Microbial community metabolism and coupled carbon and iron cycling in ferruginous environments

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Models of Precambrian microbial communities and their impact on global geochemical cycles over 3 billion years of Earth's history remain almost entirely conceptual. This is due to a lack of information from environments with biogeochemistry extensible to ferruginous oceans. Kabuno Bay, a sub-basin of Lake Kivu in East Africa, is one of the few permanently stratified iron-rich (ferruginous) environments on the planet today. Process rate measurements and tag sequencing reveal a tight coupling between the primary producing photoferrotrophic bacteria, heterotrophic iron reducers, and methanogens. This tight coupling dictates the export of Fe(III) and the production of methane. While the role of the photoferrotrophic Chlorobi in Fe(II) oxidation has been established, the pathways through which carbon is channeled from primary production to terminal oxidation, as well as the organisms responsible for each pathway, remain largely unknown. Yet, it is the flow of carbon through these pathways that dictates the relative rates of iron export and methane production in Kabuno Bay. To gain molecular level insight into coupled C and Fe cycling we conducted metagenomic analyses to map metabolic pathways at the population and community level. These pathway-centric analyses highlight key taxa, such as Candidate phyla Patescibateria and Gammaproteobacteria, that likely support fermentation and Fe recycling respectively. Additionally, we quantified specific genes within these pathways to determine their abundance. For example, heme binding outer membrane cytochromes, implicated in Fe oxidation and reduction and therefore linked C and Fe cycling, are highly abundant. Furthermore, metagenomic assembled genomes (MAGs) reveal metabolic potential that underpins these processes. Indeed, MAGs identified as Patescibateria have the metabolic potential for polysaccharide and sugar degradation. Our metagenomic analyses thus reveal mechanistic aspects of coupled C and Fe cycling that likely supported microbial communities across vast stretches of Earth's early history.