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Whole-Genome Sequencing Analysis of *Chromobacterium piscinae* Strain ND17, a Quorum-Sensing Bacterium

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Here, we report the draft genome sequence of *Chromobacterium piscinae* strain ND17. This bacterium was isolated from a fresh water sample in Malaysia and exhibits quorum-sensing activity. This first draft genome of *C. piscinae* strain ND17 will pave the way to future studies of the quorum-sensing properties of this isolate.

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Bacteria communicate to control physiological activities such as virulence determinants, competence, symbiosis, antibiotic production, and biofilm formation (1). This bacterial cell-to-cell communication is known as "quorum sensing" (QS), a term first introduced by Fuqua and colleagues (2, 3). QS is achieved by generation and response of QS signaling molecules which refer to small, self-generated signal molecules (4). QS is a function that is population density dependent (5).

Chromobacterium piscinae is a Gram-negative, aerobic, rod-shaped, motile bacterium with violet pigmentation (6). In this study, we report the whole genome of *Chromobacterium piscinae* strain ND17. *C. piscinae* strain ND17 was isolated from a fresh water sample in Malaysia. Genomic DNA was extracted by using a MasterPure DNA purification kit (Epicentre, Inc., Madison, WI, USA). Next, a NanoDrop spectrophotometer (Thermo Scientific, Waltham, MA, USA) and Qubit 2.0 fluorometer (Life Technologies, Carlsbad, CA, USA) were used to determine the quality of the DNA extracted. An Illumina MiSeq sequencer (Illumina, Inc., San Diego, CA, USA) was used to sequence the bacterium genome. An average coverage of 38.5-fold was obtained for the draft genome of 4,089,562 bp in 223 contigs with an N_{50} of 43,813. The paired-end reads were trimmed and *de novo* assembled with CLC Genomic Workbench version 5.1 (CLC Bio, Denmark). Prodigal (version 2.60) was used for gene prediction (7) and Rapid Annotation Subsystem Technology (RAST) was used for gene annotation (8). tRNA was predicted with tRNAscan SE version 1.21 (9) and rRNA with RNAmmer (10).

The G+C content of the *C. piscinae* strain ND17 genome is 62.6%. The total number of predicted genes is 3,916, of which 3,506 are protein coding genes with predicted function numbers, equivalent to approximately 90% of the total number of predicted genes. A total of 81 tRNAs, two copies of 5S rRNA, and a copy of each 16S rRNA and 23S rRNA were predicted for strain ND17. Based on the annotation result, the *C. piscinae* strain ND17 genome is comprised of 89 genes responsible for virulence, disease, and defense, where most of the genes are connected with antibiotics and toxic compounds resistance. This is the first finding reported on QS of *C. piscinae*. We hope this annotated genome of strain ND17 will be a valuable tool for better understanding the QS mechanism of *C. piscinae* strain ND17.

Nucleotide sequence accession numbers. This whole-genome-shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. JTGE00000000. The version described in this paper is the first version, JTGE01000000.

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