Draft Genome Sequence of a New Vibrio Strain with the Potential To Produce Bacteriocin-Like Inhibitory Substances, Isolated from the Gut Microflora of Scallop (Argopecten purpuratus)

Wilbert Serrano, Ulrike I. Tarazona, Raul M. Olaechea, Michael W. Friedrich

Carrera de Biología Marina, Facultad de Ciencias Veterinarias y Biológicas, Universidad Científica del Sur, Lima, Peru
Microbial Ecophysiology Group, Faculty of Biology/Chemistry and MARUM, Center for Marine Environmental Sciences, University of Bremen, Bremen, Germany

ABSTRACT A new Vibrio strain, V7A, was isolated from the intestinal tract of the Peruvian scallop (Argopecten purpuratus). Strain V7A clusters within the Mediterranei clade of the genus Vibrio and has the potential to produce bacteriocin-like inhibitory substances (BLIS). Here, we report the draft genome sequence of Vibrio mediterranei strain V7A.

Vibrios constitute a very successful and versatile group of heterotrophic rod-shaped Gram-negative bacteria known to inhabit a diversity of environments (1, 2). Although some Vibrio species have been collected from pristine waters as free-living organisms (3), they are ubiquitous in marine ecosystems living attached to plankton particles, as symbionts of marine organisms, or associated with marine bivalves (4–6). However, the major concern in the aquaculture industry is pathogenic vibrios, which are deadly for scallop larvae (7). Some species are able to produce bacteriocins, a proteinaceous compound lethal to bacterial species that inhabit the same ecological niche (8). Here, we report the draft genome sequence of Vibrio mediterranei strain V7A isolated from the gut microflora of the Peruvian scallop (Argopecten purpuratus).

As part of the study of the microbiome of A. purpuratus, strain V7A was isolated from fecal pellets extracted from a host organism. Sample collection, enrichment culture, single-colony isolation, genomic DNA extraction, and library preparation for next-generation sequencing (NGS) using the MiSeq sequencer (Illumina) were carried out as described by Serrano et al. (9). The read library contained 789,308 trimmed paired-end reads with an average coverage of 100×. The quality of the reads was determined using the FastQC tool (10), and sequence trimming was performed using Trimmomatic version 0.32 (11). De novo assembly was performed using the SPAdes genomic assembler version 3.10.1 (12) and CLC Genomics Workbench 7.0.4 (CLC bio/Qiagen). The draft genome consists of 89 scaffolds with an average length of 63,563 bp. The N50 value of the assembly was 167,754 bp, with a G+C mol% composition of the DNA of 44.1% and genome size of 5,657,141 bp. Gene prediction and annotation were performed using the online service Rapid Annotations using Subsystems Technology (RAST; http://rast.nmpdr.org) server (13). RAST identified 5,178 coding sequences, of which 1,327 were predicted to encode hypothetical proteins, and 83 predicted noncoding RNAs.

In this report, genomic species circumscription of the new isolate was achieved using the online server JSpeciesWS (14). On the basis of pairwise genome comparison, strain V7A is affiliated with the Vibrio mediterranei clade of the genus Vibrio, with Vibrio mediterranei strain NBRC 15635 as the closest relative. V. mediterranei was isolated from diverse marine environments in the Mediterranean Sea in Spain (15). Some species of
V. mediterranei have been reported to produce bacteriocin-like inhibitory substances (BLIS) against the human pathogen Vibrio parahaemolyticus (8), whereas other pathogenic strains are the causative agent of bleaching in the coral Oculina patagonica (16). An average nucleotide identity (ANI) calculation between the genome of strain V7A and other available V. mediterranei genomes from GenBank showed ANI values of 96.74 to 98.99%. These values are clearly above the accepted cutoff value for species delimitation (14). However, strain V7A was the only strain among the examined related Vibrio mediterranei strains showing 24 phage-related gene clusters, among them two types of phage tail proteins, which might be involved in the production of bacteriocins (17). Besides, strain V7A lacks gene clusters involved in the biosynthesis of secondary metabolites, such as polyketide synthase (PKS) or nonribosomal peptide synthetase (NRPS).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number PYVE00000000, with the current version PYVE01000000.

