

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Brown Rot Caused by *Monilinia polystroma* on Sweet Cherry and Almond in Italy

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Brown rot decay is an important disease of pome and stone fruits. In Italy, the main pathogens on stone fruits are *Monilinia laxa*, *M. fructigena*, and *M. fructicola* (Spitaler et al. 2022). In addition, *Monilinia polystroma* (G. Leeuwen) L. M. Kohn (van Leeuwen et al. 2002) was recently found in Italy on peach (Martini et al. 2014), pear (Martini et al. 2015), plum (Abate et al. 2018), apple (Rosati et al. 2021), and quince (Spitaler et al. 2023). In South Tyrol province, sweet cherry (*Prunus avium* L.) and almond (*Prunus dulcis* Mill. D. A. Webb), plants of the Rosaceae family with stone fruits, were observed to be frequently affected by brown rot. Affected cherries and almonds showed brown lesions, covered by yellowish or buff-colored stroma in concentric rings. Symptomatic cherries became shriveled, while symptomatic almonds remained firm. To determine the pathogen, single spore isolates were obtained from five symptomatic fruits each from a cherry orchard of the cultivar Kordia in July 2021 and almond trees of the variety Dulcis in August 2021. Both sample sites were situated in Vadena/Pfatten. Infestation in the cherry orchard, covered by a rain-protection foil, was about 1%. In almond, over 50% of the fruits of various ripening stages showed brown rot symptoms. On potato dextrose agar (PDA) at 22°C and a photoperiod of 16 h, isolates from both fruits matched the morphological characteristics of *M. polystroma* (Vasić et al. 2016) within 14 days. DNA was extracted from mycelium and the rRNA encoding gene region using ITS4 and ITS6 primers as well as a genomic sequence of unknown function using the primers UniMon_Forw and UniMon_Rev (Petróczy et al. 2012), amplified, and sequenced. MegaBLAST analysis revealed 100% identity with *M. polystroma* sequences from NCBI GenBank (rRNA encoding region: NR_154,198; genomic region: JN128836). Sequences were deposited

in GenBank under accession numbers OP642545/OP654171 (cherry) and OP642546/OP654172 (almond). Pathogenicity was confirmed with mature cherry cultivar Duroncino and almost mature almond fruit of the variety Dulcis: 16 samples each for both fruits were surface-sterilized by dipping in 75% ethanol for 10 s and subsequent rinsing with sterile water for 10 s. Mycelial plugs (3 mm) were dislodged from a 7-day old colony and inserted in a 3 mm hole into the fruits. Incubation was performed in plastic boxes under the conditions described above. PDA-inoculated fruit were used as controls. All cherries and all almonds were completely covered by brown rot lesions 7 and 15 days post inoculation, respectively. Control fruits remained symptomless. Conidia were produced in branched chains on mycelium-inoculated fruit. Conidia were one-celled, limoniform, hyaline, measuring 13.1 to 22.2 × 9.7 to 14.8 µm (cherry) and 14.1 to 20.8 × 10.7 to 15.3 µm (almond). Additionally, 16 fruits each were inoculated with 20 µl conidial suspension (5 × 10³ spores/ml) from mycelium-inoculated fruits. All cherries and all almonds were completely covered by brown rot lesions 7 and 15 days post inoculation. Control fruits remained symptomless. To confirm identity, the fungus was isolated from five spore-inoculated fruits each for cherry and almond. The isolates showed identical morphological features and sequence identity as the original isolates. To our knowledge, this is the first report of *M. polystroma* on almond, while the pathogen has already been reported on sweet cherry in Poland (Poniatowska et al. 2016). These additional host plants identified in this study suggest a broad impact of *M. polystroma* on Italian stone fruit production. Due to the economically important cultivation of stone fruit, further knowledge of the pathogen's host range will help to assign brown rot symptoms to *M. polystroma* and to improve targeted control strategies.

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