


Advancing fundamental knowledge of NLR biology to enhance crop resistance against pathogens

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	Project Information	Project Number : 23K20042 Project Period (FY) : 2023-2029 Keywords : crops, pathogens, resistance, NLR proteins

Purpose and Significance of the Research

Crop loss due to pathogen damage represents a tremendous threat to world food security. The most cost-effective and sustainable means to control crop disease is by using cultivars with resistance (*R*-) genes. The majority of *R*-genes so far studied code for Nucleotide-binding Leucine-rich repeat Receptors (NLRs), implying that a full understanding of NLR biology is instrumental to crop protection (Fig. 1). In this project, we address the following questions of NLR biology focusing on rice, wheat and cucurbit crops (Fig. 2); (1) To what extent do NLRs encoded in plant genomes (NLRome) function in SINGLETONS, PAIRS and NETWORKS? (2) What are the MECHANISMS of NLR pairs functioning together to exert resistance, and what is the structure of the higher-order protein complex? (3) How do NLRs RECOGNIZE pathogen effector molecules? (4) How can we leverage the knowledge of NLR biology in APPLICATIONS for NLR engineering and developing crops with durable resistance? (Fig. 3)

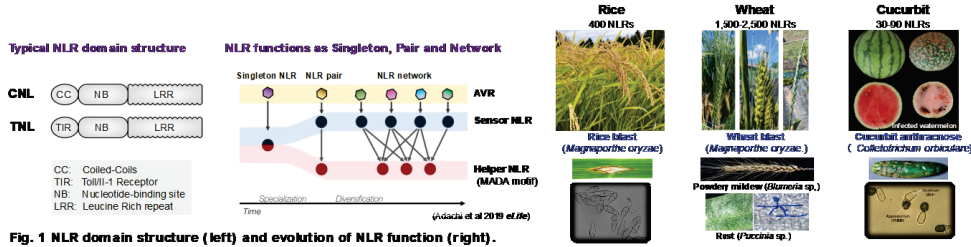


Fig. 1 NLR domain structure (left) and evolution of NLR function (right).

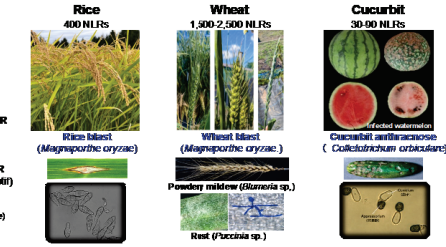


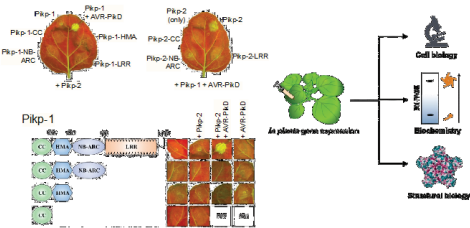
Fig. 2 Focal crops, their NLR numbers and typical pathogens.

(1) Extract NLRomes of rice, wheat and cucurbits using genomic information

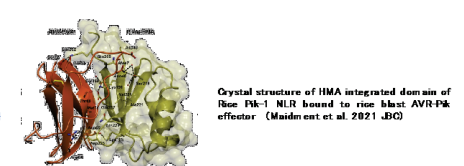
Crop	Species	Ploidy	Number of NLRs	Notes
Rice	<i>Oryza sativa</i>	2x	358	cv. Nipponbare
	<i>Oryza glaberrima</i>	2x	326	cv. CG14
Wheat	<i>Triticum aestivum</i>	6x	2426	cv. Chinese spring
	<i>Triticum burgkianum</i>	4x	1376	cv. Svevik
Cucumis melo	<i>Cucumis melo</i>	2x	53	cv. Payzawat
	<i>Cucumis sativus</i>	2x	30	cv. Chinese Long
Cucurbit	<i>Cucumis melo</i>	2x	90	Wild relative
	<i>Cucumis hystrix</i>	2x	81	Wild relative
	<i>Cucumis melo</i>	2x	81	Wild relative

