GENOME WATCH

Ocean's elevenses

Helena Seth-Smith

The recent publication of the genome sequences of two marine γ -proteobacteria from the order *Oceanospirillales* might lead to the development of new methods to detoxify oceanic contamination.

Oil pollution and algal blooms are two of the main environmental threats to the marine biosphere. An overgrowth of dinoflagellate species produces algal blooms, which deplete local oxygen levels and cause harm to many marine species. Up to three million tonnes of oil, originating from natural sources, the oil industry and tanker accidents, pollute the sea annually. Oil pollution has deleterious effects on the marine ecosystem, both short- and long-term, as polyaromatic hydrocarbons persist in the environment as toxins and carcinogens, and become incorporated into the food chain.

Hahella chejuensis is a bacterium that produces a red pigment that kills a red-tide algal species. At 7.2 Mb, the genome is the largest marine prokaryotic genome sequenced so far, and comprises 6,783 coding sequences (CDSs), with an average GC content of 54.8% (REF. 1). *Alcanivorax borkumensis* is prevalent in oil-polluted waters and uses oil hydrocarbons as carbon and energy sources. The genome of this bacterium, first reported in 2003 (REF. 2), is just 3.1 Mb and comprises 2,755 CDSs, with an average GC content of 54.7% (REF. 3).

Despite the difference in genome size these bacteria share several common features. Both species require salt for growth and encode several Na^+/H^+ antiporters, including a multi-subunit pump used to maintain the sodium motive force. This is used to power nutrient transport in both species, and flagellar rotation in *H. chejuensis*. Both genomes also encode uptake systems to scavenge nutrients from the environment. Extracellular polysaccharide (EPS) gene clusters are present in both species, with *H. chejuensis* harbouring five such gene clusters.

The difference in genome size reflects both the number of regulatory proteins in the two species (considerably more in *H. chejuensis*), and the propensity of each bacterium for the acquisition of foreign DNA. Up to 23% of the *H. chejuensis* genome might have been horizontally acquired, whereas *A. borkumensis* contains little mobile DNA.

Whereas *H. chejuensis* has complete pathways for central carbon metabolism, *A. borkumensis* lacks components of several pathways and cannot derive energy from most sugars. Instead, it feasts on the alkanes found in oil. The CDSs encoding the alkane hydroxylases AlkB_1 and AlkB_2 are found near the origin of replication, giving a higher gene dosage. In addition, P450s, rubredoxin and other oxidoreductases are implicated in

the degradation of many hydrocarbons. To enhance the bioavailability of oil and speed up alkane degradation, *A. borkumensis* produces a surfactant and the CDSs potentially involved in the synthesis of this surfactant were identified³.

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The mechanism by which *H. chejuensis* kills *Cochlodinium polykrikoides*, an important red-tide alga, was elucidated¹. A gene cluster was identified that codes for the synthesis of prodigiosin, a red pigment that rapidly lyses the alga. Extracellular hydrolytic enzymes might digest the nutrients released by lysis for uptake by *H. chejuensis*.

The information deduced from these genomes should lay the foundations for tackling the dual blights of algal blooms and oil pollution.

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doi:10.1038/nrmicro1589

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DATABASES

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Alcanivorax borkumensis | *Hahella chejuensis*
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