

REVIEW

The CGIAR–JIRCAS Partnerships for Sustainable Food Systems: Rice Blast Differential Systems and Biological Nitrification Inhibition as Examples

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Abstract

The Japan International Research Center for Agricultural Sciences (JIRCAS) working with partners such as CGIAR and its research centers, has made notable progress in creating farming solutions directed at the needs of poor farmers worldwide. This review discusses two critical achievements—development and deployment of differential systems for blast study in rice and biological nitrification inhibition (BNI). Both achievements were initiated from basic studies. Results of the research guide crop improvement programs designed to introgress rice blast resistance and BNI into target crops. Both works clearly highlight that collaboration of scientists are key to the success. The wide research networks of JIRCAS and CGIAR are effective at establishing partnerships which can tackle the complexity and geographic scale of challenges in agricultural research. CGIAR's strong presence in regions where problems occur, rich genetic resources, and strong genetic improvement programs are crucial to effective research-for-development activities to achieve agricultural sustainability. CGIAR–JIRCAS partnerships should be strengthened to bringing the benefits of science to the world's poor farmers.

Discipline: Crop Science

Additional key words: Africa Rice Center, CIAT, CIMMYT, ICRISAT, IRRI

Introduction

Reflecting the predicted expansion of the world's population and changes in food consumption patterns, global food demand is expected to increase greatly (Islam & Karim 2020). However, currently, 821 million people—more than one-ninth of the world's population—still do not have enough to eat (World Food Programme 2020). Moreover, the challenges in global environmental issues, urbanization, and malnutrition are crucial to establishing sustainable food systems. To achieve food security in terms of both quantity and quality and to minimize the burden on Earth's systems, we urgently need effective technology development and application of the latest

technology and tools in agriculture through cooperation.

The Japan International Research Center for Agricultural Sciences (JIRCAS), established in 1970 as the Tropical Agriculture Research Center, is a national research and development agency under the Ministry of Agriculture, Forestry and Fisheries (MAFF) of Japan, and plays a core role in international collaborations in agriculture, forestry, and fisheries (JIRCAS 2020a). Through the accumulation of collaborative research in developing regions over the past half century, JIRCAS has established a domestic and overseas network that conducts research-for-development (R4D) activities to serve the world's food-poor. CGIAR (formerly the Consultative Group on International Agriculture Research) established

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around the same period, and its 15 research centers (CGIAR research centers) are important partners sharing the same mission and challenges to achieve sustainable development goals.

JIRCAS holds a Memorandum of Understanding (MoU) with 11 CGIAR Research Centers (Table 1) to engage in various collaborative activities, not only in agricultural research, but also in the mobilization of human resources, knowledge, technology, products, and partnerships, both public–public and public–private. As an example, JIRCAS hosted the Japan–CGIAR Fellowship Program (2004–2013) with the support of MAFF. The Program dispatched a total of 106 young Japanese scientists and students to all 15 CGIAR research centers to support their capacity development through practical experience in applying food and environmental science to problems of development and in sharing knowledge. A survey conducted in 2013 found that 64% of fellows (excluding students) worked in research position in various universities and research institutes, including CGIAR research centers, where they helped to advance of agricultural research.

The collaboration between JIRCAS and CGIAR Research Centers has accomplished tremendous achievements over the decades. The partnerships with CGIAR have been essential parts of JIRCAS's activities, through the worldwide research network, local presence in over 100 countries, extensive gene bank with over 770 000 germplasm accessions, and leading scientists of CGIAR (CGIAR 2020). Some of the excellent works done under CGIAR–JIRCAS partnerships are presented in other papers in this special issue. In this review, we discuss two critical achievements—the development and deployment of differential systems for blast study in rice and biological nitrification inhibition (BNI), as the fruits

of collaboration among multiple CGIAR research centers and JIRCAS—to illustrate the efforts and partnerships in technology development, and discuss future prospects.

