제3주제 : Ecology, Phylogeny, and Epidemiology(3-01～3-26)

3-01. Analysis genetic diversity of *Plasmodiophora brassicae* using RFLP and RAPD(oral)

Seung Hwan Heo, Chang Soon Jang, Hyoun Kyoung Lee, Woo Chung Lee, Se Jeong Jang and Hong Gi Kim

College of Agriculture and Life Sciences, Chungnam National University, Daejeon, 305-764, Korea

Genetic diversity of *Plasmodiophora brassicae* from major chinese cabbage cultivating areas in Korea was analyzed by using PCR-RFLP and RAPD. Single spores of *P. brassicae* isolated from galls of club root made induce lesion on chinese cabbage successfully. The PCR-RFLP and RAPD by primers PbITS, URP 3, 6 and OPA 7 revealed that single spore isolates showed various DNA polymorphisms among them unrelated geographic origins. These results indicate that *P. brassicae* population in Korea showed genetic difference among them. This study could be facilitate to identify genetic characteristics of *P. brassicae* based on DNA polymorphisms between single spore isolates and to get basic information which can be used to advanced resistance breeding against club root of chinese cabbage.

3-02. Effect of Environmental Pre-treatment on Expression of Blister Rust Resistance in *Pinus monticola (oral)*

K.S. WOO[1], Y..J. Kim[1], G.I. McDonald[2], L. Fins[3]. [1]Dept. of Forest Genetic Resources, Korea Forest Research Institute, Suwon, 441-350, Korea; [2]Rocky Mountain Research Station, USDA Forest Service, Moscow, ID 83843 USA; [3]Dept. of Forest Resources, University of Idaho, Moscow, ID 83843 USA.

Levels of blister rust infection (from *Cronartium ribicola*) varied in western white pine(*Pinus monticola* Dougl.) seedlings grown in two nurseries in northern Idaho. This observation suggested the potential importance of environmental components operating on the blister rust pathosystem. In an experiment designed to test the influence of environmental conditions at two nurseries, seedlings of a single genetic source were unintentionally held in cold storage for 6 months longer at one nursery than at the other. Subsequently, these seedlings, which had been growing under nursery conditions for 7 months or 1 month, were inoculated with blister rust spores on September 9th, 1999. Infection efficiency measured on the seedlings with only 1 month of growth was 70X greater than on the seedlings that had 7 months for their new growth to mature. Results from this nursery test and infection levels of northern Idaho resistant selections in mild climates suggest that expression of genes related to rust resistance in western white pine can be manipulated by regulation of phenology. If so, several new molecular tools may be employed to enhance our understanding of environmental regulation of genes for blister rust resistance.

3-03. Morphology, Pathogenicity and Molecular analysis of *Alternaria* Isolates from Solanaceous Crops (oral)

H.S. CHO, M.S. Park, B.R. Kim and S.H. Yu Division of Applied Biology, Chemistry and Food Science, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 305-764, Korea

More than 30 isolates of *Alternaria* were obtained from various solanaceous crops in Korea. For all isolates, morphological characteristics of the conidia were determined and compared with those of representative isolates of *A. solani* and *A. tomatophila*. Pathogenicity test was performed to potato, tomato, egg plant and red pepper and molecular characteristics of them including the representative isolates were determined using sequence analyses of ITS rDNA and histone H3 gene, and URP-PCR analysis. Based on morphological characteristics, the isolates from the solanaceous crops were grouped as identical or very similar to either *A. tomatophila*(ATO), *A. solani*(ASO), and unidentified *Alternaria* sp.(ASP). Among the molecular markers used in this study, the URP-PCR analysis was found to be appropriate for taxonomic resolution of these species. Based on the conidial morphology, pathogenicity test and molecular characteristics, *A. tomatophila*(early blight of tomato) could be distinguished from *A. solani*(early blight of potato), and the *Alternaria* sp.(ASP) from potato, which was closely related to *A. solani* in conidial morphology, was considered as a new species.

3-04. Complete genome sequence analysis *Hosta virus X* and comparison to other potexviruses

M.H. Park, and K.H. Ryu
Plant Virus GenBank, PVGABC, College of Natural Science, Seoul Women's University, Seoul 139-774, Korea

A potexvirus, *Hosta virus X* (HVX-Kr), causing mosaic and mottle symptoms was isolated from hosta plants (*Hosta* spp.), and its entire genome RNA sequence was determined. in Korea using cDNA library and RACE methods. The genome of HVX encodes five open reading frames coding for viral replicase, triple gene block (TGB), and viral coat protein (CP) from the 5′ to 3′ ends, which is a typical genome structure of potexviruses. The 3-terminal region of the virus includes the TGB1 (26 kDa), TGB2 (13 kDa), TGB3 (8 kDa), and 23 kDa coat protein (CP) and the 3-nontranslated region (NTR). The CP gene of the type isolate of HVX (HVX-U) was amplified by RT-PCR and its nucleotide sequence was determined. The CPs of HVX-Kr and HVX-U had 100% and 98.9% identical amino acids and nucleotides, respectively. Most of the regions of the genome HVX had over 50% nucleotide identical to other sequenced potexviruses. This is the first report of complete genome sequence information of HVX and molecular evidence supporting the virus as a distinct species of the genus *Potexvirus*.

3-05. Pathological and molecular comparisons of five distinct species of pepper-infecting Potyviruses (oral)

H.I. Yoon, H.M. Chung, and K.H. Ryu
Plant Virus GenBank, PVGABC, College of Natural Science, Seoul Women's University, Seoul 139-774, Korea