



GENOME WATCH

'Slick' operation

Helena Seth-Smith

Recent studies on marine microorganisms and their ability to degrade oil components make for particularly poignant reading in the wake of the Deepwater Horizon rig disaster. Several groups have looked at oil-degrading bacterial communities derived from marine samples, identifying and isolating key strains, analysing transcription and investigating specific degradative enzymes.

Crude oil is made up of hydrocarbons, which can be a useful food source in marine environments. Low-level contamination of marine environments with oil occurs through natural pollution and marine traffic. Thus, some bacteria have evolved the ability to degrade these compounds. For example, the marine species *Alcanivorax borkumensis* degrades alkanes, and the genome of *A. borkumensis* str. SK2 contains several genes encoding proteins that are implicated in alkane degradation: three members of the cytochrome P450 CYP153A family and two non-haem-iron monooxygenases (AlkB)¹. Moreover, *A. borkumensis* produces biosurfactants, which emulsify oil to improve access of the degradative enzymes to their substrates. Despite this, large oil spills push natural systems far beyond their normal limits.

One approach to studying oil degradation by marine microbial consortia is to culture the bacteria with oil as the sole carbon source. Kato *et al.*² observed oil emulsification and alkane removal after 7 days of culture, with the dominant strains (14 out of 30 clones) being *Alcanivorax* spp.; *Maricaulis* spp. and *Marinobacter* spp. were also identified. Sequencing of mRNA showed that *A. borkumensis* is actively transcribing under these conditions and that the consortium produces proteins involved in cell wall and membrane biogenesis, and inorganic ion and lipid transport and metabolism, as well as proteins with roles in lipid biosynthesis, which are likely to be involved in the emulsification process.

Vila *et al.*³ sought to identify the species responsible for the degradation of different oil components using bacteria derived from the sand from the Spanish coastline affected by the Prestige fuel spill in 2002. Many crude oil components were degraded completely in 60 days, and others were notably depleted. Again, the most frequently detected bacterial species was *A. borkumensis*, with *Maricaulis* spp. and *Roseovarius* spp. also present. Specifically, *A. borkumensis* was dominant in the first week of culture with crude oil, which coincides with the degradation of aliphatic compounds; alphaproteobacteria and *Maricaulis* spp. increased in abundance later, during the polyaromatic hydrocarbon (PAH) and alkyl degradation stage. These findings were confirmed by culturing bacteria with different oil components: *A. borkumensis* was most abundant in the aliphatic compound culture, whereas other species dominated the aromatic experiment. Single PAH cultures indicated that alphaproteobacteria degrade anthracene, *Marinobacter* spp. degrade phenanthrene, fluoranthrene, benzo(a)anthracene and chrysene, and other strains break down pyrene. The isolation of the culturable bacterial species from these experiments will allow further investigation into specific catabolic genes.

Wang *et al.*⁴ investigated the presence of genes encoding candidate degradative enzymes from the CYP153A and AlkB families in bacteria isolated from 18 Atlantic samples that had been enriched with oil-degrading microorganisms. Of the 177 bacterial strains isolated (which belonged to 43 genera), 80 had gene fragments from 1 or both of these gene families. Almost half these isolates were found to be from the genus *Alcanivorax*, reinforcing it as a key oil-degrading marine bacterial genus; other prominent oil degraders included strains of *Gordonia*, *Marinobacter*, *Parvibaculum* and *Salinisphaera* species. This study identified

82 unique CYP153A family sequences and 52 unique *alkB* sequences. Thirty strains contained both a CYP153A-encoding gene and *alkB*, and some strains encoded several versions of the enzymes; for example, one strain of *Parvibaculum* has six CYP153A-encoding genes. Phylogenetic analyses of the diverse gene fragments indicate that the phylogeny of CYP153A-encoding genes correlates better than that of *alkB* with the host ribosomal RNA gene phylogeny, suggesting that *alkB* genes may be more mobile. Some of the isolated oil degraders contained neither CYP153A nor AlkB, perhaps indicating that there are other pathways for alkane degradation.

Natural degradation of oil in a marine environment is a slow process and is unlikely to have a large effect on the Deepwater Horizon rig spill, but it is reassuring to know that there are natural processes at work that may, over time, have some role in mitigating the disaster.

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Competing interests statement

The author declares no competing financial interests.

DATABASES

Entrez Genome Project: <http://www.ncbi.nlm.nih.gov/genome/prj>
Alcanivorax borkumensis

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