

First Report of Take-All on Turfgrass Caused by *Gaeumannomyces graminis* Var. *Graminis* in Korea

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Gaeumannomyces graminis Arx & Olivier comprises four varieties: *G. graminis* var. *tritici* (*Ggt*), var. *avenae* (*Gga*), var. *maydis* (*Ggm*) and var. *graminis* (*Ggg*), and all cause similar diseases on different crops or grasses. *Ggt* causes take-all of wheat, barley. *Gga* attacks oats. *Ggm* causes take-all of maize. *Ggg* causes dieback of Bermuda grass and sheath blight of rice (Freeman and Ward, 2004). *Gga*, *Ggm* and *Ggt* produce a simple, unlobed hyphopodium, but *Ggg* develops a lobed hyphopodium, as a key characteristic for identification of the pathogen (Freeman and Ward, 2004). Take-all disease of turfgrass is caused by *G. graminis* var. *graminis*, the fungus belongs to Magnaporthaceae. First report of the disease was on St. Augstengrass in 1991 in US, the pathogen has been known to successfully infect and cause disease on other turfgrasses (Krausz, 2005). Symptoms of the disease generally appear in late spring or early summer. The disease has been reported in worldwide (Hill et al., 1999) but not in Korea. In June 2011, we observed severe disease patches at a golf course (turfgrass; *Zoysia* sp.) in Giheung, Gyeonggi province (Fig. 1A). The patch was suspected as turfgrass take-all, based on the symptoms. The infected stolons and roots had typical black lesions (Fig. 1B) and yellowish foliage and brown symptoms were observed on the edge of the patch. The infected roots and stolons were washed for 2 hr running tap water and then surface-sterilized by immersion in a solution of 1% silver nitrate for 1 min, followed by rinsing twice in distilled water. Excess water was removed by filter paper then roots were cut into pieces and placed on R-PDA (Kwak et al., 2009). Dark-pigmented fungi were isolated from the roots and the stolons of the infected plants. The ITS sequences were deposited in GenBank (Accession No.

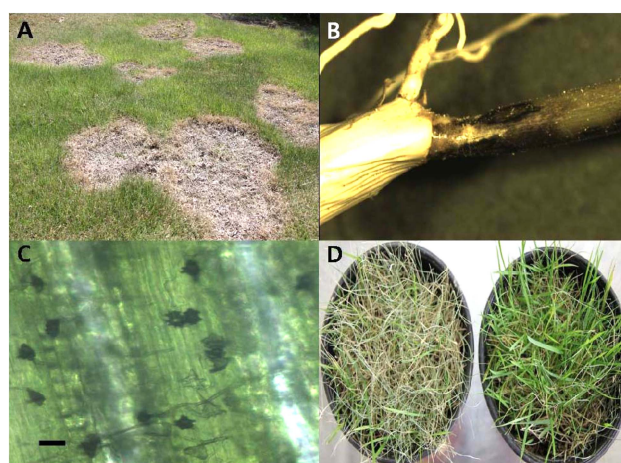


Fig. 1. (A) Severe take-all patch symptoms on Zoysiagrass. (B) Typical black lesion symptom on the stolon. (C) Hyphopodia on turfgrass coleoptiles by isolates *G. graminis* var. *graminis* TG-1. Bars indicate 20 μ m. (D) Take-all symptom was produced isolates of *G. graminis* var. *graminis* TG-1.

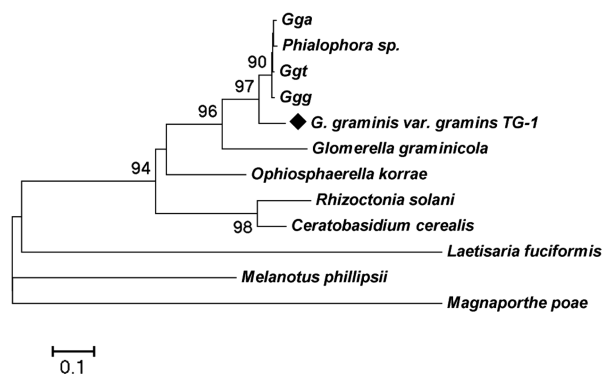


Fig. 2. Phylogenetic tree of *Gaeumannomyces* spp. based on rDNA ITS sequences. Multiple sequence alignment performed using ClustalW2. A neighbor-joining algorithm was used to generate the phylogenetic tree. The tree was constructed using the original data set and 1000 bootstrap data sets. indicated the present isolate.

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JQ303334). The fungi were identified as *G. graminis* var. *graminis* based on ITS-rDNA sequences and the phylogenetic tree (Fig. 2), avenacinase-like gene PCR reaction (data not shown) (Rachdawong et al., 2002) and morphological characteristics, such as lobed hyphopodia on coleoptiles of turfgrass (Fig. 1C). On PDA media, the optimal temperature for the pathogen hyphal growth was 20°C (3.85 mm±1 per day) (data not shown). The barely kernel inoculums (1%, v/v) of the pathogen successfully produced the take-all symptom on Zoysiagrass (Fig. 1D). To our knowledge, this is the first report of take-all disease in turfgrass and the causal pathogen, *G. graminis* var. *graminis*, in Korea.

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