

Science for Environment Policy

Micro-organism communities disrupted near world's largest ship recycling yard

Pollutants have been shown to alter the structure of bacterial communities in the coastal waters around the Alang-Sosiya shipbreaking yard in north-west India. The research analysed seawater from two sites near Alang-Sosiya and from pristine sea water taken 10 km from the coast. The results provide a clearer idea of changes to the microbial ecology near a large ship recycling yard.

The Alang-Sosiya shipbreaking yard is one of the largest in the world, accounting for nearly half of shipbreaking and recycling activities worldwide. Although ship recycling reduces the pressure on metal resources, such as iron and copper, contaminants that enter the seawater as a result of the recycling process can have a major impact on the marine environment — particularly on the microbial communities that play an important role in the nutrient cycles of local ecosystems.

The study took samples from two sites (one in Alang and one in Sosiya) during three different seasons: winter, summer and monsoon. The researchers assert the control seawater was not directly affected by anthropogenic activity, as it was taken 10 km out from the Alang-Sosiya coast.

These samples were analysed to determine their chemical content, then diluted in series and introduced to a range of high-nutrient and low-nutrient agar preparations to develop microbial communities. One of the preparations, which used BHM (Bushnell-Hass Medium) agar, contained only petroleum hydrocarbons (such as benzene) as the carbon source to determine whether organisms had locally adapted to surviving in a polluted environment.

For the purposes of identification, the DNA of the microorganisms was extracted and a 16S rRNA (ribonucleic acid) analysis was performed. This test is often used to determine if previously known or new microbes are present in a particular environment. The technique is widely used as a biomarker and in microbial ecology studies.

The results show that bacterial communities are altered as a result of human activities and waste products, but also show an amount of seasonal variation in the bacterial counts. The bacteria in the vicinity of the ship recycling yard were shown to be shifting from a *Gammaproteobacteria* (which was dominant in control samples) towards *Betaproteobacteria* and *Epsilonproteobacteria* classes — in general, towards bacteria that are known for their ability to degrade hydrocarbons.

Bacterial counts on the BHM agar, which contained petroleum-derived hydrocarbons, showed a strong difference between samples, with a high abundance of bacteria (ranging between 190 and 40 000 colony-forming units (CFU)/ml) on agar treated with samples from polluted waters and a markedly low abundance (35 CFU/ml) on unpolluted samples. The authors suggest that this could be due to the bacteria's adaptation to high concentrations of polycyclic aromatic hydrocarbons (PAHs) which the bacteria are exposed to as a result of the shipbreaking industry.

It is difficult to tell what proportion of contaminants measured in the study come directly from the shipbreaking industry, as large quantities of industrial and domestic waste flow into the Gulf of Khambat from many different river sources. However, a firm link was observed between anthropogenic pollutants in the coastal waters around Alang-Sosiya and the bacterial community structure. The control sample — 10 km away from the two main sampling sites — which was labelled by the authors as 'pristine seawater', would be affected by this pollution from other sources.

Another potential benefit of this study is that the specific microbial biodiversity discovered on the site may be of use to those looking into the bioremediation of anthropogenic pollutants.



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