**432**

Paper presented at the International Rice Congress 2023 from October 16-19 in Manila, Philippines.

# Genetic analysis for brown planthopper resistance from African rice (Oryza glaberrima and Oryza barthii)

Kaiki Baba1 , Yoshiyuki Yamagata2 , Hideshi Yasui2 , Shao-Hui Zheng 1 , Daisuke Fujita1

*1 Grad.Sch.Agr., Saga Univ., Saga, Japan. 2 Grad.Sch.Agr., Kyushu Univ., Fukuoka, Japan*

The brown planthopper (BPH: Brown planthopper, Nilaparvata lugens Stål) is one of a major insect pest of rice (Oryza sativa L.) in the tropics and temperate areas. BPH resistant varieties have been used for controlling BPH and more than 40 BPH resistance genes have been identified from cultivated and wild rice distributed in Asia. Although some African rice accessions are known to have BPH resistance, however, few genetic studies have been conducted on BPH resistance. In this study, to estimate BPH resistance genes from cultivated rice O. glaberrima (IRGC103777) and wild rice O. barthii (W747) in Africa, we analyzed BPH resistance using chromosome segment substitution lines (CSSLs) and QTL analysis. The CSSLs, OGIL1-28 (BC■F■) derived from IRGC103777 with a genetic background of the susceptible variety Taichung 65 (T65), were used for resistance tests (Yamagata et al. 2019) In addition, to detect QTL for BPH resistance from IRGC103777, F■ population derived from a cross between OGIL17 and T65 was used for QTL analysis. To evaluate BPH resistance, modified seed box screening test (MSST), antibiosis, antixenosis and tolerance tests were conducted. To analyze BPH resistance on O. barthii (W747), backcrossed lines (BC■F■) derived from W747 with a genetic background of T65 has been developed and were used for analysis. The QTLs for BPH resistance were detected using Windows QTL Cartographer and R-qtl, based on a 5% level threshold. Among OGILs, only OGIL17 showed BPH resistance by MSST. Based on three different tests for characterizing resistance mechanism, IRGC103777 had antibiosis and tolerance and OGIL17 had only antibiosis. Using the F■ population derived from a cross between OGIL17 and T65, a QTL was detected on the short arm of chromosome 6. To identify QTL for BPH resistance from W747, the backcrossed lines were analyzed and a QTL was detected on the short arm of chromosome 6. The QTLs detected from O. glaberrima and O. barthii were located in the same region on chromosome 6. These results will contribute to the reduction of BPH damage by breeding lines through pyramiding with other BPH resistance genes in the future.

*© By the International Rice Research Institute (IRRI) and is licensed for use under Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International (CC BY-NC-SA 4.0)*