

Blast Research Network for Stable Rice Production under Unfavorable Environment Condition

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Abstract

Cold stress occurs a serious damage, and blast disease always make a problem together in Temperate and rainfed lowland and upland of Tropical areas. These traits have been a set of rice breeding targets in these areas. More than 80 blast resistance genes and QTLs were reported, but several ones were founded in the same loci. Nobody can characterize well and discriminate in each resistance gene, and the genetic research situation is quite complex. One of the reasons is lack of the differential system consisting of differential varieties and blast isolates to clarify the pathogenicity and the resistance. To solve these problems, a new international standard differential variety set was developed by Japan and IRRI. These differential varieties harbor a single gene and cover for twenty four kinds of genes. These will make possible the survey of germplasm, development of differential system, and clarification of race differentiation. There are limitations to what can be achieved by only one country or organization, hence an international collaboration based on network research, which enhances the exchanges of information, rice germplasms, and blast pathogens, may be the ideal solution for it. A research project, Blast Research Network for Stable Rice Production, is conducting and targeting the distribution of differential system, the elucidation of distribution and dynamics of blast pathogens and rice resistance genes, and a survey of useful resistance germplasms. The ways and tools for durable resistant system of stable rice production will be discussed for blast disease under the unfavorable condition.

Media summary

A International standard differential system consisted differential varieties and blast pathogens were developing under a research project “Blast Research Network for Stable Rice production”.

Key Words

Blast (*Magnaporthe grisea* (Hebert) Barr.), differential system, resistance gene, network, rice (*Oryza sativa* L.)

Introduction

Japan International Research Center for Agricultural Sciences (JIRCAS) is conducting a collaborative study beginning 2006 regarding rice blast resistance based on the development and use of a new international

standard differential system, to enhance the sustainability of rice production system against the disease with the International Rice Research Institute (IRRI). The differential system is a basic tool for understanding host-pathogen interaction, which consists of the rice varieties each carrying ideally a single gene for blast resistance and the blast isolates differing in corresponding avirulence/virulence genes. They are classified based on specificity of reaction between the particular differential variety and differential blast isolates, and can be used for the identification of resistance gene(s) in the varieties and avirulence/virulence gene in the blast pathogens. To develop the new international differential system, (1) diversity studies for blast pathogens and resistance in rice varieties, (2) development of differential varieties, (3) selection of standard differential blast isolates, (4) built up the common evaluation system for pathogenicity of blast isolates, (5) new designation system for blast races, and (6) identification of novel resistance gene etc., are conducting under the network research.

Comportment of research network

The research network is consisted of a total of 11 institutes and one organization, JIRCAS, IRRI, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences (ICS-CAAS, China), China National Rice Research Institute (CNRRI, China), Yunnan Agricultural University (China), Cuu Long Rice Research Institute (CLRRI, Vietnam), Philippine Rice Research Institute (PhilRice, Philippines), Indonesian Center for Rice Research (ICRR, Indonesia), Center for Research and Development of Isotopes and Radiation Technology, National Nuclear Energy Agency (Indonesia), Agricultural Research Center in Laos, and the Rural Development of Agriculture in Korea in 2007. All institute which is interesting in the network research, can participate the annual workshop and these activities as the collaborative institute. In this network, the information and materials of blast pathogens and resistance rive varieties, and breeding tools such as the DNA markers and differential varieties as gene sources, are sharing each other, to develop the differential system in each country and to use the breeding program.

