

A-09 Corynespora Leaf Spot of *Momordica charantia* Caused by *Corynespora cassiicola* in Korea. Jin-Hyeuk Kwon, Hyeong-Jin Jee¹ and Chang-Seuk Park². Gyeongsangnam-do Agricultural Research and Extension Services, Jinju 660-360, Korea. ¹Organic Farming Technology Division, National Institute of Agricultural Science and Technology, RDA, Suwon 441-707, Korea. ²College of Agriculture and Life Sciences, Gyeongsang National University, Jinju 660-701, Korea

In November and December 2003, a corynespora leaf spot occurred severely on *Momordica charantia* at Changwon, Gyeongnam province in Korea. The causal fungus isolated from infected leaves of the plant grew well on potato dextrose agar showing gray to brown color. Solitary or catenary conidia of the fungus were obclavate to cylindrical in shape, and pale olivaceous brown or brown in color. The number of isthmus pseudosepta ranged from 4 to 20 and measured $36 \sim 186 \times 8 \sim 19 \mu\text{m}$ in size. Conidiophores were pale to light brown in color and measured $94 \sim 648 \times 3 \sim 8 \mu\text{m}$ in size. Optimal temperature for mycelial growth was 30°C. On the basis of mycological characteristics and pathogenicity to the host plant, the fungus was identified as *Corynespora cassiicola*. This is the first report on the corynespora leaf spot on *M. charantia* caused by *C. cassiicola* in Korea.

A-10 Random Amplified Polymorphic DNA and Internal Transcribed Spacer Analysis of *Didymella bryoniae* Isolated from Cucurbits. Sung Kee Hong, Weon Dae Cho, Sang Yeob Lee and Jong Kun Kim. Plant Pathology Division, National Institute of Agricultural Science and Technology (NIAST), Rural Development Administration (RDA) Suwon 441-707, Korea

The causal agent of gummy stem blight, *Didymella bryoniae* (anamorph *Phoma cucurbitacearum*), was isolated from diseased cucurbits in several locations, Korea. A total of 55 isolates were subjected to random amplified polymorphic DNA (RAPD) analysis to assess the genetic variation. The RAPD profiles indicated that all the isolates were placed in five phylogenetic group, designated URP group (URPG) I (25isolates), II (13isolates), III (6 isolates), IV (10 isolates) and V (1 isolates). On cucumber leaves, a subset of isolates of each group was pathogenic. Two PCR primer pairs specific to RAPD groups (RG1 and RG2) of *D. bryoniae* from cucurbits developed previously were used to confirm the identity of all Korea isolates. For RG1- and RG2-specific primer pairs, a positive reaction was obtained with 25isolates of URPG I and 6 isolates of URPGIII, respectively, but isolates of all other groups gave a negative result. These

results indicate that *D. bryoniae* isolates from Korea contain three additional subgroups as well as two subgroups reported previously. We also analyzed sequences of internal transcribed spacer (ITS) region for isolates of each group.

A-11 Regional distribution of two species of *Sclerotium* causing white rot of *Allium* crops and comparison of the pathogenicity between the two pathogens. Yong-Ki Kim, Mi-Kyung Kwon, Tack-Soo Kim, Hong-Sik Shim, Wan-Hae Yeh, Weon-Dae Cho, Seong-Chan Lee¹, Yong-Hwan Lee², Suk-Ju Koh² and Chan-Jung Lee³ Plant Pathology Div., National Institute of Agricultural Science and Technology, Suwon 441-707, Korea, ¹Agricultural Environment Div., National Institute of Subtropical Agriculture, jeju 690-850, Korea, ²Jeonnam Agricultural Research & Extension Services, Naju 520-715, Korea, ³Onion Experimental Station, Kyungnam Agricultural Research and Extension Services, Changryung 635-800, Korea

White rot of *Allium* crops has known to be caused by two species of *Sclerotium* in Korea. In the past time white rot of *Allium* crops was caused by only one species, an unidentified *Sclerotium* sp. forming a little larger sclerotia than those of *Sclerotium cepivorum*. However, in recent date *Sclerotium cepivorum* have isolated frequently from the diseased *Allium* crops. In this study we compared DNA profiles between the two species, and between native isolates of *Sclerotium cepivorum* isolated from Korea and a standard isolate originated from the Netherlands. It was confirmed that *Sclerotium cepivorum* isolated newly in Korea belonged to group b based on DNA profile using UP PCR described by Tyson et al in 2002. Disease survey was conducted to confirm regional distribution of two species of *Sclerotium* in main garlic cultivation areas, Chungnam, Gyungbuk, Gyungnam, Jeonnam, and Jeju provinces. The survey showed that isolation frequency of *Sclerotium cepivorum* new-isolated recently was higher in garlic cultivation regions in which garlic seeds had been exchanged frequently among garlic farmers and garlic cultivation regions. With a simple pathogenicity method using the sliced clove, the pathogenicity of the two species of *Sclerotium* isolated from garlic, onion, welsh onion and wild rocambole was compared on garlic, onion, welsh onion and wild rocambole. The same *Sclerotium* species showed similar pathogenicity regardless the kinds of *Allium* crops as isolation origins of white rot pathogens. The pathogenicity of *Sclerotium cepivorum* was much higher than that of *Sclerotium* sp. In addition the sclerotia were formed earlier on *Allium* crops infected with *Sclerotium cepivorum* than those with a native pathogen, an unidentified *Sclerotium* sp. And the