

论文

鼠尾草属药用植物及其近缘种的ITS序列分析

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摘要:

采用分子系统学方法分析鼠尾草属药用植物及其近缘种的遗传多样性, 为准确进行基源鉴定、阐明本属内的种间关系及发现新的药用资源提供分子证据。本文从野外采集的27个鼠尾草属植物叶片样品中分离提取DNA, PCR扩增ITS区及5.8S rDNA完整序列并测序, 采用Mega 3.1软件进行系统学分析。27个鼠尾草样品的ITS及5.8S rDNA区序列全长为612~617 bp, 邻接法(neighbor-Joining)构建的系统发生树部分支持了形态学的属下划分, 但对部分种的系统位置特别是三叶鼠尾草和黄花鼠尾草两个亚种的处理上与形态学划分存在明显的分歧。序列分析显示5.8S rDNA序列相当保守, 而ITS区段则在亚属间差异明显, 且原产我国的该属植物与欧美引进种明显具有不同起源。ITS系统树对于亚属和组的处理较为合理, 但对组下的划分则表现出了信息量不足, 需要其他相关证据的支持。ITS分析支持了丹参组内其他近缘种作为丹参类药材替代资源的合理性, 同时也揭示了甘西鼠尾类高山丹参在遗传上与丹参类药材的显著不同。

关键词: 鼠尾草属 ITS序列 遗传多样性

Analysis of ITS sequences of some medicinal plants and their related species in *Salvia*

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Abstract:

Molecular systematic techniques were applied to reveal the genetic diversity of medicinal plants and their related species in *Salvia*. The internal transcribed spacer (ITS) as well as 5.8S rDNA sequences of 27 samples of *Salvia* were amplified using PCR method and sequenced. Mega 3.1 was used to analyze the genetic diversity within genus. The complete sequences of ITS plus 5.8S rDNA are about 612-617 bp. A phylogenetic tree generated by Neighbor-Joining method partly supported the morphological classification within *Salvia*, but incompatible results were also obtained in the treatment of phylogenetic positions of some species such as *Salvia trijuga*, *Salvia flava* var. *flava* and *Salvia flava* var. *megalantha*. The ITS regions of present *Salvia* species showed considerable variation between subgenera in contrast with the conservative 5.8S rDNA sequences. The native *Salvia* species might have a different origin from the foreign species. The phylogenetic positions of subgenera and sections inferred by ITS analysis were comparable with that of traditional classification, while the phylogeny within sections is still doubtful due to limited information in ITS sequence and need to be further proved by other evidence. ITS analysis in this study supports the rationality of using species from *Drymosphace* section as substitute drug resources of Dan shen, but also reveals significant genetic differences between high mountain Dan shen species such as *Salvia przewalskii* with traditional Dan shen origins.

Keywords: ITS sequence genetic diversity *Salvia*

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