

Organic matter – microbial interactions in tropical peatland

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The interactive relationship between environmental conditions, organic matter (OM) composition and microbiology is central to our understanding of soil carbon cycling. Such research on tropical peatlands is limited despite their importance to the global carbon cycle through the sequestration of OM and production of methane. Here, we determine the OM composition and microbial community structure of tropical peatland and how both change during downcore peat degradation and redox change. Our work is based on both a global database of peat biomarkers, representing over 30 sites, as well as a focused transect study of San San Pond Sak (SSPS), a wetland area in the Republic of Panama. The SSPS transect spans coastal to inland settings and associated representative peatland ecosystems - mangrove, mixed tropical forest, stunted forest with sawgrass (sedge) and ombrotrophic sawgrass bog.

At SSPS, organic matter composition changes markedly with depth: pronounced and selective degradation and redox-catalysed diagenetic transformations result in aromatic-rich and cellulose- and lipid-poor organic matter. These transformations are far more rapid and dramatic than observed at most temperate and boreal peatlands, except those where significant drainage has occurred, consistent with accelerated degradation at high temperatures. OM composition also varies across the transect, albeit more subtly, with increasing abundances of alkylresorcinols and decreasing proportions of lignin in the sawgrass bog.

Both archaeal and bacterial populations also change dramatically with depth, reflecting the switch from aerobic to anaerobic conditions and perhaps the increasingly recalcitrant OM substrate. Particularly striking is the dominance of the Bathyarchaeota, a phylum of anaerobic, metabolic generalists, throughout the SSPS peatland but especially in the deeper catotelm. This indicates a major role for these archaea in the anaerobic degradation of tropical peats (and possibly, subsurface methanogenesis and autotrophy). They appear to be associated with production of glycerol monoalkyl glycerol tetraether (GMGT), butanetriol dialkyl glycerol tetraether (BDGT) and unidentified isomers of glycerol dialkyl glycerol tetraether (GDGT) lipids, whose abundances also increase with depth. Crucially, similar lipid depth profiles are nearly ubiquitous in our global database, suggesting that Bathyarchaeota are key organisms in peatland carbon metabolism, especially at depth and likely persisting into the deep subsurface.