Metagenomics of deeply buried marine sediments

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Deeply buried marine sediments make up a vast potential biosphere and contain up to one-third of all microorganisms [1]. Sediments collected on Ocean Drilling Program Leg 201, which visited the Peru Margin in 2002, have been examined by many different methods. Using different molecular and biogeochemical procedures, two vastly different views of the subsurface microbial world have emerged. Based on intact polar lipids, RNA and FISH counts, there is evidence for a dominant and active archaeal community in sediments on the Peru Margin [2, 3]. Using different techniques on similar samples, evidence also exists that the subsurface microbial population is mostly bacterial [4, 5, 6]. Our recent study tried to address the discrepancies between experiments to resolve the understanding of subsurface microbial communities.

We have obtained 61.9 Megabases of metagenomic sequence from 4 separate horizons at ODP Site 1229 on the Peru Margin. Analysis of this metagenome shows that based on small subunit ribosomal RNA in-silico biomarkers, the subsurface community is dominated by Archaea at depth, reaching 88% of the microbial community at 50 meters below seafloor. We have also analyzed the gene content of the metagenome and over 85% of the genetic sequence does not have a closely related homolog in the public databases, suggesting that the deeply buried sediments hold a vast amount of genetic diversity. In addition to this metagenomic study, we have analyzed nucleic acid retrieved from this sediment environment by quantitative polymerase chain reaction and confirm that at depth, there is an archaeal dominance of the sediment microbial populations.

The subsurface sediment of the Peru Margin is extremely unique in that it holds a vast amount of archaeal microorganisms, more than any environment previously studied. This has now been determined by both measurements of active cells and total genetic material.

References

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Hexachlorocyclohexanes trace pathways and processes in the Canadian archipelago

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Hexachlorocyclohexane (HCH) is the most abundant organochlorine pesticide in the Arctic Ocean. Most of the HCH loadings took place by atmospheric deposition until ~1980, and by ocean current transport thereafter. The α-HCH concentrations in surface water on the North American side of the Arctic Ocean are 2-4 times higher than on the Eurasian side. Measurements made on the Swedish Tundra Northwest 1999 expedition in the Canadian Archipelago showed that surface water concentrations of the HCH isomers varied by about 2-fold, with higher concentrations near the Beaufort Sea to the west and lower ones in Baffin Bay – Davis Strait at the east end. Enantiomer fractions of α-HCH,

$$EF = (+)/[(+) + (-)],$$

were less than the racemic value of 0.500 and ranged from 0.436 in the Beaufort Sea to 0.454 in Baffin Bay, indicating preferential microbial degradation of (+)α-HCH. HCH distributions in the eastern Archipelago were consistent with mixing of three water bodies with characteristic end member concentrations and EFs. Levels of α-HCH in air of the central Archipelago were 37 ± 9 pg m^{-3} and 53 ± 5 pg m^{-3} before and after the mid-July ice breakup, a significant ($p < 0.001$) increase of 30%. The concentration increase was accompanied by a reduction in the EF in air after ice breakup, from 0.495 ± 0.003 to 0.482 ± 0.010, indicating sea-to-air transfer. It is suggested that enantiomers of α-HCH in air can provide a sensitive indication of ice cover loss in the Arctic.