

# Original Research Article

## Genetic Variability and Correlation of Cassava (*Manihot esculenta* Crantz) accessions for yield and related traits

### ABSTRACT

The study was carried out in Tapioca and Castor Research Station, Yethapur, India to study the "Genetic Variability and Correlation of Cassava (*Manihot esculenta* Crantz) accessions for yield and related traits". Observations on quantitative and qualitative traits of cassava were recorded and the analysis of variability and association analysis were carried out. High Genotypic coefficients of variation (GCV) were found for LAI, height at first branching, number of leaves per plant, number of tiers, yield of tuber per plant and severity scores of CMD whereas low GCV were found for Chlorophyll content. Phenotypic Coefficients of Variation were higher than Genotypic coefficients of Variation for all the observed characters. Plant height, number of tiers, internodal length, number of leaves per plant, LAI, height at first branching, length of tubers, dry matter content, severity scores of CMD, tuber yield recorded high heritability with high GAM suggesting that these characters are under the additive gene control and selection for genetic improvement would be successful. Chlorophyll content, girth of tuber and starch content recorded high heritability coupled with moderate GAM whereas stem girth recorded moderate heritability and GAM which offers only less scope for selection that is due to non-additive gene actions. The correlation analysis results showed that yield of tuber per plant had high positive and high significant correlation with plant height, number of tubers per plant, starch content, length of tuber, girth of tuber and weight of tuber. Genetic variability and correlation analysis provides a knowledge which would be helpful in selecting the cassava accessions with greater yield potential.

*Keywords: Cassava; PCV; GCV; genetic advance; correlation; tuber yield*

### 1. INTRODUCTION

Starchy root and tuber crops are pivotal globally, serving as significant sources of carbohydrates, ranking just behind cereals. These crops, including cassava, sweet potatoes, yams, aroids (such as taro and elephant foot yam), and various minor tuber crops like arrowroot and Chinese potato, are essential for ensuring food security and bolstering economic stability in numerous regions. Annually, these crops collectively yield approximately 836 million tonnes worldwide [1]. These crops not only fulfill crucial dietary needs but also furnish raw materials for industry and significantly contribute to animal feed production [2]. The wide variety of tropical tuber crops underscores their adaptability to diverse climates, making them indispensable for maintaining agricultural diversity and enhancing global food security.

The *Manihot* genus, consisting of around 300 genera and approximately 8000 species, is considered one of the largest families among flowering plants [3]. Cassava (*Manihot esculenta* Crantz) is a highly heterozygous, perennial tropical tuber crop belongs to the family Euphorbiaceae with chromosome number  $2n=36$ , which provides source of energy for more than 800 million people worldwide [4]. Because of its diverse applications in the food industry as additives, ingredients in livestock feed, and industrial processing for the production of starch, sago, various sweeteners, and ethanol, cassava has emerged as a major crop for international trade [5]. India ranks fifth globally in cassava cultivation, following Brazil, Zaire, Nigeria, and Indonesia. The country produces 6853 thousand metric tonnes (MT) of tapioca on approximately 186 thousand hectares of land [6]. Tamil Nadu alone contributes 83.75% to India's total production. Cassava cultivation is also practiced in Kerala, Karnataka, Andhra Pradesh, Maharashtra, Assam, and Nagaland.

The Tapioca and Castor Research Station (TCRS), Tamil Nadu Agricultural University (TNAU) in Yethapur, developed cassava hybrids for evaluating and aimed to enhance the yield of this tuber crop. In this study, the assessment of genetic variability and correlation among 11 cassava hybrids and 2 check varieties helps in selecting superior cassava varieties that can significantly enhance yield through breeding strategies. These genetic variability and correlation studies are essential for discerning the range of genetic traits within the hybrids and their association with yield-related characteristics.

## 2. MATERIAL AND METHODS

### 2.1 Plant Materials and Experimental Design

The study on genetic variability and correlation on cassava accessions was carried out at Tapioca and Castor Research Station, TNAU, Yethapur. Totally 11 cassava hybrids developed from TCRS, Yethapur and 2 check varieties viz., Sree Kaveri (National Check) and YTP-2 (Local check) were evaluated in this study (Table 1).

