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GENOME ANNOUNCEMENT

# Whole-Genome Sequence of *N*-Acylhomoserine Lactone-Synthesizing and -Degrading *Acinetobacter* sp. Strain GG2

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***Acinetobacter* sp. strain GG2 is a quorum-sensing and quorum-quenching bacterium isolated from the ginger rhizosphere. It degrades a broad range of *N*-acylhomoserine lactone molecules via lactonase. The genome sequence of strain GG2 may provide insights on the regulation of quorum-sensing and quorum-quenching mechanisms in this bacterium.**

Members of the genus *Acinetobacter* are always subjects of research because they have great potentials in biotechnology and environmental sciences. *Acinetobacter* is also a well-known emerging multidrug-resistant nosocomial infectious pathogen (2). Previous reports have shown that *Acinetobacter* spp. possess either quorum-sensing (QS) or quorum-quenching (QQ) activity (2, 5, 8). However, recently, our group has reported that *Acinetobacter* sp. strain GG2, isolated from the rhizosphere of ginger (*Zingiber officinale*) growing in the Malaysian rainforest, exhibits both QS and QQ activities (3). Strain GG2 can degrade various types of *N*-acylhomoserine lactone (AHL) molecules, ranging from $C_5$-homoserine lactone ($C_5$-HSL) to $C_{14}$-HSL, via a broad-spectrum lactonase activity. The lactonase of strain GG2 degrades AHL molecules regardless of the substituent group at the C-3 position of the AHL molecules (3). Here, we sequenced the complete genome of *Acinetobacter* sp. strain GG2 as a step toward understanding the molecular regulation of QS systems and searching for the QQ gene in this bacterium.

Genomic DNA of *Acinetobacter* sp. strain GG2 was isolated using the QIAamp DNA minikit (Qiagen, Germany) per the manufacturer's instructions. The quality of DNA was examined using a Nanodrop spectrophotometer (Thermo Scientific) and a Qubit 2.0 fluorometer (Life Technologies). The whole-genome sequencing of strain GG2 was performed using the Illumina HiSeq 2000 platform after the construction of a sequencing library using the TruSeq DNA sample preparation kit, v2 (Illumina Inc., CA). This resulted in 2,466,436 filtered reads and approximately 56-fold coverage. The filtered reads were *de novo* assembled with the CLC Genomic Workbench v5.1, generating 57 contigs ($N_{50}$, 168,611 bp), containing a total of 3,890,805 bp. The G+C content of this genome is 38.4%. Gene prediction was performed using Prodigal (v2.60), and a total of 3,572 open reading frames (ORFs) were predicted (6). Annotation was performed using Blast2GO (4) against the NCBI-NR sequence database (1). One complete rRNA operon and one copy each of the 5S rRNA gene, the 23S rRNA gene, and the 16S rRNA gene were identified using RNAmmer (9). A total of 49 tRNAs were identified using tRNAscan-SE (10).

Based on Blast2GO analysis, the AHL synthase gene of *Acinetobacter* sp. strain GG2 was found in contig 3. It has a high percentage of similarity (95%) to the AHL synthase gene of *Acinetobacter* sp. strain DR1 (7). Furthermore, a putative AHL-lactonase gene that has a metallo-beta-lactamase domain was found *in silico* in contig 2.

**Nucleotide sequence accession numbers.** This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ALOW00000000. The version described in this paper is the first version, ALOW01000000.

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## REFERENCES

1. **Benson DA, et al.** 2012. GenBank. Nucleic Acids Res. **40**:D48–D53.
2. **Bhargava N, Sharma P, Capalash N.** 2010. Quorum sensing in *Acinetobacter*: an emerging pathogen. Crit. Rev. Microbiol. **36**:349–360.
3. **Chan KG, et al.** 2011. Characterization of *N*-acylhomoserine lactone-degrading bacteria associated with the *Zingiber officinale* (ginger) rhizosphere: co-existence of quorum quenching and quorum sensing in *Acinetobacter* and *Burkholderia*. BMC Microbiol. **11**:51. doi:10.1186/1471-2180-11-51.
4. **Conesa A, et al.** 2005. Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. Bioinformatics **21**: 3674–3676.
5. **Garner AL, et al.** 2012. Stereochemical insignificance discovered in *Acinetobacter baumannii* quorum sensing. PLoS One **7**:e37102. doi:10.1371/journal.pone.0037102.
6. **Hyatt D, et al.** 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics **11**:119. doi: 10.1186/1471-2105-11-119.
7. **Jung J, Baek JH, Park W.** 2010. Complete genome sequence of the diesel-degrading *Acinetobacter* sp. strain DR1. J. Bacteriol. **192**:4794–4795.
8. **Kang BR, et al.** 2004. Degradation of acyl-homoserine lactone molecules by *Acinetobacter* sp. strain C1010. Can. J. Microbiol. **50**:935–941.
9. **Lagesen K, et al.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35**:3100–3108.
10. **Lowe TM, Eddy SR.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25**: 955–964.

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