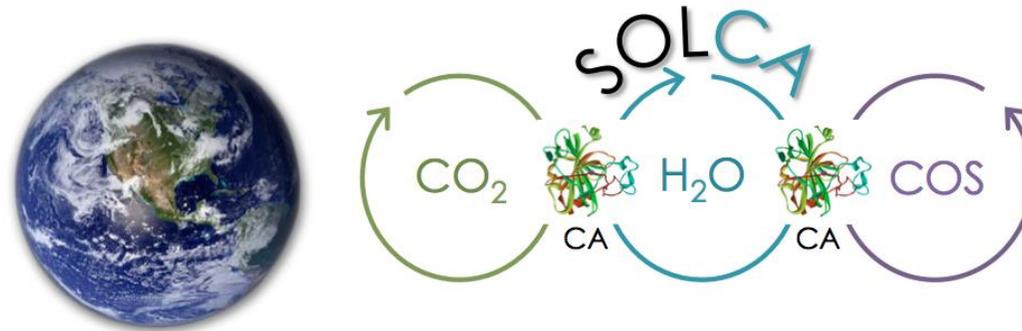


Revealing how nitrogen fertilization regulates the fluxes of COS between soil communities and the atmosphere using a functional metagenomic and metatranscriptomic approach

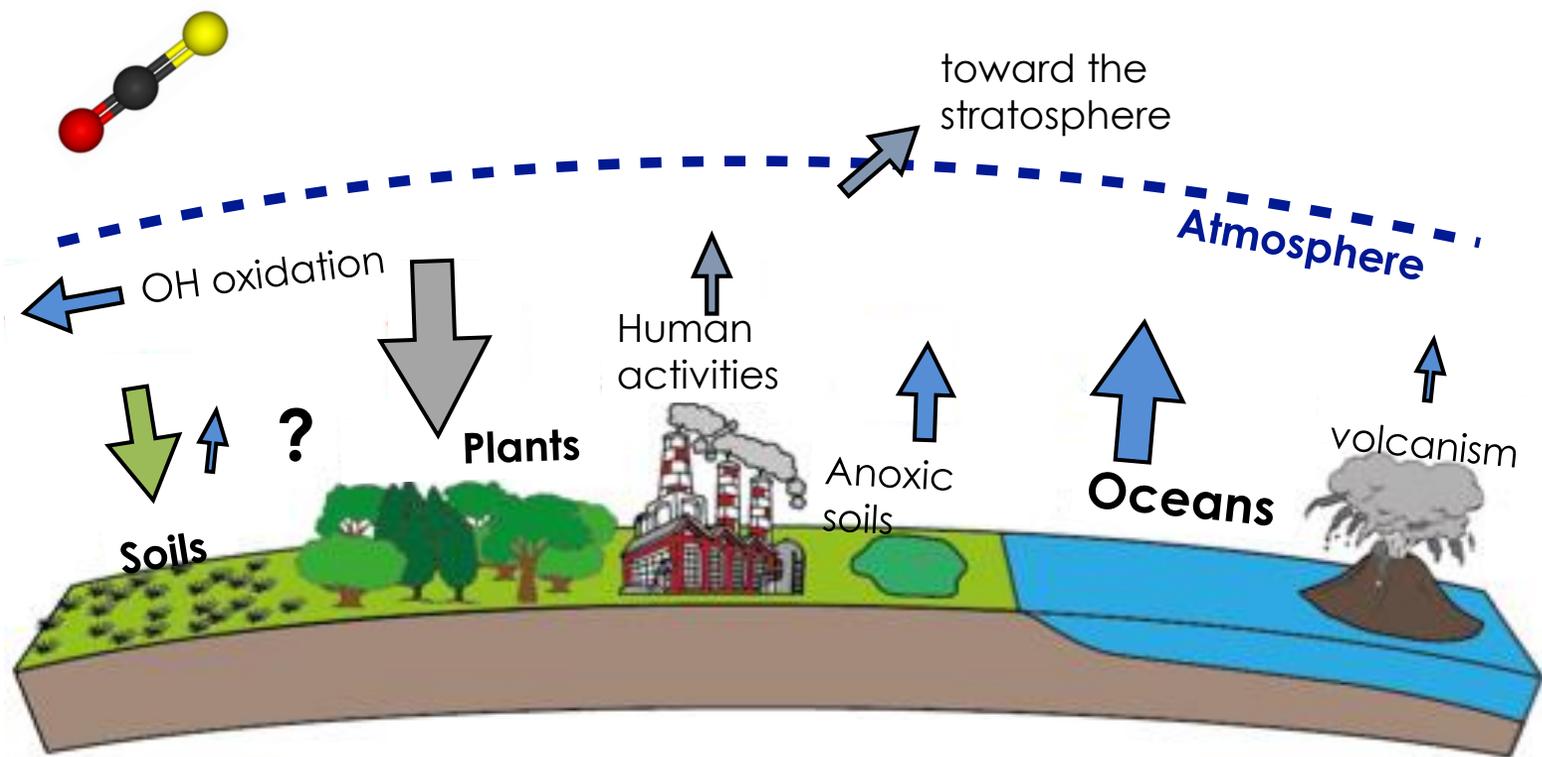


Evert van Schaik (INRAE Dijon, France)

Samuel Mondy, Mélanie Lelièvre, Marine Martin, Solène Perrin, Laura Meredith, Aurore Kaisermann, Samuel Jones, Olivier Rué, Valentin Loux, and Lisa Wingate

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Incomplete understanding of global COS budget

