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研究报告

rDNA ITS 序列在 ACCC 真菌鉴定中的应用

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摘　要：【目的】真菌无处不在，并与人类生活紧密相关。真菌的鉴定是科学研究和资源开发利用的基础。本研究从中国农业微生物菌种保藏管理中心(ACCC)随机选取已经定名的 112 株库藏真菌菌株作为实验材料，通过 DNA 测序，评估核糖体 DNA 内转录间隔区(rDNA ITS)序列在真菌属级鉴定上的应用。【方法】采用真菌 DNA 条形码 rDNA ITS 的序列测定和在 GenBank 中查寻比对的方法，对这些菌株进行属水平的鉴定复核。【结果】通过研究，供试菌株中有 80 株的属名与原鉴定相符，同时表明序列中套峰的情况降低与 GenBank 中序列比对的相似性。【结论】rDNA ITS 序列测定法可以用于真菌菌株进行属水平的鉴定复核，国家菌种保藏机构应对已入库保藏和即将入库的所有真菌菌株都进行属水平的鉴定复核，并对菌株鉴定结果作审慎处理，原定名的名称及其变更历史应以“曾用名”在数据库中保留。

关键词：真菌，DNA 条形码，鉴定，ITS，属

Applying rDNA internal transcribed spacer sequences to identify fungal strains preserved at Agricultural Culture Collection of China

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Abstract: [Objective] Fungi are found everywhere and associated closely with human life. Identification of fungi is the basis of further scientific research and commercial application of fungal resources. In this study, 112 fungal strains preserved at the Agricultural Culture Collection of China (ACCC) were randomly chosen to test the application of rDNA internal transcribed spacer (ITS) sequences in their identification at the genus level. **[Methods]** rDNA ITS was sequenced from all the strains used in this study and compared with available sequences in GenBank using a BLASTn search for their generic identification. **[Results]** Among the strains used, 80 were consistent with their original generic determinations. Polymorphisms of DNA bases or impurity of sequence chromatograms reduced the similarity in comparison with the target sequence in GenBank.

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