Genetic Diversity Assessment and Improvement of Cassava Germplasm Collected in China Using Molecular Markers

Wenquan Wang[1], Jixin Zou[2], Kaimian Li[2]

1 Institute of Tropical Biology Sciences and Technology, State Key Laboratory of Tropical Crop Biotechnology, CATAS, Haikou China 571101

2 Institute of Tropical Crop Germplasm Researches, CATAS, Danzhou China 571737

Introduction

There are about two hundred years of cultivation and evolution of cassava (Manihot esculenta Crantz) in China. Presently, cassava is an important energy sources crop in south China with consistent market demanding (Henry and Westby, 2000). Although several elite cultivars such as HN 205 have been bred and released, varieties possessed higher starch content in root- tubers, resistance to Brown leaf spot (Cercosporidium henningsii) and abiotic stresses are yet not available. Germplasm is the base of hybrid breeding. Internationally, cassava accessions have been paid more attention to carry out genetic diversity evaluation by molecular tools and enhance new genes for breeding (Fregene et al., 1997; Allem et al, 2001; Mba et al, 2001). Total 102 cassava accessions have been collected in China but few genetic structure knowledge were understood. In this research, the genetic diversity of the all accessions has been investigated using SSR and AFLP markers, and the works on developing molecular markers of high starch content and waxy also have be embarked.

Materials and Methods

Materials: The 89 accessions grown in cassava nursery of Institute of Tropical Crop Germplasm Research, CATAS have been investigation and evaluation using simple sequences repeats (SSR) amplification. All this collection was made during 50 years mostly from different district southern China and some from abroad recently.

Methods: A set of 40 SSR primers, two to three from each of 18 linkage groups of the cassava genome has been selected to employ in characterizing the land races, 19 SSR markers have been accomplished. PCR amplification, gel electrophoresis and silver staining were done as normal. Genetic distance and UPGAM trees were completed by software NTSYSpc version 2.0 (Hart, 1983). Parameters of genetic diversity and differentiation were calculated from allele data using the computer package of POPGENE32 version 1.31 (Francis C Y, 2003).

Results and Discussion

A large cassava genetic diversity with similarity coefficient 0.52 to 0.93 among 89 accessions collected in China was discovered. It’s higher than diversity took place in Nigeria, Guatemala reported (Fregene, 2003). Based on coefficient 0.70, the all accessions were ascribed into 9 groups shown in Figure.1. They are each with accessions of A (15), B (24), C (13), D (16), E (2), F (8), G (8), H (2) and I (1). The result will benefit to parents selection in cassava hybridization breeding (Mazur et al., 1999). The genetic diversity parameters, including number of genotypes sample,number of ssr loci, number of polymorphic loci, percentage of polymorphic loci,average number of allele per locus, average number of allele polymorphic loci, average gene diversity and average gene heterozygosity corrected for small samples size of the 9 groups were shown in Table 1. The average gene diversity (He) of every groups is lower from 0 to 0.2848, This indicated there is no rich diversity germplasm to used for breeding and need import alien germs to cassava breeding in China.

