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论文

射干及类似药用植物叶绿体*rbcL*基因序列分析

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摘要：

目的 对射干*Belamcanda chinensis* (L.) DC.,鸢尾*Iris tectorum* Maxim.,野鸢尾*I.dichotoma* Pall.,蝴蝶花*I.japonica* Thunb.和德国鸢尾I.germaica L.等5种药用植物进行叶绿体*rbcL*基因序列分析,并对其亲缘关系进行探讨。方法CTAB(Cetyl trimelhyl ammonium bromide,CTAB)法提取总DNA,用作者设计的引物对鸢尾科5种药用植物的叶绿体*rbcL*(ribulose 1,5-bisphosphate carboxylose Large Gene,rbcL)基因进行扩增,PCR扩增产物纯化后,用ABI310 DNA自动测序仪测序。结果获得射干和4种鸢尾属药用植物叶绿体*rbcL*基因部分序列(约750 bp),除德国鸢尾外, 其余4种药用植物的*rbcL*基因序列为首次获得;用clustal 8.0,MEGA 2.0等软件分析统计获得的目的基因片段,得到碱基突变点,遗传距离［碱基差异数(1.000～20.000)、颠换数为(0.000～9.000)、转换数为(0.000～14.000)］,根据*rbcL*基因部分序列数据建立分子系统树。结论根据叶绿体*rbcL*基因序列数据可以很好的鉴别5种鸢尾科植物。

关键词： 射干 鸢尾属 *rbcL*基因 基因序列分析 分子鉴定

rbcL sequence analysis of *Belamcanda chinensis* and related medicinal plants of *Iris*

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Abstract:

AimTo identify “Shegan” ［*Belamcanda chinensis* (L.) DC.］ and relative medicinal plants of *Iris* including *Iris tectorum* Maxim., *I.dichotoma* Pall., *I.germanica* L. and *I.japonica* Thunb. by ribulose 1,5-bisphosphate carboxylase Large Gene (*rbcL*) sequence analysis. MethodsGeneral DNA was isolated from the fresh leaves of *Belamcanda chinensis* and 4 *Iris spp*. by CTAB. A pair of primers was designed to amplify the *rbcL* gene and PCR Preps DNA kit was used to purify the PCR products. The *rbcL* sequences were determined by ABI (Applied Biosystems Inco.) Prism 310 Genetic Analyzer. ResultsA fragment of about 750 bp of *rbcL* gene from *Belamcanda chinensis* and 4 *Iris spp*. were amplified and sequenced. The *rbcL* sequences of *Iris tectorum, I.dichotoma*Pall. and *I.japonica* were reported for the first time. The *rbcL* sequences of 5 species of Iridaceae were aligned and analyzed using Clustal (Version 8.0) and MEGA (Version 2.0.) programs. The nucleotide number of difference is from 1.000 to 20.000. The tranversions is from 0.000 to 9.000 and the transitions is from 0.000 to 14.000. Phylogenetic tree based on *rbcL* partial sequence data indicated that the eleven samples of 5 species clustered separately. Conclusion The sequence variation of *rbcL* can be used to identify *Belamcanda chinensis* and 4 species of relative medicinal plants of *Iris*. The molecular phylogenetic tree accords with the classical taxonomy.

Keywords: *Iris* *rbcL* gene nucleotide sequence analyses molecular identification *Belamcanda chinensis*

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