

# 2019 Fall LIFE SCIENCES & IBB SEMINAR

## Novel Insight into Plant Immunity and Fungal Virulence from the Investigation of Rice Blast Disease

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Plant diseases are among the most serious problems in agriculture and the use of plant immunity controlled by disease resistance (R) genes is a key strategy for crop protection. The vast majority of R genes code for nucleotide-binding and leucine-rich repeat proteins (NLRs) that act as intracellular immune receptors and recognize pathogen-secreted virulence factors termed effectors. A better understanding of these NLRs and the effectors they recognize is crucial for more efficient and sustainable crop disease protection.

We study molecular mechanisms in the interaction between rice and the fungus *Magnaporthe oryzae* that causes blast disease, a particularly devastating rice disease. Based on our work on the detection of the effector proteins AVR-Pia and AVR1-CO39 from *M. oryzae* by the rice NLR RGA5, we recently developed the hypothesis that some NLRs recognize effectors through non-canonical integrated domains (IDs) that act as mimics of effector targets. AVR-Pia and AVR1-CO39 have no similarity in their amino acid sequences but possess the same three dimensional protein structure that is characteristic of the extended and particularly important family of MAX (*Magnaporthe Avr* and *ToxB*) effectors in the blast fungus. By detailed structure-function analysis, we deciphered the molecular details of the binding of AVR-Pia and AVR1-CO39 to the integrated heavy metal-associated (HMA) decoy domain of RGA5. This demonstrated that direct effector/RGA5-HMA binding is strictly required for effector recognition and acts in concert with the association of the effectors to additional sites in RGA5. Comparative genomic analysis showed that NLRs carrying integrated decoy domains are frequent and widespread. We identified them in 31 land plants, from mosses to angiosperms, and they represent, on average, 5% of the NLRs in plant genomes. Knowledge on effector recognition by integrated decoy domains can now be exploited for in silico detection of proteins targeted by effectors and potentially acting in plant immunity and for the engineering of NLRs with novel recognition specificities.

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- **Date: Sep 27 (Fri) 4:30PM**
  - **Place: Auditorium(1F), POSTECH Biotech Center**
  - **Inquiry: IBB Tel: 279-8284**