

Isolation and molecular characterization of Egyptian *Trichoderma* and assessment of their antagonistic potential against *Rhizoctonia solani*

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ABSTRACT

Morphological and molecular characterization of antagonistic ability of *Trichoderma* species was studied. Soil dilution plate method was used to isolate *Trichoderma* from rhizosphere of bean, cowpea, cucumber, wheat and faba bean plants. Based on morphological and cultural characteristics, the *Trichoderma* isolates were identified as *T. harzianum* (10 isolates), *T. koningii* (8 isolates), and *T. viride* (2 isolates). A portion of rDNA, 560-600 bp was amplified from six biocontrol isolates using ITS1 and ITS 4 primers, and was sequenced and aligned against ex-type strain sequences from TrichoBlast and established *Trichoderma* taxonomy. Molecular phylogenetic analysis were performed based on nucleotide sequences in order to examine these isolates among 15 accession numbers of *Trichoderma* spp. found in GenBank. The results indicate that the FUE3, FUE5, FUE6, FUE9 and FUE18 *Trichoderma* isolates are closely related to *Trichoderma koningii*, while FUE15 isolate is closely related to *Trichoderma harzianum*. This result was in accordance with the result obtained from morphological and cultural characteristics. Production of volatile inhibitors and mycoparasitism were investigated using *in vitro* and *in vivo* tests in dual culture PDA medium and infected soils. The percent inhibitory effect against growth of *Rhizoctonia solani* was calculated, *T. koningii* FUE3 showed the greatest antagonistic effect to the pathogen (57.77%) in vitro experiment whereas *T. koningii* FUE6 and FUE18 were gave the highest reduction 96% of disease incidence caused by *R. solani* in greenhouse conditions.

These results indicated that, interactive morphological key and a specific molecular database coupled with tools for identification of *Trichoderma* strains represent an ideal way to identify the *Trichoderma* spp., although, they need regular updates to include the rapidly increasing number of species of this genus.