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黄芪与其混伪品的ITS序列分子鉴定研究

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中文摘要：目的：研究黄芪与其混伪品之间的DNA分子鉴别方法。方法：采集不同产地的黄芪药材13份,替代品红芪2份,混伪品紫花苜蓿3份和蜀葵1份,所有样品进行总DNA的提取,PCR扩增,并对扩增产物进行测序得到相应的序列,同时从GenBank下载蓝花棘豆、锦鸡儿2种伪品的ITS序列。用MEGA 4计算其种间的K-2-P距离,最后利用ITS序列构建其系统发育树。结果：测得了19份样品的ITS序列全长,分别为蒙古黄芪646～650 bp,膜荚黄芪为646～650 bp;红芪为664 bp;紫花苜蓿为659 bp;蜀葵为728 bp,在GenBank中注册,获得登记号。通过以ITS序列重建系统进化树进行的聚类分析可以将黄芪与其混伪品有效的区分开。结论：ITS序列能够成功鉴定黄芪及其易混伪品,可以作为黄芪与其混伪品的分子鉴定方法。

中文关键词：黄芪 ITS序列 分子鉴定

Molecular identification of Astragali Radix and its adulterants by ITS sequences

Abstract:Objective: To explore a new method for identification Astragali Radix from its adulterants by using ITS sequence. **Method:** Thirteen samples of the different Astragali Radix materials and 6 samples of the adulterants of the roots of *Hedysarum polybotrys*, *Medicago sativa* and Althaea rosea were collected. ITS sequence was amplified by PCR and sequenced unidirectionally. The inter-specific K-2-P distances of Astragali Radix and its adulterants were calculated,and NJ tree and UPGMA tree were constructed by MEGA 4. **Result:** ITS sequences were obtained from 19 samples respectively, there were Astragali Radix 646-650 bp, *H. polybotrys* 664 bp, *Medicago sativa* 659 bp, *Althaea rosea* 728 bp, which were registered in the GenBank. Phylogeny trees reconstruction using NJ and UPGMA analysis based on ITS nucleotide sequences can effectively distinguish Astragali Radix from adulterants. **Conclusion:** ITS sequence can be used to identify Astragali Radix from its adulterants successfully and is an efficient molecular marker for authentication of Astragali Radix and its adulterants.

keywords: Astragali Radix ITS sequences molecular identification

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