



Genetic diversity and population structure of *Eucommia ulmoides* Oliver, an endangered medicinal plant in China

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ABSTRACT. *Eucommia ulmoides* Oliver, one of the tertiary relict species found only in China, is the only extant species of Eucommiaceae. Using inter-simple sequence repeat (ISSR) and sequence-related amplified polymorphism (SRAP) markers, we studied the genetic diversity and population genetic structure of 187 accessions from 17 *E. ulmoides* populations throughout its main distribution in China. A total of 65 bands were amplified using eight ISSR primers, of which 50 bands (76.9%) were polymorphic. Meanwhile, another 244 bands were observed using eight SRAP primer combinations and 163 (66.8%) of these were polymorphic. The analysis of molecular variation (AMOVA) indicated that 88.8 and 92.4% of the total variation resided within populations based on ISSR and SRAP analysis, respectively. Moreover, we found that the *E. ulmoides* populations were clustered into six distinct groups using ISSR and SRAP markers via the unweighted pair-group method (UPGMA). Furthermore, STRUCTURE analysis showed that these 17 populations could be classified into four groups using ISSR markers, but only two groups using SRAP markers. No

significant relevancy was observed between genetic and geographic distances among the sampled populations. The results of this study support the view that exchange of seeds among local farmers plays an important role in shaping the present genetic distribution pattern. “Core collection” is suggested for genetic diversity conservation of *E. ulmoides* in China.

Key words: Genetic diversity; Diversity conservation; ISSR; SRAP; *Eucommia ulmoides* Oliver