Biomarker and stable isotope analysis linked to methane cycling in Lake Untersee, Antarctica

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Lake Untersee, in East Antarctica is a perenially ice-covered lake (2 – 4 m) consisting of two basins; a well mixed oxic basin ca. 160 m deep and a smaller, anoxic basin ca. 100 m separated by a sil at 50 m depth. Analysis of microbial phospholipid fatty acids (PLFA) and ether lipids (archeol and GDGT-0) and their isotopic compositions was used to constrain methane cycling and the recycling of carbon within the anoxic basin water column and sediments.

High concentrations of methane (8.5 mmol/L) were present within the bottoms waters of the anoxic basin, derived from sedimentary methanogens as shown by archaeol concentrations of 25 µg/g. Methane concentrations decreased slightly towards the annoxic/oxic interface. Methane is derived from CO_2 reduction based on its isotopic composition ($\delta^{13}C$: -50‰; δD: -438‰ at 95m) and that of the corresponding DIC ($\delta^{13}C$ ca. +25‰ at 95m). Methane oxidation occured within a suboxic transition zone present at ca. 70 – 80m. Within this zone [CH_4] decreased from 7.3 mmol/L at 85 m to 0.02 mmol/L by 72 m. Concurrently, $\delta^{13}C$-CH_4 values increased, from -51‰ at 85m to -40‰ at 72m, consistent with CH_4 oxidation.

PLFA concentrations varied throughout the water column, but generally increased with depth. Between 20 and 72m, values ranged from 0.2 – 3.8 µg/L (72m: 3.5 x 10^5 cells/L). Higher biomass was observed at the bottom of the suboxic zone: 78 and 80 m were 8.5 and 12.9 µg/L respectively (80m: 1.3 x 10^6 cells/L). The increase in PLFA concentrations at the bottom of the suboxic zone, combined with depleted $\delta^{13}C_{PLFA}$ values ($\delta^{13}C$-16:1: -36.8‰ at 76m) was consistent with a methanotrophic community supported by methane derived from the sediments. PLFA concentrations of 57 µg/g (5.4 x 10^9 cells/g) and $\delta^{13}C_{PLFA}$ values of ca. -20 to -25‰ within the sediments suggests an active heterotroph population producing CO_2 via organic degradation supporting the methanogenic community.

Identification of biomarkers created by the modern, viable bacterial and archaeal community is fundamental to understanding the preservation of biomarkers within palaeo-lacustrine environments that are relevant analogues to early Earth and Mars.