

Draft Genome Sequence of *Vibrio* sp. Strain Vb278, an Antagonistic Bacterium Isolated from the Marine Sponge *Sarcotragus spinosulus*

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We report here the draft genome sequence of *Vibrio* sp. Vb278, a biofilm-producing strain isolated from the marine sponge *Sarcotragus spinosulus*, showing *in vitro* antibacterial activity. The annotated genome displays a range of symbiotic factors and the potential for the biosynthesis of several biologically active natural products.

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Vibrio species are known for their metabolic and genotypic plasticity, having widespread occurrence in marine and estuarine ecosystems as members of either planktonic (1, 2) or symbiotic communities (3, 4). To date, much research has been performed, e.g., on *Vibrio*-squid symbiosis, and a mechanistic view of this particular interaction has been achieved (5). Yet, the precise roles of *Vibrio* spp. across several foundational marine symbiotic consortia, such as coral, sponge, and seaweed holobionts, where they emerge as one of the most profuse cultivatable members (4, 6, 7), remain far from being fully understood. To gain better insight into the antimicrobial potential and life strategies of symbiotic *Vibrio* species, we sequenced the genome of *Vibrio* sp. strain Vb278, a biofilm-forming bacterium displaying *in vitro* antagonism toward *Escherichia coli* and *Staphylococcus aureus* (4).

Strain Vb278 was isolated from the marine sponge *Sarcotragus spinosulus* using marine agar medium. The animal host was sampled at 15 m depth off the coast of Galé Alta (37°04'09.6N 8°19'52.1 W), Algarve, southern Portugal (4). Genomic DNA of strain Vb278 was extracted from a pelletized, freshly grown culture (48 h of incubation at 23°C) using the Wizard genomic DNA purification kit (Promega Corporation, Madison, WI) and sequenced on an Illumina MiSeq platform at MR DNA (Shallowater, TX). The sequence output was 1.22 Gb, comprising 2 × 301-bp paired-end reads, allowing for an estimated 228× coverage of the targeted genome. The obtained sequence reads were *de novo* assembled by MR DNA into 14 contigs (longest, 1,197,025 bp) with the NGen DNA assembly software by DNASTar, Inc. The resulting draft genome sequence was annotated using the Rapid Annotation using Subsystems Technology (RAST) prokaryotic genome annotation server, version 2.0 (8). The genome is 5,359,740 bp long and has a G+C content of 44.6%. In total, 4,709 coding sequences (CDSs) were identified, in addition to 114 tRNAs and 37 rRNAs.

Vibrio sp. Vb278 presents 99.7% and 99.3% 16S rRNA gene similarity with type strains *Vibrio gigantis* LGP 13 (9) and *Vibrio crassostreae* LG 7 (10), respectively, both isolated from cultured

oysters (*Crassostrea gigas*). Its genome displays a vast repertoire of carbohydrate-degrading genes, along with the complete vibrioferrin (siderophore) biosynthesis and transport gene clusters, suggesting that strain Vb278 possesses excellent nutrient-scavenging capacities. Of note is the presence of 14 of the 18 members of the symbiotic colonization and sigma-dependent biofilm formation (polysaccharide biosynthesis) gene cluster Syp, originally described for *Aliivibrio fischeri* (formerly *Vibrio fischeri*) (11). We further identified autoinducer 2 (AI-2) production (LuxS), binding (LuxP), and sensor kinase (LuxQ) protein biosynthesis genes, type I, II IV, and VI secretion system-encoding genes, and the full bacteriocin production operon. Altogether, the genome of *Vibrio* sp. strain Vb278 features varied adaptive strategies for symbiotic living, underlying the strain's high virulence potential and host colonization aptitude.

Nucleotide sequence accession numbers. The genome sequence of *Vibrio* sp. strain Vb278 has been deposited in the DDBJ/ENA/EBI/NCBI databases under the accession no. [CVNE000000000](https://www.ncbi.nlm.nih.gov/nuclink/CP010000000). The version described in this study is CVNE000000000.1 and consists of contig sequences [CVNE010000001](https://www.ncbi.nlm.nih.gov/nuclink/CP010000001) to [CVNE010000014](https://www.ncbi.nlm.nih.gov/nuclink/CP010000014).

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REFERENCES

1. Kita-Tsakamoto K, Oyaizu H, Nanba K, Simidu U. 1993. Phylogenetic relationships of marine bacteria, mainly members of the family *Vibrionaceae*, determined on the basis of 16S rRNA sequences. *Int J Syst Bacteriol* 43:8–19. <http://dx.doi.org/10.1099/00207713-43-1-8>.
2. Mansergh S, Zehr JP. 2014. *Vibrio* diversity and dynamics in the Monterey bay upwelling region. *Front Microbiol* 5:48. <http://dx.doi.org/10.3389/fmicb.2014.00048>.
3. Preheim SP, Boucher Y, Wildschutte H, David LA, Veneziano D, Alm EJ, Polz MF. 2011. Metapopulation structure of *Vibrionaceae* among

- coastal marine invertebrates. *Environ Microbiol* 13:265–275. <http://dx.doi.org/10.1111/j.1462-2920.2010.02328.x>.
4. Esteves AI, Hardoim CC, Xavier JR, Gonçalves JM, Costa R. 2013. Molecular richness and biotechnological potential of bacteria cultured from *Irciniidae* sponges in the north-east Atlantic. *FEMS Microbiol Ecol* 85:519–536. <http://dx.doi.org/10.1111/1574-6941.12140>.
 5. McFall-Ngai MJ. 2014. The importance of microbes in animal development: lessons from the squid-vibrio symbiosis. *Annu Rev Microbiol* 68:177–194. <http://dx.doi.org/10.1146/annurev-micro-091313-103654>.
 6. Chimetto LA, Brocchi M, Thompson CC, Martins RC, Ramos HR, Thompson FL. 2008. Vibrios dominate as culturable nitrogen-fixing bacteria of the Brazilian coral *Mussismilia hispida*. *Syst Appl Microbiol* 31: 312–319. <http://dx.doi.org/10.1016/j.syapm.2008.06.001>.
 7. Wiese J, Thiel V, Nagel K, Staufenberg T, Imhoff JF. 2009. Diversity of antibiotic-active bacteria associated with the brown alga *Laminaria saccharina* from the Baltic Sea. *Mar Biotechnol* 11:287–300. <http://dx.doi.org/10.1007/s10126-008-9143-4>.
 8. Overbeek R, Olson R, Pusch 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. <http://dx.doi.org/10.1093/nar/gkt1226>.
 9. Le Roux F, Goubet A, Thompson FL, Faury N, Gay M, Swings J, Saulnier D. 2005. *Vibrio gigantis* sp. nov., isolated from the haemolymph of cultured oysters (*Crassostrea gigas*). *Int J Syst Evol Microbiol* 55: 2251–2255. <http://dx.doi.org/10.1099/ijs.0.63666-0>.
 10. Faury N, Saulnier D, Thompson FL, Gay M, Swings J, Le Roux F. 2004. *Vibrio crassostreae* sp. nov., isolated from the haemolymph of oysters (*Crassostrea gigas*). *Int J Syst Evol Microbiol* 54:2137–2140. <http://dx.doi.org/10.1099/ijs.0.63232-0>.
 11. Yip ES, Grublesky BT, Husa EA, Visick KL. 2005. A novel, conserved cluster of genes promotes symbiotic colonization and sigma-dependent biofilm formation by *Vibrio fischeri*. *Mol Microbiol* 57:1485–1498. <http://dx.doi.org/10.1111/j.1365-2958.2005.04784.x>.