

First Draft Genome Sequence of the *Acidovorax caeni* sp. nov. Type Strain R-24608 (DSM 19327)

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We report the draft genome sequence of the *Acidovorax caeni* type strain R-24608 that was isolated from activated sludge of an aerobic-anaerobic wastewater treatment plant. The closest strain to *Acidovorax caeni* strain R-24608 is *Acidovorax* sp. strain MR-S7 with a 55.4% (amino-acid sequence) open reading frames (ORFs) average similarity.

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Acidovorax isolates (*Comamonadaceae* family) are Gram-negative, aerobic bacteria with a polar flagellum and 62 to 70% G+C (1). *Acidovorax* species have been isolated from soil or water (1, 2), infected plants (3, 4), activated sludge (5–7), and clinical samples (1, 8–10). *Acidovorax radices* N35 was identified as a root-colonizing bacterium without phytopathogenic potential, which showed plant-growth-promoting activity (11). Autotrophic growth with hydrogen as an electron donor was found in *Acidovorax facilis* and some strains of *Acidovorax delafieldii* (1). Denitrification in wastewater treatment plants has been proposed to be catalyzed by members of the *Acidovorax* genus (6, 12, 13) and based on 16S rRNA gene sequence analysis, 19 denitrifiers were recently identified as *Acidovorax avenae*, *A. defluvii*, and *A. temperans* species (5).

Four novel denitrifiers were characterized as belonging to a new species termed *Acidovorax caeni* sp. nov. Here, we announce the first draft genome sequence of the *Acidovorax caeni* sp. nov. type strain R-24608 (14).

The genome was sequenced using the Illumina MiSeq platform, which generated pair-end read sequences of 250 bp. Assembly using Edena (15, 16) produced 152 contigs with a total genome size of 4,190,928 bs (63.2% G+C content, N_{50} : 78.99 Kbp, mean: 27.43 Kb) and an average of 83.9-fold coverage. Automatic annotation was performed using the RAST server version 4.0 (17), generating 3,904 features potentially assigned to protein-encoding genes (open reading frames [ORFs]).

A comparison between the draft genome of *Acidovorax caeni* strain R-24608 and the 17 genomes or draft genomes currently available for *Acidovorax* isolates, *Acidovorax* sp. JHL-3 (PRJNA195669), JHL-9 (PRJNA195668), NO-1 (18), CF 316 (19), MR-S7 (20), JS42 (PRJNA15685), KKS102 (21) and *A. citrulli* AAC00-1 (PRJNA15708), *A. citrulli* ZJU1106 (PRJNA175738), *A. avenae* ATCC 19860 (PRJNA37867), *A. avenae* RS-1 (22), *A. radices* N35 (PRJNA64465), *A. radices* N35v (PRJNA64471), *A. ebreus* TPSY (23), *A. delafieldii* 2AN (PRJNA32605), *A. oryzae* ATCC 19882 (PRJNA223028), and *A. temperans* KY4

(PRJNA270288) indicated *Acidovorax* sp. strain MR-S7 with a 55.4% (amino-acid sequence) of ORFs average similarity to be the most closely related to strain R-24608. Both strains share 1,318 ORFs with >80% similarity and 934 ORFs observed in the genome of R-24608 were absent in the genome of the strain MR-S7.

Genes involved in denitrification are encoded by nitrate respiration (*nar*), nitrite respiration (*nir*), nitric oxide respiration (*nor*), and nitrous oxide respiration (*nos*) genes (24). Strain R-24608 harbors the operon *narGHJI* and upstream two *narK* genes encoding nitrate transporter proteins as previously described (25). Nitrite respiration, encoded by the *nirSCFDLHJN* operon was found in R-24608 and we observed that this genomic organization was spread in most of the *Acidovorax* species. The operon involved in nitric oxide respiration, *norEFCBQD*, was identified downstream from the *nir* operon as previously observed in *Brucella suis* 1330 (26). Nitrous oxide respiration, encoded by the *nosDFYL* operon, was located upstream of the *nosR* gene and the catabolic subunit *nosZ* was eliminated as previously found in *Neisseria meningitidis* MC58 (27).

Nucleotide sequence accession numbers. This draft genome sequencing project has been deposited at the EMBL-EBI European Nucleotide Archive under accession numbers [CYIG010000001](https://www.ebi.ac.uk/ena/record/CYIG010000001) to [CYIG010000152](https://www.ebi.ac.uk/ena/record/CYIG010000152).

