



Genome Sequences and Metagenome-Assembled Genome Sequences of Microbial Communities Enriched on Phytoplankton Exometabolites

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ABSTRACT We report 11 bacterial draft genome sequences and 38 metagenome-assembled genomes (MAGs) from marine phytoplankton exometabolite enrichments. The genomes and MAGs represent marine bacteria adapted to the metabolite environment of phycospheres, organic matter-rich regions surrounding phytoplankton cells, and are useful for exploring functional and taxonomic attributes of phytoplankton-associated bacterial communities.

Bacteria associated with marine phytoplankton play essential roles in global carbon and nutrient cycles (1, 2). In the nutrient-rich phycosphere surrounding phytoplankton cells, the interactions among cooccurring bacteria and between bacteria and their hosts determine community composition. The phycosphere therefore represents a unique microcosm in which ecological principles of microbial community assembly can be examined (3, 4). A high-throughput synthetic phycosphere system was established (5) in which a natural coastal seawater bacterial assemblage was passaged through 8 serial transfers in a 96-well format culture system containing different mixtures of metabolites known to be released preferentially by diatoms (6, 7) or dinoflagellates (7). Here, we report the genomes and metagenome-assembled genomes (MAGs) enriched in those synthetic phycospheres, providing a resource for understanding the functional potentials of, and ecological interactions occurring in, ocean microbial communities.

The 11 bacterial strains were isolated from 2 microbial communities, 1 supplied with a mixture of 5 diatom exometabolites (xylose, glutamate, glycolate, ectoine, and dihydroxypropanesulfonate) and the other with 5 dinoflagellate exometabolites (ribose, spermidine, trimethylamine, isethionate, and dimethylsulfoniopropionate) (5). Enrichments were serially diluted, plated onto solid marine basal medium containing each of the individual metabolites, and grown at 24°C in the dark for 1 week. Single colonies were isolated to uniform morphology on half-strength yeast extract-tryptone sea salt medium. DNA extraction was carried out using the ZymoBIOMICS DNA miniprep kit, and libraries were prepared using the KAPA Hyper prep kit (Kapa Biosystems, Wilmington, MA). Illumina MiSeq (2 × 150 bp) reads were trimmed using Trimmomatic v0.38 (8), quality was assessed using QUAST (9), and *de novo* assembly was performed using SPAdes v3.12.0 (10). The 16S rRNA genes were amplified using the 27F and 1492R primers (11). Sanger sequencing performed at Genewiz (South Plainfield, NJ) confirmed the purity of the amplicons.

Metagenome sequencing (Illumina NextSeq; 1 × 150 bp) was carried out on enrichment cultures representing six diatom and six dinoflagellate exometabolite treatments. As described previously (5), reads from the six diatom or the six dinoflagellate exometabolite treatments were separately coassembled using MEGAHIT v1.1.3 (12, 13). Default parameters were used for all software unless otherwise specified. Reads were mapped to the assembly with Bowtie v2.2.9 (14) and binned into MAGs using Anvi'o v4 (15, 16) and CONCOCT (17) following published protocols (18) (<http://merenlab.org/data/tara-oceans-mags/>). The completeness and redundancy of bins were assessed

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TABLE 1 Characteristics of 11 isolate genomes and 38 MAGs obtained from serial enrichments of a coastal bacterial assemblage with metabolites from marine diatoms or dinoflagellates

