ENVIRONMENTAL MICROBIOLOGY

Right place, right time

A new bacterial strain that is capable of *in situ* biodegradation of the major environmental pollutant naphthalene has been identified.

Biogeochemical cycling, the cycling of elements from the Earth's surface to the atmosphere and back again, is driven by microorganisms. However, the complex nature of natural environments means that the identification of the specific microorganisms responsible for a particular biogeochemical process *in situ* is extremely problematic. Now, Eugene Madsen and colleagues have carried out the first contaminated-field-based trials of a technique known as stable isotope probing (SIP), which enables researchers to follow the flow of labelled carbon atoms from a substrate — in this case naphthalene — into the DNA of naturally occurring microbial populations.

At a coal-tar waste disposal site that was contaminated with naphthalene and other aromatic hydrocarbons 40 years ago, ^{13}C-labelled naphthalene was released into surface sediments and the presence of naphthalene-degrading bacteria was confirmed by monitoring the generation of ^{13}C-labelled CO_2. The DNA was extracted from the treated sediment and the ^{13}C-labelled DNA fraction was isolated using a CsCl gradient and was then used to create a 16S ribosomal RNA (rRNA) clone library. Phylogenetic analysis of the library showed that most of the clones isolated from the sediment were clustered in a group containing β-proteobacterial species, including *Acidovorax* and *Variovorax*.

Of the 92 rRNA clones isolated from the contaminated soil, 46 were identical. Serial dilutions of the contaminated soil were grown on a mineral salts medium in the presence and absence of naphthalene vapours. The naphthalene-degrading bacterium was identified as a new strain, *Polaromonas naphthalenivorans* strain CJ2. Genetic analysis revealed that strain CJ2 contains the 16S rRNA gene that was identified in the clone library. It also revealed that strain CJ2 contains a novel naphthalene dioxygenase gene that had been identified in environmental samples, but for which the bacterial 'host' has been unknown until now.

This work proves that SIP can be used in the field to detect the *in situ* metabolism of environmental pollutants. Researchers hope that the same technique can be applied to identify other useful bacteria in contaminated sediments, such as those that metabolize the carcinogenic derivatives of naphthalene, the polycyclic aromatic hydrocarbons.

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References

ORIGINAL RESEARCH PAPER Jeon, C. O. *et al.* Discovery of a bacterium, with distinctive dioxygenase, that is responsible for *in situ* biodegradation in contaminated sediment. *Proc. Natl Acad. Sci. USA* **100**, 13591–13596 (2003)

FURTHER READING Radajewski, S. *et al.* Stable-isotope probing as a tool in microbial ecology. *Nature* **403**, 646–649 (2000)

IN BRIEF

VIROLOGY

Role for influenza virus envelope cholesterol in virus entry and infection

Sun, X. & Whittaker, G. R. *J. Virol.* **77**, 12543–12551 (2003)

Lipid microdomains or 'rafts' rich in cholesterol have been identified as important budding sites for several different enveloped viruses, including HIV and influenza. Cholesterol levels in the host-cell membrane do not affect influenza virus entry, but depleting cholesterol from the envelopes of influenza virions showed that although virus morphology was unaffected, entry and infection were inhibited.

ANTI-INFECTIVES

A genetic basis for *Pseudomonas aeruginosa* biofilm antibiotic resistance

Mah, T.–F. *et al. Nature* **426**, 306–310 (2003)

Antibiotic resistance in biofilms — surface-attached microbial communities — can be 10–1,000-fold greater than planktonic bacteria. Now, Graham Walker, George O'Toole and colleagues have identified a mutant of *Pseudomonas aeruginosa* that can form biofilms but is susceptible to antibiotics. The mutated gene encodes a glucosyltransferase that is involved in the synthesis of cyclic periplasmic glucans that can sequester antibiotics, which might account for biofilm antibiotic resistance.

INDUSTRIAL MICROBIOLOGY

Innovative approach for improvement of an antibiotic-overproducing industrial strain of *Streptomyces albus*

Tamehiro, N. *et al. Appl. Environ. Microbiol.* **69**, 6412–6417 (2003)

Using a *Streptomyces albus* strain that produced industrial amounts (10 mg ml^{-1}) of salinomycin, the authors introduced drug-resistance-producing mutations. Mutants with combined resistance to streptomycin, gentamicin and rifampin produced 2.3-fold more salinomycin then the parent strain.

EVOLUTION

Evolution of genomic diversity and sex at extreme environments: fungal life under hypersaline Dead Sea stress

Kis-Papo, T. *et al. Proc. Natl Acad. Sci. USA* **100**, 14970–14975 (2003)

The Dead Sea has non-saline, saline and hypersaline microenvironments. Eviator Nevo and his team exploited this unique habitat and assessed the diversity of coding and non-coding sequences of the filamentous fungus *Aspergillus versicolor* from different niches by amplified-fragment length polymorphism (AFLP). Genomic diversity was not random, and positively correlated with increasing levels of ecological stress, but diversity was reduced in the most extreme conditions because only fit genotypes can survive. The proportion of sexual fungi correlated with the patterns of genetic diversity — studying micromycete fungi might help to unravel the answers to fundamental questions about evolution and sex.