ASSESSMENT OF GENETIC DIVERSITY IN CASSAVA (*MANIHOT ESCULENTA* CRANTZ.) GENOTYPES

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ABSTRACT

The present investigation was carried out at Department of vegetable Science, HC&RI, Dr.Y.S.R.H.U, Venkataramannagudem during 2012-13. All the 18 cassava genotypes were grouped into five clusters based on D^2 values, which exhibited no association between geographical distribution and genetic divergence. The genotypes were mainly grouped due to morphological differences but not due to geographical differences. Among the five clusters, cluster IV was largest with 7 genotypes followed by cluster I with 5 genotypes. The intra cluster distance was maximum for cluster IV (17.2) and minimum for cluster III (0.00). The maximum inter cluster distance was observed between clusters IV and V (62.40) followed by clusters II and V (55.11) indicating that there is presence of wide range of genetic diversity among the cassava genotypes. Such genotypes with wide genetic diversity based on their mean values can be utilized for breeding programmes for genetic improvement in cassava. Four characters viz. tuber dry matter content (64.05%), plant dry matter content (20.26%), height of first branching (9.15%), starch content (5.23%) contributed maximum in manifestation of diversity. Greater diversity was observed between cluster IV and V revealed that the genotypes of these clusters can be used for hybridization program to obtain better transgressive segregants to produce new varieties with desirable traits.

INTRODUCTION

Cassava (*Manihot esculenta* Crantz.) is one of the most important staple foods in human diet in the tropics and ranked as the sixth most important source of calories in the human diet worldwide (Alfredo *et al.,* 2000). It belongs to the family Euphorbiaceae, native to north - eastern Brazil. It is highly heterozygous due to its out crossing nature. It is an important food crop for more than 900 million people in the tropics and sub tropics (Nassar, 2003).

Cassava has moved from being a subsistence crop to a full commercial crop for its income generating capacity. The crop is now widely cultivated for its vast industrial potentials including flour, starch and dextrin for food, feed, confectionery, pharmaceutical, adhesives, explosives and other industrial uses. Apart from its importance as animal feed and industrial raw material, cassava has emerged as an important biofuel resource (Egesi *et al.,* 2007). Cassava has the advantage of being well adapted to a wide range of environmental stresses. It grows very well in less fertile soil in contrast to many other crops that are highly vulnerable to environmental stresses during critical stages of plant development (Ugorji, 1998).

One of the best methods to increase cassava production in developing countries like India is by the development of high yielding varieties with resistance to pests, diseases and drought. To develop a new variety there is need of the magnitude of

genetic variability in the germplasm and the vast of variability for desired characters. A good knowledge on genetic diversity or genetic similarity could be helpful in long term selection gain in plants (Kumar *et al.,* 2012). Hence, genetic variability and diversity is of prime interest to the plant breeder as it plays a key role in framing and successful breeding programme. The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generation as already reported by earlier workers (Kumar *et al.,* 1994).

Mahalanobis D^2 statistics is a powerful tool in quantifying the degree of variability at the genotype level. The utility of multivariate analysis have greatly been emphasized (Murty and Arunachalam, 1966). Several workers studied the genetic diversity, clustering pattern, relative contribution of different characters towards divergence and effectiveness of selection in cassava (Carvalho and Schaal, 2001; Raghu *et al.,* 2007; Vieira *et al.,* 2008 and Rimoldi *et al.,* 2010). So, the present experiment was formulated to study the genetic divergence and clustering pattern of the cassava genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield.

MATERIALS AND METHODS

The experimental material comprised of eighteen genotypes of cassava collected from All India Co-ordinated Research Project on Tuber crops, Venkataramannagudem, Andhra

Pradesh, were evaluated during Kharif, 2012 in a randomized block design with three replications. Timely crop management practices were adopted as recommended by CTCRI, Tiruvananthapuram to raise healthy crop. The observations were recorded on five randomly selected plants per each replication for each genotype on fourteen quantitative characters viz., petiole length (cm), number of leaves per plant, total leaf area (cm²), plant height (cm), height of first branching (cm), stem diameter (cm), number of tubers per plant , tuber length (cm), tuber diameter (cm), plant dry matter content (%), tuber dry matter content (%), starch content (%), HCN content (ppm) and tuber yield (tonnes per hectare).

Statistical analysis

Mahalanobis (1936) generalized distance (D^2) was used to determine the degree of divergence and the genotypes were grouped into clusters following Tocher's method (Rao, 1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1985).

