

Genetic divergence of Malaysian upland rices revealed by microsatellite markers

ABSTRACT

Molecular markers are useful tools for evaluating genetic diversity and determining cultivar identity. A total of 50 upland rice accessions, 24 from Peninsular Malaysia and 26 from West Malaysia (Sabah state) were investigated using 10 microsatellite (SSR) markers distributed across the rice genome to study the genetic diversity. A total of 49 alleles were detected across the 50 accessions. The number of alleles per locus ranged from 2 to 11 with an average of 4.9. The average Polymorphism Information Content (PIC) value was 0.710. A dendrogram was constructed using Jaccard's similarity coefficient, and accessions were clustered into 7 groups. The most of the accessions were clustered according to their geographical origin. Shannon's information index ranged from 0.5269 to 2.0050. Nei's gene diversity (h) ranged from 0.3432 to 0.8273. Overall gene flow was 0.0011. In order to develop suitable upland rice varieties, accessions 03838, 03835, 07537, 07538, 03826, 07574, 07588, 07585, 07540, 07575, 07541, 07543, 07544, 07576, 07571, 07539, 03825, 03830 could be used as parents for future breeding program in Malaysian environment.

Keyword: Genetic diversity; Microsatellite; Molecular marker; Upland rice