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Genetic diversity of *Rhizoctonia solani* associated with potato tubers in France

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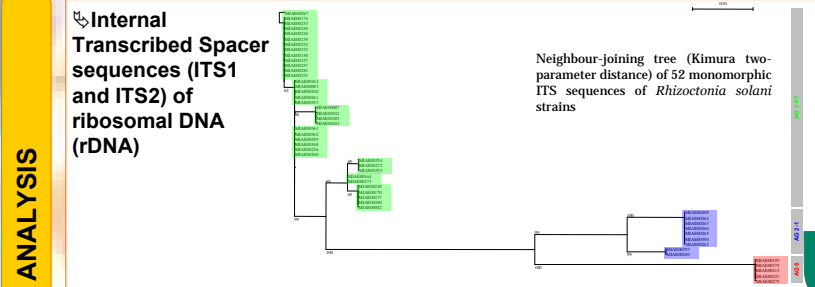
The **hidden polymorphism** of a fungal group can be revealed thanks to the use of different molecular approaches. In the case of *Rhizoctonia solani* (teleomorph *Thanatephorus cucumeris*, Kühn, 1858), the diversity of 73 French strains isolated from potato tubers grown in the mains potato seed production 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).

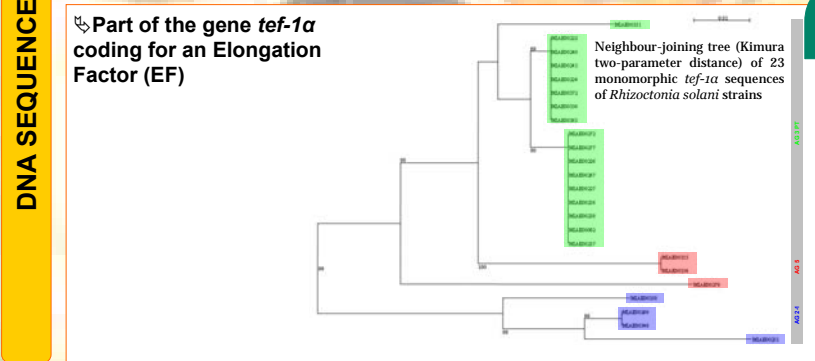


A sclerotia (black scurf)
B skinning
C enlarged lenticels
Alterations where *R. solani* was isolated



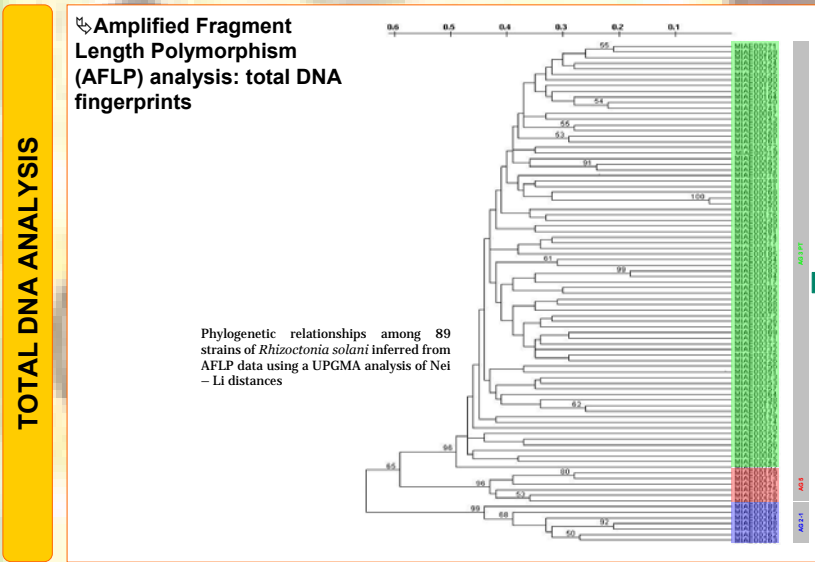
i Classical (= microscopic) method used to determine AG is laborious, time-consuming and requires technical training.

C2 type (= killing reaction) anastomosis based on the fusion of the hyphal tips of two compatible individuals belonging to the same AG (McNish *et al.*, 1993)



	AG ¹ diversity		Number of types	
	inter-	intra-	monomorphic	polymorphic
ITS	+	+/-	10	29
EF	+	+	7	30

¹ Anastomosis Group



- ▶ Significant diversity
 - ▶ No particular structure of the studied populations
 - ▶ No relation between the genetic profiles of the strains and their geographical origin
- Level of polymorphism**

METHODOLOGICAL 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.

SCIENTIFIC 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