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REFERENCES

- Willems A, Falsen E, Pot B, Jantzen E, Hoste B, Vandamme P, Gillis M, Kersters K, De Ley J. 1990. *Acidovorax*, a new genus for *Pseudomonas facilis*, *Pseudomonas delafieldii*, E Falsen (EF) group 13, EF group 16, and several clinical isolates, with the species *Acidovorax facilis*

- comb. nov., *Acidovorax delafieldii* comb. nov., and *Acidovorax temperans* sp. nov. *Int J Syst Bacteriol* 40:384–398. <http://dx.doi.org/10.1099/00207713-40-4-384>.
2. Choi J-, Kim M-, Roh SW, Bae J-W. 2010. *Acidovorax soli* sp. nov., isolated from landfill soil. *Int J Syst Evol Microbiol* 60:2715–2718. <http://dx.doi.org/10.1099/ijs.0.019661-0>.
 3. Gardan L, Dauga C, Prior P, Gillis M, Saddler GS. 2000. *Acidovorax anthurii* sp. nov., a new phytopathogenic bacterium which causes bacterial leaf-spot of Anthurium. *Int J Syst Evol Microbiol* 50:235–246. <http://dx.doi.org/10.1099/00207713-50-1-235>.
 4. Gardan L, Stead DE, Dauga C, Gillis M. 2003. *Acidovorax valerianellae* sp. nov., a novel pathogen of lamb's lettuce [*Valerianella locusta* (L.) L-terr]. *Int J Syst Evol Microbiol* 53:795–800. <http://dx.doi.org/10.1099/ijs.0.02404-0>.
 5. Heylen K, Vanparys B, Wittebolle L, Verstraete W, Boon N, De Vos P. 2006. Cultivation of denitrifying bacteria: optimization of isolation conditions and diversity study. *Appl Environ Microbiol* 72:2637–2643. <http://dx.doi.org/10.1128/AEM.72.4.2637-2643.2006>.
 6. Hoshino T, Terahara T, Tsuneda S, Hirata A, Inamori Y. 2005. Molecular analysis of microbial population transition associated with the start of denitrification in a wastewater treatment process. *J Appl Microbiol* 99:1165–1175. <http://dx.doi.org/10.1111/j.1365-2672.2005.02698.x>.
 7. Schulze R, Spring S, Amann R, Huber I, Ludwig W, Schleifer K, Kämpfer P. 1999. Genotypic diversity of *Acidovorax* strains isolated from activated sludge and description of *Acidovorax defluvii* sp. nov. *Syst Appl Microbiol* 22:205–214. [http://dx.doi.org/10.1016/S0723-2020\(99\)80067-8](http://dx.doi.org/10.1016/S0723-2020(99)80067-8).
 8. Malkan AD, Strollo W, Scholand SJ, Dudrick SJ. 2009. Implanted-port-catheter-related sepsis caused by *Acidovorax avenae* and methicillin-sensitive *Staphylococcus aureus*. *J Clin Microbiol* 47:3358–3361. <http://dx.doi.org/10.1128/JCM.01093-09>.
 9. Shetty A, Barnes RA, Healy B, Groves P. 2005. A case of sepsis caused by *Acidovorax*. *J Infect* 51:e171–e172. <http://dx.doi.org/10.1016/j.jinf.2004.12.014>.
 10. Vanechoutte M, Janssens M, Avesani V, Delmee M, Deschaght P. 2013. Description of *Acidovorax wautersii* sp. nov. to accommodate clinical isolates and an environmental isolate, most closely related to *Acidovorax avenae*. *Int J Syst Evol Microbiol* 63:2203–2206. <http://dx.doi.org/10.1099/ijs.0.046102-0>.
 11. Li D, Rothballer M, Schmid M, Esperschütz J, Hartmann A. 2011. *Acidovorax radialis* sp. nov., a wheat-root-colonizing bacterium. *Int J Syst Evol Microbiol* 61:2589–2594. <http://dx.doi.org/10.1099/ijs.0.025296-0>.
 12. Etchebehere C, Errazquin I, Barrandeguy E, Dabert P, Moletta R, Muxi L. 2001. Evaluation of the denitrifying microbiota of anoxic reactors. *FEMS Microbiol Ecol* 35:259–265. <http://dx.doi.org/10.1111/j.1574-6941.2001.tb00811.x>.
 13. Mechichi T, Stackebrandt E, Fuchs G. 2003. *Alicyclophilus denitrificans* gen. nov., sp. nov., a cyclohexanol-degrading, nitrate-reducing beta-proteobacterium. *Int J Syst Evol Microbiol* 53:147–152. <http://dx.doi.org/10.1099/ijs.0.02276-0>.
