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M13-microsatellite PCR and rDNA sequence markers for identification of *Trichoderma* (Hypocreaceae) species in Saudi Arabian soil

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ABSTRACT. Seven fungal isolates were identified as pan-global *Hypocrea*/*Trichoderma* species, from section *Trichoderma*, on the basis of their morphology. These species were *H. lixii*/*T. harzianum* and *H. orientalis*/*T. longibrachiatum*. PCR-based markers with primer M13 (core sequence of phage M13) and internal-transcribed spacer sequences of ribosomal DNA were used to confirm the identity of the two *Trichoderma* species. Sequence identification was performed using the TrichOKEY version 2.0 barcode program and the multilocus similarity search database TrichoBLAST. Sequences from the ribosomal DNA internal-transcribed spacer regions showed limited variation among the *Trichoderma* species. This analysis divided the isolates into two main groups. Grouping the isolates based on cluster analysis of their DNA profiles matched the grouping based on morphological taxonomy. Molecular data obtained from analyses of gene sequences are essential to distinguish phonetically cryptic species in this group and to establish phylogenetic relationships.

Key words: *Trichoderma*; Phytopathogenic fungi; PCR;
Biological control