Rice blast differential system

Rice (*Oryza sativa* L.) supports half of the world's population. Its stable supply and productivity improvement are vital to achieving food security in the developing world. JIRCAS's collaboration with the International Rice Research Institute (IRRI) dates back to 1979 in a series of projects. The results have appeared in many publications, and various breeding materials and technologies have been developed under the IRRI–Japan Collaborative Research Project (IJCRP), Phases I–VII (funded by MAFF), from 1984 to 2020 (JIRCAS 2019). Among the numerous outputs, advances in the genetics, genomics, and control of rice blast disease are significant.

Blast disease, caused by the fungus *Pyricularia oryzae* Cavara, affects rice production in all rice-growing regions and causes major yield losses (Bonman & MacLill 1988, Ou 1985, Latterell & Rossi 1986). While chemical control is effective, the use of resistant cultivars is still the most practical and economical way to control the disease, especially for farmers who are resource poor.

The relationships between resistance in rice cultivars and virulence of blast isolates can be explained by gene-for gene theory (Flor 1971), and the information about the virulence of rice blast isolates is important in genetic studies and breeding of resistant cultivars. Studies of the inheritance of resistance to blast disease have been conducted since 1922, but the establishment of a system for differentiating blast fungus races in Japan by Goto in 1965 led to systematic studies (Gurdev & Jena 2007). A set of differential varieties (DVs) is important material for

Table 1. CGIAR Research Centers with which JIRCAS holds a Memorandum of Understanding

CGIAR centers		Period*		
Africa Rice Center	AfricaRice	1998	-	Current
International Maize and Wheat Improvement Center	CIMMYT	1992	-	Current
International Center for Agricultural Research in the Dry Areas	ICARDA	1987	-	Current
International Center for Tropical Agriculture	CIAT	1983	-	Current
International Crop Research Institute for the Semi-Arid Tropics	ICRISAT	1994	-	Current
International Food Policy Research Institute	IFPRI	2004	-	Current
International Institute of Tropical Agriculture	IITA	1989	-	Current
International Rice Research Institute	IRRI	1979	-	Current
International Water Management Institute	IWMI	1988	-	Current
International Livestock Research Institute	ILRI	1984	-	Current
World Agroforestry	ICRAF	1997	-	Current

* The period include some gap years

breeding for blast resistance and for studies of pathology. With the knowledge of resistance genes in each variety among the DVs, the pathogenicity (races) of blast isolates can be distinguished from the reaction patterns or as qualitative differences in reactions to different races.

Under IJCRP Phase III (1994–1999), Phase IV (1999–2004), and Phase V (2005–2009), IRRI and JIRCAS developed four sets of international DVs including monogenic lines (MLs) and near-isogenic lines (NILs) (Table 2). As the first set of international DVs, MLs were developed with the genetic background of a susceptible Chinese Japonica Group cultivar, Lijiang-xin-tuan-heigu (LTH), which is compatible with all of the blast isolates evaluated at IRRI at that time (Tsunematsu et al. 2000). This set of MLs contains 23 blast resistance genes derived from 27 donor cultivars.

Following to MLs, three near-isogenic lines (NILs) were developed with the genetic background of LTH (LTH NILs, Telebanco-Yanoria et al. 2010a) as the advance DV for MLs, Indica Group cultivar CO 39 (CO 39 NILs, Telebanco-Yanoria et al. 2010b), and the

universal susceptible line US-2 (Kobayashi et al. 2007). CO 39 harbors the additional resistance gene *Pia* in the genetic background. US-2, which was derived from a cross between an Indonesian landrace, Kencana, and Indica Group cultivar, Takanari, is easy to cultivate and suitable under the environment of tropical area. Moreover, the NILs were more uniform than the MLs. The introgression of several segments on the genome chromosome regions of DVs corresponding to the locations of blast resistance genes was identified, but addition segments were also still remained in the other chromosome region(s).

