

**Disease Reports**

## Powdery Mildew of Crenate Deutzia Caused by *Erysiphe deutziae* in Korea

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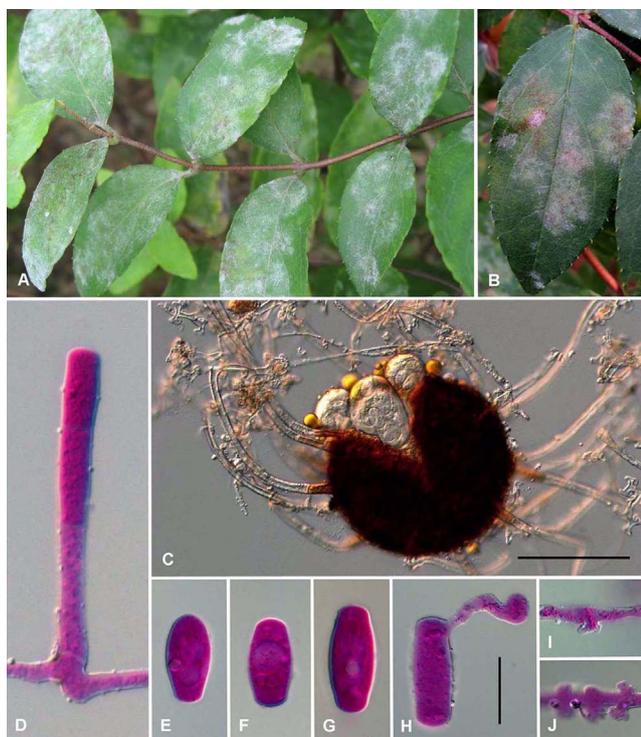
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Crenate deutzia (*Deutzia crenata* Sieb. & Zucc.) is a common ornamental shrub belonging to the Hydrangeaceae. In July 2007, powdery mildew infections were first noticed in a garden of National Agrobiodiversity Center, Suwon, Korea. Powdery mildew lesions on leaves and non-lignified stems were conspicuous, especially when growing in the shade (Fig. 1A). The leaves exhibited chlorotic circular patches, sometimes forming reddish discolorations (Fig. 1B). Production of chasmothecia was found starting from September and continued into November. Voucher specimens are kept at Korea University (KUS-F24694, F24779).

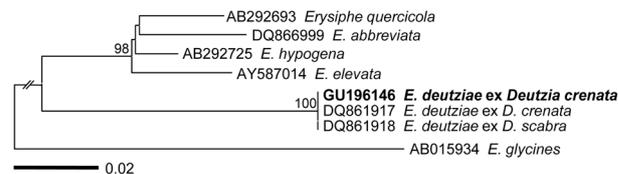
White superficial colonies developed with abundant sporulation. Hyphal appressoria were lobed, single or opposite in pairs. Conidiophores were 55-98×7.5-10 μm, composed of 3-4 cells, straight or slightly flexuous at the base, and producing conidia singly. Conidia were ellipsoid to barrel-shaped, 25-34×12.5-16.5 μm, devoid of conspicuous fibrosin bodies, and producing perihilar germ tubes. First formed conidia were rounded at the apex and subtruncate at the base. Chasmothecia were 90-135 μm in diam.,

blackish brown, depressed globose. Appendages were about 8-14 in number, substraight to mildly bent, 4-5 times dichotomously branched, apex recurved, 1-3-septate. Asci were 3-6 per chasmothecium, 42-52×36-45 μm, 6-8-spored. Ascospores were oval, 18-22×12.5-15 μm (Fig. 1C-J). The observations were in full agreement with previous records of *Erysiphe deutziae* (Bunkina) U. Braun & S. Takam. (Nomura, 1997; Bolay et al., 2005).

To confirm the identity of the fungus, the complete ITS region of rDNA from KUS-F24694 was amplified with primers ITS5 and P3 as described by Takamatsu et al. (2009) and directly sequenced. The resulting sequence of 560 bp was deposited in GenBank (GU196146). Phylogenetic analysis was performed using MEGA4 with neighbor-joining method (using Tajima-Nei model). The Korean isolate showed 100% similarity with two sequences of *E. deutziae* found on *D. crenata* and *D. scabra* Thunb. from the UK (DQ861917 and DQ861918, respectively). Therefore, the sequence analysis verified the pathogen to be *E. deutziae*.



**Fig. 1.** Powdery mildew symptoms and *Erysiphe deutziae* on *Deutzia crenata*. (A) Infections on the young shoot. (B) Reddish discoloration of the lesions. (C) Chasmothecium producing several asci with 6-8 ascospores each. (D) Conidiophore. (E) First formed conidium. (F&G) Conidia. (H) Germinating conidium. (I&J) Hyphal appressoria. Each structure in D-J was stained with lactofuchsin. Bar=100 μm for C and 20 μm for D-J.



**Fig. 2.** Phylogenetic relationship between *Erysiphe deutziae* on *Deutzia* and related *Erysiphe* species, 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.

*Erysiphe deutziae* is the only powdery mildew fungus known from *Deutzia* spp. This fungus has been recorded from Russian Far East and Japan (Nomura, 1997) and recently from Europe with new epidemic spread in France, Germany, Poland, Switzerland and the UK (Bolay et al., 2005; Denton and Henricot, 2007) on several species of *Deutzia*. There has been no previous record of *E. deutziae* from Korea, where several native and introduced species of *Deutzia* are growing. This is the first record of this fungus as well as its host plant in Korea.

### References

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