

Draft Genome Sequence of *Arthrobacter* sp. Strain SPG23, a Hydrocarbon-Degrading and Plant Growth-Promoting Soil Bacterium

Panagiotis Gkorezis,^a Eric M. Bottos,^b Jonathan D. Van Hamme,^b Sofie Thijs,^a Francois Rineau,^a  Andrea Franzetti,^c Maria Balseiro-Romero,^d Nele Weyens,^a Jaco Vangronsveld^a

Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium^a; Department of Biological Sciences, Thompson Rivers University, Kamloops, British Columbia, Canada^b; Department of Environmental Sciences, University of Milano-Bicocca, Milan, Italy^c; Department of Soil Science and Agricultural Chemistry, University of Santiago de Compostela, Campus Vida, Santiago de Compostela, Spain^d

We report here the 4.7-Mb draft genome of *Arthrobacter* sp. SPG23, a hydrocarbonoclastic Gram-positive bacterium belonging to the Actinobacteria, isolated from diesel-contaminated soil at the Ford Motor Company site in Genk, Belgium. Strain SPG23 is a potent plant growth promoter useful for diesel fuel remediation applications based on plant-bacterium associations.

Received 3 November 2015 Accepted 4 November 2015 Published 23 December 2015

Citation Gkorezis P, Bottos EM, Van Hamme JD, Thijs S, Rineau F, Franzetti A, Balseiro-Romero M, Weyens N, Vangronsveld J. 2015. Draft genome sequence of *Arthrobacter* sp. strain SPG23, a hydrocarbon-degrading and plant growth-promoting soil bacterium. *Genome Announc* 3(6):e01517-15. doi:10.1128/genomeA.01517-15.

Copyright © 2015 Gkorezis et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Jaco Vangronsveld, jaco.vangronsveld@uhasselt.be.

Members of the genus *Arthrobacter* have been associated with the degradation of compounds, such as 4-chlorophenol (1), polychlorinated biphenyls (2, 3), pentachloronitrobenzene, (4), 2-nitrobenzoate (5), atrazine (6), 2,4-dinitrotoluene (7), *para*-nitrophenol (8), 4-bromophenol (9), phenanthrene, and phthalates (10, 11). Genome sequence data indicate that several strains of *Arthrobacter* are capable of degrading aromatic compounds, including *Arthrobacter* sp. YC-RL1 (12), *Arthrobacter* sp. W1 (13), and *Arthrobacter* sp. strain SJCon (14).

Using gas chromatography (GC) (model 450; Agilent Technologies) coupled to mass spectrometry (MS) (model 220; Agilent Technologies), *Arthrobacter* sp. SPG23 was found to degrade up to 25% of diesel range organics over 10 days. Partial 16S rRNA gene sequence data and phenotypic profiling indicate that SPG23 is related to *Arthrobacter* sp. FB24 (GenBank accession no. CP000454).

For sequencing, genomic DNA was extracted with a Qiagen blood and tissue kit (Qiagen NV, Hilden, Germany), and an Ion Torrent PGM was used to generate a whole-genome shotgun using methods described by Thijs et al. (15).

In total, 912,912 reads (mean length, 214 bases) generated 196 Mb of data in Torrent suite 4.2.1, which were assembled into 38 contigs using MIRA 4.0.5 (16), giving a consensus length of 4,703,830 bp at 40.0× coverage (largest contig, 432,818 bp; N_{50} , 216.99 bp). Open reading frame (ORF) prediction and gene annotation were carried out using the PGAP (NCBI) pipeline (17). The contigs were ordered in Mauve (18) using the *Arthrobacter* sp. FB24 genome as a reference.

The SPG23 genome consists of a single circular chromosome (66.3% G+C content), including 3,902 coding genes that were arranged into pathways using Pathway Tools (19, 20), 280 pseudogenes, 15 rRNAs (5S, 16S, and 23S), 52 tRNAs, and 1 noncoding RNA (ncRNA).

Annotation has predicted gene-coding clusters for alkane degradation (5 genes), benzene degradation (9 genes), and naphthalene (8

genes). Genes for plant growth-promoting traits are present, affirming the results from phenotypic assays that determined that these are involved in symbiotic nitrogen fixation, siderophore biosynthesis, and inorganic phosphorus solubilization and uptake.

Based on both its hydrocarbon-degrading and plant growth-promoting capacities, *Arthrobacter* sp. SPG23 is a promising candidate as an inoculant to stimulate the phytoremediation of petroleum-contaminated sites.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JYCN00000000. The version described in this paper is version JYCN01000000.

ACKNOWLEDGMENTS

This work was supported by the Hasselt University BOF project 06G02 and the Methusalem project 08M03VGRJ.