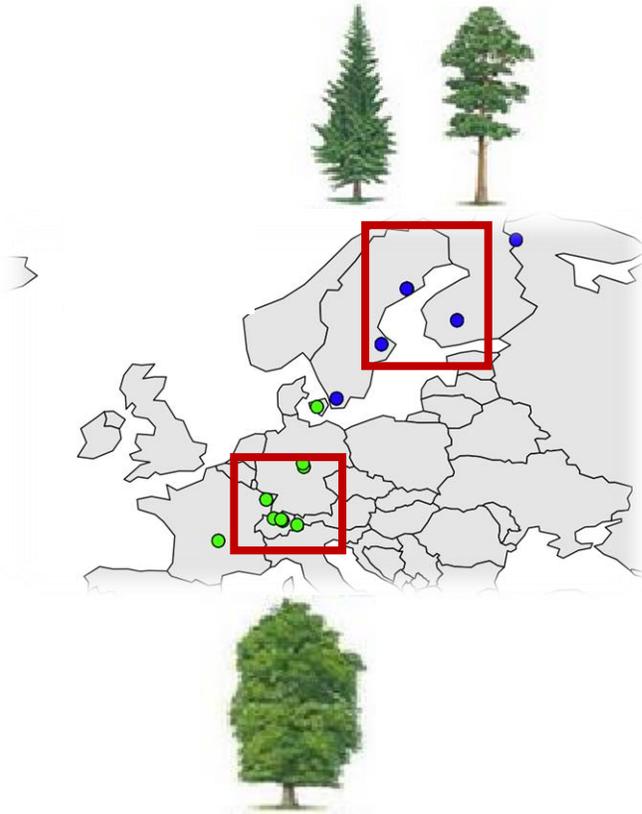


Recent interest in the seasonal and spatial variability of atmospheric COS has intensified as its use as an atmospheric tracer of biosphere productivity in the carbon cycle has recently been demonstrated. However, some uncertainties remain.

Our work aims to clarify this work using **COS gas exchange** measurements combined with genetic approaches to study the **microbial community composition** and **activity of the carbonic anhydrase** enzyme, that fixes COS.

How do soils contribute to budget?

