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GENOME SEQUENCES

Draft Genome Sequences of 10 Bacteria from the Marine *Pseudoalteromonas* Group

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ABSTRACT Here, we report the draft genome sequences of 10 marine *Pseudoalteromonas* bacteria that were isolated, assembled, and annotated by undergraduate students participating in a marine microbial genomics course. Genomic comparisons suggest that 7 of the 10 strains are novel isolates, providing a resource for future marine microbiology investigations.

The genus *Pseudoalteromonas* comprises numerous marine species that are found in association with marine plants and animals (1). Some *Pseudoalteromonas* species produce compounds that inhibit the fouling of marine surfaces by invertebrates and algae (2), while others stimulate the metamorphosis of tubeworms, urchins, and corals (3). Many pseudoalteromonads possess the ability to produce diverse specialized metabolites (4–6), providing an understudied resource for biotechnology.

To engage undergraduates in discovery-based research, 10 purified isolates were cultured, and their genomes were sequenced, assembled, annotated, and analyzed by students participating in a marine microbial genomics (MMG) course at San Diego State University. The strains were collected from various marine organisms or objects using sterile cotton swabs (Table 1). A single colony of each strain was obtained on marine agar 2216 (BD Difco, Franklin Lakes, NJ, USA) and incubated at 25°C for 24 to 48 h. Colonies were transferred to marine broth 2216 and incubated for 24 to 48 h at 25°C before storage and DNA isolation. Genomic DNA was extracted using a Quick-DNA fungal/bacterial miniprep kit (Zymo Research, Irvine, CA, USA). 16S rRNA gene (27F-1492R) Sanger sequencing (Eton Biosciences, San Diego, CA, USA) classified all strains as being within the *Pseudoalteromonas* genus (>98% identity, >97% coverage). DNA was submitted to the Microbial Genome Sequencing Center (Pittsburgh, PA, USA) for library preparation (Illumina DNA prep kit; San Diego, CA, USA) and whole-genome sequencing (NextSeq 550; Illumina), producing 2 × 150-bp paired-end reads. Reads were trimmed using Trim Galore v0.6.1 (7), assembled using Unicycler v0.4.8 (8), integrated in PATRIC v3.6.9 (9), and annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.1 (10) with default parameters. General features of each genome are listed in Table 1.

To identify and compare the genomes of the newly sequenced strains with their nearest publicly available genomes, we used the Mash/MinHash search (9, 11) and calculated the average nucleotide identity (ANI) using EZBioCloud (12). Of the 10 genomes, 7 possessed ANI values that are below the 95% threshold that delineates species (13), suggesting that they are novel isolates (Table 1). When grown on marine agar 2216, all strains possessed pigmentation (Table 1) (14). When analyzed using antiSMASH v5.0 (15), the genomes were found to possess from 2 to 25 specialized

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TABLE 1 Genome features and metadata of 10 *Pseudoalteromonas* strains[a,b]

Strain	Closest strain, assembly accession no.	ANI (%)	Genome size (Mb)	N_{50} (bp)	GC (%)	No. of raw reads	No. of contigs	Coverage (×)	Colony pigment	No. of specialized metabolite gene clusters	*macB* E value	*macS* E value	*macT* E value	Isolation origin	Isolation location	SRA accession no.	Genome accession no.
MMG001	*Pseudoalteromonas luteoviolacea* H33-S, GCF_001625695.1	99.4	6.19	166,341	42.0	4,233,854	155	164	Purple	25	0	0	2E-109	Tubeworm	Quivera Basin, San Diego	SRR14127474	JAGJEM000000000
MMG002	*Pseudoalteromonas luteoviolacea* H33-S, GCF_001625695.1	99.4	6.19	166,863	41.9	3,534,634	151	136	Purple	25	0	0	2E-109	Tubeworm	Quivera Basin, San Diego	SRR14127473	JAGJEL000000000
MMG005	*Pseudoalteromonas aurantia* S3895, GCA_005887285.1	78.6	5.66	173,183	40.7	2,304,625	96	98	Orange	21	0	0	2E-59	Tubeworm	Quivera Basin, San Diego	SRR14127467	JAGJEK000000000
MMG006	*Pseudoalteromonas* sp. S3178, GCA_005886985.1	92.7	4.27	184,297	39.4	2,153,867	61	123	Brown	6	NS	NS	NS	Sediment	Silver Strand, San Diego	SRR14127466	JAGJEJ000000000
MMG007	*Pseudoalteromonas* sp. S3178, GCA_005886985.1	92.6	4.08	210,295	39.5	1,278,590	64	81	Brown	5	NS	NS	NS	Intertidal boulder	Bird Rock, San Diego	SRR14127465	JAGJEI000000000
MMG009	*Pseudoalteromonas luteoviolacea* NCIMB1944, GCF_001625565.1	91.9	6.51	469,158	42.2	4,505,820	75	173	Purple	16	0	0	7E-105	Aquarium filter	Aquarium, San Diego	SRR14127464	JAGJEH000000000
MMG010	*Pseudoalteromonas* sp. H103, GCF_001469205.1	77.2	3.57	204,150	38.2	1,477,062	39	107	Pink	2	NS	NS	NS	Sea snail	Sunset Cliffs, San Diego	SRR14127463	JAGJEG000000000
MMG012	*Pseudoalteromonas* sp. MSK9-3, GCA_003590335.1	79.1	5.44	56,381	40.7	1,307,359	261	62	Orange	20	0	4E-134	2E-59	Yellow sponge	Sunset Cliffs, San Diego	SRR14127462	JAGJEF000000000
MMG013	*Pseudoalteromonas citrea* S2233, GCA_005887445.1	78.6	5.84	153,003	40.8	1,538,911	145	68	Green	17	0	8E-135	2E-59	Yellow sponge	Sunset Cliffs, San Diego	SRR14127461	JAGJEE000000000
MMG019	*Pseudoalteromonas luteoviolacea* IPB1, GCF_001696455.1	98.9	5.94	309,281	42.7	3,759,179	75	170	Purple	17	0	0	3E-96	Coral	Water Factory, Curacao	SRR14127460	JAGJED000000000

[a] ANI values are calculated with respect to the closest strain. The MAC protein sequences MacB (WP_039609830.1), MacS (WP_039609824.1), and MacT (WP_039609826.1) were searched against the genomes using tBLASTn (20).
[b] NS, not significant.

metabolite biosynthesis gene clusters (Table 1). Strains MMG009 and MMG019 possess the brominated marine pyrroles/phenols (*bmp*) gene cluster (16, 17), which can produce a compound capable of stimulating the metamorphosis of coral larvae (18). Of the 10 genomes, 7 were found to possess *macB*, *macS*, and *macT* genes that compose phage tail-like contractile injection systems (Table 1), which promote tubeworm metamorphosis and other host-microbe interactions (19). These genome sequences provide a valuable resource for studying the ecology of *Pseudoalteromonas* bacteria and advancing natural product biotechnology.

Data availability. The genome sequencing and assembly projects have been deposited in DDBJ/EMBL/GenBank under BioProject number PRJNA716944. See Table 1 for the SRA and GenBank accession numbers.

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