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Genetic Diversity among Nile Delta Isolates of *Rhizoctonia solani* Kühn Based on Pathogenicity, Compatibility, Isozyme Analysis and Total Protein Pattern

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Abstract: The present study obtained 12 isolates from *Rhizoctonia solani* Kühn isolated from Cotton L., Trifolium L. and Vicia faba L. from different localities in the Nile Delta of Egypt. All strains were pathogenic and caused seed rot, wilt, stunting, and pre-emergence and post-emergence damping-off. The isolated strains produced different forms of infection cushions that ensure the pathogenicity of these strains. SDS-PAGE of the 12 *R. solani* isolates showed that although the *R. solani* isolates were isolated from very divergent host plants, the total soluble protein patterns among them were similar. Isozyme analysis revealed higher polymorphism among *R. solani* isolates using the EST isozyme. The cluster analysis based on isozyme data showed that the *R. solani* isolates fell into 4 distinct groups, whereas the dendrogram resulting from cluster analysis based on the compatibility test and other morphological characteristics of pathogen infection cushion showed that all *R. solani* isolates were placed into 3 main distinct groups.

 [Keywords](#)
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Key Words: Genetic diversity, *Rhizoctonia solani*, SDS-PAGE, isozymes, anastomoses

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