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# Whole-Genome Analysis of Quorum-Sensing *Burkholderia* sp. Strain A9

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***Burkholderia* spp. rely on *N*-acyl homoserine lactone as quorum-sensing signal molecules which coordinate their phenotype at the population level. In this work, we present the whole genome of *Burkholderia* sp. strain A9, which enables the discovery of its *N*-acyl homoserine lactone synthase gene.**

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Bacteria communicate through signaling molecules, a cell-cell communication known as quorum sensing (QS) (1, 2). *N*-Acyl homoserine lactone (AHL) is one of the common QS signaling molecules synthesized by *Proteobacteria* (3). *Burkholderia* spp. are pathogens often found in the lungs of cystic fibrosis patients, and uses AHL as the QS signaling molecule to communicate not only within the same species but also between the bacterial community residing in the human lung upon infection (4–6). The QS property of *Burkholderia* sp. strain A9 has been confirmed, but the gene responsible for its AHL production remains unknown (7). In view of this, we performed whole-genome sequencing of *Burkholderia* sp. strain A9 with the ultimate goal of searching for its AHL synthase gene.

*Burkholderia* sp. strain A9 was isolated from soil using a KGM medium and routinely maintained on a Luria-Bertani medium (7, 8). Bacterial genomic DNA was extracted with MasterPure DNA purification kit (Epicenter, USA) and subjected to next generation sequencing (NGS) sample preparation with a Nextera DNA library preparation kit (Illumina, USA) (9, 10). The sequencing library was quantified using Qubit 2.0 (Invitrogen, USA) and qualified with Bioanalyzer (Agilent, USA). The NGS was performed on MiSeq (Illumina, USA) (10). Sequencing raw reads were trimmed and assembled using CLC Genomic Workbench (v7.5) (11). Subsequently, the genome was annotated using NCBI prokaryotic annotation pipeline (v2.9) and BLAST against the NCBI nonredundant (NR) database (12, 13).

A total of 1.8 million reads were generated in this sequencing project. The draft genome of *Burkholderia* sp. strain A9 was assembled into 98 contigs with an  $N_{50}$  of 136,739 bp resulting in a genome size of 3.46 Mbps. The average coverage of this genome is 32-fold, and the G+C content is 65.62%. A total of 3,010 coding DNA sequences (CDS) were identified from this genome. The genome sequence of *Burkholderia* sp. strain A9 contains 3,128 genes, 89 pseudogenes, 5 rRNAs, and 23 tRNAs.

Our previous study confirmed that *Burkholderia* sp. strain A9 produces AHLs, namely, *N*-hexanoylhomoserine lactone and

*N*-octanoylhomoserine lactone (7). In this genome study, an AHL synthase gene with a length of 609 bp was determined by analysis of the genome sequence. It is located at 194,270 to 194,878 bp of contig 16. The AHL-based QS of *Burkholderia* spp. regulates the expression of its extracellular proteins production, siderophores production, biofilm maturation, and swarming ability (14–16). Thus, with the availability of this whole-genome information, future work can focus on the importance of the QS of environmental *Burkholderia* sp. strain A9.

**Nucleotide sequence accession numbers.** The draft genome of *Burkholderia* sp. strain A9 was deposited into DDBJ/EMBL/GenBank under accession no. JSZN00000000. The version described in this paper is the first version, JSZN01000000.

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## REFERENCES

- Bassler BL. 2002. Small talk: cell-to-cell communication in bacteria. *Cell* 109:421–424. [http://dx.doi.org/10.1016/S0092-8674\(02\)00749-3](http://dx.doi.org/10.1016/S0092-8674(02)00749-3).
- Waters CM, Bassler BL. 2005. Quorum sensing: cell-to-cell communication in bacteria. *Annu Rev Cell Dev Biol* 21:319–346. <http://dx.doi.org/10.1146/annurev.cellbio.21.012704.131001>.
- Pappas KM, Weingart CL, Winans SC. 2004. Chemical communication in *Proteobacteria*: biochemical and structural studies of signal synthases and receptors required for intercellular signalling. *Mol Microbiol* 53: 755–769. <http://dx.doi.org/10.1111/j.1365-2958.2004.04212.x>.
- Venturi V, Friscina A, Bertani I, Devescovi G, Aguilar C. 2004. Quorum sensing in the *Burkholderia cepacia* complex. *Res Microbiol* 155:238–244. <http://dx.doi.org/10.1016/j.resmic.2004.01.006>.
- Riedel K, Arevalo-Ferro C, Reil G, Görg A, Lottspeich F, Eberl L. 2003. Analysis of the quorum-sensing regulon of the opportunistic pathogen *Burkholderia cepacia* H111 by proteomics. *Electrophoresis* 24:740–750. <http://dx.doi.org/10.1002/elps.200390089>.
- Eberl L, Tümmler B. 2004. *Pseudomonas aeruginosa* and *Burkholderia*

