Session : *INTERACTIONS MOLECULAIRES*

Poster n° 1

Distribution and origin of the rice blast resistance gene *Pi33*

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Few reports on the distribution of resistance genes to plant pathogens within a species are available. Because of its genetic structuration, *Oryza sativa* can be an interesting model for such a study. We were interested in the interaction between the resistance gene to blast *Pi33* and its corresponding avirulence gene *ACE*1. Although *Pi33* was not cloned, its allele(s) conferring resistance can be identified by inoculation of pairs of isogenic strains of *Magnaporthe grisea* differing only for *ACE1*.
One-hundred-eighty-three varieties of *O. sativa* were inoculated with isogenic strains. Twenty-three varieties of the Indica subspecies (mainly modern semi-dwarf varieties) carrying a resistance allele of *Pi33* were identified representing 21,6 percent of the Indica varieties tested. None of the 45 Japonica varieties tested carried the resistance allele.
In order to identify the original donors of *Pi33*, the genealogies of the varieties carrying *Pi33* were examined. In addition, 28 parental lines from IR64 were tested to seek the donor of resistance for this variety. Two possible origins of resistance could be identified: Tsai Yuan Chung and the wild rice *O. rufipogon*. These two candidates were confirmed as possible sources of resistance by genotyping and sequencing. It appears that both resistance sources were commonly used in breeding programmes leading to modern semi-dwarf Indica varieties.
The presence of *Pi33* in *O. rufipogon* led us to the hypothesis that *Pi33* existed before domestication. This hypothesis was confirmed by the detection of *Pi33* in *O. latifolia* (CCDD genome), O. barthii (AA) and diverse accessions of *O. rufipogon* (AA).