Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Aspergillus versicolor* Associated with Fruit Rot Disease of Tomato (*Solanum lycopersicum*) from India

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Funding: The first author acknowledges ICMR, New Delhi for awarding ICMR SRF fellowship (file no. ICMR-SRF award no: 45/69/2018-PHA/BMS/OL) and the third author thanks CSIR, New Delhi for the award of CSIR-Research Associate Fellowship. Plant Dis. 106:1300, 2022; published online as <https://doi.org/10.1094/PDIS-07-21-1461-PDN>. Accepted for publication 9 October 2021.

Tomato (*Solanum lycopersicum* L.) is an important vegetable crop and cultivated throughout India. During 2019–20, Karnataka produced 2,163 metric tons of tomato, accounting for 10.51% of total production (<https://agricoop.gov.in/horticulture-reports>). During a survey conducted in September 2019, characteristic fruit rot symptoms associated with tomato were severe at the harvest stage and caused by a characteristic mold. The necrotic lesions on infected fruit were covered with black fungal fruiting bodies. The incidence of new fruit rot disease was estimated around 12 to 14% in an area of 18 ha (~62 fields) surveyed in the southern Karnataka region. The fruit rot was characterized by lesions appearing, which later enlarged into a necrosis stage and rotting. In total, 20 samples were used for isolation. Infected fruit rot samples were surface sterilized with 2% NaOCl for 2 min, rinsed thrice in sterile distilled water, and plated on potato dextrose agar (PDA) medium amended with chloramphenicol (40 mg/liter). The plates were incubated at 28 ± 2°C and pure cultures were obtained by hyphal tipping. Fungal colonies expressed on PDA medium produced sulcate and centrally raised sporulating structures. The colony on PDA developed as white in the beginning and later turned to yellow

green, often intermixed with flesh to pink exudates. Conidiophores were hyaline or slightly pigmented with smooth walls. Vesicles were subglobose to ellipsoidal and phialides were borne on metulae. Conidia were globose, brownish, and conspicuously echinulate. On the basis of microscopic and cultural characteristics, the causative pathogen was identified to be *Aspergillus versicolor* (Jurjevic et al. 2012). Further molecular characterization was also done by amplifying the internal transcribed spacer (ITS) region using the universal ITS1/ITS4 primer pair with three representative isolates (White et al. 1990). Genomic DNA was isolated using CTAB using a 15-day-old culture followed by PCR amplification using the ITS1/ITS4 primer pair and sequencing. The generated sequence analysis revealed 100% (561/561 bp) sequence similarity through nBLAST analyses with the reference sequences of *A. versicolor* (KU318417.1 and MT798844.1) from the GenBank database. The representative sequences of ITS-rDNA for three isolates (namely, *A. versicolor* NCM_1, NCM_2, and NCM_3) were deposited in GenBank (accession nos. MZ520551.1 to MZ520553.1). Pathogenicity tests were conducted on 10 healthy mature fruits (tomato F1 hybrid INDAM 3003) using prick inoculation (conidial suspension 3 × 10⁶ conidia ml⁻¹). Tomato fruit (*n* = 5) inoculated with only sterile water served as controls. The experiments were conducted in triplicates of 10 fruits each and repeated three times (Mahadevakumar et al. 2019). Within 7 days postinoculation, fruit rot symptoms were observed on all inoculated fruit, which showed a characteristic lesion similar to the field observations. The control fruit remained asymptomatic even after 10 days. The pathogen was reisolated from diseased fruit and its identity was confirmed based on micromorphological examinations and cultural features. *A. versicolor* has been reported as a postharvest fungal pathogen on various other vegetable crops (Aidoo 1993). Tomato fruit rots are reported to be a major problem (Nizamani et al. 2021). However, no reports are available for the association of *A. versicolor* with fruit rot of tomato from India (Farr and Rossman 2021). To the best of our knowledge, this is the first report of *A. versicolor* associated with fruit rot of tomato from India.

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The author(s) declare no conflict of interest.

Keywords: *Aspergillus versicolor*, fruit rot, molecular diagnosis, *Solanum lycopersicum*, new disease report

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