

PHYLOGENETIC RELATIONSHIP OF *Trichoderma* ISOLATES FROM PADDY FIELDS OF MAZANDARAN PROVINCE BASED ON SEQUENCE ANALYSIS OF *tef1 α* GENE *

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Abstract

Fungi belonging to genus *Trichoderma* are well known for their effectiveness in the biological control of different plant pathogenic fungi, inducing systemic resistance in crops and for promoting plant growth. Phylogeny of 81 *Trichoderma* isolates (with emphasis on some biocontrol strains) belonging to six species obtained from paddy fields in Mazandaran province, was studied by partial sequence analyses of the translation elongation factor 1- α (*tef1 α*) gene. Data were analyzed by Neighbor-Joining, Maximum Parsimony and Minimum Evolution methods. For each analysis, one consensus tree was used out of all generated phylograms. Phylogenetic trees of the 41 *Trichoderma* isolates inferred by all methods and programs were similar. Results showed that 14 *tef1 α* haplotypes can be recognized for *T. harzianum* (the most frequent species in rice fields) isolates grouped into five clades. Therefore, this complex species presented the highest intraspecific diversity when compared to other species in this study. In contrast, only two haplotypes were recognized for *T. virens*, the second most prevalent species. Furthermore, sequence analyses revealed three and two haplotypes for *T. atroviride* and *T. hamatum*, respectively. Results indicated that biological control strains represented various haplotypes and placed in different clades along with other native isolates. Consequently, a specific *tef1 α* haplotype related to antagonism could not be distinguished. In addition, there was no correlation between *tef1 α* haplotype and the geographic location and thus different species and haplotypes were isolated from the same sampling sites.

Keywords: Biodiversity, Rice, Biological control, Haplotype, Iran.

See Persian text for figures and tables (Pages ۱۳۹-۱۴۹).

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