

**Study on the defense genes related to whitebacked planthopper and brown planthopper in rice (*Oryza sativa* L.)**Yoon Hee Jang<sup>1</sup>, Sopheap Yun<sup>1</sup>, Hak Yoon Kim<sup>2</sup>, Kyung-MinKim<sup>1\*</sup><sup>1</sup>School of Applied Biosciences, College of Agriculture & Life Science, Kyungpook National University, Daegu, 41566, Korea<sup>2</sup>Department of Global Environment, Keimyung University, Daegu, 42601, Korea**[Introduction]**

Resistance rice used through a number molecular mechanisms and biochemical to counter offset the pest attack. The whitebacked planthopper (WBPH) *Sogatella furcifera* Horváth and brown planthopper (BPH) *Nilaparvata lugens* Stál are the most serious and damage in rice (*Oryza sativa* L.). The governed through one dominant and one recessive gene which segregate independently of each different revealed that a single dominant gene governs resistance (Nair et al., 1982). The recessive genes in cluster C on chromosome 6 which might confer resistance to both BPH and WBPH (Ramesh et al., 2014). The whitebacked planthopper (WBPH) is the most devastating rice pests (An et al., 2015). In this study, we identify the QTLs association resistance varieties to defense WBPH and BPH. To evaluated the genes resistance related WBPH and BPH. Developed evidence natural product for rice protection.

**[Materials and Methods]**

Resistance rice used through a number molecular mechanisms and biochemical, to counter offset the pest attack. The whitebacked planthopper (WBPH) *Sogatella furcifera* Horváth and the brown planthopper (BPH) *Nilaparvata lugens* Stál are the most serious and damage in rice (*Oryza sativa* L.) Four selection varieties of ‘Cheonghcheong/Nagdong’ doubled haploid (CNDH) populations, Samgangbyeo/Nagdongbyeo doubled haploid (SNDH) with resistance Drimi 3 and susceptible TN1. In the present study, C-7, C-9 was sprayed and infested WBPH, BPH with rice.

**[Results and Discussions]**

QTLs analysis identified the resistance rice on the regions in map base genetic. Reverse transcription PCR (RT-PCR) and quantitative real time PCR (qPCR), the amplification of the OsF3H1, OsCM, OsWRKY45 and OsNPR1 the defense genes related resistance with WBPH and BPH, were used. The results showed that, WBPH doesn't like C-7 and C-9 of rice. QTLs were detected on chromosomes 4, 7, 8, and chromosome 12. The QTLs detected with qWBPH4, qWBPH7, qWBPH8-1, qWBPH8-2, and qWBPH12. QTLs evaluated association with RM280-RM6990, RM248-RM1134, RM23230-RM3689, RM17699-RM264, and RM1226-RM12. The RT-PCR was determined resistance rice and C-7, C-9 useful for rice resistance. The results, the level evaluation relative genes expression was low expression in resistance Drimi 3 and sprayed C-7, C-9. Further, qPCR were amplified 4 genes OsF3H1, OsCM, OsWRKY45 and OsNPR1. The results, genes expression relative of resistance plant was low expression in control plant and low expression when we were prayed C-7, C-9 in susceptible plant. The rice susceptible and infested WBPH or BPH were high expression. Moreover, the accumulation is relative expression for compare the accurate of susceptible rice and sprayed C-7, C-9 during 1 day, 2 days, and 3 days. In addition, susceptible rice cans growth better after sprayed C-7 and C-9 as the natural product. These consequences point out that genes defense association to rice resistance with WBPH and BPH.

**[Acknowledgements]**

This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ013647032018), Rural Development Administration, Republic of Korea.

\*Corresponding author: Tel. +82-53-950-5711, E-mail. kkm@knu.ac.kr