Complete Genome Sequence of the Type Strain

Cupriavidus necator N-1$^\text{V}$$^\dagger$

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Here we announce the complete genome sequence of the copper-resistant bacterium Cupriavidus necator N-1, the type strain of the genus Cupriavidus. The genome consists of two chromosomes and two circular plasmids. Based on genome comparison, the chromosomes of C. necator N-1 share a high degree of similarity with the two chromosomal replicons of the bioplastic-producing hydrogen bacterium Ralstonia eutropha H16. The two strains differ in their plasmids and the presence of hydrogenase genes, which are absent in strain N-1.

Cupriavidus necator N-1, the type strain of the genus Cupriavidus, was isolated from soil and described as a nonobligate predator of soil bacteria and fungi (1, 4). A characteristic of this betaproteobacterium is resistance against (heavy) metals. Analyses of the 16S rRNA gene sequence indicated that the bioplastic-producing “Knallgas” bacterium Ralstonia eutropha H16, reclassified as Cupriavidus necator H16 (1, 2, 3, 5), is closely related to C. necator N-1.

Whole-genome shotgun sequencing of C. necator N-1 genome was performed by using a 454 GS-FLX system (Roche 454 Life Science, Mannheim, Germany). Four shotgun and one paired-end pyrosequencing runs resulted in 32-fold coverage. The initial assembly yielded 64 scaffolds containing 1,004 contigs. PCR-based techniques and Sanger sequencing of the products were used to close remaining gaps. The final genome sequence of C. necator N-1 (8,480,857 bp) comprises two chromosomes of 3,872,936 (chromosome 1) and 2,684,606 (chromosome 2) bp and two circular plasmids of 1,499,175 (pBB1) and 409,240 bp (pBB2). Chromosomes 1 and 2 harbor 3,646 and 2,468 predicted protein-encoding genes, respectively. In addition, three and two rRNA operons were located on chromosomes 1 and 2, respectively. The two plasmids contain 1,424 (pBB1) and 409 (pBB2) putative protein-encoding genes. The main set of tRNA genes (57) was located on chromosome 1, whereas seven tRNA genes were found on chromosome 2 and two on each of the plasmids.

The genome of C. necator N-1 differs in size and the number of replicons from the genome of R. eutropha H16, which consists of two chromosomes (4,052,032 and 2,912,490 bp) and one megaplasmid (452,156 bp) adding up to a total size of 7,416,678 bp (2, 3). Bidirectional BLAST analysis revealed that 81% (2,951) and 67% (1,653) of the putative genes located on chromosome 1 and chromosome 2 of C. necator N-1 show orthologous counterparts in the genome of R. eutropha H16 (e-value less than 1e-20). The percentage of orthologous genes located on pBB1 and pBB2 was only 10 and 19%, respectively. While C. necator N-1 harbors one cbb operon coding for enzymes of autotrophic CO$_2$ fixation, R. eutropha H16 hosts two copies of the cbb operon. The genome of C. necator N-1 shares four operons encoding different formate dehydrogenases (chromosome 1, fds and fdh operons; chromosome 2, fdo and fdw operons), but putative genes encoding H$_2$-oxidizing hydrogenases, which enable strain H16 to grow lithoautotrophically (2), were not detected in C. necator N-1. Complete sets of genes required for polyhydroxyalkanoate metabolism, degradation of benzoate, 4-hydroxybenzate, phenol, and chlorinated aromatic compounds, and the gentisate pathway were identified in the C. necator N-1 genome. N-1 was described as a copper-resistant bacterium, leading to the genus designation Cupriavidus (1, 5). Putative genes coding for copper resistance proteins (copABCD) and a copper efflux P-type ATPase (copF) belong to the genomic repertoire of C. necator N-1. The biological activity of these genes remains to be investigated.

Nucleotide sequence accession numbers. The complete sequences of the C. necator N-1 chromosomes and plasmids have been deposited in GenBank under accession numbers CP002877 (chromosome 1), CP002878 (chromosome 2), CP002879 (pBB1), and CP002880 (pBB2).

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REFERENCES