

Interactions

Plantes

Microorganismes

Environnement

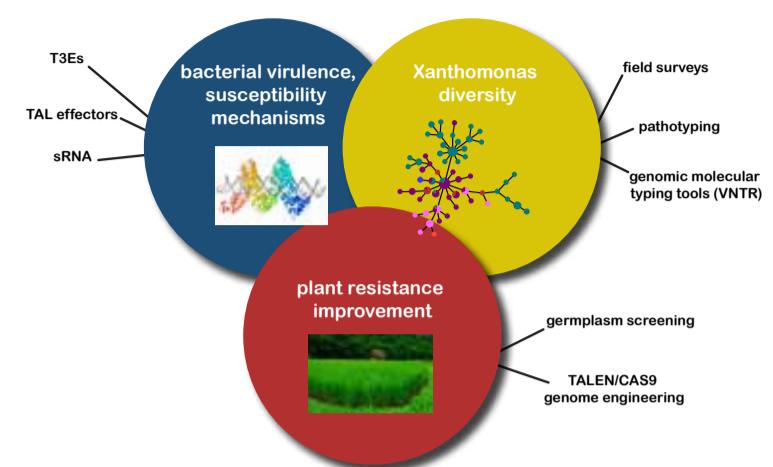


Team 3 : GTIPP

Genomics & Transcriptomics of Plant-Procaryotes Interactions

Objectives

- Decipher epidemic processes involved in **disease emergence**
- Understand **bacterial pathogenicity** mechanisms
- Comprehend **plant resistance** mechanisms
- Propose **durably resistant** plant material for breeding



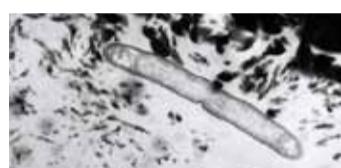
Models

One major bacterial model: *Xanthomonas*

- pathogenic on more than 140 plants**, high host and tissue specialization
- a unique and complex **pathogenicity process**: specific proteins are injected inside the plant cell, where they hijack the plant metabolism to the benefit of the bacteria

Different complementary economically important pathosystems

- Xanthomonas oryzae* pv. *oryzae* & pv. *oryzicola* on rice
- Xanthomonas citri* pv. *citri* on citrus
- Xanthomonas phaseoli* pv. *manihotis* on cassava
- Xanthomonas vasicola* pv. *musacearum* on banana
- pathovars of *Xanthomonas translucens* on cereals



Molecular epidemiology, population genetics, pathotyping, diagnostics
X. musacearum, *X. oryzae*, *X. manihotis*, *X. translucens*

Diversity & evolution of T3SS & T3E
X. citri, *X. oryzae*, *X. translucens*

Diversity & evolution of TAL effectors
X. citri, *X. oryzae*, *X. translucens*, *X. manihotis*

Functions & targets of TAL effectors
X. oryzae, *X. manihotis*, *X. citri*, *X. translucens*

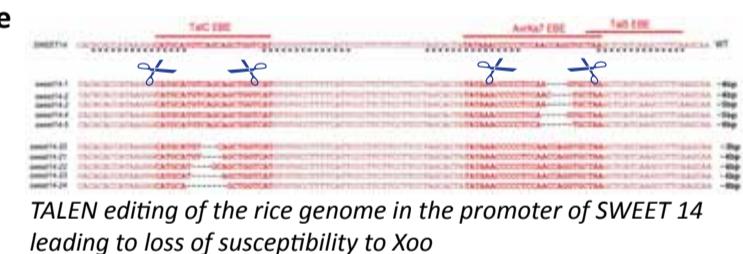
Roles of sRNA in rice susceptibility
X. oryzae

Resistance engineering: germplasm screening, genome editing
rice, cassava



Major results

- Involvement in several *Xanthomonas* sequencing projects (FNX consortium): more than 100 genomes, which provide indispensable data for our research
- Development of **MLVA typing** tools for population analysis and epidemiological monitoring
- Development of a WEB platform for automatic **classification & annotation** of TALE, and for **plant target prediction**
- Identification of plant small RNAs induced by bacteria (TE3) that may **suppress rice immunity**
- Identification of **loss of susceptibility resistance gene** in rice (*xa41*)
- Characterization of SWEET sugar transporters as **major susceptibility targets** of *Xoo* in rice
- Identification of UPTAL2, an ERF transcription factor, as a **new susceptibility gene** specific of African *Xoo* strains
- Design of new resistance alleles of rice to BLB (*X. o. pv. oryzicola*) by **genome editing**
- Design of **artificial TALEs** for the analysis of TALE plant targets



Projects & funding

- ANR (XANTHracing, Xanthomix, CROpTAL, PIXIES)
- Bill & Melinda Gates Foundation (TALENted_Rice)
- Agropolis (Plant Epidemiosurveillance, PAIX, MUSEOVIR, MICERES)
- Rice Agri-Food system (MENERGEP)
- PEERS (YUCATAL)
- Région Languedoc-Roussillon (Projet Chercheur d'avenir)
- Post-doctoral & doctoral fellowships (NSF, ERASMUS, Beachell-Borlaug, MESR)
- EU (Marie Curie IOF : RXomics)



Publications & tools

- Databases & bioinformatic tools:
 - www.xanthomonas.org
 - QueTAL, TALVEZ
- 18 publications in 2015 in journals with IF>3 with more than 60% in partnership with collaborators in the South



Partners

- LMI Patho-Bios (Burkina-Faso) ; JEAI CoANA (Mali)
- CIAT, IRRI, CRP RTB, CRP RICE, AfricaRice, Bioversity International, IITA, FERA...
- U. of Colorado, Cornell U. (USA), U. de los Andes, U. Nacional (Colombie), U. Catholique Louvain (Belgique), Leibniz Universität Hannover (Allemagne), U. Exeter (UK), Agriculture Genetics Institute (Vietnam)

Teaching & training

- Master courses (~20h/year SupAgro Montpellier and U. Montpellier)
- Coorganization of the course 'Biologie Intégrative des Systèmes Microbiens Parasitaires' (25h) Master DIPHE and DEMPI (UM)
- Teaching 'Biotechnologies Végétales et Microbiennes', 'Phytopharmacie et Protection des Végétaux' at U. Cheikh-Anta-Diop (Sénégal)
- in 2015: 3 PhD defenses, 3 post-docs, 4 visiting scientists, 7 PhD students



Our team is deeply involved in the FNX network started in 2008 (INRA SPE). This network is a major tool for cooperation, project management and for the international visibility of the French *Xanthomonas* community

- LIPM (INRA, CNRS, UPS), Toulouse
- IPME (IRD, CIRAD, UM), Montpellier
- BGPI (INRA, CIRAD, SupAgro), Montpellier
- EMERSYS (INRA, AgroCampus Ouest, U. Angers), Angers
- PVBMT (CIRAD, U. Réunion), La Réunion