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Draft genome sequences of two *Halobacteriovorax* strains isolated from Apalachicola Bay, Florida

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ABSTRACT Predatory bacteria are common in aquatic environments and associated with eukaryotic hosts. Here, we report draft genome sequences for two marine isolates, *Halobacteriovorax* sp. strains GFR7 and GFR8, that were isolated from Dickerson Bay in Apalachicola Bay, Florida, USA.

KEYWORDS BALO, marine microbiology, predatory bacteria

Halobacterivorax (formerly *Bacteriovorax*) are obligate bacterial predators within marine and brackish habitats (1–5). Taxa within this genus are considered "keystone species" due to their predicted top-down structuring role (1).

Here, we introduce the genomes of two *Halobacteriovorax* strains, GFR7 and GFR8, that were isolated from Dickerson Bay in Apalachicola Bay, Florida, USA near the Gulf Specimen Marine Laboratory (30.025614°N, 84.382839°W). Water samples were collected, stored on ice, and transported to Florida A&M University. Strains were isolated from PP20 agar plaques on *Vibrio vulnificus* prey. To acquire genomic DNA, plaques were generated and resuspended in 40 mL of freshly grown *V. parahaemolyticus* culture. Once cleared, cultures were filtered twice through 0.45 µm syringe filters. Filtrates were centrifuged at 21,300 × *g* for 20 min to pellet, and then DNA was extracted with an Invitrogen PureLink Genomic DNA Kit according to manufacturer instructions (Thermo Fisher Scientific). DNA quantity and quality were determined using a Nanodrop spectrophotometer. gDNA samples were then sent to SeqCenter, LLC (Pittsburgh, PA) for Illumina whole-genome sequencing using the Illumina DNA Prep Kit. Sequencing was performed on an Illumina NovaSeq X Plus sequencer and resulted in paired-end 150 bp reads: 2,926,628 and 3,073,590 paired reads for GFR7 and GFR8, respectively (Table 1). Default parameters were used for all software, unless otherwise specified. Raw reads had a Phred Q30 score of 95.5% for GFR7 and 94.7% for GFR8 (6). Raw reads were assembled into contigs using Unicycler (7) on the Galaxy (8) (usegalaxy.org version 25.1.rc1) public server. Contigs were uploaded into Geneious Prime 2025.0.3, extended, and combined using the default map to reference and *de novo* assembly actions. Genomes were annotated via the Prokka Pipeline (9, 10) on Galaxy (8); upon upload to National Center for Biotechnology Information (NCBI), data were reanalyzed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (11).

The final draft genomes of GFR7 and GFR8 are 3,420,318 and 3,420,369 bp long, respectively, in three contigs, have 120× and 125× genome coverage, an N50 of with 2,950,718 and 2,950,716 bp, respectively, and a G+C content of 37% for each strain (Table 1). We determined that contig 1 was a closed plasmid via the Unicycler Assembler (7) on Galaxy (8) manually and using the map to reference feature by checking that the overhanging mapped reads from each contig end matched one another. A total of 3,318 and 3,320 DNA coding regions were identified, including 3,272 and 3,274 encoding putative proteins and 38 encoding RNAs, respectively, for GFR7 and GFR8. We predicted functions for 2,103 for GFR7 and 2,105 for GFR8 of these proteins, while the other

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TABLE 1 Sequencing statistics for GFR7 and GFR8[a]

Strain	Total reads	Genome size (bp)	N50 (bp)	Avg. coverage	G/C content	Coding regions	Putative proteins
GFR7	2,926,628	3,420,318	2,950,718	120x	37%	3,318	3,272
GFR8	3,073,590	3,420,369	2,950,716	125x	37%	3,320	3,274
Individual contig information							
	Contig 1 accession	**Contig 1 size (bp); circularized**	**Contig 1 size (bp); circularized**	**Contig 2 accession**	**Contig 2 size (bp)**	**Contig 3 accession**	**Contig 3 size (bp)**
GFR7	JBPBLS010000001.1	97,014	97,014	JBPBLS010000002.1	372,586	JBPBLS010000003.1	2,950,718
GFR8	JBPBLR010000001.1	97,014	97,014	JBPBLR010000003.1	372,639	JBPBLR010000002.1	2,950,716

[a]Contigs are shown ordered smallest to largest.

1,207 proteins were assigned as hypothetical for both strains using Prokka on Galaxy (8). RefSeq Masher (12) determined that the most closely related genome on NCBI was *Bacteriovorax* sp. BAL6_X (PRJNA210328), with 91.5% ANI to GFR7 and GFR8, suggesting these strains are in the same genus. BAL6_X was deposited in NCBI in 2013, after which the *Bacteriovorax* genus was reclassified as *Halobacteriovorax* (3).

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Lauren Speare, Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Resources, Writing – original draft, Writing – review and editing | Macey N. Coppinger, Data curation, Methodology, Resources, Writing – original draft, Writing – review and editing | Grisel Fierros-Romero, Methodology, Resources | Henry N. Williams, Methodology, Resources

DATA AVAILABILITY

These genome sequences of GRF7 and GRF8 are available in GenBank under accession no. SAMN48918368 and SAMN48918369, respectively, in the BioProject number PRJNA1272625. Cultures of GFR7 and GFR8 are available upon request.

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