Disease Reports

Powdery Mildew of *Momordica charantia* Caused by *Podosphaera fusca* in Korea

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Bitter melon (*Momordica charantia* L.), also known as bitter gourd, is widely cultivated in tropical and subtropical regions for its edible immature fruit, which is used both as a vegetable and for medicinal purposes. Recently, in the southern part of Korea, this vine has also been planted in parks to grow over and through pergolas, in order to provide a shady tunnel for people to enjoy. In October 2009, a severe outbreak of powdery mildew occurred on this plant, localized to a private garden in Gimhae, Korea. Powdery mildew infections were prominent on leaves, which were visibly covered by thin white mycelial mats with abundant conidia (Fig. 1A). No chasmothecia formation was found until the vine died.

Detailed microscopic examination of a representative sample (KUS-F24827) was made to identify the pathogen. Hyphae were colorless, septate, branched and up to 6 µm wide. Hyphal appressoria were indistinct, nearly absent. Conidiophores were unbranched, cylindrical, 90-230 µm long and 9-12 µm wide, composed of a foot cell and three to eight barrel-shaped conidia formed in chains, foot cells slightly swollen at the base and constricted at the branching point (Fig. 1B). Conidia were oval to ellipsoid, 24-38 × 14-22 µm and containing distinct fibrous bodies (Fig. 1C). These structures are typical of the powdery mildew *Oidium* subgenus *Euoidium*, anamorph of the genus *Podosphaera*. The measurements and characters of taxonomic value coincide with those of *Podosphaera fusca* (Fr.) U. Braun & Shishkoff [syn. *Sphaerotheca fusca* (Fr.) S. Blumer] as described by Braun (1987).

Fig. 1. Powdery mildew infections on *Momordica charantia*, caused by *Podosphaera fusca*. **A:** Heavily infected leaf. **B:** Conidiophore (bar = 50 µm). **C:** Conidia (bar = 20 µm).

To confirm the identity of the causal fungus, the amplification and sequencing of the complete ITS rDNA of the isolate was performed using primers ITS5 and P3, as described by Ito and Takamatsu (2010). The resulting sequence of 475 bp was deposited in GenBank (accession no. HM070403). Phylogenetic analysis was carried out using MEGA4 with neighbor-joining method and Tajima-Nei distance model. Comparison with the sequences available in the GenBank database revealed that the ITS sequence share 100% similarity with sequences of *P. fusca* as well as other *Podosphaera* species belonging to the subsection *Magnicellulatae* of the genus *Podosphaera* section *Sphaerotheca*, of which species delimitations remain unclear (Ito and Takamatsu, 2010). In the phylogenetic tree (Fig. 2), the present isolate infecting *M. charantia* was well nested within a clade comprising reference isolates of *P. fusca*, retrieved from GenBank.

Fig. 2. Phylogenetic relationship among *Podosphaera fusca* isolates including powdery mildew fungus infecting *Momordica charantia*, inferred by neighbor-joining method using the ITS rDNA region. Numbers above the branches represent the bootstrap values. Bar = Number of nucleotide substitutions per site.

Two species of powdery mildew fungi have been recorded on *M. charantia* (see Farr and Rossman, 2010): *Golovinomyces cichoracearum* (syn. *Erysiphe cichoracearum*) from USA and China and *Podosphaera fusca* (syn. *P. fuliginea*) from China, India and Japan. In Korea, Lee et al. (1982) recorded *Oidium* sp. as powdery mildew fungus on this plant, without further description. Actually, the occurrence of powdery mildew on this crop has been noticed and occasionally associated with crop loss, especially those grown in polythene tunnels in Korea (JHK, unpublished data). This is the first confirmed report in Korea of a *P. fusca* infection of *M. charantia*.

References

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