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plant disease

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DISEASE NOTES

First Report of *Colletotrichum acutatum* Causing Anthracnose in *Feijoa sellowiana* in Italy

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Feijoa sellowiana Berg (syn. *Acca sellowiana* [O. Berg] Burret) is an evergreen tree cultivated worldwide as an ornamental tree and for its edible fruits. In summer to autumn of 2015 and 2016, anthracnose-like symptoms were observed on mature fruits and leaves of feijoa in gardens and a commercial orchard located in Bari and Matera Provinces of southern Italy. Around 10 to 20% of trees were affected. Mature fruits had dark, sunken lesions, which often became covered by pink conidial masses and progressed to a fruit rot. Leaves exhibited chlorotic lesions that progressed to brown spots and sunken necrotic areas. Small pieces of symptomatic plant tissues from the margin of the lesions and were surface disinfested, plated in Petri dishes containing potato dextrose agar (PDA), and incubated at 25°C. After 10 days, the resulting colonies were transferred to PDA to obtain pure cultures. A fungus with pink, flat colonies was consistently isolated on PDA. Conidia produced by the pure isolates were hyaline, smooth-walled, aseptate, and cylindrical to fusiform. One hundred conidia were measured, and their dimensions ranged from 11.5 to 19 µm (mean = 15.2 µm) × 2.7 to 4.0 µm (mean = 3.4 µm). On the basis of conidia morphology (Damm et al. 2012), the causal agent was identified as *Colletotrichum acutatum* (J.H. Simmonds) species complex. For further identification of the species, total DNA was extracted from 10 representative isolates, and a multilocus sequence analysis was carried out. Sequences of rDNA-ITS (ITS), partial actin (ACT), chitin synthase (CHS-1), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and β-tubulin-2 (TUB2) were amplified using corresponding primers. The obtained sequences were deposited in GenBank under the following accession numbers: ITS (LT745886, LT745887, and LT972205 to LT972210), ACT (LT976516 to LT976525), CHS-1 (LT976833 to LT976842), GAPDH (LT976492 to LT976501), and TUB2 (LT976506 to LT976515). The deposited sequences showed high identity percentages (99 to 100%) with *C. acutatum* sequences present in GenBank (KX069826, KX069821 for ITS; JQ005839, KY171912 for ACT; MF979822, KY856133 for CHS-1; KX069805, KM252191 for GAPDH, and GU183311,

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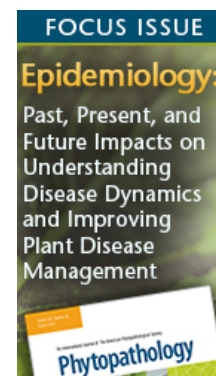
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GU183314 for TUB2). Phylogeny inferred from combined datasets of the five genes and *C. acutatum* species-complex sequences from GenBank revealed that all feijoa isolates were included in the *C. acutatum* subclade (100% branch bootstrap support value after 1,000 replicates). Koch's postulates were fulfilled by spraying a spore suspension (5×10^4 conidia/ml) from monoconidial colonies of 10 sequenced isolates on 50 leaves and inoculating 30 μ l of the same spore suspension on 50 wounded mature feijoa fruit. As controls, 10 leaves and 10 mature feijoa fruit were inoculated with sterile distilled water. Following inoculation, leaves and fruits were maintained in a growth chamber at $25 \pm 1^\circ\text{C}$. Pathogenicity tests were carried out twice. Symptoms identical to those observed in the field appeared within 10 to 15 days on inoculated leaves and fruits but not on controls. *C. acutatum* was always reisolated from inoculated fruits and leaves and identified by both conidia morphology and molecular methods. The infection of feijoa plants by *C. acutatum sensu lato* has been previously reported in Auckland, New Zealand (Lardner et al. 1999). To our knowledge, this is the first report of *C. acutatum* on feijoa plants in Italy.



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Section:

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