

Characterization of the Genetic Diversity of *Rhizoctonia solani* Associated with Potato Tubers in France

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Abstract:

The plant pathogenic soil-borne fungus *Rhizoctonia solani* causes severe damages in crops all around the world. Tubers of potato are frequently affected by *R. solani* leading to the downgrading of the production. Generally the isolates involved in the sclerotia occurring at the surface of the tuber are assigned to the anastomosis group (AG) 3 but a more precise characterization of the diversity of this deleterious group is needed to set up appropriate control strategies. The diversity of 73 French isolates from the mains potato seed production areas and 31 isolates originating from 9 other countries was assessed according to 3 molecular approaches. Three phylogenetic trees were built up based on the sequences of the internal transcribed spacer (ITS) region and the gene *tef-1 α* as well as the comparison of the total DNA fingerprints of each strain established by amplified fragment length polymorphism (AFLP). The determination of the AGs of *R. solani* based on the sequencing of the ITS region showed 3 different AGs among our collection (60 AG 3, 8 AG 2-1 and 5 AG 5). Grouping of the isolates belonging to the same AG was confirmed by the sequencing of the gene *tef-1 α* used for the first time to study the genetic diversity of *R. solani*. About 42 % of the ITS sequences and 73 % of the gene *tef-1 α* sequences contained polymorphic sites where several nucleotides are possible, suggesting that the cells of *R. solani* strains contain several copies of ITS and gene *tef-1 α* within the same nucleus or between different nuclei. Phylogenetic trees showed a greater genetic diversity within AGs in *tef-1 α* sequences than in ITS sequences. The AFLP analyses showed an even greater diversity among the strains demonstrating that the French strains of *R. solani* isolated from potatoes were not a clonal population. Moreover, there was no relationship between the geographical origins of the strains or the potato variety from which they were isolated and their genetic diversity. This important and under evaluated genetic diversity as the lack of population structure suggest important genetic mixings leading to a constant evolution within *R. solani* and could explain the difficulties to control it successfully.

Key words: amplified fragment length polymorphism, anastomosis group, elongation factor, internal transcribed spacer, polymorphic site