

RESEARCH NOTE

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Occurrence of Violet Root Rot on Membranous Milk Vetch Caused by *Helicobasidium mompa* in Korea

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Severe violet root rot occurred in a field of membranous milk vetch in Bonghwa, Korea, in October 2010. Two fungal isolates from the diseased plants were identified as *Helicobasidium mompa* based on their morphological, cultural, and molecular characteristics. This is the first report that *H. mompa* causes violet root rot on membranous milk vetch in Korea.

KEYWORDS : *Helicobasidium mompa*, Membranous milk vetch, Violet root rot

Membranous milk vetch [*Astragalus membranaceus* (Fisch.) Bunge.] is a perennial herbaceous plant belonging to the family Leguminosae. The plant has been used as a medicinal plant in Korea. In October 2010, membranous milk vetch plants showing wilt, chlorosis and premature defoliation were found in a field in Bonghwa, Korea (Fig. 1A). The affected plants were uprooted and roots covered with reddish purple mycelia were exposed (Fig. 1B). The outer layers of the diseased roots were peeled easily and the interior tissues exhibited soft rot (Fig. 1C).

Helicobasidium sp. isolates IY1041 and IY1045 were obtained at the margin of mycelia grown from the diseased roots on water agar and cultured on potato dextrose agar (PDA). Colonies of the isolates were well grown on PDA at 23~25°C, and reached 50~53 mm in diameter in 3 wk. Colonies were filamentous, irregular, and fluffy, with abundant aerial mycelia, brownish white on top surface, and deep purplish red on reverse side (Fig. 1D and 1E). The fungal hyphae produced branches at right and acute angles to the main hypha. The hyphal branches were slightly constricted at the branch origin and there was often a septum close to the branch origin (Fig. 1F). Hyphal width measured 5.2~6.0 µm in the main hyphae and 3.5~3.9 µm in young hyphal branches. No teleomorph stage was produced in culture. Morphological and cultural characteristics of present isolates were similar to those of the genus *Helicobasidium* described previously [1, 2]. However, it was difficult to accurately identify the *Helicobasidium* isolates to the species level.

To overcome the weakness of conventional identification techniques, the ribosomal DNA internal transcribed spacer (rDNA ITS) regions from the present isolates were amplified using the primers ITS1/ITS4 and the resulting products were sequenced. The sequences were deposited in GenBank with accession numbers JN542565 and JN542566. An ITS-based phylogenetic tree was constructed by the neighbor-joining method with Kimura's two-parameter distance model using MEGA ver. 4.0. The phylogenetic tree placed present isolates in the same clade with *Helicobasidium mompa* Tanaka isolates from Chinese mulberry tree (AB097270), asparagus (AY292428) and apple tree (AB056573), and clearly distinguished from other two *Helicobasidium* species, *Helicobasidium purpureum* (Tul.) Pat. and *Helicobasidium longisporum* Wakef. in GenBank (Fig. 2). The result confirmed that *Helicobasidium* sp. isolates from membranous milk vetch were *H. mompa*, which causes violet root rot on a broad range of host plants [1].

Pathogenicity tests were made on membranous milk vetch plants according to modified root box method [3]. The plants grown for 2 mon were inoculated using mulberry fragments colonized with *H. mompa* isolates and then kept in a greenhouse at 25°C for 2 mon. *H. mompa* isolates produced hyphal masses on surface of the roots and incited root rots with age. However, no symptoms developed on control plants inoculated with only sterilized mulberry fragments. The pathogen was re-isolated from the inoculated plants.

