Atmospheric Methane over the past 400 million years

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Long term variations in atmospheric CH_4 concentration, excluding short bursts from hydrate reservoirs, have been estimated for the past 400 Ma. We constructed a steady state model that combines estimates of wetland CH_4 emission, based on the percentage abundance of coal basin sediments and original global rates of clastic sedimentation, with a Cambridge 2-D chemistry-transport model to determine loss by reaction with OH radical. The results [1] indicate that tropospheric CH_4 concentrations reached exceptionally high values of ~12,000 ppb during the Permo-Carboniferous, when tropical swamplands were widespread, fell to minimum levels (~100 ppb) during the Triassic 'coal gap', averaged around 2000-4000ppb during the Mesozoic and < 1000 ppb in the Cenozoic. The high Permo-Carboniferous levels made an appreciable methane contribution to mean earth surface temperature (see Figure) that allowed for lack of glaciation in paleo-Siberia while still permitting continent-wide glaciation in the southern hemisphere. The moderately high Mesozoic CH_4 levels were due partly to CO_2-driven warming resulting in increased CH_4 release from wetlands. Other than during the Permo-Carboniferous, over the rest of Phanerozoic history methane appears to have played a secondary role to atmospheric CO_2 and the evolution of the Sun in driving climate change.

[1] Beerling *et al.* (2009) *Am J. Sci.* **309**, 97-113.

Microbial metal reduction: Insights from genomics and transcriptomics

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Microbial metal reduction can be catalyzed by metal- and sulfate-reducing bacteria. In particular, *Shewanella oneidensis* MR-1, a metal-reducing bacterium (MRB), and *Desulfotomaculum reducens* MI-1, a Gram positive sulfate-reducing bacterium (SRB), have been shown to couple growth to Fe(III) reduction and to reduce U(VI). The mechanisms of Fe(III) and U(VI) reduction by *S. oneidensis* have been studied extensively using biochemical, transcriptomic and mutagenic approaches and have been shown to involve periplasmic and outer-membrane *c*-type cytochromes for both metals. The genome of *S. oneidensis* contains 42 *c*-type cytochromes which account for the metabolic versatility of this organism. In contrast, the mechanism of metal reduction by *D. reducens* remains unknown. Recent results have shown that U(VI) and Fe(III) reduction in *D. reducens* proceed through different pathways as vegetative cells grow with Fe(III) and spores reduce U(VI) with no apparent metabolic benefit. Reduction by spores requires the presence of spent growth medium suggesting the requirement for an endogenous factor to reduce U(VI). Furthermore, Fe(III) reduction by *D. reducens* differs significantly from that in *S. oneidensis* as the former lacks an outer membrane. In addition, the *D. reducens* genome only encodes for a single triheme *c*-type cytochrome annotated as a nitrite reductase. A transcriptomic study targeting Fe(III) reduction in *D. reducens* was conducted in order to investigate the role of the single *c*-type cytochrome and that of the nine hydrogenases in the genome. In addition, a second transcriptomic study was conducted to evaluate the effect of U(VI) on the metabolism of fermentatively-grown *D. reducens* cells.We report the results of these transcriptomic studies and compare them to previous results for *S. oneidensis*.