

[Grant-in-Aid for Specially Promoted Research]

Exploring rice NLRome - pathogen effector interactions to enhance food security

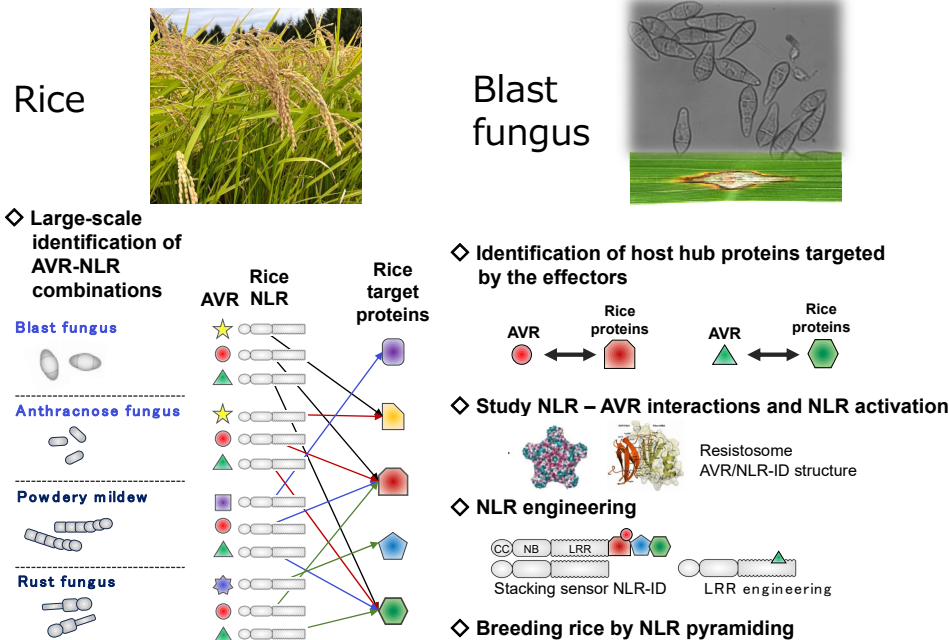


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Purpose and Background of the Research

● Outline of the Research

In rice, blast disease caused by a fungus *Magnaporthe oryzae* accounts for 30% production loss globally, equivalent of feeding 60 million people (Nalley et al. 2016), pointing to the necessity of effective disease control. Plants are equipped with resistance genes mainly encoding Nucleotide-binding Leucine-rich repeat Receptor proteins (NLRs). In this project, we carry out a systematic search for rice NLRs and cognate pathogen effectors (avirulence effectors = AVR) that are recognized by the NLRs. We will perform a multi-faceted research to understand the mechanisms of NLR-AVR interactions, AVR-host target interactions and NLR activation. The obtained knowledge will be harnessed to engineer NLRs and breed rice cultivars with durable blast resistance. Success of the research will provide deep insights into the function of NLRs in general and will contribute to the world food security.



Elucidating the diversity and function of rice NLRome by multi-faceted approaches → Contributing to rice disease control and world food security

Figure 1. Scheme of the research project

Expected Research Achievements

Based on our accumulating knowledge on rice NLRs, we carry out a project with the objectives of exploring the whole set of NLRs (NLRome) of rice with a goal of understanding general rule of NLR-AVR interactions and achieving durable resistance of rice against the rapidly evolving blast disease.

To this end, we set the following six sub-objectives:

- Isolation of a large number of pathogen AVR**s recognized by rice: Using *M. oryzae* as vector, we screen effector candidate genes of various fungal pathogens to identify ~100 AVR effectors that trigger resistance in rice cultivars.
- Isolation of rice NLRs cognate of the AVR**s: Using a high-throughput forward genetics approach, we isolate ~50 rice NLRs that recognize the AVR.
- Identification of host effector targets of the AVR** effectors: Host target proteins of the AVR effectors will be identified by the methods of biochemistry and their molecular interactions will be studied.
- Understand mechanisms of AVR recognition by NLR and NLR activation**: Molecular interactions between NLR and AVR will be studied for singleton NLRs focusing on LRR, and paired NLRs focusing on sensor NLR Integrated Domains (IDs). We study activation mechanisms of the three paired NLRs (Pia/Pias, Pii, Pik) as well as novel NLRs identified in this project by biochemistry and structure approaches.
- Engineering of NLRs**: We engineer ID of sensor NLR of Pias/Pia-paired NLRs to extend its recognition specificities by ID stacking.
- Developing rice varieties with durable resistance against disease**: Based on the knowledge obtained through 1-2, we develop rice varieties harboring multiple NLRs recognizing conserved AVR effectors, thereby achieving durable resistance against wide range of blast pathogens.

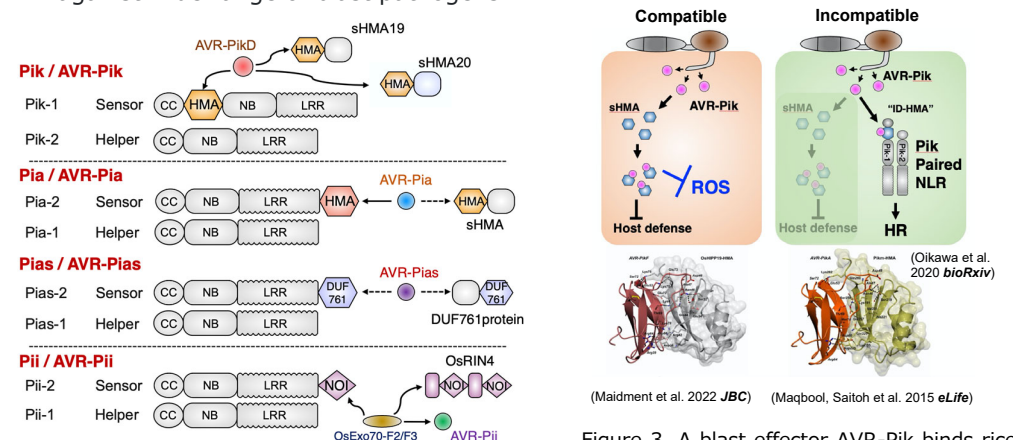


Figure 2. Examples of molecular interactions among the rice NLRs, rice blast AVR effectors, and their rice target proteins so far studied by the PI's research group.

Figure 3. A blast effector AVR-Pik binds rice sHMA proteins and stabilizes them to potentially suppress ROS, thereby enhancing virulence (compatible). During rice evolution, HMA domain was integrated to Pik NLR (ID-HMA), which binds AVR-Pik and induce HR-mediated resistance (incompatible).

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<http://www.crop-evolution.kais.kyoto-u.ac.jp>
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