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Genetic diversity studies in cassava (*Manihot esculenta* Crantz) under coastal salinity conditions of Karaikal

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Abstract

Genetic diversity among 33 cassava genotypes was worked out using Mahalanobis D statistic. Based on D² analysis, the genotypes were grouped into eight clusters, where the cluster VII possessed higher number (10) of genotypes followed by cluster I (7), cluster IV (5), cluster VIII (3), cluster II (2), cluster III (2), cluster IV (2) and cluster V (2). Clustering pattern revealed that geographical diversity was not associated with genetic diversity that is, genotypes collected from same location were grouped into different clusters.

Keywords: Cassava, genetic diversity, D² analysis, clusters

Introduction

Cassava (*Manihot esculenta* Crantz) or tapioca which belongs to the family Euphorbiaceae is a diploid (2n = 36). High degree of variability exists among the genotypes for earliness, tuber yield, harvest index, dry matter content, branching habit, leaf area, starch, HCN etc. Globally cassava is grown in an area of 18.57 million ha producing 230.27 million tonnes with 12.4t.ha⁻¹ of productivity (Kanagarasu *et al.*, 2014) [3]. The edible root supply energy for more than 500 million people world-wide (Ceballos *et al.*, 2006) [1]. The present study was undertaken to find out genetic variability among the different characters studied.

Materials and Methods

The present investigation was conducted in the Department of Horticulture, Pandit Jawaharlal Nehru college of Agriculture and Research institute, Karaikal during 2014 - 2015. Totally 33 genotypes were collected from different geographical location and utilized for study.

Among 33 genotypes collected for the study, 22 genotypes were collected from CTCRI, Thiruvananthapuram, seven varieties from different district of Kerala and four varieties from different district of Tamil Nadu

The experiment was laid out in a Randomized Block Design (RBD) with two replications. The main field was ploughed thoroughly and the stem cuttings were planted in the ridge and furrows of 75 cm width at a spacing of 75 cm. The cultural operations and plant protection measures were followed as per the package of practices recommended for cassava (CTCRI, Thiruvananthapuram)

The observations of five randomly selected plants were recorded. Observation was taken for yield and yield contributing characters. The characters were namely plant height, number of leaves plant⁻¹, length of the petiole, internodal length, number of tubers per plant, individual tuber weight, dry matter content of the tubers, tuber length, tuber girth, tuber length diameter ratio, harvest index, top root ratio, leaf area, net assimilation rate, crop growth rate, starch, HCN content, total sugar, reducing sugars, non-reducing sugars, tuber yield plant⁻¹.. The recorded data was subjected to statistical analysis and genetic diversity was worked out following Mahalanobis (1936) [4] genetic distance (D²) extended by Rao (1952) [5] to clustering in Tocher's method.

Result and Discussion

The analysis of variance exhibited significant difference among the genotypes for all the characters. The genotypes were clustered based on diversity analysis. The D² values were worked out. By the application of clustering technique, the 33 genotypes were grouped into eight different clusters (Table 2).

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Among the eight clusters it was observed that cluster VII was the largest with 10 genotypes followed by cluster I (7), cluster IV (5), cluster VIII (3), cluster II (2), cluster III (2), cluster IV (2) and cluster V (2).

The highest intra cluster distance of 235.96 was observed in VI cluster followed by cluster VII (147.51), whereas the lowest distance of 7.45 was observed in cluster I. This is indicative of the fact that the genotypes included in these cluster are very diverse.

The minimum inter cluster distance was found between cluster III and cluster IV (70.39). Revealing closer relation among the genotypes included in the clusters. Maximum inter

cluster distance was observed between cluster II and cluster VIII as 370.37 followed by cluster IV and cluster VI (365.54) (Table 3). The relative contribution for each character towards genetic divergence was estimated by the individual characters. The character, yield plant⁻¹ contributed the maximum contribution of 72.53 per cent, towards the genetic divergence followed by non-reducing sugars (17.04), reducing sugars (2.84), net assimilation rate (1.51), plant height (1.51), HCN content (1.32), total sugar (0.94), leaf area (0.56), tuber girth (0.56), dry matter content of the tubers (0.37), starch (0.37). The other traits exhibited very less contribution towards genetic divergence. (Table 1).

Table 1: Relative contribution of different characters to genetic diversity in cassava.

