Morphology, Molecular Phylogeny and Pathogenicity of *Colletotrichum panacicola*
Causing Anthracnose of Korean Ginseng

Kyung Jin Choi¹, Wan Gyu Kim¹, Hong Gi Choi¹, Hyo Won Choi¹, Young Kee Lee¹, Byung Dae Lee³, Sang Yeob Lee⁴ and Sung Kee Hong*¹

¹Crop Protection Division, National Academy of Agricultural Science (NAAS), RDA, Suwon 441-707, Korea
²Department of Agricultural Biology, Chungnam National University, Daejeon 305-704, Korea
³Bioresource Development Institute, Herbking Inc. Hankyang University, Arneong 456-749, Korea
⁴Agricultural Microbiology Team, NAAS, RDA, Suwon 441-707, Korea

(Received on December 6, 2010; Accepted on February 7, 2011)

*Corresponding author. Phone) +82-31-290-0415, FAX) +82-31-290-0453 E-mail) sukhong@korea.kr

*Colletotrichum panacicola* isolates were obtained from anthracnose lesions of Korean ginseng and compared with four *Colletotrichum* species in morphology, molecular phylogeny and pathogenicity. Based on morphological characteristics, *C. panacicola* was easily distinguished from *Colletotrichum gloeosporioides* but not from *C. destruendum* and *C. coccodes*. A phylogenetic tree generated from ribosomal DNA-internal transcribed spacer sequences revealed that *C. panacicola* is remarkably distinguished from *C. gloeosporioides* and *C. coccodes* but not from *C. higginsianum* and *C. destruendum*. However, molecular sequence analysis of three combined genes (actin + elongation factor-1α + glutamine synthetase) provided sufficient variability to distinguish *C. panacicola* from other *Colletotrichum* species. Pathogenicity tests showed that *C. panacicola* is pathogenic to Korean ginseng but not to other plants. These results suggest that *C. panacicola* is an independent taxon distinguishable from *C. gloeosporioides* and other morphologically similar *Colletotrichum* species.

Keywords: Anthracnose, *Colletotrichum gloeosporioides*, *Colletotrichum panacicola*, Korean ginseng

In Korea, *Colletotrichum panacicola* recorded as a causal pathogen of Korean ginseng anthracnose (Takimoto, 1919) has been considered to be a synonym of *Colletotrichum gloeosporioides* without any basis that these two species are the same taxon. Accordingly, there is a need for a comprehensive approach for confirming the taxonomical position of *C. panacicola*. This study was conducted to compare morphology, molecular phylogeny and pathogenicity of *C. panacicola*, *C. gloeosporioides* and morphologically similar *Colletotrichum* species.

Materials and Methods

Isolation of pathogenic fungi. *Colletotrichum* isolates were obtained from leaves or fruits of Korean ginseng, Chinese cabbage, radish, soybean, potato, tomato and chili pepper with symptoms of anthracnose. The symptomatic tissues were surface-sterilized by immersion in 1% NaOCl for 1 minute followed by two rinses in sterile distilled water. The blotted tissues were transferred to water agar (WA) plates and incubated at 25°C for 3 days. Conidia produced on the tissues were suspended with sterile distilled water, streaked on WA plates and incubated at 25°C for 18 to 24 hours. Monoconidial isolates were obtained from germinating spores on WA and transferred to potato dextrose agar (PDA) slants.

Morphological and cultural characteristics. The *Colletotrichum* isolates were cultured on PDA plates in darkness at 23°C for 7 days. The culture plates were transferred into an incubator with alternating cycles of 12 h NUV light and 12 h darkness for another week to induce conidial production. The conidia harvested from each isolate were mounted in water and their morphological features were examined using a light microscope. To observe appressorial formation, a drop of conidial suspension (5 × 10⁵ conidia·mL⁻¹) was dropped on sterilized slide glass in petri-plates with water-
soaked filter paper and kept at 25 °C for 16 to 24 hours. Mycelial growth and colony features of the isolates were examined on PDA plates kept in darkness at 26 °C for a week. The colony colors were described using the Munsell renovation color system (Nippon Shikisai Co. Ltd.).

