



## GENETIC VARIABILITY AND GENETIC ADVANCE OF ELITE VARIETIES OF CASSAVA (*Manihot esculenta Crantz*)

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### Abstract

The present study was conducted in National Root Crops Research Institute, Umudike, Nigeria to access the genetic variability, phenotypic and genotypic coefficient of variation, heritability and genetic advance during year 2017/2018 cropping season of eight elite cassava genotypes. In this experiment, analysis of variance indicated that significant variation was present among the cassava genotypes for all the traits under study. The highest genotypic (GCV) and phenotypic coefficient of variation (PCV) were exhibited by cassava green mite severity indicating that direct selection can be effective for yield improvement in the populations under study. Relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study indicating environmental influence on the traits. Moderate heritability and high genetic advance were observed in the cassava green mite, cassava mosaic disease and fresh root weight. The combination of the high heritability and high genetic advance provide the clear image of the trait in the selection process.

**Keywords:** Genetic advance, heritability, GCV, PCV, and coefficient of variability

### Introduction

Cassava (*Manihot esculenta Crantz*) is a perennial woody shrub, mostly grown as an annual crop that belongs to the family *Euphorbiaceae*. It is grown throughout the lowland tropics in the world (El-Sharkawy, 2003). It is suggested that the crop originated in South America, but has spread throughout tropical areas of Africa during the period of slave trade by the Portuguese explorers in the sixteenth century (Adeniji et al., 2007). The crop is an important staple food and animal feed in tropical and sub-tropical Africa, Asia and Latin American countries. Cassava is grown in almost all the agro-ecological zones of Nigeria as a major source of low cost carbohydrates for the populations, and it also provides regular income for farmers in Nigeria. Genetic improvement of cassava is pivoted on the strength of genetic diversity within the crop species. Adequate variability provides options from which selections are made for improvement and possible hybridization. Genotypic coefficient of variation and phenotypic coefficient of variation had been used as an effective tool to determine the relationships among agronomic traits in genetically diverse population for enhanced progress in crop improvement (Bello et al. 2010). Heritability assumes that individuals more closely related are more likely to resemble one another than distant ones (Falconer and Mackay, 1996). Heritability estimate assists breeders to allocate resources necessary to effectively select for

desired traits, and to achieve maximum genetic gain with little time and resources (Smalley et al. 2004). Genetic advance explains the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. It also indicates the presence of additive genes in the trait and further suggest reliable crop improvement through selection of such traits. Estimates of heritability with genetic advance are more reliable and meaningful than individual consideration of the parameters (Nwangburuka et al., 2012). Continuous improvement of cassava is imperative for the increased competition for the crop. This can be achieved through effective selection of suitable parent materials of significant genetic variability. The objective of the present study was to estimate the genetic variation, heritability and genetic advance in the elite cassava and to evaluate suitable selection criteria for further breeding.

### Materials and Methods

The present study was conducted at National Root Crops Research Institute, Umudike, Abia State, Nigeria. The germplasm comprises of CR346, NR090191, NR8082, TMEB419, TMS000070, TMS30572, TMS980581 and TMS982101. The experiment was carried out in a randomized complete block design with three replications in a cropping season. In each plot, an intra-row spacing of 0.8m, and inter-row spacing of 1m

were maintained to accommodate four rows of five plants per plot. All recommended agricultural practices for cassava production were followed.

#### Data collection

Plant height, plant architecture, dry matter content, fresh root weight, cassava green mite severity and cassava mosaic disease severity were evaluated on the plants in the net plots following IITA (1990) to evaluate the genotypes.

#### Data analysis

##### Analysis of variance (ANOVA)

The data collected for each trait was subjected to analysis of variance (ANOVA) using randomized complete block design to test the variations among genotypes. The analysis of variance was calculated using R software version 3.4 (R core team, 2013) and significant means were compared using least significant difference at P0.05 and 0.01