Isolate or MAG	Taxonomic classification ^a	Size G+C (Mb) content (%)	No. of reads	Coverage (x)	No. of contigs (bp)	N ₅₀ cont (%) ^b	Compl cont (%) ^b	SRA accession no.	GenBank accession no.	Closest genome (GenBank accession no.) ^c	ANI or AAI (%)
Isolates											
HF1	<i>Marivivens donghaensis</i>	3.34 60.8	317,066	14.2	24	292,199 99.7/0.8		SRRT1481811	JAATOP0000000000	<i>Marivivens</i> sp. JLT3646 NZ (CP018572)	66.7 ^f
HF2	<i>Thalassospira lucentensis</i>	4.50 53.2	477,674	15.9	13	758,710 100.0/0.0		SRRT1481803	JAATOV0000000000	<i>Thalassospira lucentensis</i> MCCC 1A00383	84.4 ^g
HF7	<i>Pseudoceanicola</i> sp.	4.27 64.9	312,562	11.0	74	103,803 98.5/0.8		SRRT1481802	JAATOW0000000000	<i>Pseudoceanicola antarctica</i> (GCA_002786285)	67.7 ^f
HF9A	<i>Phaeobacter</i> sp.	4.27 62.2	256,104	9.0	262	30,359 99.3/1.5		SRRT1481810	JAATOX0000000000	<i>Phaeobacterium scottomollicae</i> (GCA_003003215)	79.9 ^f
HF9B	<i>Vibrio diazotrophicus</i>	4.39 43.3	256,880	8.8	193	47,679 99.8/2.6		SRRT1481807	JAATOR0000000000	<i>Vibrio diazotrophicus</i> NBRC 103148	91.0 ^g
HF15	<i>Thalassospira</i> sp.	4.29 54.5	412,760	14.4	25	551,637 100.0/0.0		SRRT1481809	JAAVKI0000000000	<i>Thalassospira indica</i> NZ (CP031555)	88.0 ^g
HF17	<i>Vibrio campbellii</i>	5.66 45.5	273,858	7.3	459	21,883 99.7/1.2		SRRT1481808	JAATOC0000000000	<i>Vibrio campbellii</i> NZ (CP019293)	97.8 ^g
HF18	<i>Salipiger thiooxidans</i>	5.26 67.5	272,102	7.8	1,007	9,637 95.4/2.8		SRRT1481806	JAATOS0000000000	<i>Salipiger thiooxidans</i> (GCA_9001020275)	97.8 ^g
HF31	<i>Celeribacter</i> sp.	3.60 59.9	605,892	25.2	13	522,533 99.2/0.5		SRRT1481805	JAATOT0000000000	<i>Celeribacter ethanolicus</i> NZ (CP022196)	84.5 ^g
HF66	<i>Pseudoalteromonas</i> sp.	4.39 40.7	692,080	23.6	48	210,054 100.0/0.4		SRRT1481804	JAATOU0000000000	<i>Pseudoalteromonas shioyasakiensis</i> (GCA_001550135)	91.6 ^g
HF70	<i>Vibrio hepatarius</i>	4.71 45.9	382,864	12.2	74	168,419 100.0/0.9		SRRT1481812	JAATOO0000000000	<i>Vibrio hepatarius</i> (GCA_001274785)	92.6 ^g
MAGs^d											
HF-Dia02	<i>Oceanospirillaceae</i>	4.47 42.0	423,160	14.2	283	24,277 86.5/3.0		SRRT1451986	JABXIF0000000000	<i>Marinomonas polaris</i> DSM 16579	81.6 ^g
HF-Dia03	<i>Rhodobacteriales</i>	3.64 53.4	1,038,613	42.8	201	31,207 95.0/0.8		SRRT1451960	JABXHV0000000000	<i>Labrenzia suaedae</i> (GCA_900142725)	64.5 ^f
HF-Dia04	<i>Cryomorphaceae</i>	3.29 45.4	302,680	13.8	182	29,213 97.9/9.7		SRRT1451963	JABXHS0000000000	<i>Phaeocystidibacter luteus</i> (GCA_008933115)	82.4 ^g
HF-Dia05	<i>Flavobacteriales</i>	2.53 40.3	1,017,060	60.3	97	147,211 93.1/2.7		SRRT1451996	JABXHN0000000000	<i>Arenibacter aquaticus</i> (GCA_003957295)	59.6 ^f
HF-Dia07	<i>Alteromonadaceae</i>	5.10 47.9	16,809,600	494.4	123	84,748 99.9/2.8		SRRT1451997	JABXHM0000000000	<i>Alteromonas alba</i> (GCA_002993365)	77.4 ^f
HF-Dia11	<i>Flavobacteriales</i>	2.94 32.3	429,240	21.9	98	76,707 98.3/1.1		SRRT1451994	JABXHX0000000000	<i>Tenacibaculum</i> sp. DSM 106434	65.1 ^f
HF-Dia12	<i>Gammaproteobacteria</i>	3.42 40.8	517,560	22.7	285	17,653 93.4/2.2		SRRT1451988	JABXID0000000000	<i>Psychrosphaera saromensis</i> (GCA_002954545)	64.2 ^f
HF-Dia14	<i>Gammaproteobacteria</i>	3.64 51.8	485,333	20.0	287	19,154 95.1/4.9		SRRT1451964	JABXHR0000000000	<i>Thiohalobacter thiocyanaticus</i> NZ (AP018052)	46.4 ^f
