Entry No. 8RGS-0037

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetics of Biotic interactions: Stress tolerance, Mitigation and Microbiome
Endorsement email	:
Genetics of Biotic interactions Stress tolerance Mitigation and MicrobiomeKeyword 1	: blast blight
Genetics of Biotic interactions Stress tolerance Mitigation and Microbiome Keyword 2	: fungi
Genetics of Biotic interactions Stress tolerance Mitigation and MicrobiomeKeyword 3	:
Title of Entry	: Pathogen effector recognition by paired rice NLR immune receptors and decoy domains
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Nucleotide-binding domain and leucine-rich repeat containing proteins (NLRs) are important receptors in plant immunity and allow specific recognition of pathogen effectors. Based on our work on the detection of the Magnaporthe oryzae effectors AVR-Pia and AVR1-CO39 by the rice NLR RGA5, we recently developed the hypothesis that some NLRs recognize effectors by integrated decoy domains (Cesari et al., 2013; Cesari et al., 2014; Kroj et al., 2016). 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 the direct RGA5-HMA/effector binding is strictly required for effector recognition but only of moderate affinity and acts in concert with the association of the effectors to additional sites in RGA5 (Ortiz et al., 2017). This combination of integrated decoy domains with additional independent effector-NLR interactions seems to confer robust effector recognition that is resilient to effector mutations. I will also present first results on how knowledge on the molecular details of effector recognition by integrated decoy domains can be exploited for the modification of the recognition spectrum of NLRs. 1. S. Césari et al., Plant Cell. 25, 1463–81 (2013). 2. S. Césari, et al., Front. Plant Sci. 5, 606 (2014) 3. T. Kroj et al., New Phytol. 210, 618–626 (2016). 4. D. Ortiz et al., Plant Cell, 29, 156–168 (2017).

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