

**S7-3**

## **Analysis of Rice Blast Infection and Resistance-inducing Mechanisms via Effectors Secreted from *Magnaporthe oryzae***

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Rice blast, caused by the fungal pathogen *Magnaporthe oryzae*, is one of the most destructive diseases of rice worldwide. The rice - *M. oryzae* pathosystem has become a model in the study of plant - fungal interactions due to its economic importance and accumulating knowledge. During the evolutionary arms race with *M. oryzae*, rice plants evolved a repertoire of Resistance (R) genes to protect themselves from diseases in a gene-for-gene fashion. *M. oryzae* secretes a battery of small effector proteins to manipulate host functions for its successful infection, and some of them are recognized by host R proteins as avirulence effectors (AVR), which turns on strong immunity. Therefore, the analysis of interactions between AVRs and their cognate R proteins provide crucial insights into the molecular basis of plant - fungal interactions. Rice blast resistance genes *Pik*, *Pia*, *Pii* comprise pairs of protein-coding ORFs, *Pik-1* and *Pik-2*, *RGA4* and *RGA5*, *Pii-1* and *Pii-2*, respectively. In all three cases, the paired genes are tightly linked and oriented to the opposite directions. In the *AVR-Pik/Pik* interaction, it has been unraveled that AVR-Pik binds to the N-terminal coiled-coil domain of *Pik-1*. *RGA4* and *RGA5* are necessary and sufficient to mediate *Pia* resistance and recognize the *M. oryzae* effectors AVR-Pia and AVR1-CO39. A domain at the C-terminus of *RGA5* characterized by a heavy metal associated domain was identified as the AVR-binding domain of *RGA5*. Similarly, physical interactions among *Pii-1*, *Pii-2* and AVR-Pii are being analyzed.