 14. Heylen K, Lebbe L, De Vos P. 2008. *Acidovorax caeni* sp. nov., a denitrifying species with genetically diverse isolates from activated sludge. *Int J Syst Evol Microbiol* 58:73–77. <http://dx.doi.org/10.1099/ijs.0.65387-0>.
 15. Hernandez D, Francois P, Farinelli L, Osteras M, Schrenzel J. 2008. *De novo* bacterial genome sequencing: millions of very short reads assembled on a desktop computer. *Genome Res* 18:802–809. <http://dx.doi.org/10.1101/gr.072033.107>.
 16. Hernandez D, Tewhey R, Veyrieras J-B, Farinelli L, Osteras M, Francois P, Schrenzel J. 2014. *De novo* finished 2.8 Mbp *Staphylococcus aureus* genome assembly from 100 bp short and long range paired-end reads. *Bioinformatics* 30:40–49. <http://dx.doi.org/10.1093/bioinformatics/btt590>.
 17. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formisano K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
 18. Huang Y, Li H, Rensing C, Zhao K, Johnstone L, Wang G. 2012. Genome sequence of the facultative anaerobic arsenite-oxidizing and nitrate-reducing bacterium *Acidovorax* sp. strain NO1. *J Bacteriol* 194:1635–1636. <http://dx.doi.org/10.1128/JB.06814-11>.
 19. Brown SD, Utturkar SM, Klingeman DM, Johnson CM, Martin SL, Land ML, Lu T-YS, Schadt CW, Doktycz MJ, Pelletier DA. 2012. Twenty-one genome sequences from *Pseudomonas* species and 19 genome sequences from diverse bacteria isolated from the rhizosphere and endosphere of *Populus deltoides*. *J Bacteriol* 194:5991–5993. <http://dx.doi.org/10.1128/JB.01243-12>.
 20. Miura T, Kusada H, Kamagata Y, Hanada S, Kimura N. 2013. Genome sequence of the multiple- β -lactam-antibiotic-resistant bacterium *Acidovorax* sp. strain MR-S7. *Genome Announc* 1(4):e00412-13. <http://dx.doi.org/10.1128/genomeA.00412-13>.
 21. Ohtsubo Y, Maruyama F, Mitsui H, Nagata Y, Tsuda M. 2012. Complete genome sequence of *Acidovorax* sp. strain kks102, a polychlorinated-biphenyl degrader. *J Bacteriol* 194:6970–6971. <http://dx.doi.org/10.1128/JB.01848-12>.
 22. Xie G-L, Zhang G-Q, Liu H, Lou M-M, Tian W-X, Li B, Zhou X-P, Zhu B, Jin G-L. 2011. Genome sequence of the rice-pathogenic bacterium *Acidovorax avenae* subsp. *avenae* RS-1. *J Bacteriol* 193:5013–5014. <http://dx.doi.org/10.1128/JB.05594-11>.
 23. Byrne-Bailey KG, Weber KA, Chair AH, Bose S, Knox T, Spanbauer TL, Chertkov O, Coates JD. 2010. Completed genome sequence of the anaerobic iron-oxidizing bacterium *Acidovorax ebreus* strain tpsy. *J Bacteriol* 192:1475–1476. <http://dx.doi.org/10.1128/JB.01449-09>.
 24. Philippot L. 2002. Denitrifying genes in bacterial and archaeal genomes. *Biochim Biophys Acta* 1577:355–376. [http://dx.doi.org/10.1016/S0167-4781\(02\)00420-7](http://dx.doi.org/10.1016/S0167-4781(02)00420-7).
 25. Marger MD, Saier MH Jr. 1993. A major superfamily of transmembrane facilitators that catalyze uniport, symport and antiport. *Trends Biochem Sci* 18:13–20. [http://dx.doi.org/10.1016/0968-0004\(93\)90081-W](http://dx.doi.org/10.1016/0968-0004(93)90081-W).
 26. Loisel-Meyer S, Jimenez de Bagues MP, Basseres E, Dornand J, Kohler S, Liautaud J-, Jubier-Maurin V. 2006. Requirement of *norD* for *Brucella suis* virulence in a murine model of in vitro and in vivo infection. *Infect Immun* 74:1973–1976. <http://dx.doi.org/10.1128/IAI.74.3.1973-1976.2006>.
 27. Barth KR, Isabella VM, Clark VL. 2009. Biochemical and genomic analysis of the denitrification pathway within the genus *Neisseria*. *Microbiol* 155:4093–4103. <http://dx.doi.org/10.1099/mic.0.032961-0>.