Autotrophic nitrate reduction coupled to oxidation of Fe(II) phases by a *Gallionellaceae* sp.-dominated microbial community enriched from a pyrite-rich aquifer

NATALIA JAKUS¹, NIA BLACKWELL¹, ADRIAN MELLAGE¹, DANIEL STRAUB¹, CARMEN HOESCHEN², MARKUS MAISCH¹, JAMES M. BYRNE³, CARSTEN W MUELLER⁴, PETER GRATHWOHL¹, SARA KLEINDIENST¹ AND ANDREAS KAPPLER¹

¹University of Tuebingen

²Technical University Muenchen

³University of Bristol

⁴University of Copenhagen

Presenting Author: natalia.jakus@geo.uni-tuebingen.de

Autotrophic denitrification coupled to pyrite oxidation is thought to drive natural attenuation of nitrate in aquifers. However, laboratory-based cultivation of autotrophic nitratereducing iron-oxidizing (NRFeOx) microorganisms is challenging, and so far little is known about the identity of subsurface-inhabiting NRFeOx bacteria, their physiology, metabolic makeup, and the mechanisms of oxidation of solid Fe(II) sources. Here, we used culture-dependent studies supported by NanoSIMS analysis, SEM imaging and reactionmodeling to evaluate the rates, the extent and mechanisms of $Fe^{2+}_{(aq)}$, siderite (FeCO₃), and pyrite (FeS₂) oxidation coupled to nitrate reduction by an autotrophic NRFeOx culture enriched from a fractured limestone aquifer containing Fe(II) minerals. Additionally, we applied metagenomics to elucidate putative electron transfer pathways in nitrate reduction and Fe(II) oxidation. During incubation with $\mathrm{Fe}^{2+}_{(aq)}$, and siderite, the NO3 reduced/Fe(II)oxidized ratios were close to a stoichiometric ratio of 0.2, suggesting that complete Fe(II)-dependent denitrification occurred. While growing on pyrite, only a fraction of nitrate (25.8%) was reduced due to direct oxidation of structural Fe(II), and the rest was coupled to the oxidation of S⁰ present as a residue from pyrite synthesis. The 16S rRNA gene sequencing revealed that the culture was dominated (ca. 62% relative abundance) by a so far uncultured organism belonging to the family Gallionellaceae (known Fe(II)-oxidizers). The unclassified Gallionellaceae sp., apart from having a cytochrome Cyc2 gene, putatively involved in extracellular electron transfer from Fe(II), also possesses narGHJI, nirKS, and norBC, a complete set of genes necessary to reduce NO_3^- to N_2O . It lacks, however, the nosZ gene and genes involved in S-cycling (sox), suggesting that NRFe oxidation in pyrite-containing aquifers requires multiple inter-species metabolic hand-offs. These findings highlight the importance of chemolithoautotrophic Gallionellaceae in linking biogeochemical cycles of N and Fe and has implications for predicting the fate of nitrate in freshwater ecosystems poor in organic carbon.