REFERENCES

1. Westerberg K, Elvang AM, Stackebrandt E, Jansson JK. 2000. *Arthrobacter chlorophenolicus* sp. nov., a new species capable of degrading high concentrations of 4-chlorophenol. *Int J Syst Evol Microbiol* 50: 2083–2092. <http://dx.doi.org/10.1099/00207713-50-6-2083>.
2. Abramowicz DA. 1990. Aerobic and anaerobic biodegradation of PCBs: a review. *Crit Rev Biotechnol* 10:241–249. <http://dx.doi.org/10.3109/07388559009038210>.
3. Stella T, Covino S, Burianová E, Filipová A, Křesinová Z, Voříšková J, Větrovský T, Baldrian P, Cajthaml T. 2015. Chemical and microbiological characterization of an aged PCB-contaminated soil. *Sci Total Environ* 533:177–186. <http://dx.doi.org/10.1016/j.scitotenv.2015.06.019>.
4. Wang Y, Wang C, Li A, Gao J. 2015. Biodegradation of pentachloronitrobenzene by *Arthrobacter nicotianae* DH19. *Lett Appl Microbiol* 61: 403–410. <http://dx.doi.org/10.1111/lam.12476>.
5. Arora PK, Sharma A. 2015. New metabolic pathway for degradation of 2-nitrobenzoate by *Arthrobacter* sp. SPG. *Front Microbiol* 6:551. <http://dx.doi.org/10.3389/fmicb.2015.00551>.
6. Ying Z, Zhang Q, Chao N, Ge S, Zhao J, Miao H, Bo C. 2015. Biodegradation of atrazine by free and immobilized cells of *Arthrobacter* sp. strain DNS10. *Environ Eng Manag J* 14:819–826.
7. Küce P, Coral G, Kantar Ç. 2015. Biodegradation of 2,4-dinitrotoluene

- (DNT) by *Arthrobacter* sp. K1 isolated from a crude oil contaminated soil. *Ann Microbiol* 65:467–476. <http://dx.doi.org/10.1007/s13213-014-0880-5>.
8. Sahoo NK, Pakshirajan K, Ghosh PK. 2011. Batch biodegradation of *para*-nitrophenol using *Arthrobacter chlorophenolicus* A6. *Appl Biochem Biotechnol* 165:1587–1596. <http://dx.doi.org/10.1007/s12010-011-9379-8>.
 9. Sahoo NK, Pakshirajan K, Ghosh PK. 2014. Biodegradation of 4-bromophenol by *Arthrobacter chlorophenolicus* A6 in batch shake flasks and in a continuously operated packed bed reactor. *Biodegradation* 25: 265–276. <http://dx.doi.org/10.1007/s10532-013-9658-x>.
 10. Wen Z, Gao D, Wu W. 2014. Biodegradation and kinetic analysis of phthalates by an *Arthrobacter* strain isolated from constructed wetland soil. *Appl Microbiol Biotechnol* 98:4683–4690. <http://dx.doi.org/10.1007/s00253-014-5568-z>.
 11. Vandera E, Samiotaki M, Parapouli M, Panayotou G, Koukkou AI. 2015. Comparative proteomic analysis of *Arthrobacter phenanthrenivorans* Sphe3 on phenanthrene, phthalate and glucose. *J Proteomics* 113: 73–89. <http://dx.doi.org/10.1016/j.jprot.2014.08.018>.
 12. Ren L, Shi Y, Jia Y, Yan Y. 2015. Genome sequence of *Arthrobacter* sp. YC-RL1, an aromatic compound-degrading bacterium. *Genome Announc* 3(4):e00749-15. <http://dx.doi.org/10.1128/genomeA.00749-15>.
 13. Jiang Y, Qu Y, Xu P, Tang H. 2015. Genome sequence of a versatile aromatic hydrocarbon-degrading bacterium, *Arthrobacter* sp. W1. *Genome Announc* 3(2):e00387-15. <http://dx.doi.org/10.1128/genomeA.00387-15>.
 14. Vikram S, Kumar S, Vaidya B, Pinnaka AK, Raghava GPS. 2013. Draft genome sequence of the 2-chloro-4-nitrophenol-degrading bacterium *Arthrobacter* sp. strain SJCon. *Genome Announc* 1(2):e00058-13. <http://dx.doi.org/10.1128/genomeA.00058-13>.
 15. Thijs S, Van Hamme J, Gkorezis P, Rineau F, Weyens N, Vangronsveld J. 2014. Draft genome sequence of *Raoultella ornithinolytica* TNT, a trinitrotoluene-denitrating and plant growth-promoting strain isolated from explosive-contaminated soil. *Genome Announc* 2(3):e00491-14. <http://dx.doi.org/10.1128/genomeA.00491-14>.
 16. Chevreur B, Pfisterer T, Drescher B, Driesel AJ, Muller WEG, Wetter T, Suhai S. 2004. Using the miraEST assembler for reliable and automated mRNA transcript assembly and SNP detection in sequenced ESTs. *Genome Res* 14:1147–1159. <http://dx.doi.org/10.1101/gr.1917404>.
 17. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity GM, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of Standard Operating Procedures (SOPs) for (meta)genomic annotation. *Omics* 12: 137–141. <http://dx.doi.org/10.1089/omi.2008.0017>.
 18. Rissman AI, Mau B, Biehl BS, Darling AE, Glasner JD, Perna NT. 2009. Reordering contigs of draft genomes using the Mauve aligner. *Bioinformatics* 25:2071–2073. <http://dx.doi.org/10.1093/bioinformatics/btp356>.
 19. Caspi R, Altman T, Billington R, Dreher K, Foerster H, Fulcher CA, Holland TA, Keseler IM, Kothari A, Kubo A, Krummenacker M, Latendresse M, Mueller LA, Ong Q, Paley S, Subhraveti P, Weaver DS, Weerasinghe D, Zhang P, Karp PD. 2014. The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. *Nucleic Acids Res* 42:D459–D471. <http://dx.doi.org/10.1093/nar/gkt1103>.
 20. Karp PD, Paley S, Romero P. 2002. The Pathway Tools software. *Bioinformatics* 18(Suppl 1):S225–S232. http://dx.doi.org/10.1093/bioinformatics/18.suppl_1.S225.