

GENOME ANNOUNCEMENTS

Genome Sequences of *Pelagibaca bermudensis* HTCC2601^T and *Maritimibacter alkaliphilus* HTCC2654^T, the Type Strains of Two Marine *Roseobacter* Genera[∇]

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***Pelagibaca bermudensis* HTCC2601^T and *Maritimibacter alkaliphilus* HTCC2654^T represent two marine genera in the globally significant *Roseobacter* clade of the *Alphaproteobacteria*. Here, we present the genome sequences of these organisms, isolated from the Sargasso Sea using dilution-to-extinction culturing, which offer insight into the genetic basis for the metabolic and ecological diversity of this important group.**

Organisms from the *Roseobacter* clade of the *Alphaproteobacteria* are numerically significant in the world's oceans and have been found in a wide range of habitats (1, 3). Using previously described high-throughput dilution-to-extinction culturing (6, 13), the marine *Roseobacter* strains *Pelagibaca bermudensis* HTCC2601^T and *Maritimibacter alkaliphilus* HTCC2654^T were isolated in low-nutrient heterotrophic medium (LNHM) (4) from surface water collected at the Bermuda Atlantic Time-Series Study (BATS) site in the western Sargasso Sea (5, 9). As the type strains for two genera of this globally prolific *Roseobacter* group, *P. bermudensis* and *M. alkaliphilus* were selected for shotgun genome sequencing at the J. Craig Venter Institute through the Moore Foundation Microbial Genome Sequencing Project (<http://www.moore.org/microgenome>). Draft genomes of *P. bermudensis* and *M. alkaliphilus*, with 103 and 46 contigs, respectively, were annotated and analyzed through the Joint Genome Institute IMG/M website (<http://img.jgi.doe.gov/cgi-bin/pub/main.cgi>) (10).

The draft genomes of *P. bermudensis* and *M. alkaliphilus* comprise 5,425,920 and 4,529,231 bases, 5,522 and 4,764 predicted open reading frames (ORFs), and 66.44% and 64.13% G+C content, respectively. The *P. bermudensis* genome is predicted to contain 56 tRNA genes, five 5S rRNA genes, four 16S rRNA genes, and five 23S rRNA genes, and that of *M. alkaliphilus* 49 tRNA genes and one each of the 5S, 16S, and 23S rRNA genes. Both genomes have putative genes for complete glycolysis and Entner-Doudoroff pathways, a complete tricarboxylic acid cycle, and predicted metabolic pathways for the

oxidation of C₁ compounds. Both have predicted genes for the synthesis of most essential amino acids and some vitamins and cofactors. Each has putative genes for the utilization of fructose, sucrose, and mannose, confirmed in physiological testing of *P. bermudensis* (5) but not for *M. alkaliphilus* (9). *P. bermudensis* contains a predicted complete RuBisCO complex, unique to the sequenced *Roseobacter* species (12, 15), a complete assimilatory nitrate reduction pathway, and several type VI secretion genes. *M. alkaliphilus* is predicted to have complete nitrate reduction pathways to both N₂ and ammonia and most type IV secretion genes. Both are predicted to have complete *sec* pathways and large numbers of ABC transporters (362 in *P. bermudensis* and 224 in *M. alkaliphilus*), similar to other *Roseobacter* strains (15).

M. alkaliphilus was named because of its alkaline growth optimum at pH 10. Na⁺/H⁺ antiporters have been shown to be involved in conferring alkaliphilic phenotypes for a variety of organisms by increasing internal cellular H⁺ concentrations in alkaline conditions where Na⁺ is present (2, 7, 8, 14, 16, 17). As expected, the genome of *M. alkaliphilus* contains two putative Na⁺/H⁺ antiporters, one homologous to *nhaP*, important for alkaliphily in several strains (2, 16, 17), and another located adjacent to predicted ABC transporter genes for capsular polysaccharide export.

Nucleotide sequence accession numbers. The draft genome sequences of *Pelagibaca bermudensis* HTCC2601^T and *Maritimibacter alkaliphilus* HTCC2654^T are available in GenBank under the accession numbers AATQ00000000 and AAMT00000000, respectively. Data annotated independently by GenDB (11) are accessible in the Marine Microbial Genomics database at Oregon State University (<http://bioinfo.cgrb.oregonstate.edu/microbes/>).

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