S. No	Characters	Number of first rank	Percentage of contribution
1	Plant height	8	1.5152
2	Numbers of leaves plant ⁻¹	0	0
3	Length of the petiole	0	0
4	Internodal length	0	0
5	Number of tubers per plant	0	0
6	Individual tuber weight	0	0
7	Dry matter content of tubers	2	0.3788
8	Tuber length	0	0
9	Tuber girth	3	0.5682
10	Length diameter ratio of the tuber	0	0
11	Harvest index	0	0

Table 2: Clustering pattern of 33 genotypes of cassava

Cluster	Number of genotypes	Genotypes	Origin
I	7	M.E-1 (CO1) M.E-2 (CO 2) M.E-4 (CO 4) M.E-5 (MVD 1) M.E-6 (M 4) M.E-12(SREE PRAKASH) M.E-20 (SREE APOORVA)	Triuchirapalli, Tamilnadu Thiruvapur, Tamilnadu IITA, Ibadan, Nigeria CIAT Tamilnadu CTCRI, Sreekariyam CTCRI, Sreekariyam
II	2	M.E-18 (SREE PADMANABHA) M.E-21 (9S-127)	CTCRI, Sreekariyam CTCRI, Sreekariyam
III	2	M.E-26 (KALPAKA), M.E-29 (VELLAYANI HRASWA)	CTCRI, Sreekariyam KAU, Vellayani
IV	2	M.E-15 (SREE VIJAYA), M.E-25 (CR-43-7)	CTCRI, Sreekariyam CTCRI, Sreekariyam
V	2	M.E-17 (SREE PRABHA) M.E-3 (CO 3)	CTCRI, Sreekariyam CTCRI, Sreekariyam
VI	5	M.E-7 (H 97), M.E-8 (H165) M.E-9 (H 226), M.E-10 (SREE SAHYA), M.E-11 (SREE VISHAKAM)	CTCRI, Sreekariyam CTCRI, Sreekariyam CTCRI, Sreekariyam CTCRI, Sreekariyam CTCRI, Sreekariyam
VII	10	M.E-13 (SREE HARSHA) M.E.-14 (SREE JAYA) M.E-16 (SREE REKHA) M.E-19 (SREE ATHULYA) M.E-22 (CI- 800) M.E-23 (CR-43-2) M.E-24 (CR-24-4) M.E-27 (MALABAR LOCAL) M.E-28 (CTRL) M.E-30 (KOZHICODE LOCAL)	CTCRI, Sreekariyam CTCRI, Sreekariyam CTCRI, Sreekariyam CTCRI, Sreekariyam CTCRI, Sreekariyam CTCRI, Sreekariyam CTCRI, Sreekariyam Palakkad, Kerala Ranni, Kottayam Calicut, Kerala
VIII	3	M.E-31 (PATHANAMTHITTA LOCAL) M.E-32 (RED MIXTURE) M.E-33 (BLACK MIXTURE)	Pathanamthitta, Kerala Kottayam, Kerala Kottayam, Kerala
Total = 8 clusters	Total = 33		

Table 3: Average inter and intra cluster D² values of cassava

Cluster	I	II	III	IV	V	VI	VII	VIII
I	1154.54 (7.45)	1323.77 (115.0)	827.84 (90.98)	712.24 (84.39)	1582.28 (125.78)	12807.04 (357.86)	1912.76 (138.3)	9851.58 (313.87)
II		242.84 (49.28)	1165.85 (107.98)	687.23 (82.9)	2284.57 (151.14)	16604.95 (407.49)	2379.11 (154.24)	13717.44 (370.37)
III			275.78 (52.51)	495.6 (70.39)	909.93 (95.39)	11287.13 (335.96)	1319.05 (114.85)	7917.79 (281.38)
IV				282.43 (53.14)	1477.27 (121.54)	13362.46 (365.54)	1671.62 (129.29)	10351.6164 (321.73)
V					309.52 (55.63)	8132.46 (285.17)	384.31 (117.65)	7097.81 (266.41)
VI						2176.06 (235.96)	10328.26 (321.37)	5446.71 (233.38)
VII							176.06 (147.51)	7922.86 (281.47)
VIII								00.00 (00.00)

Intra cluster distance: Diagonal values

Inter cluster distance: Off-diagonal values

D values: Values in parenthesis

Conclusion

Present investigation revealed that wide range of genetic divergence was noticed among the 33 genotypes of cassava studied, and this divergence of the genotypes may be taken into account for selecting the parents for hybridization and future breeding program. The characters such as tuber yield plant⁻¹, tuber girth, dry matter content of the tubers, non-reducing sugar, reducing sugars, net assimilation rate, plant height, HCN content, total sugar, leaf area, starch should also be considered while selecting parents for hybridization as they are important contributors of genetic divergence.

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