Occurrence and molecular characterization of rice viruses

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The 3 known rice viruses that occur in Korea are *rice dwarf virus*(RDV), *rice stripe virus*(RSV) and *rice black-streaked dwarf virus*(RBSDV). *Rice dwarf virus*, a member of the family *Reoviridae*, has a genome composed of 12 segmented dsRNAs designatedas S1 to S12 with an increasing order of mobility in polyacrylamide gel electrophoresis (PAGE). RDV isolate were collected from several locations in Korea, Japan, China, Philippines and Nepal. Genomic dsRNA segment profiles in PAGE differed among the isolates. This was the case even among isolates from the same region. The full-length S12 of Korean isolates was cloned and sequenced. It is 1,066 nucleotide long, with the longest open reading frame starting at nucleotide 42 and terminating at nucleotide 978. Nucleotide sequence identities were 94 to 99% with those of another isolates. Three open reading frames previously reported were present in RDV-Kor isolate, and the sequence identities were 83 to 98% for P12, 89 to 98% for P12OPa. In order to locate P12, ultrathin sections of RDV-infected rice plant were labelled by the anti-P12 polyclonal antibody and the protein A-gold complex. When thin sections from infected tissues were treated with a preimmune serum, nonspecific gold labelling was not observed, nor did labelling occurred in the absence of the primary antiserum from the standard incubation procedure. Gold particles were observed with P12 throughout the cytoplasm of infected leaves, although labelling was not uniform. Densely labelled areas frequently occurred in patches in the cytoplasm where slightly electron-dense. Sections from healthy tissues exhibited no significant labelling. Immunocytochemical studies showed P12 accumulated in the cytoplasm of infected cells.

Rice stripe virus, which causes severe damage to rice in Korea, Japan and China, is a type member of the *tenuivirus* group and is transmitted by the small brown planthopper, *Laodelphax striatellus*, in a persistant manner. Until now, occurrence of RSV is limitted insouthern part of Korea. However recently the occurrence of RSV is increasing and spreading in central part of Korea including chungcheongdo and kyonggido province. It is very difficult to distinguish RSV symptoms on virus symptom from physiological damage of rice. The symptoms induced of infected plants includegeneral leaf striping, yellowing, a distinct white coloring of the leaf stripes. We detected RSV viral RNA using reverse transcripion(RT)-PCR. The result of RT-PCR, we

observed specfic band including RSV-polymerase (1,023bp) and CP(968 bp) in both host of rice and insect vector.

Rice black-streaked dwarf virus, a member of the genus *Fijivirus* within the family *Reoviridae*, is propagatively transmitted to rice, maize, barley and wheat in a persistent manner by the planthopper *Laodelphax striatellus*. The genome composed of 10 segmented dsRNAs designated as S1 to S10 with an increasing order of mobility in polyacrylamide gel electrophoresis (PAGE). The first major incidence of RBSDV was high in 1975~1976 in Korea. Except for these periods of high incidence, the occurrence of RBSDV was local, and the incidence was generally low. Until now, occurrence of RBSDV is limitted in Kyeongsang provinces in Korea. However recently the occurrence of RBSDV is increasing and spreading in Jeonra provinces including Gochang-gun. We isolated RBSDV from rice fields and analysed their genomic dsRNAs by using PAGE. The genomic dsRNA patterns were 10 segments in PAGE. we extracted dsRNA from infected leaves and detected RBSDV by reverse transcription(RT)-PCR using specific primer of S10. The result of RT-PCR, we observed specific band including of S10 RBSDV. In 2004, occurrence of RBSDV increased in rice including Gochang-gun of southwestern part. However, this year, the occurrence of RBSDV is increasing and spreading in maize in the same locations. We extracted viral genomic dsRNA from infected maize leaves and analyzed dsRNA pattern by polyacrylamide gel(PAGE). Also we detected RBSDV by reverse transcription (RT)-PCR using specific primer of S7, S8, S10 from genomic dsRNA. The genomic dsRNA patterns were 10 segments in PAGE. The result of RT-PCR, we observed specific band of RBSDV S7. S8, S10.