Genetic studies of resistance to green rice leafhopper (Nephotettix cincticeps Uhler) in the relative species of rice (Oryza sativa L.)

ニン, ワー, テイン

氏　　名　：ニン　ワー　テイン

論文題名　：Genetic studies of resistance to green rice leafhopper (Nephotettix cincticeps Uhler) in the relative species of rice (Oryza sativa L.)（イネの近縁種が保有するツマグロヨコバイ抵抗性に関する遺伝学的研究）

区　　分　：甲

論　文　内　容　の　要　旨

In the present study, genetic studies conducted to elucidate the genetic basis of resistance to green rice leafhopper in two relative species of rice; *O. longistaminata* (wild type) and *O. glaberrima* (cultivated from).

In chapter I, a total of 65 *O. longistaminata* accessions evaluated the GRH resistance using the ratoon leaves to identify the resistance responses of *O. longistaminata* accessions. Evaluation of 65 *O. longistaminata* accessions showed the unique pattern of high resistance to the GRH except 5 accessions evaluated as susceptible. These evaluation results provide the new germplasm sources for insect resistance (especially planthoppers). For population development, *O. sativa* cultivar “Nipponbare” (susceptible to the GRH) and *O. longistaminata* accession W1413 (resistance to the GRH) was crossed and developed 28 BC_3F_3 ILs to analyze the GRH resistance. After screening of 28 ILs, four ILs showed the range of nymph mortality from moderate to high resistance to the GRH while other 24 ILs evaluated as susceptible to the GRH.

From the evaluation of ILs in chapter I, four ILs resulted out as the candidate ILs to do the genetic mapping. Among them, three ILs have enough seeds for QTL analysis. Therefore, three candidate ILs and three sister plants of these ILs used for QTL detection in chapter II. Three significant QTLs on the short arm of chromosome 4 (*qGRH4*), the long arm of chromosome 5 (*qGRH5*) and the long arm of chromosome 11 (*qGRH11*) detected in five BC_3F_3 populations and the effects of these QTLs come from the W1413 parent. Moreover, these three QTLs and another novel QTL on the long arm of chromosome 2, *qGRH2* were validated using the seven BC_3F_4 populations. Total of four alleles successfully identified from *O. longistaminata* for GRH resistance. The correspondence of chromosomal position of *qGRH4*, *qGRH5* and *qGRH11* was similar with those of the previously reported genes; *Grh6*, *Grh1* and *Grh2*, respectively. In addition, four NILs carried each QTL, three PYLs carried two QTLs and one PYL carried four QTLs were selected from the BC_3F_3 mapping populations and assessed for GRH resistance. The resistance level of PYL carried four QTLs was similar to the original parent, W1413. Thus, resistance of *O. longistaminata* to GRH can be explained by at least four QTLs.

In chapter III, a total of 140 *O. glaberrima* accessions sources from IRRI were regarded as resistant to the GRH by antibiosis test at the seedling stage. Total of 135 *O. glaberrima* accessions showed high nymph mortality and resistant to the GRH. Other five accessions did not show completely susceptible to the GRH (NM range between 20-40%). Based on this evaluation, it can conclude that all African *O. glaberrima* accessions (sourced from IRRI) showed a unique resistance source to the GRH. To understand the genetic basis of GRH resistance from *O. glaberrima*, BC_1F_1 population derived from a cross between *O. glaberrima* accession, IRGC103777 (resistant to the GRH) and *O. sativa* T65 (susceptible to the GRH) in IRGC103777

background analyzed for GRH resistance and five significant QTLs were detected in recent study. To validate one significant QTL on the long arm of chromosome 9, *qGRH9* confirmed in the four BC_3F_4 populations. Another new significant QTL was detected on chromosome 2, *qGRH2* in BC_3F_4 population and validated in BC_3F_5 population. However, the *qGRH2* effect observed and detected when *qGRH9* region carried heterozygous and homozygous of T65 alleles. *qGRH9* candidate region narrowed down between RM6707 and RM6797 (1.7 cM interval) and tightly linked with RM24827 that is between the RM6707 and RM6797. In addition, two sets of ILs with two genetic backgrounds derived from the bi-parental crosses between *O. sativa* cultivar T65 and *O. glaberrima* acc. IRGC103777 used to confirm the GRH resistance. All ILs in IRGC103777 showed high resistance to the GRH except two ILs (IL 7 and IL 8) that carried T65 homozygous segments in the *qGRH9* candidate region. In contrast, GRH resistance from the set of ILs in T65 genetic background illustrated very low nymph mortality so there was no resistance to the GRH in this set of ILs. The evaluation of two sets of ILs confirmed that GRH resistance derived from *O. glaberrima* was not completed with one major QTL, *qGRH9* effect; other additional QTL (*qGRH2*) supported to this resistance. Moreover, the genetic interaction of additive by additive (AA) observed between the *qGRH2* and *qGRH9*. The effect of *qGRH9* mask the effect of *qGRH2* and observed the digenic interaction at 1% significant level (P=0.0310) at two way ANOVA using the R statistics. AA interaction was calculated by orthogonal contrast of R statistics and significant at 0.01 level (P=0.0021), but other interactions of AD, DA, and DD was not significant.

This dissertation thesis described the genetic basis of GRH resistance derived from the two relative species of rice; *O. longistaminata* and *O. glaberrima*. Based on the results of chapter II and III, the genetic basis of these species was controlled by two or more QTLs for GRH resistance.