

rice quality are undergoing.

3-18. New method for sclerotial isolation of *Sclerotium* spp. from infested soil

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White rot on *Allium* species recently had a high incidence as increased cultivating areas of tropical garlic types in Korea. Two types of *Sclerotium* have been known as causal agents producing different size and shapes of sclerotia in infested fields. We developed a new method for isolation of two types of sclerotia from infested field soils that can be used for ecological study of *sclerotium* spp. and establishment of control strategy. Soil samples collected from heavily infested fields were evenly mixed and placed on a automatic sieve shaker connected with tap water. After 10 min. of shaking, residues on 0.5mm and 0.25mm sieve were separately collected and suspended with 70% sugar solution, which method floats sclerotia in aqueous layer. Then, floated fraction was carefully separated and mixed with a same volume of 1% sodium hypochlorite solution to differentiate with organic materials. This method provides direct count of sclerotia under dissecting microscopy.

3-19. Pathogenic and Molecular Characteristics of *Agrobacterium vitis* strains isolated from Grapevine in Korea

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Agrobacterium vitis is a causal agent of crown-gall disease on grapevine. In Korea, grapevine variety (GeoBong) have severely been infected by the bacteria since stems of the variety were buried in soil for overwintering. Infection ratio over 70-80% was observed on 7 years old GeoBong grapevine in Ansung and Cheonan. PCR specific primers for *A. vitis* strains were designed using nucleotide sequences of *vir A* gene in Ti-Plasmid, *pheA* gene in chromosomal DNA and a URP-PCR polymorphic band. Three hundred bacterial strains were isolated from the different 80 galls formed on GeoBong grapevine in Cheonan and Ansung of Korea and were screened to identify *A. vitis* using the three specific PCR primers for *Agrobacterium vitis*. Twenty-four bacterial strains that are detected by the primers were further confirmed by pathogenicity and biochemical methods. To investigate the genomic diversity of the bacterial strains, twenty primers of 20 mer referred to universal rice primers (URP) were applied for PCR fingerprinting. Of them, URP2R and URP2F primers could effectively be used to detect polymorphism within the bacterial strains.

3-20. Characterization of the host reaction of some citrus plants with *Xanthomonas*

***axonopodis* pv. *citri*, causing citrus bacterial canker disease.**

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Relative degree of resistance of citrus to *Xanthomonas axonopodis* pv. *citri*, the causal bacterium of canker, was investigated. Growth rate of a bacterium in leaf tissues after infiltration, disease incidence, and percent of lesion area were compared. By using growth rate $[(GR=(A_t - A_{t-1})/A_{t-1})]$ host plants were differentiated into susceptible and resistant. Growth rates reached to peak at 40 hrs after inoculation and then declined. The growth rate in leaf tissues of a moderately susceptible cultivar, *Citrus sinensis* var. Lane late(sweet orange), was the highest, and those of *C. unshiu* × *C. sinensis*(kiyomi), *C. junos*(yuzu), [*Citrus. unshiu* × *C. sinensis*) × *C. reticulata*(shiranuhi), and *C. unshiu*(satsuma mandarin) were similar. This result indicates that the growth rate of the bacterium in leaf tissues can be effectively used for evaluation of disease resistance for citrus plants to *X. axonopodis* pv. *citri*. The disease on sweet orange occurred earlier than relatively resistant citrus plants tested. The percent of lesion area on leaf was also higher in sweet orange than those of satsuma mandarin, shiranuhi and kiyomi, and yuzu. The disease severity was highest on sweet orange and followed by kiyomi, shiranuhi, satsuma mandarin, and yuzu.

3-21. Dispersal of *Xanthomonas axonopodis* pv. *citri*, the Causal Bacterium of Citrus Canker, on Unshiu Orange.

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Dispersal of *Xanthomonas axonopodis* pv. *citri*, causing citrus bacterial canker disease on Unshiu orange was investigated at previously infested plots at Seogwipo in Jeju island of Korea. The bacterial pathogen overwintered in lesions started to multiply at late May, and disease firstly observed one month after detection of phage from lesions. The disease gradually increased, however, it dispersed non-directionally to nearby plants from inoculum sources. Diseased plants were aggregated to form a cluster throughout the experiment. Population dynamics of phage on symptomless leaf surface and the disease severity were compared in the nursery. Increase of phage population on symptomless leaf surface preceded one month to that of the disease severity. Population of phage increased constantly from late July to October, however, the disease severity decreased from late August to late October. It was assumed that the decrease of disease severity might be due to disease-induced defoliation.

3-22. Characterization of disease outbreak pattern of transgenic potato plants with the coat protein gene of Potato leaf roll virus.