PROGRAM

ABSTRACTS

and

PARTICIPANT DIRECTORY

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A novel molecular typing system for pathogenic xanthomonads

Alejandra Munoz Bodnar,[1] Karine Durand,[2] Christian Vernière,[3] Olivier Pruvost,[3] Marie-Agnès Jacques,[2] Valérie Verdier,[1] and Ralf Koebnik[1]

[1]Laboratoire Génome et Développement des Plantes, Université de Perpignan via Domitia – CNRS – IRD, 34394 Montpellier; [2]UMR Pathologie végétale, INRA – INH – Université d'Angers, 49071 Beaucouzé; [3]UMR Peuplement Végétaux et Bioagresseurs en Milieu Tropical, CIRAD – Université de La Réunion, 97410 Saint-Pierre; FRANCE

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associated sequences (*cas*) form hypervariable loci which are widely distributed in prokaryotes. The repetitive region is characterized by short interspersed unique spacer sequences which often match to bacteriophage-derived DNA, thus providing immunity against foreign genetic elements, in particular bacteriophages. Bacteria of the genus *Xanthomonas* cause diseases on over 400 different host plants, including many economically important crops, such as rice, wheat, citrus, and banana plants. We screened more than 300 strains of *Xanthomonas*, representing ten different species (44 pathovars), for the presence of CRISPR loci. Only a few pathovars were found to possess a CRISPR locus, among them *X. axonopodis* pv. *vasculorum*, *X. axonopodis* pv. *cassavae*, *X. campestris* pv. *raphani, X. citri* pv. *citri*, *X. oryzae* pv. *oryzae* (*Xoo*), *X. translucens*, and *X. vasicola* pv. *musacearum*. Presence/absence of CRISPR loci appeared to be conserved at the pathovar level, except for *Xoo*. The apparent absence of CRISPR loci from African *Xoo* isolates confirms previous results showing that African *Xoo* isolates form a phylogenetic group that is distant from the Asian *Xoo* group. Comparative genomics suggested that the common ancestor of all xanthomonads had two CRISPR loci which in most species/pathovars got lost during evolution. Based on DNA sequence information about the terminal spacers of 32 Asian *Xoo* CRISPR loci we postulate that the common ancestor of these strains had all the spacers which are nowadays still found in a few strains and that some spacers got lost during evolution in some *Xoo* lineages. This work represents the first proof of concept of CRISPR analysis as a molecular tool for high-resolution strain typing, phylogenetic studies, and global surveillance of a phytopathogen.

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A conserved 22-amino-acid peptide of *Xanthomonas oryzae* pv. *oryzae* – a candidate for AvrXa21?

Guillaume Robin, Jean Paul Brizard, Thierry Mathieu, Ralf Koebnik

Laboratoire Génome et Développement des Plantes, Université de Perpignan via Domitia – CNRS – IRD, UMR 5096, 34394 Montpellier, France

The Gram-negative bacterium *Xanthomonas oryzae* pathovar *oryzae* (*Xoo*) causes bacterial leaf blight (BLB) of rice, one of the most devastating diseases of rice worldwide. Until now, about 30 resistance genes against BLB have been isolated from domesticated or wild rice species, among them *Xa21*. *Xa21* was the first rice disease resistance gene to be cloned. It encodes a receptor-like kinase which is thought to detect a small molecule, called AvrXa21, which is produced from *Xoo*. Eight *rax* genes (required for AvrXa21 activity), organized in four operons, have been identified in *Xoo*. Yet, the molecular nature of AvrXa21 is still unknown. Since *Xa21* is one of the most important resistance genes that has been used in several breeding programmes, characterization of the AvrXa21 molecule and understanding of the ligand-receptor interaction would be extremely useful for future breeding programmes and for studies of the defense response in rice. By *in silico* analysis, we have identified a candidate *avrXa21* gene within the *raxSTAB* operon. This candidate gene shares overlapping stop/start codons with its upstream and downstream genes, *raxST* and *raxA*, respectively. It encodes a 22-amino acid peptide with a central double-glycine motif which is characteristic for small peptides secreted by a subfamily of ABC transporters, including RaxA. DNA sequence analysis shows that this small gene is strictly conserved within *X. oryzae* and that a similar peptide might be produced by other *Xanthomonas* species, such as *X. axonopodis* and *X. translucens*. We will show our latest results on the role of the candidate *avrXa21* gene in the pathogen-plant interaction.