



A new disease, bacterial fruit rot of jujube, caused by *Xanthomonas arboricola* in Korea

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Jujube (*Zizyphus jujuba*) is an economically important crop in Korea. Jujube fruits are used as an ingredient in Korean cooking and as a medicine. A fruit rot of jujube was observed in fields in the Boeun District and in Kyungsan City, Korea in 2008 and 2009. Initial symptoms on fruit included small, circular reddish to black spots which turned deep brown to red brown as they expanded (Figs. 1A, 1B). The surface of affected areas eventually became sunken, while internal tissues turned deep brown (Figs. 1C, 1D). Ten bacterial isolates were obtained from the diseased fruits (surface-sterilised in 70% ethanol for 1 min) by plating on trypticase soy agar. All isolates were Gram-negative aerobic rods with a single flagellum. Colonies were yellow and raised with smooth margins on peptone sucrose agar.

To complete Koch's postulates, detached jujube fruits (cv. Bokjoe) wounded with a razor blade were spot-inoculated with 5 µl of a cell suspension containing 10⁵ cfu/ml (five fruits per isolate). The fruits were maintained in a plastic box with high humidity at 28°C. Inoculated surfaces turned brown in 24 hrs followed by internal discoloration within 25 days. Bacteria were reisolated and their identities confirmed by metabolic fingerprinting using the Biolog Microbial Identification System, version 4.2 (Biolog Inc., Hayward, CA, USA), and re-inoculation of fruits as described above. No symptoms were noted on two fruits inoculated with sterile distilled water (Fig. 2). The *gyrB* region was partially sequenced to aid in identification of three isolates, BC2927, BC2928 and BC3042, using PCR primers reported by Young *et al.* (2008). A 860-bp fragment of the *gyrB* of the three isolates was compared with sequences of the reference strains of the genus *Xanthomonas* available in the GenBank. The isolates were clustered with *X. arboricola* pathovars, and clearly separated all the pathovars in a phylogenetic tree generated by the neighbour-joining method in the MEGA software, version 4.1 (Fig. 3) (Tamura *et al.*, 2007). The *gyrB* sequence from the isolates had distance indices of 0.014, 0.017, 0.017, 0.037, 0.013, 0.016, and 0.020, as

determined by the Jukes-Cantor model, with sequences of the reference strains of *X. arboricola* pvs. *juglandis*, *pruni*, *corylina*, *populi*, *celebensis*, and the *X. arboricola* strains from *Capsicum* spp. (Myung *et al.*, 2010; Young *et al.*, 2008), respectively. On the basis of the sequence, the three isolates were identified as *X. arboricola*. The disease is named bacterial fruit rot. To our knowledge, this is the first report of bacterial fruit rot of jujube caused by *X. arboricola*. Further studies are required to determine the pathovar status of the strain. Further spread of the pathogen is expected to have an economic impact on fruit production in Korea. Nucleotide sequence data are available under the following GenBank Accession Nos.: GU120086, GU120087 and GU120085 for *gyrB* of isolates BC2927, BC2928 and BC3042, respectively.

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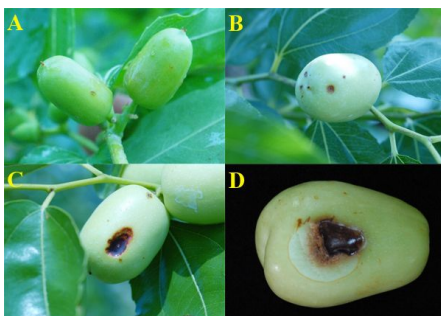


Figure 1



Figure 2

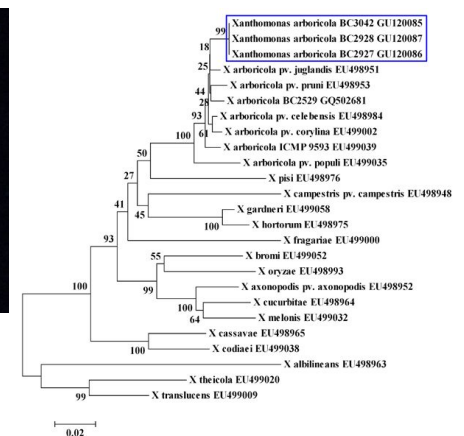


Figure 3

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