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# Complete Genome Sequences of the Chemolithoautotrophic *Oligotropha carboxidovorans* Strains OM4 and OM5

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**We report on genome sequencing of *Oligotropha carboxidovorans* strain OM4 and resequencing of strain OM5. The genomes of both are composed of one chromosome and two plasmids. The presence of two plasmids in the OM5 genome is inconsistent with the previously published sequence, for which only one plasmid was described (D. Paul, S. Bridges, S. Burgess, Y. Dandass, and M. Lawrence, BMC Genomics 11:511, 2010).**

*Oligotropha carboxidovorans* OM4 and OM5 (formerly described as *Pseudomonas carboxydovorans*) are chemolithoautotrophic members of the *Alphaproteobacteria*. Both strains were isolated in 1978 from wastewater in Göttingen, Germany (3), and can utilize carbon monoxide or hydrogen and carbon dioxide as sole energy sources (2). It has been previously shown for strain OM5 that the essential genes for utilization of these substrates are encoded by the 133-kb plasmid pHCG3 (1).

The genome sequences of strains OM5 and OM4 were determined by a combination of Sanger sequencing of shotgun libraries and pyrosequencing (OM5) using a 454 GS-FLX system (Roche 454 Life Sciences, Mannheim, Germany) and pyrosequencing only (OM4). PCR-based techniques and Sanger sequencing of the products were used to close remaining gaps.

The manually curated and annotated final genome sequence of strain OM5 consists of a 3,595-Mbp chromosome, a 133-kbp plasmid (pHCG3), and a 167-kbp plasmid (pOC167). The number of replicons of strain OM4 is identical to that of strain OM5. OM4 harbors one chromosome (3,539 Mbp) and two plasmids of 133 (pHCG3b) and 167 kbp (pOC167b). The genomes of strains OM5 and OM4 share an overall sequence identity of 99%. The sequences of plasmids pOC167 and pOC167b are identical, and those of pHCG3 and pHCG3b differ by 5 bases. However, the chromosome of OM5 possesses two unique regions, of 53 and 7.7 kbp. The 7.7-kb region contains hypothetical and phage-related genes and might represent a prophage. The 53-kb region includes gene clusters for dissimilatory nitrate reduction (*narGHJI*) and nitrous oxide reduction (*nosRZDFYL*), transporters, and biosynthesis proteins, but putative genes encoding phage-related proteins were not detected. Since the corresponding region in OM4 consists only of the *narI* gene and genes encoding a transposase, an integrase, and an interrupted pseudogene that is complete in OM5, it is tempting to speculate that OM5 is the ancestor of OM4.

The sequence of the OM5 genome reported here differs from the one reported earlier (4, 5), in which only plasmid pHCG3 was described. The sequence of plasmid pOC167 has been found but has been assembled into the chromosome. The plasmids pOC167 (OM5) and pOC167B (OM4) encode typical plasmid-related traits, such as replication initiation proteins RepA, RepB, and RepC, transport proteins, efflux pumps, and resistance proteins, as well as components of a type IV secretion system. Interestingly, the plasmid contains regions of 16.5 and 4.2 kbp which show high homology to regions of 18 and 4.5 kbp, respectively, on the chromosome. These regions appear to be suitable for homologous recombination. Correspondingly, the pOC167 sequence of the published OM5 genome has been integrated in this area of the chromosome (4, 5). We verified the presence of plasmids pOC167 (OM5) and pOC167b (OM4) by PCR-based approaches.

**Nucleotide sequence accession numbers.** The complete sequences of *O. carboxidovorans* OM4 and OM5 chromosomes and plasmids have been deposited in GenBank under accession numbers CP002821 (OM4 chromosome), CP002822 (pHCG3b), CP002823 (pOC167B), CP002826 (OM5 chromosome), CP002827 (pHCG3), and CP002828 (pOC167).

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