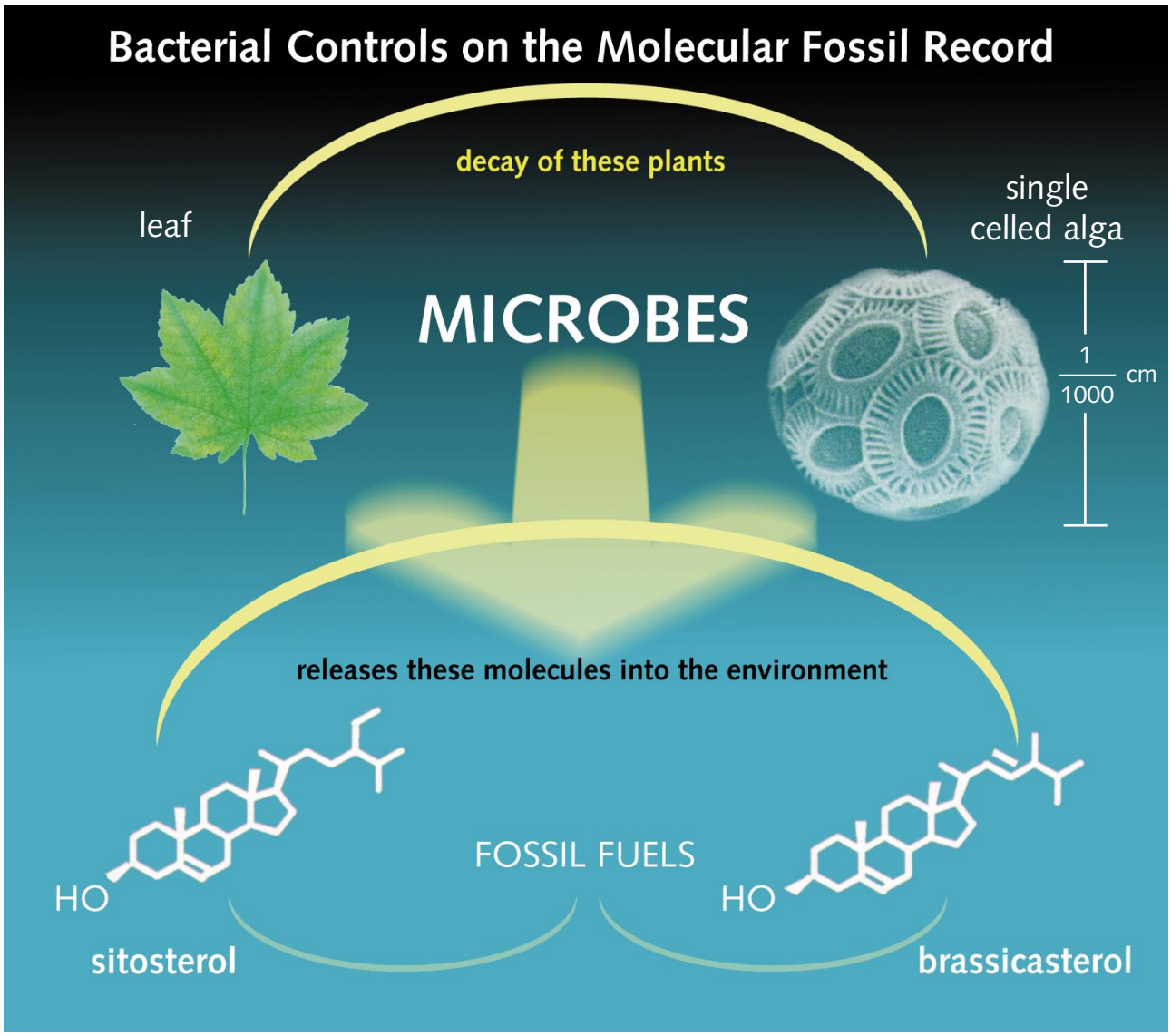
Simulating bacterial decay



How do biological molecules survive for millions of years, despite the activity of microbes that cause decay? We have developed a way to simulate thousands of years of bacterial decay of leaves and algal cells in just a few months in the laboratory. 'Ideal' conditions are provided to stimulate bacterial populations. Our method may help to reconstruct past environments from the small amounts of surviving molecules, as we can directly relate the type and amount of fossil molecules to the original living organisms.

