





# Draft Genome Sequence of *Nereida* sp. Strain MMG025, Isolated from Giant Kelp

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**ABSTRACT** Here, we report the draft genome sequence of *Nereida* sp. strain MMG025, isolated from the surface of giant kelp and assembled and analyzed by undergraduate students participating in a marine microbial genomics course. A genomic comparison suggests that MMG025 is a novel species, providing a resource for future microbiology and biotechnology investigations.

To engage undergraduates in discovery-based research, novel marine bacteria were isolated and cultured and their genomes sequenced, assembled, annotated, and analyzed by students in a marine microbial genomics (MMG) course at San Diego State University. Strain MMG025 was isolated from the surface of a giant kelp, *Macrocystis pyrifera*, from the La Jolla Tide Pools, CA, USA (32.8411°N, 117.2817°W), using a sterile cotton swab. A single colony was obtained on marine agar 2216 (BD Difco, Franklin Lakes, NJ, USA) and incubated at 28°C for 72 h. The colonies were transferred to marine broth 2216 and incubated for 72 h at 25°C before storage, DNA isolation, and imaging by scanning electron microscopy (SEM) (Fig. 1).

Genomic DNA was extracted using a Quick-DNA fungal/bacterial miniprep kit (Zymo Research, Irvine, CA, USA). Using 16S rRNA gene amplification with the primers 27F-1492R (1) and Sanger sequencing (Eton Biosciences, San Diego, CA, USA), the closest strain was identified as *Nereida ignava* CECT 5292 (identity, 97.99%; E value, 0.0). 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 platform; Illumina), producing 2 × 150-bp paired-end reads. The reads were trimmed using Trim Galore v0.6.5 (2), assembled using Unicycler v0.4.8 (3) integrated in PATRIC v3.6.12 (4), and annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.1 (5) with default parameters. MMG025 has a 3.1-Mb genome, a total GC content of 56% with 40 contigs at 242.493× coverage, and an  $N_{50}$  value of 628,545 bp, with 3,260 predicted coding sequences. Default parameters were used except where otherwise noted.

A phylogenetic analysis revealed that strain MMG025 falls into the genus *Nereida* (Fig. 1), which is part of the *Roseobacter* group, in the family *Rhodobacteraceae* and class *Alphaproteobacteria* (6–9). Comparing strain MMG025 with *Nereida ignava* CECT 5292 yields an average nucleotide identity (ANI) value of 72.47% (4, 10, 11), a distance that is below the 95% threshold that delineates species (12), suggesting that MMG025 is a new species. We designate the current isolate *Nereida* sp. strain MMG025.

Species within and related to the *Nereida* genus have been found in association with diverse marine eukaryotes. *Nereida ignava* CECT 5292 is related to an uncultured gall symbiont from red algae (7). Related species from the genus *Octadecabacter* were isolated from an ascidian or compose 70 to 80% of the microbiome of a brittle star (13, 14). *Roseobacter*

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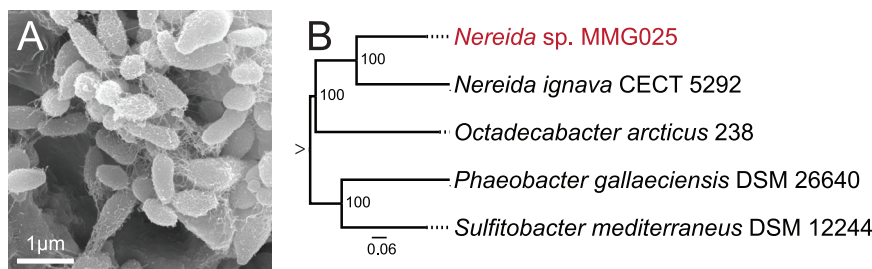
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The authors declare a conflict of interest.

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**FIG 1** (A) Scanning electron micrograph of *Nereida* sp. MMG025. Bacteria were fixed onto coverslips with 2.5% glutaraldehyde, 4% paraformaldehyde, 0.15% Alcian blue, 0.0075% lysine, and 0.1 M cacodylate buffer. The coverslips were dehydrated and critical point dried prior to coating with 6 nm platinum. Images were obtained on an FEI Quanta 450 variable pressure SEM. (B) Maximum likelihood phylogeny constructed using the codon tree method through PATRIC with 100 single-copy genes and proteins identified using cross-genus families (PGfams) (10, 21–27). The phylogeny root is indicated by an arrow for clarity. The GenBank accession numbers of the sequences used in this analysis are as follows: [CVPC000000000](https://www.ncbi.nlm.nih.gov/nuccore/CVPC000000000) (*Nereida ignava* CECT 5292), [CP003744](https://www.ncbi.nlm.nih.gov/nuccore/CP003744) (*Octadecabacter arcticus* 238), [CP006967](https://www.ncbi.nlm.nih.gov/nuccore/CP006967) (*Phaeobacter gallaeciensis* DSM 26640), and [QBKU000000000](https://www.ncbi.nlm.nih.gov/nuccore/QBKU000000000) (*Sulfitobacter mediterraneus* DSM 12244).

species are associated with algae and reef-building corals, where they are thought to play important roles in global sulfur cycling, in part through the degradation of dimethylsulfoniopropionate (DMSP) (15). We found that strain MMG025 harbors a homolog of the DMSP demethylase gene *dmdA* (identity, 80%; query coverage, 100%; E value, 0) (16). Because of their natural occurrence with plants and animals and antagonistic properties against pathogenic bacteria, *Roseobacter* species are promising candidates for use as probiotics in aquaculture or for environmental restoration (17–20). The isolation and genome sequence of *Nereida* sp. MMG025 provides a valuable resource for studying the ecology of *Roseobacter* bacteria and serves as an asset for biotechnology applications.

**Data availability.** The genome sequencing and assembly project for strain MMG025 has been deposited at DDBJ/EMBL/GenBank under BioProject accession number [PRJNA716944](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA716944), the raw sequencing data under SRA accession number [SRR17607627](https://www.ncbi.nlm.nih.gov/sra/SRR17607627), and the whole-genome sequence under GenBank accession number [JAKFZN000000000](https://www.ncbi.nlm.nih.gov/nuccore/JAKFZN000000000).

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