Session : *INTERACTIONS MOLECULAIRES*

Poster n° 2

Cloning of *Pi33*, the rice resistance gene corresponding to the cloned avirulence gene *ACE1* of *Magnaporthe grisea*

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The *Oryza sativa-Magnaporthe grisea* pathosystem is of economic importance but it is also a model for the plant-fungus interaction studies. A gene-for-gene system was described for this pathosystem. However, the number of specific interactions characterized at the molecular level is still restricted. After cloning the avirulence gene *ACE1* of *M. grisea* (Böhnert et al. 2004, Plant Cell), we undertook the positional cloning of the corresponding resistance gene *Pi33*. *Pi33* was localised on chromosome 8 of rice in two independent crosses (Berruyer et al. 2003, TAG). A fine mapping allowed us to place the gene between two markers distant of 240 kb. In this area, a cluster of 9 candidate genes was identified by analysis of the sequence of Nipponbare (which is deprived of *Pi33*). This analysis was confirmed by the sequencing of two BAC clones covering the same region in IR64 (which carries a resistance allele of *Pi33*). To identify the gene among the candidates, several strategies were developed. Silencing experiments by RNAi were started. Partial sequences of the different candidates were compared between varieties with or without *Pi33*. Polymorphism of flanking markers was also characterized. Finally, expression of the candidates was measured by RT-PCR in varieties with or without *Pi33*.