

<http://www.fgsc.net/26thFGC/26FGCProgramAndAbstracts.pdf>

**26th Fungal Genetics Conference at Asilomar**  
**March 15-20 2011**  
**Fungal Genetics Reports volume 58 - supplement**

Ribot C, Cesari C, Hirsch J, Fournier E, Tharreau D, Vallet J, Lebrun MH, Kroj T. 2011. Deciphering Effector Function in the /Magnaporthe oryzae /- Rice Interaction. Poster présenté à la 26th Fungal Genetics Conference, 15-20 mars 2011, Asilomar, USA. p.259

595. Deciphering Effector Function in the Magnaporthe oryzae - Rice Interaction. Cécile Ribot<sup>1</sup>, Stella Cesari<sup>1</sup>, Judith Hirsch<sup>1</sup>, Elisabeth Fournier<sup>1</sup>, Didier Tharreau<sup>1</sup>, Julie Vallet<sup>2</sup>, Marc-Henri Lebrun<sup>2</sup>, Thomas Kroj<sup>1</sup> 1BGPI, INRA-CIRAD-SUPAGRO, Montpellier, France; 2MAP,CNRS-UCB-INSA-BCS, Lyon, France.

Effectors are central to virulence in all pathogenic organisms and to their adaptation to specific hosts. However, the role and molecular function of fungal effector proteins is largely unknown. A better understanding of fungal effectors is necessary for a deeper understanding of fungal pathogenicity and for new perspectives in the development of durably resistant crops. Therefore, we perform systematic and targeted analysis of effectors of the causal agent of blast disease, the ascomycete fungus *Magnaporthe oryzae*, which is the most important rice pathogen and a model for the investigation of the molecular basis of fungal pathogenicity. Genome wide expression analysis allowed us the identification of ~100 effector candidates, secreted specifically during infection. Results from the functional analysis of promising candidates will be presented. Investigation of their localization during infection by life cell imaging studies and in vitro translocation assays indicate their translocation into host cells by unknown mechanisms. In addition, two hybrid screens and over expression studies in rice are beginning to shed light on targeted host proteins and host processes.