**Extraction of genomic DNA, amplification and phylogenetic analysis.** *Colletotrichum* isolates were cultured in potato dextrose broth at 25 °C for 4 days. The mycelial mats were lyophilized for 16 hours and homogenized at 5,800 rpm for 40 seconds using the Precellys® 24 (Bertin technologies). Genomic DNA was extracted with a modified CTAB method (Stewart and Via, 1993). The internal transcribed spacer (ITS) region of rDNA was amplified with primers ITS1 and ITS4 (White et al., 1990). Actin, elongation factor -1 alpha (EF-1α), and glutamine synthetase (GS) genes were amplified with primer sets ACT-512F/ACT-783R (Carbone and Kohn, 1999), EF1-526F/EF1-1567R (Rehner, 2001), and GSF1/GSR1 (Guerber et al., 2003), respectively. The PCR reactions were performed in a total volume of 50 μl including 100ng genomic DNA, 5 μl of 10× PCR buffer containing 25 mM MgCl₂, 0.2 mM dNTP, 0.2 μM of each primer and 1 unit of Taq DNA polymerase (Takara Bio Inc.) using a DNA Engine Tetrad® 2 (Bio-Rad laboratories Inc.). Thermal conditions were programmed for 35 cycles of denaturation (94 °C for 50 sec), annealing (60 °C for 1 min) and extension (72 °C for 1 min 20 sec). PCR products were purified with Wizard® SV gel and PCR clean-up system (Promega) following manufacturer's instructions. The eluted DNAs were cloned into pGEM-T easy vector (Promega) and transformed into *Escherichia coli* JM109. True transformants were selected and sequenced with 3730XL DNA Analyzer (Applied Biosystem). Two phylogenies were generated from the ITS region sequences and from the combined data of actin, EF1-α and GS genes. Sequence alignments were performed using Clustal X version 2.0.10 (Thompson et al., 1997). Nucleotide sequences of *Colletotrichum* isolates were deposited in GenBank (http://www.ncbi.nlm.nih.gov) and are listed in Table 1. Phylogenetic trees were constructed by neighbor-joining method (Saitou and Nei, 1987) with pairwise deletion parameters of Kimura's two-parameter model (Kimura, 1980) using MEGA version 4.0 (Tamura et al., 2007). Confidence of phylogenetic trees was supported with bootstrap method for 1,000 replicates (Felsenstein, 1985).

**Pathogenicity assay.** Tri-folia leaves of 4-year old ginseng, leaves of 3-week old tomato cultivar ‘seokwang’, leaves of 3-week old soybean cultivar ‘daepoong’ and leaves of 3-week old radish cultivar ‘taeguam’ were used for pathogenicity assays. Leaves were wounded with blunt pencil tips or left unwounded. Fifteen μl of conidia suspension (5 × 10⁵ conidia·ml⁻¹) was used to inoculate wounded and unwounded sites of the leaves. The inoculated leaves were placed in plastic containers (230 × 295 × 55 mm) layered with moist paper towels, and kept at 26 °C (± 1 °C). Disease severity on ginseng, radish and tomato was based on lesion diameter measured 5 days after inoculation and disease severity on soybean was based on lesion diameter measured 10 days after inoculation on soybean.

### Results

**Morphological and cultural characteristics.** Three *C. panacicola* isolates from leaves and fruits of Korean ginseng, two *Colletotrichum higginsianum* isolates from Chinese cabbage and radish, *Colletotrichum destructivum* isolate from soybean, two *C. coccodes* isolates from potato and tomato, and two *C. gloeosporioides* isolates from chili pepper were used to compare their morphological and cultural characteristics (Table 1). Remarkable differences in conidial morphology between *C. panacicola*...
Colletotrichum panacicola Causing Anthracnose of Korean Ginseng

