

PLANT RESISTANCE SUSTAINABILITY

International Conference — 2012



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Scientific Programme and Abstracts

Sessions

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

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

Session 2: Sustainable and integrated breeding and deployment of genetic 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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New insights on virulence and evolutionary dynamics of the *Ralstonia solanacearum* species complex –keys and challenges in the search of durable resistance in *solanaceae*

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Abstract

Bacterial wilt, caused by the soilborne betaproteobacterium *Ralstonia solanacearum*, is a major disease of solanaceous crops, throughout tropical and subtropical areas, and emerging in temperate regions. If genetic resistance is still considered as the most promising control measure, breeding for resistance to *Ralstonia solanacearum* (*Rsol*), has been hindered for decades by the scarcity of high level resistance sources, strong genotype x environment interactions, and the huge genomic and phenotypic plasticity of the pathogen. *Ralstonia solanacearum* is a species complex composed of four phylotypes related to geographical origins (I: Africa-Asia, II: American, III: Africa, IV: Indonesia). Solanaceae-pathogenic strains belong to all four phylotypes, but most epidemiologically active strains belong to phylotype I, IIA, IIB, and III, phylotype I being the most widespread lineage.

Extensive screenings of resistant accessions of tomato, eggplant and pepper towards a worldwide *R.sol* core-collection, lead to formalize grain Solanaceae-*Rsol* interactions into six main virulence profiles, and allowed to identify highly resistant accessions, mainly in eggplant and pepper. Among them, the eggplant MM960 was demonstrated to carry a phylotype I-resistance major dominant gene (*Ers1*) and

two partial resistance QTLs with strain-specific expression. We identified patterns of strain –specificity, but found no evidence of phylotype-specificity; phylotype I containing four of the six pathoprofiles.

Searching for durable resistance implies both the identification of bacterial genes responsible for avirulence and virulence, and assessment of the pathogen evolutionary potential. Considering “immune” accessions (five eggplants, two peppers, one tomato) giving true incompatible interactions (no wilt and no colonization), we then searched for genetic factors associated with bacterial virulence and avirulence using comparative genomics hybridization (CGH) data. We thus identified 61 type III effectors fairly to highly associated to avirulence to eggplants Dingras, SM6, Ceylan, Surya, and MM960, peppers CA8 and Perennial, and tomato HW7996. Interestingly, some of these effectors were elsewhere shown to contribute to bacterial fitness. Focusing on the accessions MM960 and Dingras, less than 10 genes were highly associated with avirulence, among which *popP2*, avirulence gene interacting with the RRS1-R resistance gene in *Arabidopsis thaliana*.

We inferred evolutionary dynamics of the *R.solanacearum* species complex (RSSC) at a global scale, performing multi-locus sequence analysis (MLSA) and gene genealogies on a worldwide collection. Although recombination was found ubiquitous within the RSSC, we observed phylotype-specific recombination rates and demographic histories. Phylotype I (and, to a lesser extent, phylotype III) is highly recombinogenic, and carries molecular signatures of a recent and rapid demographic expansion. Phylotype II is actually composed of two evolutionary lineages, one (IIA) being moderately recombinogenic and expanding, and the other (IIB) being clonal and poorly expanding. Taken together, these findings strongly suggest that phylotype I is the most prone to adapt rapidly to new hosts and varieties, thank to its recombination and mutation rates, capacity to disseminate, and large virulence range.

To decipher evolutionary dynamics leading to adaptation at the local, field scale, an experimental evolution trial is in course to monitor the impact of *Ers1*-carrying eggplant MM960 successive crops on the population structure and putative avirulence genes evolution.

Keywords: population genetics, virulence, *Solanum*

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