Fossil fuels, so vital to modern life, come from plants which grew millions of years ago. Most of this plant material was broken down by microbes, the small fraction which survived ultimately formed present day deposits. As well as being crucial sources of energy these deposits contain fossil molecules which provide a unique source of information about past life on our planet and how this responded to climate change. How have these biomarker molecules survived at all?

Although bacterial decay of dead organisms is extensive, it is incomplete. Less than 0.1% of biological molecules escape decay, but this is out of a total of 50 billion tonnes produced each year. This preserved material – including fossil fuel deposits – contains some very reactive compounds, which should be easily broken down by microbes. It is these 'fossil' molecules which provide the most information about conditions and environments in the geological past.

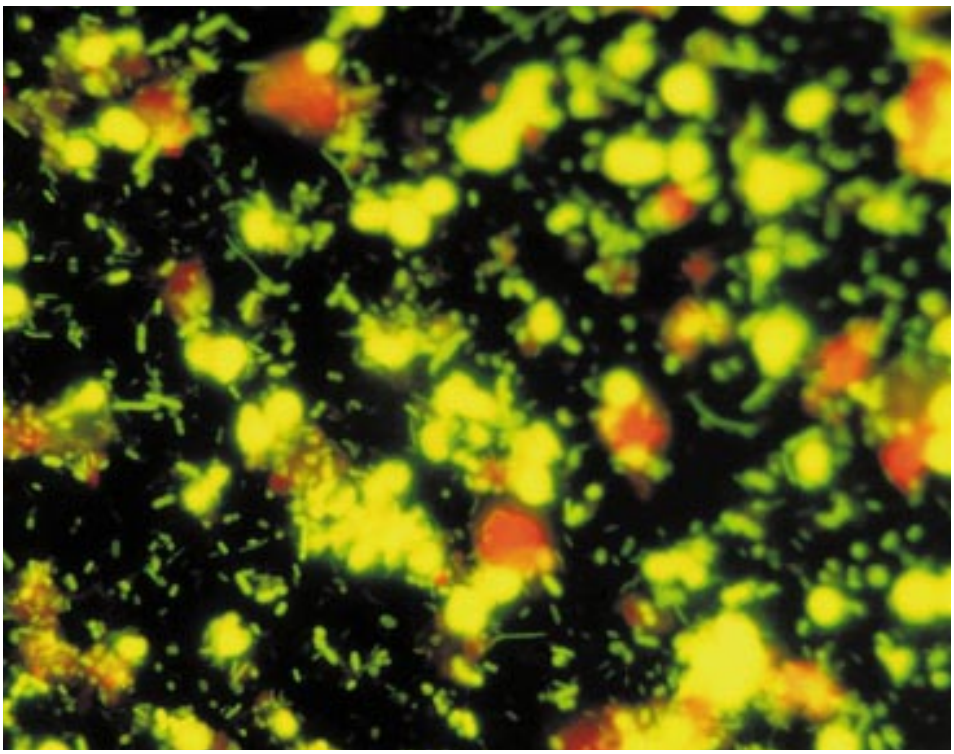
We wanted to know how reactive molecules are preserved as molecular fossils, in order to interpret this unique reservoir of information. We simulated the natural decay of tree leaves and algae in our laboratory, so that we could see how bacteria break down biological material. Chemical reactions that take thousands of years in the environment can be studied in months to years in our laboratory by providing the bacteria with ideal conditions.