Those four sets of international DVs target 23 resistance genes: *Pia*, *Pib*, *Pish*, *Pit*, *Pii*, *Pi3*, *Pi5(t)*, *Pik-s*, *Pik*, *Pik-p*, *Pik-h*, *Pik-m*, *Pi1*, *Pi7(t)*, *Piz*, *Piz-5*, *Piz-t*, *Pi9(t)*, *Pita*, *Pita-2*, *Pi12(t)*, *Pi19(t)*, and *Pi20(t)* (Fukuta et al. 2009). The reaction patterns of these DVs relative to representative blast isolates from Japan and the Philippines, as well as their morphological and agronomical characters, have been reported, along with their genetic characterization, and the chromosome components and introgression of chromosome segments

Table 2. Differential varieties developed by IRRI–Japan Collaborative Research Project

		Differential variety for blast resistance			
Target gene	Chr.	Monogenic line (Tsunematsu <i>et al.</i> 2000)	LTH NILs (Telebanco-Yanoria <i>et al.</i> , 2010a)	CO 39 NILs Telebanco-Yanoria <i>et al.</i> , 2010b)	US-2 NILs (Unpublished)
		Genetic background			
		Japonica Group	Japonica Group	Indica Group harboring <i>Pia</i>	Indica Group
<i>Pish</i>	1	2	-	4	1
<i>Pib</i>	2	1	1	1	-
<i>Pit</i>	1	1	-	-	-
<i>Pia</i>	11	2	1	-	2
<i>Pii</i>	9	1	-	-	1
<i>Pi3</i>	9	1	1	-	1
<i>Pi5 (t)</i>	9	1	-	1	1
<i>Pik-s</i>	11	2	3	1	2
<i>Pik-m</i>	11	1	-	1	1
<i>Pi1</i>	11	1	-	1	1
<i>Pik-h</i>	11	1	1	1	1
<i>Pik</i>	11	1	1	2	1
<i>Pik-p</i>	11	1	-	1	1
<i>Pi7 (t)</i>	11	1	1	1	1
<i>Pi9 (t)</i>	6	1	1	-	1
<i>Piz</i>	6	1	-	-	1
<i>Piz-5 (Pi2)</i>	6	1	1	1	1
<i>Piz-t (Pi40 (t))</i>	6	1	-	1	1
<i>Pita-2</i>	12	2	1	3	1
<i>Pi12 (t)</i>	12	1	-	-	1
<i>Pita (Pi4 (t))</i>	12	3	3	2	4
<i>Pi19 (t)</i>	12	1	-	-	-
<i>Pi20 (t)</i>	12	1	-	-	1
Total		29	15	21	25

harboring resistance genes.

As a tool to identify blast resistance genes in rice and to characterize the pathogenicity of the blast isolates under the gene-for-gene theory (Flor 1971), the MLs and NILs have been distributed to more than 15 countries through IJCRP and the International Network for Genetic Evaluation of Rice, and have been used for pathological studies of blast fungus in Japan, Korea, China, Vietnam, Cambodia, Laos, Thailand, Malaysia, Indonesia, the Philippines, Bangladesh, India, Kenya, West African countries and so on, and as the donor cultivars for resistance genes. NILs are used in various studies as the most suitable material for blast race differentiation (JIRCAS 2019). The LTH NILs make it easier to evaluate inoculations test owing to their uniform morphological traits. The CO 39 NILs, adapted to tropical conditions, can be compared with materials with the LTH genetic background. Those NILs with LTH and CO 39 backgrounds could supply genes to improve the blast resistance of Japonica and Indica Group cultivars, respectively.

Following the successful development of the international DVs, in 2006 JIRCAS established the Blast Research Network for Stable Rice Production with national agricultural research systems in participating countries (Korea, China, Vietnam, the Philippines, Indonesia, Laos, Cambodia, Thailand, Bangladesh, Kenya, Ethiopia, and Japan), universities (Yunnan Agricultural U., China; Nagoya University; Hirosaki University, Japan), and two CGIAR research centers (IRRI and Africa Rice Center (AfricaRice) which covers the countries in West Africa) (Fig. 1). The aim of the network is to establish a durable system to control blast disease. Through the activities of the network, an international differential system was proposed and established as a basic tool for studying host–pathogen interactions. The established international differential system comprises the sets of DVs, standard differential blast isolates (SDBIs) selected from the collaborative countries in Asia and Africa, and the methods to evaluate pathogenicity of blast isolates based on of reaction patterns

to the DVs against blast isolates and designate blast races (Hayashi & Fukuta 2009). From a matrix of reactions of DVs and SDBIs (Fig. 2), the international differential system can identify the pathogenicity of blast fungi and the genotypes of resistance genes in rice cultivars on the basis of the gene-for-gene theory.

