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Draft Genome Sequence of *Clavibacter michiganensis* subsp. *nebraskensis* Strain DOAB 397, Isolated from an Infected Field Corn Plant in Manitoba, Canada

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In 2014, the pathogen *Clavibacter michiganensis* subsp. *nebraskensis* was isolated from symptomatic corn leaves in Manitoba, Canada. We report the draft genome sequence of *C. michiganensis* subsp. *nebraskensis* DOAB 397, consisting of 3.059 Mb with 73.0% G+C content, 2,922 predicted protein-coding sequences, 45 tRNAs, 3 rRNAs, and 37 pseudogenes.

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Clavibacter michiganensis subsp. *nebraskensis* (CMN) is the causal agent of Goss's wilt and blight disease of corn. The disease was first reported in 1969 in south-central Nebraska, USA, but became sporadic after partially resistant cultivars were identified in field corn (1). Goss's wilt has reemerged and is spreading rapidly in major corn-growing regions of the United States and Canada. This pathogen is a concern to corn growers given the potential high yield losses (up to 50%) that could be incurred from systemic infections as well as its phytosanitary risk to nonendemic international trade partners such as Europe and China. In 2014, we isolated *Clavibacter michiganensis* subsp. *nebraskensis* DOAB 397 from symptomatic corn leaves in Manitoba, Canada, confirming the establishment of the disease in this Canadian province. We report the draft genome sequence of *Clavibacter michiganensis* subsp. *nebraskensis* DOAB 397. Genomic DNA shearing, library preparation, and the whole-genome shotgun sequence of *Clavibacter michiganensis* subsp. *nebraskensis* DOAB 397 were performed by the Génome-Québec Innovation Centre (Montreal, Canada). The draft genome was determined by paired-end sequencing using Illumina MiSeq technology (Génome-Québec, Montreal, Canada). A total of 1,078,908 paired-end reads, each 250 bp in length, totaling 269,727,000 bp, were obtained. The quality of the reads was checked by using FastQC version 0.11.3 (2). *De novo* assembly was performed using ABySS version 1.5.2 (3) at different *k*-mer values (75–113). A *k*-mer value of 97 gave the best assembly quality (no misassembled scaffolds) based on QUAST version 2.3 (4). Scaffolds with length <300 bp were discarded. The draft genome comprises 28 scaffolds (minimum, 3,207 bp; maximum, 428,173 bp; N_{50}, 142,187 bp; total size, 3,059,794 bp). The G+C content of the draft genome is 73.0% with an overall estimated coverage of 89×.

The 28 scaffolds of *Clavibacter michiganensis* subsp. *nebraskensis* DOAB 397 were ordered and oriented based on the complete genome sequence of the type strain, *Clavibacter michiganensis* subsp. *nebraskensis* NCPPB 2581^T (NC_020891) using the CAR software (5). The NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) revealed that the draft genome of *Clavibacter michiganensis* subsp. *nebraskensis* DOAB 397 contains 2,922 predicted protein-coding sequences, 45 tRNAs, 37 pseudogenes, 3 rRNAs, and 1 other RNA. Compared to PGAAP, CMG-Biotools (6) predicted 2,903 genes based on Prodigal (7), whereas RNAmmer version 1.2 (8) predicted 3 rRNAs containing one copy each of 16S rRNA, 5S rRNA, and 23S rRNA. The number of predicted tRNAs genes was confirmed by tRNAscan-SE version 1.3.1 software (9). Analysis of the draft genome of strain DOAB 397 revealed that it has 14 more genes than the complete genome sequence of *Clavibacter michiganensis* subsp. *nebraskensis* NCPPB 2581^T, the type strain isolated in 1969. A more detailed analysis of strain DOAB 397 will be included in a future publication.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LAKL00000000. The version described in this paper is the first version, LAKL01000000.

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