

Draft Genome Sequence of *Pantoea* sp. Strain A4, a *Rafflesia*-Associated Bacterium That Produces *N*-Acylhomoserine Lactones as Quorum-Sensing Molecules

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***Pantoea* sp. strain A4 is a Gram-negative bacterium isolated from the *Rafflesia* flower. We present here, for the first time, the genome sequence of *Rafflesia*-associated *Pantoea* sp. strain A4, which exhibited quorum-sensing activity.**

Rafflesia is an endophytic holoparasite flowering plant found mostly in Southeast Asia, and it is one of the world's largest flowers (1, 2). A member of the genus *Pantoea* has been reported to synthesize quorum-sensing signaling molecules, i.e., *N*-acylhomoserine lactones (AHLs) (9), that regulate several phenotypes, such as virulence factor production, cell aggregation (8), and biofilm formation (7). Here we present the genome sequence of *Pantoea* sp. strain A4, an AHL-producing bacterium isolated from *Rafflesia cantleyi* in the tropical rain forest of Peninsular Malaysia. We sequenced the complete genome of *Pantoea* sp. strain A4 as a step toward understanding the molecular regulation of the quorum-sensing system in this bacterium.

The total genomic DNA of *Pantoea* sp. strain A4 was isolated using the QIAamp DNA Mini kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. The quality of the DNA was examined using a Nanodrop spectrophotometer (Thermo Scientific) and a Qubit 2.0 fluorometer (Life Technologies). Whole-genome sequencing of *Pantoea* sp. strain A4 was performed using the Illumina HiSeq 2000 (Illumina, Inc.) platform. This resulted in 577,857,447 filtered reads with an average read length of 77.94 bp and approximately 108.25-fold coverage. The filtered reads were *de novo* assembled with CLC Genomic Workbench version 5.1, generating 72 contigs (N₅₀, 224,734.58). The genome contains a total of 5,331,108 bp with a G+C content of 52.91%. Gene prediction was performed using Prodigal (version 2.60), and a total of 4,793 open reading frames were predicted (4) and annotated by comparison with the NCBI nonredundant database (3). A total of 43 tRNAs were predicted using tRNAscan-SE (v.1.21) (6), and the rRNAs were predicted using the RNAmmer 1.2 server (5).

From the BLAST results, *Pantoea* sp. strain A4 possesses two AHL synthase genes, of which the first is similar to *eanI* of *Pantoea ananatis* (identity score of 74%) and the other is similar to *phzI* of *Pantoea* sp. (identity score of 79%). The genome sequence of *Pantoea* sp. strain A4 may provide novel insight into the quorum-sensing regulation mechanism of this bacterium.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/

GenBank under accession no. [ALXE000000000](https://www.ncbi.nlm.nih.gov/nuclot/ALXE000000000). The version described in this paper is the first version, [ALXE010000000](https://www.ncbi.nlm.nih.gov/nuclot/ALXE010000000).

ACKNOWLEDGMENTS

K.-G. Chan thanks the University of Malaya for the financial support awarded (High Impact Research Grant A000001-50001).

We thank Sonny Wong (Malaysian Nature Society) for his assistance during the field sampling of the *Rafflesia* flower.

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Received 30 August 2012 Accepted 17 September 2012

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doi:10.1128/JB.01619-12