

云南西双版纳野生与栽培绞股蓝根内丛枝菌根真菌的分子多样性

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Molecular diversity of arbuscular mycorrhizal fungi in wild and cultured *Gynostemma pentaphyllum* roots in Xishuangbanna, Southwest China.

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摘要

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摘要

采用巢式-PCR、DNA克隆测序技术,对西双版纳地区野生与栽培绞股蓝根内丛枝菌根真菌(AMF)进行群落结构多样性研究.试验共获得551个含有丛枝菌根真菌18S rDNA片段的克隆子,经限制性片段长度多态性分析,得到100个RFLP类型,将其划分为20个序列类型,分属于7个科.将20个序列类型的相关序列与GeneBank数据库进行比对,有5个可以鉴定到种,分别为 *Glomus viscosum*、*Claroideoglossum etunicatum*、*Racocetra tropicana*、*Acaulospora spinosa*、*Acaulospora mellea*.与 Maarj AM 数据库中序列进行比对,12个可鉴定为虚拟分类分子种,其中7个未在孢子形态学鉴定方法中获得.西双版纳地区野生与栽培绞股蓝根内丛枝菌根真菌群落组成差异极显著.野生绞股蓝根内Glo₂、Amb₁、Para₁为优势类群,而栽培绞股蓝根内Glo₃、Glo₈、Glo₁₀、Div₁为优势类群. Claroideoglomeraceae和Ambisporaceae仅在野生样本中出现,而Diversisporaceae仅在栽培样品中出现.

关键词: 丛枝菌根真菌 绞股蓝 多样性 RFLP分析 巢式-PCR

Abstract:

By using nested-PCR, DNA cloning, and sequencing techniques, this paper studied the diversity of the community structure of arbuscular mycorrhizal fungi (AMF) in wild and cultured *Gynostemma pentaphyllum* roots. A total of 551 clones containing 18S rDNA genes of AMF were obtained from the roots. After the analysis of the restriction fragment length polymorphism, 100 different RFLP types were obtained, which were further divided into 20 AMF phylotypes belonging to seven families. The comparison of the sequences of 20 AMF phylotypes with the GenBank database showed that there were 5 AMF phylotypes having high similarity to the sequences of reported AMF species *Glomus viscosum*, *Claroideoglossum etunicatum*, *Racocetra tropicana*, *Acaulospora spinosa*, and *Acaulospora mellea*, respectively. These sequences were then assessed for the similarities against the Maarj AM database, and 12 phylotypes showed high similarity to the corresponding molecular virtual taxa, of which, 7 phylotypes were not obtained by the morphological identification of soil asexual spores. Statistical analysis indicated that there were significant differences in the AMF community between wild and cultured *G. pentaphyllum* roots. The analysis of relative abundance data indicated that Glo₂, Amb₁, and Para₁ were the dominant phylotypes in wild *G. pentaphyllum* roots, while Glo₃, Glo₈, Glo₁₀, and Div₁ were the prevalent phylotypes in cultured ones. Claroideoglomeraceae and Ambisporaceae were only detected in wild *G. pentaphyllum* roots, and Diversisporaceae was only identified in cultured ones.

Key words: arbuscular mycorrhiza *Gynostemma pentaphyllum* diversity RFLP nested-PCR.

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