



12th European Foundation for Plant Pathology (EFPP)

& 10th French Society for Plant Pathology (SFP)

CONFERENCE



**DEEPEN KNOWLEDGE IN PLANT
PATHOLOGY FOR INNOVATIVE
AGRO-ECOLOGY**

BOOK OF ABSTRACTS



May 29 - June 2 2017
Dunkerque - Malo-les-Bains - FRANCE

Session 3
Oral 26

Genomic study shows endemic and pandemic rice blast lineages and lineages between rice and setaria infecting gene pools

Thierry¹ M, Rieux² A, Ravel¹ S, Cros-Arteil³ S, Adreit¹ H, Milazzo¹ J, Terauchi⁴ R, Ios⁵ R, Tharreau¹ D, Fournier² E, Gladieux³ P.

¹CIRAD, UMR BGPI, Montpellier, France; ²CIRAD, UMR PVBMT, St Pierre de la Reunion, France; ³INRA, UMR BGPI, Montpellier, France; ⁴Iwate Biotechnology Research Center, Kitakami, Iwate, Japan; ⁵ANSES, Malzéville, France.

The rice blast fungus *Magnaporthe oryzae* is the most damaging rice pathogen, and a textbook example of widely distributed, rapidly adapting pathogen, despite limited genetic diversity. The aim of our study was to elucidate the factors and evolutionary changes underlying the emergence, diversification and spread of *M. oryzae* on rice. Analyses of population structure based on Infinium-genotyping of 5300 SNPs for 970 isolates collected on rice on the five continents identified 13 lineages within *M. oryzae*. Three lineages were pandemic in multiple continents and one of them was the only lineage detected in Europe. Multiple lineages with more restricted distributions in sub-Saharan Africa and Asia were also identified. Whole genome resequencing of a subset of 80 rice-infecting isolates combined with 12 isolates collected on *Setaria* millet revealed several lineages with intermediate positions between the previously identified rice- and *Setaria*-infecting gene pools, questioning the *Setaria* origin of rice-infecting *M. oryzae* and suggesting that the emergence of rice blast may be more recent than previously thought. Because the sequenced isolates were collected between 1973 and 2009 and recombination is limited, we will use dated tips to calibrate tree nodes within a phylogenetic framework to elucidate the timing of emergence and global dispersal of *M. oryzae*. Most lineages were highly clonal, but we found evidence for recombination in a widely distributed lineage infecting upland rice in Yunnan, Laos and Thailand. We will use genome scans for genetic exchanges to test the hypothesis that recombining lineages are more likely to receive genetic material from other lineages. Our work provides a population-level genomic framework for defining molecular markers to assist in the control of rice blast and for investigating the molecular underpinnings of phenotypic and fitness differences between divergent lineages.

Keywords : *Magnaporthe*, *Setaria*, Rice, Population genomics, Recombination, Gene flow