Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium buharicum* Causing Root Collar Rot on *Abelmoschus sagittifolius* in Vietnam

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In Vietnam, Sam Bo Chinh (*Abelmoschus sagittifolius* [Kurz]) is a valuable medicinal plant due to its health benefits and potential pharmacological properties and is one of the high-value crops (Bay and Thong 2025; Nguyen et al. 2024; Vo et al. 2023). In June 2023, sudden wilting, root collar rot, and plant death were observed on *A. sagittifolius* in Thua Thien Hue Province, Vietnam. To isolate the causal pathogen, symptomatic plant samples were collected from Sam Bo Chinh farms in Thua Thien Hue, Dong Thap, and Quang Binh provinces, where yield losses were estimated at 30 to 60%. Infected root collars were surface sterilized with 70% ethanol for 1 min and 1% sodium hypochlorite for 2 min. After removing the outer bark, the samples were sprayed with 70% ethanol, briefly flame-sterilized, and then plated on potato dextrose agar (PDA) supplemented with 100 µg/ml of streptomycin and ampicillin. Plates were incubated at 25°C for 5 days. Single-spore cultures of three isolates produced white, dense, cottony hyphae on PDA; the reverse was beige to yellowish and 62.5 to 68.3 mm in diameter after 7 days. On carnation leaf agar, these strains produced macroconidia, chlamydospores, and conidiophores consistent with the *Fusarium* genus (Barnett and Hunter 1987; Paul et al. 2024). Macroconidia were falcate, slender, and slightly curved, with a beaked apical cell and a foot-shaped basal cell. No microconidia were observed. Thick-walled chlamydospores were formed singly, in pairs, or in chains and were 8.5 to 9.0 µm in diameter. Conidiophores were monophialidic and polyphialidic. For molecular identification, the translation elongation factor 1-alpha (*tef1*) and the second largest subunit of RNA polymerase II (*RPB2*) were amplified using the primer pairs EF1/EF2 (Carbone and Kohn 1999) and 7cf/11aR (O'Donnell et al. 2022), respectively. BLAST analyses were then performed against NCBI and FUSARIUM-ID version 2.0 databases (Geiser et al. 2004). The *tef1* sequences (PX432120 to PX432122) and the *RPB2* sequences (PZ135593 to PZ135595) clustered with *Fusarium buharicum* reference strains, supported by high bootstrap values (99 to 100%) in the phylogenetic analysis. To assess pathogenicity, 4-month-old plants were inoculated by placing 5-mm-diameter mycelial plugs from 14-day-old cultures at the root collar region, whereas nonfungal PDA plugs were used for negative controls. Plants were incubated at 100% humidity for 24 h and then transferred to a growth chamber at 25°C with a 12-h photoperiod. Five to seven days after inoculation, leaf chlorosis and necrotic lesions developed on the root collar, resembling those in naturally infected plants. All three fungal isolates caused typical root collar rot symptoms with a 100% disease incidence within 7 days, while control plants remained healthy. To fulfill Koch's postulates, diseased tissues were cultured on PDA for 7 days, and the original fungal strains were successfully reisolated and identified as *F. buharicum*. To our knowledge, this is the first report of root collar rot on Sam Bo Chinh caused by *F. buharicum* in Vietnam, highlighting the need to consider this pathogen in disease management strategies.

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