



Draft Genome Sequences of *Salinivibrio proteolyticus*, *Salinivibrio sharmensis*, *Salinivibrio siamensis*, *Salinivibrio costicola* subsp. *alcaliphilus*, *Salinivibrio costicola* subsp. *vallismortis*, and 29 New Isolates Belonging to the Genus *Salinivibrio*

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ABSTRACT The draft genome sequences of 5 type strains of species of the halophilic genus *Salinivibrio* and 29 new isolates from different hypersaline habitats belonging to the genus *Salinivibrio* have been determined. The genomes have 3,123,148 to 3,641,359 bp, a G+C content of 49.2 to 50.9%, and 2,898 to 3,404 open reading frames (ORFs).

The genus *Salinivibrio*, within the class *Gammaproteobacteria*, family *Vibrionaceae*, currently includes four species, one of them with three subspecies. Members of this genus are moderately halophilic bacteria, growing in the presence of 0 to 25% NaCl, and inhabit salted meats, brines, and hypersaline environments (saline lakes and salterns) (1–6). The members of the genus *Salinivibrio* grow optimally at ca. 7.5% NaCl, 37°C (range, 17 to 55°C), and pH 7.5 (range, pH 5 to 11). Therefore, they have developed cellular mechanisms to thrive under extreme conditions, such as high salt concentrations, alkaline pH values, UV radiation, or the presence of arsenic and other metals (3, 7, 8). *Salinivibrio costicola* subsp. *costicola* is considered a representative model for studies on moderately halophilic bacteria, and it has been used for osmoregulation and other physiological studies (9, 10). The genome of this bacterium, as well as those of *Salinivibrio* spp. S10B, S34, and S35, have already been published (8, 11); here, we report the draft genome sequences of the other species or subspecies of this genus, as well as of 29 new strains isolated from pond water of different salterns located in Spain and Puerto Rico (Table 1).

The draft genome sequences of the 34 strains were determined using a whole-genome shotgun strategy (12) with two Illumina sequencing systems, Illumina MiSeq (2 × 300-bp paired-end reads) (Swansea University, United Kingdom) and Illumina HiSeq (2 × 100-bp paired-end reads) (Macrogen, South Korea). The sequencing depth ranged between 7- and 100-fold coverage of the entire genome, and the resulting genome assemblies possessed N_{50} values between 9,975 and 311,807 bp. All reads were assembled in a range of 22 to 513 contigs ($\geq 1,000$ bp) using A5-MiSeq (13) and were used to identify open reading frames (ORFs) and provide a functional annotation of predicted proteins, rRNAs, and tRNA genes. Genome annotation was performed using RAST (14).

Received 1 March 2017 Accepted 20 March 2017 Published 6 July 2017

Citation López-Hermoso C, de la Haba RR, Sánchez-Porro C, Bayliss SC, Feil EJ, Ventosa A. 2017. Draft genome sequences of *Salinivibrio proteolyticus*, *Salinivibrio sharmensis*, *Salinivibrio siamensis*, *Salinivibrio costicola* subsp. *alcaliphilus*, *Salinivibrio costicola* subsp. *vallismortis*, and 29 new isolates belonging to the genus *Salinivibrio*. Genome Announc 5: e00244-17. <https://doi.org/10.1128/genomeA.00244-17>.

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TABLE 1 Features of the 34 draft genomes of *Salinivibrio* strains sequenced

