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DISEASE NOTES

First Report of *Phytophthora capsici* as Causal Agent of Snap-bean (*Phaseolus vulgaris*) Pod Decay in Brazil

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Citation

Snap-bean is a main vegetable crop in small-scale agricultural systems in Brazil. In 2012, pods displaying water soaked lesions with white mold followed by pod decay and rotting were observed (~5% incidence) in surveys of open-field grown crops in a commercial vegetable-producing sector in Brazlândia-DF, Brazil. Six isolates were obtained using 10% clarified V8 medium amended with 30 mg/liter of rifampicin. Analyses under light microscopy revealed coenocytic hyphae; papillated and pyriform sporangia with long pedicels. The sporangia (n = 50) were 47.8 µm (33 to 56 µm) × 30.3 µm (24 to 41 µm); oogonia were 37.3 µm (32 to 44 µm), and antheridia were 14.2 × 13.1 µm. Chlamydospores were not observed. These characteristics were in agreement with *P. capsici* description. All isolates were able to grow on V8 medium at 35°C, which discriminated them from *P. tropicalis* (Aragaki and Uchida 2001). The snap-bean isolates were paired with *P. capsici* A1 and A2 mating type testers in V8 medium. All isolates produced oospores only with the A2 isolates. In pathogenicity assays, intact pods were sprayed with monosporangium-derived suspensions (2 × 10^4 zoospores/ml) until run-off. Isolates induced similar symptoms on pods 4 days after inoculation and *P. capsici* was reisolated from these pods. All isolates induced crown rot after inoculation (2 × 10^4 zoospores/ml) of snap-bean 'Fortuna' (50% incidence) and *Capsicum annuum* 'Ikeda' (100% incidence) seedlings, whereas *C. annuum* 'CM 334' displayed no symptoms (Reifschneider et al. 1992). All isolates showed similar phenotypic attributes, thus only two isolates (PCva-01 and PCva-02) were selected for sequencing of the internal transcribed spacer (ITS) region. Total DNA was extracted from pure colonies using a modified CTAB method (Boiteux et al. 1999) and used as template in PCR assays with the ITS-1 (5′-TCCGTAGGTGAACCTGCGG-3′) and ITS-4 (5′-TCCTCCGCTTATTGATATGC-3′) primer pair (White et al. 1990). BLASTn alignments of the PCva-01 (GenBank accession no. KT818615) and PCva-02 (KT818616) amplicon sequences (~750 bp) showed 100% identity, and they shared 99 to 100% identity with a subset of publically available *P.*

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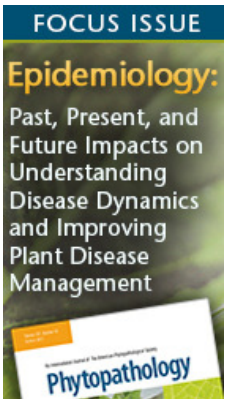
capsici ITS sequences (*n* > 100), including isolates described on *P. vulgaris* (GU011684) and *P. lunatus* L. (DQ464043). This combination of data allowed us to classify the snap-bean isolates as *P. capsici*. This pathogen has been reported infecting snap-bean pods elsewhere (Gevens et al. 2008). However, to our knowledge, this is the first record of *P. capsici* naturally infecting this crop in Brazil. Soil infested with *P. capsici* is the most likely initial source of inoculum. Susceptible crops such as squashes (*C. moschata*) and bell peppers are often cultivated in this area. The confirmation of snap-bean as an alternative host of *P. capsici* is an important information for establishing effective disease management strategies.



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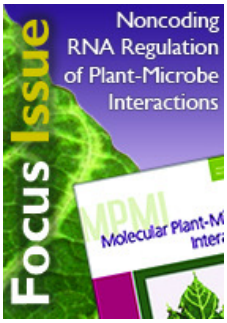

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