



Genome Sequence of *Roseovarius mucosus* Strain SMR3, Isolated from a Culture of the Diatom *Skeletonema marinoi*

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ABSTRACT We present the genome of *Roseovarius mucosus* strain SMR3, a marine bacterium isolated from the diatom *Skeletonema marinoi* strain RO5AC sampled from top layer sediments at 14 m depth. Its 4,381,426 bp genome consists of a circular chromosome and two circular plasmids and contains 4,178 coding sequences (CDSs).

Roseovarius mucosus strain SMR3 was isolated from a culture of the chain-forming diatom *Skeletonema marinoi*. The diatom strain (RO5AC) was established from a germinated resting cell embedded in sediment. Sediment was collected with a box corer in Öresund, Sweden (55°59.16' N, 12°44.02' E), in May 2010. The genome was sequenced on one single-molecule real-time (SMRT) cell using the PacBio RSII system (Pacific Biosciences, Menlo Park, CA, USA), which produced 83,546 uncorrected reads totaling 756.4 Mbp. Reads were assembled using Falcon version 1.7.5 (<https://github.com/PacificBiosciences/FALCON> [1]) with a seed read length of 7,000 bp, and circularization of contigs 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 resulting assembly contained three circular contigs totaling 4,381,426 bp, with average read coverage of 144.99×.

The chromosome is 4,170,996 bp long with a G+C content of 60.9%, plasmid pSMR3-1 is 180,135 bp (G+C 60.1%) and plasmid pSMR3-2 is 30,295 bp (G+C 58.3%). The two identical 16S rRNA sequences found in the chromosome have 99.8% identity with that of *R. mucosus* DSM 17069^T (accession no. AONH01000000). Sequences identical to the SMR3 16S sequences were also found at three locations in *Roseovarius* sp. TM1035 (accession no. NZ_ABCL00000000). A phylotaxonomic analysis using PhyloPhlAn version 0.99 (3), comparing the SMR3 strain to all whole-genome sequenced strains in the family *Rhodobacteraceae* available at the NCBI RefSeq ftp site (<ftp://ftp.ncbi.nlm.nih.gov/genomes/refseq/bacteria/>), showed it to be sister to *Roseovarius* sp. TM1035, and together with *Roseovarius mucosus* strain DSM 17069^T forming a clade with 100% bootstrap support. Annotation was performed using Prokka version 1.12beta (4), which predicted 4,178 coding sequences (CDSs) (3,542 with a functional prediction and 636 hypothetical proteins), 3 pseudogenes, 46 tRNAs, 6 rRNAs, 5 noncoding RNAs (ncRNAs), and 1 tmRNA.

Roseovarius mucosus strain SMR3 contains two phosphatidylcholine synthase genes (ROSMUCSMR3_00993 and ROSMUCSMR3_02532), and both an acyl-homoserine-lactone synthase and *luxR* gene (ROSMUCSMR3_00613 and ROSMUCSMR3_00149, respectively; both involved in quorum sensing), all of which are suggestive of a symbiotic or pathogenic relationship with a eukaryote (reviewed in references 5 and 6). There is also evidence of interaction in the form of horizontal gene transfer between

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R. mucosus strain SMR3 and other bacteria within the *S. marinoi* microbiome. The pSMR3-2 plasmid shares 100% sequence identity, over the full length of the plasmid, with interrupted regions of a *Loktanella* sp. plasmid found in the same *S. marinoi* culture. These interruptions can primarily be accounted for by transposase genes on the *Loktanella* sp. plasmid.

Accession number(s). This whole-genome project has been deposited in GenBank under the accession numbers [CP020474](#), [CP020475](#), and [CP020476](#), as part of BioProject No. PRJNA380207.

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REFERENCES

- Gordon D, Huddleston J, Chaisson MJ, Hill CM, Kronenberg ZN, Munson KM, Malig M, Raja A, Fiddes I, Hillier LW, Dunn C, Baker C, Armstrong J, Diekhans M, Paten B, Shendure J, Wilson RK, Haussler D, Chin C-S, Eichler EE. 2016. Long-read sequence assembly of the gorilla genome. *Science* 352:aae0344. <https://doi.org/10.1126/science.aae0344>.
- Chin C-S, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Non-hybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563–569. <https://doi.org/10.1038/nmeth.2474>.
- Segata N, Börnigen D, Morgan XC, Huttenhower C. 2013. PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. *Nat Commun* 4:2304. <https://doi.org/10.1038/ncomms3304>.
- Seemann T. 2014. Prokka: Rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
- Sohlenkamp C, López-Lara IM, Geiger O. 2003. Biosynthesis of phosphatidylcholine in bacteria. *Prog Lipid Res* 42:115–162. [https://doi.org/10.1016/S0163-7827\(02\)00050-4](https://doi.org/10.1016/S0163-7827(02)00050-4).
- Miller MB, Bassler BL. 2001. Quorum sensing in bacteria. *Annu Rev Microbiol* 55:165–199. <https://doi.org/10.1146/annurev.micro.55.1.165>.