Differential system and it's application

As a new international differential variety set, monogenic lines, which were introduced only a single resistance gene in the genetic background and targeted 24 kinds resistance genes, *Pia*, *Pib*, *Pii*, *Pik*, *Pik-h*, *Pik-m*, *Pik-p*, *Pik-s*, *Pish*, *Pit*, *Pita*, *Pita-2*, *Piz*, *Piz-t*, *Piz-5*, *Pi1*, *Pi3*, *Pi5(t)*, *Pi7(t)*, *Pi9(t)*, *Pi11(t)*, *Pi12(t)*, *Pi19(t)*, and *Pi20(t)*, was developed by IRRI-Japan Collaborative Research Project (Tsunematsu et al. 2000). Three other differential variety sets with different genetic backgrounds, Chinese Japonica-type rice, Lijiangxintuanheigu (LTH), an Indica-type rice, CO 39, and an universal susceptible rice, US-2, have been also developing (Tabel 1, Kobayashi et al., 2007).

These differential varieties will make possible to character the blast isolate which collected in field, and to develop the differential system and a new designation method of blast races. In the participate countries, Korea, China, Indonesia, Philippines Vietnam, and Laos, the collection and characterizations of blast isolates are doing and comparing the pathogenicities based on the reactions to monogenic lines as a common differential sets. These results will show the differentiation and geographical distribution of blast

racess and in the grovel level. The diversity study for blast pathogen from Tropical to Temperate region is showing that several specific reactions to several differential varieties (resistance genes) and dramatic differentiations of blast races in the boundary between North and South China are observed.

Table 1. Generation of differential variety series with blast resistance genes developed at IRRI in 2005

Targeted gene	Recurrent backcross parents			
	Monogenic line	Near isogenic line		
	LTH	LTH	CO39	US-2
<i>Pi a</i>	BC ₁ F ₂₀	BC ₆ F ₁₅	-	BC ₆ F ₇
<i>Pi b</i>	BC ₁ F ₁₅	BC ₆ F ₁₄	BC ₆ F ₁₄	-
<i>Pi i</i>	BC ₁ F ₂₀	BC ₃ F ₁	BC ₄ F ₁	BC ₃ F ₁
<i>Pi k</i>	BC ₁ F ₂₀	BC ₆ F ₁₄	BC ₆ F ₁₄	BC ₆ F ₈
<i>Pi k-h</i>	BC ₁ F ₁₅	BC ₆ F ₁₄	BC ₆ F ₁₄	BC ₆ F ₇
<i>Pi k-m</i>	BC ₁ F ₁₆	BC ₂ F ₁	BC ₆ F ₁₄	BC ₄ F ₁
<i>Pi k-p</i>	BC ₁ F ₂₀	BC ₃ F ₁	BC ₆ F ₁₄	BC ₆ F ₇
<i>Pik-s</i>	BC ₁ F ₂₀	BC ₆ F ₁₄	BC ₆ F ₁₄	BC ₆ F ₇
<i>Pi sh</i>	BC ₁ F ₂₀	BC ₃ F ₁	BC ₆ F ₁₄	BC ₃ F ₁
<i>Pi t</i>	BC ₁ F ₆	-	-	-
<i>Pi ta</i>	BC ₅ F ₁₆	BC ₆ F ₁₆	BC ₆ F ₁₄	BC ₆ F ₈
<i>Pi ta-2</i>	BC ₁ F ₁₆	BC ₆ F ₁₅	BC ₆ F ₁₄	BC ₄ F ₁
<i>Pi z</i>	BC ₁ F ₂₀	BC ₃ F ₁	-	BC ₄ F ₁
<i>Pi z-5</i>	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₆ F ₁₄	BC ₄ F ₁
<i>Pi z-t</i>	BC ₁ F ₂₀	BC ₆ F ₁₅	BC ₆ F ₁₂	BC ₆ F ₈
<i>Pi 1</i>	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₆ F ₁₄	BC ₆ F ₇
<i>Pi 3</i>	BC ₂ F ₁₈	BC ₆ F ₁₆	BC ₄ F ₁	BC ₄ F ₁
<i>Pi 5 (t)</i>	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₆ F ₁₄	BC ₆ F ₈
<i>Pi 7 (t)</i>	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₆ F ₁₄	BC ₆ F ₇
<i>Pi 9 (t)</i>	BC ₃ F ₁₈	BC ₆ F ₁₆	BC ₃ F ₁	BC ₆ F ₇
<i>Pi 11</i>	BC ₂ F ₁₈	-	BC ₄ F ₁	-
<i>Pi 12 (t)</i>	BC ₂ F ₁₈	BC ₃ F ₁	BC ₄ F ₁	BC ₆ F ₇
<i>Pi 19</i>	BC ₁ F ₁₇	BC ₁ F ₁	BC ₁ F ₁	BC ₁ F ₁
<i>Pi 20 (t)</i>	BC ₁ F ₁₆	BC ₂ F ₁	BC ₃ F ₁	BC ₃ F ₁