RESULTS AND DISCUSSION

In the present study, hierarchical cluster analysis based on fourteen quantitative characters allocated the eighteen genotypes of cassava into five clusters (Fig.1). The magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated by the high inter-cluster and low intra cluster D^2 values. Clustering based on the studied traits separated the genotypes into five clusters (Table 1). The cluster divergence was proved by the high inter-cluster and low intra cluster D^2 values. Cluster IV consisted of maximum number of genotypes (7) followed by cluster I (5) while cluster II had three genotypes whereas cluster V had two genotypes and the remaining cluster IV was solitary cluster. The grouping pattern did not showed any relationship between genetic divergence and geographic diversity. These results are in accordance with the findings of Omprakash and Vijay (2013) in tomato and Garje *et al.* (2013) in green gram.

The mean intra and inter cluster D^2 values among the five clusters are presented in the Table 2. and Fig. 2. The intra cluster distance ranged from 0.00 to 17.2, where maximum

distance was reported in cluster IV (17.2) followed by cluster I (12.21). Cluster III showed no intra-cluster D^2 value as it had only one genotype.

In the present investigation inter cluster D^2 values ranged from 17.52 to 62.40. This high range of D^2 values showed the presence of good amount of diversity in the material used for the present study. Minimum inter-cluster D^2 value was observed between the cluster I and II (17.52) indicated close relationship among the genotypes included in these clusters. Maximum inter-cluster D^2 value was observed between the cluster IV and V (62.40) followed by cluster II and V (55.11) indicated that the genotypes belonging to these groups were genetically most divergent and the genotypes included in these clusters can be used as parents in hybridization programme to get higher heterotic hybrids from the segregating population. Several studies have reported morphological characterization to determine the genetic diversity among cassava genotypes (Sambatti *et al.,* 2001; Raghu *et al.,* 2007; Vieira *et al.,* 2008; Benesi *et al.,* 2010; Rimoldi *et al.,* 2010; Asare *et al.,* 2011).

Cluster analysis classified the 18 genotypes into five clusters showing random distribution of the genotypes. This can be
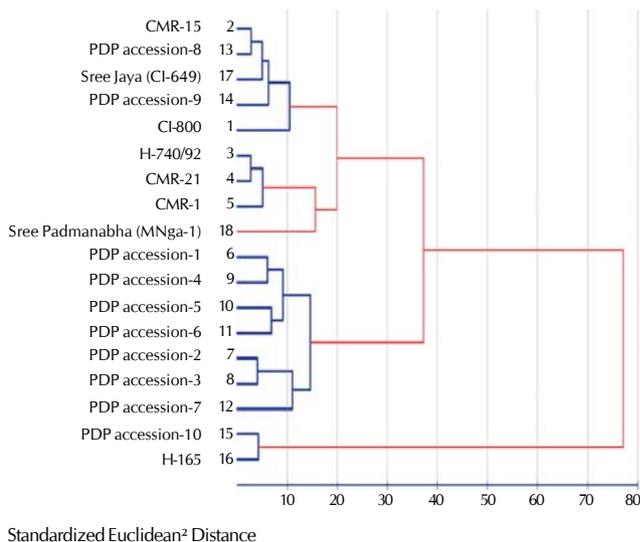

Standardized Euclidean² Distance

Figure 1: Euclidean average linkage dendrogram

Table 1: Clustering pattern of cassava genotypes (Ward's method)

Cluster	No. of genotypes	Genotypes
I	Five	CMR-15, PDP accession-8, Sree Jaya, PDP accession-9, CI-800
II	Three	H-740/92, CMR-21, CMR-1
III	One	Sree Padmanabha (MNga-1)
IV	Seven	PDP accession-1, PDP accession -4, PDP accession-5, PDP accession-6, PDP accession-2, PDP accession-3, PDP accession -7
V	Two	PDP accession-10, H-165

Table 2: Average intra (bold) and inter-cluster D^2 values for five clusters in cassava genotypes. (Ward's method)

Clusters	I	II	III	IV	V
I	**12.21**	17.52	26.23	23.31	48.60
II		**7.77**	23.38	22.52	55.11
III			**0.00**	35.15	39.35
IV				**17.25**	62.40
V					**8.46**

justified by the fact that cassava has a reproductive system which favors out crossing, and this plant can also be propagated vegetatively, which facilitates the dispersion of genotypes, the exchange among farmers. An intense exchange system of varieties has been documented among farmers growing cassava (Sambatti *et al.,* 2001).

