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论文

中国不同地区蛇床的rDNA ITS序列分析

蔡金娜;周开亚;徐珞珊;王峥涛;沈曦;王义权;李晓波

1.中国药科大学生药学研究室,南京 210038;南京师范大学江苏省资源生物技术重点实验室,南京 210097 摘要:

目的:探讨不同分布区的蛇床Cnidium monnieri的ITS序列变异与其地理分布和化学成分的相关性。方法:设计2对引物,Pf+Pb及P5.8S ITS1+P5.8S ITS2,PCR扩增产物纯化后用银染法或ABI 310测序。结果:得到核糖体DNA中的ITS及5.8S rDNA完全序列,18S和26S rDNA部分序列,共约700 bp。5个地点样品的ITS-1及ITS-2的序列大小分别为210~217 bp和219~224 bp。ITS-1碱基序列的遗传距离0.00~1.93%,ITS-2碱基序列的遗传距离0.46~2.34%,ITS-1较为保守。以NJ法根据ITS-2序列数据重建系统发生树。哈尔滨样品聚为一组,衡水与德州样品和郑州与高淳样品各自聚为一组。结论:ITS-2序列的变异与中国产蛇床的纬度分布相关,而其与蛇床化学型的关系尚需作进一步研究。

关键词: 蛇床; rDNA内转录间隔区; 纬度

RIBOSOMAL DNA ITS SEQUENCE ANALYSES OF *CNIDIUM MONNIERI* FROM DIFFERENT GEOGRAPHICAL ORIGIN IN CHINA

Wang Yiquan; Cai Jinna; Zhou Kaiya; Xu Luoshan; Wang Zhengtao; Shen Xi; and Li Xiaobo

Abstract:

AIM: To study the correlation between ITS sequence variation of *Cnidium monnieri* and geographical distribution and chemo-type of the plant. METHODS: Two pairs of primers Pf+Pb and P5.8S ITS1+P5.8S ITS2 were designed. The PCR products were purified and sequenced by silver staining DNA sequencing technique and ABI 310. RESULTS: Complete sequence of ITS and 5.8S rDNA, and partial sequence of 18S rDNA and 26S rDNA of *Cnidium monnieri* were obtained. They totaled about 700 bp. The sequences of ITS-1 and ITS-2 ranged from 210 bp to 217 bp and 219 bp to 224 bp; respectively. Pairwese sequence divergences of the samples ranged from 0% to 1.93% in ITS-1, and from 0.46% to 2.34% in ITS-2. The ITS-1 is more conservative. Phylogenetic tree based on ITS-2 sequence data (225 aligned sites) indicated that the Harbin samples, Hengshui and Dezhou samples, and Zhengzhou and Gaochun samples clustered separately. CONCLUSION: The sequence variation of ITS-2 is correlated to latitude distribution of *Cnidium monnieri* in China. Further studies are needed to clarify the relation between ITS sequence variation and chemo-type of *Cnidium monnieri*.

Keywords: rDNA internal transcribed spacer latitude Cnidium monnieri

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