Hello everyone. Today I’d like to present you the study I took part in, that aimed to understand the influence of light on soil microbial communities and the consequences for soil COS exchange. I’ll start off by a bit of context, our hypotheses, and then we’ll jump into the experimental protocol that we implemented to answer them. Finally we’ll discuss the results and what can be drawn from them.

Carbonyl sulfide, abbreviated as COS, is an atmospheric trace gas. It is the most abundant sulfur compound naturally present in the atmosphere, with a mean concentration of around 0.5 ppb. COS is naturally absorbed by terrestrial plants alongside with CO2 through the activity of an enzyme, carbonic anhydrase, or CA. Because of this, COS atm concentrations decrease during the photosynthetic season. This makes COS a great proxy to estimate gross primary production at the ecosystem scale. However, doing so implies that plants are the major contributors to COS fluxes within their ecosystem.

This is an issue, because it is known that soils are also significant COS contributors. CA is an enzyme shared across a wide range of organisms, including soil microorganisms. This leads to biotic COS uptake by soils. On the other hand, soils can also emit COS through both biotic and abiotic pathways that remains to be fully determined.

COS consumption by soil microorganisms depends on many factors, including local COS concentration, temperature, soil moisture, and light. Our study focused on this last parameter. So what did we do ?

Soils with different physico chemical parameters were sampled in 4 locations across France, the croplands DBZ and LG, the orchard TL and the pine forest LB. I’ll be refering to these locations with the term “soil type”. At each location, we filled 6 jars with soil, then we incubated them in stable conditions in a controlled climate chamber. Half of them were incubated in the light, while the other half was incubated in the dark. After 40 days of incubation, gas exchange measurements were performed to see if the soil of each jar acted as sinks or sources for CO2 and COS.

For the next step, 1g of soil was sampled out of each jar and, after DNA extraction, submitted to quantitative PCR to assess the number of gene copies per microbial OTU, as a proxy to estimate their abundance. The extracted DNA also underwent DNA metabarcoding to associate it to identified OTUs using online databases.

We were looking to test three hypotheses. First, we expected that the composition of phototroph communities would differ in light conditions compared with dark conditions. Specifically, we expect an increase in the abundance of obligatory phototrophic organisms, and a decrease in that of shade tolerant cyanobacteria. Then, we expected that these shifts in the composition of phototroph communities would affect in return the one of heterotrophic communities. More specifically, we expected that the increase in the abundance of phototrophs with light would also lead to an increase in the abundance of parasites or predators of algae, or copiotrophic organisms, which are capable of rapidly exploiting the resources of their environment. Finally, we expected that shifts in the composition of microbial communities altogether would have repercussions on COS fluxes, with phototrophs being linked with COS uptake, and certain other key OTU being linked to their role already assigned in the litterature. **X**

From our experimental protocol, we obtained 3 abundance tables, one for each group of organisms, which are phototrophs, bacteria and fungi. I joined the internship at this point, so I was in charge of the statistical analyses. Here’s what I did. I started with permanovas to see if soil types and light treatments significantly influenced microbial community composition. I did that at the lowest taxonomic level available, which was the genus level. For all the remaining analyses, I used the class level, which was easier to handle while maintaining reasonable accuracy. I also performed a mixed effect linear model to understand if soil types and light treatments influenced CO2 and COS balance in soils. For this one, I didn’t use a classic permanova because I wanted to take into account the position of the jar in the climate chamber, since there could be variation depending if the jar was closer or not to lights or air inlets.

To visualize the variation between the different soil communities and how much of this variation could be explained by environmental variables, I used a canonical correspondence analysis. But how did microbial community composition influence COS fluxes ? To answer this question, I used a generalized linear latent variable model that allowed me to correlate the different microbial classes with soil COS fluxes. Finally, I built a network analysis to unveil potential interactions between members of microbial communities.

Now let’s start by investigating our first hypothesis. It appeared that all soils presented significantly different phototroph community composition in light conditions compared with dark conditions, except LG which is highlighted in red.

To keep looking at phototrophs communities, we should now analyse the phototrophs CCA. If we look at the different environmental parameters, we can see that there is a trend.

The effect of light is mainly represented on the y axis

While other factors such as pH and sand content, related to soil type, are represented on the x axis.

