Chronology of atmospheric deposition of Arsenic inferred from reconstructed sedimentary records

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In a pristine lake, sedimentary records of arsenic (As) differed markedly between basins that were either perennially oxic or seasonally anoxic. Differences included: i) As concentrations increased sharply upward close to the sediment surface in the perennially oxic basin, whereas they decreased in the seasonally anoxic basin; ii) the magnitude and position of major subsurface As maxima differed between the two basins. To explain these sediment profiles, we measured As in porewaters then used a one-dimensional transport-reaction equation to estimate As concentrations at the time of deposition as well as subsequent additions or removal of As at various sediment depths. By multiplying As concentrations at the time of deposition and sediment mass accumulation rates, we were able to estimate variations in As fluxes at the sediment surface over the last two centuries. These fluxes were then transformed into atmospheric As deposition fluxes by applying a correction using the ratio of expected to measured unsupported ^{210}Pb inventories at the sampling sites. The resulting chronological profiles of atmospheric fluxes of As deposition were similar in both basins, and were consistent with both the history of specific markers for coal combustion and direct historical measurements of As in dry and wet atmospheric deposition

Stable carbon isotope fractionation in sulfur oxidizing and heterotrophic bacteria native to an acid mine tailings pond

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This study identifies unique carbon isotope signatures associated with autotrophic and heterotrophic microbial communities that may be used to determine carbon cycling relationships *in situ* for acid mine drainage (AMD) sites. Stable carbon isotope ratios (δ^{13}C) of carbon sources, bulk cells, and membrane phospholipids (PLFA) were measured for pure strains of the sulfur oxidizing bacteria *Acidithiobacillus ferrooxidans* and *Acidithiobacillus thiooxidans,* and for autotrophic and heterotrophic laboratory enrichment cultures from 2002 and 2003, from a previously described oxidation pond at the Strathcona Tailings Treatment System [1,2]. Biosynthetic carbon isotope fractionation factors were determined for unique PLFA biomarkers produced by autotrophic and heterotrophic cultures. The autotrophic enrichment cultures were indistinguishable from the pure strains in PLFA distribution and δ^{13}C. Bulk cellular material in all autotrophic cultures was depleted in δ^{13}C by 5.6‰ to 10.9‰ relative to carbon source, indicating that these cultures are carbon limited. Individual PLFA in autotrophs were further depleted 8.2‰ to 14.6‰ compared to the bulk cell isotope composition, which are some of the largest biosynthetic isotope fractionation factors reported in the literature. Heterotrophic bulk cellular material was not fractionated in δ^{13}C relative to carbon source. The 2002 heterotrophic enrichment produced PLFA which were up to 3‰ depleted relative to carbon source, in contrast to the 2003 enrichment, which produced PLFA that were up to 3‰ enriched relative to carbon source. These PLFA biomarkers and associated isotope signatures represent a new approach that can potentially elucidate microbial community structure and carbon cycling in AMD environments.

[1] Bernier & Warren (2005) *Geobiology* **3**, 115-133.
[2] Bernier & Warren (2007) *GCA* **71**, 5684-5697.