HF-Dia15	<i>Rhizobiales</i>	3.97 45.9	304,367	11.5	295	19,983 91.4/3.0		SRRT1451989	JABXIC0000000000	<i>Terasakiella pusilla</i> DSM 6293 (GCA_000688235)	68.8 ^f
HF-Dia17	<i>Oceanospirillales</i>	3.38 51.2	22,932,173	1,017.7	418	10,263 91.2/3.3		SRRT1451974	JABXHP0000000000	<i>Marinobacterium mangrovicola</i> (GCA_004339595)	62.1 ^f
HF-Dia18	<i>Rhodobacteraceae</i>	4.51 63.1	24,212,687	805.3	409	15,672 93.0/5.3		SRRT1451991	JABXIA0000000000	<i>Leisingera daeponensis</i> DSM 23529	86.7 ^g
HF-Dia21	<i>Oceanospirillales</i>	4.53 40.5	1,265,380	41.9	96	99,744 99.2/0.4		SRRT1451993	JABXHY0000000000	<i>Pleionea mediterranea</i> (GCA_003148745)	62.4 ^f
HF-Dia22	<i>Flavobacteria</i>	4.70 40.8	463,733	14.8	179	42,273 98.6/1.4		SRRT1451985	JABXHO0000000000	" <i>Candidatus</i> <i>Fluviicola riflensis</i> " (CP022585)	56.2 ^f
HF-Dia23	<i>Tenacibaculum</i> sp.	3.20 31.7	424,533	19.9	86	70,967 98.5/0.8		SRRT1451962	JABXHT0000000000	<i>Tenacibaculum discolor</i> (GCA_003664185)	97.8 ^g
HF-Dia27	<i>Oceanospirillales</i>	3.64 45.2	2,817,360	116.1	196	31,979 98.3/2.6		SRRT1451965	JABXHQ0000000000	<i>Pleionea mediterranea</i> (GCA_003148745)	64.1 ^f
HF-Dia28 ^e	<i>Ruegeria pomeroyi</i>	4.51 64.0	60,900,033	2,025.5	200	33,165 97.6/2.2		SRR9668573	JABXIZ0000000000	<i>Ruegeria pomeroyi</i> DSS-3	100.0 ^g
HF-Dia32	<i>Flavobacteriales</i>	3.09 45.8	861,080	41.8	76	69,153 97.7/0.5		SRRT1451995	JABXHW0000000000	<i>Phaeocystidibacter luteus</i> (GCA_008933115)	67.2 ^f
HF-Dia38	<i>Cyclobacteriaceae</i>	3.39 40.8	2,743,640	121.4	460	8,688 86.7/4.1		SRRT1451992	JABXHZ0000000000	<i>Algoriphagus kandelae</i> (GCA_004571135)	82.1 ^g
HF-Dia39	<i>Marivivens</i> sp.	2.49 56.7	7,811,960	470.6	142	23,748 95.1/1.0		SRRT1451961	JABXHU0000000000	<i>Marivivens</i> sp. JLT3646 NZ (CP018572)	97.2 ^g
HF-Dia40	<i>Vibrionaceae</i>	4.24 46.3	7,453,920	263.7	357	16,672 96.6/2.1		SRRT1451990	JABXIB0000000000	<i>Vibrio hepatarius</i> (GCA_001274785)	92.6 ^g
HF-Din01	<i>Salipiger</i> sp.	4.40 68.0	10,301,867	351.2	701	7,265 86.8/2.7		SRRT1451976	JABXIO0000000000	<i>Salipiger thiooxidans</i> (GCA_900102075)	98.0 ^g
HF-Din02	<i>Methylcytoseae</i>	4.09 48.4	13,224,333	485.0	69	276,225 100.0/1.0		SRRT1451984	JABXIG0000000000	<i>Terasakiella pusilla</i> DSM 6293	79.0 ^f
HF-Din03 ^e	<i>Ruegeria pomeroyi</i>	4.54 64.0	36,062,733	1,191.5	78	105,484 98.7/0.7		SRR9668574	JABXIV0000000000	<i>Ruegeria pomeroyi</i> DSS-3	100.0 ^g
HF-Din05	<i>Gammaproteobacteria</i>	3.45 45.4	425,500	18.5	223	24,639 93.7/2.2		SRRT1451969	JABXIU0000000000	<i>Pseudoalteromonas phenolica</i> O-BC30 GCA 004103265	48.7 ^f
HF-Din08	<i>Oceanospirillaceae</i>	5.78 58.6	3,787,827	98.3	249	42,217 98.1/2.0		SRRT1451978	JABXIM0000000000	<i>Marinobacterium rhizophilum</i> DSM 18822	68.5 ^g
HF-Din09	<i>Flammovirgaceae</i>	4.04 42.1	2,308,187	85.7	543	9,559 92.8/2.7		SRRT1451975	JABXIP0000000000	<i>Roseivira spongicola</i> (GCA_004103265)	81.4 ^f
HF-Din10	<i>Alphaproteobacteria</i>	3.00 54.3	1,760,000	88.0	309	14,274 81.9/1.7		SRRT1451968	JABXIV0000000000	<i>Hankyongella ginsenosidimutans</i> WT-2-3 (CP039704)	50.2 ^f
HF-Din11	<i>Vibrio campbellii</i>	5.63 45.3	36,542,453	973.6	92	123,020 100.0/0.1		SRRT1451983	JABXIH0000000000	<i>Vibrio campbellii</i> NZ (CP019293)	97.9 ^g
HF-Din12	<i>Oceanospirillales</i>	2.58 41.6	1,683,880	97.9	62	69,368 98.1/4.1		SRRT1451973	JABXIQ0000000000	<i>Kangiaella profunda</i> NZ (CP025120)	63.5 ^f

