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Draft genome sequence of *Maricaulis maris* DSM 4734 isolated from filtered polluted sea water

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Running title

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Abstract

Here, we report the genome of *Maricaulis maris* DSM 4734 isolated from filtered polluted seawater. The whole genome was 3568848 bp long, with a GC content of 63.14%, and resistance to 12 antibiotics.

Announcement

Maricaulis maris is a rod-shaped, gram-negative, oligotrophic bacterium found in seawater and marine environments. The genome was studied to understand how bacteria change morphologically due to environmental stimuli. This process is known as differentiation, and *M. maris* was chosen due to the high predictability of differentiation processes in *M. maris* (1). *M. maris* is the type strain and was isolated from filtered polluted seawater collected from various locations across the Pacific Ocean, including Washington state and the California coast. After the seawater was incubated for two months, a surface film formed. Bacteria were collected from this surface film and were cultured at 30℃ on a medium of peptone, yeast extract, and agar. *M. maris* is a prosthecate bacterium, meaning it has appendages called prosthecae or stalks that are an extension of the cell membrane and act as a holdfast, aiding in adhesion (1). 16s rRNA gene sequencing was used to classify the isolate as *M. maris* (NCBI Accession Number: GCA_003634045) (2).

All genomes were sequenced at the DOE Joint Genome Institute (JGI) using Illumina

technology. An Illumina standard shotgun library was constructed and sequenced using the Illumina HiSeq–2000 1TB platform, which generated 5,660,802 reads with a read type of 2x151 bp. The Raw Illumina sequence was filtered for quality using BBTools per SOP 1061. 200 base pairs were trimmed from the sequence at all contig ends, and the contigs were discarded if the length was less than 1 kbp or the read coverage was less than 2. There was a total number of 5,712,362 raw sequence reads resulting in 862,566,662 bp. After trimming, the final draft assembly contained 3,568,848 bp. The software used for the genome assembly includes BBTools, which was used to remove known process artifacts and contaminants and left 10,000,000 subsample reads. SPAdes (spades/3.10.1) was used to read the subsamples. Prodigal was then used to predict coding sequences on each scaffold, and the output protein sequences were aligned to NCIB using LAST. The annotation was standard according to the JGI Microbial Genome Annotation Pipeline (2). The genome was complete with a contamination value of 0.19 (3).

Feature	Finding
Length (bp)	3568848
Status	Complete
No. of Scaffolds	12
Scaffold N50	2236752
Average fold coverage (x)	241.69
GC content (%)	63.14%
No. of genes	3413
No. of protein-coding genes	3360
No. of rRNAs	5
No. of tRNAs	43

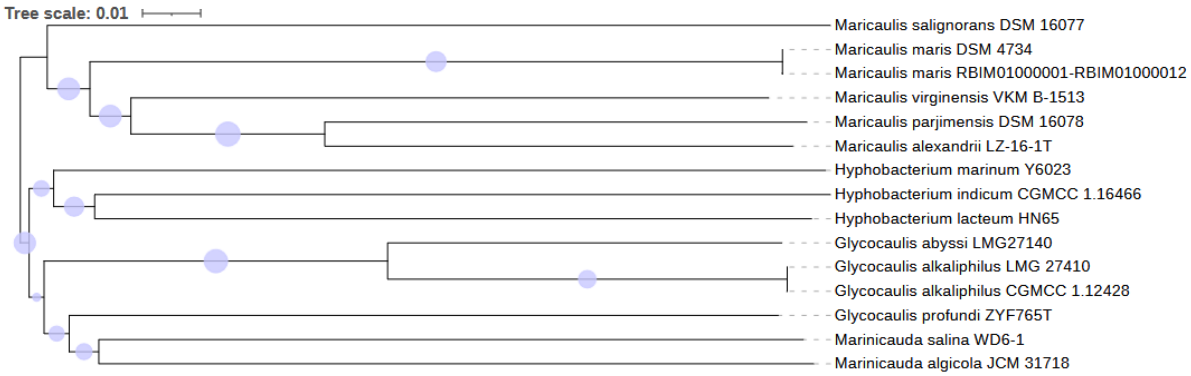

Figure 2. Tree inferred with FastME 2.1.6.1 [7] from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of the GBDP distance formula d5. The numbers above the branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 77.4 %. The tree was rooted at the midpoint [8].

To determine whether or not *Maricaulis maris* has antibiotic resistance, the Comprehensive Antibiotic Resistance Database (CARD) version 4.0.0 was used (4). It was determined that our isolate is resistant to numerous amount of Antibiotics, including macrolide, aminoglycoside, aminocoumarin, tetracycline, glycylcycline, fluoroquinolone, penicillin β-lactam, peptide, carbapenem, diaminopyrimidine, phenicol, and nitroimidazole. Finally, we identified a secondary metabolite production using antiSMASH version 7.0 and found that *M. maris* could produce an antibiotic (5). There is a presence of a well-structured terpene biosynthetic gene cluster between 85,917-106,734bp.

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