Previously, several differential systems have been also developed and used in the Philippines (Telebanco-Yanoria et al. 2008), Bangladesh (Khan et al. 2016), Vietnam (Nguyen et al. 2020), Laos (Xangsayasane et al. 2020), and Indonesia (Kadeawi et al. 2021) to develop and distribute the basic tools for pathological and breeding research works. As proposed by Hayashi and Fukuta (2009), the sets of DVs are now available and distributed among the partners to evaluate and classify blast isolates. The genetic variations among blast races have been clarified in each country and at the global level, along with the distribution of highly diverse races in tropical and temperate countries of Asia and Africa (Mekwatanakarn et al. 2000, Chen et al. 2001, Telebanco-Yanoria et al. 2008, Zeigler et al. 1995, Odjo et al. 2014, Kawasaki-Tanaka et al. 2016, Khan et al. 2016). With blast isolates collected by the Blast Research Network for Stable Rice Production, 30 isolates, which correspond to 23 resistance genes in the DVs, are now nominated as international SDBIs (unpublished data).

The differential system is a useful tool which to clarify resistance genes. Fukuta et al. (2007) found some limited kinds of blast resistance genes among 42 IRRI-bred rice cultivars using it. In the other hand, Telebanco-Yanoria (2008) found wide variation in resistance based on the reactions to 20 SDBIs from the Philippines in 992 accessions collected around the world. Using different system, Fukuta et al. (2019) found the outbreaks of virulent blast races to the resistance genes of three major varieties—Basmati 217, Basmati 370, and ITA310—in Kenya and several accessions including IR 2793080-1, showed resistance to all SDBIs used. A set of near isogenic lines with the genetic background of a rainfed lowland Indica



Fig. 1. Kickoff meeting of Blast Research Network for Stable Rice Production at International Rice Research Institute in August 2006. Participants from Australia, China, Japan, Korea, Egypt, India, Indonesia, the Philippines, Thailand, and the USA and from IRRI, CIAT, the French Agricultural Research Centre for International Development (CIRAD), and JIRCAS discussed the use of differential systems for protection from blast disease.

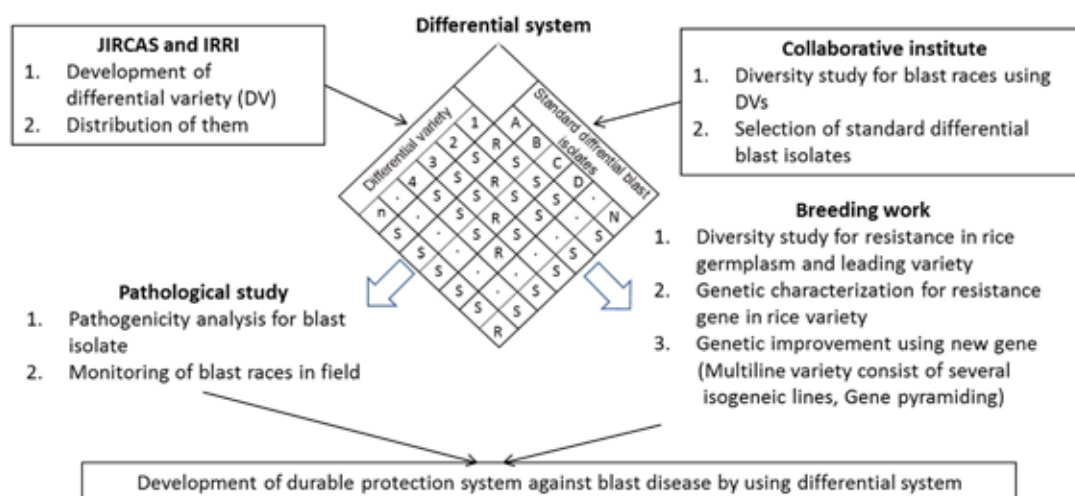


Fig. 2. Development of the differential system for rice blast studies and its application. The differential system consists of differential varieties (DVs) and standard differential blast isolates (SDBIs). The pathogenicity of blast isolates and the resistance of rice cultivars are estimated by comparison with a matrix of reaction patterns.

