DISEASE NOTE

FIRST REPORT OF *PANTOEA STEWARTII* subsp. *STEWARTII* CAUSING JACKFRUIT BRONZING DISEASE IN MEXICO

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"Jackfruit bronzing", an emerging disease affecting jackfruit (Artocarpus heterophyllus) caused by the bacterium Pantoea stewartii, had only been reported in the Philippines and Malaysia. It is characterized by yellow-orange to reddish discoloration of affected pulps and rags (Gapasin et al., 2014; Zulperio et al., 2017). In autumn 2016, the disease was suspected in major growing areas in Nayarit, Mexico, where jackfruits with typical fruit bronzing symptoms were observed and collected. The fruits were excised and the sampled tissues were disinfected with 1% sodium hypochlorite (2 min), then rinsed with sterilized water and placed on Luria-Bertani (LB) agar medium. Ten bacterial isolates with characteristics particular to Pantoea spp. (Gapasin et al., 2014) and resembling the *P. stewartii* subsp. *stewartii* (Smith) Mergaert et al. (ATCC8199) type strain, showing round, vellow pigmented, smooth, translucent colonies, Gramnegative and rod-shaped cells and positive for catalase, protease and amylase production, were obtained and selected for further examination. The cpsD and hrpS genes obtained from a typical Mexican bacterial isolate from jackfruit JM-5´ (deposited in the Bacterial Collection of the Autonomus University of Nayarit) (GenBank accession Nos. KY965964 and KY965965) with primers specific to Pantoea stewartii (CPSL1-CPSR2c and HRP1d-HRP3c; Coplin et al., 2002) showed 98-99% similarity to reference strains of P. stewartii subsp. stewartii (EU215384, AB894429-27, AF282857). Furthermore, sequence analysis of a 16S rDNA region (KY965963), amplified with bacterial universal primers FD1-RD1 (Weisburg et al., 1991), showed that our JM-5' bacterial isolate was 99% identical to Pantoea stewartii subsp. stewartii (KM508073, HG792421). Phylogenetic analyses of sequences were conducted, using MEGA 7 software, by the Maximum Likelihood method. The cspD and 16S rDNA sequences were compared with the available sequences for these genes in genomes of *P. stewartii* subsp. *stewartii*, while the *hrpS* gene sequence was compared against brpS sequences of phytopatogenic bacteria available in the database, including that of P. stewartii subsp. stewartii. Dinoroseobacter shibae (CP000830) was included as an outgroup. Analysis based on cspD sequence indicated that Mexican bacterial isolates clustered together in the clade of *P. stewartii* subsp. *stewartii*. Moreover hrpS and 16S rDNA sequences obtained from our bacterial isolate JM-5' grouped respectively with brpS and 16S rDNA genes from available genomes of *P. stewartii* subsp. stewartii. Pathogenicity tests showed characteristic symptoms of fruit bronzing disease 14 days post inoculation in jackfruits inoculated by injection with a bacterial suspension (10 ml, 108 cfu ml⁻¹). No symptoms were observed in control fruits inoculated with sterile water. Bacteria re-isolated from inoculated jackfruits were identical to the original isolate showing the morphological, biochemical and microscopic characteristics described above. Furthermore the PCR analyses of the cpsD and hrpS genes revealed that JM-J1, IM-I6, IM-I11 re-isolates generated amplicons with similar sizes to those obtained from the P. stewartii subsp. stewartii ATCC8199 type strain. Based on morphological, biochemical, physiological, pathogenicity tests and molecular analyses, we conclude that Mexican bacterial isolates from Jackfruit can be identified as *Pantoea stewartii* subsp. *stewartii*. This is the first record of jackfruit bronzing disease in Mexico.

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