results six *Gymnosporangium* species were identified. Three species, *G. asiaticum*, *G. clavariiforme* and *G. yamadae*, were previously described in Korea, while the other three species, *G. cornutum*, *G. globosum*, and *G. japonicum* were new to Korea. Here we present the detailed morphological descriptions, distribution, host ranges and keys to species in both aecial and telial stages of each species. Some morphological characteristics related with telial formation on trees were newly identified; witches brooms for *G. asiaticum*, small galls for *G. yamadae* and telial formations on trunk for *G. japonicum*. Geographically G. *asiaticum* and *G. yamadae* distributed widely throughout Korea, while the others were collected only at the limited locations. Eight *Juniperus* species as telial hosts and fifteen Rosaceous plants as aecial hosts were confirmed to be new in Korea.

4-21. Verification of aecial host ranges of four *Gymnosporangium* species based on artificial inoculation.

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Aecial host ranges of four *Gymnosporangium* species causing cedar-apple rust diseases, *G. asiaticum*, *G. cornutum*, *G. japonicum* and *G. yamadae*, were investigated through artificial inoculation. Thirteen species of nine genera among Rosaceous plants, which have been reported as aecial hosts in Korea, were inoculated with fresh teliospores spores in early days of May of 2000 and of 2001, respectively. In the results, we re-confirmed that there was highly specific relationship between the rust species and aecial hosts and report new aecial hosts of four *Gymnosporangium* species. Teliospores of *G. cornutum* collected from *Juniperus rigida* successively produced spermogonia and aecia only on *Sorbus alnifolia*, the first report on host alteration of *G. cornutum* in Korea. Positive responses by teliospores of *G. japonicum* from *J. chinensis* of Suwon and from *J. chinensis* var. *horizontalis* of Jeju island were obtained only on *P. villosa*. *Crataegus pinnatifida* was confirmed as a new aecial host of *G. asiaticum*. Until this time, *G. yamadae* was believed to have *Malus* as the aecial host. However, teliospores of *G. yamadae* collected from *J. chinensis* var. *kaizuka* successively formed spermogonia and aecia on the leaves of *Chaenomeles lagenaria*, *C. sinensis*, *Pyrus pyrifolia* var. *culta*, *P. ussuriensis*, *Malus pumila* and *M. sileboldii*. The date for maturation of spermogonia and aecia, and symptom development varied according to the rust fungi and aecial host plants, respectively.

4-22. Rapid Identification of Potato Scab Causing *Streptomyces* spp. from Soil Using Pathogenicity Specific Primers.

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The plant-pathogenic species *S. scabies*, *S. acidiscabies*, and *S. turgidiscabies* cause the scab disease of potato and produce the phytotoxins, thaxtomins. necl, a gene conferring a necrogenic phenotype, is involved in pathogenicity and physically linked to the thaxtomin A biosynthetic genes. Identification of the pathogenic strains of *Streptomyces* from soil was performed through the polymerase chain reaction by using specific pathogenicity primer sets derived from the necl gene sequences of *Streptomyces scabies*. The DNA was extracted from soil using a bead-beating machine and modifications of the FastPrep system. The DNA was suitable for direct use in the PCR. The PCR products showed the bands of approximately 460 bp. This methods can be very usuful in identifying species responsible for scab diseases and studying on the ecology of plant-pathogenic *Streptomyces* spp.

4-23. Detection of *Xanthomonas axonopodis* pv. *citri*, the causal agent of bacterial canker on Unshiu orange fruits using bacteriophage in Korea.

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A technique for detection of *Xanthomonas axonopodis* pv. *citri*, a causal bacterium of canker on Unshiu orange fruits, was developed using bacteriophage. Procedure for the detection was designed on the basis of the previous reports that one group(CP_1) of *X. axonopodis* pv. *citri* bacteriophage and corresponding two lysotypes distributed in Korea. First, fruit surface was washed with sterile distilled water and pellet was obtained from centrifugation. The pellet was resuspended in Wakimoto's potato semi-synthetic broth medium and divided equally into two parts. One part was heated in boiling water to kill bacterial cells. Bacteriophages(CP_1) were respectively added into two parts and 0.1 ml from each part was mixed with soft agar medium. After incubation for 18 hrs at 25℃, the causal bacterium of canker was determined based on plaques formed on the medium. This procedure can be effectively used for detection of living bacterial pathogen on fruit surfaces of Unshiu orange.

4-24. Characterization of *Xanthomonas axonopodis* pv. *glycines* plasmids

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To characterize plasmids in *Xanthomonas axonopodis* pv. *glycines*, we isolated plasmids pAG1 from the strain AG1 and pXAG81 and pXAG82 from the strain 8ra, respectively, and sequenced three plasmids. The size of plasmids, pAG1, pXAG81, and pXAG82 was 15,149-base pairs (bp), 26,727-bp, and 1,496-bp, respectively. Fifteen and twenty six possible open reading frames (ORFs) were present in pAG1 and pXAG81, respectively. Only one ORF homologous to a *rep* gene of *Xylella fastidiosa* was present in pXAG82. pAG1 contained genes homologous to *avrBs3, tnpA, tnpR, repA, htrA*, three *parA* genes, *M.XmaI, R.XmaI,* and six hypothetical proteins.