



GENOME WATCH

Deep-sea striving

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This month's Genome Watch highlights a recent article that used single-cell genomics to characterize uncultivated archaea present in marine sediments.

The surface of the ocean floor is covered with sedimentary deposits generated by the gradual accumulation of both organic and inorganic matter that settles through the water

column. Deep oceanic sediments are generally characterized by cold, dark, anoxic conditions that, despite appearing hostile from a human point of view, harbour large numbers of microbial cells derived from all three domains of life. The mechanisms used by microorganisms to survive in such limiting environmental conditions are only partially understood. Detrital proteins are thought to be the most abundant form of organic matter present,

and it was generally thought that bacteria were responsible for the degradation of this carbon source. Now, ground-breaking recent work by Lloyd *et al.*¹ indicates that archaea also have a role in this process.

Archaea were originally thought of as extremophiles, but are now known to inhabit a diverse array of environmental niches, including mammalian intestines². To uncover the role of

archaea on the ocean floor, Lloyd *et al.*¹ sampled marine sediment near the Danish coast. Profiling using 16S rRNA gene sequencing and quantitative PCR revealed that uncultured archaea belonging to the miscellaneous crenarchaeotal group (MCG) and marine benthic group D (MBG-D) were abundant. As neither of these groups is currently amenable to culture, individual microbial cells were instead recovered from sediment samples using fluorescence-activated cell sorting (FACS), and genomic DNA from these sorted cells was amplified using multiple displacement amplification (MDA). Amplified genomes were then taxonomically screened by sequencing the 16S rRNA genes. This revealed that the authors had recovered one MCG cell and three individual MBG-D cells, which they then submitted for whole-genome sequencing using a combination of 454, Illumina and Ion Torrent technologies.

One of the limitations of MDA is that it introduces amplification bias, and this was reflected in the results. Genome assemblies ranged from 0.59 to 1.04 Mb in size, and on the basis of the presence or absence of known universally conserved archaeal genes, the authors estimated that their genome coverage ranged from 31.8% to 70.3%. Nonetheless, this level of coverage was still sufficient to give novel insights into both the phylogenetic placement and functional capabilities of the previously uncharacterized archaeal groups. Both groups were found to be only distantly related to previously characterized archaea, and the genomes suggest that the MBG-D cells form part of a new order within the phylum Euryarchaeota, whereas the MCG cell belongs to a completely distinct archaeal phylum.

Analysis of protein-coding sequences revealed that these archaea might generate energy for growth through protein degradation. The archaeal cells were shown to encode

extracellular peptidases such as clostripain, gingipain, papain and pyroglutamyl peptidase. The authors measured the activity of gingipain and clostripain in sediment samples, and both seemed to be highly active. In addition to these extracellular peptidases, all four cells seem to encode mechanisms for transporting the resulting peptides into the cell and for subsequent intracellular breakdown of amino acids. The MCG cell also appears to have the genetic machinery for the degradation of D-amino acids, which are typically found in bacterial cell walls. This suggests that the archaeon can survive by feeding on cell wall amino acids released by dead and decaying bacteria, representing an efficient way of recycling organic material within an environment where energy sources are limited.

Homologues of the extracellular peptidase-encoding genes were also identified in metagenomic data sets from marine sediments collected in California and Alaska, USA. The presence of these homologues suggests that archaeal degradation of marine sediment proteins is a geographically widespread phenomenon. Thus, this work offers new insights into the functions of sediment-dwelling archaea and, as the sea bed is the most abundant source of organic carbon on Earth, highlights the important role that these archaea might have in the global carbon cycle.

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2. DeLong, E. F. Everything in moderation: archaea as 'non-extremophiles'. *Curr. Opin. Genet. Dev.* **8**, 649–654 (1998).

Competing interests statement

The author declares no competing financial interests.

