

【Grant-in-Aid for Scientific Research (S)】

Biological Sciences (Agricultural Sciences)



Title of Project : Towards Understanding Molecular Interactions of Rice and the Blast Fungus *Magnaporthe Oryzae*

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Research Project Number : 15H05779 Researcher Number : 50236981

Research Area : Genetics and Breeding

Keyword : Breeding, Plant Pathology, Host, Pathogen, Coevolution

【Purpose and Background of the Research】

Blast disease caused by the Ascomycete fungus *Magnaporthe oryzae* is not only the most devastating disease of rice but also belongs to the group of seven most destructive diseases/pests of crops worldwide (Pennisi, E. 2010, Science). Breeding of resistant rice cultivars is the most cost

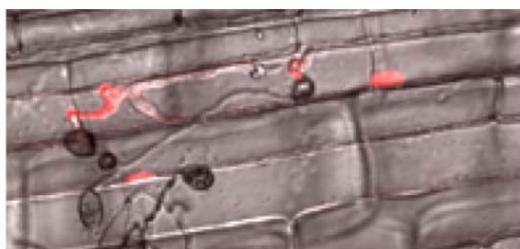


Figure 1 Blast fungus invading rice cells

effective way to control the disease.

Blast pathogen secretes a battery of effector proteins into rice cells to facilitate its invasion. It is hypothesized that effectors perturb host resistance and metabolism, paving the way for pathogens to establish in the host environment. However, their molecular functions are largely unknown. Certain effectors are recognized by host surveillance system, by the products of *R* (*Resistance*)-genes, in most cases coding for cytosolic Nucleotide-Binding Leucine Rich Repeat Receptors (NLRs). Effectors recognized by *R*-gene products are called avirulence effectors (AVRs). We cloned three AVRs, *AVR-Pia*, *AVR-Pii* and *AVR-Pik*, from the blast pathogen, as well as isolated their cognate *NLR* genes *Pia* and *Pii* from rice. *Pik* was isolated by Ashikawa and colleagues (Ashikawa *et al.* 2008, Genetics). Notably, all the three NLRs are composed of a pair of proteins encoded by two tightly linked genes. In this project, we will investigate the structure and function of the three AVRs, as well as elucidate their molecular interactions with NLRs. We will also address how the each NLR pair functions to trigger resistance.

【Research Methods】

We will attempt to identify the target proteins in rice for the three AVRs of *M. oryzae* and to understand their functions. AVR-target protein interactions as well as AVR-NLR interactions will be studied at the protein structure levels. Additionally, molecular interactions and functions of the NLRs pairs will be addressed. We will also exploit whole genome information of *M. oryzae* and rice to isolate novel pathogen effectors and their host target proteins.

【Expected Research Achievements and Scientific Significance】

By comparing the three AVR-NLR combinations, we will strive to unravel the shared mechanisms of AVR recognition by NLR. Identification of effector target proteins will facilitate the identification of novel rice susceptibility genes, which in turn allows us to develop blast resistant rice cultivars by introgression breeding. Successful accomplishment of the project should provide us with the fundamental understanding of organismal coevolution processes.

【Publications Relevant to the Project】

- Yoshida, K., Saitoh, H. *et al.* (2009) Association genetics reveals three novel avirulence genes from the rice blast fungal pathogen *Magnaporthe oryzae*. *Plant Cell* 21:1573-1591.
- Okuyama, Y., Kanzaki, H. *et al.* (2010) A multifaceted genomics approach allows the isolation of the rice *Pia*-blast resistance gene consisting of two adjacent NBS-LRR protein genes. *Plant J.* 66:467-479.

【Term of Project】 FY2015-2019

【Budget Allocation】 151,500 Thousand Yen

【Homepage Address and Other Contact Information】

<http://genome-e.ibrc.or.jp/home>