Group cultivar, IR 49830-7-1-2-2 for targeting resistance genes; *Pish*, *Pi3*, *Pi5(t)*, *Pik*, *Pi7(t)*, *Piz-5*, *Pi9(t)*, and *Pita-2*, were also developed as a multiline variety (Koide et al. 2011). The breeding material will be one of useful tools for developing of durable protection system to blast disease in the future.

The international differential system developed by JIRCAS through the collaboration with IRRI and partners, including the AfricaRice, has enabled global surveys of the distribution of blast races and the identification of useful genetic resources for genetic improvement. Through strong international partnerships, the analysis of such data will help guide elastic blast control and stable rice production.

Biological nitrification inhibition (BNI)

The loss of nitrogen (N) from farmland is a serious problem, as it both reduces the economic efficiency of farming and damages ecosystems through N pollution (Gilbert 2011). Agriculture is now the world's largest contributor to global greenhouse gas (GHG) emissions (Gilbert 2011). A major portion of GHG emissions from agriculture is associated with the production of N fertilizers and their application to farmland (Vermeulen et al. 2012). The Paris Agreement under the United Nations Framework Convention on Climate Change (UNFCCC) envisions a 70% reduction in GHG emissions by 2050 (IPCC 2014). It is now urgent to develop new technologies to reduce N losses, N-fertilizer use, and GHG emissions from agriculture to make production systems ecologically and environmentally friendly and sustainable in the long

term.

More than 70% of N applied in agriculture is lost before the crop has a chance to take it up and convert it into protein (Tian et al. 2020). One main reason for such a low N-use efficiency (NUE) is a set of soil microbial processes that convert ammonium-N (less mobile) into nitrate-N (highly mobile), termed 'nitrification'. Nitrate is susceptible to transformation to N_2O and NO through another microbial process called 'denitrification' (Fig. 3).

Nitrification and denitrification are responsible for most N losses from farmland (through nitrate leaching and gaseous N emissions) and thus the low NUE (Doran 2002; Subbarao et al. 2012). Modern crop management practices have accelerated soil nitrifier activity and result in the rapid formation of soil nitrates from N fertilizers (urea is rapidly converted into ammonium within 24 h in soil, which is then converted into nitrates). Controlling soil nitrifier activity and reducing nitrification rates are thus crucial to reducing N losses and improving NUE. Although synthetic nitrification inhibitors were discovered in the 1950s, they are not widely used in production agriculture owing to the lack of consistent benefit and their low cost-effectiveness. Controlling soil nitrification is thus a major challenge in agriculture.

A research partnership initiated in 2000 by JIRCAS with the International Center for Tropical Agriculture (CIAT) has resulted in the development of a new area of research, termed 'biological nitrification inhibition' (BNI), a plant function whereby root systems produce nitrification inhibitors that suppress soil nitrifier activity (Subbarao et al. 2015, 2017). BNI is a mechanism evolved in natural ecosystems where protecting soil-nitrogen

JIRCAS expanded BNI research into wheat in 2015. Researchers identified *Leymus racemosus*, a wild wheat relative with high BNI capacity in its roots that could be used as a genetic source to improve the BNI capacity of wheat (Subbarao et al. 2007). JIRCAS and the International Maize and Wheat Improvement Center (CIMMYT) identified the Lr#n chromosome as the controlling center for the BNI trait, through pre-breeding strategy. The second research partnership, from 2015 to 2020, led to the transfer of the chromosomal region controlling the BNI trait into cultivated wheats. The research will continue with the long-term goal of developing BNI-enabled modern wheat cultivars that can suppress soil nitrifier activity and reduce N losses from wheat farming. The first generation BNI-enabled wheat cultivars are expected to be developed shortly. These new BNI wheats will require extensive field evaluations to assess the potential of BNI to improve N recovery and NUE in wheat production systems.

