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Draft Genome Sequence of a Quorum-Sensing Bacterium, *Dickeya* sp. Strain 2B12, Isolated from a Freshwater Lake

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***Dickeya* sp. strain 2B12 was isolated from a freshwater lake in Malaysia. Here, we report the draft genome sequence of *Dickeya* sp. 2B12 sequenced by the Illumina MiSeq platform. With the genome sequence available, this genome sequence will be useful for the study of quorum-sensing activity in this isolate.**

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All members of the *Enterobacteriaceae* family that are pathogenic to plants, both pectolytic (*Erwinia carotovora* and *Erwinia chrysanthemi*) and nonpectolytic (*Erwinia amylovora*), were assigned into a new genus, *Erwinia*, in 1917 (1). Despite the original notion that *Erwinia chrysanthemi* is a pathogen of chrysanthemum (2), and thus named as such, it was later discovered to infect a wide range of plant hosts (3, 4). *E. chrysanthemi* strains were classified into several pathovars according to pathogenicity on host plants and biochemical and physiological differences (5). This species was later transferred into a new genus called *Dickeya*, which now comprises eight species (*D. chrysanthemi*, *D. dadantii*, *D. dianthicola*, *D. dieffenbachiae*, *D. zeae*, *D. paradisiaca*, *D. solani*, and *D. aquatica*) (1, 2, 6). Here, we present a draft genome sequence of *Dickeya* sp. strain 2B12, isolated from a fresh lake water sample.

The genome of *Dickeya* sp. 2B12 was sequenced by an Illumina MiSeq sequencer with a 150-bp read chemistry. In brief, genomic DNA of *Dickeya* sp. 2B12 was extracted from an overnight culture using a Master Pure DNA purification kit (Epicentre, Inc., Madison, WI, USA). The quality and quantity of the DNA was assessed via a NanoDrop spectrophotometer (ThermoScientific, Waltham, MA, USA) and a Qubit 2.0 fluorometer (Life Technologies, Carlsbad, CA, USA). Then, 50 ng of DNA was used to construct a sequencing library using a Nextera DNA sample prep kit (Illumina, San Diego, CA, USA) according to the manufacturer's protocol. The library was quantified by a Qubit 2.0 fluorometer and Bioanalyzer high-sensitivity chip (Agilent Technologies, Santa Clara, CA, USA). A sequencing run was set up to generate 2 × 150 base-paired reads.

The raw reads were trimmed at Q30, resulting in 1,745,868 reads with an average length of 144.3 bp. The reads were assembled *de novo* using CLC Genomic Workbench 6 (CLC Bio, Denmark), giving 120 contigs with an N_{50} of 92,830 bp, constituting a genome size of 4,349,822 bp. The assembled genome has a GC content of 54.5%. There are 107 contigs with an average coverage of 30×, and the average coverage across the genome is 46.7×. This

genome was annotated using Rapid Annotation using Subsystem Technology (RAST), version 2.0 (7), which revealed the presence of 3,965 coding sequences and 77 RNA genes, with 59% of the coding sequences (CDS) covered by the subsystem in the RAST server. The *Dickeya* sp. 2B12 harbors putative pectate lyase and cellulase genes in its genome, which suggest the potential of *Dickeya* sp. 2B12 as a plant pathogen, a well-known role performed by other members of *Dickeya* spp. (1, 2). Interestingly, a pair of *luxI*/*luxR* homologues was also present in the genome in contig 11, suggesting the adaptation of a quorum-sensing system to regulate gene expression in this bacterium.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JSYG00000000](https://www.ncbi.nlm.nih.gov/nuclink/JSYG00000000). The version described in this paper is the first version.

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