Genetic Variability and Heritability Estimation in Cassava (*Manihot esculenta* Crantz)

Systematic study and evaluation of cassava germplasm is of great importance for current and future agronomic and genetic improvement of cassava. Estimates of genetic variance and heritability are of great importance in plant breeding programmes. Plant breeders have made efforts to use heritability estimates as an indication of selection pressure to a segregating population (Burton and Devane, 1953). Assessment of variability present in any crop species is an essential pre-requisite for formulating an effective breeding programme. The genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance and include dominance and epitasis (non-allelic interaction). Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance. Estimation of genetic variability does not give a clear indication of the possible improvement that can be achieved through selection and it should be used in conjunction with heritability and genetic advance. So proper evaluation of genetic resources is essential to understand and estimate the genetic variability and heritability. Hence an attempt was made in the present investigation to assess the variability in cassava genotypes with the help of genetic parameters like phenotypic and genotypic coefficient of variation, heritability and genetic advance.

Twenty genotypes of cassava were collected from different parts of Andhra Pradesh. These genotypes were planted in randomized block design with three replications during 2011-2012 at the Horticultural Research Station, Venkatramannagudem, Dr. Y.S.R. Horticultural University, Andhra Pradesh, India. The distance between the rows and between the plants were 90 cm. Chemical fertilizers were applied to supply NPK @ 60:60:60 kg ha^{-1} in three split doses. Data was recorded for eight characters from ten plants for plant height, stem girth, leaf area, number of leaves, number of tubers per plant, tuber girth, tuber yield per plant and starch content.

The data was computed to determine the extent of variability present in the genotypes. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953). Phenotypic and genotypic variance were calculated according to Lush (1949). Heritability in the broad sense was estimated as per Allard (1960). The range of heritability in broad sense was classified as low (less than 30%), moderate (30-60%) and high (more than 60%) as suggested by Johnson et al. (1955). Genetic advance was estimated as per the formula proposed by Lush (1949) and Johnson et al. (1955). The range of genetic advance as per cent of mean was classified as low (less than 10%), moderate (10-20%) and high (more than 20%) as suggested by Johnson et al. (1955).

Significant differences were observed among the accessions for all the characters like plant height, stem girth, leaf area, number of leaves, number of tubers, tuber girth, tuber yield and starch content. Plant height, leaf area per plant and number of leaves showed high phenotypic as well as genotypic variances. In general the genotypic coefficient of variation was lower than the phenotypic coefficient of variation (Table 1) for all the characters studied, indicating the influence of environment on the expression of these characters. The data further indicated that characters like leaf area, number of leaves and tuber yield showed high values for phenotypic and genotypic coefficient of variation. High values of GCV for these characters suggest better scope of improvement by selection. The stem girth showed the lowest coefficient of variation at phenotypic and genotypic levels. Similar results were reported for these traits with respect to PCV and GCV (Surya Kumari and Anuradha, 2000).

Table 1. Estimates of genetic variability in cassava

Characters	Mean	Range	Variance		H²	GA as % of mean	PCV	GCV
			Genotypic Vg	Phenotypic Vp				
Plant height (cm)	311.05	212.0-401.6	1469.04	2334.73	62.92	20.13	15.53	12.32
Stem girth (cm)	8.17	7.0-9.9	0.41	0.53	77.88	14.30	8.91	7.87
Leaf area (cm²)	402.95	172.4-630.3	20028.84	20122.77	99.53	72.18	35.20	35.12
Leaf number	895.55	241.6-2175.6	246581.20	248158.60	99.36	113.86	55.63	55.45
Tuber number	14.71	6.0-25.0	17.14	20.51	83.56	52.98	30.78	28.14
Tuber girth (cm)	15.45	11.2-20.1	4.08	6.56	62.11	21.22	16.59	13.07
Tuber yield (t ha⁻¹)	27.60	15.8-52.4	85.17	142.20	72.96	62.82	49.54	47.24
Starch (%)	26.78	19.8-33.4	14.75	14.89	99.09	29.41	14.41	14.34

However, it is not possible to determine the amount of heritable variation with the help of genotypic coefficient of variation alone. Burton (1952) suggested that the study of genotypic coefficient of variation along with heritability estimates is needed to obtain the best results on the extent of heritable variation. The heritability estimates ranged from 62.1% to 99.5% thus revealing high heritability for the characters studied. In the present study, high heritability estimates were observed for leaf area, number of leaves, number of tubers per plant and starch content indicating importance of additive genetic variance for these characters. Johnson et al. (1955) pointed out that high heritability value does not always indicate greater genetic progress. Swarup and Chaugle (1982) and Jones et al. (1985) reported that heritability estimates along with genetic gain are usually more efficient than heritability values alone in predicting the final outcome of selection.

The expected genetic advance as per cent of mean varied from 14.3 to 113.86. The genetic advance was maximum for number of leaves, leaf area and number of tubers. A low value of genetic advance was observed for plant height. Birader et al. (1978) also reported that plant height in cassava had low values of genetic advance and heritability. High heritability and high genetic advance as per cent of mean were observed for these traits indicating the presence of additive gene action in the inheritance of these traits and simple selection will be highly rewarding for improving these characters.

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[1]AICRP on Tuber Crops, Horticultural Research Station, Venkatramannagudem, West Godavari District 534 101, Andhra Pradesh
[2]Horticultural Research Station, Venkatramannagudem, West Godavari District, Andhra Pradesh
[3]Department of Agronomy, Horticultural College and Research Institute, Venkatramannagudem 534 101, Andhra Pradesh
Corresponding author: P. Ashok, e-mail: hortashok@gmail.com

P. Ashok[1]
M. Rajasekhar[2]
K. Sasikala[3]