Contribution of microbial core-collections and exploitation of polygenic resistances to the development of Phytophthora control strategies in solanaceous crops

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PLANT RESISTANCE SUSTAINABILITY

International Conference 2012

La Colle-Sur-Loup (France)
October 16th-19th, 2012

INRA

Scientific Programme and Abstracts

Sessions

Session 1: Impact of plant disease resistance on the structure and evolution of pathogen populations

Session 2: Sustainable and integrated breeding and deployment of genetic resistance

Session 3: From plant-pathogen molecular interactions to the durability of resistance

Session 4: Socio-economic issues related to the use of resistant varieties and their deployment in agro-systems

Invited Speakers

Philippe Baret, Université Catholique de Louvain, Belgium - **James Brown**, John Innes Centre, England - **Marion Desquilbet**, INRA, France - **Sylvain Gandon**, CNRS, France - **Benoit Moury**, INRA, France - **Chris Mundt**, Oregon State University, USA - **Laura Rose**, Heinrich-Heine University, Germany - **Walter Rossing**, Wageningen University, The Netherlands - **Peter Thrall**, CSIRO Plant Industry, Australia

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Metaprogramme on Sustainable Management of Crop Health (SMaCH)

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biogemma PEPFL SAKATA syngenta VEGEPOLYS Add on vegetal value

Contribution of microbial core-collections and exploitation of polygenic resistances to the development of *phytophthora* control strategies in solanaceous crops

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Abstract

Oomycetes form a diverse group of fungus-like eukaryotic microorganisms that include saprophytes as well as pathogens of animals and some of the most devastating pathogens of dicotyledonous plants. Among them, few species of the genus *Phytophthora*, such as ***P. capsici* and *P. infestans* cause enormous economic damage on** Solanaceous crops**. Major genes have been identified in tomato to confer resistance against *P. infestans*, but were rapidly overcome by virulent populations. Pepper resistance towards *P. capsici* is provided by several quantitative trait loci (QTLs). Efficient exploitation of such polygenic resistance sources in plant breeding programs requires a good evaluation of their spectrum and durability. This requires a precise knowledge of the diversity of pathogen populations (with a focus on virulence, aggressiveness and host range) and some of their adaptive traits, such as changes in virulence or adaptation to prevalent cultivars. Theoretically, the use of *Phytophthora* core-collections reflecting the overall intraspecific diversity would help to assess the *a priori* durability of resistance sources.**

We initiated a study to evaluate the potential sustainability of polygenic pepper and tomato resistances to *Phytophthora*. It implied i) to estimate the diversity of *P. infestans* and *P. capsici* collections and their evolution over time; ii) to develop diverse quantitative and qualitative pathogenic assays to identify the various components underlying polygenic resistances. Collections included isolates from various geographic origins. Genetic diversity was investigated using a combination of neutral markers and genes under positive selection. First results on *P. capsici* reveal significant variations in the structure and dynamics of regional populations, and suggest that *P. capsici* core-collections may be of local interest. We also showed that *P. infestans* populations are diverse but structured. Hence, strains isolated on tomato or potato differ at the genotypic and phenotypic levels. The use of *P. infestans* core-collections in breeding programs therefore requires gaining knowledge on the structure and epidemiological characteristics of natural pathogen populations collected on tomato.

Keywords: Resistance, *Phytophthora spp.*, pepper, tomato, core-collection, plant breeding.