Based on that, we can see that we have this soil, the cropland DBZ, that is very strongly affected by light

As well as this other soil, the orchard TL.

And then we have the two other soils, that are more affected by soil type than by light. Even if the pine forest LB, on the right, is stil significantly affected by light, it is not the case for the cropland LG, on the left, as I said before.

So going back to the cropland DBZ, we can see that there are great differences in phototroph community composition between light and dark conditions. In the dark, DBZ phototroph communities are dominated by unidentified phototrophs. Indeed, unfortunately, the pipeline was not able to identify these organisms at the class level, but only at the phylum level. As such they belonged to the cyanobacteria phylum. And on the other hand, in the light, we can see that many classes of obligatory phototrophs, such as Trebouxiophyceae or Bacillariophyceae, increased in abundance at the expense of these shade tolerant cyanobacteria.

And about the same thing is happening in the orchard TL soils.

However, in the pine forest LB soils, that were the most acidic soils sampled, we’re going from communities heavily dominated by Chlorophyceae in the dark to more diverse communities In the light, notably including the class Zygnemophyceae, which was exclusive to these dark soils in our study.

Secondly, we wondered if these changes would affect heterotrophic communities. Looking at this network analysis, we can see that the abundance of fungi from the class Chytridiomycetes, known for their algae parasitic behaviour, was positively associated with the ones of several green algae, which were Mediophyceae, Pedinophyceae and Ulvophyceae.

There were also copiotrophic organisms whose abundances were positively associated with the ones of several classes of phototrophs. For instance, Sphingobacteria and Flavobacteria, two classes identified in the litterature as copiotrophic, were positively associated with 4 different classes of phototrophs.

Finally, how did variations in microbial communities composition affect COS fluxes in soils ? Here we’re looking at the phototrophic classes correlated with either COS emission or consumption. Consumption is related with negative values on the x axis, and emission with positive values. In the litterature, phototrophs are commonly associated with COS uptake, and since this analysis was meant to show correlation and not causality, we didn’t acknowledge algae correlated with COS emission.

However, one class of mosses correlated with COS uptake, Takakiopsida. Mosses are known for being potent COS consumers.

Now looking at the bacteria, several classes were correlated with COS uptake. And these classes were already identified as strong consumers in the litterature. Both of these classes displayed positive associations with another phototroph class in our network analysis, meaning that their effect could be enhanced in the light. However, both of these bacterial classes displayed correlation with COS uptake both in light and dark conditions.

Finally, here is the same plot, but for fungal classes. First, in contrast with our expectations, the yeasts Mortierellomycetes were not correlated with COS emission in our study. On the other hand, Sordariomycetes was associated with COS emission, which is at odds with the litterature. However, Leotiomycetes appeared correlated with COS uptake in the dark.

The abundance of this class of fungi appeared correlated with the one of the phototrophic class Chrysophyceae, meaning that changes in phototroph community composition could affect the consumption of COS by this fungi.

Thus, to summarize our findings, the composition of phototroph communities differed indeed in light conditions compared with dark conditions. Mixotrophic cyanobacteria dominated in the dark, while obligatory phototrophs developped in the light.

Then, these shifts in the phototroph community composition did affect heterotrophic community composition. In the light, several fungi and bacteria supposedly benefited from the increased presence of phototroph, either by parasiting them or by making good use of the increased environmental ressources.

And finally, many soil microbes were associated as playing an important role in soil COS balance. However, there was inconsistencies, probably due to the use of the class level, which can lack precision. Moreover, it is still difficult to asses the effect of light on microbial classes linked with COS emission or uptake, since they were often linked both in light and dark.

So to further explore the effect of light on COS fluxes related to soil microbial communities, it is important to keep improving pipelines for a better identification of soil communities members. And at the same time, this would allow us to function at lower and more precise taxonomic levels, to discover potential interactions that remained hidden until now and to better define the role of the different actors within soil microbial communities.

Much remains to be discovered about soil microbial communities, especially regarding phototrophic organisms. And, with the right tools in hand, it now definitely seems relevant to continue to explore how they shape communities through the action of light. This will allow us to estimate more precisely both spacially and temporally the contribution of soils to this black box that are COS fluxes in land ecosystems, and thus continue to understand the dynamics of the contemporary carbon cycle.