**Table. 1 Details and sources of Cassava accessions**

Accessions	Source	Accessions	Source
TCS 1	TCRS, Yethapur	TCS 8	TCRS, Yethapur
TCS 2	TCRS, Yethapur	TCS 9	TCRS, Yethapur
TCS3	TCRS, Yethapur	TCS 10	TCRS, Yethapur
TCS 4	TCRS, Yethapur	TCS 11	TCRS, Yethapur
TCS 5	TCRS, Yethapur	Sree Kaveri (National Check)	CTCRI, Thiruvananthapuram
TCS 6	TCRS, Yethapur	YTP 2 (Local check)	TCRS, Yethapur
TCS 7	TCRS, Yethapur		

These accessions were grown in Randomized Block Design and they were replicated thrice, with the spacing of 90x90 cm apart. The plot was ploughed and tilled finely. Following the standard recommendation of crop production guide (2020), fertilizers were applied at rates of 45:90:120 kg/ha with 25 tonnes of FYM as basal dressing. Setts, 15 cm in length with 6-8 nodes, were taken from 12-month-old parent stem. In the third month, weeding, hoeing, and earthing up were done. A top dressing of 45:0:120 kg/ha of NPK was applied during earthing up. Observations on plant height, stem girth, number of tiers, intermodal length, number of leaves per plant, Leaf Area Index (LAI), chlorophyll content, height at first branching, number of tubers per plant, length of tuber, girth of tuber, yield of tuber per plant, dry matter content, starch content, severity score of CMD (Cassava Mosaic Disease) were recorded. Genetic parameters such as coefficients of variation viz., (Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), broad-sense heritability, and genetic advance were calculated.

Phenotypic coefficient of variation and Genotypic coefficient of variation is calculated as given by [7].

$$\text{Phenotypic coefficient of variation (\%)} = \frac{\text{Phenotypic variance}}{\text{Mean value of trait}} \times 100$$

$$\text{Genotypic coefficient of variation (\%)} = \frac{\text{Genotypic variance}}{\text{Mean value of trait}} \times 100$$

PCV and GCV estimates were categorized into low (0-10%), moderate (10-20%), and high (>20%) ranges following the criteria established by [8].

Broad-sense heritability ( $h^2b$ ) was determined using the formula proposed by [9] and [10].

$$\text{Broad-sense heritability (} h^2b \text{)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Broad-sense heritability ( $h^2b$ ) were categorized into low (0-30%), moderate (30-60%), and high (>60%). Genetic advance was calculated using the formula provided by [9].

$$\text{Genetic advance as percent mean} = (\text{Genetic advance} / \text{Grand mean}) \times 100$$

Genetic advance as percent mean estimates were categorized into low (0-10%), moderate (10-20%), and high (>20%) ranges. The equation provided by [11] was utilized to calculate simple correlations. The statistical analysis was carried out in R 4.1.2 Software using the package 'agricolae' for genetic variability and 'corrplot' for correlation analysis.

### 3. RESULTS AND DISCUSSION

#### 3.1. Genetic parameters

##### 3.1.1. Phenotypic and Genotypic Coefficient Variation

The amount of variability available within the genotype indicates the potentiality that could be exploited further. A larger phenotypic coefficient of variation was found than its genotypic coefficient of variation indicating that the major role of genetic factors in the expression of variability of these characters. There is only marginal difference found between the characters between PCV and GCV taken in study. Among characters studied number of tiers, internodal length, number of leaves per plant, Leaf area index, height at first branching, severity scores of CMD and tuber yield per plant showed high PCV and GCV. These are in accordance with [12], [13], [14] and [15]. Plant height, stem girth, number of tubers, length of tuber, girth of tuber, dry matter content content and starch content showed moderate GCV and PCV whereas chlorophyll content showed low GCV and PCV. The traits with lower PCV and GCV show that it has limited potential for improvement.

##### 3.1.2. Heritability and Genetic Advance

Genetic advance represents the inherited improvement in offspring compared to the original population due to selection, providing insight into the efficacy of selection processes. Due to the influence of environmental factors on traits, the magnitude of genetic advance can vary significantly. Therefore, genetic advance as a percentage of the mean was computed to predict the potential genetic gain, facilitating relative comparisons of traits under varying environmental conditions. Traits with high genetic advance have high heritability indicate a significant proportion of additive genetic variance, leading to higher genetic gains through selection [16]. High genetic advance with low heritability indicates that while selection can improve the trait, these gains may be driven more by non-additive genetic effects or environmental factors. Thus, achieving the trait's full potential may require managing both environmental conditions and genetic selection [17]. In general, most traits exhibited high heritability values, emphasizing their potential for effective breeding programs.

