Tomato soil pathogens(*Phythopthora* spp.) analyed high rates in series culture soil and existed in culture parts. To make a diagnosis of *Phythopthora* sp. and Its concentration, potato slices were manufactured to a round shape(2.5cm) or retangular form(1x4cm). and then, The potato slices dipped into diagnostic reagents with an antibiotic substance for 2~4hours. Potato slices treated with a few reagents varied into 15cm depths in innoculated soils for 24hrs. Mycelium of the *Phytophthora* root rot fungus, *Phytophthora capsici*, were produced easily on potato slice. We collected many potato slice samples on diseased fields in various area. After storage of 24hrs in 20 ℃ incubater, White mycelium of *phytophthora* sp. formed on potato slice surface. Dilute concentrations of *Phytophthora* sp. was detected very low contents(1×10^1sporangia/g). But expressing *Phytophthora* root rots on potato slice did not developed larger lesions upon storage time in room temperature. These results suggest that the use of potato slice in a series of soil cultural system may still serve as efficient means of diagnosis of *Phytophthora* root rots in the absence of control measures.

4-13. Development of PCR-Based Sequence Characterized DNA Markers for the Identification and Detection, Genetic Diversity of *Didymella bryoniae* with Random Amplified polymorphic DNA(RAPD)

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Gummy stem blight pathogen is very difficult not only to monitor the inoculum levels prior to host infection, and also it is destructive and hard to control in field condition. We have applied RAPD technique to elucidate the genetic diversity of the genomic DNA of *Didymella bryoniae* and also to generate specific diagnostic DNA probe useful for identification and detection. The 40 primers produced clear bands consistently from the genomic DNA of twenty isolates of *Didymella bryoniae*, and two hundred seventy-three amplified fragments were produced with 40 primers. The combined data from 273 bands was analyzed by a cluster analysis using UPGMA method with an arithmetic average program of NTSYS-PC (Version 1.80) to generate a dendrogram. At the distance level of 0.7, two major RAPD groups were differentiated among 20 strains. RAPD group (RG) I included 8 isolates from watermelon except one isolate from melon. RAPD group (RG) IV included 12 isolates from squash, cucumber, watermelon and melon.. In amplification experiment with SCAR specific primer RG1F-RG1R resulted in a single band of 650bp fragment only for 8 isolates out of 20 isolates that should be designated as RAPD Group I. However, same set of experiment done with RGIIF-RGIIR did not result in any amplified product.. Our attempts to detect intraspecific diversity of ITS region of rDNA by amplifying ITS region and 17s rDNA region for 20 isolates and restriction digestion of amplified fragment with 12 enzymes did not reveal polymorphic band. In order to develop RAPD markers for RGIV specific primer, a candidate PCR fragment(≒1.4kb) was purified and Southern hybridized to the amplified fragment RGIV isolates. This promising candidate probe recognized only RGIV isolates