Microbes degrade oil from Deepwater Horizon spill

Marine microorganisms responded to the Deepwater Horizon oil spill by boosting the abundance of species capable of breaking down crude oil, according to new research. This method of ‘bioremediation’ could help manage crises in deep sea environments, where other clean-up methods are ineffective.

Nearly 5 million barrels of crude oil were spilled into the Gulf of Mexico following the Deepwater Horizon explosion in April 2010. Initially, most of the oil was found to be trapped in a deep sea plume at around 1000-1200m, but oil is now barely detectable at this depth. Scientists have therefore been uncertain as to the ultimate fate of the oil in the marine ecosystem.

In the new study, researchers used GeoChip-based metagenomic technologies (which comprises an array of gene probes that can be used to detect a large number of functional genes at one time) to test the hypothesis that the microbial communities living in the sea played an important part in degrading the oil and thus reducing the long-term effects on marine life. The scientists took eight seawater samples from within the plume and five samples from outside the plume, all between 1099-1219m deep. For each sample, they analysed the genes present in the microbial population using GeoChip and compared the results to the presence of benzene, toluene and other hydrocarbons found in crude oil.

The results revealed a dramatically different microbial community composition - the abundance of each species - in the plume samples compared to non-plume samples from the same depth. The difference was more closely linked to the concentration of different hydrocarbons than to temperature or to phosphate or iron, which microbes need to grow.

When the scientists looked at the DNA of the microbial species present, they found that genes responsible for breaking down potentially toxic constituents of oil, such as toluene and Poly Aromatic Hydrocarbons (PAH), were enriched in the plume samples compared to the non-plume samples. For example, they found 19-26 alk b genes - which oxidise alkanes - in the oil-contaminated samples compared to 11-15 in the non oil-contaminated samples. Genes responsible for the release of phosphate in seawater were higher in plume samples compared to non-plume samples, indicating enhanced microbial activity. Genes involved in generating methane, chemically reducing sulphate and assimilating iron from seawater – processes that are associated with microbial breakdown of hydrocarbons – were also up to ten times more abundant in the plume samples.

Some genes, particularly for breaking down PAHs, were found only in the plume samples while some other genes were found only in the non-plume samples. This suggests that the microbial community underwent a dramatic change in response to the oil spill, selecting against some resident species and favouring those that contained genes for hydrocarbon breakdown. This confirms previous research that microbes capable of hydrocarbon breakdown become dominant following an oil spill.

The full impact on the marine ecosystem in the Gulf of Mexico now needs to be further assessed by monitoring changes in the resident microbial community alongside chemical analysis of the seawater and other factors that may influence the ultimate fate of the oil, such as ocean currents.

The natural ‘bioremediation’ capability of resident microbial communities to mitigate the ecological impact of oil spills should help design appropriate emergency response measures to deal with incidents that occur in the deep sea, say the researchers. At such depths, current technology is unable to remove oil and gas directly and chemical dispersants are also ineffective.

Contact: jzhou@ou.edu
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