AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

Draft Genome Sequence of *Pseudoruegeria* sp. SK021, a Representative of the Marine *Roseobacter* Group, Isolated from North Sea Sediment

Marion Pohlner,[a] Ian Marshall,[b] Lars Schreiber,[b] Heribert Cypionka,[a] Bert Engelen[a]

Institute for Chemistry and Biology of the Marine Environment, University of Oldenburg, Oldenburg, Germany[a]; Department of Bioscience, Center for Geomicrobiology, Aarhus University, Aarhus, Denmark[b]

ABSTRACT *Pseudoruegeria* sp. SK021 is a member of the *Roseobacter* group, isolated under aerobic conditions from North Sea sediment. The draft genome comprises 3.95 Mb and contains 3,747 protein-coding sequences. Although the strain is nonmotile under laboratory conditions, the entire set of genes for the formation of a flagellar apparatus was found.

Received 27 April 2017 **Accepted** 2 May 2017 **Published** 15 June 2017

Citation Pohlner M, Marshall I, Schreiber L, Cypionka H, Engelen B. 2017. Draft genome sequence of *Pseudoruegeria* sp. SK021, a representative of the marine *Roseobacter* group, isolated from North Sea sediment. Genome Announc 5:e00541-17. https://doi.org/10.1128/genomeA.00541-17.

Address correspondence to Bert Engelen, engelen@icbm.de.

The *Roseobacter* group is globally distributed in the marine environment and represents a significant part of pelagic and benthic microbial communities (1–3). Their broad metabolic versatility make roseobacters successful in a variety of habitats (4, 5). In coastal sediments, roseobacters can constitute up to 10% of all cells (6). Although 28% of all described species in this group are of benthic origin (7), the metabolic properties of roseobacters in sediments are poorly understood. *Pseudoruegeria* sp. SK021, analyzed in this study, was isolated from surface sediment of the North Sea (7.1667 E, 57.8145 N) at a water depth of 181 m below sea level (8). It is closely related to *P. aestuarii* and represents a new benthic member of this genus.

Pseudoruegeria sp. SK021 was grown on marine broth agar (Difco) amended with dimethyl sulfide (100 μM) and lactate (5 mM) at 20°C. DNA was extracted using the innuPREP DNA mini kit (Analytik Jena) and a sequencing library was prepared using the Nextera XT kit (Illumina). Genome sequencing was performed using the Illumina MiSeq platform with the MiSeq reagent kit version 3 and generated approximately 3.8 million reads, representing ~0.98 Gb of data (fastq-stats version 1.01, http://expressionanalysis.github.io/ea-utils). Reads were trimmed and adapters removed using Trimmomatic version 0.36 (9) with the following parameters: CROP:288, HEADCROP:19, SLIDINGWINDOW:4:20, MINLEN:100, ILLUMINACLIP:bbmap/adapters.fa:2:40:15. Paired reads were assembled with SPAdes version 3.9.1 (10) using "--careful" and multiple *k*-mer sizes (*-k* 21, 33, 55, 77, 99, 127). Only contigs with a G+C content of 40 to 68%, an average read coverage $>$ 7.5×, and a minimum size of 200 bp were retained to eliminate potential contamination. After decontamination, the assembled draft genome of *Pseudoruegeria* sp. SK021 had a total length of 3,948,746 bp, 128 contigs (>500 bp), and approximately 245-fold coverage. The average G+C content was 60.17% and the N_{50} length was 94,596 bp, as determined by QUAST version 4.3 (11). Genome completeness was 99.27%, estimated by CheckM version 1.0.7 (12) using marker genes for the family *Rhodobacteraceae*. Annotation by Prokka version 1.12-beta (13), on the basis of three published and annotated genomes of *Pseudoruegeria* spp., identified 3,747 protein-coding sequences, 3 rRNA-encoding sequences (5S, 16S, 23S rRNA), and 48 tRNAs. Even though *Pseudorugeria* sp. SK021 is nonmotile, genes for the formation of the complete flagellar apparatus were found in the annotated genome,

including genes for the motor switch (e.g., FliG, FliM, MotA), the basal body (e.g., FlgB, FlgC), the different rings (FliF, FlgH, FlgI), the flagellar hook (e.g., FlgE, FlgK, FlgL), and the flagella itself (flagellin). Although motility is not essential in sediments, the presence of flagellar genes shows that the strain might be motile under specific conditions.

