

研究报告

## 珍稀濒危植物夏蜡梅遗传多样性的ISSR分析

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**摘要** 利用ISSR分子标记技术,对濒危植物夏蜡梅10个居群的遗传多样性进行了分析.结果表明:夏蜡梅种的遗传多样性较高,多态位点百分率为73.08%,Shannon指数为0.3097,Nei指数为0.1987;而居群水平的遗传多样性较低,多态位点百分率平均为23.65%,Shannon指数平均为0.1251,Nei指数平均为0.0839.AMOVA分子差异分析显示:居群间遗传分化程度高,57.11%的变异存在于居群间,42.89%存在于居群内,基因分化系数( $G_{st}$ )为0.5779;居群间的基因流为0.3651.生境的片断化使居群间的基因流受阻,可能是导致居群间高遗传分化和居群水平低遗传多样性的主要原因.10个居群间的平均遗传距离为0.1471.利用UPG-MA法对10个居群进行聚类,结果是天台县内的2个居群、临安市内的8个居群各组成一大类群.

**关键词** [夏蜡梅](#) [天然居群](#) [遗传多样性](#) [遗传分化](#) [ISSR](#)

分类号

## ISSR analysis on genetic diversity of endangered relic shrub *Sinocalycanthus chinensis*

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### Abstract

By using inter-simple sequence repeat (ISSR) markers technique, this paper studied the genetic diversity of ten populations of endangered relic shrub *Sinocalycanthus chinensis*. The results showed that at species level, the percent age of polymorphic loci ( $P$ ) was 73.08%, Shannon's index ( $h$ ) was 0.3097, and Nei's gene diversity ( $I$ ) was 0.1987, indicating a high level of genetic diversity, but at population level, they were 23.65%, 0.1251 and 0.0839, respectively, suggesting a low level of genetic diversity. The analysis of molecular variance (AMOVA) demonstrated that there was a relatively high level (57.11%) genetic variation among the populations, with the gene differentiation coefficient ( $G_{st}$ ) and gene flow being 0.5779 and 0.3651, respectively. The high genetic differentiation among populations and the low genetic diversity within populations could be attributed to the habitat fragmentation and the limited gene flow among populations. Through cluster analysis, the ten populations of *S. chinensis* were classified into two groups, with the eight populations in Lin'an City forming a group and other two in Tiantai County forming another group.

**Key words** [Sinocalycanthus chinensis](#) [natural population](#) [genetic diversity](#) [genetic differentiation](#) [ISSR](#)

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