Measuring the variability of soil CO₂ fluxes



500 ppt, 18°C and 30% WHC

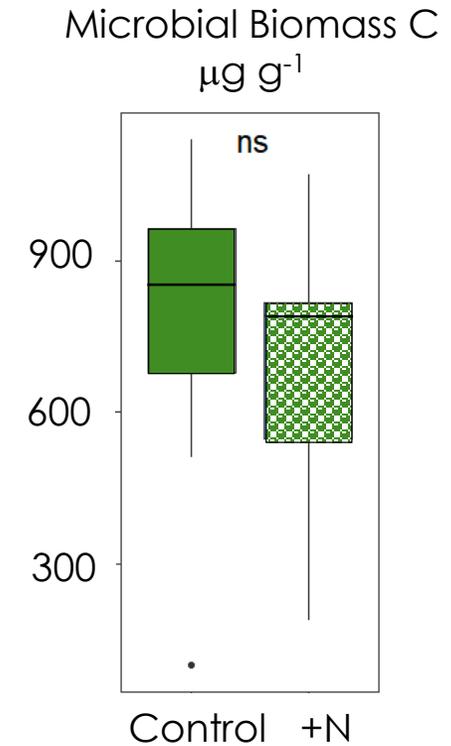
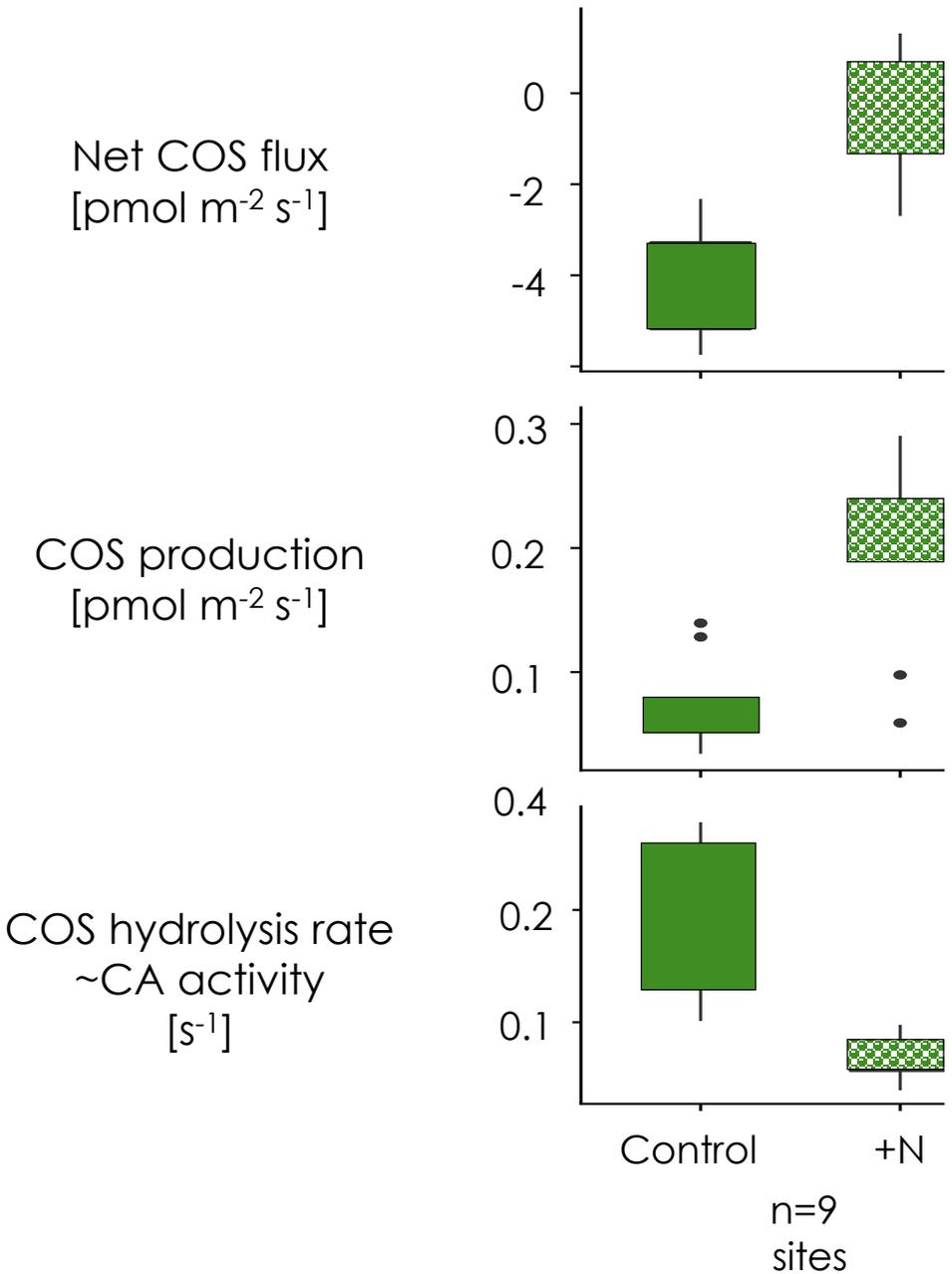


Soils were collected across a European transect of biomes and land uses.