Accession number(s). The genome was uploaded to IMG under Genome ID 2711768631. Furthermore, this whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number MTBG00000000. The version described in this paper is the first version, MTBG01000000.

ACKNOWLEDGMENTS

We acknowledge Saranya Kanukollu and Jana Schmidt (both University of Oldenburg), for isolating the strain and for providing support during the cultivation, and Britta Poulsen (Aarhus University) for performing the Illumina MiSeq sequencing. This study was funded by the Deutsche Forschungsgemeinschaft (DFG) within the Transregional Collaborative Research Center TRR51 and the Graduate School of Science and Technology, University of Oldenburg. Furthermore, the Aarhus University Graduate School of Science and Technology, the Danish National Research Foundation (grant no. DNRF104), an ERC Advanced Grant MICROENERGY (grant no. 294200), and a Marie Curie IIF fellowship "ATP_adapt_low_energy" (both European Union Seventh Framework Programs) supported this work financially.

REFERENCES

1. Buchan A, González JM, Moran MA. 2005. Overview of the marine *Roseobacter* lineage. Appl Environ Microbiol 71:5665–5677. https://doi.org/10.1128/AEM.71.10.5665-5677.2005.
2. Giebel HA, Brinkhoff T, Zwisler W, Selje N, Simon M. 2009. Distribution of *Roseobacter* RCA and SAR11 lineages and distinct bacterial communities from the subtropics to the Southern Ocean. Environ Microbiol 11:2164–2178. https://doi.org/10.1111/j.1462-2920.2009.01942.x.
3. Selje N, Simon M, Brinkhoff T. 2004. A newly discovered *Roseobacter* cluster in temperate and polar oceans. Nature 427:445–448. https://doi.org/10.1038/nature02272.
4. Wagner-Döbler I, Biebl H. 2006. Environmental biology of the marine *Roseobacter* lineage. Annu Rev Microbiol 60:255–280. https://doi.org/10.1146/annurev.micro.60.080805.142115.
5. Brinkhoff T, Giebel HA, Simon M. 2008. Diversity, ecology, and genomics of the *Roseobacter* clade: a short overview. Arch Microbiol 189:531–539. https://doi.org/10.1007/s00203-008-0353-y.
6. Lenk S, Moraru C, Hahnke S, Arnds J, Richter M, Kube M, Reinhardt R, Brinkhoff T, Harder J, Amann R, Mußmann M. 2012. *Roseobacter* clade bacteria are abundant in coastal sediments and encode a novel combination of sulfur oxidation genes. ISME J 6:2178–2187. https://doi.org/10.1038/ismej.2012.66.
7. Pujalte MJ, Lucena T, Ruvira MA, Arahal DR, Macián MC. 2014. The family *Rhodobacteraceae*, p 439–512. *In* Rosenberg E, DeLong EF, Lory S, Stackebrandt E, Thompson FL (ed), The prokaryotes: alphaproteobacteria and betaproteobacteria, 4th ed. Springer Verlag, Berlin.
8. Kanukollu S, Wemheuer B, Herber J, Billerbeck S, Lucas J, Daniel R, Simon M, Cypionka H, Engelen B. 2016. Distinct compositions of free-living, particle-associated and benthic communities of the *Roseobacter* group in the North Sea. FEMS Microbiol Ecol 92:11. https://doi.org/10.1093/femsec/fiv145.
9. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.
10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
11. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086.
12. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Res 25:1043–1055. https://doi.org/10.1101/gr.186072.114.
13. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.