

Genomic study on resistance to green rice leafhopper (*Nephotettix cincticeps* Uhler) of rice landraces (*Oryza sativa* L.) in Myanmar

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(ミャンマーにおけるイネ在来品種 (*Oryza sativa* L.) のツマグロヨコバイ (*Nephotettix cincticeps* Uhler) 抵抗性に関するゲノム科学的研究)

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Thesis Summary

Green rice leafhopper (GRH, *Nephotettix cincticeps* Uhler) is a serious insect pest of rice in the temperate regions of Asia. Utilization of host plant resistance is one of the most effective strategy to mitigate insect pest infestation. The resistance of varieties carrying single resistance gene is easy to break down due to evolution of new biotypes. Therefore, it is still need to explore new resistance genes and integrate them into the rice cultivars to combat the virulent GRH populations. The rice landraces in Myanmar is one of the precious genetic reservoir for rice improvement for the agronomically important genes such as abiotic and biotic stress resistance. The objective of this thesis is to study the genetic basis of conferring resistance to GRH in landraces of Myanmar rice.

First of all, 224 rice accessions of Myanmar landraces were evaluated for GRH resistance at the seedling stage in Chapter I. A total of 188 accessions were moderate to high resistance to GRH. Based on the phenotypic data for nymph mortality of GRH, GWAS was conducted to identify the genomic regions associated with GRH resistance. GWAS identified three maker-trait associations (MTAs) including MTA4, MTA5 and MTA11 on chromosome 4, 5 and 11 respectively. Among them, MTA4 adjacent to *GRH6* and MTA5 adjacent to *GRH1* explained in major part GRH resistance in Myanmar landraces. In addition, MTA11 that will be likely a novel QTL conferring resistance to GRH was observed.

In Chapter II, analysis of haplotypes revealed that the genomic haplotypes HapMTA4A, Hap*GRH6A*, Hap*GRH1A*, and HapMTA11A mainly explained GRH resistance. Combination of haplotype analysis revealed that 47 accessions with one or more resistant haplotypes at major reported genes (Hap*GRH6A* and Hap*GRH1A*) explained high resistance to GRH, 32 accessions with the resistance haplotype only at MTA11 (HapMTA11A) showed moderate to high resistance. There were several resistance accessions without carrying resistance haplotypes at any detected locus speculating that the resistance of these accessions may derived from unknown QTL and they are the candidate donors for identifying novel QTLs conferring resistance to GRH. The distribution of resistance haplotypes revealed that accessions harboring resistance haplotypes at major known genes (HapMTA4A, Hap*GRH6A*, and Hap*GRH1A*) were mainly distributed in Southern Myanmar, and MTA11 was mainly responsible for GRH resistance in the landraces in mountainous areas.

In Chapter III, to validate the QTLs detected in GWAS, QTL analysis was conducted in F₂ populations derived from the cross between T65 or IR24 and resistance Myanmar accessions. The donor parents were selected as representatives of each haplotype. The *qGRH11* was validated from the donors carrying resistance haplotype at MTA11 and it was located 2.3 Mbp far from *GRH2* at the MTA11 region speculating that *qGRH11* was likely a novel QTL conferring resistance to GRH.

In Chapter IV, I conducted gene cloning of *GRH6*, that is a major factor of GRH resistance of landraces in Myanmar, using the *O. nivara* accession WK56 as donor to identify the causal locus of *GRH6*

and characterize it. Complementation test revealed WK56 allele at the GRH6 region correspond to GRH resistance and designated as *GRH6-WK56*. Expression analysis explained *GRH6-WK56* was highly induced by GRH infestation and conferred resistance to GRH by inhibiting the sucking of phloem sap.

The present study identified the genetic factors affecting resistance to GRH in landraces in Myanmar by GWAS and revealed those two major genes previously identified and one novel QTL conferred resistance to GRH. The accessions carrying resistance haplotypes at the detected loci were estimated by haplotype analysis. The haplotype information of donor parents facilitated in validation of QTL using bi-parental population. Finally, map-based cloning of *GRH6* identified the causal locus of *GRH6*. Our findings would facilitate the elucidation of the molecular mechanism of GRH resistance and provide essential haplotype-based genetic information for the development of GRH-resistant rice cultivars.