

研究论文

附子野生资源群体遗传多样性的RAPD分析

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摘要 应用RAPD标记分析了分布在附子主产区四川、重庆、陕西及湖北16个野生乌头种群的遗传变异。24个引物共检测到643个RAPD位点, 多态位点602个, 总的多态位点百分率达93.5%。Shannon多样性和Nei遗传分化结果一致显示重庆酉阳种群和重庆城口种群遗传多样性最高, 四川盐源种群和陕西勉县种群的遗传多样性最低。Shannon指数测出的种群内的遗传变异(57.6%)略占优势, 群体间的遗传分化达到42.4%; Nei基因分化系数(GST)达40.0%; 分子方差分析(AMOVA)发现群体间遗传变异仅为25.37%; 种群每代迁移数Nm为0.756。Nei相似性系数的UPGMA分析结果显示该地区的野生乌头分布上有一定的地域性, 特别是同为附子道地产地江油供种的北川、安县和青川种群间遗传关系密切, 说明种质资源在道地药材形成中具有重要作用。研究结果表明, 附子主要栽培地区的乌头野生种群之间存在较大的遗传分化, 遗传多样性较高, 遗传种质资源较丰富, 存在一定的特异性资源, 为进一步开发利用乌头(川乌、附子)提供了丰富的种质资源。

关键词 附子(乌头); 遗传多样性; RAPD标记; 种群分化; 野生种群

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RAPD analysis of genetic diversity in the wild populations of *Aconitum carmichaeli* Dexb. (Ranunculaceae) in China

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Abstract *Chuanwu (Aconitum carmichaeli* Dexb. (Ranunculaceae)) is a traditional Chinese medicinal herb, widely used for its pharmacological effects, including anti-inflammation and pain relief. This herb has been cultivated in China for medical use for over 1000 years and is mainly grown in Sichuan and Shanxi provinces in China. We have examined the genetic diversity and genetic differentiation in 16 wild populations of *A. carmichaeli* from HengDuan and QingBa Mountains in Southwest China using random amplified polymorphic DNA (RAPD) markers. A total of 643 discernible loci were obtained for all populations using 24 primers, and 93.5% of these loci were polymorphic (PPL=93.5%). POPOGENE analysis indicated that the genetic diversity by Shannon index among populations was 42.4% and Nei's gene diversity coefficient (GST) was 40.0%. AMOVA also found the genetic diversity among population was 25.37%. It was found that the genetic variation was relatively greater within populations compared to that among populations. The estimated gene flow from GST(Nm) was 0.756. Wind and insect pollination played important roles in the sexual reproduction of wild *A. carmichaeli*, resulting in a high level of out-crossing. Out-crossing and tuber reproduction were the main causes of high genetic diversity and abundant genetic differentiation in *A. carmichaeli* genetic resources. Calculations of Shannon diversity and Nei genetic differentiation consistently indicated that the Chongqing Youyang and Chongqing Chengkou populations possessed the greatest genetic diversity, where as Sichuan Yanyuan and Shanxi Mianxian populations possessed the lowest genetic diversity. The results of UPGMA and Nei's analysis indicated that the genetic make-up of these wild populations of *A. carmichaeli* showed regional diff

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erences. The populations in a region including Beichuan, Anxian and Qingchuan were quite closely related. The high medical quality variety Jiangyou FUZI (*Radix Aconiti Lateralis Preparata*) is from this region and the tuber of this variety is usually used as seeds in cultivation. This research has indicated that there is rich germplasm resource of *A. carmichaeli* and there are large genetic diversities among its wild populations; both are important for selecting *A. carmichaeli* varieties that may have better medical quality.

Key words *Aconitum carmichaeli* Dextb.; genetic diversity; population differentiation; RAPD; wild population

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