We observed a remarkably quick removal of organic matter, with half gone in a single week. But despite this rapid initial decay, some very reactive molecules are still preserved at low concentrations even after several years. Finding out how biological molecules decay will help us to understand the global carbon cycle, and to reconstruct the climates of the past.

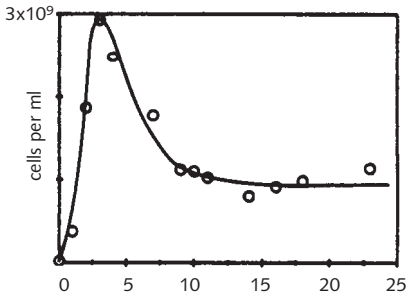
The Ancient Biomolecules Initiative is a five-year programme to understand the fate of biological molecules in archaeological and fossil materials, and to explore the applications of this new knowledge. The Initiative is funded by the Natural Environment Research Council.

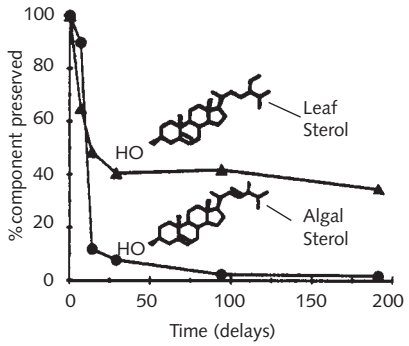
Natural Environment Research Council

Simulating bacterial decay: the science in detail



A photomicrograph taken after 3 days of inoculation, illustrating how bacterial populations are monitored in our experiments. Small green rods are bacteria, larger yellow 'blobs' are algae and red indicates clay particles. The graph below shows the rapid growth in bacterial population with a fall after about 3 days.





Results from an oxic microbial decay study comparing the extent of degradation of sterols in higher plant leaves with that for algal cells. Percentage abundance is relative to the start of the experiment. The leaf sterol exhibits the greatest long term preservation potential, explaining why higher plant lipids are better preserved than algal lipids in environments, even when they make a low overall contribution to biomass.

Methods

We can condense geological time using microbial model systems which are reproducible and which reflect degradation patterns in the natural environment. This is an extremely powerful tool for unravelling preservational controls on the molecular fossil record and the global sedimentary carbon cycle.

Careful monitoring of microbiological and chemical changes together with biomarker degradation patterns tells us what controls decay and preservation. Repeat experiments under changed conditions can test the impact of possible controlling factors (eg presence or absence of oxygen, amount of decay material, presence of surfaces and nutrients).

Bacterial populations increase rapidly as they degrade plant material (by over 100-fold within 5 days) which coincides with rapid degradation of lipid biomarkers (about half being removed within 7 days). Subsequently, bacterial populations decrease, but are still elevated ten-fold compared to initial concentrations.

Lipid degradation also slows down, and for some compounds a threshold is reached where no further degradation occurs for up to two years, despite the initial rapid breakdown. This replicates the preservation of labile compounds observed in geological deposits. Our laboratory degradation experiments can be used to predict the preservation potential of biomarkers in the environment.

Research highlights

Increasing the amount of starting material increases proportionally the amount of labile lipids preserved. The quantity of material reaching the sediment may be a major control on preservation, with implications for whether primary productivity or sediment redox conditions determine the amount of organic matter preserved in sediments.

Bacterial degradation is not limited by nutrients or inhibitory compounds, since adding more bacteria or a labile compound to decay experiments at 'threshold' stimulates bacterial activity.

All lipid biomarkers are degraded. Differences in their degradation rate result in considerable modification of the original biomarker signature and the ratios of certain compounds. This has implications for the use of such ratios in palaeoclimatic reconstruction.

It has been suggested that inorganic particles play an important role in protecting organic matter from bacterial degradation. But experiments without sediment particles also reached stable lipid concentrations and no further decay occurred.

Similar lipids in leaves and algae are degraded to different extents. Although it is well known that molecular structure, especially chain length, affects preservation potential of biomarkers this is evidently not the only control.

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