



Genetic diversity and differentiation of the endangered and endemic species *Sauvagesia rhodoleuca* in China as detected by ISSR analysis

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ABSTRACT. *Sauvagesia rhodoleuca* (Ochnaceae) is an endangered plant that is endemic to southern China. The levels of genetic variation and patterns of population structure in *S. rhodoleuca* were investigated using inter-simple sequence repeat markers. Eleven primers were used to amplify DNA samples from 117 individuals, and a total of 92 loci were detected. Our results indicated that genetic diversity was quite low both at the species level (percentage of polymorphic bands (PPB) = 41.30%, Nei's gene diversity (h) = 0.1331, and Shannon information index (I) = 0.2028) and the population level (PPB = 16.30-28.26%, h = 0.0496-0.1012, and I = 0.0756-0.1508). A high level of genetic differentiation among populations was detected based on Nei's genetic diversity analysis (0.4344) and analysis of molecular variance (47.03%). The low genetic diversity within population and high population

differentiation of *S. rhodoleuca* were assumed to result largely from limited gene flow, genetic drift, inbreeding, and clonal growth. Conservation strategies for this endangered species are proposed based on the genetic data.

Key words: Endangered plant; Inter-simple sequence repeat; *Sauvagesia rhodoleuca*; Genetic diversity; Genetic differentiation