Traits such as plant height, number of tiers, internodal length, number of leaves per plant, leaf area index, height at first branching, number of tubers, length of tuber, girth of tuber, starch content, dry matter content, severity scores of CMD incidence, tuber yield per plant recorded high heritability coupled with high genetic advance as a percentage of mean. The results indicate that these characteristics exhibit significant selection responses and are predominantly governed by additive genetic mechanisms. The finding is in the line of [18] in cassava, [14], [15] and [19] in cassava. The character stem girth shows moderate heritability coupled with genetic advance as percentage of mean whereas chlorophyll content showed high heritability with moderate genetic advance as percentage of mean. It is rational to infer that non-additive genetic factors govern this trait, making selection for such traits less productive. Heritability is positively influenced by the environment rather than genotype alone, thus direct selection methods may not be effective. However, improvements can be achieved through hybridization or utilizing transgressive segregants in heterosis breeding programs.

**Table 2. Genotypic and phenotypic coefficient of variations, heritability, genetic advance and genetic advance as percent mean of Cassava accessions**

Parameters	Genotypic coefficient of variations	Phenotypic coefficient of variations	Heritability %	Genetic advance value % means
Plant height	12.42	14.76	70.82	21.53
Stem Girth	13.32	19.93	44.71	18.35
Number of tiers	40.24	41.48	94.09	80.40
Internodal Length	25.42	26.03	95.31	51.11

<b>Number of leaves per plant</b>	49.65	57.16	75.44	88.83
<b>LAI</b>	73.35	78.66	86.95	140.90
<b>Chlorophyll content</b>	6.63	8.54	60.32	10.61
<b>Height at first branching</b>	54.24	54.66	98.46	110.88
<b>Number of tubers</b>	13.92	15.31	82.60	26.06
<b>Length of tubers</b>	17.43	19.99	76.07	31.32
<b>Girth of tubers</b>	15.89	17.71	80.49	29.36
<b>Dry matter content</b>	15.12	15.23	98.53	30.92
<b>Starch content</b>	11.61	11.75	97.72	23.65
<b>Severity scores of CMD Incidence</b>	26.97	28.07	92.36	53.40
<b>Tuber yield per plant</b>	33.30	35.87	86.20	63.69

### 3.2. Correlation studies

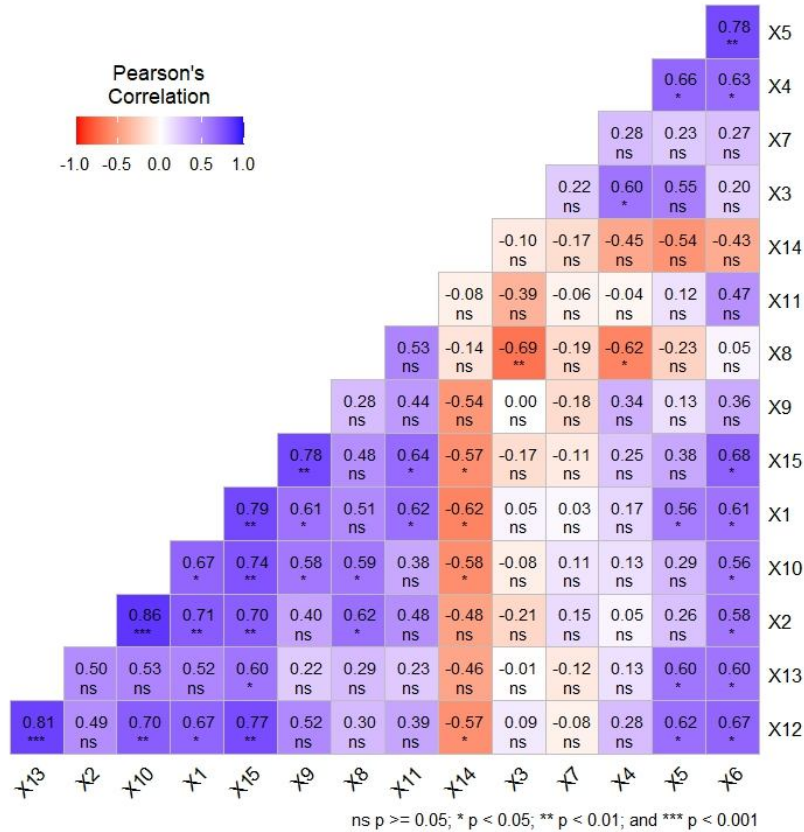
The genetic enhancement of tuber yield, a primary focus for plant breeders, is governed by multiple genes. According to Graffing (1956), any changes in tuber yield must coincide with alterations in one or more traits, although modifications in individual components do not necessarily affect the overall yield. This is because of diverse degrees of positive and negative correlations among yield, its components, and their interrelationships. In this context, simple correlation coefficients between tuber yield and its components were computed (Table. 2).

