic gain recorded for plant height and stem girth indicate that, these characters are primarily under genetic control and selection for them can be achieved through their phenotypic performance (Makame, 1995).

The low broad sense heritability recorded for dry matter (5.23) and root size (11.4) indicate that, these characters are greatly influenced by the environment and direct selection of these characters will be ineffective (CIAT, 1995). Locations had no significant ($P < 0.05$) contribution in variation on dry matter content as it can be proved by its low contribution of 3.92%. Genotypes showed highly significant ($P < 0.001$) contribution (24.33%) to variations in root dry matter content (Table 4). The contribution of variation of the locations coupled with insignificant G x E interaction, and the main effects of the replicates suggests that, dry matter content is not much influenced by the environment as by genetic differences. These results agree with other studies of Perez *et al.,* (2001), who reported that dry matter content in cassava roots is likely to be controlled by one or a few major genes.

Table 2: Estimates of parameters of variability for yield and yield components for cassava in the trial sites

Variable	Mean	δ^2g	δ^2ph	δ^2l	GCV (%)	PCV (%)	h^2_b(%)	EGA (%)
Plant height	130.3217	738.3795	1012.8815	274.5019	20.8507	24.4208	72.9	36.6731
Number of branches	2.6506	0.1799	0.6306	0.4507	15.9997	29.9587	28.52	17.6022
Root size	0.2528	0.0029	0.0249	0.022	20.969	61.9131	11.47	14.6298
Roots per plant	4.3889	1.3886	3.0938	1.7052	26.8494	40.0767	44.88	37.0549
Stem girth	4.4354	0.7554	1.0884	0.333	19.596	23.5217	69.41	33.6305
Root Dry matter (%)	37.6309	0.5327	10.1789	9.6462	1.9395	8.4782	5.23	0.914

Where: δ^2g = variance due genotypic, δ^2ph = variance due to phenotypic, δ^2l = variance due location, GCV (%) = genotypic coefficient of variation, PCV (%) = phenotypic coefficient of variation, h^2b = broad heritability, EGA (%) = expected genetic advance.

Table 4: Dry Matter Analysis of variance

Source of Variation	Degree of Freedom	Sum of Squares	% SS Contribution	Mean Squares	v.r.	F probability
REP stratum	2	1.214		0.607	0.07	
LOCATION	2	87.812	3.92	43.906	5.21	0.077
Residual	4	33.738		8.435	1.93	
WEEDING	1	0.377		0.377	0.09	0.779
SITE.WEEDING	2	22.338		11.169	2.56	0.157
Residual	6	26.2		4.367	0.51	
GENOTYPE	11	545.31	24.33	49.574	5.84	<.001
SITE.GENOTYPE	22	220.37		10.017	1.18	0.276
WEEDING.GENOTYPE	11	71.928		6.539	0.77	0.669
SITE.WEEDING.GENOTYPE	22	111.817		5.083	0.6	0.918
Residual	132	1119.822		8.483		
Total	215	2240.925				

3.3 Genetic Correlations

Significant positive genotypic correlations were observed between plant height and stem girth (r = 0.5900***), plant height and roots per plant (r = 0.4463***) and stem girth and roots per plant (r = 0.5046***) (Table 3). These results are in accordance with the report of Aina *et al.,* (2009) who reported that plant height, stem girth, and number of roots per plant is positively correlated. Furthermore, the above highly correlated traits had positive correlations with root yield. This suggests that, improvement of root yield can therefore be achieved through selection of these highly correlated characters, as increase in mean value of any one of these characters would significantly increase the means of others (Mahungu, 1983). Insignificant association between both dry matter and root size with all variables indicated that, yield improvement through direct selection of dry matter or root size as a single character would be impractical. This agrees with previous report by Akinwale *et al.,* (2009), who reported the same.

Table 3: Genetic correlations between variables influencing yield in cassava as observed in a combined analysis

	PHT	BPL	RSZ	SGH	DM	RPL	HI	YLD
PHT	1.0000	-0.02570	0.10970	0.5900 ***	-0.05730	0.4463 ***	0.3005 ***	0.5436***
BPL		1.0000	-0.06060	0.03350	-0.04100	0.2441 ***	0.1762 **	0.0947
RSZ			1.0000	-0.00620	0.07370	0.0033	0.08330	0.1969
SGH				1.0000	-0.15480 *	0.5046 ***	0.09280	0.3874***
DM					1.0000	-0.00100	0.02690	0.0472
RPL						1.0000	0.2647 ***	0.7053***
HI							1.0000	0.3025***
YLD								1.000

Significance Levels	0.05	0.01	0.005	0.001
If correlation (r = >)	0.1335	0.1749	0.1903	0.2224

5.0 Conclusion

This study had shown substantial genetic variability for different agronomic traits studied and that improvement of root yield can significantly be achieved through selection based on various yield components instead of one.

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