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Since the demonstration that the transgenic plants expressing tobacco mosaic virus(TMV) coat protein(CP) gene showed resistance to TMV infection, there have been numerous attempts to produce virus-resistant plant by introducing of a part of or modified viral genome. This study was conducted to investigate the characterization and variability of disease outbreak of transgenic potato(T-potato) with the CP gene of potato leaf roll virus(PLRV) in an isolated field from 2000 to 2002. In the field inspection, incidence of PLRV on T-potato showed only 3.5%, while non-transgenic potato(N-potato) revealed 13.4%. Infection rate of PLRV was considerably low on T-potato with 4.2% compared to 15.4% of N-potato in ELISA tests. Those of potato virus M, potato virus Y and potato virus X on both potatoes were not statistically different. Infection of potato virus A was not observed on both potatoes. Incidence of potato late blight caused by *Phytophthora infestans* on T-potato and N-potato did not differ each other with 52.7%, and 50.8%, respectively. Mating type of the causal fungus isolated from both potatoes was all A1 types. Results indicates that the CP gene of PLRV affects specifically to the virus in the transgenic potato.

3-23. Molecular pathological interactions between Apple stem grooving virus (ASGV) and its fungi.

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Apple stem grooving virus (ASGV) belongs to *Capillovirus* and infects pome fruits. Transmission mode of ASGV is known by grafting and mechanical inoculation into susceptible hosts, not by any other natural vectors. But we have observed the spread of ASGV in the field without mechanical inoculation or grafting. Transmission seems to be occurred from tree-to-tree and tree-to-susceptible herbaceous plants along but not across ditches in the field. In order to ascertain this possibility, various fungi were isolated and cultured from ASGV-infected plants and 69 isolates were characterized. By means of RNA dot-blot hybridization and PCR analysis, 3 isolates were sorted out for further studies. The isolates were identified to *Talaromyces sp.* and belonged to *Phenicillium* by morphological characteristics and molecular markers. As an experimental host, 10 kidney beans (*Phaseolus vulgaris*) were screened and Kyunggi-5 was selected for virus amplification and symptom development. Kyunggi-5 infected by fungi which seemed to carry ASGV showed the typical disease symptoms and viral coat protein genes were detected from

all tested plants. To confirm the Koch's rule, fungi cultured from inoculation origins of kidney bean were grown on PDA media and re-inoculated to hosts. The fungi isolated from inoculation origins induced the typical disease symptoms on hosts. However virus free fungi did not induce any sympom on the experimental hosts. This bioassay showed that these typical symptoms were caused by virus, not fungi.

3-24. Comparison of viral population of pathologically and geographically different areas of Southern provinces and Jeju, Korea

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The objective of this work was to analyze the population of sequence variants of *citrus tristeza virus* (CTV) isolates in Korea and to make the phylogeny trees of CTV in Korea. We also tried to analyze and find the mild strain of CTV to apply for the cross protection. The CTV isolates from yuzu (C. Junos) collected from different geographic areas of Southern provinces such as Namhae-Do, Kerche-Do, Bosung, Wan-Do and Koheung and Jeju-Do, Korea were used for SSCP analysis. The SSCP profiles of the cDNAs obtained by RT-PCR with primers specifically designed for the p20 of the CTV population. The SSCP profiles obtained from 150 PCR products in yuzu contained two or three DNA bands, whereas, in some case, others contained four or more bands of similar intensity. The pathologically mild isolates of CTV usually yielded two DNA bands by SSCP profiles, whereas the SSCP profiles of the most virulent isolates contained more than two DNA bands. Plants shown severe stem pitting were corresponded to those plants with typical SSCP profiles of severe strains, and vice versa. This results indicate that the primers designed for SSCP analysis can be used for distinguishing the mild strains from severe strains of CTV.

3-25. Genetic diversity of *Fusarium graminearum* from rice in Korea

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Fusarium graminearum (telomorph: *Gibberella zeae*), an important fungal pathogen of cereal crops with ubiquitous geographic distribution, produces mycotoxins on diseased crops that has threaten human and animal health. Recently severe epidemics of scab diseases of barley and rice by this fungus occurred in Korea, causing serious economic losses. To determine genetic diversity of *F. graminearum* from rice in Korea, a total of 269 isolates were obtained from Southern part of Korea during 2001-2002. A phylogenetic tree of the isolates was constructed by using amplified fragment length polymorphism (AFLP). Population structure of the rice isolates consists of a single lineage (lineage 6). Frequency of female fertility among these isolates was relatively low (37%) compared to that among lineage 7 isolates from Korean corn. PCR amplification using chemotype specific primers