

Genome Sequences of Two *Pseudoalteromonas* Strains Isolated from the South China Sea

Zhenshun Zeng, Shikun Dai, Yunchang Xie, Xinpeng Tian, Jie Li, Xiaoxue Wang

Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China

Two *Pseudoalteromonas* strains, SCSIO 04301 and SCSIO 11900, were isolated from the South China Sea, and both strains form biofilms. Here we present the draft genome sequences of these two strains, which will aid the study of marine microbes that are adapted to marine sediments or are associated with eukaryotic hosts.

Received 21 March 2014 Accepted 25 March 2014 Published 17 April 2014

Citation Zeng Z, Dai S, Xie Y, Tian X, Li J, Wang X. 2014. Genome sequences of two *Pseudoalteromonas* strains isolated from the South China Sea. *Genome Announc.* 2(2): e00305-14. doi:10.1128/genomeA.00305-14.

Copyright © 2014 Zeng et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Xiaoxue Wang, xxwang@scsio.ac.cn.

Pseudoalteromonas (*Gammaproteobacteria*, *Alteromonadales*, *Alteromonadaceae*), a genus of *Gammaproteobacteria*, was differentiated from the *Alteromonas* genus in 1995 according to the difference in small-subunit rRNA gene sequences (1). *Pseudoalteromonas* is widespread in marine environments and has become an organism of interest to the fields of ecological and pharmaceutical sciences due to its influence on biofilms and its ability to synthesize bioactive molecules (2). So far, draft genome sequences of over 40 *Pseudoalteromonas* strains have been released to public databases, and three strains have complete whole-genome sequences.

Here we present the genome sequences of two *Pseudoalteromonas* strains, *Pseudoalteromonas lipolytica* SCSIO 04301 and *Pseudoalteromonas* sp. strain SCSIO 11900. SCSIO 04301 was isolated from sediment at 63 m deep in the South China Sea (18°0'N, 109°42'E), and SCSIO 11900 was isolated from the surface mucus layer of the coral at 4 m deep in the South China Sea (18°13'N, 109°28'E). The 16S rRNA sequences of SCSIO 04301 share 100% similarity with *Pseudoalteromonas lipolytica* LMEB 39 (3), while SCSIO 11900 is most closely related to the deep-sea sediment-adapted strain *Pseudoalteromonas* sp. SM9913 (4). The SCSIO 04301 and SCSIO 11900 strains are nonpigmented. Similar to other *Pseudoalteromonas* strains, both strains produce large amounts of extracellular polymeric substances and form pellicles and biofilms.

Sequences were obtained using the Illumina HiSeq 2000 sequencing platform; 680 Mb and 677 Mb of clean data were produced for the SCSIO 04301 and SCSIO 11900 genomes, respectively. SOAPdenovo (version 1.05) (5, 6) was used to assemble the reads after filtering. The assembled result was then locally assembled and optimized according to paired-end and overlap relationships. The sizes of the genomes were estimated by k-mer analysis, the GC contents were calculated by GC-depth analysis, and the protein-coding open reading frames (ORFs) were predicted by Glimmer (7, 8) (version 3.02). For RNA prediction, rRNA was predicted by the rRNA database and RNAmmer (9) (version 1.2) and tRNA was predicted by tRNAscan (10).

Based on the assembled results, the genome size of SCSIO

04301 is 4.7 Mb and the GC content is 41.26%. The number of scaffolds is 12 and the total coverage over the genome is 145-fold. For SCSIO 11900, the genome size is 3.7 Mb, with a GC content of 40.45%. The number of contigs is 22, and the total coverage over the genome is 183-fold. A total of 4,215 ORFs, 95 tRNAs, and 6 rRNAs are predicted for SCSIO 04301, and a total of 3,515 ORFs, 89 tRNAs, and 26 rRNAs are predicted for SCSIO 11900. Two chromosomes were found for both SCSIO 04301 and SCSIO 11900, and the circularizations of the small chromosomes were confirmed again by PCR and subsequent DNA sequencing. A comprehensive study combined with comparative genome analysis and phenotypic analysis is under way to explore the relationships between genetic variation and phenotypic variation of *Pseudoalteromonas* strains in different ecological niches.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers [JDVB00000000](https://accession.ddbj.go.jp/acc/showacc.cgi?acc=JDVB00000000) for SCSIO 04301 and [JEMJ00000000](https://accession.ddbj.go.jp/acc/showacc.cgi?acc=JEMJ00000000) for SCSIO 11900.

ACKNOWLEDGMENTS

This work was supported by the National Basic Research Program of China (grant 2013CB955701) and by the National Science Foundation of China (grant 31290233).

REFERENCES

1. Gauthier G, Gauthier M, Christen R. 1995. Phylogenetic analysis of the genera *Alteromonas*, *Shewanella*, and *Moritella* using genes coding for small-subunit rRNA sequences and division of the genus *Alteromonas* into two genera, *Alteromonas* (emended) and *Pseudoalteromonas* gen. nov., and proposal of twelve new species combinations. *Int. J. Syst. Bacteriol.* 45:755–761. <http://dx.doi.org/10.1099/00207713-45-4-755>.
2. Holmström C, Kjelleberg S. 1999. Marine *Pseudoalteromonas* species are associated with higher organisms and produce biologically active extracellular agents. *FEMS Microbiol. Ecol.* 30:285–293. <http://dx.doi.org/10.1111/j.1574-6941.1999.tb00656.x>.
3. Xu XW, Wu YH, Wang CS, Gao XH, Wang XG, Wu M. 2010. *Pseudoalteromonas lipolytica* sp. nov., isolated from the Yangtze River estuary. *Int. J. Syst. Bacteriol.* 60:2179–2181. <http://dx.doi.org/10.1099/ijs.0.017673-0>.
4. Yan BQ, Chen XL, Hou XY, He H, Zhou BC, Zhang YZ. 2009. Molecular analysis of the gene encoding a cold-adapted halophilic subti-

- lase from deep-sea psychrotolerant bacterium *Pseudoalteromonas* sp. SM9913: cloning, expression, characterization and function analysis of the C-terminal PPC domains. *Extremophiles* 13:725–733. <http://dx.doi.org/10.1007/s00792-009-0263-1>.
5. Li RQ, Li YR, Kristiansen K, Wang J. 2008. SOAP: short oligonucleotide alignment program. *Bioinformatics* 24:713–714. <http://dx.doi.org/10.1093/bioinformatics/btn025>.
 6. Li R, Zhu H, Ruan J, Qian W, Fang X, Shi Z, Li Y, Li S, Shan G, Kristiansen K, Li S, Yang H, Wang J, Wang J. 2010. De novo assembly of human genomes with massively parallel short read sequencing. *Genome Res.* 20:265–272. <http://dx.doi.org/10.1101/gr.097261.109>.
 7. Delcher AL, Harmon D, Kasif S, White O, Salzberg SL. 1999. Improved microbial gene identification with GLIMMER. *Nucleic Acids Res.* 27: 4636–4641. <http://dx.doi.org/10.1093/nar/27.23.4636>.
 8. Delcher AL, Bratke KA, Powers EC, Salzberg SL. 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. *Bioinformatics* 23:673–679. <http://dx.doi.org/10.1093/bioinformatics/btm009>.
 9. Lagesen K, Hallin P, Rødland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res.* 35:3100–3108. <http://dx.doi.org/10.1093/nar/gkm160>.
 10. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25: 955–964. <http://dx.doi.org/10.1093/nar/25.5.0955>.