Species names, ploidy levels and the number of NLRs in their genomes

(2) Understanding NLR activation mechanisms



(3) Understanding recognition mechanisms of pathogen AVR by NLRs



(4) Enhancing crop protection by NLR engineering and NLR breeding

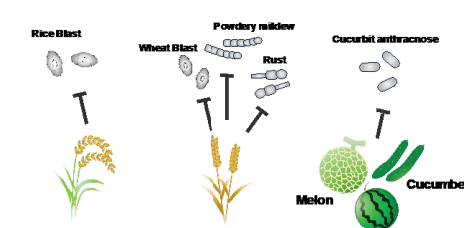


Fig. 3 Outline of the NLR Biology project.

Organization of the Project Team

PI Terauchi has been working on plant genomics and rice-*Magnaporthe* interactions. Co-Is of Japan side are experts in disease resistance research of respective crops. The main UK collaborator Prof. S. Kamoun (TSL), Fellow of the Royal Society, is a world-leading scientist with strong expertise in all aspects of plant-microbe interactions, including NLR and effector biology. The other UK collaborators are also world top class experts in the field (Fig. 4).

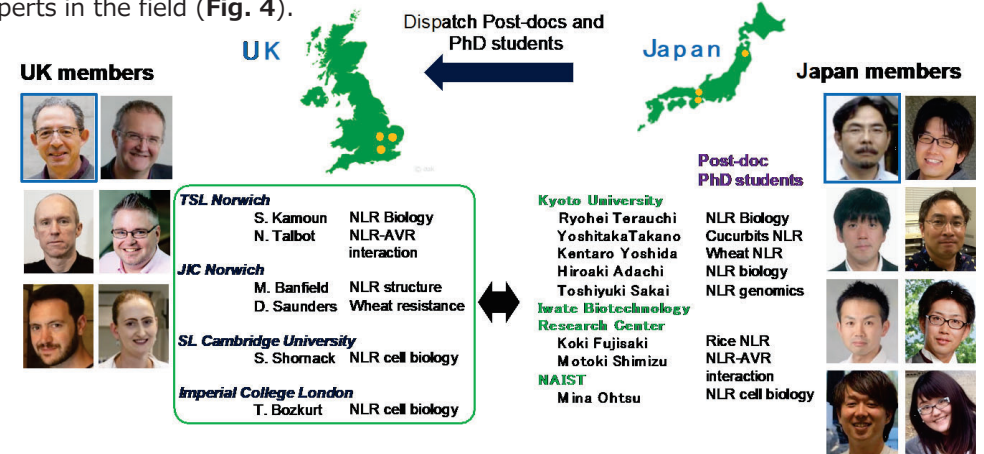


Fig. 4 Scientists involved in the NLR Biology international collaboration.

Plan for Fostering Early-career Researchers

With the project, we aim to foster Japanese early-career scientists so that they become competent and independent researchers to lead the future research fields of plant immunity, plant resistance breeding, plant genomics and microbe genomics. We will allocate 70% of the total budget specifically for fostering early-career researchers, and incorporate post-docs and PhD students in the project. A total of eight highly competent young postdocs from around Japan are engaged in the projects (1) to (4). We also select a total of eight competent PhD students to be involved in the project. Up to 12 among them will be sent to the UK laboratories and spend 3 – 24 months to carry out NLR Biology research together with the UK members (Fig. 5).

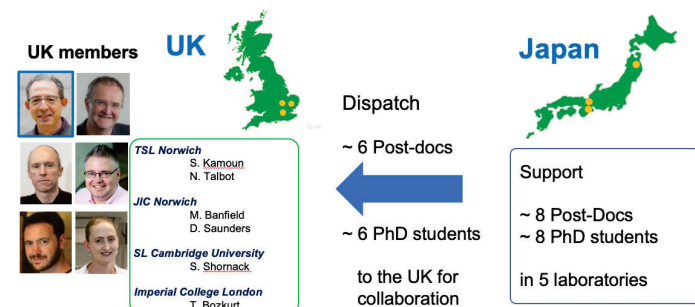


Fig. 5 Plan of dispatching young Japanese scientists to the UK for NLR Biology studies.