

Targeted genomic detection of biosynthetic pathways: anaerobic production of hopanoid biomarkers by a common sedimentary microbe

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ABSTRACT

The lipid biomarker principle requires that preservable molecules (molecular fossils) carry specific taxonomic, metabolic, or environmental information. Historically, an empirical approach was used to link specific taxa with the compounds they produce. The lipids extracted from numerous, but randomly cultured species provided the basis for the interpretation of biomarkers in both modern environments and in the geological record. Now, with the rapid sequencing of hundreds of microbial genomes, a more focused genomic approach can be taken to test phylogenetic patterns and hypotheses about the origins of biomarkers. Candidate organisms can be selected for study on the basis of genes that encode proteins fundamental to the synthesis of biomarker compounds. Hopanoids, a class of pentacyclic triterpenoid lipid biomarkers, provide an illustrative example. For many years, interpretations of biomarker data were made with the assumption that hopanoids are produced only by aerobic organisms. However, the recent discovery of ^{13}C -depleted hopanoids in environments undergoing anaerobic methane oxidation and in enrichment cultures of anammox planctomycetes indicates that some hopanoids are produced anaerobically. To further examine the potential distribution of hopanoid biosynthesis by anaerobes, we searched publicly available genomic databases for the presence of squalene-hopene cyclase genes in known obligate or facultative anaerobes. Here we present evidence that *Geobacter sulphurreducens*, *Geobacter metallireducens*, and *Magnetospirillum magnetotacticum*, all bacteria common in anoxic environments, have the appropriate genes for hopanoid biosynthesis. We further show that these data accurately predict that *G. sulphurreducens* does produce a variety of complex hopanoids under strictly anaerobic conditions in pure culture.

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