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Page 2171

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DISEASE NOTES

A Root Rot of Chickpea Caused by Isolates of the *Fusarium solani* Species Complex in Brazil

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ABSTRACT

Chickpea (*Cicer arietinum* L.) has great potential for increased cultivation in Brazil. Approximately 20% of chickpea plants (cv. Cícero) displayed vascular wilt and root rot in surveys conducted in 2011 to 2012 in three commercial fields (5 to 20 ha) in Cristalina-GO (Goiás State) and Brasília-DF (Federal District). Diseased stems were cut into small (2 to 3 mm) pieces, washed with tap water, disinfested with 70% ethanol for 1 minute, rinsed in sterilized water, transferred to PDA medium, and incubated at 25°C (12/12 h dark/light cycle). Fungal colonies displayed a beige color with an average mycelial growth rate of 2.3 mm/day. Three representative monosporic isolates (FUS 236, FUS 285, and FUS 286) were selected randomly and characterized. Isolates formed kidney-shaped, 0- to 2-septate microconidia (24 to 43 × 2 to 6 μm) on 21 × 168 μm long monophialides; macroconidia (23 to 45 × 4 to 5 μm) were falcate (3- to 5-celled), and chlamydospores (5.0 to 10.5 μm) were ovoid, bicellular, and terminal. These characteristics fit those of the *Fusarium solani* (Mart.) Sacc. species complex, FSSC (Summerell et al. 2003). A PCR assay was done using DNA extracts of all three isolates with the primers EF1 and EF2 targeting the translation elongation factor (TEF)-1α region (Mbofung et al. 2007). The amplicons (~700 bp each) were purified and sequenced. The sequences of FUS 285 (KJ849238) and FUS 286 (KJ849239) were approximately 99% homologous with the TEF-1α sequence of *F. solani* isolates (e.g., KP267463), whereas FUS 236 (KJ956787) displayed 96% homology to the TEF-1α sequence of *F. falciforme* (KF020508) and 92% homology with that of *F. solani* (DQ247551). Bayesian inference analyses of available FSSC sequences revealed clustering of FUS 285 and FUS 286 sequences in a unique phylogenetic lineage (0.99

posterior probability), whereas the FUS 236 was a sister lineage of *F. falciforme*. The root dip inoculation method of [Cabral et al. \(2014\)](#) was carried out to assess pathogenicity of the three isolates. Apical root segments (2 cm) were cut from the plants and the root system of each plant dipped for 5 min into a spore suspension (2×10^6 microconidia/ml) of the appropriate isolate. Independent assays were conducted with each isolate using 4 to 6 'Cícero' seedlings/isolate. Noninoculated control seedlings and inoculated seedlings were transplanted into sterilized soil in a greenhouse (23 to 35°C). Inoculated plants displayed root rot 30 days after inoculation, and no symptoms were observed on control plants. Fungi typical of the FSSC were reisolated as described above from the inoculated plants, but not from the control plants. Reisolates from inoculated plants were subjected to sequencing using the same primers and they displayed sequences identical to that of the original isolates, thus fulfilling Koch's postulates. These isolates from chickpea may have been introduced into Brazil via contaminated seeds or represent endemic populations previously reported to affect other leguminous crops in Brazil ([Aoki et al. 2003](#)). Chickpea was reported as a host of FSSC isolates in the Americas, Europe, and the Middle East. However, this is the first report of FSSC isolates on chickpea in Brazil.

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