

Genome Sequence of *Cupriavidus metallidurans* Strain H1130, Isolated from an Invasive Human Infection

Pieter Monsieurs,^a Ann Provoost,^a Kristel Mijndonckx,^a Natalie Leys,^a Christiane Gaudreau,^b Rob Van Houdt^a

Unit of Microbiology, Belgian Nuclear Research Centre (SCK-CEN), Mol, Belgium^a; Microbiologie Médicale et Infectiologie, Centre Hospitalier de l'Université de Montréal (CHUM)-Hôpital Saint-Luc, Montréal, Québec, Canada^b

***Cupriavidus metallidurans* H1130 was repeatedly isolated from different blood culture sets taken from a patient suffering from significant nosocomial septicemia. Here, we announce the H1130 genome sequence for use in comparative analyses and for exploring the adaptation and pathogenic potential of this bacterium.**

Received 5 November 2013 Accepted 15 November 2013 Published 12 December 2013

Citation Monsieurs P, Provoost A, Mijndonckx K, Leys N, Gaudreau C, Van Houdt R. 2013. Genome sequence of *Cupriavidus metallidurans* strain H1130, isolated from an invasive human infection. *Genome Announc.* 1(6):e01051-13. doi:10.1128/genomeA.01051-13.

Copyright © 2013 Monsieurs et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Rob Van Houdt, rob.van.houdt@sckcen.be.

Cupriavidus metallidurans strains are frequently isolated from industrial sites linked to mining, metallurgic, and chemical industries (1–3), as well as from other anthropogenic environments not typified by metal contamination, such as spacecraft-related environments (4). *C. metallidurans* strains are Gram-negative, peritrichously flagellated bacterial rods with an oxidative metabolism (5) and are characterized by multiple metal resistances (1, 4, 6–8). Many of the metal resistance determinants are shared by all *C. metallidurans* strains, irrespective of the isolation type and location of a strain (6), and a substantial number of these determinants are carried by native megaplasmids like pMOL28 and pMOL30 of type strain CH34 (9). *C. metallidurans* strains do display substantial differences in their mobile gene pools (6), which include genomic islands (GIs), integrative and conjugative elements, transposons, and insertion sequence (IS) elements (10, 11).

C. metallidurans isolates are increasingly being recovered from medically relevant sources, such as patients with cystic fibrosis (12) and human cerebrospinal fluid (e.g., strain CCUG43015, deposited directly to the Culture Collection, University of Göteborg). Recently, the first case of invasive infection by *C. metallidurans* was reported (13). Four out of 5 blood culture sets taken over a period of 6 days from a patient with signs of sepsis were positive for a Gram-negative rod that was identified as *C. metallidurans* (GenBank accession no. GU230889). The genome of this isolate, designated H1130, was sequenced for comparative analyses and for exploring the adaptation and pathogenic potential of this bacterium.

Full-genome sequencing of *C. metallidurans* H1130 was performed by BaseClear (Leiden, The Netherlands) on the Illumina HiSeq 2000 platform using a paired-end sequencing library (50 nucleotides) (Illumina, Inc.), with an average insert size of 328 nucleotides (nt). The reads were filtered to remove low-quality reads, resulting in a total of 6,894,135 paired reads (7.03 Gbp). The genome of *C. metallidurans* H1130 was estimated to be 7,225,099 bp, which was sequenced with >98-fold genome coverage. *De novo* assembly of the paired reads was performed using two different

genome assembly tools, Velvet (hash length, 37; minimal contig length, 500; minimal coverage cov_cutoff, 6) and ABySS (parameter k set to 45), resulting in 683 and 1,099 contigs, respectively. Both assemblies were integrated using the Minimus software, resulting in a total of 118 assembled contigs.

Three replicons were identified, namely, 1 chromosome, 1 secondary chromosome or chromid (presence is phylogenetically linked [14]), and 1 megaplasmid (based on megaplasmid extraction analysis; for the method, see Mijndonckx et al. [4]). Genome annotation through the MicroScope platform (15) revealed 7,012 protein-encoding genes, 72 tRNA genes, and 24 rRNA genes, with a 63.5% G+C content.

Nucleotide sequence accession number. This project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AXBU00000000](https://www.ncbi.nlm.nih.gov/nuccore/AXBU00000000).

ACKNOWLEDGMENTS

This work was supported by the European Space Agency (ESA-PRODEX) and the Belgian Science Policy (Belspo) through the COMICS project (no. C90356).