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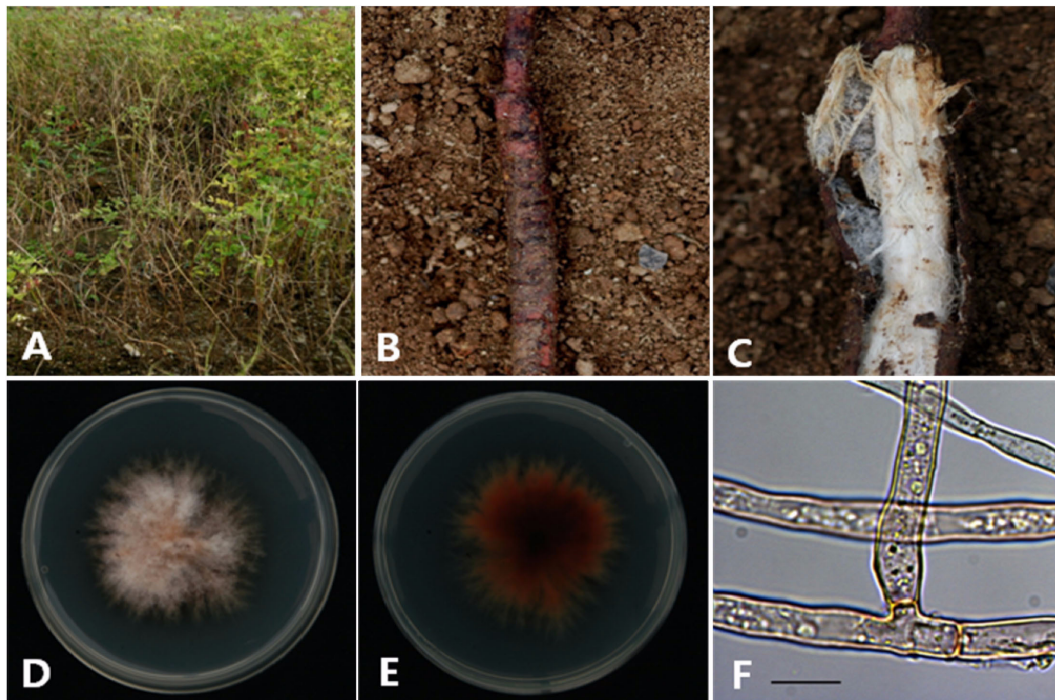


Fig. 1. Violet root rot symptoms of membranous milk vetch caused by *Helicobasidium mompa* in the field and cultural features of the pathogen. A, Wilt of the affected plants; B, Reddish purple discoloration on the surface of a diseased root; C, Soft rot on a diseased root; D, E, Colonies on the top and reverse side of the pathogen grown on potato dextrose aga; F, Hyphae (scale bar = 10 μ m).

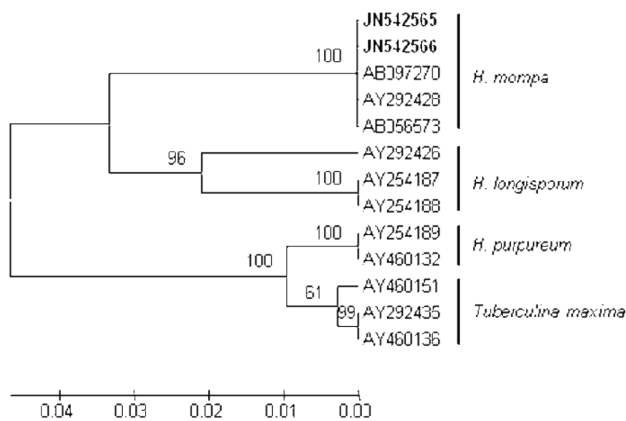


Fig. 2. Neighbor-joining tree based on sequences of rDNA internal transcribed spacer regions of *Helicobasidium mompa* isolates and related species. The numbers above the nodes represent bootstrap values of > 60% out of 1,000 bootstrap replication. The bar represents number of nucleotide substitutions per site.

H. mompa, *H. purpureum* [synonym: *Helicobasidium brebissonii* (Desm.) Donk] and *H. longisporum* are considered as valid species assigned to the genus *Helicobasidium* [1, 4, 5]. *H. mompa* is distinguished from closely related species based on morphological characteristics of the basidiospores and rDNA ITS sequences [1, 2, 4]. The fungus has been recorded as a pathogen causing

violet root rot on 13 plants including apple tree, peanut and mulberry tree in Korea [6], and on more than 100 plant species in Japan, China, Taiwan, Malaysia, Indonesia and South Africa [5, 7]. Especially, the fungus causes serious damage on apple trees in east Asian countries such as Korea, Japan and China. Therefore, the fungus on membranous milk vetch could serve as a source for spread of violet root rot to neighboring economically important crops. Although *H. mompa* was recorded on membranous milk vetch in China [7], but no detailed description for the fungus was given there. This is the first report that *H. mompa* causes violet root rot on membranous milk vetch in Korea.

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