

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/submit/submit) to [CYIG010000152](https://www.ebi.ac.uk/ena/submit/submit).

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