Strain	Genome size (bp)	Place of isolation	N ₅₀ (bp)	No. of contigs	Sequencing depth (x)	% G+C	No. of ORFs	Sequencing technology	DDBJ/ENA/GenBank accession no.
<i>S. costicola</i> subsp. <i>alcaliphilus</i> DSM 19052	3,326,316	Campania, Italy	74,560	104	74	49.3	3,114	Illumina HiSeq	MUFR000000000
<i>S. costicola</i> subsp. <i>vallismortis</i> DSM 8285	3,478,614	Death Valley, USA	196,230	44	83	49.7	3,218	Illumina HiSeq	MUF000000000
<i>S. proteolyticus</i> DSM 19052	3,603,496	Bakhtegan Lake, Iran	143,067	51	11	49.8	3,338	Illumina MiSeq	MUFP000000000
<i>S. sharmensis</i> DSM 18182	3,326,895	Ras Mohammed Park, Egypt	229,272	40	35	50.4	3,028	Illumina MiSeq	MUFC000000000
<i>S. siamensis</i> JCM 14472	3,442,185	Nakornnayok, Thailand	114,651	61	17	50.3	3,126	Illumina MiSeq	MUFB000000000
<i>Salinivibrio</i> sp. AL184	3,398,626	Santa Pola, Alicante, Spain	198,024	42	100	50.3	3,132	Illumina HiSeq	MUEK000000000
<i>Salinivibrio</i> sp. AR640	3,256,021	Aragonesas, Huelva, Spain	87,861	60	31	49.3	2,962	Illumina MiSeq	MUFD000000000
<i>Salinivibrio</i> sp. AR647	3,281,043	Aragonesas, Huelva, Spain	311,807	22	22	49.3	3,002	Illumina MiSeq	MUFE000000000
<i>Salinivibrio</i> sp. IB282	3,226,186	Isla Bacuta, Huelva, Spain	40,759	157	11	50.7	3,021	Illumina MiSeq	MUET000000000
<i>Salinivibrio</i> sp. IB560	3,492,326	Isla Bacuta, Huelva, Spain	11,814	65	28	50.5	3,194	Illumina MiSeq	MUEM000000000
<i>Salinivibrio</i> sp. IB563	3,483,818	Isla Bacuta, Huelva, Spain	42,363	173	16	50.5	3,276	Illumina MiSeq	MUEN000000000
<i>Salinivibrio</i> sp. IB574	3,612,537	Isla Bacuta, Huelva, Spain	106,472	69	9	49.8	3,385	Illumina MiSeq	MUFN000000000
<i>Salinivibrio</i> sp. IB643	3,123,148	Isla Bacuta, Huelva, Spain	79,381	91	20	49.4	2,898	Illumina MiSeq	MUFF000000000
<i>Salinivibrio</i> sp. IB868	3,440,756	Isla Bacuta, Huelva, Spain	206,501	30	29	50.5	3,112	Illumina MiSeq	MUEW000000000
<i>Salinivibrio</i> sp. IB870	3,437,860	Isla Bacuta, Huelva, Spain	138,190	42	26	50.5	3,104	Illumina MiSeq	MUEX000000000
<i>Salinivibrio</i> sp. IB872	3,641,359	Isla Bacuta, Huelva, Spain	82,702	102	11	49.8	3,398	Illumina MiSeq	MUFO000000000
<i>Salinivibrio</i> sp. IC202	3,608,911	Isla Cristina, Huelva, Spain	72,723	111	25	50.5	3,404	Illumina MiSeq	MUEO000000000
<i>Salinivibrio</i> sp. IC317	3,278,261	Isla Cristina, Huelva, Spain	21,208	236	8	50.9	3,116	Illumina MiSeq	MUEP000000000
<i>Salinivibrio</i> sp. MA351	3,308,854	La Malahá, Granada, Spain	95,545	59	25	49.3	3,000	Illumina MiSeq	MUEG000000000
<i>Salinivibrio</i> sp. MA421	3,535,899	La Malahá, Granada, Spain	94,274	70	26	50.4	3,251	Illumina MiSeq	MUER000000000
<i>Salinivibrio</i> sp. MA427	3,263,514	La Malahá, Granada, Spain	9,975	513	7	49.3	3,296	Illumina MiSeq	MUFH000000000
<i>Salinivibrio</i> sp. MA440	3,421,552	La Malahá, Granada, Spain	59,971	102	35	49.5	3,107	Illumina MiSeq	MUFJ000000000
<i>Salinivibrio</i> sp. MA607	3,352,168	La Malahá, Granada, Spain	87,592	68	26	49.2	3,043	Illumina MiSeq	MUFK000000000
<i>Salinivibrio</i> sp. ML198	3,433,707	Es Trenc, Mallorca, Spain	163,752	44	24	50.4	3,134	Illumina HiSeq	MUEZ000000000
<i>Salinivibrio</i> sp. ML277	3,446,273	Es Trenc, Mallorca, Spain	117,752	73	31	50.4	3,146	Illumina MiSeq	MUEL000000000
<i>Salinivibrio</i> sp. ML290	3,523,661	Es Trenc, Mallorca, Spain	168,056	36	15	50.2	3,224	Illumina MiSeq	MUEY000000000
<i>Salinivibrio</i> sp. ML318	3,361,480	Es Trenc, Mallorca, Spain	65,785	96	14	50.7	3,080	Illumina MiSeq	MUEQ000000000
<i>Salinivibrio</i> sp. ML323	3,233,876	Es Trenc, Mallorca, Spain	132,870	63	16	50.8	2,960	Illumina MiSeq	MUES000000000
<i>Salinivibrio</i> sp. ML328A	3,392,891	Es Trenc, Mallorca, Spain	172,729	38	55	50.5	3,124	Illumina HiSeq	MUEU000000000
<i>Salinivibrio</i> sp. ML331	3,545,121	Es Trenc, Mallorca, Spain	128,351	60	86	50.4	3,262	Illumina HiSeq	MUEV000000000
<i>Salinivibrio</i> sp. PR5	3,456,024	Cabo Rojo, Puerto Rico	68,288	105	23	49.9	3,141	Illumina MiSeq	MUFK000000000
<i>Salinivibrio</i> sp. PR6	3,443,918	Cabo Rojo, Puerto Rico	165,099	49	28	50.4	3,140	Illumina MiSeq	MUFA000000000
<i>Salinivibrio</i> sp. PR919	3,489,646	Cabo Rojo, Puerto Rico	33,984	176	14	49.9	3,269	Illumina MiSeq	MUFL000000000
<i>Salinivibrio</i> sp. PR932	3,497,261	Cabo Rojo, Puerto Rico	90,599	74	31	49.9	3,171	Illumina MiSeq	MUFM000000000