ACKNOWLEDGMENT
This work was funded by the Peruvian governmental agency for innovation in science and technology, Innovate Peru, under contract 330-PNICP-BRI-2015.

REFERENCES
1. Thompson FL, Iida T, Swings J. 2004. Biodiversity of vibrios. Microbiol Mol Biol Rev 68:403–431. https://doi.org/10.1128/MMBR.68.3.403-431.2004.
2. Thompson CC, Thompson FL, Vicente A, Swings J. 2007. Phylogenetic analysis of vibrios and related species by means of atpA gene sequences. Int J Syst Evol Microbiol 57:2480–2484. https://doi.org/10.1099/ijs.0.65223-0.
3. Teo J, Suswanto A, Poh CA. 2000. Novel β-lactamase genes from two environmental isolates of Vibrio harveyi. Antimicrob Agents Chemother 44:1309–1314. https://doi.org/10.1128/AAC.44.5.1309-1314.2000.
4. Rehnstam-Holm AS, Godhe A, Hännström K, Raghunath P, Saravanana V, Collin B, Karunasagar I, Karunasagar I. 2010. Association between phytoplankton and Vibrio spp. along the southwest coast of India: a mesocosm experiments. Aquat Microb Ecol 58:127–139. https://doi.org/10.3354/ame01360.
5. Zamborsky DG, Nishiguchi NK. 2011. Phylogeographical patterns among Mediterranean sepiolid squids and their Vibrio symbionts: environments drives specificity among sympatric species. Appl Environ Microbiol 77:642–649. https://doi.org/10.1128/AEM.02105-10.
6. Romalde JL, Dieguez AL, Lasa A, Balboa S. 2014. New Vibrio species associated to molluscan microbiota: a review. Front Microbiol 4:413. https://doi.org/10.3389/fmicb.2013.00413.
7. Dubert J, Barja JL, Romalde JL. 2017. New insights into pathogenic vibrios affecting bivalves in hatchery: present and future prospects. Front Microbiol 8:762. https://doi.org/10.3389/fmicb.2017.00762.
8. Carraturo A, Raieta K, Ottaviani D, Russo GL. 2006. Inhibition of Vibrio para-haemolyticus by a bacteriocin-like inhibitory substance (BLIS) produced by Vibrio mediterranei 1. J Appl Microbiol 101:234–241. https://doi.org/10.1111/j.1365-2672.2006.02099.x.
9. Serrano W, Tarazona U, Olaechea RM, Friedrich MW. 2017. Draft genome sequence of Vibrio sp. strain V1B isolated from the gut microbiota of the scallop Argopecten purpuratus. Genome Announc Sci 01130-17. https://doi.org/10.1128/genomeA.01130-17.
10. Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. http://www.bioinformatics.babraham.ac.uk/projects/fastqc.
11. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for illumine sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.
12. Bankhead A, Nukr S, Antipov D, Gurevich AA, Dowkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prijibelski AD, Pyshkin AV, Sirokin AV, Vyahhi N, Tesler G, Aleksyev MA, Pevzner PA. 2012. SPAdes: a new algorithm and its application to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
13. Overbeek R, Olson R, Puich GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). Nucleic Acids Res 42:D206–D214. https://doi.org/10.1093/nar/gkt1226.
14. Richter M, Roselló-Mora R, Oliver Glöckner F, Peplies J. 2016. JSpeciesWS: a web server for prokaryotic species circumscription based on pairwise genome comparison. Bioinformatics 32:929–931. https://doi.org/10.1093/bioinformatics/btv681.
15. Pujalte M, Garay E. 1986. Proposal of Vibrio mediterranei sp. nov.: a new marine member of the genus Vibrio. Int J Syst Bacteriol 36:278–281. https://doi.org/10.1099/00207713-36-2-278.
16. Rubio-Portillo E, Yarza P, Peñalver C, Ramos-Esplá AA, Antón J. 2014. New insights into Oculina patagonica coral diseases and their associated Vibrio spp. communities. ISME J 8:1794–1807. https://doi.org/10.1038/ismej.2014.33.
17. Casjens S. 2003. Prophages and bacterial genomes: what have we learned so far? Mol Microbiol 49:277–300. https://doi.org/10.1046/j.1365-2958.2003.03580.x.