

Genetic diversity of aromatic rice germplasm revealed by SSR markers

ABSTRACT

Aromatic rice cultivars constitute a small but special group of rice and are considered the best in terms of quality and aroma. Aroma is one of the most significant quality traits of rice, and variety with aroma has a higher price in the market. This research was carried out to study the genetic diversity among the 50 aromatic rice accessions from three regions (Peninsular Malaysia, Sabah, and Sarawak) with 3 released varieties as a control using the 32 simple sequence repeat (SSR) markers. The objectives of this research were to quantify the genetic divergence of aromatic rice accessions using SSR markers and to identify the potential accessions for introgression into the existing rice breeding program. Genetic diversity index among the three populations such as Shannon information index (H') ranged from 0.25 in control to 0.98 in Sabah population. The mean numbers of effective alleles and Shannon's information index were 0.36 and 64.90%, respectively. Similarly, the allelic diversity was very high with mean expected heterozygosity (H_e) of 0.60 and mean Nei's gene diversity index of 0.36. The dendrogram based on UPGMA and Nei's genetic distance classified the 53 rice accessions into 10 clusters. Analysis of molecular variance (AMOVA) revealed that 89% of the total variation observed in this germplasm came from within the populations, while 11% of the variation emanated among the populations. These results reflect the high genetic differentiation existing in this aromatic rice germplasm. Using all these criteria and indices, seven accessions (Acc9993, Acc6288, Acc6893, Acc7580, Acc6009, Acc9956, and Acc11816) from three populations have been identified and selected for further evaluation before introgression into the existing breeding program and for future aromatic rice varietal development.

Keyword: Genetic diversity; Aromatic rice; Germplasm; SSR markers

