

An Ecosystem Model for Predicting the Methane Flux Into the Archean Atmosphere

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Atmospheric methane may have played a significant role in warming the surface of early Earth. Photochemical calculations suggest that a CH_4 flux comparable to the present biological flux could have produced methane mixing ratios on the order of 10^{-3} – high enough to offset low solar luminosity even at today’s low CO_2 level. Methane may also be a useful biomarker molecule in the atmospheres of early-Earth type extrasolar planets. For both these reasons, it would be useful to be able to estimate the methane flux on the early Earth. Abiotic sources of methane can be estimated by comparing with modern (submarine) volcanic fluxes. The biotic source is more difficult to compute, as it would have depended on the nature of the Archean ecosystem. Methanogens were most likely only one component of a diverse microbial ecosystem that evolved, continuously exploiting metabolic strategies in response to ongoing reductive and oxidative geologic and ecosystem processes. Sequence acquisition of prokaryotic genomes in their entirety provides the means for identifying lateral gene transfer and gene duplication events. This information can be used to reconstruct the evolutionary histories of metabolic pathways, setting time constraints on the various events relative to their appearance in the molecular record. One can then use this information to model the nature of the dominant microbial community during periods of ecosystem transition as indicated by the geologic record. We describe an integrated approach to evaluating the Archean biosphere through *i*) computer modeling of the early environment, *ii*) phylogenetic reconstruction of genes and pathways for major contributing species of extinct and/or extant C_1 metabolizing microbes and *iii*) a mixed-effect modeling strategy to predict microbial interactions in flux with an ecosystem.