Draft Genome Sequence of Acinetobacter johnsonii C6, an Environmental Isolate Engaging in Interspecific Metabolic Interactions

Kaas, Rolf Sommer; Mordhorst, Hanne; Leekitcharoenphon, Pimlapas; Jensen, Jacob Dyring; Haagensen, Janus Anders Juul; Molin, Søren; Pamp, Sünje Johanna

Published in:
Genome Announcements

Link to article, DOI:
10.1128/genomeA.00155-17

Publication date:
2017

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):

General rights
Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.
Draft Genome Sequence of *Acinetobacter johnsonii* C6, an Environmental Isolate Engaging in Interspecific Metabolic Interactions

Rolf Sommer Kaas,a Hanne Mordhorst,a Pimlapas Leekitcharoenphon,a Jacob Dyring Jensen,a Janus A. J. Haagensen,b Søren Molin,b Sünje Johanna Pampa

Research Group for Genomic Epidemiology, Technical University of Denmark, Kongens Lyngby, Denmarka; Novo Nordisk Center for Biosustainability, Technical University of Denmark, Kongens Lyngby, Denmarkb

**ABSTRACT** *Acinetobacter johnsonii* C6 originates from creosote-polluted groundwater and performs ecological and evolutionary interactions with *Pseudomonas putida* in biofilms. The draft genome of *A. johnsonii* C6 is 3.7 Mbp and was shaped by mobile genetic elements. It reveals genes facilitating the biodegradation of aromatic hydrocarbons and resistance to antimicrobials and metals.

*A. johnsonii* C6 (formerly, *Acinetobacter* sp. strain C6) was isolated in 1994 from a microbial community of a creosote-contaminated aquifer at a gasworks in Fredensborg, Denmark (1, 2). Creosotes are mixtures of chemicals formed during natural gas production, which can contain aromatic hydrocarbons and a variety of heterocycles. Despite their toxicity, creosotes were used as medical treatment against infections, toothache, gastrointestinal, and respiratory complications.

*A. johnsonii* C6 forms biofilms and participates in interspecific interactions, including metabolic interactions, with *Pseudomonas putida* (3–6). The genetic determinants for these activities are largely unknown. Here, we report the draft genome sequence of *A. johnsonii* C6. It was generated using Illumina MiSeq sequencing (2 × 250 cycles), yielding 593,389 raw read pairs and a depth of coverage of ~68×. The reads were trimmed and filtered using bbduk2 (BBMap 35.82) (http://jgi.doe.gov/data-and-tools/bbtools/) and assembled using SPAdes 3.7.0 (7). Contigs smaller than 500 bp or with coverage below 2× were removed. The draft genome is 3,705,435 bp in 26 contigs, with a G+C content of 41.7%. It contains 3,543 genes, as predicted using Prodigal (8), 77 tRNA genes, and one rRNA operon (16S, 23S, 5S). The 16S rRNA gene sequence had >99% sequence similarity to *A. johnsonii* XBB1 (accession no. NZ_CP010350.1), *A. johnsonii* ATCC 17909T (accession no. Z93440.1), and *A. johnsonii* DSM 6963 (accession no. X81663.1) (9–11). Putative functions for predicted proteins were assigned using PROKKA 1.1 and by comparing sequences to the public databases Pfam, KEGG, InterPro, and CARD (12–16), followed by submission-ready file conversion (https://bitbucket.org/RolfKaas/gff3_to_ena_embl).

*A. johnsonii* C6 encodes proteins predicted to convert aromatic hydrocarbons, such as benzyl alcohol, benzoate, fluorobenzoate, dihydroxybenzoate, methylcatechol, methylbenzyl alcohol, hydroxybenzaldehyde, hydroxymethylnaphthalene, naphthalenemethanol, benzene, toluene, chlorobenzene, and cyclohexanol. Previously, it was shown that this strain could grow on toluene, benzyl alcohol, and benzoate (4, 5).

A number of antimicrobials, as well as heavy metals (e.g., arsenate, mercury, tellurite, copper, and chromate), may be tolerated by *A. johnsonii* C6, mainly facilitated by proteins involved in their efflux, transport, reduction, and functions encoded by anti-
biotic resistance genes, such as \( \text{bla}_{\text{OXA-334}} \) (OXA-211 family) and \( \text{catB} \). In vitro assays revealed that \textit{A. johnsonii} C6 was resistant to chloramphenicol, trimethoprim, cefoxitin, and quinupristin-dalfopristin. \textit{A. johnsonii} C6 may produce secondary metabolites, and it harbors biosynthetic gene clusters for a siderophore, aryl polyene, bacteriocin, and unknown metabolites, based on predictions by antiSMASH (17).

The \textit{A. johnsonii} C6 draft genome encodes 19 proteins containing GGDEF and/or EAL domains involved in c-di-GMP metabolism, and proteins involved in motility (pili), and secretion (type II secretion system [T2SS], T6SS, secretory-signal recognition particle [Sec-SRP], and Tat), suggesting dynamic interactions with their environment, including with other microorganisms. The presence of features related to plasmids, phages, and insertion sequence (IS) elements suggests that mobile genetic elements have shaped the evolution and ecology of \textit{A. johnsonii} C6.

The genome sequence of \textit{A. johnsonii} C6 will facilitate the understanding of its physiology, evolution, and interaction with \textit{P. putida}. Studies on \textit{A. johnsonii} could also provide new insight into the biodegradation of aromatic hydrocarbons and resistance to antimicrobials and toxic metals, with relevance to environmental biotechnology.

**Accession number(s).** The draft genome sequence of \textit{A. johnsonii} C6 is available from DDBJ/ENA/GenBank under the accession number FUUY00000000.

**ACKNOWLEDGMENTS**

The support from Frank M. Aarestrup and the National Food Institute at the Technical University of Denmark are greatly appreciated.

**REFERENCES**


