

Co-differentiation of blast races and rice varieties in Japan

JIRCAS, through its project titled “Blast Research Network for Stable Rice Production,” has clarified the diversity of blast (*Pyricularia oryzae* Cavara) races and the genetic variation of resistance in rice (*Oryza sativa* L.) cultivars of Asia and Africa.

To develop a durable protection system against blast disease, which has caused serious damage to rice production in all rice cultivation areas of the world, the diversities of blast races and the variations of resistance in rice cultivars were examined. This is important for understanding and defining the relationships between the races and cultivars in order to provide basic information.

In Japan, we found multiple evidence of co-differentiation of blast races and rice cultivars, based on pathogenicity studies of blast isolates collected and genetic analysis for resistance of rice cultivars in each region.

The pathogenicity of 310 blast isolates was evaluated based on the reactions to 23 differential varieties, which harbor a single resistance gene in each genetic background and susceptible control, Lijiangxintuanheigu(LTH). It was then classified into three cluster groups, I, Ila and I Ib. Blast isolates in group I were mainly virulent to resistance genes of *Pik* alleles, and were distributed with higher frequencies in Hokkaido, Tohoku, Kanto and Hokuriku, compared with the other regions. Those in group Ila did not show virulence to *Pik* alleles' genes, and were distributed in all regions of Japan. Those in group I Ib were not virulent against *Pik* alleles' genes and *Pii*, *Pi3* and *Pi5(t)*, and the distributions were limited to Hokuriku, Tokai, Chugoku/Shikoku and Kyushu.

A total of 350 rice accessions were classified into four cluster groups, A1, A2, B1 and B2, based on the resistance reactions to blast isolates from Japan and the Philippines. A1 was the most susceptible among the four groups, and included differential varieties and LTH only. The most resistant group was B2 followed by B1 and A2. Many accessions of group B1 were expected to harbor the *Pik* alleles' genes in the genetic backgrounds, and these were cultivated with higher frequencies in Hokkaido and Tohoku than in other regions. The highest resistance group B2 was found with high frequency in Kanto region.

Blast races and resistance of rice accessions varied in each region of Japan, and the differentiations of blast races corresponded with the variations of rice varieties in each region. In particular, the relationships between virulent blast races for *Pik* alleles' genes and rice accessions with *Pik* alleles' genes were found in Hokkaido and Tohoku regions. These results indicated that blast races were differentiated on the basis of resistance genes in rice varieties.

(Y. Fukuta, S. Yanagihara, N. Hayashi [National Institute of Agrobiological Sciences], A. Kawasaki-Tanaka [Tottori University])

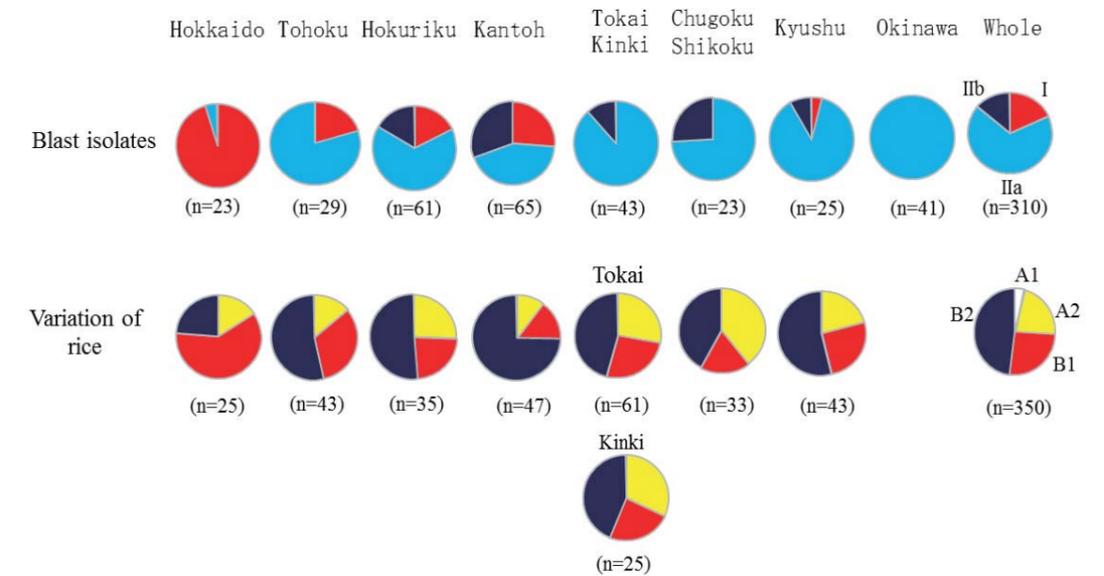


Fig. 1. Genetic variation of blast races and resistance in rice cultivars in each region of Japan. Virulent blast isolates for resistance genes of *Pik* alleles, which were classified into cluster group I (red color), were dominant in Hokkaido and Tohoku regions. These *Pik* alleles' genes were included mainly in the rice cultivar's group blast isolates (B1), and higher frequencies were shown in Hokkaido and Tohoku compared with the other regions. These data on blast races and rice accessions were modified from Kawasaki-Tanaka et al. (2016, Plant Disease 100: 816-823) and Kawasaki-Tanaka and Fukuta (2014, Breeding Science 64: 183–192), respectively.