##### Estimates of variance components

The variability present in the population was estimated by the mean, phenotypic and genotypic variance and coefficient of variation. To estimate the phenotypic and genotypic variance, genotypic and phenotypic coefficients of variation were estimated following Syukur *et al.* (2012) thus;

$$\text{Genetic variance (Vg)} = \frac{\text{MSG} - \text{MSE}}{r}$$

Environmental Variance = Error Mean Square (EMS)

$$\text{Phenotypic variance (Vp)} = \frac{\text{Vg} + \text{Ve}}{r}$$

Genotypic and Phenotypic coefficient of Variation was calculated as

$$\text{GCV (\%)} = \frac{\sqrt{\text{Vg}}}{x} * 100$$

$$\text{PCV (\%)} = \frac{\sqrt{\text{Vp}}}{x} * 100$$

Where, GCV% = Genotypic coefficient of variation; Vg = Genotypic variance; PCV % = Phenotypic coefficient of variation; Vp = Phenotypic variance; Ve = Environmental variance (error mean square from the analysis of variance); MSG = Mean square of genotypes; MSE = Error mean square; r = number of replications

PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973).

Less than 10% = Low

10-20% = Moderate

More than 20 % = High

Broad sense heritability ( $H^2$ ) of the all traits were calculated according to the formula as described by Allard (1960) as follows:

$$H^2 = \text{Vp}/\text{Vg} * 100$$

The heritability ( $H^2$ ) was categorized as suggested by Johnson *et al.* (1955).

0-30% = Low

31-60% = Medium

61% and above = High

The expected Genetic Advance for each trait was calculated as;

$$\text{GK} = K * \sqrt{\text{Vp}} * H^2$$

Expected genetic advance percentage of mean was calculated according to Shukla *et al.* (2006) thus;

$$\text{GA\%} = \frac{\text{GA}}{X} * 100$$

where K = standardized selection differential constant (2.06) at 5% selection intensity, and

x = grand mean of a trait.

The genetic advance as percent over mean was categorized as suggested by Johnson *et al.* (1955).

Less than 10% = Low

10-20% = Moderate

More than 20 % = High

#### Results and Discussion

The analysis of variance showed that genotype mean squares for all traits studied were highly significant (Table 1). It reflected the existense of large variability among tested genotypes and this variability can be further utilized in the cassava improvement program. Genotype NR090191 had the lowest CGM severity score of 1.47, while genotype TMS980581 had the highest severity of 2.56. Genotype TMS000070 had the lowest CMD severity score of 1.00, while the most severed genotype TMS30572 had a score of 2.94. The highest dry matter content (38.61%) was found in genotype CR346, while the least dry matter content (32.36%) was found in genotype TMS982101. The highest root weight of 52.61kg was observed in TMS000070, while the lowest value of 9.46kg was recorded for genotype NR8082. Genotype TMEB419 had the best architecture of 3.5, while genotype TMS982101 had the worst architecture (2.3). TMEB419 attained maximum plant height (147.21cm), while TMS30572 had the minimum plant height value of 114.96cm.

Genotypic coefficient of variance, phenotypic coefficient of variance, broad sense heritability and response to the selection for six recorded traits are shown in Table 3. The knowledge of nature and magnitude of the variability among the genotypes for the traits is a very important prerequisite for making simultaneous selection on more number of traits to make significant improvement in cassava. The genotypic coefficients of variation (GCV) ranged from 5.05 for dry matter content to 39.01 for cassava green mite severity. Similarly, phenotypic coefficients of variation (PCV) ranged from 7.97 for dry matter content to 49.5 for cassava green mite severity. In this study, the GCV values were lower than that of PCV, indicating that the environment had an important role in the expression of

these traits. According to Deshmukh *et al.* (1986), PCV and GCV values greater than 20% are regarded as high, whereas, values less than 10% are considered to be low, and values between 10 and 20% to be medium. Based on this argument, cassava green mite severity recorded high GCV and PCV. Fresh root weight recorded high PCV and medium GCV. This observation agrees with the earlier findings of Aina (2007), Cock (1985), and Akinyele and Odiyi (2007). It indicates that selection may be effective based on these characters with high and medium PCV and GCV values, and their phenotypic expression would be a good indication of genetic potential.