The traits such as plant height, stem girth, number of tubers, length of tuber showed highly significant and positive genotypic correlation with yield of the tuber per plant. These reports are in agreement with findings [12] in cassava. Starch content also showed highly significant and positive correlation with tuber yield per plant which is in line with the report of [14] and [20] in cassava. However, it is contrary to the report of [12]. Leaf area index, girth of the tuber, dry matter content is significant and positively correlated with tuber yield which is in accordance with the result of [21] in cassava. Severity scores of CMD are significant and negatively correlated with tuber yield which is in the line of the report of [22] in cassava. The starch content showed a highly significant and positive correlation with the dry matter content. This is in accordance with the study of [23] in potato.

Leaf area index is positively correlated with plant height, stem girth, internodal length, length of tuber, starch content and dry matter content. Number of tubers is positively correlated with plant height and length of the tuber. Cassava mosaic disease severity score showed a negative correlation with plant height, length of tuber and starch content is in accordance with the results of [24].

Identifying traits that show both a positive and significant correlation with yield and are interconnected would be advantageous in a breeding program focused on enhancing multiple characteristics concurrently. Consequently, selecting for these traits in high-yielding accessions would lead to the identification and release of superior individual plant selections, paving the way for the development of new and improved varieties in the future.

**Table.2. Pearson correlation matrix of different cassava quantitative traits**



- X1- Plant height (cm)
- X2- Stem girth (cm)
- X3- Number of tiers
- X4- Internodal length (cm)
- X5- Number of leaves per plant
- X6- Leaf area index
- X7- Chlorophyll content (SPAD value)
- X8- Height at first branching (cm)
- X9- Number of tubers
- X10- Length of tuber (cm)
- X11- Girth of tuber (cm)
- X12- Starch content (%)
- X13- Dry matter content (%)
- X14- Severity scores of CMD
- X15- Tuber yield per plant (Kg)

#### 4. CONCLUSION

Based on this study, it is concluded that in breeding programs focused on enhancing multiple traits simultaneously, traits with positive and significant correlations with yield, as well as with each other, are particularly desirable. Traits such as plant height, number of tubers per plant, starch content, tuber length, girth, and weight contribute significantly to the increase in tuber yield per plant and exhibit mutual correlations. The greatest levels of genotypic and phenotypic variation were observed in traits like the leaf area index (LAI), height at first branching, number of leaves per plant, number of tiers, tuber yield per plant, and CMD (Cassava Mosaic Disease) severity scores. High heritability and genetic advancement were noted in traits such as plant height, number of tiers, internodal length, number of leaves per plant, LAI, height at first branching, tuber length, dry matter content, CMD severity scores, and tuber yield. These traits are reliable predictors of tuber production and can serve as key markers for yield in the selection process.

#### Disclaimer (Artificial intelligence):

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

#### REFERENCES

[1] FAOSTAT. 2013, <http://faostat3.fao.org>.

