

黄芩种质资源ISSR遗传多样性的分析及评价

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收稿日期 修回日期 网络版发布日期 接受日期

摘要

采用ISSR分子标记技术对6个野生或栽培居群共147份黄芩种质进行遗传多样性分析和评价。分析结果表明, 51个ISSR引物中筛选出18条扩增条带清晰、重复性好和多态性高的引物, 共扩增出485条清晰的条带, 其中466条具有多态性, 平均多态性位点比率为96.08%, 平均Nei's基因多样性指数和Shannon's信息指数分别为0.244 4和0.388 9, 等位基因数(N_a)和有效等位基因数(N_e)分别为1.993 8和1.383 9, 遗传分化指数 G_{st} =0.122 3, 遗传一致度(I)和遗传距离(D)分别为0.951 5和0.050 1, 说明收集的黄芩种质资源在总体上具有较高的遗传多样性, 不同居群间存在一定的遗传分化和基因交流, 遗传变异主要存在于居群内。分子聚类结果表明, 同一地区的种质并没有按照收集来源完全聚类, 可能与种质不同起源或民间栽培引种有关。在DNA分子水平揭示黄芩种质资源的遗传多样性水平, 将为进一步黄芩种质资源评价、保存和新品种选育等利用提供依据。

关键词 [黄芩; 种质资源; ISSR; 遗传多样性; 聚类分析](#)

分类号 [S567.2](#)

Analysis and Evaluation on Genetic Diversity of *Scutellaria baicalensis* G. by ISSR Markers

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Abstract

To study the genetic diversity of *Scutellaria baicalensis* G., 147 individuals from six populations were analyzed by inter-simple sequence repeat (ISSR). Eighteen primers were selected to produce highly reproducible ISSR bands. Among 485 amplified bands, 466 showed polymorphism, the percentage of polymorphic bands reached 96.08%. Nei's gene diversity index and Shannon information index were 0.244 4 and 0.388 9, respectively. Number of alleles (N_a) and effective number of alleles (N_e) were 1.993 8 and 1.383 9, respectively. G_{st} was 0.123 3, genetic identity (I) and genetic distance (D) were 0.951 5 and 0.050 1, respectively. The results showed that the collected germplasm resources of *S. baicalensis* had a high genetic diversity in general. There was a certain genetic differentiation and gene flow among different populations and the genetic variation was mainly within populations. Molecular clustering results showed that the same region germplasms were not clustered completely following the collection source. It may be related to folk culture introduction or less than normal for ISSR primers. The genetic diversity of *S. baicalensis* germplasm resources can provide a basis for the evaluation, preservation and breeding of new varieties in the future.

Key words [Scutellaria baicalensis G.; germplasm; ISSR; genetic diversity; cluster analysis](#)

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