Goldschmidt 2026 Abstract
https://doi.org/10.46427/gold2026.38103

Uncovering Novel Iron- and Nitrogen-Cycling Microorganisms in a Peatland Through Metagenomics and Metatranscriptomics

RENE L HOOVER[1], CARL-ERIC WEGNER[2,3], ZANDER HUMAN[3], REBECCA COOPER[3], KIRSTEN KUESEL[3] AND **CLARA S CHAN**[1]

[1]University of Delaware
[2]Heinrich Heine University
[3]Friedrich Schiller University Jena

Iron redox cycling is a key driver of soil and water quality, yet we have limited knowledge of the diversity of iron oxidizing and reducing microorganisms and their links to nutrient cycling due to the lack of general functional marker genes for both pathways. Here, we use genome-resolved metagenomics and metatranscriptomics to uncover novel iron-cycling microorganisms, their genomic potential, and transcriptional activity in a model Fe-rich peatland, the Schlöppnerbrunnen fen. Our analysis revealed approximately half the microbial community had a potential for iron oxidation or iron reduction. We found two novel clades of Gallionellaceae (RI-121 and CAITJF01) alongside known iron oxidizing microorganisms (FeOM) *Gallionella* and *Sideroxydans*. We also identified an abundant Archaea with a highly expressed *cyc2* iron oxidase gene, that can also be considered a novel iron oxidizer. Although known iron-reducing microorganisms (FeRM) like *Geobacter* were present in low abundance, many other taxa with iron reductase genes were detected, including Acidobacteriota. These findings indicate both well-known and novel organisms contribute to iron oxidation in the fen, while reduction is primarily by previously unknown iron-reducers. These iron-cyclers showed potential for impacting nitrogen transformations, hosting and expressing genes for coupling iron oxidation to nitrate reduction (NDFO) or iron reduction to ammonia oxidation (Feammox). The results suggest that iron energy metabolisms are more pervasive in peatlands than previously known, promoting nitrogen cycling and removal and thus have greater, undocumented effects on biogeochemical cycles.

Given the pervasiveness of iron, it is likely that Fe oxidation and reduction metabolisms are more common than currently known and go beyond canonical taxa. Our work creates a roadmap for identifying novel iron oxidizers and iron reducers and their activities along oxic-anoxic gradients. Careful analysis of iron oxidation/reduction genes plus geochemistry improved detection of these iron cyclers, including novel taxa. A more complete documentation of iron oxidizers and iron reducers will enable better understanding and prediction of how iron cycling drives nutrient transformations across various environments.