

Genome Sequences of *Oceanicola granulosus* HTCC2516^T and *Oceanicola batsensis* HTCC2597^{TV}

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Genome sequences from the prolific *Roseobacter* clade in the *Alphaproteobacteria* are beginning to reveal the genetic basis for the diverse lifestyles of these organisms. Here we present the genome sequences of *Oceanicola granulosus* HTCC2516^T and *Oceanicola batsensis* HTCC2597^T, two marine *Roseobacter* species isolated from the Sargasso Sea using dilution-to-extinction culturing, whose genomes encode for significant differences in metabolic potential.

Members of the *Roseobacter* clade are ecologically and physiologically diverse, occupying a wide variety of lifestyles (1, 2, 7). *Oceanicola granulosus* HTCC2516^T and *Oceanicola batsensis* HTCC2597^T were isolated by dilution-to-extinction culturing in low-nutrient heterotrophic media (LNHM) (4) from water collected at the Bermuda Atlantic Time-Series Study (BATS) station in the Sargasso Sea (3, 5). The genomes were shotgun sequenced by the J. Craig Venter Institute as part of the Moore Foundation Microbial Genome Sequencing Project (<http://www.moore.org/microgenome>). Draft genomes of *O. granulosus* and *O. batsensis* containing 85 and 23 contigs, respectively, were annotated analyzed through the Joint Genome Institute IMG/M website (<http://img.jgi.doe.gov/cgi-bin/pub/main.cgi>) (6). The draft genomes of *O. granulosus* and *O. batsensis* comprised 4,039,111 and 4,437,668 bases, 3,855 and 4,261 predicted open reading frames (ORFs), and 70.41% and 66.10% G+C contents, respectively. The *O. granulosus* genome is predicted to contain 55 tRNA genes, two 5S rRNA genes, four 16S rRNA genes, and two 23S rRNA genes; that of *O. batsensis* is predicted to contain 45 tRNA genes, one each of the 5S and 16S rRNA genes, and two 23S rRNA genes.

The sequencing of these and other *Roseobacter* genomes has directly affected the *Oceanicola* phylogeny. Recent phylogenetic studies of the *Alphaproteobacteria* and the *Roseobacter* clade specifically have established that the *Oceanicola* genus is not monophyletic (1, 7, 11). Not surprisingly, the two genomes reveal different potential capabilities for these two organisms. *O. granulosus* is predicted to possess several genes necessary for the Calvin cycle, including the large (but not the small) RuBisCo (ribulose-1,5-bisphosphate carboxylase) subunit. Both strains tested negative for fructose utilization (3) but contain putative genes necessary for this metabolism. Consistent with physiological tests showing glucose utilization, *O. granulosus* is predicted to have complete glycolysis, pentose-phosphate, and Entner-Doudoroff (ED) pathways. *O. batsensis*

has only a putative ED pathway, but did not utilize glucose (3). Both strains were characterized as nonmotile (3), and *O. batsensis* has no *che* gene homologs, but *O. granulosus* is predicted to have most flagellar and *che* gene homologs. *O. granulosus* has putative genes for an *aa*₃-type cytochrome *c* oxidase, and *O. batsensis* is predicted to have both *aa*₃- and *cbb*₃-type cytochrome *c* oxidases, the latter potentially conferring an adaptive advantage over a greater range of oxygen concentrations (8, 9).

Both organisms are predicted to have most Sec pathway genes. *O. batsensis* contains several putative type IV secretion genes and 6 putative TonB receptors. Each has many predicted ABC transporter genes: 239 in *O. granulosus* and 193 in *O. batsensis*. Both organisms were observed to form polyhydroxybutyrate (PHB) in culture (3), and both organisms contain putative genes necessary for PHB synthesis (see reference 10 and references therein), including predicted copies of PHB or polyhydroxyalkanoate (PHA) polymerases and several acetyl coenzyme A (acetyl-CoA) acetyltransferases, and *O. batsensis* has a predicted acetoacetyl-CoA reductase.

Nucleotide sequence accession numbers. The draft genome sequences of *Oceanicola granulosus* HTCC2516^T and *Oceanicola batsensis* HTCC2597^T are available in GenBank under accession no. AAOT00000000 and AAMO00000000, respectively. Data annotated independently by GenDB are accessible in the Marine Microbial Genomics database at Oregon State University (<http://bioinfo.cgrb.oregonstate.edu/microbes/>).

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