Genetic diversity assessment of Saccharum species and elite cultivars from China using SSR Markers

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Jun Liang1, Mo Leixing1, Deng Zhinian2, Yuanwen Wei2 and Yangrui Li2

1. Sugarcane Research Center, Chinese Academy of Agricultural Sciences/Guangxi Sugarcane Research Institute, Nanning 530007, China
2. Guangxi Key Laboratory of Subtropical Bioresources Conservation and Utilization, Guangxi University, Nanning 530004, China

Abstract

Genetic diversity amongst 52 sugarcane clones including Saccharum species and cultivars (used for breeding and commercial production since the beginning of 20th century) had been assessed using 21 Simple Sequence Repeat (SSR) markers. The PCR products visualized using Capillary Electrophoresis (CE), instead of using traditional agarose gel electrophoresis, elaborated the expressions for use in the software. Use of 21 SSR primers resulted in amplification of 327 distinguishable SSR markers with an average of 15.6 bands per primer ranging from 7-24. A total of 141 distinctive SSR alleles were scored, which have been used for construction of fingerprinting database and assessment of the genetic diversity. The UPGMA algorithm with SSR markers showed four distinguishable clusters of genetically similar species and varietal clones. The highest genetic homology was 87%, observed between ROC 16 and TY 1 and few other closely related cultivars. Further, the use of CE in combination with PCR brought most of the sugarcane clones, bred using the genetically similar parents in long course of time, in one cluster. The results indicated that using SSR markers in combination with CE is an efficient tool for fingerprinting database construction and assessment of genetic diversity. Occurrence of most cultivated clones in just 4 clusters indicated the exploitation of similar genetic database for the breeding purposes. The breeding programs should be tailored to exploit the wide range of germplasm using Saccharum species to get good varieties especially for disease or insect-pest resistance.

Fig.1 Homology tree of 52 sugarcane cultivars based on 141 SSR loci

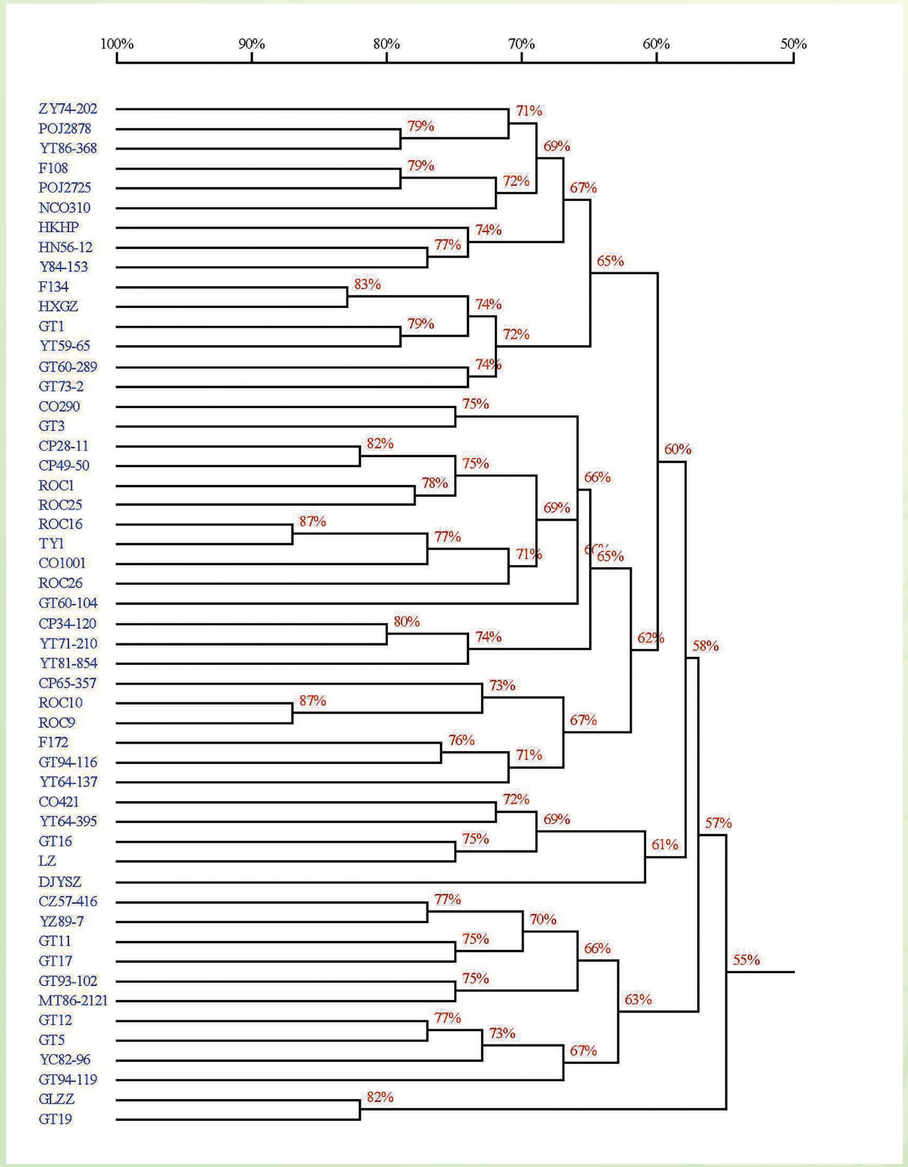

Fig.2 Dendrogram of 52 sugarcane cultivars based on SSR markers