



Evaluation of genetic diversity in *Piper* spp using RAPD and SRAP markers

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ABSTRACT. Random amplified polymorphic DNA (RAPD) and sequence-related amplified polymorphism (SRAP) analysis were applied to 74 individual plants of *Piper* spp in Hainan Island. The results showed that the SRAP technique may be more informative and more efficient and effective for studying genetic diversity of *Piper* spp than the RAPD technique. The overall level of genetic diversity among *Piper* spp in Hainan was relatively high, with the mean Shannon diversity index being 0.2822 and 0.2909, and the mean Nei's genetic diversity being 0.1880 and 0.1947, calculated with RAPD and SRAP data, respectively. The ranges of the genetic similarity coefficient were 0.486-0.991 and 0.520-1.000 for 74 individual plants of *Piper* spp (the mean genetic distance was 0.505 and 0.480) and the within-species genetic distance ranged from 0.063 to 0.291 and from 0.096 to 0.234, estimated with RAPD and SRAP data, respectively. These genetic indices indicated that these species are closely related genetically. The dendrogram generated with the RAPD markers was topologically different from the dendrogram based on SRAP markers, but the SRAP technique clearly distinguished all *Piper* spp from each other. Evaluation of genetic variation levels of six populations showed that

the effective number of alleles, Nei's gene diversity and the Shannon information index within Jianfengling and Diaoluoshan populations are higher than those elsewhere; consequently conservation of wild resources of *Piper* in these two regions should have priority.

Key words: *Piper*; Genetic diversity; Molecular marker; RAPD; SRAP