Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Athelia rolfsii* (= *Sclerotium rolfsii*) Causing Foot Rot Disease of Chia (*Salvia hispanica*) in India

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Salvia hispanica L. (Lamiaceae), commonly called “chia,” is an important food crop that has gained significance in recent times globally due to its nutritive value. During a field survey (Mysore district, Karnataka, October 2021), chia fields were found associated with a characteristic foot rot disease. Further, the presence of mycelial structures along with sclerotial bodies was recorded near the stem-soil interface on the infected plants. The disease incidence ranged from 15 to 21% in an area of approximately 15 hectares of chia fields. The symptoms initially appeared as tan lesions near the stem soil interface and the lesions were colonized by the fast-growing mycelium. As the disease progressed, the plants toppled due to death of the stem–root interface region. Infected plants from KM Halli and DMG Halli ($n = 30$) were sampled and associated fungal pathogens isolated on potato dextrose agar (PDA; HiMedia Lab, Mumbai). Fungal mycelia developing from the infected tissues were inoculated onto fresh PDA plates to obtain pure cultures for further identification. Fungal colonies with dense, aerial whitish-cottony mycelia with uniformly globoid sclerotia (0.5 to 2.9 mm) were observed after 10 to 12 days of incubation at room temperature. Sclerotia were white at first and turned brown with age. The average number of sclerotia produced per plate ranged from 150 to >280 ($n = 10$). To further confirm the identity of the

isolates, three representative isolates (SrSh1, SrSh5, and SrSh10) 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 was obtained and later sequenced from both directions. The consensus sequences were analyzed through a BLASTn search that revealed 100% (643/643 bp) sequence similarity with reference sequences of *Athelia rolfsii* (*Sclerotium rolfsii*) from GenBank (KY640622 and AB075298). A phylogenetic tree obtained by the neighbor-joining method using MEGAX showed a common clade with the reference sequences, thus confirming the identification based on sequence analysis and molecular phylogeny. Representative sequences of *A. rolfsii* isolates SrSh1, SrSh4, and SrSh7 were deposited in GenBank (accession nos. OM021878 to OM021880). Based on etiology, morphological, cultural, and molecular data, the pathogen was identified as *A. rolfsii* (Curzi) Tu & Kimbrough (Syn: *S. rolfsii* Sacc.) (Mahadevakumar et al. 2016, 2018; Mordue 1974). Pathogenicity tests were conducted by inoculating the sclerotial bodies near the stem–soil interface of chia plants grown in a greenhouse at $28 \pm 2^\circ\text{C}$ and 70% relative humidity. Briefly, 60 healthy plants were inoculated with sclerotia and covered with polythene bags for 2 days and removed later. Plants ($n = 20$) inoculated without any sclerotia were treated as controls. The development of characteristic foot rot disease was observed 6 to 8 days post inoculation. A total of 38 plants showed the foot rot symptoms while control plants remained healthy. The identity of the fungus was confirmed by morphology and molecular sequence analysis after reisolation. Chia is an important food crop and in recent times has been regarded as a superfood. Although *A. rolfsii* is known to be associated with many crops, this is the first report in chia. Therefore, to the best of our knowledge, this is the first report of foot rot disease caused by *A. rolfsii* on chia in India. Early diagnosis of this disease will help farmers to adopt suitable management practices to avoid loss.

References:

- Mahadevakumar, S., et al. 2016. Eur. J. Plant Pathol. 145:215.
- Mahadevakumar, S., et al. 2018. Eur. J. Plant Pathol. 151:1081.
- Mordue, J. E. M. 1974. CMI descriptions of pathogenic fungi and bacteria. No. 410.
- White, T. J., et al. 1990. Page 315 in: PCR Protocols: A Guide to Methods and Applications. Academic Press, San Diego, CA.

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