The draft genomes were estimated to contain between 3,123,148 and 3,641,359 bp, with a G+C content between 49.2 and 50.9% and a range of 2,898 to 3,404 putative ORFs (Table 1).

Genes involved in osmoregulation mechanisms included ectoine and hydroxyectoine synthesis genes, transporters for betaine, and other compatible solutes, like proline and choline. A complete set of genes encoding RecBCD helicase/nuclease and UvrABC endonuclease holoenzymes were found; these genes are involved in the recombinational repair of DNA double-strand breaks. Enzyme-encoding genes involved in anaerobic respiration were found, such as arsenate reductase (*asrR*) and flavodoxin reductase (FIR). These halophilic bacteria are widely isolated from aquatic hypersaline environments and salted food products. Thus, the availability of their genome sequences, combined with other physiological and biochemical data, will advance our understanding of haloadaptation and other stress defense mechanisms of halophilic bacteria to extreme conditions.

Accession number(s). The draft genome sequences of the 34 strains of *Salinivibrio* have been deposited in DDBJ/ENA/GenBank with accession numbers listed in Table 1.

ACKNOWLEDGMENTS

This work was funded by the Spanish Ministry of Science and Innovation (grant CGL2013-46941-P), with FEDER funds (to A. Ventosa) and wgs-aqua.net project funded by BBSRC/NERC as part of the sustainable aquaculture call (BB/Mo26388/1) (to E. Feil). C. López-Hermoso was the recipient of a postgraduate fellowship from the Spanish Ministry of Education, Culture and Sports.

