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Microbially mediated methane oxidation across a 4.1 million year soil chronosequence

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A soil chronosequence is a group of soils that differ in age but have similar parent materials and have formed under similar conditions of climate, vegetation and geomorphic position. The soils of the Hawaiian archipelago have formed from the same basaltic parent material, only differing in development age as the Pacific plate moves across a stationary convective plume (Chadwick *et al*., 1999). The Hawaiian soils represent a model soil chronosequence with near constancy in geology, topography, climate and biota dating back 4.1 Ma, a uniquely wide time range. Previous detailed characterization of the chronosequence has explored multiple aspects of the soil's development including variations in soil mineralogy and organic carbon with time studied (Torn *et al*., 1997).

Methane oxidizing bacteria (Methanotrophs) occur in every soil order, and are an important sink for atmospheric CH_4 in well aerated soils. The quantity of C cycled via methanotrophic bacteria in soils is globally significant yet the fate of methane derived carbon remains largely unknown and unquantified. There is generally good agreement regarding the magnitude of the soil CH_4 sink determined by methane flux measurements and process modeling. More poorly characterised aspects of the soil CH_4 sink include: (i) the physical and biological controls that influence the mechanism of CH_4 oxidation in soils; (ii) the fate of oxidized CH_4 carbon; (iii) the proportion of C from CH_4 oxidation that is sequestered as organic C or released as CO_2.

In this study, phospholipid fatty acid stable isotope probing (PLFA-SIP) has been used to investigate the development and variability of microbial activity during ecosystem development across a broad range of different soils. Specifically, a time series $^{13}CH_4$ labeling study was conducted to investigate CH_4 oxidation and C uptake by soil methanotrophs via $^{13}CH_4$ PLFA-SIP (Maxfield *et al*., 2006). CH_4 oxidation rates were also determined and compared with methanotroph C uptake. A combination of PLFA analysis and phylogenetic profiling were used to evaluate total soil microbial biomass and shifts in the wider microbial community structure.

Considerable variability was observed in the microbial communities across the soil chronosequence. CH_4 oxidation activity broadly followed SOM content increasing with soil development before decreasing again in the most highly weathered soils. Uptake of CH_4-C was observed into specific PLFAs. Bacteria similar to known type II methanotrophs mediated CH_4 oxidation although active methanotrophic populations were small relative to the high C content of some of the mid-aged soils (Maxfield *et al*., 2009).

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