# Disease Note

## Diseases Caused by Fungi and Fungus-Like Organisms

### First Report of Fusarium Wilt Disease Caused by *Fusarium equiseti* on Grafted Watermelon in Korea

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In Korea, most grafted watermelons are a fusion of bottle gourd (*Lagenaria siceraria*) as a rootstock and watermelon (*Citrullus lanatus*) as a scion-stock (Lee et al. 2010). Currently, we have collected several samples from grafted watermelon displaying symptoms of yellowing, withering, and wilting leaves. When the symptomatic stem was excised, browning vascular tissues were observed due to the colonization of a fungal pathogen. From the samples obtained, 25 fungal isolates were identified as species of *Fusarium*. Among 25 isolates, 18 were identified as *F. oxysporum*, four as *F. solani*, and three as *F. equiseti*. Initial assessment showed that one of the *F. equiseti* isolates (NIHHS 16-126) was highly virulent to rootstock. Interestingly, this is the first time *F. equiseti* has been identified as pathogenic to grafted watermelon. The NIHHS 16-126 isolate was collected from a watermelon cultivation field in Buyeo-gun (36.25951°N, 126.92044°E) county. The disease was estimated to infect approximately 10% of the watermelon plants cultivated in this area. The NIHHS 16-126 isolate was examined to confirm its identity. On potato dextrose agar, colonies appeared yellowish-brown while the aerial mycelium was whitish to peach in color. Macroconidia were relatively long (20.21 to 51.13 × 2.30 to 4.5 µm, n = 50), with 3 to 6 septa, curved, and with conidiophores with monophialides. However, microconidia formation was not observed. These morphological characteristics resemble *F. equiseti* characters as described by Hyun et al. (2019). For molecular identification, an internal transcribed spacer of ribosomal DNA (*ITS-rDNA*), elongation factor-1α (*EF-1α*), and beta-tubulin (*β-tub*) genes were sequenced using primer pairs ITS1/ITS4 (White et al. 1990), EF1-728F/EF1-986R (Glass and Donaldson 1995), and Bt2a/Bt2b (Carbone and Kohn 1999). BLASTn analysis revealed that the *ITS-rDNA* (LC648248), *EF-1α* (LC648250), and *β-tub* (LC648249) sequences were 99 to 100% identical to *F. equiseti* reference sequences (KF515650, KF747331, and KF747330) infecting *Avicennia marina* in China (Lu et al. 2014). Phylogenetic analysis of concatenated *ITS-rDNA*, *EF-1α*, and *β-tub* sequences showed that this isolate clustered in the same clade as *F. equiseti*, confirming its identity as *F. equiseti*. For the inoculation, roots of 12-day-old seedlings (watermelon and bottle gourd, n = 10 each) were dipped in a conidial suspension ($1 \times 10^6$ conidia/µl) for 30 min. Inoculated seedlings were planted in the soil before being transferred to the greenhouse (temperature: 30°C; daylight: 14 hours). Control plants were inoculated with sterile water. After 21 days post-inoculation, all inoculated bottle gourd seedlings (n = 10) wilted and eventually died. In contrast, none of the inoculated watermelons or control seedlings were affected. Re-isolation of three fungal isolates (infected root) showed that their morphology and gene marker sequences were identical to the original isolates, thus fulfilling Koch's postulates. Bottle gourd is the most preferred rootstock for grafted watermelons among Korean farmers due to its ability to resist *Fusarium* spp. infection. Therefore, the identification of *F. equiseti* as a fungus that is pathogenic to rootstock is crucial information to manage fusarium wilt disease among grafted watermelon. To our knowledge, this is the first report confirming *F. equiseti* infection in grafted watermelon plants in Korea.

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