and *C. gloeosporioides* were observed (Fig. 1; Table 2). *C. panacicola* isolates were straight or slightly unilaterally curved, with a round apex and a subconical base, measuring 11.2–20.5 × 3.3–4.8 μm, with a mean range of 16.4–18.3 × 4.0–4.4 μm, matching well with previous descriptions of the fungi (Nakata and Takimoto, 1922). *C. gloeosporioides* isolates were usually straight, broad cylindrical with rounded both ends or pointed to one end, measuring 10.0–22.9 × 3.8–6.5 μm, with a mean range of 13.6–16.4 × 4.6–5.2 μm, matching well with previous descriptions of the fungi (Gunnell and Gubler, 1992). There were no clear morphological differences among *C. panacicola*, *C. higginsianum*, *C. coccodes* and *C. destructivum*. The conidia of four species in common are elongated fusiform, usually pointed to one end and also in their size overlapped each other except *C. coccodes* in conidial width is somewhat wider than the other three species (Fig. 1; Table 2). The results of conidial morphology agreed well with previous descriptions for the respective species (Nakata and Takimoto, 1922; Sutton, 1980; 1992).

Morphology of conidial appressoria was compared among the *Colletotrichum* species. The appressorial shape of *C. panacicola* showed minor differences to that of *C. gloeosporioides* and their size overlapped to a significant degree. *C. panacicola* isolates were usually irregularly lobed, sometimes clavate and measured 6.0–11.3 × 4.4–7.9 μm, with a mean range of 7.8–8.6 × 5.5–6.3 μm. *C. gloeosporioides* isolates were clavate, ovate or irregularly lobed, and measured 6.5–10.1 × 5.3–7.8 μm, with a mean range of 8.1–8.5 × 6.0–6.9 μm. There were no clear differences in appressorial morphology among *C. panacicola*, *C. higginsianum*, *C. coccodes* and *C. destructivum* (Fig. 1; Table 2).

*Colletotrichum* colonies on PDA were compared. There were clear differences in colony morphology between *C. panacicola* and *C. gloeosporioides* (Fig. 1). *C. panacicola* isolates were 67 to 70 mm after 7 days, consisting of sparse aerial mycelium, grayish yellow brown to dark olive green in the central region and yellowish white towards the margin, whereas *C. gloeosporioides* were 83 to 85 mm after 7 days, consisting of floccose aerial mycelium and grayish yellow green on the surface. Colonies of *C. higginsianum*, *C. destructivum* and *C. coccodes* showed also distinct differences. *C. higginsianum* isolates C97027 and C08122 were 68 to 73 mm after 7 days, dark yellowish brown or yellowish gray on center of surface and dark yellowish brown or dull orange in reverse side. *C. destructivum* isolate C08077 was 62 to 63 mm, olive color in the central region and pale orange towards the margin on top side, yellowish brown on reverse side. *C. coccodes* isolates C07046 and C96002 were 42 to 49 mm and grew slowly, olive or dark olive gray on top and reverse side.

**Analysis of rDNA-ITS and combined genes (actin + EF1-α + GS) sequences.** Size polymorphism and sequence similarity derived from the sequences of rDNA-ITS region and combined multi-locus genes were investigated. The length of the rDNA-ITS from *Colletotrichum* species ranged from 487 bp to 500 bp and yield 507 aligned nucleotide positions for all species included in the alignment. The nucleotide size for alignment was 499 bp in both *C. panacicola* and *C. higginsianum*, 487 bp in *C. gloeosporioides* and 500 bp in *C. destructivum*. Comparative analysis of the rDNA region containing the two internal transcribed spacers (ITS1 and ITS2) and 5.8S rRNA gene revealed that nucleotide sequences of the 5.8S in all tested taxa were highly conserved but those of their ITS regions
were variable. In particular, nucleotide variations of the ITS1 (6.7%) were two times higher than those of ITS2 (3.2%). The difference of nucleotide variations between ITS1 and ITS2 was consistent with results of previous research (Cano et al., 2004; Sreenivasaprasad et al., 1996).

The ITS sequences from *C. panacicola* isolates shared homology of 87.3–87.5% with *C. gloeosporioides* isolates, 92.9 to 93.1% with *C. coccodes* isolates. However, the sequences showed high level of homology of 99.0–99.5% with *C. higginsianum* and *C. destructivum*.