JIRCAS is the convener of the International BNI Research Consortium, initiated in 2014 (JIRCAS 2020b). The first meeting was held to bring together collaborators involved in BNI research with JIRCAS, with the participation of three CGIAR research centers. Membership has now grown to 20 research institutes in Asia, Europe, the USA, and Mexico (Deshpande 2017, Fig. 4). The fourth BNI Consortium meeting, scheduled for October 2021, will host up to 50 research collaborators. As the membership grows, it creates opportunities to bring in diverse research skills, in addition to expanding the funding sources to develop BNI research. The development of BNI technology involves the genetic improvement of BNI capacity in the root systems of major

crop and pasture species to develop low-nitrifying, low-N₂O-emitting production systems. The long-term goal of BNI research is to reduce N loss from farmland and to improve the sustainability of crop production systems. When fully developed and deployed, BNI technology will become an integral part of ‘green technology’ for farming, a technology that is designed to be eco-friendly (Subbarao et al. 2013a, 2017). The three case-studies described above show the progress of BNI technology development at JIRCAS and the role of CGIAR research centers in shaping research to reduce N losses in agriculture.

Prospects

JIRCAS and its partners have made notable progress in creating farming solutions directed at the needs of poor farmers worldwide (JIRCAS 2020a).

The differential system is a basic research tool for use in plant pathology and rice breeding (Kobayashi et al. 2009). It has generated knowledge of dominant blast races, genetic variations in resistance, and rice genotypes, and will lead to further genetic improvements of leading rice cultivars. By learning from nature to understand BNI, evolved in nature for protection of soil-nitrogen in natural ecosystems, we can introduce these mechanisms (i.e. plant traits) into the managed ecosystems such as agriculture. JIRCAS’s long-term goal of BNI research is to introduce/improve BNI-capacity in root systems of staple crops, starting from wheat, sorghum and possibly maize in the near future (Subbarao et al. 2009, 2015, 2017). The potential effects of climate change on the impacts of plant pathogens on food security have been discussed (Fones



Fig. 4. 3rd BNI international consortium meeting organized by JIRCAS in 25-26 October 2018 at Tsukuba. A total 40 attendees from participating organizations of the consortium, including 11 from CGIAR research centers (CIAT, CIMMYT, ICRISAT, ILRI), 10 from overseas universities / institutes (UK, USA, China, Austria, France, Germany), and 6 from Japanese institutes, were discussed the progress and future direction of BNI research for deployment to agro-ecosystems.

et al. 2020; Zayan 2020). N losses from agricultural production contribute to detrimental effects on water, soil, air, and human health (Bowles et al. 2018). The technologies developed and networks of scientists formed in the two activities reviewed are useful tools with which to tackle these challenges.

A crucial aspect of both activities is that the scientists in JIRCAS as the coordinating organization and in multiple CGIAR research centers and other national partners have worked together to develop and apply the technologies in order to solve agricultural problems in developing regions. The complexity and geographical scale of the challenges in agricultural research require holistic approaches through multi-stakeholder partnerships to achieve innovative solutions. Recognizing the value that can be created through collaboration and partnerships in all projects to achieve agricultural sustainability, JIRCAS is committed to working with its partners (JIRCAS 2020a).

It is clear that the public investment in agricultural R4D has elicited high returns and fostered the growth of poor farmers (World Bank 2007, Fuglie & Heisey 2007, Pardey & Alston 2011). Among various partners, CGIAR and its centers are recognized as the most successful of the global institutional innovators (World Bank 2007, Alston et al. 2020). Its strong presence in regions where problems occur, rich genetic resources, and strong genetic improvement programs are essential parts of these R4D activities. However, since agricultural research is “slow magic”, a cumulative endeavor, steady implementation, and sustained investment are necessary (Pardey & Beintema 2001). As well as international partners, it is also important to have the participation of national partners and the private sector to sustain the on-ground activities. The wide research networks created by CGIAR and JIRCAS are key to effective partnerships to tackle the various problems facing agriculture.

Over 50 years, the CGIAR–JIRCAS partnerships have bridged the world of science with various disciplines to meet the needs of poor farmers. By acting together, JIRCAS and CGIAR can continue to bring the benefits of science to the world’s poor farmers, making sustainable food production a reality.

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