



HAL
open science

Genetic diversity of*[i]* *Rhizoctonia solani**[/i]* associated with potato tubers in France

Marie Fiers, Véronique Edel-Hermann, Cécile Héraud, Nadine Gautheron, Catherine Chatot, Yves Le Hingrat, Karima Bouchek-Mechiche, Christian Steinberg

► To cite this version:

Marie Fiers, Véronique Edel-Hermann, Cécile Héraud, Nadine Gautheron, Catherine Chatot, et al.. Genetic diversity of*[i]* *Rhizoctonia solani**[/i]* associated with potato tubers in France. 12. International Conference on Culture Collections (ICCC12), Sep 2010, Florianopolis, Brazil. 1 p., 2010. hal-01190295

HAL Id: hal-01190295

<https://hal.science/hal-01190295>

Submitted on 1 Sep 2015

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



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

Marie FIERIS¹, Véronique EDEL-HERMANN¹, **Cécile HERAUD¹**, Nadine GAUTHERON¹, Catherine CHATOT², Yves LE HINGRAT³, Karima BOUCHEK-MECHICHE¹, Christian STEINBERG^{1*}

¹INRA-National Institute of Agronomical Research/University of Burgundy

UMR 1229 MSE Microbiology of Soil and Environment
17 rue Sully, F-21000 Dijon, Dijon, France.

² Gemicopa R&D, Kerguivarch, 29520 Châteauneuf du Faou, France

³ FNPPPT, Roudouhir, 29460 Hanvec, France

*E-mail : christian.steinberg@dijon.inra.fr

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

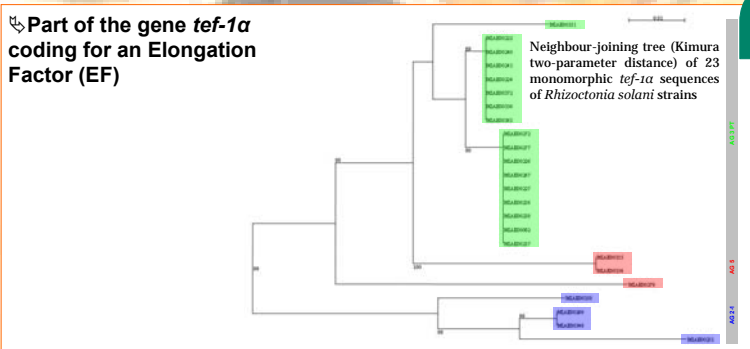
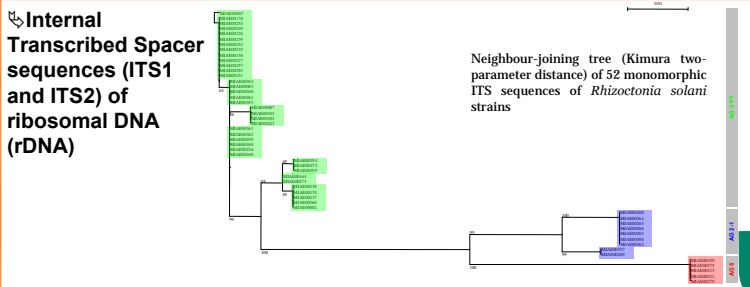
ITS region, sequencing of a part of the gene *tef-1α*, and AFLP analysis of the total DNA.

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

DNA SEQUENCE ANALYSIS



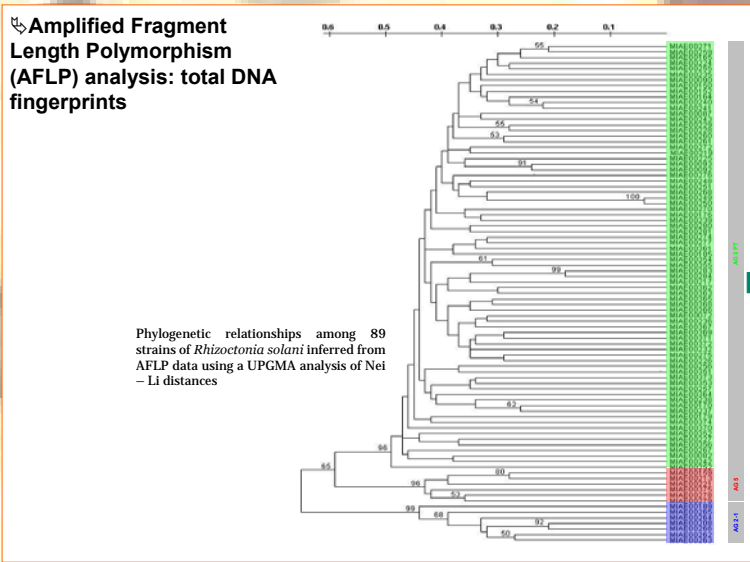
i Classical (= microscopic) method used to determine AG is laborious, time-consuming and requires technical training.

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

TOTAL DNA ANALYSIS



- ▶ 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