

CLASSIFICATION AND GENETIC VARIABILITY OF RHIZOCTONIA ISOLATES ASSOCIATED WITH SUGAR BEET IN IRAN

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The soilborne necrotrophic fungus *Rhizoctonia solani* is of relevance for agriculture, causing several diseases on more than 27 plant families. Sugar beet is one of the most economically important crops that is suffering from *Rhizoctonia* diseases causing significant yield losses every year in sugar beet growing area in the world. The complexity associated to correct identification of *Rhizoctonia* species, anastomosis groups (AGs) and subgroups by using traditional methods justifies the efforts to use molecular markers for isolate characterization. In this study, molecular methods were used to classify different taxonomic groups of *Rhizoctonia* isolates causing sugar beet root and crown rot, also to investigate the genetic variability of the isolates. Application of species-specific primers designed for amplification of rDNA-ITS region revealed that all of the 45 isolates obtained from sugar beet crowns and roots were *R. solani*. Analysis of rDNA-ITS polymorphisms revealed that 38 isolates belonged to AG2-2 IIIB, 4 were AG2-2 IV, and 3 were AG5 but this method did not show any molecular variation within each subgroup. Genetic structure of the isolates was investigated using repetitive element-PCR. The similarity matrices were analysed using unweighted pair group method with arithmetic mean (UPGMA) clustering method in combination with Jaccard's similarity coefficient and the obtained dendrogram showed small genetic distances within the isolates. Correlation was observed between resulted grouping of the isolates and their taxonomic identification. Analysis of molecular variances revealed that geographic origin is not an important factor affecting genetic structure of *R. solani* populations obtained from sugar beet and new genotypes have been introduced into a region over time.