

 中文标题  

## 利用ISSR-PCR方法分析单叶蔓荆居群的遗传多样性

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中文摘要: 目的: 对山东和江西单叶蔓荆的4个居群80个样本进行资源考察和种内遗传变异情况分析。方法: 利用ISSR分子标记技术。结果: 从100条ISSR引物中筛选出15条特异性强、稳定性好的引物进行ISSR分析, 共获得129个位点, 其中多态位点数115个, 多态位点百分率为89.15%。利用PopGene软件进行分析, 结果表明居群之间的平均多态位点百分率为71.89%, Shannon表型多样性指数(D)平均值为0.220 4, 具有较高的遗传多样性。结合聚类分析和地理变异规律把种群划分为2个大的种群组: 山东居群组和江西居群组。结论: 以上结果可为单叶蔓荆种质资源的保护和利用以及物种分化研究提供依据。

中文关键词: [单叶蔓荆](#) [ISSR-PCR](#) [遗传多样性](#)

### Genetic diversity analysis of *Vitex trifolia* var. *simplicifolia* populations with inter-simple sequence repeats (ISSR) technique

Abstract: Objective: To investigate 4 populations of 80 samples of *Vitex trifolia* var. *simplicifolia* collected from Shandong and Jiangxi province and analyze their intraspecific genetic variance. Method: Inter-simple sequence repeat (ISSR) technique was applied for the study. Result: Fifteen specific and stable primers were selected from 100 primers. A total of 129 sites were generated, and 115 of them (89.15%) were polymorphic. The data analyzed by PopGene demonstrated that the average polymorphic site percentage among the four populations was 71.89%. The average Shannon's information index was 0.220 4. According to cluster analysis and the law of geographic variation, the populations were classified into two large groups: the Shandong group and the Jiangxi group. Conclusion: These results will provide the information for protection and utilization of *V. trifolia* var. *simplicifolia* and also further data for the study of genetic variation and species differentiation of *V. trifolia* var. *simplicifolia*.

Keywords: [Vitex trifolia](#) var. [simplicifolia](#) [ISSR-PCR](#) [genetic variation](#)

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