**Table 2. Morphology of Colletotrichum panacicola and other Colletotrichum species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Isolate</th>
<th>Colony Diameter a (mm)</th>
<th>Color b Top</th>
<th>Color Reverse</th>
<th>Conidium Shape c</th>
<th>Size (µm) Mean</th>
<th>Shape d Size (µm) Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>C. panacicola</em></td>
<td>C08048 69 DOG(138) DOG(138)</td>
<td>F, TAB 14.3–19.9 × 4.0–4.7</td>
<td>17.0 × 4.4</td>
<td>IRL, CL 6.0–8.9 × 4.8–7.9</td>
<td>7.9 × 6.3</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>C08061 68 DOG(138) DOG(138)</td>
<td>F, TAB 11.2–19.1 × 3.3–4.7</td>
<td>16.4 × 4.0</td>
<td>IRL, CL 6.5–9.6 × 4.4–6.5</td>
<td>7.8 × 5.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>C08087 68 DOG(138) DOG(138)</td>
<td>F, TAB 15.1–20.5 × 3.8–4.8</td>
<td>18.3 × 4.3</td>
<td>IRL, CL 6.3–11.3 × 4.9–6.4</td>
<td>8.6 × 5.5</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>C. higginsianum</em></td>
<td>C97027 68 YG(68) DYB(76)</td>
<td>F, TAB 15.7–22.7 × 3.9–4.9</td>
<td>19.0 × 4.4</td>
<td>IR, OV 6.2–9.2 × 4.9–6.9</td>
<td>7.8 × 6.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>C08122 70 YG(68) YG(68) DO(75)</td>
<td>F, TAB 15.3–22.2 × 3.7–5.0</td>
<td>19.1 × 4.4</td>
<td>OV, IR 5.8–10.1 × 4.8–7.0</td>
<td>7.4 × 5.5</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>C. destructivum</em></td>
<td>C08077 62 O(105) O(105) PO(60) YW(92)</td>
<td>F, TAB 13.8–19.4 × 3.6–4.7</td>
<td>16.8 × 4.0</td>
<td>OV, CL 7.8–12.2 × 6.2–9.9</td>
<td>9.6 × 7.4</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>C. coccodes</em></td>
<td>C07046 45 O(105) O(105)</td>
<td>F, TAB 13.2–23.0 × 4.0–5.7</td>
<td>18.4 × 4.7</td>
<td>IR, CL 7.0–12.4 × 4.5–7.4</td>
<td>8.7 × 5.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>C96002 49 DOG(138) DOG(138)</td>
<td>F, TAB 12.7–17.4 × 4.0–5.6</td>
<td>15.3 × 4.6</td>
<td>IR, CL 6.3–10.8 × 4.2–6.4</td>
<td>8.2 × 5.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>C. gloeosporioides</em></td>
<td>C07008 85 O(105) DOG(138)</td>
<td>C, ROB 11.2–16.9 × 3.8–5.5</td>
<td>13.6 × 4.6</td>
<td>CL, OV 6.5–10.1 × 5.3–6.6</td>
<td>8.5 × 6.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>C07009 83 DG(144) DOG(138)</td>
<td>C, TAO 10.0–22.9 × 4.4–6.5</td>
<td>16.4 × 5.2</td>
<td>OV, IR 7.3–9.1 × 6.1–7.8</td>
<td>8.1 × 6.9</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

a Colony diameter was measured 7 days after inoculation.
b A serial number of Munsell renovation color system today’s color/300, DG: dull green, DO: dull orange, DOG: dark olive green, DYB: dark yelowish brown, GYB: yelowish brown, PO: pale orange, O: olive, YB: yelowish brown, YG: yelowish gray, YW: yelowish white.
c C: cylindrical; F: fusiform; TAB: tapered to both ends; TAO: tapered to one end; ROB: rounded both ends.

The ITS sequences from *C. panacicola* isolates shared homology of 87.3–87.5% with *C. gloeosporioides* isolates, 92.9 to 93.1% with *C. coccodes* isolates. However, the sequences showed high level of homology of 99.0–99.5% with *C. higginsianum* and *C. destructivum*.

