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.

pXAG81 contained genes homologous to *avrBs3, tnpA, tnpR, repA, htrA,* two *parA* genes, *pemI, pemK, mobA, mobB, mobC, mobD, mobE, trwB, traF, traH, ISxac2,* and eleven hypothetical proteins. Based on DNA sequence analysis, we presume that pXAG81 is a conjugal plasmid. Interestingly, we found 0.5-kb truncated avirulence gene similar to *avrXacE3* on the right border of *avrBs3* homolgs of pAG1 and pXAG81. Two hundred twenty five isolates were analyzed to find *avrBS3* or *tra* gene homologs by Southern hybridization. The numbers of *avrBs3* homolog varied from 3 in AG1 to 8 in AG166. Two hundred seventeen isolates appeared to carry conjugative plasmids (pXAG81 type), and thirty eight isolates appeared to carry non-conjugative plamids (pAG1 type). This indicated that *avrBs3* gene homologs might be spread by conjugation in *X. axonopodis* pv. *glycines.*

### 4-25. Rapid identification of *Burkholderia glumae* from diseased seeds

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Bacterial grain rot by *Burkholderia glumae* cause severe damage in seedling and grain of rice after heading season. This seed-borne pathogen play a role as first infection agent that could be cause disease following cropping season. Until now the direct isolation of the bacteria has some trouble by interference of other bacteria existed inside seed. This study established convenient identification method as simple isolation with KB medium from seed showing symptom and using PCR identification. By this isolation method, *B. glumae* was isolated from 40 to 50% in brown rice and inner hull, however, there were saprophytic bacteria and fungi outer hull. In PCR identification with Ogf4 and Ogr3 primer to these 25 isolates, the amplified products were presented in all of the collections but not in 10 saprophytic germs. The isolation rate was constant to 3 months stored seeds. This result provide a rapid and convenient isolation and identification of *B. glumae.*

### 4-26. Phytoplasma specific primer for detection of jujube witches' broom group(16SrV) in Korea and China

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In order to diagnose and differentiate jujube witches' broom (JWB) phytoplasma rapidly, oligonucleotide primer pair, 16Sr(V) F/R, for polymerase chain reactions (PCRs) was designed on the basis of 16S rRNA sequences of JWB phytoplasma. The PCR employing phytoplasma universal primer pair P1/P7 consistently amplified DNA in all tested phytoplasma isolates. But no phytoplasma DNA was detected in healthy jujube seedlings. The nested PCR, the primer pair 16S(V) F/R, about 460 bp fragment, amplified DNA in all tested JWB and related phytoplasmas including LiWB phytoplasma of the 16S rRNA group V, but no DNA amplification was detected from other