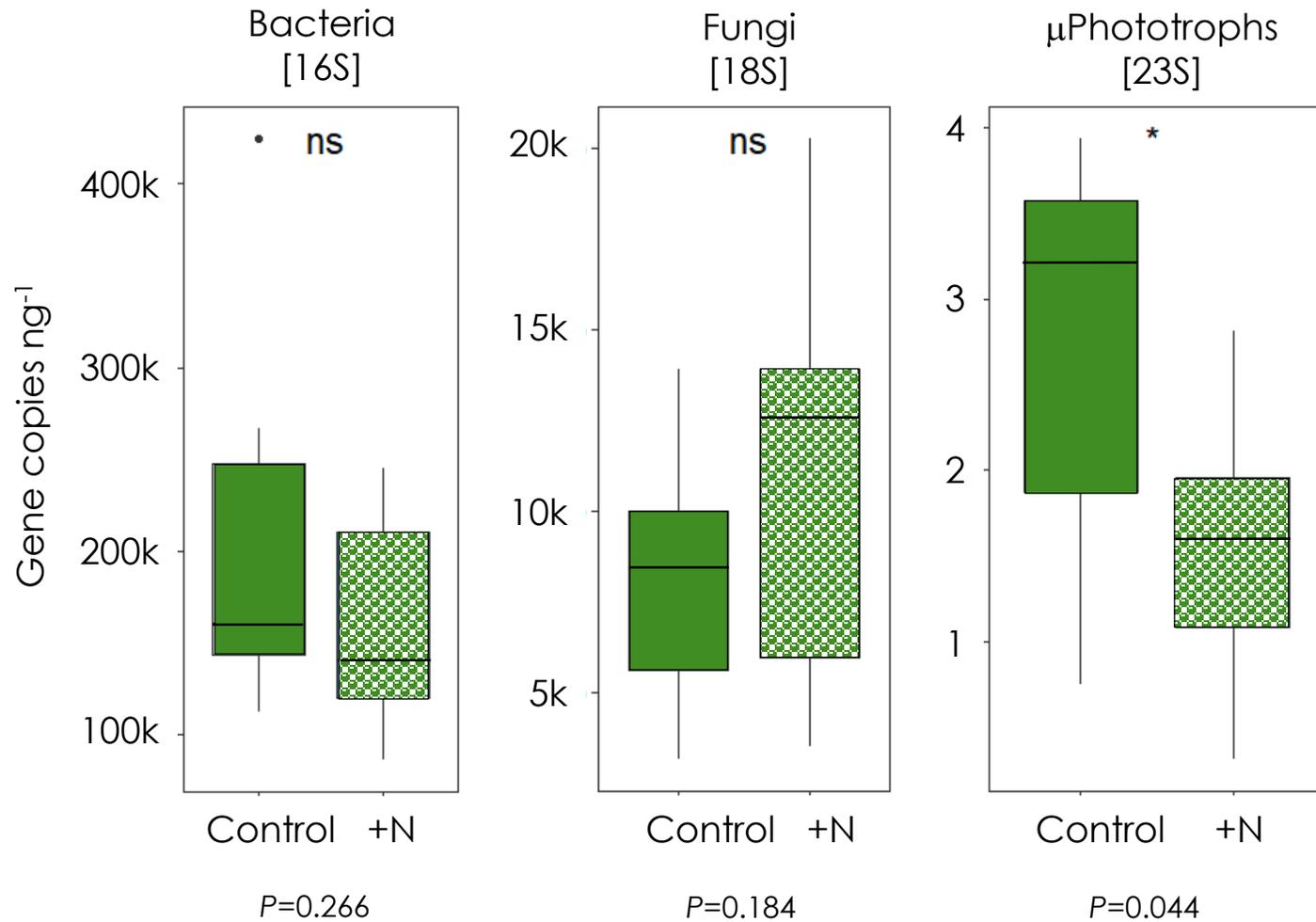
For each forest site, soils were sieved, re-packed in climate-controlled microcosms and partitioned CO₂ fluxes were estimated.

For 9 of the sites there were 3 control microcosms and 3 microcosms that received N additions.

