

研究报告

浙江省境内七子花天然种群遗传多样性研究

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摘要

利用RAPD技术对浙江省境内的七子花9个天然种群遗传多样性和遗传分化进行研究.结果表明, 12种随机引物对180棵植物进行检测, 共得到164个可重复的位点.多态位点百分率在14.60%~27.44%(平均为20.73%),以括苍山种群最高, 其次是四明山种群, 最低是观音坪种群. Shannon指数和Nei指数均反映出七子花各种群具有较低的遗传多样性,但遗传分化明显. Shannon指数显示种群内遗传多样性只占总遗传多样性的27.28%, 而种群间遗传多样性却占72.72%; Nei指数表明种群内的遗传变异较小, 种群间的遗传变异较大, 种群间的遗传分化系数为0.7157. 七子花种群间的基因流为0.1987, 遗传相似度平均为0.7306, 遗传距离平均为0.3150, 各种群间的遗传分化明显. 根据遗传距离聚类分析, 大致可以将9个七子花种群分为东部和西部两大类群.

关键词 [七子花; 天然种群; 遗传多样性; 遗传分化; RAPD](#)

分类号

Genetic diversity of *Hepatacodium miconioides* natural populations in Zhejiang Province

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Abstract

Hepatacodium miconioides is the Class II protected plant species in China. This paper studied the genetic diversity and differentiation of its nine natural populations in Zhejiang Province by using random amplified polymorphic DNA (RAPD) technique. Twelve random primers were selected in the amplification, and 164 repetitive loci were produced. The percentage of polymorphic loci in each *H. miconioides* population ranged from 14.60% to 27.44%, with an average of 20.73%. Among the test populations, Kuochangshan population had the highest percentage of polymorphic loci, Simingshan population took the second place, and Guanyinping population had the lowest one. As estimated by Shannon index, the genetic diversity within *H. miconioides* populations accounted for 27.28% of the total genetic diversity, while that among *H. miconioides* populations accounted for 72.72%. The genetic differentiation among *H. miconioides* populations as estimated by Nei index was 0.7157. The genetic differentiation estimated by Nei index was generally consistent with that estimated by Shannon index, i.e., the genetic differentiation among populations was relatively high, but that within populations was relatively low. The gene flow among *H. miconioides* populations was relatively low (0.1987), and the genetic similarity ranged from 0.6557 to 0.8119, with an average of 0.7306. The highest genetic distance among populations was 0.4229, while the lowest one was 0.2083. All the results showed that there was a distinct genetic differentiation among *H. miconioides* populations. The genetic distance matrix of nine test populations was calculated by using the method, and the clustering analysis

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was made by using the unweighted pair group method with arithmetic mean (UPGMA). The cluster analysis suggested that the nine populations of *H. miconioides* in Zhejiang Province could be divided into two groups, i.e., eastern Zhejiang group and western Zhejiang group.

Key words

[Hepatacodium miconioides](#) [Natural population](#) [Genetic diversity](#)
[Genetic differentiation](#) [RAPD](#)

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