Genetic diversity of Rhizoctonia solani associated with potato tubers in France
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The hidden polymorphism of a fungal group can be revealed thanks to the use of different molecular approaches. In the case of Rhizoctonia solani (teleomorph Thanatephorus cucumeris, Kühn, 1858), the diversity of 73 French strains isolated from potato tubers grown in the main potato seed production areas in France and 31 strains isolated in 9 other countries was assessed. Three molecular tools are proposed to investigate different levels of diversity within this fungal collection: sequencing of the ITS region, sequencing of a part of the gene tef-1α, and AFLP analysis of the total DNA.

The isolates are stored in the collection “Microorganisms of Interest for Agriculture and Environment” (MIAE, INRA Dijon, France, see Heraud et al., Poster 24 Area 4 for more details).

Keywords: amplified fragment length polymorphism, anastomosis group, elongation factor, internal transcribed spacer, molecular tools.

### DNA SEQUENCE ANALYSIS

#### Amplified Fragment Length Polymorphism (AFLP) analysis: total DNA fingerprints

Phylogenetic relationships among 89 strains of Rhizoctonia solani inferred from AFLP data using a UPGMA analysis of Nei – Li distances.

### TOTAL DNA ANALYSIS

#### Neighbour-joining tree (Kimura two-parameter distance) of 32 monomorphic ITS sequences of Rhizoctonia solani strains.

#### Neighbour-joining tree (Kimura two-parameter distance) of 23 monomorphic tef-1α sequences of Rhizoctonia solani strains.

### SCIENTIFIC CONCLUSIONS

- **Validation of the molecular method** to determine AG.
  - **Target sequences DNA vs. Total DNA analysis highlight different but complementary informations:**
    - Sequencing: rapid access to AG (sub-)group
    - AFLP: high discrimination between strains.

### METHODOLOGICAL CONCLUSIONS

- **High intra-species and intra-AG diversity** of the French strains of *R. solani*.
- **Constant evolution of the genomes** according to the genetic events in the environment.
- **Polymorphic sites** within strains probably due to several copies of ITS and gene tef-1α within the same nucleus or between different nuclei of *R. solani* strains.

**Keywords**: amplified fragment length polymorphism, anastomosis group, elongation factor, internal transcribed spacer, polymorphic group.