

Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Athelia rolfsii* (= *Sclerotium rolfsii*) Associated with Foot Rot Disease of *Chrysanthemum morifolium* in India

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Chrysanthemum morifolium L. is an important flower crop grown in different parts of Karnataka for its striking cut flowers and international market value. During a field survey (Mysore district, Karnataka, February 2022), chrysanthemum fields were found infected with foot rot disease. The presence of white mycelial structures with sclerotia was recorded near the stem-soil interface. The disease incidence ranged from 10 to 12% over an area of approximately 10 ha. The infected plants showed quick wilt, yellowing and toppling of the entire plant. Infected plants from Doddamaragowdanahally and Rayanahally ($n = 15$) were collected, and the associated fungal pathogen isolated after surface sterilization with NaOCl (1%) on potato dextrose agar (PDA) amended with chloramphenicol (50 mg/liter). Fungal mycelia developed from the infected tissues were inoculated on fresh PDA plates to obtain pure cultures for further identification. Fungal colonies with dense, aerial whitish-cottony mycelia with uniformly globose sclerotia (0.28 to 4.2 mm) were observed after 15 days of incubation ($28 \pm 2^\circ\text{C}$). Sclerotia were white in the beginning and turned brown at maturity. The average number of sclerotia produced per plate ranged from 240 to > 480 ($n = 10$). To further confirm the identity of the isolates, two representative isolates

(CmSr1 and CmSr2) were subjected to molecular identification based on ITS-rDNA sequences. Briefly, genomic DNA was isolated from 12-day-old cultures using the CTAB method and ITS-rDNA was amplified using ITS1-ITS4 primers (White et al. 1990). An expected amplicon of > 650 bp (ITS) was obtained and later sequenced from both directions. The consensus sequences were analyzed through BLASTn search, which revealed 100% sequence similarity with reference sequences of *Athelia rolfsii* (*S. rolfsii*) from GenBank database (MT127465, MN974137, KC292637; identity 656/656; 0 gaps). A phylogenetic tree obtained by the neighbor-joining method using MEGAX shared a common clade with the reference sequences retrieved and computed, thus confirming the identification based on sequence analysis and molecular phylogeny. The representative sequence of *A. rolfsii* isolates CmSr1 and CmSr2 was deposited in GenBank (accession nos. ON456153 and ON456154, respectively). Based on etiology, morphological, cultural and molecular data, the pathogen was identified as *A. rolfsii* (Curzi) Tu & Kimbrough (Syn: *Sclerotium rolfsii* Sacc.; Mordue 1974; Mahadevakumar et al. 2016, 2018). Plants ($n = 60$) were inoculated with sclerotial bodies (2 sclerotia/plant) near the stem-soil interface in a greenhouse and covered with polythene bags (at $27 \pm 2^\circ\text{C}$ and 80% RH). Noninoculated plants ($n = 20$) served as controls. The development of foot rot disease was observed 8 days after inoculation. A total of 48 plants showed foot rot symptoms and 12 inoculated plants and all control plants remained healthy. The identity of the fungus was confirmed by morphological and cultural characters after reisolation. *C. morifolium* is an important flower crop in Karnataka. *A. rolfsii* is known to be associated with blight and collar rot of *Chrysanthemum* spp. from Kerala (Beena et al. 2002), but no species (host) identity was provided. Therefore, to the best of our knowledge, this is the first report of foot rot disease caused by *A. rolfsii* on *C. morifolium* in India. Early diagnosis of this disease will help farmers to adopt suitable management practices to avoid loss.

References:

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