COS uptake reduced with +N but not microbial biomass



However +N did cause decreases in the size of the phototroph community



μphototrophs relatively small community
23S:16S = 1:100,000
23S:18S = 7:100

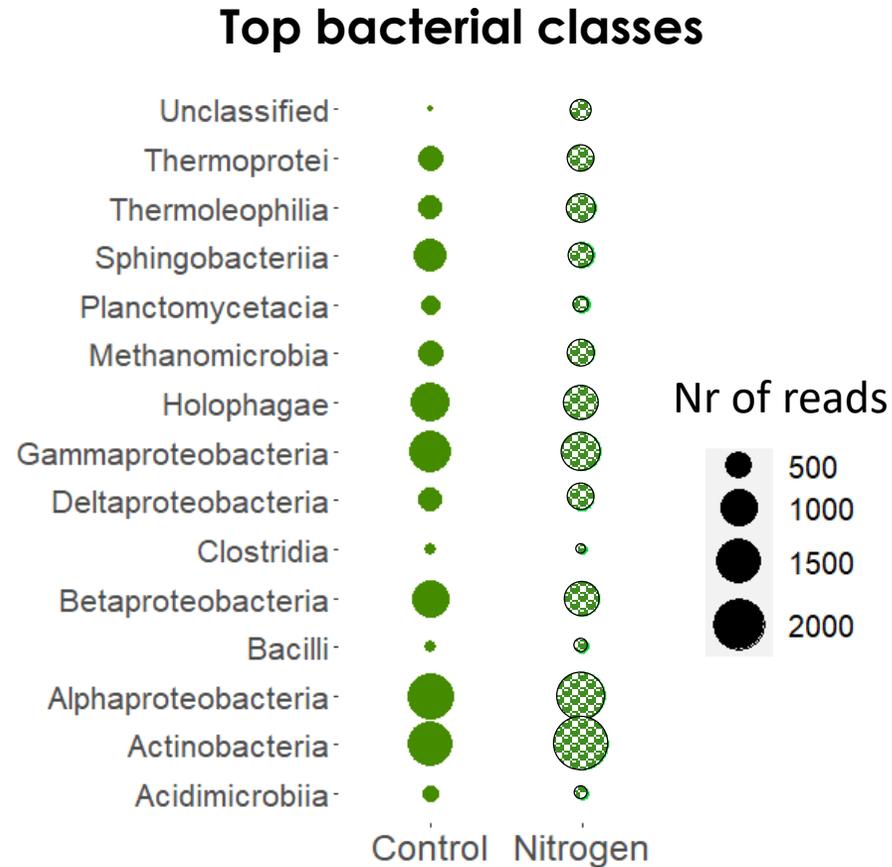
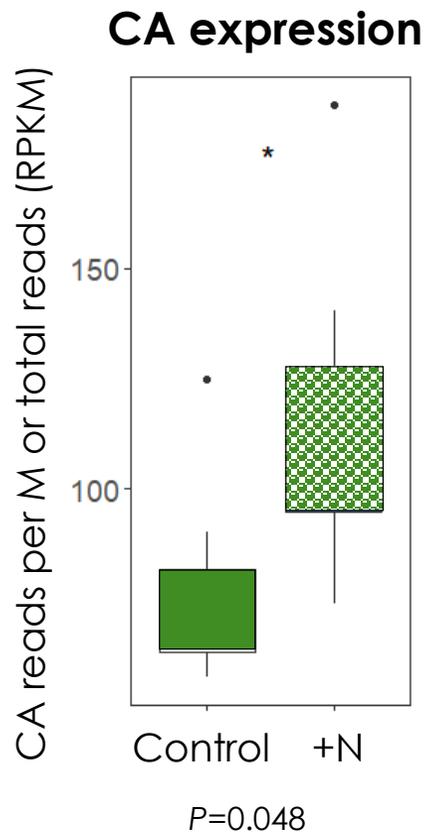
Even though fungal and microbial communities are small compared to bacteria, they have been reported as having an important role on COS flux

See display D484 | EGU2020-20422

For more details refer to Djemiel *et al.*, Scientific Reports, 2020
<http://microgreen-23sdatabase.ea.inra.fr/>
<https://www.nature.com/articles/s41598-020-62555-1>

&
Meredith *et al.*, ISME, 2018
<https://www.nature.com/articles/s41396-018-0270-2>

Carbonic anhydrase expression also responded to nitrogen



n=9
sites

Soils can function either as a source or a sink of COS. Disentangling which bacteria are involved in either of these two processes will require further analyses of our data.

Further analyses should reveal

- why CA expression goes up
- which species are either consuming less or producing more COS when we add N.

Conclusions and prospects

- We hope to clarify which microbial species might have a key role in COS production and fixation.
- Important factors to tease apart will be:
 - The effects of biome and land use
 - Clarification of the roles of bacteria, fungi and algae on the COS flux
- Furthermore we hope to utilise the metagenome and metatranscriptome dataset fully to:
 - Assign (specific) CA gene variations to specific genera
 - Study of other genetic pathways that may have an effect on COS fluxes

Thanks

Dr. Lisa Wingate (INRA Bordeaux)

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Dr. Samuel Mondy

Mélanie Lelievre

Solène Perrin

Marine Martin

Celine Faivre-Primot



Dr Laura Meredith (UA, Tucson, Arizona)



Migale platform

Olivier Rue

Valentin Loux



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