Data on broad sense heritability estimates are also presented in Table 3. Heritability values are helpful in predicting the expected progress to be achieved through the process of selection. Genetic coefficient of variation along with heritability estimate provides a reliable estimate of the amount of genetic advance to be expected through phenotypic selection (Wright, 1921). Heritability ranged from 34.83% for plant architecture to 91.37% for cassava mosaic disease severity. According to Singh (2001), heritability values greater than 80% are very high, 60-79% as moderately high, 40-59% as medium and values less than 40% as low. Accordingly, heritability estimate was very high (>80%) for cassava mosaic disease severity (91.37%). Similarly, Akinwale *et al.* (2010) reported high heritability values for cassava mosaic disease. Very high heritability indicates selection will be effective. Johnson *et al.* (1955) classified genetic advance as percentage of mean (GAM); values from 0-10% as low, 10-20% as moderate and 20% and above as high. Based on this delineation, the range for GAM was from 10.10% for plant architecture to 42.62% for cassava green mite severity. Medium genetic advance as percentage of mean were observed in all the traits evaluated expect for cassava green mite severity with high genetic advance as percentage of mean of 42.62%. Dry matter contents had medium heritability estimates and low genetic gain; this can be attributed to non additive gene action.

Traits like; cassava mosaic disease, cassava green mite severity and fresh root weight, had high heritability, high Phenotypic coefficients of variation (PCV), Genotypic coefficients of variation (GCV), and high genetic advance as a percent of mean, which are very important for selection than heritability estimates alone. In addition, estimation of heritability and genetic advance as percent of average performance is also needed to assess the extent of genetic gain expected from effective selection. Heritability in the broad sense include: both additive and epistatic gene effects, it will be reliable only when it is accompanied with high genetic advance (Ramesh and Arumugam, 2013).

### Conclusion

Assessment of variability is therefore a prerequisite for crop improvement to judge the potential of the population as a base for genetic improvement. Significant variability has been observed among

cassava genotypes and selection of desirable characters will lead to progress in plant genetic improvement. The traits evaluated in this study could be used as good criteria for selection in the cassava improvement because these traits had moderate to high genotypic coefficient of variation, heritability estimate and genetic advance as percent of the mean.

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**Table 1: Analysis of variance for traits evaluated in cassava genotypes**

Source of variation	DF	CMDS	CGMS	Plant height	Plant architecture	DMC	Fresh root weight
MSS	7	7.75***	3.21***	2858.26***	2.14***	68.79***	3769.6***
Error	14	0.07	0.18	553.02	0.19	23.14	671.4

\*\* Highly Significant at 0.01% level \* Significant at 0.05% level. DF = Degree of freedom; CMDS = Cassava mosaic disease; CGMS = Cassava green mite severity; DMC = Dry matter content

**Table 2: Performance Mean of genotypes for some morphological traits in cassava**

	CGMS	CMDS	DMC	Fresh root weight	Plant architecture	Plant height
CR346	1.86	1.19	38.61	27.61	2.78	146.26
NR090191	1.47	1.04	33.24	29.38	2.82	147.21
NR8082	1.75	1.59	33.33	9.46	3.00	137.48
TMEB419	2.03	1.19	33.77	27.25	2.94	143.16
TMS000070	2.50	1.00	32.97	52.61	3.00	114.96
TMS30572	2.50	2.94	33.90	24.33	2.56	117.07
TMS980581	2.56	1.06	34.98	46.77	3.50	130.49
TMS982101	2.50	1.06	32.36	47.94	2.33	120.72
Mean	2.15	1.38	34.14	33.17	2.87	132.17
Min	1.47	1.00	32.36	9.46	2.33	114.96
Max	2.56	2.94	38.61	52.61	3.50	147.21
SEM	0.08	0.07	0.42	2.95	0.07	2.25
CV (%)	42.23	56.82	14.64	106.85	27.69	20.38

CMDS = Cassava mosaic disease; CGMS = Cassava green mite severity; DMC = Dry matter content

**Table 3: Variability, heritability and expected genetic advance of some relevant morphological traits of cassava**

Trait	PCV (%)	GCV (%)	H <sup>2</sup>	GAM (%)
CGMS	49.50	39.01	42.00	42.62
CMDS	10.31	6.40	91.00	19.41
DMC	7.97	5.05	69.00	11.33
Fresh root weight	21.35	18.90	42.00	18.49
Plant architecture	14.08	13.10	35.00	10.10
Plant height	9.47	8.33	75.00	14.67

CMDS = Cassava mosaic disease; CGMS = Cassava green mite severity; DMC = Dry matter content; PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation