



Conservation and population genetic diversity of *Curcuma wenyujin* (Zingiberaceae), a multifunctional medicinal herb

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ABSTRACT. *Curcuma wenyujin* is an important multifunctional medicinal herb in China. Currently, populations of *C. wenyujin* are decreasing, and wild individuals have almost disappeared from their natural habitats. Moreover, little is known regarding the molecular characteristics of this plant. In this study, we investigated the genetic diversity and variation of five populations of *C. wenyujin*, using random amplified polymorphic DNA (RAPD) and inter-simple sequence repeat (ISSR) markers. We found that the percentages of polymorphic loci (*PPL*) at the species level (98.25% by RAPD and 100% by ISSR) were significantly higher than those at the population level (66.32% by RAPD and 67.14% by ISSR). The highest values of *PPL*, expected heterozygosity, and Shannon's information index were in Pop1, while the lowest values were in Pop2. Both DNA markers revealed a short

genetic distance between Pop1 and Pop2 (0.1424 by RAPD and 0.1904 by ISSR). Phylogenetic trees produced similar results, with Pop1, Pop2, and Pop5 in one group and Pop3 and Pop4 in another. There were no significant correlations between their genetic distances and their geographical distances. The highest genetic diversity was in Pop1 and the lowest was in Pop2, and genetic diversity at the species level was relatively low, but much higher than that at the population level. We recommended the establishment of a germplasm bank, *in situ* conservation, and propagation of wild individuals. The present study will improve the evaluation, protection, and utilization of the population resources of *C. wenyujin*.

Key words: *Curcuma wenyujin*; Population; Phylogenetic analysis; Inter simple sequence repeat (ISSR); Genetic diversity; Random amplified polymorphic DNA (RAPD)