Genome Sequences of Two Freshwater Betaproteobacterial Isolates, *Limnohabitans* Species Strains Rim28 and Rim47, Indicate Their Capabilities as Both Photoautotrophs and Ammonia Oxidizers

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Betaproteobacterial genus *Limnohabitans* represents an important part of freshwater bacterioplankton. Here, we report genome sequences of two *Limnohabitans* isolates, Rim28 and Rim47. They contain a complete photosynthesis gene cluster, RuBisCO, CO dehydrogenase, ammonia monooxygenase, and sulfur-oxidizing genes, which indicates a great metabolic versatility of the *Limnohabitans* species.

Limnohabitans is a recently established betaproteobacterial genus (3, 6), encompassing species formerly described as the *Rhodospirillum* sp. BAL47 cluster (13) or the R-BT065 cluster (10). These organisms represent one of the most important bacterial groups in many freshwater habitats (8). In spite of the accumulating ecological data (4, 7, 9, 10), little is known about its metabolism and genome composition. Here, we report the whole genome sequences of two *Limnohabitans* isolates, Rim28 and Rim47, which were isolated from the Římov reservoir (Czech Republic) (5) with the aim of elucidating the physiological potential of this ecologically important group.

The strains were grown under aerobic conditions. After DNA extraction and preparation of a 300-bp library, the genome sequencing was performed with Illumina HiSeq 2000. About 9.0 GB of raw data of 101-bp paired-end reads was generated from each sample. The sequence quality control and trimming were conducted on the Galaxy server (2). The reads were *de novo* assembled using SeqMan NGen 4.0 (Dnastar Inc., Madison, WI). Annotation was performed with the RAST server (1).

The draft genomes of *Limnohabitans* spp. Rim28 and Rim47 consisted of 73 and 230 contigs with N_{50} values of 236,333 bp and 183,460 bp and with a total size of 3.41 and 3.03 Mb, containing 3,342 and 2,877 open reading frames (ORFs) and 40 and 46 tRNAs, respectively. The G+C content of both genomes was 58.5%. Each genome contained single copies of 5S, 16S, and 23S rRNA genes, forming a complete rRNA operon. Sequence identities of the 16S and 23S rRNA genes of the two strains were 98.8% and 98.6%, respectively.

A complete photosynthesis gene cluster (PGC) was found in both genomes with an identical gene organization of *crtEF-bchCXYZ-pufBALMC-crtADC-pucBAC-crtBI-puhE-acsF-puhCBA-lhaA-bchMLHBNF-aerR-ppsR-bchGPODI*. The PGC size was 58.6 kb for Rim28 and 46.0 kb for Rim47. Nucleotide sequence identities of the same genes of the two PGCs were between 84% and 89%. The PGC gene organization of the two *Limnohabitans* strains differs from other purple phototrophic bacteria sequenced so far (12). However, it was similar to an incomplete PGC found in the environmental fosmid clone DelRiverFos 06H03 obtained from the Delaware River (11).

The genomes contain genes encoding ribulose-1,5-bisphosphate carboxylase (RuBisCO) and carbonic anhydrases, which in-

dicates the metabolic potential for autotrophic carbon fixation. There are nitrogen cycling-related genes encoding ammonia transporter and ammonia monooxygenase, nitrate transporter, nitrate reductase, nitrite reductase, urea transporter, and urease. In addition, there are the *soxBXAZYDCR* gene cluster, which contains sulfur-oxidizing-related genes, and the *coxMSLGDEF* gene cluster, encoding carbon monoxide dehydrogenase and related accessory proteins. These findings suggest a great metabolic versatility in the *Limnohabitans* species (5, 6). A more detailed genome analysis and experimental verification of the identified metabolic pathways will provide further insights about the physiology of this ecologically important group.

Nucleotide sequence accession numbers. The *Limnohabitans* species Rim28 and Rim47 genome sequences have been deposited at DDBJ/EMBL/GenBank under the accession numbers [ALKN000000000](#) and [ALKO000000000](#), respectively. The versions described here are the first versions, ALKN01000000 and ALKO01000000.

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