Fig. 2. A neighbor-joining tree derived from sequences of rDNA-ITS region of *Colletotrichum* spp. Numbers on nodes (> 60%) represent bootstrap values (%) from 1000 replicates. A phylogenetic tree was conducted using MEGA 4.0 with Kimura-two parameter model. The letters in parentheses refer to isolate numbers. Bar represents 0.01 substitutions per site.
Analysis of the combined data set of multi-locus sequences (actin + EF1-α + GS) revealed that the length of *Colletotrichum* species ranged from 2318 to 2377 bp, with alignment of 2553 bp. The size of the nucleotide sequence for alignment was 2349 bp in *C. panacicola* isolates, 2358 to 2365 bp in *C. higginsianum*, 2332 to 2341 bp in *C. gloeosporioides* and 2377 bp in *C. destructivum*. In the sequences of combined multi-locus gene, *C. panacicola* isolates showed similarity of 62.4–62.6% with *C. gloeosporioides*, 71.2–71.5% with *C. coccodes*, 97.8–98.1% with *C. higginsianum* and 95.2–95.3% with *C. destructivum*.

**Phylogenetic relationships.** Phylogenetic analysis based on the sequences of rDNA-ITS showed that *C. panacicola* is clearly differentiated from *C. gloeosporioides* and *C. coccodes* with a high bootstrap support of 100% but from *C. higginsianum* and *C. destructivum* with bootstrap support less than 60% (Fig. 2).

Sequences analysis of combined multi-locus genes provided higher resolution among the five *Colletotrichum* species than ITS (Fig. 3). *C. panacicola* was distinctly separated from the other *Colletotrichum* species with bootstrap support of 100% and was positioned far from *C. gloeosporioides* and *C. coccodes*. The *Colletotrichum* species which were not significantly differentiated in an ITS-based phylogenetic tree, *C. panacicola*, *C. higginsianum* and *C. destructivum* were also further separated each other with bootstrap support of 100%. Taken together, a phylogenetic tree derived from the sequences of combined multi-locus genes led to much higher resolution for the delimitation of *C. panacicola* from other species than ITS.

**Pathogenicity.** Pathogenicity of the five *Colletotrichum* species was tested on their host and on other plants (Table 3). *C. panacicola* isolates on the leaves of Korean ginseng induced circular dark brown lesions 4 days after inoculation. The lesions developed and no major differences in pathogenicity were observed among the isolates. Disease

![Fig. 3. A neighbor-joining tree derived from sequences of combined multi-locus gene (actin+EF1-α+GS) of *Colletotrichum* spp. Numbers on nodes (>60%) represent bootstrap values (%) from 1000 replicates. A phylogenetic tree was conducted using MEGA 4.0 with kimura-two parameter model. Bar represents 0.05 substitutions per site.](image)

**Table 3. Pathogenicity of *Colletotrichum* spp. to leaves of several crops by artificial inoculation**

<table>
<thead>
<tr>
<th>Species</th>
<th>Isolate</th>
<th>Ginseng</th>
<th>Radish</th>
<th>Tomato</th>
<th>Soybean</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>W</td>
<td>UW</td>
<td>W</td>
<td>UW</td>
</tr>
<tr>
<td><em>C. panacicola</em></td>
<td>C08048</td>
<td>++</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td></td>
<td>C08061</td>
<td>++</td>
<td>++</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td></td>
<td>C08087</td>
<td>+++</td>
<td>++</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td><em>C. higginsianum</em></td>
<td>C97027</td>
<td>+</td>
<td>−</td>
<td>+++</td>
<td>++</td>
</tr>
<tr>
<td></td>
<td>C08122</td>
<td>−</td>
<td>−</td>
<td>++</td>
<td>+</td>
</tr>
<tr>
<td><em>C. destructivum</em></td>
<td>C08077</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td><em>C. coccodes</em></td>
<td>C96002</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td></td>
<td>C7046</td>
<td>−</td>
<td>−</td>
<td>++</td>
<td>+</td>
</tr>
<tr>
<td><em>C. gloeosporioides</em></td>
<td>C7008</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td></td>
<td>C7009</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Control</td>
<td></td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
</tbody>
</table>

*Disease severity* on ginseng, radish and tomato was determined on the basis of lesion diameter measured 5 days after inoculation and observed 10 days after inoculation on soybean, respectively. −, < 3.5 mm lesion; +, 3.5–7.0 mm lesion; ++, 7.0–10.5 mm lesion; ++++, > 10.5 mm lesion

*a* wounded

*b* unwounded
severity on leaves with the wound treatment was slightly higher or similar to that of the unwounded leaves. No symptoms developed on the leaves of other hosts including radish, tomato and soybean.

