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学位論文要旨
Dissertation Abstract

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学位論文題目： Studies on rice genes involved in RNA silencing: defence against pathogens including viruses
Title of Dissertation

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RNA-dependent RNA polymerases (RDRs) and suppressor of gene silencing 3 (SGS3) play key roles in gene silencing in plants. I investigated rice homologs of the genes *OsRDR1* and *OsSGS3*b to analyze any roles of the genes in rice to viral, bacterial and fungal pathogens. Rice mutant lines produced by the insertion of retrotransposon Tos17 or a mutagen were used. The double mutant of two genes (*OsRDR1/OsSGS3b*) was produced by crossing. I also produced the overexpressed lines of *OsRDR1* and *OsSGS3*b. These lines were inoculated with *Cucumber mosaic virus* (CMV), *Rice necrosis mosaic virus* (RNMV), *Xanthomonas oryzae pv. oryzae* and *Magnaporthe oryzae*, respectively. Among these lines, the double mutant line showed the highest susceptibility to all pathogens tested. Single mutant lines were more susceptible than the wild type. Microarray analysis of the mutant lines showed down-regulation of defense related and signaling pathway related genes. These results suggest that *OsRDR1* and *OsSGS3*b have a positive defense role against viral, bacterial and fungal pathogens, implicating RNA silencing as a defense against not only viruses but also bacterial and fungal pathogens. RNA-dependent RNA polymerases (RDRs) play key roles in gene silencing. I analyzed the rice RDR6 gene in response to viral, bacterial and fungal pathogens. A rice mutant line of *OsRDR6/ROL* was inoculated with CMV, RNMV, *X. oryzae pv. oryzae* and *M. oryzae*, respectively. Compared with wild type (WT), the mutant lines showed a higher level of viral RNA accumulation and more severe symptoms caused by bacterial and fungal pathogens. These results suggest that the *OsRDR6*-mediated RNA silencing pathway participates in defense against not only viruses, but also bacterial and fungal pathogens.

The complete nucleotide sequence of *rice necrosis mosaic virus* (RNMV) RNA1 was determined to be 7,178 nts long with one large open reading frame, potentially encoding a polyprotein of 258 kDa with the features of a typical bymovirus.The nucleotide sequence showed 56% identity to barley mild mosaic virus (BaMMV) and 46% to oat mosaic virus, barley yellow mosaic virus and

wheat yellow mosaic virus. RNA2 was 3,579 nts long, encoding 110 kDa polyprotein, and showed 42% and 35/26% identity to BaMMV and others, respectively. Phylogenetic analysis showed that bymoviruses were classified into two subgroups.