

Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

Bisifusarium lunatum Causing Cladode Soft Rot in Pear Cactus (*Nopalea cochenillifera*) in Brazil

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Cactus pear variety Miúda (*Nopalea cochenillifera* L. Salm-Dyck) is an important crop for the Northeast region of Brazil, composing one of the main sources of animal feed. By April 2021, cladode rot caused death of several cactus pear plants in a production area located in Itaporanga, Paraíba State, Brazil (7°21'55.35"S, 38°11'38.68"W). The infected cladodes showed brown circular necrotic spots and soft rot with perforations that extended throughout the cladode, followed by tipping over and death of the infected

plants. The incidence of the disease ranged from 10 to 30% of the plants. *Bisifusarium* strains were isolated and cultured on potato dextrose agar (PDA) and synthetic nutrient-poor agar (SNA). The colonies were purple in color on PDA. On SNA, macroconidia ($n = 100$) were abundant, hyaline, slightly falcate, and three-septate, measuring 11.0 to 23.1×2.3 to $4.1 \mu\text{m}$. Microconidia ($n = 100$) were oval and generally aseptate, measuring 4.1 to 8.7×2.3 to $3.0 \mu\text{m}$. Conidiogenic cells formed into short monophialides. Chlamydospores were not observed. According to these morphological features, the pathogen was initially identified as *Bisifusarium lunatum* (Gryzenhout et al. 2017). For further confirmation of the identification, the partial sequences of translation elongation factor 1- α (*TEF1- α*) and the second largest subunit of RNA polymerase II (*RPB2*) genes were sequenced for a representative isolate (CMA 34; GenBank accession nos. OR536502 for *TEF1- α* and OR553509 for *RPB2*) and compared with other *Bisifusarium* species from the GenBank database. Subsequently, it was subjected to a phylogenetic analysis of maximum likelihood, including previously published sequences. According to BLAST searches, the *TEF1- α* and *RPB2* sequences were 99% (637/640 nt) and 100% (312/312 nt) similar to *B. lunatum* (COUFAL0213: *TEF1- α* [MK640219] and *RPB2* [MK301291]), respectively. The isolate was also clustered in a clade containing the ex-type of *B. lunatum* with 100% support (SH-aLRT and UFboot), being confidently assigned to this species. The pathogenicity test was performed as described by Medeiros et al. (2015) by using healthy 2-month-old cactus pear seedlings ($n = 10$) cultivated in a greenhouse. Sterile toothpicks were distributed over colonies of the representative isolate grown on PDA at $25 \pm 2^\circ\text{C}$ for 7 days. Seedling cladodes were stuck with the toothpicks, moistened with sterile water, and covered with transparent plastic bags for 24 h, thus simulating a humid chamber. Following 3 months, all control plants (stuck with sterile toothpicks) remained healthy, whereas those inoculated with the representative isolate exhibited rot symptoms. This test was performed two times. *B. lunatum* was reisolated from symptomatic cladodes and identified as previously described, thus fulfilling Koch's postulates. To our best knowledge, this is the first report of *B. lunatum* causing soft rot on *N. cochenillifera* in Brazil. Besides *N. cochenillifera*, this species was also reported on *Opuntia ficus-indica* in India (Gryzenhout et al. 2017), which raises concern regarding its ability to infect other forage sources for cattle feed in Brazilian semiarid regions. The present study highlights that the precise identification of *B. lunatum* is a key factor to adjust control strategies and management of the disease to prevent the spread of this disease to other crops.

References:

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