Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Coniella granati* Associated with Dieback of Rose (*Rosa* sp.) in India

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Rose (*Rosa* sp.) is an important floricultural crop largely cultivated in the Karnataka state of southern India. A field survey conducted in the Devanahalli, Bangalore rural area during October 2019 revealed rose plants (cv. Arka Pride) showing dieback symptoms with a disease incidence of 7% in a 30-ha rose field. Dieback was characterized by the development of necrotic lesions that started at the tips of shoots and progressed downward, leading to the death of young shoots. Pycnidia were found on young shoots showing necrotic lesions. Dieback-affected shoots (n = 10) 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 with white aerial mycelia along with pycnidia were observed on eight samples. Colony growth rate was at 4.2 ± 0.4 mm/day with an average colony diameter of 47.2 ± 3.8 mm after 7 days (periods of 12 h of light and 12 h of darkness). Pycnidia were solitary and globose. Conidia were hyaline, single celled, ellipsoid to fusiform, and measured 12.4 to 16.78 by 3.2 to 5.1 µm (n = 50). Based on cultural and morphological features, the fungus was identified as *Coniella granati* (Mahadevakumar et al. 2019; Van Niekerk et al. 2004). Furthermore, two representative isolates (NLD-2021-1 and NLD-2021-2) were used for molecular identification based on barcoding of ITS-rDNA, LSU, and *tef1* regions amplified using primer pairs described by Alvarez et al. (2016). PCR-amplified products were sequenced and the consensus sequences were analyzed through BLASTn search, which showed that ITS (NLD-2021-1: 611/611 bp, MH860368 and NLD-2021-2: 573/573 bp, KU147239), LSU (NLD-2021-1: 783/906 bp, MH872113 and NLD-2021-2: 844/1,172 bp, KX833400), and *tef1* (NLD-2021-1 and NLD-2021-2: 548/548bp, KX833682) sequences shared 100% sequence similarity with *C. granati*. The nucleotide sequences were deposited in GenBank with the accession numbers ITS: MW898436 and MW898437, LSU: MZ895475 and MZ895476, and *tef1*: MW916275 and MW916276. The phylogenetic tree constructed based on combined ITS-LSU-*tef1* loci confirmed that the sequences shared a common clade with *C. granati*. Furthermore, pathogenicity tests were conducted twice on healthy rose plants (Arka Pride; 60 days old after grafting) maintained in a greenhouse at 28 ± 2°C and 70% relative humidity. Whole-plant inoculation was followed by spraying the conidial suspension (10 ml/plant) of *C. granati* (NLD-2021-1) (3×10^6 conidia/ml, amended with Tween20 at 2%) on 15 plants. In total, 10 healthy plants inoculated with sterile distilled water amended with Tween20 at 2% served as the control. Inoculated plants were covered with polythene bags for 48 h to maintain relative humidity. Dieback symptoms were observed on young shoots after 15 to 18 days post inoculation (DPI) and control plants remained disease free after 15 DPI. The pathogen was reisolated on PDA from 10 diseased plants and identity was confirmed through morphological methods. *C. granati* is an important phytopathogen known to cause dieback and twig blight of pomegranate globally, as well as other economically important crops (Cintora-Martínez et al. 2017). No reports are available on the association of *C. granati* with dieback of rose (Farr and Rossman 2021), which should help in developing appropriate disease management strategies.

References:
Alvarez, L. V., et al. 2016. Stud. Mycol. 85:1.
Cintora-Martínez, E. A., et al. 2017. Australas. Plant Dis. Notes 12:1.
Farr, D. F., and Rossman, A. Y. 2021. Fungal Databases. Syst. Mycol. Microbiol. Lab., USDA-ARS. Retrieved 3 July 2021 from https://nt.ars-grin.gov/fungaldatabases/
Mahadevakumar, S., et al. 2019. J. Plant Pathol. 101:787.
Van Niekerk, J. M., et al. 2004. Mycol. Res. 108:283.

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