

GENOME WATCH

Vying over spilt oil

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This month's Genome Watch explores the diverse microbial community involved in the bioremediation of oil spills.

The Deepwater Horizon (DWH) oil rig explosion in the Gulf of Mexico in April 2010 led to the accidental release of at least 4 million barrels of crude oil. The resulting deep-sea hydrocarbon plume was one of the largest spills in recorded history and it caused drastic changes in the microbial communities, some of which contributed to the bioremediation of the spill. Within this noxious habitat, a group of indigenous microorganisms that mostly belonged to the class Gammaproteobacteria thrived. Culture-independent analyses of these bacteria identified many lineages such as the Oceanospirillales, including *Oleispira* spp., which can metabolize hydrocarbons at extremely low temperatures. Other enriched genera included the alkane degrader *Alcanivorax* spp., as well as *Cycloclasticus* spp. and *Pseudoalteromonas* spp., which can break down aromatic hydrocarbons¹.

The characteristics of the DWH microbial response varied substantially over time. Samples taken over the course of the oil spill indicated that a succession of hydrocarbon degraders were responsible for the rapid DWH bioremediation¹. Whereas Oceanospirillales were predominant 1 month after the explosion, plume samples that were taken in June were enriched in *Colwellia* spp. and *Cycloclasticus* spp., and methylotrophs were most abundant in later samples. This succession of hydrocarbon-degrading bacteria corresponded to a relative decline in saturated hydrocarbons and an increase in the more persistent aromatic hydrocarbons over time¹.

Using metagenomic and metatranscriptomic analyses, Mason *et al.*² further showed that an enrichment of genes encoding proteins involved in aliphatic hydrocarbon

degradation accompanied the early rise of Oceanospirillales. By contrast, genes encoding proteins that have a role in the breakdown of benzene, toluene and polycyclic hydrocarbons were downregulated. As Oceanospirillales are particularly recalcitrant to laboratory cultivation, the authors used single-cell sequencing to determine draft genomes from two representative isolates. These genomes were highly enriched for factors that are involved in alkane degradation, chemotaxis and motility, which suggests that Oceanospirillales can quickly aggregate and scavenge hydrocarbon nutrients.

The two Oceanospirillales species that were analysed are closely related to *Oleispira antarctica*, which is the only cultured species among this bacterial family. Kube *et al.*³ recently sequenced the complete 4.4 Mb genome of *O. antarctica* and uncovered multiple genes encoding proteins that are linked to alkane oxidation, motility and siderophore production. Consistent with the ability of *O. antarctica* to adapt to an extreme-cold habitat, the genome also harbours two genetic systems that are responsible for the synthesis of osmoprotectants. In addition, 12.2% of the *O. antarctica* genome consists of mobile genomic islands, which is a much higher value than that reported in other oil degraders. The authors therefore proposed that *O. antarctica* may participate in horizontal gene transfer more often by functioning as a donor of mobile vectors in other bacteria. Interestingly, only a small fraction of the intracellular enzymes that were cloned from *O. antarctica* had a true psychrophilic profile, as most showed maximal activity at 20–35°C. Nevertheless, the suboptimal activity of these

enzymes at deep-sea temperatures might actually be sufficient to outcompete other microbial community members, making *O. antarctica* a highly successful oil degrader.

In another recent report, Chauhan *et al.*⁴ sequenced the genomes of five bacteria that were isolated from the tissues and mantle fluid of oysters residing in contaminated DWH reefs. The draft genomes of the isolated bacteria harboured several factors involved in aliphatic and aromatic hydrocarbon degradation, which indicates that even bacteria that colonize the surrounding reef ecosystems may possess the capacity to metabolize crude oil.

Each year, millions of gallons of oil are released into natural environments worldwide. By applying genomic approaches to understand the enzymatic processes and community dynamics of oil-degrading bacteria, valuable insights that inform ongoing bioremediation efforts can be gained.

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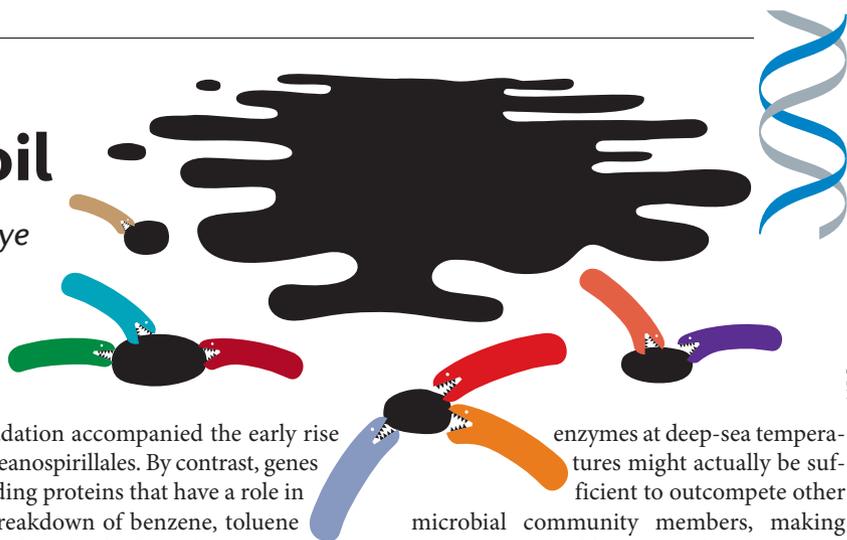
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Competing interests statement

The authors declare no competing interests.



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