The cluster mean of 18 genotypes presented in the Table 3. revealed that the mean value of clusters varied in magnitude

Table 3: Clusters means for fourteen characters in 18 cassava genotypes (Ward's method)
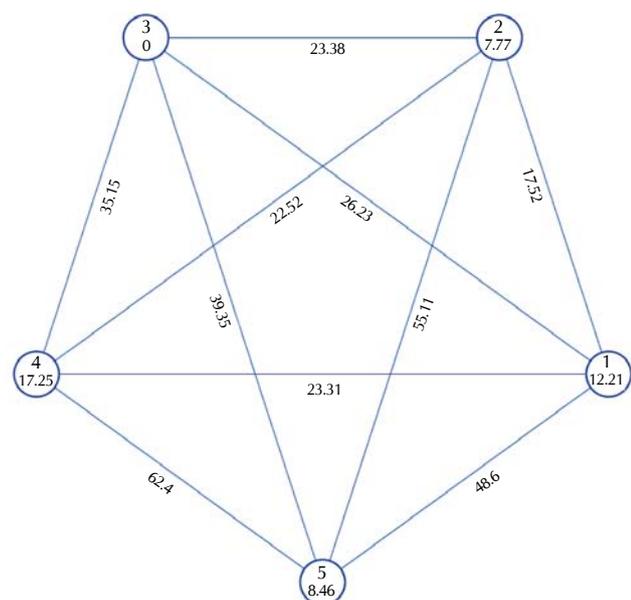
Cluster	Petiole length (cm)	Number of leaves / plant	Total leaf area (cm²)	Plant height (cm)	Height of first branching (cm)	Stem diameter (cm)	Number of tubers / plant	Tuber length (cm)	Tuber diameter (cm)	Plant dry matter content (%)	Tuber dry matter content (%)	Starch content (%)	HCN content (ppm)	Tuber yield (t.ha⁻¹)
I	34.27	3293.40	267563.20	486.00	123.49	9.78	15.40	34.89	19.46	27.93	35.27	25.23	90.13	32.51
II	35.78	3813.33	194610.17	516.67	149.86	8.23	18.33	38.66	18.10	29.54	46.50	22.57	79.82	30.61
III	32.56	4142.33	316466.56	430.00	124.70	10.51	17.67	52.01	22.32	32.63	44.76	25.57	56.67	38.13
IV	37.99	1583.67	212274.16	412.86	192.65	8.86	16.14	40.31	19.05	27.32	38.64	22.63	84.59	29.44
V	44.01	4187.17	615591.88	481.67	154.85	12.04	22.67	41.04	24.48	33.31	37.93	27.65	190.58	43.00

Table 4: Percent contribution of different characters towards diversity in cassava genotypes

S. No.	Character	No. of times ranked 1st	Percent contribution
1	Petiole length (cm)	0	0.00
2	Number of leaves/ plant	1	0.65
3	Total leaf area (cm²)	0	0.00
4	Plant height (cm)	0	0.00
5	Height of first branching(cm)	14	9.15
6	Stem diameter (cm)	1	0.65
7	Number of tubers/ plant	0	0.00
8	Tuber length (cm)	0	0.00
9	Tuber diameter (cm)	0	0.00
10	Plant dry matter content (%)	31	20.26
11	Tuber dry matter content (%)	98	64.05
12	Starch content (%)	8	5.23
13	HCN content (ppm)	0	0.00
14	Tuber yield per hectare (t/ha)	0	0.00

Mahalanobis euclidean² distances (not to the scale)

Figure: 2 Diagram showing intra and inter cluster distances among 5 clusters

for all the fourteen characters under this study. Cluster I did not exhibited high mean performance for any of the fourteen characters. Cluster II recorded the high mean performance for plant height (516.67 cm) and tuber dry matter content (46.50%). Cluster III exhibited the high mean performance for

tuber length (52.01 cm), whereas low mean performance for HCN content (56.67ppm). Cluster IV registered the high mean performance for height of first branching (192.65 cm). Cluster V showed high mean performance for petiole length (44.01 cm), number of leaves per plant (4187.17), total leaf area (615591.88 cm²), stem diameter (12.04 cm), number of tubers per plant (22.67), tuber diameter (24.48 cm), plant dry matter content (33.31%), starch content (27.65%) and the most important economic trait, tuber yield per hectare (43.00 t/ha) followed by cluster III (38.13 t/ha). It reveals that genotypes included in this cluster are useful in the improvement of tuber yield in cassava genotypes.

The percentage contribution of different important traits towards the genetic divergence is presented in Table. 4 revealed that among all the characters tuber dry matter content (64.05%) pre-dominantly contributed maximum towards genetic divergence followed by plant dry matter content (20.26%), height of first branching (9.15%). These observations were in accordance with Carvalho and Schaal, 2001.

AKNOWLDEGEMENT

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