Genome Sequence of Salegentibacter mishustinae KCTC 12263, Containing a Complete Subtype I-B CRISPR-Cas System

Fei Zhang, Wenxin Lin, Rui Zhang, Qiang Zheng, Nianzhi Jiao
State Key Laboratory of Marine Environmental Science, Institute of Marine Microbes and Ecospheres, Xiamen University, Xiamen, People’s Republic of China

Salegentibacter mishustinae KCTC strain 12263 was isolated from the sea urchin Strongylocentrotus intermedius inhabiting the Sea of Japan. Here, we report the draft genome sequence of Salegentibacter mishustinae KCTC 12263. It comprises ~3.78 Mb in 38 contigs with a G+C content of 36.5%, and a total of 3,490 protein-coding genes were obtained. One complete CRISPR-Cas gene cluster was identified in the genome, which shows the strategy against invasive genetic elements of the strain.

Interestingly, one clustered regularly interspaced short palindromic repeat (CRISPR) was identified in the genome by using CRISPRFinder (13). CRISPR functions as adaptive immune systems against invaders such as viruses and plasmids (14–16). The CRISPR system in Salegentibacter mishustinae KCTC 12263 begins at position 587432 and ends at position 590615 in the whole genome (LKTP01000001), and has a conserved region (DR) of ATTCCAGACCACTTCAA to TTAGAAACTTAGATTGAAAAC and 43 spacers. The CRISPR-Cas system in Salegentibacter mishustinae KCTC 12263 contains cas8, cas7, cas5, and cas3 genes, which makes it a typical subtype I-B. The genes encoding information-processing subsystems Cas1, Cas2, and Cas4 are all present in the system and are thought to be involved in spacer integration during the adaption stage and thus active in repelling foreign genetic elements (17).

We reported the Salegentibacter mishustinae genome and provided primary information on its adaptation and metabolism. CRISPR-Cas system was identified in the genome and predicted to belong to subtype I-B and active, which shows the strategy against foreign nucleic acids of the strain. Further experimental evidences to support the prediction deduced from the genome sequence would provide a better understanding for the genus Salegentibacter.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LKTP01000000. The version described in this paper is the first version, LKTP01000000.

FUNDING INFORMATION
This work, including the efforts of Qiang Zheng, was funded by China National Marine Science Talent Training Base (2015Z01). This work, including the efforts of Qiang Zheng, was funded by Innovation and Entrepreneurship Training Program of Xiamen University (2014X0058). This work, including the efforts of Qiang Zheng, was funded by Fundamental Research Funds for the Central Universities (2013121051). This work, including the efforts of Nianzhi Jiao, was funded by National Natural Science Foundation of China (Grant 41306027).
Science Foundation of China (NSFC) (91428308). This work, including the efforts of Nianzhi Jiao, was funded by State Oceanic Administration (SOA) of China (GASI-03-01-02-05).

REFERENCES

1. McCammon SA, Bowman JP. 2000. Taxonomy of Antarctic Flavobacterium species: description of Flavobacterium gillisiae sp. nov., Flavobacterium tegetincola sp. nov., and Flavobacterium xanthum sp. nov., nom. rev. and reclassification of [Flavobacterium] salegens as Salegentibacter salegens gen. nov., comb. nov. Int J Syst Evol Microbiol 50:1055–1063. http://dx.doi.org/10.1099/00207713-50-3-1055.

2. Nedashkovskaya OL, Kim SB, Vancanneyt M, Shin DS, Lysenko AM, Shevchenko LS, Krasokhin VB, Mikhailov VV, Swings J, Bae KS. 2006. Salegentibacter agarivorans sp. nov., a novel marine bacterium of the family Flavobacteriaceae isolated from the sponge Artemisia sp. Int J Syst Evol Microbiol 56:833–887. http://dx.doi.org/10.1099/ijs.0.64167-0.

