



入侵植物紫茎泽兰叶斑真菌多样性及其致病性研究

屠然^{1,2}, 黎亚洁^{1,3}, 李颖^{1,2}, 杨明攀¹, 张汉波^{1,2}

1. 云南大学生命科学学院, 云南昆明 650091;
2. 云南省生物资源保护与利用重点实验室(省部共建国家重点实验室培育基地)云南大学, 云南昆明 650091;
3. 中国科学院研究生院, 北京 100049

A study on the diversity and pathogenicity of the phyllosphere fungi on the invasive plant *Eupatorium adenophorum*

TU Ran^{1,2}, LI Ya-jie^{1,3}, LI Ying^{1,2}, YANG Ming-zhi¹, ZHANG Han-bo^{1,2}

1. School of Life Science, Yunnan University, Kunming 650091, China;
2. Laboratory for Conservation and Utilization of Bio-Resource, Yunnan University, Kunming 650091, China;
3. Graduate University, Chinese Academy of Sciences, Beijing 100049, China

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摘要 从云南、广西等12个地区的紫茎泽兰和其他8种植物叶片上共分离得到47个真菌菌株。根据菌落、菌丝以及孢子形态,结合18SrRNA基因限制性酶切片段长度多态性(RFLP)分型和序列测定分析,47个菌株共分为19个类群,系统发育关系与 *Aspergillus niger*, *Cladosporium cladosporioides*, *Sporisorium reilianum*, *Colletotrichum lupini*, *Alternaria sp.*, *Sporobolomyces roseus*, *Dothideomycete sp.*, *Phoma sp.*, *Filobasidium elegans*, *Aureobasidium pullulans*, *Rhodotorula slooffiae*, *R. glutinis*, *Penicillium decumbens*, *Pestalotiopsis maculans*, *Cryptococcus aureus*, *Bimuria novae-zelandiae*, *Xylariaceae sp.* 类似。这些菌株中仅有5个对紫茎泽兰离体叶片表现致病性,在系统发育树上分别和 *Myrothecium sp.*, *C. lupini*, *Alternaria sp.*, *C. cladosporioides*, *Dothideomycete sp.* 聚类。有2个 *R. glutinis* 菌株对马铃薯和白菜有致病作用,但对紫茎泽兰没有致病力。

关键词: 紫茎泽兰 叶面 真菌多样性 致病性 18SrRNA基因

Abstract: Forty-seven phyllosphere fungal strains were isolated from 12 populations of an invasive plant *Eupatorium adenophorum* and 8 other plants in Yunnan and Guangxi provinces of China. Based on the characters of their colonies, hyphae and spore morphology, as well as the analysis of 18SrRNA gene restriction fragment length polymorphism (RFLP) and DNA sequencing, the strains were divided into 19 groups, phylogenetically close to *Aspergillus niger*, *Cladosporium cladosporioides*, *Sporisorium reilianum*, *Colletotrichum lupini*, *Alternaria sp.*, *Sporobolomyces roseus*, *Dothideomycete sp.*, *Phoma sp.*, *Filobasidium elegans*, *Aureobasidium pullulans*, *Rhodotorula slooffiae*, *R. glutinis*, *Penicillium decumbens*, *Pestalotiopsis maculans*, *Cryptococcus aureus*, *Bimuria novae-zelandiae*, *Xylariaceae sp.*. Only 5 strains, which clustered together with *Myrothecium sp.*, *C. lupini*, *Alternaria sp.*, *C. cladosporioides* and *Dothideomycete sp.* in the phylogenetic tree, were pathogenic to the detached leaves of *E. adenophorum*. Two strains from *R. glutinis* were nonpathogenic to *E. adenophorum* but pathogenic to cabbages and potatoes.

Key words:

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通讯作者: 张汉波(1970-),男,云南人,教授,主要从事微生物生态学方面的研究。

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电话: 0871-5033829(传真) 5031498 5031662 E-mail: yndxxb@ynu.edu.cn yndxxb@163.com