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Poster Abstract – C.11

MOLECULAR ANALYSIS OF RICE DEFENCE RESPONSES TO BLAST INFECTION

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Plants have constantly to face a wide range of microbial attacks in the natural environment. Therefore, they developed a sophisticated machinery to perceive external signals and optimally respond to pathogens. A common facet of plant defence responses is the fine tuning of a large number of genes by transcriptional factors and the prompt expression of a battery of defence genes, such as pathogenesis related proteins (PR proteins), peroxidases and chitinases. Our focus is the study of molecular mechanisms leading to rice resistance to host and non-host *M. grisea* strains.

A high-throughput system for rice infection with *M. grisea* strains, to appraise the resistance/susceptibility of rice varieties was developed in our laboratory. Our system called *BLASTETS* enables to inoculate rice plantlets of different varieties with *M. grisea* strains (by spraying with conidial suspensions) and rapidly and reliably screen macroscopic phenotypes (pathogen lesions, resistance necrosis) on rice leaves after five days incubation in a dedicated growth chamber in controlled conditions.

Among transcriptional factors, it has been already shown that WRKY genes are implicated in plant defence responses in tobacco, barley, *A. thaliana* and rice. We characterized a panel of rice WRKY genes in response to host and non-host *Magnaporthe grisea* strains, to highlight differences between host and non-host resistance reactions. We also analysed the expression of defence genes in selected Italian rice cultivars ranging from highly-susceptible to completely resistant to study their response to blast. The aim of this scientific activity was to investigate a potential correlation between the resistance/susceptibility of the Italian rice cultivars and the expression levels of selected defence genes.

Expression of thirty *Os*WRKY candidate genes was quantified by Real Time PCR after infection with FR13 (host strain) BR29 and BR32 (non-host strains) at 12, 24 and 48 hours post infection (hpi). Most of the up-regulated genes were found to be expressed in response to host infection and only a few by both host and non-host strains, whereas only two genes were induced specifically by non-host *M. grisea* strains.

To study the expression of rice defence genes we selected the chitinase class III and β-1,3-glucanase due to their well-recognised antifungal activity and peroxidase 22.3 given its role in reinforcing the cell wall. We also included PR1 and PBZ1 genes, as they are known markers of the

activation of defence responses upon blast infection. We quantified the expression of the five defence genes by Real Time PCR before and after infection with two host Italian strains of *M. grisea.* In resistant cultivars we observed a strong induction of several defence genes at once after blast infection. In contrast, in the susceptible cultivars we did not observe any variation of expression, confirming the role of these defence genes in resistance to blast.

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