



First report of bacterial stalk rot of sweet corn caused by *Dickeya zeae* in Korea

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Sweet corn (*Zea mays*) is one of the most important crops in Korea. In Goesan District, Korea in 2007 it was cultivated on 1,178.7 ha and produced 9,725 tonnes (<http://www.goesan.go.kr>). Bacterial stalk rot of sweet corn (cv. Daehak) was observed at fields in Goesan District in July 2008. The internodes of diseased plants were tan to brown, and soft rot with a foul odour was evident in the inner parts of stems (Fig. 1). The infected plants had collapsed with blighted leaves and easily removable tops. Tissues showing these symptoms and leaf spot lesions were surface-sterilized in 70% ethanol for one minute; from these six bacterial isolates were obtained on trypticase soy agar (TSA). Colonies were gray-white and slightly raised with smooth margins on nutrient agar. The bacterial isolates exhibited the biochemical characteristics of the family Enterobacteriaceae. They were Gram-negative, oxidase negative, catalase positive, fermentative, rod shaped, motile, and facultatively anaerobic. All isolates were preliminary identified as *Pectobacterium chrysanthemi* (Biolog similarity index of a range of 0.65 to 0.73 48hr after inoculation) with the Biolog Microbial Identification System, version 4.2 (Biolog Inc., Hayward, CA). Their identities were confirmed by PCR using primers corresponding to *pel* genes as described by Nassar *et al.* (1996). A 1,449-bp fragment of 16S rDNA from the six isolates shared 98% similarity with one of *P. chrysanthemi* LMG2804^T in the GenBank database (Accession No. Z96093). The *recA* region was partially sequenced to aid in identification of two isolates, BC2879 and BC2880, using PCR primers reported by Parkinson *et al.* (2009). A 481-bp fragment was compared with sequences available in the GenBank database. The isolates clustered with *Dickeya zeae* PII subclade in a phylogenetic tree generated by the neighbour-joining method in the MEGA software, Version 4.1 (Fig. 2) (Tamura *et al.*, 2007). The *recA* sequence from the isolates had distance indices of 0.002, 0.045, and 0.154 as determined by the Jukes-Cantor model, with sequences of strains of *D. zeae* NCPPB1863 (PII subclade) (FJ217086), *D. zeae* NCPPB2538^T (PI subclade) (FJ216967), and *D. chrysanthemi* NCPPB402^T (FJ216968), respectively. On the basis of the *recA* sequence, the isolates were identified as *D. zeae*. Nucleotide sequence data are available under the following accession numbers: FJ571651, GQ461741, GQ461742, GQ461743, GQ461744, and GQ461745 for 16S rDNA of isolates BC2877, BC2878, BC2879, BC2880, BC2881 and BC2882, respectively; and HM852143, and HM852144 for

recA of isolates BC2879 and 2880, respectively.

Koch's postulates were completed with inoculation of four-week-old intact sweet corn plants of cv. Danokusu (three plants per isolate) with 100 µl of cell suspensions containing 10⁸ cfu/ml. Plants were inoculated after a pinprick at the base of an internode of the stem and then incubated in a greenhouse at 28°C and at 80% relative humidity. All isolates induced stem infection and leaf blight similar to symptoms observed in natural infections two weeks after inoculation (Fig. 3). The bacterium was re-isolated from symptomatic stems of sweet corn plants. No symptoms were noted on plants inoculated with sterilized distilled water. To our knowledge, this is the first report of bacterial stalk rot of sweet corn caused by *D. zeae* in Korea. Similar disease symptoms in corn had been reported in different countries (Boewe, 1949; Reifschneider & Lopes, 1982). Further spread of the pathogen is expected to have a high economic impact in sweet corn production in Korea.

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References

- Boewe GH, 1949. Bacterial stalk rot of corn in Illinois. *Plant Disease Reporter* **33**, 342-343.
- Nassar AA, Darrasse A, Lemattre M, Kotoujansky A, Dervin C, Vedel R, Bertheau Y, 1996. Characterization of *Erwinia chrysanthemi* by pectinolytic isozyme polymorphism and restriction fragment length polymorphism analysis of PCR-amplified fragment of *pel* genes. *Applied and Environmental Microbiology* **62**, 2228-2235.
- Reifschneider FJB, Lopes CA, 1982. Bacterial top and stalk rot of maize in Brazil. *Plant Disease* , 519-520.
- Tamura K, Dudley J, Nei M, Kumar S, 2007. MEGA 4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology and Evolution* **24**, 1596-1599. [doi:10.1093/molbev/msm092]



Figure 1

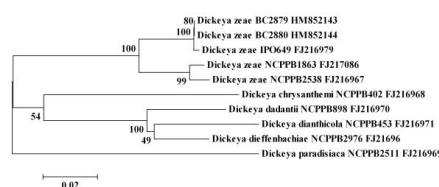


Figure 2

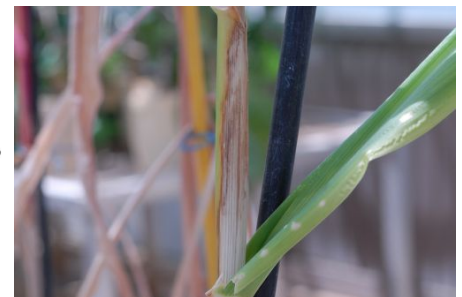


Figure 3

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