

大豆根际土壤真菌分子生物学鉴定方法

接伟光¹, 张 勇¹, 蔡柏岩², 白 莉¹, 王丽阳², 李二平³

(1. 黑龙江东方学院 食品与环境工程学部, 黑龙江 哈尔滨 150086; 2. 黑龙江大学 生命科学学院, 分子生物学重点实验室, 黑龙江 哈尔滨 150080; 3. 东北林业大学 生命科学学院, 黑龙江 哈尔滨 150040)

摘要:以大豆根际土壤为研究对象,采用湿筛倾析-蔗糖离心法分离大豆根际土壤真菌孢子。应用 Nested-PCR 技术扩增其 28S rDNA D1/D2 区域,并结合 DNA 测序、系统发育分析,对其进行分类鉴定。结果表明:筛选出的大豆根际土壤真菌孢子 DT-1 与土壤真菌 (AB438763) 有较高的序列同源性,为 97%; DT-2 与 *Mucor racemosus* (Y213713) 有较高的序列同源性,为 99%。此方法适用于大豆根际土壤真菌的鉴定,并且能够快速准确地得到试验结果。

关键词:土壤;真菌;大豆;Nested-PCR

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Molecular Identification of the Fungi in the Rhizospheric Soil of Soybean

JIE Wei-guang¹, ZHANG Yong¹, CAI Bai-yan², BAI Li¹, WANG Li-yang², LI Er-ping³

(1. Department of Food and Environment Engineering, Heilongjiang East University, Harbin 150086, Heilongjiang; 2. Key Laboratory of Microbiology, College of Life Sciences, Heilongjiang University, Harbin 150080, Heilongjiang; 3. College of Life Sciences, Northeast Forestry University, Harbin 150040, Heilongjiang, China)

Abstract: The fungi in the rhizospheric soil of soybean played a vital role in the formation of soil fertility, the spread of soil-borne diseases, the occurrence of allelopathy, etc. In particular, soybean root rot caused by soil fungi has become a major disease which result in soybean production declined dramatically in China. Therefore, the rapid identification of the fungi in rhizospheric soil of soybean has great significance in preventing and curing fungal diseases of soybean. In this study, the fungal spores were isolated from soybean rhizospheres following a procedure including wet sieving, decanting, and separation in a sucrose gradient. Nested-PCR was conducted to specifically amplify the large-subunit (28S) rDNA D1/D2 domain sequences. They were identified from sequencing, and phylogenetic analysis. It showed that sequence alignment of the DT-1 28S rDNA D1/D2 domain sequence to fungi sequences in the database revealed that DT-1 shared 97% homology with the corresponding DT-1 sequence; DT-2 clusters shared 99% homology with the corresponding *Mucor racemosus* (Y213713) sequence. Results demonstrate that the method can get results quickly and accurately, and is suitable for identification of fungi in rhizospheric soil of soybean.

Key words: Soil; Fungi; Soybean; Nested-PCR

土壤是微生物生活的大本营,其中的微生物不仅数量巨大,而且种类极多,包括细菌、放线菌、真菌、藻类等。土壤微生物种类及数量在很大程度上影响并决定着土壤肥力的形成、植物营养的转化、土传病害的传播、化感作用的发生等^[1-5]。研究和利用植物根际丰富的微生物资源库,正受到人们的重视^[6]。

大豆是我国重要的油料作物之一,是人们生活中的植物蛋白和油份的重要来源^[7-8]。长期以来,国内大豆的种植存在大面积连作现象,而黑龙江地区的大豆连作现象尤其严重,由此导致大豆根腐病

频发,造成大豆减产,因此提高大豆产量以满足不断增长的市场需求已迫在眉睫^[9-12]。

大豆根腐病主要是由多种土壤习居真菌复合侵染引起,可以导致发病的真菌有多种,主要包括尖孢镰刀菌、半裸镰刀菌、粉红粘帚菌、立枯丝核菌、疫霉菌和腐霉菌等。目前,土壤微生物学研究方法均有不足之处,如有的微生物不能纯培养,应用 DGGE 进行研究获得的基因信息较少等,限制了对土壤微生物的研究。

该研究将寡营养活体微生物丛枝菌根 (Arbuscular mycorrhiza, AM) 真菌的分子生物学鉴定方

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第一作者简介:接伟光(1981-),男,硕士,讲师,主要从事微生物生态学研究。E-mail: jiewiguang2007@126.com。

通讯作者:蔡柏岩(1968-),男,教授,主要从事生态学研究。E-mail: caibaiyan@126.com。

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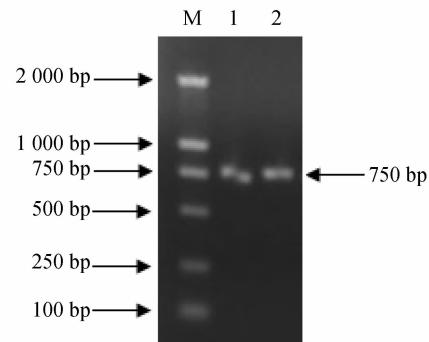
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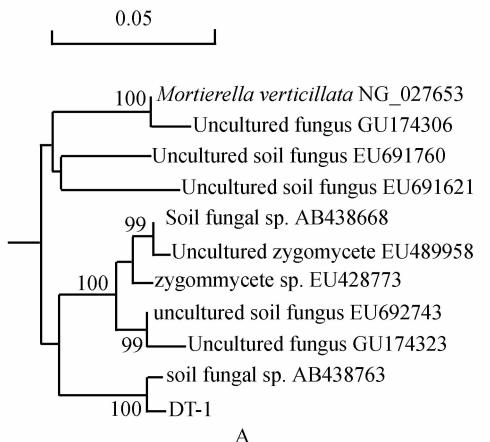
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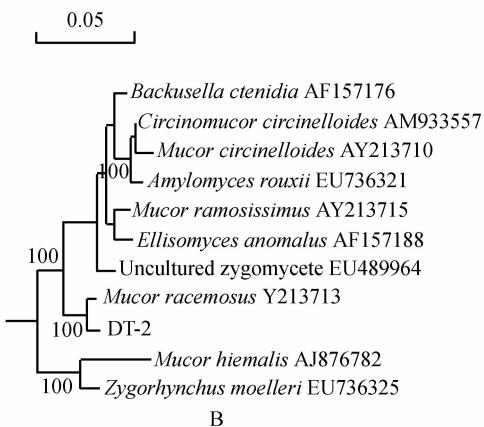


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