3. Nedashkovskaya OL, Suzuki M, Vancanneyt M, Cleenwerck I, Zhukova NV, Vysotskii MV, Mikhailov VV, Swings J. 2004. Salegentibacter holothuriorum sp. nov., isolated from the edible holothurian Apostichopus japonicus. Int J Syst Evol Microbiol 54:1107–1110. http://dx.doi.org/10.1099/ijs.0.02987-0.

4. Ying J-Y, Liu Z-P, Wang B-J, Dai X, Yang S-S, Liu S-J. 2007. Salegentibacter catena sp. nov., isolated from sediment of the South China sea, and emended description of the genus Salegentibacter. Int J Syst Evol Microbiol 57:219–222. http://dx.doi.org/10.1099/ijs.0.04658-0.

5. Nedashkovskaya OL, Kim SB, Lysenko AM, Mikhailov VV, Bae KS, Kim IS. 2005. Salegentibacter mishustinae sp. nov., isolated from the sea urchin Strongylocentrotus intermedius. Int J Syst Evol Microbiol 55:235–238. http://dx.doi.org/10.1099/ijs.0.03297-0.

6. Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res 18:221–229. http://dx.doi.org/10.1101/gr.07492.107.

7. Salzberg SL, Delcher AL, Kasif S, White O. 1998. Microbial gene identification using interpolated Markov models. Nucleic Acids Res 26:544–548. http://dx.doi.org/10.1093/nar/26.2.544.

8. Borodovsky M, McIninch J. 1993. GENMARK: parallel gene recognition for both DNA strands. Comput Chem 17:123–133. http://dx.doi.org/10.1016/0097-8485(93)85004-V.

9. Lukashin AV, Borodovsky M. 1998. GeneMark.hmm: new solutions for gene finding. Nucleic Acids Res 26:1107–1115. http://dx.doi.org/10.1093/nar/26.4.1107.

10. Angiuoli SV, Gussman A, Klinke W, Cochrane G, Field D, Garrity GM, Kodira CD, Kyripides N, Madupu R, Markowitz V, Tatusova T, Thompson N, White O. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta) genomic annotation. Omics J Integr Biol 12:137–141. http://dx.doi.org/10.1089/omi.2008.0017.

11. 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/25.5.955.

12. Lagesen K, Hallin P, Rodland EA, Staerfeldt HH, Gough J, Borghesi L, Rognes T, Ussery DW. 2007. tRNAscan-SE: consistent and rapid annotation of tRNA genes. Nucleic Acids Res 35:3100–3108. http://dx.doi.org/10.1093/nar/gkm160.

13. Grissa I, Vergnaud G, Pourcel C. 2007. CRISPRFinder: a web tool to identify clustered regularly interspaced short palindromic repeats. Nucleic Acids Res 36:3420–3425. http://dx.doi.org/10.1093/nar/gkm600.

14. Barrangou R, Fremaux C, Deveau H, Richards M, Boyaval P, Moineau S, Romero DA, Horvath P. 2007. CRISPR provides acquired resistance against viruses in prokaryotes. Science 315:1709–1712. http://dx.doi.org/10.1126/science.1138140.

15. Brouns SJ, Jore MM, Lundgren M, Westra ER, Slijkhuis RJ, Snijders AJ, Lagesen K, Hallin P, Rognes T, Ussery DW. 2013. CRISPRFinder: a web tool to identify clustered regularly interspaced short palindromic repeats. Nucleic Acids Res 41:52–57. http://dx.doi.org/10.1093/nar/gkt352.

16. Sorek R, Lawrence CM, Wiedenheft B. 2013. CRISPR- mediated adaptive immune systems in bacteria and archaea. Annu Rev Biochem 82:237–266. http://dx.doi.org/10.1146/annurev-biochem-072911-172315.

17. Makarova KS, Haft DH, Barrangou R, Brouns SJ, Charpentier E, Horvath P, Moineau S, Mojica FJ, Wolf YI, Yakunin AF, van der Oost J, Koonin EV. 2011. Evolution and classification of the CRISPR–Cas systems. Nat Rev Microbiol 9:467–477. http://dx.doi.org/10.1038/nrmicro2577.