博士論文要約（Summary）

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連合農学研究科
専攻 Course： Tropical bioresource and plant resource production science
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タイトル **Title**	Genetic and breeding studies for resistance to brown planthopper (*Nilaparvata lugens* Stål) in the genetic background of japonica rice (*Oryza sativa* L.)

キーワード **Key words**: marker-assisted selection, BPH resistance genes, NILs, PYL, gene mapping

Chapter 1

"Introduction and purpose"

Rice (*Oryza sativa* L.) is the calorie source for half of the global population and one of the staple foods for people living in Asia. Rice production is drastically reduced by several insect pests, including brown planthopper (BPH) *Nilaparvata lugens* Stål (Homoptera: Delphacidae), the most destructive pest in rice. To reduce BPH damage, the utilization of host plant resistance in rice has been an effective approach. However, BPH populations have sufficient ability to overcome specific BPH resistance genes in a resistant cultivar but are durable to varieties which carried multiple BPH resistance genes. Heat tolerance commercial *japonica* rice 'Sagabiyori', with superior grain quality 'Special A' rating, and highly soluble starch in the stem, is highly susceptible to BPH. Therefore, our first study aimed to enhance the BPH resistance of 'Sagabiyori'.

"Materials and method"

We developed seven near-isogenic lines (NILs) carrying *BPH2*, *BPH17-ptb*, *BPH32*, *BPH3*, *BPH17*, *BPH20* and *BPH21* in the 'Sagabiyori' genetic background through marker-assisted selection (MAS). Then, we characterized the resistance level of NILs against two BPH populations Hadano-1966 and Koshi-2013 with different resistance tests.

"Results"

Most lines were more resistant to the Hadano-1966 BPH population than 'Sagabiyori'. However, the lines that carry *BPH2*, *BPH17-ptb*, *BPH20*, *BPH21* and *BPH32* were not effective to Koshi-2013 with high virulence. However, the resistance levels of lines carrying *BPH17* and *BPH3* (derived

from ‘Rathu Heenati’) indicated higher resistance to Koshi-2013 than ‘Sagabiyori’.

“Conclusion and Consideration”

Understanding the genetic basis and resistance mechanism remains important even for low or non-effective resistance genes. Moreover, less effective genes are also useful for pyramiding with other BPH resistance genes to enhance the resistance level. Despite the developed NILs in this study being strengthened for developing PYLs including valuable materials for breeding efforts related to BPH resistance into commercial Japanese rice varieties.

Chapter 2

“Introduction and purpose”

Monogenic resistance is vulnerable to rapid adaptation by pest populations. BPH populations have sufficient genetic variability to enable them to overcome specific resistance genes in a resistant cultivar over several generations. The development of cultivars carrying multiple BPH resistance genes might be an effective way to enhance BPH resistance. Therefore, NILs for *BPH3* (Saga-*BPH3*) and *BPH17* (Saga-*BPH17*) have been developed in the first study. However, the intervals of flanking markers for *BPH3* and *BPH17* were large, and we have limited information on markers tightly linked to *BPH3* and *BPH17* within the ‘Sagabiyori’ genetic background. The objectives of the second study are 1) to identify markers closely linked to *BPH3* and *BPH17* within the ‘Sagabiyori’ genetic background; 2) to clarify the effect of pyramiding for *BPH3* and *BPH17* and characterize the resistant level against current virulent BPH populations.

“Materials and method”

We used homozygous recombinant lines those were derived from the corresponding NILs for substitution mapping against low virulence BPH population Hadano-1966. Besides, we developed Saga-*BPH3+17* to characterize through different tests against virulence BPH populations Koshi-2013 and Koshi-2020.

“Results”

In the second study, *BPH3* was delimited between RM3132 and RM589 on chromosome 6, and

BPH17 between RM16493 and RM16531 on chromosome 4. We developed an InDel marker for *BPH3* region (BPH32 dete 1) as well as identified closely linked SSR and InDel (I534 and I729) markers for *BPH17* region within the 'Sagabiyori' genetic background. In addition, developed Saga-*BPH3+17* exhibited a higher level of resistance against Koshi-2013 and Koshi-2020.

"Conclusion and Consideration"

Therefore, the markers information and materials developed in the second study would be efficiently applicable for future BPH breeding studies on commercial Japanese rice varieties.

Chapter 3

"Introduction and purpose"

Currently, researchers have identified and mapped at least 45 loci for BPH resistance, designated as *BPH1* to *BPH45*, distributed across all 12 chromosomes of rice. However, the known BPH resistance genes remain effective against BPH populations with lower virulence (biotype 1), many genes have been overcome by specific BPH populations. Hence, it remains crucial to identify new BPH resistance loci and evaluate their resistance mechanisms. Therefore, the objective of the third study is to identify BPH resistance locus from 'Rathu Heenati' other than *BPH3* and *BPH17*.

"Materials and method"

The populations derived from a cross between T65 and 'Rathu Heenati'. Initially, the resistance lines that did not carry both of *BPH3* and *BPH17* were utilized for QTL analysis. For characterization, we used the Hadano-1966 through different resistance tests.

"Results"

Through QTL analysis, we detected *qBPH3.1* on chromosome 3. The *qBPH3.1* conferred resistance at the early seedling stage and contributed to the strong resistance of 'Rathu Heenati'.

"Conclusion and Consideration"

Therefore, the durable resistance of traditional cultivars 'Rathu Heenati' was controlled by at least three different genes and mechanisms. Additionally, the development of a durable resistance variety by introducing three resistance genes would contribute to reducing BPH damage in Japan.