Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Root Rot Disease in Green Gram (*Vigna radiata*) Caused by *Ectophoma multirostrata* in India

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A disease survey was conducted in green gram (*Vigna radiata*) growing areas of Bharuch, Gujarat, India, in February 2020. Root rot was observed on cultivar NVL-585 in 30 fields surveyed, with 15 to 20% disease incidence. Infected plants showed foliar chlorosis, brown discoloration, dark black brittle roots with necrotic lesions, and sometimes died. The root rot causal agent was isolated on potato dextrose agar (PDA) from 25 symptomatic samples collected from 10 diseased plants and pure cultures were obtained using the single hyphal tip method. The cultures were grayish black with a smooth texture. Conidia were single celled, elliptical to oval in shape, and 5.2 to 6.5 µm ($n = 25$) in length and 2.7 to 3.4 µm in width. Plastic pots (15 cm in diameter) were filled with autoclaved soil (1.5 kg/pot) inoculated with a 15-day-old culture of the fungus at 3 g/kg (10^8 CFU/g). After 7 days, the local green gram cultivar HUM 16 was sown into the pots. Seedlings were thinned to 10 per pot. Chlorosis of leaves, rotting of roots, and even plant

death were observed at 20, 30, and 40 days after seeding. The experiment was conducted twice to fulfill Koch's postulates. The fungus was reisolated from the root rot samples, and identical colony morphology was observed as seen previously. Based on the cultural characteristics and conidial morphology, the fungus belonged to *Ectophoma* sp. (Boerema et al. 2004). ITS, D1 and D2 regions of LSU, and β -tubulin were used for molecular identification. The BLASTn analysis of ITS, the D1 and D2 region of the LSU gene, and β -tubulin gene sequences of isolate G80 showed 100% similarity with accession number MH858623 (Vu et al. 2012), 99.82% similarity with MH870612 (Vu et al. 2012), and 100% similarity with MN983939 (Hou et al. 2020). The gene sequence was submitted to NCBI GenBank, with accession numbers for ITS, the D1 and D2 region of LSU, and β -tubulin of MW165415, MW813868, and LC656357, respectively. The pathogen was previously reported from other hosts such as *Fuchsia* $\times$ *hybrida*, *Origanum vulgare*, *Lavandula angustifolia*, *Cicer arietinum*, and *Coriandrum sativum*. It can cause substantial economic damage to a wide range of commercially important crops. To the best of our knowledge, this is the first report of *E. multirostrata* causing root rot disease of green gram in India.

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