The 3rd YAU-JICA TCP Special Lecture

Speaker: Hideshi Yasui
(Professor, Faculty of Agriculture, Graduate School, Kyusyu University)
Date and Time: 14:00 Saturday, 30 April, 2016
Venue: JICATCP Meeting Room, ELB-1, YAU

Genetic studies on planthopper resistance in rice and their application to plant breeding and plant protection

Hideshi Yasui
Faculty of Agriculture, Graduate School, Kyushu University, 6-10-1, Hakozaki, Higashi, Fukuoka 812-8581, Japan

Abstract

The planthopper species are serious insect pests in rice paddy in Asia. The brown planthopper, *Nilaparvata lugens* and the whitebacked planthopper, *Sogatella furcifera* are the most serious insect pests in both tropical and temperate Asia. Several major genes and quantitative trait loci associated with resistance to rice planthopper species have been identified. Here, we present (1) the identification of the genes conferring resistance to planthopper species, (2) development of rice near-isogenic lines carrying resistance genes through marker-assisted selection, and (3) gene pyramiding for several insect-resistance genes. The resistance genes were identified using resistant accessions of cultivated and wild relatives of rice. These resistance genes were transferred to a *japonica* genetic background of Taichung 65 through marker-assisted selection. Resulting near-isogenic lines were crossed each other to give rise to the pyramided lines carrying insect-resistance genes. This strategy for gene pyramiding must be useful in rice improvement to develop the lines with broad-spectrum and durable resistance in rice.

The durability is one of the most important features in the deployment of host-plant resistance. The virulence of the brown planthopper to near-isogenic and pyramided lines carrying the brown planthopper-resistance genes has been monitored against several Asian populations of the brown planthopper. Accumulated knowledge of this monitoring brown planthopper in the past half century will be discussed for future plan for rice improvement and rice protection. In addition, incorporating favorable alleles with elite genetic background through marker-assisted selections was discussed.

Finally, I will give a talk a little about the 2016-2022-year plan of the proposed project. The outcome of this program will be leveraged to create an international agribio education and research network and platform for Japan and ASEAN countries.