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Revealing how nitrogen fertilisation regulates the fluxes of COS and CO₂ between soil communities and the atmosphere using a functional metagenomic and metatranscriptomic approach

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Recent interest in the seasonal and spatial variability of atmospheric COS has intensified as its use as an atmospheric tracer of biosphere productivity in the carbon cycle has recently been demonstrated. The key link between the COS and CO₂ cycles in the biosphere is a family of enzymes called the carbonic anhydrases (CA) that catalyse both the hydration of CO₂ and the hydrolysis of COS in both plants and soil microbes. Recently studies have demonstrated that the variability in soil COS and CO₂ fluxes are modified significantly by fertilisation with inorganic N, indicating a strong coupling between soil carbon (C), nitrogen (N) and sulphur (S) cycling (Kaisermann et al., 2018). However, it is currently not clear whether the observed changes in COS and CO₂ gas exchange were principally driven by important shifts in the microbial community size, structure or function or some combination of the three.

To elucidate the underlying mechanism(s) we used a functional metagenomic and metatranscriptomic approach coupled with climate controlled gas exchange measurements on soils. A set of 6 soils collected from boreal and temperate sites were sieved and re-packed in microcosms and incubated in the lab for 2 weeks at 23°C and 30% water holding capacity in the dark. For each site half the microcosms were fertilised with 5 mg N in the form of NH₄NO₃ at the start of the incubation period. At the end of the incubation period soil COS, CO₂ fluxes were measured, and soil samples transported at -80°C to the Genosol platform for DNA and RNA extraction. For each soil microcosm we quantified the abundance of bacterial, fungal and algal genes in each community using 16S, 18S and 23S amplicon sequencing. After assembling and cross-mapping the metagenomes and metatranscriptomes we used a HMM model (Meredith et al. 2018) to estimate and comparatively assess the abundance of CA genes between the different sites and treatments.

Our results indicate that the N treatment caused a relative increase in the abundance of fungi in N treated soils compared to those in the control. Generally, we also found that the total number of CAs in soils shifted when treated with N compared to the controls and that the β-D CA sub-family

were the most prevalent CAs in all of the soils. In our presentation we will demonstrate how both the community structure and the abundance of CAs were modified upon N fertilisation and provide vital clues on the most likely mechanism(s) controlling COS and CO₂ fluxes in soil communities and the significance of these results for interpreting atmospheric signals.

Kaisermann, Aurore, Sam P. Jones, Steven Wohl, Jérôme Ogée, and Lisa Wingate. 2018 Nitrogen Fertilization Reduces the Capacity of Soils to take up Atmospheric Carbonyl Sulphide. *Soil Systems* 2 (4), 62 doi.org/10.3390/soilsystems2040062

Meredith, Laura K, Jérôme Ogée, Kristin Boye, Esther Singer, Lisa Wingate, Christian von Sperber, Aditi Sengupta, et al. 2018. "Soil Exchange Rates of COS and CO¹⁸O Differ with the Diversity of Microbial Communities and Their Carbonic Anhydrase Enzymes." *ISME Journal*, 2018. <https://doi.org/10.1038/s41396-018-0270-2>.