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

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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.