(Modified from Kobayashi et al., 2007)

Telebanco-Yanoria et al. (2007) selected blast isolates from the Philippines and success the characterization of these pathogenecities using the monogenic lines. These are used for the standard differential blast isolates to identify the resistance gene in rice varieties. Telebanco-Yanoria et al. tried to clarify the diversity of resistance using 922 varieties. They were classified into six groups based on the reaction patterns to standard differential blast isolates (Telebanco-Yanoria et al. 2007) and geographical differentiations of the variety groups were found (Figure 1. in press). In the network, these diversity studies for blast pathogens and resistance of rice varieties are carrying out in the regional and global levels.

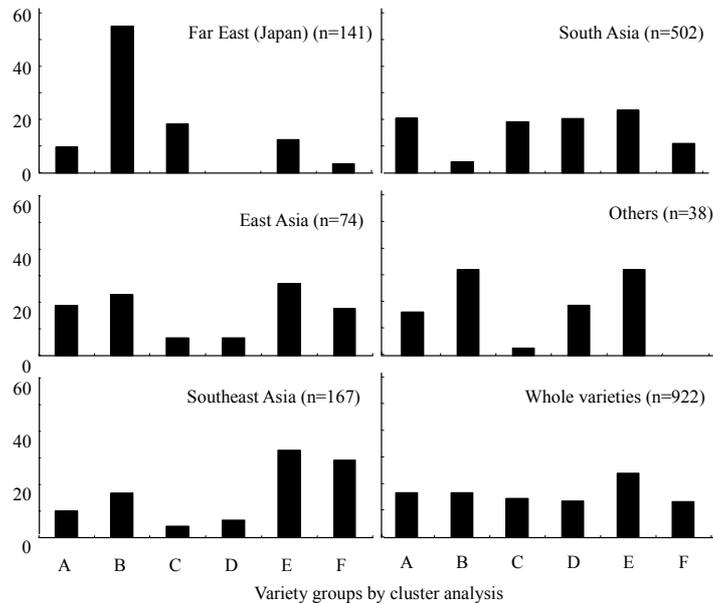


Figure 1. Diversity of blast resistance in rice varieties

A new method with systematic, expandable, and easily understandable the relationships between races and resistance genes is also proposing to built up a international standard designation and classification of blast races. Blast isolates were characterized by reactions to monogenic lines, which were divided into five groups, (1) LTH and 4 lines for *Pia*, *Pish*, *Pib*, and *Pit*, (2) 3 lines of *Pii* locus region, (3) 7 lines of *Pik* region, (4) 4 lines of *Piz* region, and (5) 7 lines of *Pita* region. Each group is consist of some units allocated with 3 differential lines and applied the codes, 1, 2, and 4, for comparative reactions of blast isolates, respectively. A blast race is characterized the sum of codes in combinations of three varieties' reactions in each unit by Gilmour method. Through the development of differential system for blast resistance, these international standard tools, differential variety sets, differential blast isolates sets, designation system of blast races, evaluation method for resistance, and information of resistance gene and marker aided breeding, will be shared under the network, and then the advance tools and methods, such as, partial resistance gene, development of multiline variety, and pyramiding used efficient resistance genes, will make possible to use for durable protection system to blast disease

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