Abstract

Assembling the marine metagenome, one cell at a time

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Determining the genetic makeup of predominant microbial taxa with specific metabolic capabilities remains one the major challenges in microbial ecology and bioprospecting, due to the limitations of current cell culturing and metagenomic methods. The complexity of microbial communities and intraspecies variations poses obstacles for the assembly of individual genomes from metagenomic shotgun libraries. Here we report the use of single cell genomics to access the genome of two uncultured proteorhodopsin-encoding flavobacteria from Gulf of Maine. High throughput fluorescence-activated sorting of single cells, whole genome amplification via multiple displacement amplification and PCR-screening enabled shotgun sequencing of these single amplified genomes (SAGs) yielding 1.9 Mbp (17 contigs) and 1.5 Mbp (21 contigs) draft genomes for the two flavobacteria. In contrast to cultured strains, the two uncultured flavobacteria genomes were excellent Global Ocean Sampling (GOS) metagenome fragment recruiters, demonstrating their numerical significance in the ocean. Annotation revealed genome streamlining and diversified energy sources of the two uncultured microorganisms, including biopolymer degradation, proteorhodopsin photometabolism, and H_2 oxidation. These features may be indicative for specific adaptations to the marine environment and for the absence of related microorganisms in cultures.

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