



Magnaporthe oryzae effectors AVR-Pia and AVR1-CO39 reveal structural homology

Karine de Guillen, Diana Ortiz-Vallejo, Jérôme Gracy, Elisabeth E. Fournier, Thomas T. Kroj, André Padilla

► To cite this version:

Karine de Guillen, Diana Ortiz-Vallejo, Jérôme Gracy, Elisabeth E. Fournier, Thomas T. Kroj, et al.. Magnaporthe oryzae effectors AVR-Pia and AVR1-CO39 reveal structural homology. 3. Annual Conference of the COST Action Sustain (FA1208), Feb 2016, Banyuls-sur-Mer, France. 97 p. hal-02738986

HAL Id: hal-02738986

<https://hal.inrae.fr/hal-02738986>

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.

***Magnaporthe oryzae* effectors AVR-Pia and AVR1-CO39 Reveal Structural Homology**

Karine de Guillen¹, Diana Ortiz-Vallejo², Jérôme Gracy¹, Elisabeth Fournier², Thomas Kroj² and André Padilla¹

1 CBS Centre de Biochimie Structurale, INSERM U1054, CNRS UMR5048, University of Montpellier, Montpellier, France

2 BGPI Biologie et Génétique des Interactions Plantes-Pathogènes, INRA- CIRAD - Montpellier SupAgro, Montpellier, France

Plant pathogen genomes co-evolve with their host genomes to overcome the plant resistance mechanisms through generation of a variety of isolates. The causal agent of rice blast, *Magnaporthe oryzae*, the major Rice pathogen, is responsible of economically significant crop losses. During the infection stage the fungus secretes small proteins acting as virulent factors, called effectors, some of them being translocated inside host cells. Among them, avirulent effectors are recognized by the plant immune system through cytoplasmic receptor proteins that activates “effector triggered immunity” mediating the resistance answer. Here, we solved the NMR structures of two such effectors of *M.oryzae*: AVR-Pia and AVR1-CO39. Structurally, they share a common three-dimensional architecture, also found in *M. oryzae* AVR-Piz-t effector and *Pyrenophora tritici repens* toxin ToxB, pathogenic for wheat. Sequence comparison search of fungi protein databases based in the 3D structures and sequence alignments, revealed new possible members of this sub-class of plant pathogen effectors.