- [2] Chandrasekara A, Josheph Kumar T. Roots and Tuber Crops as Functional Foods: A Review on Phytochemical Constituents and Their Potential Health Benefits. *International Journal of Food Science*. 2016; 3631647. doi: 10.1155/2016/3631647.
- [3] Rahman AHMM and Akter M. Taxonomy and medicinal uses of Euphorbiaceae (Spurge) family of Rajshahi, Bangladesh. *Research in Plant Sciences*. 2013; 1:74–80
- [4] McCallum EJ, Anjanappa RB, Gruissem W. Tackling agriculturally relevant diseases in the staple crop cassava (*Manihot esculenta*). *Current Opinion in Plant Biology*. 2017;38(8):50-58.
- [5] FAO: Special report 2022 FAO/WFP crop and food security assessment mission (CFSAM) to the LAO people's democratic republic. 2022; ISBN 978-92-5-137705-5
- [6] <https://static.pib.gov.in/WriteReadData/specificdocs/documents/2022/jul/doc202271470601.pdf>
- [7] Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*. 1973; 60: 1093-1096
- [8] Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. 1955; 47: 314-318.
- [9] Hanson GH, Robinson HF, Comstock RE. Biometrical studies of yield segregating population of Korean lespedeza. *Agronomy Journal*. 1956; 48:268-272.
- [10] Burton GW. Quantitative inheritance in grasses. In: *Proceedings of 6 th International Grassland Congress, Pennsylvania State College, USA*. 1952 August 23, 277- 283.
- [11] Weber CR, Moorthy, B.R. Heritability and non heritability relationships and variability of oil content and agronomic characters in the F2 generation of soybean crosses. *Agronomy Journal*.1952; 44: 202-209.
- [12] Revathi BS, Sivan S, Arya K, Sheela MN, Prakash S, Muthusamy S. Genetic diversity analysis of Indian Cassava (*Manihot esculenta* Crantz) accessions using morphological and molecular markers. *South African Journal of Botany*.2023;161; 347-357. 10.1016/j.sajb.2023.08.027.
- [13] Koundinya AVV, Ajeesh BR, Hegde V, Sheela MN, Mohan C, Asha KI. Genetic parameters, stability and selection of cassava genotypes between rainy and water stress conditions using AMMI, WAAS, BLUP and MTSI. *Scientia Horticulturae*. 2021; 281. 109949. 10.1016/j.scienta.2021.109949.
- [14] Babu Rao B, Ashok P, Ramanandam G, Sasikala K. Studies on genetic variability, heritability and genetic advance for quantitative traits in cassava (*Manihot esculenta* Crantz). *The Bioscan*.2016; 11(3):1991-94.
- [15] Polamuri A, Rajasekhar M. and Sasikala K. Genetic variability and heritability estimation in cassava (*Manihot esculenta* Crantz). *Journal of Root Crops*. 2013; 39(2): 230-231.
- [16] Devi ND, Mariappan S. Genetic variability, heritability and genetic advance for yield and its components snake gourd (*Trichosanthes anguina* L.). *African Journal of Agricultural Research*. 2013; 8(28): 3857-3859.
- [17] Singh M, Kumar K, Singh RP. Study of coefficient of variation, heritability and genetic advance in hybrid rice. *ORYZA- An International Journal on Rice*. 2007; 44(2): 160-162.
- [18] Peprah BB, Parkes E, Manu-Aduening J, Kulakow P, Van Biljon A, Labuschagne M. Genetic variability, stability and heritability for quality and yield characteristics in provitamin A cassava variety. *Euphytica*. 2020; 216: 1-13.
- [19] Akinwale MG, Akinyele BO, Dixon AG, Odiyi AC. Genetic variability among forty-three cassava genotypes in three agro-ecological zones of Nigeria. *Journal of Plant Breeding and Crop Science*. 2010;2(5):104-9.
- [20] Ntawuruhunga P and Dixon A. Quantitative variation and interrelationship between factors influencing cassava yield. *Journal of Applied Biosciences*. 2010; 26: 1594-02.
- [21] Njoku DN, Mbah EU. Assessment of yield components of some cassava (*Manihot esculenta* Crantz) genotypes using multivariate analysis such as path coefficients. *Open Agriculture*. 2020;5(1):516-28.
- [22] Akinwale MG, Akinyele BO, Dixon AGO. and Odiyi AC. Genetic variability among forty-three cassava genotypes in three agro-ecological zones of Nigeria. *Journal of Plant Breeding Crop Science*.2010; 2(5): 104–09.
- [23] Abebe T, Wong S, Taychasinpitak T. Dry matter content, starch content and starch yield variability and stability of potato varieties in amhara region of Ethiopia. *Kasetsart Journal - Natural Science*. 2012; 46: 671–683.
- [24] Elegba W, Appiah AS, Azu A, Agyei-Amponsah J, Afful N, Agbemavor S, Owureku-Asare M, Quaye B, Danso K. Effect of mosaic virus diseases on dry matter content and starch yield of five cassava (*Manihot esculenta* Crantz) accessions in Ghana. *African Journal of Biotechnology*.2013; 12: 4310-4316. 10.5897/AJB12.2958.

UNDER PEER REVIEW