



Genetic diversity and structure of the threatened species *Sinopodophyllum hexandrum* (Royle) Ying

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ABSTRACT. *Sinopodophyllum hexandrum* is an important medicinal plant that has been listed as an endangered species, making the conservation of its genetic diversity a priority. Therefore, the genetic diversity and population structure of *S. hexandrum* was investigated through inter-simple sequence repeat analysis of eight natural populations. Eleven selected primers generated 141 discernible fragments. The percentage of polymorphic bands was 37.59% at the species level, and 7.66-24.32% at the population level. Genetic

diversity of *S. hexandrum* was low within populations (average $H_E = 0.0366$), but higher at the species level ($H_E = 0.0963$). Clear structure and high genetic differentiation were detected between populations using unweighted pair groups mean arithmetic and principle coordinate analysis. Clustering approaches clustered the eight sampled populations into three major groups, and AMOVA confirmed there to be significant variation between populations (63.27%). Genetic differentiation may have arisen through limited gene flow ($N_m = 0.3317$) in this species. Isolation by distance among populations was determined by comparing genetic distance versus geographical distance using the Mantel test. The results revealed no correlation between spatial pattern and geographic location. Given the low within-population genetic diversity, high differentiation among populations, and the increasing anthropogenic pressure on this species, *in situ* conservation measures, in addition to sampling and *ex situ* preservation, are recommended to preserve *S. hexandrum* populations and to retain their genetic diversity.

Key words: *Sinopodophyllum hexandrum*; Genetic diversity; Population structure; Conservation