First Confirmed Report on Powdery Mildew of *Phlox paniculata* Caused by *Golovinomyces magnicellulatus* in Korea

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Garden phlox (*Phlox paniculata* L.), belonging to the Polemoniaceae, is a perennial plant with large heads of blossoms, providing great garden color and fragrance in summer. The plant is native to North America and known to be introduced in Korea at the beginning of the 20th century. Various horticultural varieties are widely planted for ornamental purposes in Korea. Powdery mildew infections on leaves (Fig. 1A) and inflorescence (Fig. 1B) are rather common and troublesome in gardening of this plant in Korea. However, the identity of the causal fungus has not been determined due to lack of teleomorphic state.

In August 2009, powdery mildew lesions with abundant chasmothecia were found on *P. paniculata* for the first time in Andong, Korea (Fig. 1C). Further surveys in several localities in Korea including Yeongwol, Jeongseon and Yanggu showed that this powdery mildew fungus is commonly found in these places with mature chasmothecia. The phenomenon was rather surprising, because only anamorphic state of powdery mildew has been found on this plant (Kwon and Park, 2003; Shin, unpublished data). The voucher specimens are kept at Korea University (KUS-F24480, F24739).

The conidiophores were 70-240 µm long and producing 2-6 immature conidia in chains with sinuate edge-line. Conidia were ellipsoid or doliiform, 25-35 × 12.5-17.5 µm, and without distinct fibroin bodies. Chasmothecia were dark brown, spherical, 100-150 µm in diam. and contained several asci (Fig. 1D). Appendages were mycelioid, 12-28 per chasmothecium, 0.5-2.5 times as long as the chasmothecal diam., 1-5-septate. Asci were stalked, 55-75 × 25-37 µm and 2-spored. Ascospores were ellipsoid-ovoid and 22-32 × 15-22 µm. These morphological characteristics are in good agreement with those of previous records of *Golovinomyces magnicellulatus* (Braun, 1987; Tanda, 1997).

The complete ITS rDNA of the two isolates was amplified with primers ITS5 and P3 and directly sequenced. The sequences obtained were identical to each other and deposited in GenBank (accession nos. GU945756, GU945757). Phylogenetic analysis was carried out using MEGA4 with neighbor-joining method (using Tajima-Nei distances). Comparison with the sequences available in the GenBank database revealed that the ITS sequences share 100% similarity (512/512 bp) with a sequence of *G. magnicellulatus* on *P. paniculata* (AF011303) from Japan and 99% (510/512 bp) with that of *G. magnicellulatus* on the same host (AF011303) from the USA. Therefore, the sequence analysis confirmed the identity of the pathogen as *G. magnicellulatus*.

Fig. 1. Symptoms of powdery mildew on leaves (A) and inflorescence (B) of *Phlox paniculata* infected with *Golovinomyces magnicellulatus*. (C) Close-up view of powdery mildew lesions on leaf of *P. paniculata*. Note the numerous blackish structures, overwintering chasmothecia of *G. magnicellulatus*, on the powdery mildew colonies. (D) A chasmothecium containing several 2-spored ascii (Bar = 100 µm).

![Fig. 1](image_url)

Fig. 2. Phylogenetic relationship between *Golovinomyces magnicellulatus* on *Phlox paniculata* and other *Golovinomyces* species, inferred by neighbor-joining method using DNA sequence of the ITS rDNA region. Numbers above the branches represent the bootstrap values. Bar = number of nucleotide substitutions per site.

Powdery mildew on *P. paniculata* caused by *G. magnicellulatus* was recorded from North America and extended to Europe (Braun, 1987) and recently found in Japan (Tanda, 1997). Powdery mildew on this plant in Korea was first recorded as *Oidium* sp. by Kwon and Park (2003). Their description and figures suggest that the fungus is an anamorphic state of *G. magnicellulatus*. Therefore, the present work is the first well-founded report of *G. magnicellulatus* on *Phlox* in Korea although this pathogen is likely to have been present for years before now.

References


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