



# Complete Genome Sequence of *Loktanella vestfoldensis* Strain SMR4r, a Novel Strain Isolated from a Culture of the Chain-Forming Diatom *Skeletonema marinoi*

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**ABSTRACT** We report here the genome sequence of *Loktanella vestfoldensis* strain SMR4r, isolated from the marine diatom *Skeletonema marinoi* strain RO5AC. Its 3,987,360-bp genome consists of a circular chromosome and two circular plasmids, one of which appears to be shared with an *S. marinoi*-associated *Roseovarius* species.

The chain-forming diatom *Skeletonema marinoi* strain RO5AC associates with a large number of bacterial species, and efforts are ongoing to determine their roles in the diatom-microbe holobiont. *Loktanella vestfoldensis* strain SMR4r is one such bacterium which has been found as a result. The diatom strain was established from a germinated resting cell embedded in top-layer sediment, collected from 14 m depth with a box corer in May 2010 from Öresund, Sweden (55°59.16'N, 12°44.02'E). The bacterial genome was sequenced using PacBio RS II technology (Pacific Biosciences, Menlo Park, CA, USA) on one single-molecule real-time (SMRT) cell, producing 81,585 uncorrected reads totaling 845.4 Mbp. Falcon version 1.7.5 (<https://github.com/PacificBiosciences/FALCON>) (1) was used to assemble the reads (seed read length, 17,100 bp), and contig circularization was confirmed by joining the corresponding ends and realigning the reads using the RS\_Resequencing.1 protocol on SMRT Portal version 2.3.0 (Pacific Biosciences) (2). The final assembly contained three circular contigs totaling 3,987,360 bp (average read coverage, 177.86×).

The chromosome is 3,836,950 bp long, with a G+C content of 60.8%; plasmid pSMR4r-1 is 111,030 bp (G+C content, 57.4%), and plasmid pSMR4r-2 is 39,380 bp (G+C content, 58.2%). Strain SMR4r's two identical 16S rRNA sequences have 99.8% identity with the three 16S sequences of *L. vestfoldensis* strain DSM 16212<sup>T</sup> (GenBank accession number NZ\_ARNL000000000). A phylotaxonomic analysis using PhyloPhlAn version 0.99 (3), comparing strain SMR4r to all whole-genome-sequenced Rhodobacteraceae strains on NCBI's RefSeq site (<ftp://ftp.ncbi.nlm.nih.gov/genomes/refseq/bacteria/>), showed it to be a sister to *L. vestfoldensis* strain DSM 16212<sup>T</sup> (100% bootstrap support). Annotation using Prokka version 1.12beta (4) predicted 3,936 coding sequences (CDSs; with 3,267 proteins having a functional prediction and 669 labeled as hypothetical), 8 pseudogenes, 45 tRNAs, 6 rRNAs, 19 noncoding RNAs (ncRNAs), and 1 transfer-messenger RNA (tmRNA).

*Loktanella vestfoldensis* strain SMR4r contains genes for both phosphatidylcholine synthase (LOKVESSMR4R\_00456) and acyl-homoserine-lactone synthase (LOKVESSMR4R\_01736, involved in quorum sensing), suggesting interaction with a eukaryote (reviewed in references 5 and 6). *Loktanella vestfoldensis* strain SMR4r may also be able to digest dimethylsulfoniopropionate (DMSP), an organosulfur compound produced by many phytoplankton and used by some bacteria (7); when the annotated genome of strain SMR4r was examined in Pathway Tools version 20.5 (8), three of the five enzymes in the

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DMSP degradation superpathway were found, two of which, *dmdA* (LOKVESSMR4R\_00811) and *dmdC* (LOKVESSMR4R\_00511 and LOKVESSMR4R\_02869), are noted by Pathway Tools as being unique to this pathway.

There is also evidence that strain SMR4r interacts with another *S. marinoi*-associated bacterial species. Plasmid pSMR4r-2 contains interrupted regions accounting for the entirety of the *Roseovarius mucosus* strain SMR3 plasmid pSMR3-2 (GenBank accession number CP020476), with 100% sequence identity (9). These additional regions in pSMR4r-2 contain three transposase genes, two DNA invertase genes, and an additional mercuric reductase gene.

**Accession number(s).** This whole-genome project has been deposited in GenBank under the accession numbers [CP021431](#), [CP021432](#), and [CP021433](#), as part of BioProject number PRJNA380207.

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