

## Ocean acidification: Been there, done that

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### Introduction

Amidst the uncertainties associated with the environmental effects of accumulating fossil-fuel CO<sub>2</sub> is one certainty: as atmospheric *p*CO<sub>2</sub> increases, the pH and saturation state of surface seawater with respect to aragonite and calcite are declining, and will continue to do so as long as we continue to pump CO<sub>2</sub> into the atmosphere. The observed trends in ocean chemistry can be quite confidently projected into the future [1] using models of various levels of complexity. Moreover, Earth history provides case studies of sudden addition of CO<sub>2</sub> to the atmosphere and their environmental consequences that confirm these projections and reveal the inner workings of the carbon cycle as it responds to perturbation.

### Déjà vu

The best studied carbon perturbation in Earth history is the Paleocene-Eocene Thermal Maximum (PETM). Indeed, among the paleoclimate community the PETM has become the poster-child for the dramatic consequences of ocean acidification. The onset of the PETM is rapid, within a few thousand years, and its effects sustained for nearly 200 k.y. [2]. The carbonate compensation depth (CCD) of the ocean shoaled markedly, but there is scant evidence for surface-water acidification. Simulations of the event using the intermediate complexity model Genie (<http://www.genie.ac.uk/>) demonstrate the critical importance of rate of addition: 6800 Pg CO<sub>2</sub> added to the atmosphere over 10,000 years leads to substantial seafloor carbonate dissolution, but surface waters remain highly supersaturated. Shortening the emission time to 1,000 years drives surface water calcite saturation states in the tropics from 4-7 to ~2-3 and in higher latitudes to below 1.5, in some places becoming undersaturated. This faster rate of CO<sub>2</sub> emission thus has more severe consequences for surface-dwelling calcifying organisms. However, at 6.8 Pg per year it has already been exceeded by current fossil fuel use.

[1] Zeebe *et al.* (2008) *Science* **321**, 51-52. [2] Rohl *et al.* (2007) *Geochem. Geophys. Geosys.* **8**, doi:10.1029/2007GC001784.

## The *bamA* gene: A general functional marker for the anaerobic degradation of aromatic compounds

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In anaerobic bacteria, aromatic growth substrates such as BTEX are channelled to the central intermediate benzoyl-CoA, which is then dearomatized to a cyclic dienoyl-CoA [1]. After a series of  $\beta$ -oxidation-like reactions 6-oxocyclohexenoyl-CoA (6-OCH) is formed. This intermediate serves as substrate for a ring opening hydrolase, referred to as BamA (bam = benzoic acid metabolism), yielding the aliphatic 6-OH-pimelyl-CoA. Even on the nucleotide level, *bamA* genes are highly conserved in all aromatic compound degrading anaerobes [2]. We established an assay with degenerated primers targeting the *bamA* gene from all known aromatic compound anaerobic bacteria. Two benzene contaminated aquifers were analyzed using *in situ* microcosms (BACTRAP<sup>®</sup>), loaded with benzene and incubated for five months at two different sites. The combined application of both, *bamA* and 16S-RNA analysis identified a *Geobacter* species as the only dominating species at one site, whereas at another site a species distantly related to *Azoarcus* sp. dominated.

The *bamA* gene probe provides a new and widely applicable tool for the detection of all types of anaerobic bacteria capable of degrading a wide variety of aromatic compounds. Its potential use for monitoring anaerobic biodegradation processes and for the identification of novel anaerobic, microorganisms with the capacity to degrade aromatic compounds is discussed.

[1] Boll (2005) *J. Mol. Microbiol. Biotechnol.* **10**, 132-42.

[2] Kuntze *et al.* (2008) *Environ. Microbiol.* **10**, 1547-56.