Indian J. Genet., **62**(3): 242-244 (2002)

Variability and genetic diversity in exotic germplasm of cassava (*Manihot esculenta* Crantz)

Santha V. Pillai

Central Tuber Crops Research Institute, Thiruvananthapuram 695 017

(Received: January 2002; Revised: July 2002; Accepted: July 2002)

Abstract

Seventy three exotic collections of cassava (*Manihot esculenta* Crantz) germplasm were evaluated for 10 yield and quality characters. Eight out of ten characters showed high variability. Following nonhierarchical Euclidean cluster analysis all the 73 genotypes were grouped into six clusters with variable number of genotypes. Accessions of heterogenous origin or place of release often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes. On the basis of the data on genetic divergence and the mean performance of yield and other traits seven diverse and superior genotypes were selected for use in breeding.

Key words : Cassava, variability, genetic diversity, germplasm, cluster analysis

Introduction

Cassava (*Manihot esculenta* Crantz) is a tropical tuber crop grown in 16 million hectares spread across the continents of Asia, Africa and South America. About 160 million tons of cassava tubers are produced globally to meet the food requirement of the low-income group and to sustain a lucrative starch industry. The Central Tuber Crops Research Institute (CTCRI), Thiruvananthapuram is holding a germplasm collection of more than 1600 accessions, about half of them being exotic. These are collected mainly from International Institute of Tropical Agriculture (IITA), Nigeria, International Centre for Tropical Agriculture (ICTA), Colombia, Bangkok, Madagascar, Ghana, Uganda, Fiji and Ceylon. As most of the accessions are infected with cassava mosaic disease (CMD) emphasis is to be given to CMD free accessions in the future breeding program. Accordingly, 73 CMD free genotypes were taken up for the study.

It is essential that sufficient variability for economic traits exists in the germplasm for profitable utilization following recombination breeding. The importance of genetic diversity in selecting plants for recombination breeding in crops to recover transgressive segregants has been repeatedly emphasised by many workers [1-3]. The genetic diversity of selected plants is not always based on factors such as geographical diversity or place of release [4-6]. Hence, characterisation of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as D^2 statistics and nonhierarchical Euclidean cluster analysis [7-9]. These procedures characterise genetic divergence using the criterion of similarity or dissimilarity based on the aggregate effect of a number of economically important characters. In view of these, 73 cassava genotypes were evaluated in this study to determine the magnitude of variability in the population for yield and yield components, to determine the grouping pattern of genotypes in different clusters and to identify genetically diverse and economically desirable genotypes for exploitation in a breeding program aimed at improving tuber yield of cassava.

Materials and methods

The experimental material consisted of 73 exotic accessions collected from Nigeria, Ghana, Madagascar, Uganda, Gabon, Taiwan, Fiji and Sri Lanka. These accessions were evaluated in the main farm of Central Tuber Crops Research Institute, Thiruvananthapuram, Kerala, which is located in the south west coast of India (latitude 11.5 N and longitude 75.2E). This location receives an annual rainfall of 2000-4000 mm. The temperature ranges from 20°C to 36°C with relative humidity ranging from 65 to 98 per cent. The clones were planted in single row evaluation plots of 5 m length, the plant-to-plant and row-to-row distance being 1 m. The experiment was replicated twice. Recommended package of practices were followed to raise a good crop. Data on 10 characters were recorded from 5 plants per replication and the average was taken for analysis.

The mean, coefficient of variation and correlation coefficient of variation were calculated as per the standard statistical procedures. The Euclidean cluster analysis [8, 9] was conducted to estimate the intra-and inter-cluster distances and to group the genotypes into different clusters. The whole statistical analysis was carried out using the computer software SPAR (Indian Agricultural Statistics Research Institute, New Delhi).

Results and discussion

The estimates of mean, coefficient of variation and correlation coefficient are given in Table 1. The population under study possesses high variation for most of the characters except starch per cent and girth of tuber. The highest variability was observed for weight of shoot (69.74%) followed by cyanogen content (66.74%) and tuber yield (54.85%). Starch content and girth of tuber showed low variability of 18.78and 19.00, respectively. The high variability for shoot weight is apparent from the stand of the crop where absolutely non-branching to highly branching types are observed. The maximum number of branches was 9 and the average was 5.69. Majority of the accessions is highly branching type. The cyanogen content in fresh tissue ranged from less than one to 125 ppm. The mean of the population is 42.37, well within the safe limit. Cyanogen is the bitter principle in cassava and it is considered a negative character. This population consists of 12 accessions having very low cyanogen, less than 10 ppm. This gives scope for selecting or breeding varieties with very low cyanogen content. Tuber yield *per se* showed sufficient variability with a mean value of 1.75. Accessions yielding as high as 5 kg per plant are also available.