- cepacia* in cystic fibrosis: genome evolution, interactions and adaptation. *Int J Med Microbiol* 294:123–131. <http://dx.doi.org/10.1016/j.ijmm.2004.06.022>.
7. Chen JW, Koh C-L, Sam C-K, Yin W-F, Chan K-G. 2013. Short chain *N*-acyl homoserine lactone production by soil isolate *Burkholderia* sp. strain A9. *Sensors (Basel)* 13:13217–13227. <http://dx.doi.org/10.3390/s131013217>.
  8. Wong C-S, Yin W-F, Choo Y-M, Sam C-K, Koh C-L, Chan K-G. 2012. Coexistence of quorum-quenching and quorum-sensing in tropical marine *Pseudomonas aeruginosa* strain MW<sub>3</sub>A. *World J Microbiol Biotechnol* 28:453–461. <http://dx.doi.org/10.1007/s11274-011-0836-x>.
  9. Han-Jen RE, Wai-Fong Y, Kok-Gan C. 2013. *Pandoraea* sp. RB-44, a novel quorum sensing soil bacterium. *Sensors (Basel)* 13:14121–14132. <http://dx.doi.org/10.3390/s131014121>.
  10. Chan X-Y, Chua KH, Yin W-F, Puthuchery SD, Chan K-G. 2014. Whole-genome analysis of *Aeromonas hydrophila* strain 187, exhibiting quorum-sensing activity. *Genome Announc* 2(6):e01360-14. <http://dx.doi.org/10.1128/genomeA.01360-14>.
  11. Chan XY, Chua KH, Puthuchery SD, Yin W-F, Chan K-G. 2012. Draft genome sequence of an *Aeromonas* sp. strain 159 clinical isolate that shows quorum-sensing activity. *J Bacteriol* 194:6350. <http://dx.doi.org/10.1128/JB.01642-12>.
  12. NCBI Resource Coordinators. 2013. Database resources of the national center for biotechnology information. *Nucleic Acids Res* 41:D8–D20. <http://dx.doi.org/10.1093/nar/gks1189>.
  13. McCulloch JA, de Oliveira VM, de Almeida Pina AV, Pérez-Chaparro PJ, de Almeida LM, de Vasconcelos JM, de Oliveira LF, da Silva DEA, Rogez HLG, Cretenet M, Mamizuka EM, Nunes MRT. 2014. Complete genome sequence of *Lactococcus lactis* strain AI06, an endophyte of the Amazonian açai palm. *Genome Announc* 2(6):e01225-14. <http://dx.doi.org/10.1128/genomeA.01225-14>.
  14. Huber B, Riedel K, Hentzer M, Heydorn A, Gotschlich A, Givskov M, Molin S, Eberl L. 2001. The cep quorum-sensing system of *Burkholderia cepacia* H111 controls biofilm formation and swarming motility. *Microbiology* 147:2517–2528.
  15. Sokol PA, Sajjan U, Visser MB, Gingues S, Forstner J, Kooi C. 2003. The CepIR quorum-sensing system contributes to the virulence of *Burkholderia cenocepacia* respiratory infections. *Microbiology* 149:3649–3658. <http://dx.doi.org/10.1099/mic.0.26540-0>.
  16. Aguilar C, Friscina A, Devescovi G, Kojic M, Venturi V. 2003. Identification of quorum-sensing-regulated genes of *Burkholderia cepacia*. *J Bacteriol* 185:6456–6462. <http://dx.doi.org/10.1128/JB.185.21.6456-6462.2003>.