**GENOME ANNOUNCEMENT**

**Genome Sequence of *Pectobacterium carotovorum* subsp. *carotovorum* Strain PCC21, a Pathogen Causing Soft Rot in Chinese Cabbage**

Tae-Ho Park, a Beom-Soon Choi, b Ah-Young Choi, b Ik-Young Choi, b Sunggi Heu, c and Beom-Seok Park d

Department of Horticulture, Daegu University, Gyeongsan, Republic of Korea a; National Instrumentation Center for Environmental Management, Seoul National University, Seoul, Republic of Korea b; Microbial Safety Division, National Academy of Agricultural Science, Rural Development Administration, Suwon, Republic of Korea c; and Genomics and Functional Bio-Material Division, National Academy of Agricultural Science, Rural Development Administration, Suwon, Republic of Korea d

*Pectobacterium carotovorum* is a plant-pathogenic enterobacterium responsible for soft rot in various commercially important plants. Here we report the complete genome sequence and automatic annotation of strain PCC21.

In summary, the analysis of the unclosed genome sequence of *P. carotovorum* subsp. *carotovorum* showed a genome size of 4,842,771 bp, with a mean GC content of 52.18%, and it is comparable to the published genome sizes of closely related species, which range from 3.8 to 5.1 Mbp (1, 4, 6, 9, 10). The coding regions accounted for 86.1% of the total sequence, and 4,263 annotated coding sequences (CDSs) had an average length of 978 bp. Finally, 22 rRNA operons and 76 tRNA sequences were identified in the chromosome and, among the 4,263 CDSs, 82 (2.3%) had no matches in the current NCBI database.

**Nucleotide sequence accession number.** The sequence has been deposited in GenBank under accession number CP003776.

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**REFERENCES**