Table 1. Estimates of mean and coefficient of variation for 10 characters and the correlation coefficient of tuber yield per plant with nine other characters.

S. No.	Character	Mean	PCV (%)	Correlation with yield
1	Tuber yield/plant(kg)	1.75	54.85	1
2	No. tubers/plant	4.75	45.89	0.60**
3	One tuber wt. (kg)	0.28	49.39	0.05
4	Length of tuber (cm)	25.66	35.12	0.08
5	Girth of tuber (cm)	15.63	19.00	0.04
6	Starch per cent	28.66	18.78	0.03
7	Cyanogen (ppm)	42.37	66.74	(-)0.01
8	Height of plant (cm)	110.10	28.49	0.08
9	No. branches	5.69	37.32	0.22
10	Weight of shoot (kg)	2.71	69.74	0.80**

**Significant at 1% level of probability

The highest positive correlation with yield was also shown by weight of shoot (0.80). This was followed by number of tubers per plant (0.60). High correlation existing between number of tubers and yield was reported by other workers as well [10-14]. Cyanogen, the negative character showed negative correlation with yield, though not significant.

Table 2. Distribution pattern of 73 accessions in to 6 clusters

Cluster No.	No. of genotypes	Sl. No. and country of collection
1	17	39, 48, 53, 59, 62, 63, 64, 65, 66, 67(Nigeria); 6, 8, 10, 12, 13 (Mada.); 31 (Thai); 49 (Colombia)
2	12	33, 46, 68 (Nigeria); 22, 23, 27 (Ghana); 17, 19 (Uganda); 50, 52 (Colombia); 30 (Fiji); 20(Guyana)
3	19	29, 35, 36, 38, 40, 42, 43, 47, 55, 56, 57, 60, 71, 72 (Nigeria); 9, 15 (Mada.); 16 (Fiji); 25 (Ghana); 51 (Colombia)
4	6	41, 45, 54, 58, 69 (Nigeria); 32 (Taiwan)
5	9	28, 37, 61, 70 (Nigeria); 7, 11 (Mada.); 24, 26 (Ghana); 18 (Uganda)
6	10	63, 68, 75, 80, 82, 145 (Mada.); 34, 44, 73 (Nigeria); 21 (Sri Lanka)

The accessions under study clustered into six groups comprising of varying number of members (Table 2). The number of genotypes per cluster ranged from 6 to 19. Accessions from same country are scattered in different clusters. Accessions from Nigeria, the biggest contributor, are scattered in all the clusters. This indicates the possibility of a common ancestral relationship of the genotypes. South America is considered as the centre of origin of the crop. From there it spread to Africa and Asia through the navigators. Notwithstanding this there is a tendency for a number of genotypes from the same country entering into specific clusters. Here again accessions from Nigeria show preference for cluster 3(14) and cluster 1(10). Similarly accessions from Madagascar show preference to cluster 6(6) and 1(5) whereas those from Ghana prefer cluster 2 and 5. Preferential clustering of accessions of same country to specific zymogram clusters was reported by Santha Pillai *et al.*, [I5]. Lefvre and Charrior [16] working on African cassava germplasm found that cassava varieties from different geographic origin have different enzyme profiles.

Table 3. Estimate of average intra and inter-cluster distances for 6 clusters involving 73 genotypes of cassava.

Cluster	1	2	3	4	5	6
1	**2.02**					
2	2.69	**2.11**				
3	2.17	2.86	**2.22**			
4	4.00	4.35	3.97	**2.30**		
5	3.42	3.43	3.43	4.97	**2.71**	
6	3.51	3.76	3.94	3.09	3.93	**2.58**

The data on inter- and intra-cluster distances are given in Table 3. Cluster 5 showed maximum intra cluster distance (2.71) followed by cluster 6 (2.58). Cluster number 1 showed the minimum distance of 2.02. The maximum inter-cluster distance existed between cluster 5 and 4 (4.97) followed by that between

Table 4. List of diverse and superior genotypes selected from different clusters

Sl.No.	Acc. No. of genotype	Cluster No.	Desirable characters
1	Ce 393	4	**Y(2.66)**, S(31), C(34)
2	Ce 329	4	Y(1.80), S(29), **C(10)**
3	Ce 88	5	Y(1.15), **S(35)**, C(33)
4	Ce 111	5	Y(1.75), **S(34)**, C(40)
5	Ce 480	1	**Y(2.60)**, S(33), **C(15)**
6	Ce 127	1	Y(2.25), **S(35)**, C(42)
7	Ce 135	6	**Y(2.66), S(36)**, C(54)

Y-Tuber yield per plant(kg), S-Starch per cent,
C-Cyanogen content(ppm)
Bold indicates superior characters.