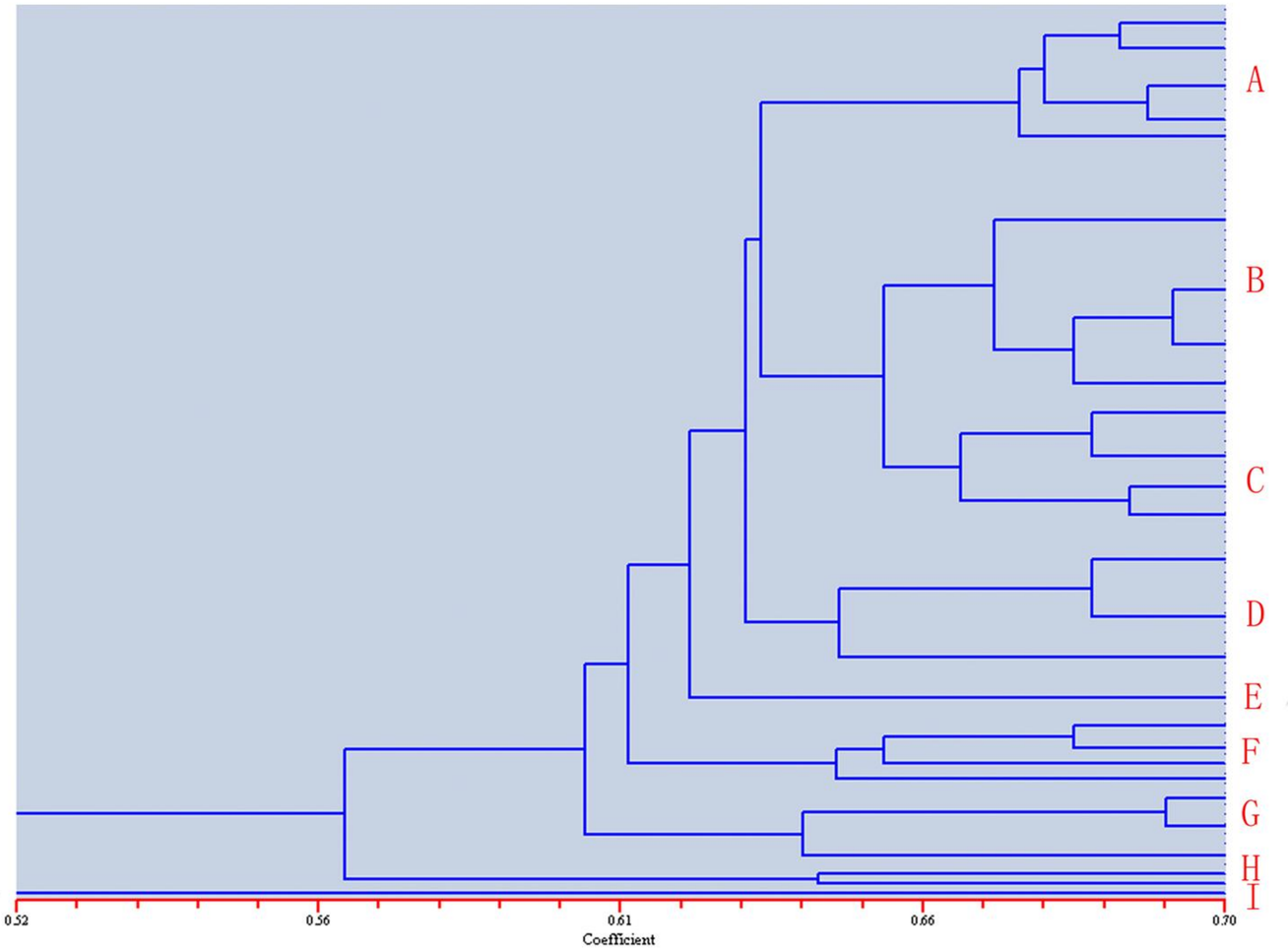
Conclusion

There is a higher genetic variation among the total germplasm collection from China but the inner- group gene diversity is small due to the asexually propagated reason. The molecular differentiation amongst land races agreed to some phenotypes of part accessions but not to others. This is the first time revealed the genetic structure of germplasm nursed in China. It's important to search more original cassava land races to breed desirable cultivars.

Future Perspectives

1. Analyze genetic diversity in the 89 accessions with all 40 SSR markers.
2. Make crosses between land races each in groups with larger genetic distance.
3. Establish another cassava molecular genetic map saturated step by step with markers.
4. Developing linkage markers of important genes such as starch content, waxy and yield characters and utilizing to MAS.

Fig 1 UPGAM tree for the nine groups of cassava land races in China based on Nei's unbiased genetic distance



References

Allem A. C., Mendes R. A., Salomao A. N. and M. L. Burle. 2001, The primary gene pool of cassava (Manihot esculenta Crantz subspecies esculenta, Euphorbiaceae), Euphytica 120(1): 115-126

Francis C Y, Timothy B. 2003, POPGENE version 1.31: Microsoft Window-Based Freeware for Population Genetic Analysis, Department of Renewable Resources, University of Alberta, Edmonton, Canada

Fregene M et al., 1997, A molecular genetic map of cassava (Manihot esculenta Crantz), Theor Appl Genet 95: 43-441

Fregene M et al., 2003, Simple sequence repeat marker diversity in cassava landraces: genetic diversity and differentiation in an asexually propagated crop Theoretical and Applied Genetics 107(6): 1083-1093

Table.1 Intra-population and inter-population estimates of genetic diversity parameters of cassava land races from China

population	n	#loc.	#loc_P	PLP	K	K_P	He	I
A	15	61	52	85.25	6.70	7.87	0.2848	0.4266
B	24	61	54	88.52	10.05	11.15	0.2805	0.4269
C	13	61	51	83.61	5.66	6.34	0.2667	0.4058
D	16	61	53	86.89	6.46	7.16	0.2792	0.4220
E	2	61	15	24.59	0.90	3.67	0.1019	0.1487
F	8	61	47	77.05	2.39	3.40	0.2198	0.3448
G	8	61	45	73.77	4.07	5.39	0.2735	0.4056
H	2	61	22	30.07	0.95	2.52	0.1494	0.2181
I	1	61	61	100	0.52	0.52	0	0
MEAN				72.1944	4.1889	5.3356	0.2062	0.3109
STD				26.5120	3.2787	3.2056	0.1013	0.1541

N: number of genotypes sample; # loc: number of ssr loci;

loc.P: number of polymorphic loci; PLP: percentage of polymorphic loci;

K: average number of allele per locus; K_P: average number of allele polymorphic loci;

He: average gene diversity Nei's (1973);

I: average gene heterozygosity corrected for small samples size [Lewontin (1972)]

STAFFS:

Wenquan Wang*

Kaimian Li

Jixin Zou

Cheng LU

Wenli ZU

Jie li

Qingrong Yao

*Email:WQUANW@hotmail.com

TEL:086-898-66894533

FAX:086-898-66890978

CBN-VI