（学位第３号様式）

学 位 論 文 要 旨

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題　目	Genetic and breeding studies for brown planthopper (*Nilaparvata lugens* Stål) resistance in cultivated rice (*Oryza sativa* L. and *Oryza glaberrima* Steud.) (栽培イネ（*Oryza sativa* L.および *Oryza glaberrima* Steud.）におけるトビイロウンカ（*Nilaparvata lugens* Stål）抵抗性の遺伝・育種学的研究)

Rice (*Oryza sativa* L.) is a widely cultivated cereal crop and staple food for over half the global population. However, insect pests, particularly the brown planthopper (BPH), *Nilaparvata lugens* Stål, cause significant damage to rice in Asia, resulting in substantial yield loss. Utilization host-plant resistance is a cost-effective and eco-friendly approach for the control of BPH.

In the first study, to estimate effective combinations among eight BPH resistance genes (*BPH32*, *BPH17-ptb*, *BPH20*, *BPH17*, *BPH3*, *BPH25*, *BPH26* and *qBPH6*), eight near-isogenic lines with the genetic background of an Indica Group rice variety 'IR64' (IR64-NIL) were developed using marker-assisted selection (MAS). The genome recoveries of these NILs ranged from 89.3% to 98.8% and agronomic traits of them were similar to those of 'IR64'. In modified seed box screening test (MSST), resistance level of IR64-NILs was higher than that of 'IR64'. In antibiosis test, high adult mortalities of BPH (from 56.0% to 97.0%) were observed among NILs, in comparison with that of 'IR64'. Among IR64-NILs, the line carrying *BPH17* showed the highest resistance level at all tests against BPH population, Koshi-2013.

In the second study, to enhance BPH resistance and gauge the effectiveness of gene pyramiding against strongly virulent BPH, we developed pyramided lines (PYLs) in the genetic background of 'IR64' carrying BPH resistance genes. We developed six IR64-PYLs (*BPH3+BPH17*, *BPH32+BPH17*, *BPH32+BPH20*, *BPH3+BPH17-ptb*, *BPH20+BPH3*, and *BPH17-ptb+BPH32*) through MAS. To assess the resistance of the IR64-PYLs, we conducted antibiosis test, honeydew test, and MSST using strongly virulent BPH populations (Koshi-2013 and Koshi-2020). The level of BPH resistance increased in all six IR64-PYLs compared to both 'IR64' and the corresponding NILs in MSST. Among them, IR64-*BPH3+BPH17* and IR64-*BPH32+BPH17* exhibited the highest resistance to BPH. However, the resistance level of most IR64-PYLs was not significantly higher than that of the corresponding NILs in antibiosis test.

In the third study, to identify the resistance gene for BPH in *Oryza glaberrima* Steud., we screened *O. glaberrima* accessions and conducted QTL analysis for BPH resistance. *O. glaberrima* accessions showed a medium level of resistance in both antibiosis test and MSST against BPH at initial screening. Furthermore, QTL analysis using GILs revealed the presence of one QTL for damage score and other QTL for honeydew area on chromosome 6S. The QTL for damage score, *qBPH6*, was located between markers RM19285 and RM19288, with a PVE of 34.7%. The other QTL for the honeydew area, *qHOD6*, was located between markers RM19274 and RM19285, with a PVE of 25.2%. Through confirming substituted chromosomal segments from *O. glaberrima* in GILs, the *qBPH6* was delimited between RM3132 and RM19359 on chromosome 6 with a physical distance of approximately 1.41 Mbp. Furthermore, the lines carrying the *qBPH6* showed the antibiosis mechanism for BPH resistance.

IR64-NILs and PYLs with BPH resistance genes could be valuable breeding lines for enhancing resistance levels by gene pyramiding and multiline variety. Additionally, the *qBPH6* identified in GILs could be effectively introgressed through marker-assisted selection into the elite rice variety for durable resistance and subsequently minimizing the BPH outbreaks in Asia.