(Continued on next page)

TABLE 1 (Continued)

Isolate or MAG	Taxonomic classification ^a	Size (Mb)	G+C content (%)	No. of reads	Coverage (x)	No. of contigs	N ₅₀ (bp)	Compl (%) ^b	SRA accession no.	GenBank accession no.	Closest genome (GenBank accession no.) ^c	ANI or AAI (%)
HF-Din13	Campylobacteraceae	2.76	28.4	1,264,080	68.7	38	142,008	99.2/1.2	SRR11451982	JABXII0000000000	<i>Haliarcobacter bivaiviorum</i> strain LMG 26154 (CP031217)	85.2 ^g
HF-Din14	Rhodobacteraceae	3.53	59.9	13,734,053	583.6	64	109,963	98.9/0.5	SRR11451979	JABXIL0000000000	<i>Celeribacter halophilus</i> (GCA_003254175)	82.0 ^g
HF-Din16	Flavobacteriia	1.81	37.0	97,740	8.1	234	9,657	83.0/2.3	SRR11451970	JABXIT0000000000	<i>Maribacter cobaltidurans</i> NZ (CP022957)	57.8 ^f
HF-Din17	Gammaaproteobacteria	4.03	44.2	354,640	13.2	487	12,701	85.8/4.3	SRR11451967	JABXIW0000000000	<i>Pleionea mediterranea</i> (GCA_003148745)	49.3 ^f
HF-Din19	Flavobacteriales	2.37	29.8	260,700	16.5	69	52,100	97.9/1.4	SRR11451981	JABXIU0000000000	<i>Polaribacter porphyrae</i> (GCA_002954685)	68.7 ^f
HF-Din21	Kordiimonadaceae	3.62	53.6	1,908,947	79.1	96	81,569	97.1/1.8	SRR11451971	JABXIS0000000000	<i>Kordiimonas lipolytica</i> (GCA_001550065)	76.8 ^f
HF-Din22	Cyclobacteriaceae	3.65	40.7	1,498,933	61.6	38	178,308	99.6/0.6	SRR11451977	JABXIN0000000000	<i>Algoriphagus kandeliae</i> (GCA_004571135)	81.1 ^g
HF-Din24	Gammaaproteobacteria	3.50	44.0	22,920,333	982.3	151	35,787	98.5/2.3	SRR11451980	JABXIK0000000000	<i>Oceanobacter kriegii</i> DSM 6294 (GCA_000422845)	54.6 ^f
HF-Din29	Gammaaproteobacteria	2.11	49.9	753,973	53.6	305	8,218	82.8/2.9	SRR11451972	JABXIR0000000000	<i>Spongibacter marinus</i> DSM 19753 (GCA_000422345)	51.2 ^f

^a Taxonomic classification of isolates is based on >98% similarity of 16S rRNA genes or >98% similarity of *hsp60* genes (*Vibrio* only). Taxonomic classification of metagenome-assembled genomes (MAGs) is based on the lowest taxonomic level with a *P* value of ≤0.015 as calculated in MIGA using the TypeMat database, in which average nucleotide identity (ANI) is generally reported for similarities of ≥85%, and average amino acid identity (AAI) is reported if the ANI is <85%.

^b Compl, completeness level; cont, contamination level.

^c Closest genome was determined by MIGA analysis using the TypeMat database.

^d MAGs that start with HF-Dia are assembled from the six diatom metagenomes, while MAGs that start with HF-Din are assembled from the six dinoflagellate metagenomes.

^e Previously published (5).

^f AAI.

^g ANI.

using CheckM v1.0.12 (19). Only bins with >80% completeness and <10% redundancy are reported here (Table 1). The taxonomic classifications of the MAGs were inferred using the Microbial Genome Atlas (MiGA) (<http://microbial-genomes.org/>) using the TypeMat database (20).

Data availability. All data are deposited under GenBank BioProject number PRJNA553557. The raw reads of the genomic data for the isolates are deposited under SRA accession numbers SRR11481802 to SRR11481812. The original raw reads of the metagenomic data used for MAG assembly are deposited under SRA accession numbers SRR11434620 to SRR11434631. The assemblies for isolates and MAGs are deposited under the GenBank accession numbers listed in Table 1; the versions described in this paper are the first versions.

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We declare no competing interests.

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