REFERENCES

- Mellado E, Moore ERB, Nieto JJ, Ventosa A. 1996. Analysis of 16S rRNA gene sequences of *Vibrio costicola* strains: description of *Salinivibrio costicola* gen. nov., comb. nov. *Int J Syst Bacteriol* 46:817–821. <https://doi.org/10.1099/00207713-46-3-817>.
- Romano I, Gambacorta A, Lama L, Nicolaus B, Giordano A. 2005. *Salinivibrio costicola* subsp. *alcaliphilus* subsp. nov., a haloalkaliphilic aerobe from Campania region (Italy). *Syst Appl Microbiol* 28:34–42. <https://doi.org/10.1016/j.syapm.2004.10.001>.
- Huang CY, Garcia JL, Patel BKC, Cayol JL, Baresi L, Mah RA. 2000. *Salinivibrio costicola* subsp. *vallismortis* subsp. nov., a halotolerant facultative anaerobe from Death Valley, and emended description of *Salinivibrio costicola*. *Int J Syst Evol Microbiol* 50:615–622. <https://doi.org/10.1099/00207713-50-2-615>.
- Amoozegar MA, Schumann P, Hajighasemi M, Fatemi AZ, Karbalaie-Heidari HR. 2008. *Salinivibrio proteolyticus* sp. nov., a moderately halophilic and proteolytic species from a hypersaline lake in Iran. *Int J Syst Evol Microbiol* 58:1159–1163. <https://doi.org/10.1099/ijs.0.65423-0>.
- Romano I, Orlando P, Gambacorta A, Nicolaus B, Dipasquale L, Pascual J, Giordano A, Lama L. 2011. *Salinivibrio sharmensis* sp. nov., a novel haloalkaliphilic bacterium from a saline lake in Ras Mohammed Park (Egypt). *Extremophiles* 15:213–220. <https://doi.org/10.1007/s00792-010-0349-9>.
- Chamroensaksri N, Tanasupawat S, Akaracharanya A, Visessanguan W, Kudo T, Itoh T. 2009. *Salinivibrio siamensis* sp. nov., from fermented fish (pla-ra) in Thailand. *Int J Syst Evol Microbiol* 59:880–885. <https://doi.org/10.1099/ijs.0.001768-0>.
- Garcia MT, Ventosa A, Ruiz-Berraquero F, Kocur M. 1987. Taxonomic study and amended description of *Vibrio costicola*. *Int J Syst Bacteriol* 37:251–256. <https://doi.org/10.1099/00207713-37-3-251>.
- Gorriti MF, Dias GM, Chimetto LA, Trindade-Silva AE, Silva BS, Mesquita MM, Gregoracci GB, Farias ME, Thompson CC, Thompson FL. 2014. Genomic and phenotypic attributes of novel salinivibrios from stromatolites, sediment and water from a high altitude lake. *BMC Genomics* 15:473. <https://doi.org/10.1186/1471-2164-15-473>.
- Oren A. 2002. Halophilic microorganisms and their environments. Kluwer Academic Press, London, United Kingdom.
- Oren A. 2002. Diversity of halophilic microorganisms: environments, phylogeny, physiology, and applications. *J Ind Microbiol Biotechnol* 28:56–63. <https://doi.org/10.1038/sj/jim/7000176>.
- Dikow RB, Smith WL. 2013. Genome-level homology and phylogeny of *Vibrionaceae* (*Gammaproteobacteria: Vibrionales*) with three new complete genome sequences. *BMC Microbiol* 13:80. <https://doi.org/10.1186/1471-2180-13-80>.
- Fleischmann RD, Adams MD, White O, Clayton RA, Kirkness EF, Kerlavage AR, Bult CJ, Tomb JF, Dougherty BA, Merrick JM, McKenney K, Sutton GG, FitzHugh W, Fields CA, Gocayne JD, Scott JD, Shirley R, Liu LI, Glodek A, Kelley JM, Weidman JF, Phillips CA, Spriggs T, Hedblom E, Cotton MD, Utterback T, Hanna MC, Nguyen DT, Saudek DM, Brandon RC, Fine LD, Fritchman JL, Fuhrmann JL, Geoghagen NS, Gnehm CL, McDonald LA, Small KV, Fraser CM, Smith HO, Venter JC. 1995. Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd. *Science* 269:496–512. <https://doi.org/10.1126/science.7542800>.
- Coil D, Jospin G, Darling AE. 2015. A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. *Bioinformatics* 31:587–589. <https://doi.org/10.1093/bioinformatics/btu661>.
- 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. <https://doi.org/10.1093/nar/gkt1226>.