

## Abstract of Poster Presentation

### **Involvement of horizontal gene transfer in the emergence of new pathotypes of *Ralstonia solanacearum***

B. COUPAT-GOUTALAND (1), A. Guidot (2), P. Prior (2), X. Nesme (3), F. Bertolla (3)

(1) Université de Lyon, Université Lyon 1, UMR CNRS 5557 Ecologie Microbienne, VILLEURBANNE, FRANCE; (2) CIRAD-INRA, Pôle de Protection des Plantes (3P), Bios UMR C53 – Ligne Paradis, Saint Pierre Cedex, La Réunion, FRANCE; (3) Université de Lyon, Université Lyon 1, UMR CNRS 5557, USC INRA 1193 Ecologie Microbienne, VILLEURBANNE, FRANCE

Presenter's E-mail: bcoupat@univ-lyon1.fr

*Ralstonia solanacearum* is a widely distributed phytopathogenic bacterium that is known to invade more than 200 host species, mainly in tropical areas. *R. solanacearum* has been described as a highly flexible organism capable of counteracting plant resistance, leading to the emergence of a new pathological variant. We propose to investigate the fundamental role of horizontal gene transfer (HGT) in its genome evolution. In the *R. solanacearum* species complex, the natural ability to transform has been described as an ubiquitous physiological trait. Eighty percent of strains distributed in all phylotypes - likely species - have the ability to acquire free plasmids and/or genomic DNA (Coupat *et al.*, 2008, FEMS Microbiol Ecol 66:14-24). Extent and number of transfer events were also evaluated by using selective antibiotics markers as well as by comparative genomic hybridization with DNA microarrays. Results showed that replacements might involve DNA fragments up to 90 kb and multiple integration events into the *R. solanacearum* genome. In addition, inter-phylotype HGT studies showed that transformants were able to acquire large DNA blocks (30 kb) containing pathogenicity determinants from the DNA donor (Guidot *et al.*, 2009, ISME J. doi :1038/ismej.2009.14). The natural transformation mechanism thus appears as one of the main forces for the generation of emergent pathogens. We confirmed that a recombinant strain, which was found to be more virulent on tomato than its wild type parental strain, has acquired a type III effector which was not present in the wild type parental genome.