Polymorphic DNA) in both potato and tomato isolates of *P. infestans*. Cluster analysis showed high level genetic variation in potato isolates of *P. infestans* than tomato isolates. *P. infestans* isolates were observed genetic diversity among them but not grouped among isolates related mating type and metalaxyl response. These results exhibited that *P. infestans* isolates showing genetic difference among them were distributed in Korea.

3-12. Genetic characteristics of *Phytophthora capsici* mutants induced by dimethomorph

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Phytophthora blight, caused by *P. capsici*, is very important disease of pepper. Many fungicides to control of Phytophthora blight have been developed, but most of fungicides disappeared in short periods. Nowadays dimethomorph was known as one of the most effective to control of this disease. *P. capsici* isolates from pepper fields were collected and surveyed their growth in dimethomorph amended V8 medium in order to evaluate their fungicides resistance. The fungicide resistant isolates were not founded among them. Most of the sensitive isolates were inhibited perfectly in V8 medium amended with 10ppm dimethomorph. Mutants of *P. capsici* by dimethomorph, was grown very well in 250ppm. The difference of pathogenicity, colony morphology, drug response, RT-PCR results was identified between sensitive and resistance isolates. This study should be provided a basic information about the occurrence of dimethomorph resistant isolates and genetic changes in *P. capsici* population.

3-13. Phylogenetic analysiccccccccc of the genus *Stemphylium* based on elongation factor -1 alpha and calmodulin gene squences

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The importance and diversity of the genus *Stemphylium* highlights the need for accurate identification of species. However, many *Stemphylium* isolates have been misidentified due to the use of spore size as the only identifying character. Molecular phylogenetic analyses were performed on fifty-four isolates covering 9 *Stemphylium* species collected in Korea. Phylogenetic analysis of the translation elongation factor -1 alpha (EF-1<alpha>) and the calmodulin gene sequence data showed that *Stemphylium* species were segregated into seven distinct groups, most of which correlated with species identified by morphology. Analysis of EF-1<alpha> in particular was useful for establishing well- supported relationships among the species of *Stemphylium*.

3-14. Complete genome sequence of *Fusarium hypovirus* DK21 strain and genomic diversity of dsRNA mycoviruses isolated from *Fusarium graminearum*

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We tested for the presence of double-stranded RNA (dsRNA) mycovirus in 827 *Fusarium graminearum* isolated from diseased barley and maize. dsRNA mycoviruses with various sizes were isolated. Of them, it was previously reported that dsRNA from DK21 isolate had pronounced morphological changes, including reduction in mycelial growth, increased to red pigmentation, reduced virulence and sporulation. (Chu et al., Appl. Environ. Microbiol. 2002). For better understanding of this hypovirulence associated with DK21 dsRNA virus, we determined the complete nucleotide sequence of dsRNA genome and named *Fusarium hypovirus* DK21 strain (Fhv-DK21). Genomic RNA of Fhv-DK21 was determined to be 6625 nucleotides in length excluding the poly (A) tail and contained three putative open reading frame. RNA-dependent RNA polymerase (RdRp) and helicase domain were expected in ORF A, 54 to 4709 nucleotide position. ORF B, 4752 to 5216 nucleotide position, and ORF C, 5475 to 6578 nucleotide position, were predicted to encode 16.7kDa and 41.3kDa protein respectively each. We could not detect any conserved domains from these two proteins. Phylogenetic analysis showed Fhv-DK21 was related to *Cryphonectria hypovirus* 3. Ten additional isolates were found that were infected with dsRNA mycoviruses. These mycoviruses contain 2 to 4 different segments of dsRNAs with the size range of approximately 1.7 to 10-kbp in length. The presence of dsRNAs isolates did not affect colony morphology and were transmissible through conidia and ascospore with incidence of 30~100%. These results indicate that there is genomic diversity of dsRNA mycoviruses that infect *F. graminearum* isolates and that impact of virus infection on host's morphology and virulence is determined by the interaction between dsRNAs and the fungal host, not by the mere presence of the dsRNAs

3-15. Factors affecting the occurrence of wilt of strawberry caused by *Fusarium oxysporum* f. sp. *fragariae* in Korea.

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The occurrence of Fusarium wilt in strawberry fields in Korea was assessed from 2001 to 2003. Fusarium wilt was found from June to August in nursery beds, from September to October after planting in production beds, and from January to March during harvest. The symptoms seen were root rots, discolored vascular tissue in the crown and deformation and yellowing of central leaflets. The disease occurred in up to 30% of plants in 37 of 214 fields surveyed. *Fusarium oxysporum* Schlecht. ex Fr. f. sp. *fragariae* was frequently isolated from cvs. Dochiodome, Maehyang, Redpearl, Samaberry and Akihime. Factors affecting the occurrence of Fusarium wilt were investigated; infested soils had high salt concentrations, low pH, OM, average P2O5 and exchangeable. Fusarium wilt was more frequent following conventional basal fertilization than after non-nitrogen basal fertilization and more frequent following the use of NH4-N than after NO3-N.