REFERENCES

1. Goris J, De Vos P, Coenye T, Hoste B, Janssens D, Brim H, Diels L, Mergeay M, Kersters K, Vandamme P. 2001. Classification of metal-resistant bacteria from industrial biotopes as *Ralstonia campinensis* sp. nov., *Ralstonia metallidurans* sp. nov. and *Ralstonia basileensis* Steinle et al. 1998 emend. *Int. J. Syst. Evol. Microbiol.* 51:1773–1782.
2. Brim H, Heyndrickx M, de Vos P, Wilmotte A, Springael D, Schlegel HG, Mergeay M. 1999. Amplified rDNA restriction analysis and further genotypic characterisation of metal-resistant soil bacteria and related facultative hydrogenotrophs. *Syst. Appl. Microbiol.* 22:258–268.
3. Diels L, Mergeay M. 1990. DNA probe-mediated detection of resistant bacteria from soils highly polluted by heavy metals. *Appl. Environ. Microbiol.* 56:1485–1491.
4. Mijndonckx K, Provoost A, Ott CM, Venkateswaran K, Mahillon J, Leys N, Van Houdt R. 2013. Characterization of the survival ability of *Cupriavidus metallidurans* and *Ralstonia pickettii* from space-related environments. *Microb. Ecol.* 65:347–360.
5. Vandamme P, Coenye T. 2004. Taxonomy of the genus *Cupriavidus*: a tale of lost and found. *Int. J. Syst. Evol. Microbiol.* 54:2285–2289.

6. Van Houdt R, Monsieurs P, Mijndonckx K, Provoost A, Janssen A, Mergeay M, Leys N. 2012. Variation in genomic islands contribute to genome plasticity in *Cupriavidus metallidurans*. *BMC Genomics* 13:111. doi:10.1186/1471-2164-13-111.
7. Mergeay M, Monchy S, Vallaeyts T, Auquier V, Benotmane A, Bertin P, Taghavi S, Dunn J, van der Lelie D, Wattiez R. 2003. *Ralstonia metallidurans*, a bacterium specifically adapted to toxic metals: towards a catalogue of metal-responsive genes. *FEMS Microbiol. Rev.* 27:385–410.
8. Mergeay M. 2000. Bacteria adapted to industrial biotopes: the metal resistant *Ralstonia*, p 403–414. In Storz G, Hengge-Aronis R (ed), *Bacterial stress responses*. ASM Press, Washington, DC.
9. Monchy S, Benotmane MA, Janssen P, Vallaeyts T, Taghavi S, van der Lelie D, Mergeay M. 2007. Plasmids pMOL28 and pMOL30 of *Cupriavidus metallidurans* are specialized in the maximal viable response to heavy metals. *J. Bacteriol.* 189:7417–7425.
10. Van Houdt R, Monchy S, Leys N, Mergeay M. 2009. New mobile genetic elements in *Cupriavidus metallidurans* CH34, their possible roles and occurrence in other bacteria. *Antonie van Leeuwenhoek* 96:205–226.
11. Mijndonckx K, Provoost A, Monsieurs P, Leys N, Mergeay M, Mahillon J, Van Houdt R. 2011. Insertion sequence elements in *Cupriavidus metallidurans* CH34: distribution and role in adaptation. *Plasmid* 65:193–203.
12. Coenye T, Spilker T, Reik R, Vandamme P, Lipuma JJ. 2005. Use of PCR analyses to define the distribution of *Ralstonia* species recovered from patients with cystic fibrosis. *J. Clin. Microbiol.* 43:3463–3466.
13. Langevin S, Vincelette J, Bekal S, Gaudreau C. 2011. First case of invasive human infection caused by *Cupriavidus metallidurans*. *J. Clin. Microbiol.* 49:744–745.
14. Van Houdt R, Mergeay M. 2012. Plasmids as secondary chromosomes. In Bell E, Bond J, Klinman J, Masters B, Wells R (ed), *Molecular life sciences: an encyclopedic reference*. Springer-Verlag, Heidelberg, Germany. <http://www.springerreference.com/docs/html/chapterdbid/333639.html>.
15. Vallenet D, Belda E, Calteau A, Cruveiller S, Engelen S, Lajus A, Le Fèvre F, Longin C, Mornico D, Roche D, Rouy Z, Salvignol G, Scarpelli C, Thil Smith AA, Weiman M, Médigue C. 2013. MicroScope—an integrated microbial resource for the curation and comparative analysis of genomic and metabolic data. *Nucleic Acids Res.* 41:D636–D647. doi:10.1093/nar/gks1194.