



HAL
open science

Mode of action and engineering of a rice NLR immune receptor for broader recognition specificity of *Magnaporthe oryzae* effectors

Stella Cesari

► **To cite this version:**

Stella Cesari. Mode of action and engineering of a rice NLR immune receptor for broader recognition specificity of *Magnaporthe oryzae* effectors. New Phytologist Symposium. Next generation scientists 2019, Jul 2019, Dublin, Ireland. hal-02734456

HAL Id: hal-02734456

<https://hal.inrae.fr/hal-02734456>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

**Mode of action and engineering
of a rice NLR immune receptor
for broader recognition
specificity of *Magnaporthe
oryzae* effectors.**

Plenary lecture

STELLA CESARI

14:00–14:50

*INRA, UMR BGP, Campus International de Baillarguet, TA A-54/K,
34398, Montpellier, France*

Plant nucleotide-binding domain and leucine-rich repeat containing proteins (NLRs) are intracellular immune receptors that specifically recognize pathogen effectors and induce immune responses. Based on our work on the detection of the *Magnaporthe oryzae* effectors AVR-Pia and AVR1-CO39 by the rice NLR RGA5, we developed the hypothesis that some NLRs recognize effectors through non-canonical integrated domains (IDs) that act as effector target decoys. We unravelled the molecular details of AVR-Pia and AVR1-CO39 binding to the integrated heavy metal-associated (HMA) domain of RGA5 through detailed structure-function analyses. Our results revealed that direct effector/HMA domain interactions are required for the specific recognition of both effectors by RGA5. However, the binding affinity between these effectors and the HMA domain is moderate but may be reinforced by additional associations of effectors on other sites in RGA5. This combination of effector-binding to IDs and to additional sites in the NLR seems to confer robust effector recognition. Here, I will also discuss how our knowledge of the molecular details of effector recognition by NLRs carrying IDs can be exploited to extend the recognition spectrum of plant immune receptors. Briefly, I have introduced point mutations in the HMA domain of RGA5 to investigate the possibility of modifying the recognition specificity of this receptor and enable the detection of AVR-PikD, another *M. oryzae* effector.