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GENOME ANNOUNCEMENT

Genome Sequence of the Marine Bacterium *Marinobacter hydrocarbonoclasticus* SP17, Which Forms Biofilms on Hydrophobic Organic Compounds

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***Marinobacter hydrocarbonoclasticus* SP17 forms biofilms specifically at the interface between water and hydrophobic organic compounds (HOCs) that are used as carbon and energy sources. Biofilm formation at the HOC-water interface has been recognized as a strategy to overcome the low availability of these nearly water-insoluble substrates. Here, we present the genome sequence of SP17, which could provide further insights into the mechanisms of enhancement of HOCs assimilation through biofilm formation.**

Hydrophobic organic compounds (HOCs) encompassing lipids, hydrocarbons, and some organic pollutants are widely distributed in the environment but are weakly soluble in water and as a consequence poorly available for assimilation by heterotrophic bacteria. Biofilm formation at the HOC-water interface is a strategy employed by *Marinobacter hydrocarbonoclasticus* SP17 (ATCC 49840) to overcome the low bioavailability of HOCs. SP17 was isolated from chronically oil-contaminated sediment for its ability to use alkanes as the sole carbon and energy source (5). *M. hydrocarbonoclasticus* is a Gram-negative, aerobic, motile, nonspore-forming, and rod-shaped bacterium (5). It exhibits extreme halotolerance (0.08 to 3.5 M NaCl) and synthesizes ectoine as an osmoprotectant (2, 3).

SP17 adheres and forms biofilms on alkanes and produces an extracellular-surface-active compound (2, 6). Physiological and proteomic studies revealed that biofilm formation is an efficient strategy to colonize hydrophobic interfaces (1, 11, 12). SP17 forms biofilms at the interface between aqueous-phase and HOC substrates like *n*-alkanes, fatty alcohols, or apolar lipids, such as wax esters and triacylglycerols. In contrast, biofilms were not observed on the nonmetabolizable compounds (n-C_{32} alkanes, pristane, and heptamethylnonane) and glass or plastics (7). The discrimination between metabolizable and nonmetabolizable compounds indicates that at some level, biofilm formation is controlled by the presence of a nutritive interface. Adhesion and biofilm formation could be a behavioral strategy to acquire carbon and energy from HOCs contained in marine aggregates.

The sequencing of the *M. hydrocarbonoclasticus* SP17 genome was obtained using a conventional whole-genome shotgun strategy with three libraries (3-, 10-, and 25-kb fragments) on ABI3730 sequencers. Assembly was done using the Phred/Phrap/Consed software package (www.phrap.org) with primer walking, PCR, and *in vitro* transposition technology (Template generation system II kit; Finnzyme, Espoo, Finland) as finishing steps, yielding a single contig molecule without gaps. Automatic genome annotation was performed using the MAGE annotation server (9, 10) followed by manual annotation. The genome of SP17 encompasses a unique chromosome with a similar G+C content (57.43%) to but a smaller size (3989,480 bases) than that of the other *Marinobacter* genomes (ranging between 4,333 and 4,894 kb) (4, 8, 13). The SP17 genome contains 3 rRNA operons, 50 tRNA genes, and 3807 protein-coding sequences (CDSs) (967.89-bp average length, 91.74% coding density). It carries multiple genes known to be involved in biofilm formation, including four pilus gene clusters and three clusters of polysaccharide biosynthesis genes, as well as the *lap* genes. The SP17 genome encodes 58 proteins containing GGDEF, EAL, or HD-GYP domains, which are involved in the metabolism of the intercellular signaling molecule, c-di-GMP, whose concentration regulates the transition between sessile and biofilm lifestyles.

Further in-depth analysis of this genome and comparison with the genomes of *Marinobacter aquaeolei*, the heterotypic synonym of SP17, and other *Marinobacter* species could provide valuable information on the molecular mechanisms of biofilm formation on HOCs and more generally on strategies of colonization of nutritive surfaces in marine environments.

Nucleotide sequence accession number. The complete genome sequence of *M. hydrocarbonoclasticus* strain SP17 has been deposited in GenBank under accession no. FO203363.

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