The lesions on leaves of Korean ginseng inoculated with C. gloeosporioides isolates C07008 and C07009 did not appear. C. higginsianum C97027 and C. coccodes C96002 showed weak responses on wounded leaves of Korean ginseng, while C. higginsianum, C. coccodes and C. destructivum produced lesions on leaves of their host plants.

Discussion

C. panacicola was first described by Takimoto (1919). Later, Nakata and Takimoto (1922) provided a detailed description for the causal fungus of leaf blight of Korean ginseng. However, the species in Korea has been regarded as a synonym of C. gloeosporioides, a species complex encompassing diverse groups of strains and biotypes (Yu, 1992; Yu and Ohh, 1993). In addition, Mcpartland and Hosoya (1998) found that morphology of C. panacicola is similar to that of C. coccodes (Wallr.) Hughes.

C. panacicola could be distinguished from C. gloeosporioides using conidial morphology but not from C. higginsianum, C. destructivum and C. coccodes. C. panacicola could also be distinguished from C. gloeosporioides using colony features. The former grew slower than the latter, and both species showed different colony colors. Colony radial growth of C. panacicola, C. higginsianum and C. destructivum was not informative for their speciation, but colony colors revealed difference among them. In short, although conventional methods can be used for identification of the five Colletotrichum species, they provided limited information to delimitate C. panacicola from other morphologically similar Colletotrichum species (Talhinhas et al., 2005; Whitelaw-Weckert et al., 2007).

To overcome limitations of morphological approaches for determination of Colletotrichum species, molecular techniques have been employed (Guerber et al., 2003; Johnston and Jones, 1997; Lubbe et al., 2004; Talhinhas et al., 2002). Although ITS regions have known to be potentially in formative regions for phylogenetic studies at species level, they were not informative enough to resolve relationships among the C. panacicola and its morphologically similar species Moriwaki et al. (2002) revealed that C. destructivum was not separated from C. higginsianum, C. linicola and C. fuscum based on the sequences of ITS1 region. In addition, Sreenuivasaprasad et al. (1996) reported that C. destructivum and C. linicola were not differentiated based on ITS1 sequences.

The sequence data from the three independent loci (actin + EFL-α + GS) were combined and used to complement the rDNA-ITS sequencing. A phylogenetic analysis derived from combined multi-locus sequences revealed that C. panacicola is not only differentiated from C. gloeosporioides and C. coccodes but also sufficiently differentiated from C. higginsianum and C. destructivum with 100% bootstrap support. Analysis using the combined dataset has been used for recognition of fungal species, including Fusarium spp. (O’Donnell et al., 1998).

In this study, the phylogenetic tree based on sequences of the combined genes provided much better resolution for delimitation of C. panacicola from other Colletotrichum species than the rDNA-ITS regions.

Artificial inoculation of Colletotrichum species revealed that C. panacicola is pathogenic on leaves of Korean ginseng but C. gloeosporioides is not. Accordingly, C. panacicola was confirmed as a major pathogen causing anthracnose in Korean ginseng. Colletotrichum isolates from radish, tomato and soybean induced severe symptoms on their host plants by artificial inoculation but weak or no symptoms on other host plants. C. panacicola and other Colletotrichum species used in this study showed host specificity. Taxonomy of Colletotrichum species based on the host specificity has been accepted as a criterion to characterize species by previous workers (Farr et al., 2006; Lubbe et al., 2004; Nirenberg et al., 2002; Sutton, 1980). Although C. coccodes was isolated from soil planted with American ginseng (Panax quinquefolium L.) in Wisconsin, pathogenicity of the fungus on ginseng was not described (Mepartland, 1985). C. coccodes isolate C96002 produced lesions on wounded leaves of Korean ginseng. However, whether the fungus in fields actually causes ginseng anthracnose or not is unclear and requires further investigation.

In conclusion, this work clearly demonstrates that C. panacicola is an independent taxon distinguishable from C. gloeosporioides and other morphologically similar Colletotrichum species based on their morphological, cultural and molecular characteristics and pathogenicity.

References

Colletotrichum panacicola Causing Anthracnose of Korean Ginseng