2 and 4 (4.35). The intercluster distance was the least between cluster 1 and 2 (2.17). Inter crossing of superior genotypes from distant clusters is expected to throw a wide spectrum of variability. Accordingly seven superior genotypes from these distant clusters as well as from other clusters were selected for inclusion in the breeding program (Table 4). While selecting genotypes for a superior character, the scores of other characters were kept above the mean. Similar approach was followed by other workers in wheat [17], barley [18] and oat [19]. However, in cassava selection of plants for breeding program can be made only within the limitations set by flowering habit and therefore, the list given here includes only flowering types.

References

1. **Murty B. R. and Anand I. J.** 1966. Combining ability and genetic divergence in some varieties of *Linum usitatissimum*. Indian J. Genet., **26**: 21-26.
2. **Jatsara D. S. and Paroda R. S.** 1983. Genetic divergence in wheat. Indian J. Genet., **43**: 63-67.
3. **Cox T. S. and Murphy J. P.** 1990. Effect of parental divergence on F_2 heterosis in winter wheat crosses. Theor. Appl. Genet., **79**: 241-250.
4. **Murty B. R. and Arunachalam V.** 1966. The nature and divergence in breeding systems in some crop plants. Indian J. Genet., **26**: 188-198.
5. **Bhat G. M.** 1970. Multivariate analysis approach to selection of plants for hybridisation aimed at yield improvement in self-pollinated crops. Aust. J. Agric. Res., **21**: 1-7.
6. **Garg D. K. and Gautam P. L.** 1988. Evaluation of collections of wheat (*Triticum* spp.) germplasm. Genetica Agr., **42**: 255-262.
7. **Mahalanobis P. C.** 1936. On the generalised distance in statistics. Proc. Nat. Sci. India. **2**: 49-55.
8. **Beale E. M. L.** 1969. Euclidean cluster analysis. Proc. 37th session of the International Statistical Institute.
9. **Spark D. N.** 1973. Euclidean cluster analysis Algorithm As. 58. Applied Statistics, **22**: 126-130.
10. **Rajendran P. G., Lakshmi K. R. and Unnikrishnan M.** 1987. Genetic and path coefficient analysis in cassava. *In*: Proc. Nat. Symp. Production and Utilization of Tropical Tuber Crops. Nov. 27-29, 1985, CTCRI, Trivandrum, 1-7.
11. **Magoon M. L., Krishnan R. and Lakshmi K.** 1972. Association of plant and tuber characters with yield of cassava. Tropical Root and Tuber Crops Newsletter No. **5**: 29-30.
12. **IITA. 1974**. IITA Root and Tuber Crops Program. Annual Report, IITA, Ibadan, Nigeria: 125-152.
13. **Mahungu N. M., Chedda H. R., Akeriova M. E. and Hahn S. K.** 1994. Correlated response and use of selection index in cassava. Tropical root crops in a developing country. Acta Horticultura, **380**: 114-117.
14. **Balakrishnan S. and Thamburaj.** 1993. Association and path analysis studies in cassava. South Indian Horticulture, **41**(I): 47-48.
15. **Santha Pillai V., Potty V. P., Sundaresan S. and Dinesh V.** Genetic diversity in CMD free accessions of cassava expressed in terms of esterase isozyme polymorphism. *In*: Proc. Int. Meet. Tropical Tuber Crops. Dec. 9-12, 1996. CTCRI, Trivandrum, 238-242.
16. **Lefvre F. and Charrier A.** 1993. Isozyme diversity within Aftican *Manihot* germplasm. Euphytica, **66**: 73-80.
17. **Johnson V. A., Mattem P. J., Schmidt J. W. and Stroike J. E.** 1973. Genetic advance in wheat protein quantity and composition. *In*: E. R. Sears and L. M. S. Sears (Ed). Proc. 4th Int. Wheat Genet. Symp . Missouri Agric Exp Stn., Columbia: 547-556.
18. **Barbacki S., Kurhanska G., Surma M. and Adamsky T.** 1976. Transgressions in barley (*Hordeum sativum* Jess). 3. Transgressions in crude protein in grains of hybrid Impala x Himalaya. Genet. Polonica, **17**: 35-40.
19. **Cox T. S. and Frey K. J.** 1985. Complementary genes for high protein percentage from *Avena sativa* and *Avena sterilis* L. Crop Sci., **25**: 106-109.