



# High-Quality Draft Single-Cell Genome Sequence of the NS5 Marine Group from the Coastal Red Sea

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**ABSTRACT** The uncultured NS5 marine group represents one of the most ubiquitous flavobacterial bacterioplankton associated with marine blooms in the pelagic ocean. Here, we present a single-cell genome sampled from coastal waters in the Red Sea that represents the first high-quality draft genome sequence within the NS5 lineage.

The uncultured NS5 marine group (also known as ARC11) represents one of the most ubiquitous flavobacterial bacterioplankton in the pelagic ocean (1–3). Their biomass can reach  $6 \times 10^3$  cells per ml (4), and their abundance is strongly correlated with marine phytoplankton blooms (4–6). Therefore, members of this group are currently considered indicator species for coastal bacterioplankton communities (3). However, to date no member of NS5 has been cultivated or sequenced.

Although the biogeography of this group has been extensively captured in environmental 16S rRNA gene surveys (3–7), information regarding the potential metabolism and ecology of NS5 members in the pelagic ocean currently remains fragmentary. However, environmental fosmids carrying 16S rRNA gene sequences affiliated with NS5 suggest capabilities for degrading high-molecular-weight organic matter such as proteins and polysaccharides (2, 8). Here, we report on a nearly complete single-cell genome (*Bacteroidetes* bacterium SCGC AAA795-G10) of an NS5 member from the coastal waters of the central Red Sea.

Surface seawater samples were collected from Red Sea coastal waters near King Abdullah University of Science and Technology (KAUST) Harbor (22°18'23.20''N, 39°6'10.71''E) in February 2012, where the temperature was 25°C and salinity was 39‰. Single cells were sorted and amplified using the REPLI-g kit (Qiagen) at the Single Cell Genomics Center in the Bigelow Laboratory for Ocean Sciences as described in Ngugi et al. (9).

A paired-end sequence library (101 bp  $\times$  2) of the single-cell amplified genome (SAG) was prepared using the TruSeq DNA library kit and sequenced using an Illumina HiSeq sequencer at the Bioscience Core Laboratory at KAUST. Sixty-five million reads were quality trimmed using Trimmomatic v0.32 (10) and assembled into contigs with SPAdes v3.9.0 (11), applying the error correction and single-cell modes. Genome completeness was estimated using CheckM (12). Carbohydrate active enzymes were predicted using the dbCAN server (13).

The SAG comprises 106 contigs totaling 1.93 Mbp ( $N_{50}$  value of 1.06 Mbp; 1,900 $\times$  coverage) with a DNA G+C content of 31.8%. Based on operational standards for SAGs (14), this SAG is of high quality, with 92.1% completeness and 0.5% contamination. It contains 1,746 protein-coding genes and 33 RNA-coding genes, including 1 rRNA operon, as annotated with PGAAP (15) and the RAST server (16). The 16S rRNA gene sequence shows 99% identity to environmental genomic DNA fosmid sequences from the North Atlantic Ocean (2, 8) and the Peruvian coastal margin (GenBank accession number EU795293) and only 95% identity to Arctic fosmids (EU795086 and EU795252). The SAG encodes 37 predicted glycoside hydrolases (GH); among these are

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endo- $\beta$ -glucanases (GH16 and GH74),  $\alpha$ -fucosidases (GH29 and GH95),  $\alpha$ -amylases (GH13), glucosidases (GH3 and GH63), and mannan endo- $\alpha$ -1,2-mannosidase (GH99), indicating the capacity to degrade marine polysaccharides. However, no putative proteorhodopsin-encoding genes were detected, as is the case in some flavobacteria (17). This genome provides a suitable genetic resource for study of the transcriptional landscape of microbial biopolymer degradation in the pelagic sea.

**Accession number(s).** This whole-genome shotgun project has been deposited in GenBank under accession number [QFDA0000000](https://doi.org/10.1093/femsec/fv099). The version described here is QFDA01000000.

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