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Genetic Diversity among Wild Resources of the Genus *Boehmeria* Jacq. from West China Determined Using Inter-simple Sequence Repeat and Rapid Amplification of Polymorphic DNA Markers

Li-jun Liu[1)], Zu-Qing Meng[2)], Bo Wang[1)], Xu-xia Wang[1)], Jin-Yu Yang[1)] and Ding-xiang Peng[1)]

1) College of Plant Science and Technology, Huazhong Agricultural University
2) Tibet Agricultural and Animal Husbandry College

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Abstract: Ramie (*Boehmeria nivea* L.Gaud) is planted as an important fiber crop in China. Randomly amplified polymorphic DNA (RAPD) and inter-simple sequence repeat (ISSR) markers were used for the first time for the detection of genetic polymorphism of 37 ramie accessions (29 wild genotypes and 8 commercial varieties) collected from various geographical regions of West China. The objectives of this study were: 1) to examine the genetic diversity of four species in genus *Boehmeria* Jacq.: *B. clidemioides var. diffusa*, *B. nivea* L. Gaud, *B. longispica* Steud, and *B. macrophylla* Hornem; and 2) to determine the genetic distance of the four species by these methods. *Laportea cuspidata* (Wedd.) Friis was used as an outgroup species. The results showed that 375 (17 monomorphic fragments) strips were amplified by 31 RAPD primers, while 266 (10 monomorphic fragments) strips by 18 ISSR primers. On the average, each RAPD and ISSR primer amplified 12.1 and 14.8 strips, respectively. Based on the appearance of the markers, the genetic relationships were analyzed using unweighted pair-group method of arithmetic average cluster analysis (UPGMA) and the genetic Dice coefficients were calculated. Clustering analysis indicated that the 37 accessions were classified into four clusters which belong to 3 sections (including Section *Phyllostachys*, Section *Tilocnide* and Section *Duretia*). The overall grouping pattern of clustering corresponded well with traditional botanical taxonomy. Principal component analysis (PCA) confirmed the patterns of genetic diversity observed among the species. These results suggested that RAPD and ISSR were efficient approaches suitable for taxonomic analysis of ramie wild materials. The results provided valid guidelines for collection, conservation, and characterization of *Boehmeria* genetic resources.

Keywords: *Boehmeria*, ISSR marker, RAPD marker, Taxonomic analysis, UPGMA

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