



# Genetic diversity of *Toona sinensis* Roem in China revealed by ISSR and SRAP markers

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**ABSTRACT.** *Toona sinensis* Roem has an important value as a type of traditional vegetable and Chinese medicinal herb, and is also a valuable source of wood in China. In this study, we used the inter-simple sequence repeat (ISSR) and sequence-related amplified polymorphism (SRAP) markers to assess the level and pattern of genetic diversity in five domesticated *T. sinensis* populations in China. Our results indicated a relatively low level of genetic diversity both at species ( $H_s = 0.1662, 0.2098$ , respectively) and population levels ( $H_s = 0.0978, 0.1145$ , respectively). Molecular variance analyses revealed a relatively high degree of differentiation among populations ( $G_{ST} = 0.3901, 0.4498$ ), and low levels of gene flow ( $N_m = 0.7816$  and  $0.6116$ ). We divided the five populations into two groups by cluster analysis: group one consists of populations collected from the south part of China (e.g., Yuxi, Yunan Province and Zuanjiang, Chongqing Municipality), and group two contains those cultivated in north part of China (e.g., Hengshui, Hebei Province, Jinan and Rizhao, Shandong Province). The correlation of genetic

relationships among populations fits well with their geographical distribution (Mantel test;  $r = 0.7236$  and  $0.6789$ , respectively). Asexual propagation, limited gene flow and geographic isolation are most likely the key factors associated with the observed genetic structure of *T. sinensis* grown in China. The present study indicated that both ISSR and SRAP markers were effective and reliable for assessing the degree of *T. sinensis* genetic variations.

**Key words:** *Toona sinensis* Roem; Genetic diversity; ISSR; SRAP