Impact of rising temperature and inputs of terrestrial organic matter on bacterial communities in aquatic habitats: insight from mesocosm experiments

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1 Context

While inland waters (e.g., lakes, streams, wetlands) cover only ~1 % of the surface of the Earth, they are estimated to mineralize and bury ~2.7 $PgC \cdot yr^{-1}$, i.e. roughly the size of the terrestrial carbon sink for anthropogenic emissions [1].

Climate change may cause longer periods of droughts followed by intense rainfalls that could increase terrestrial Organic Matter (tOM) inputs to inland waters, along with higher temperatures [2].

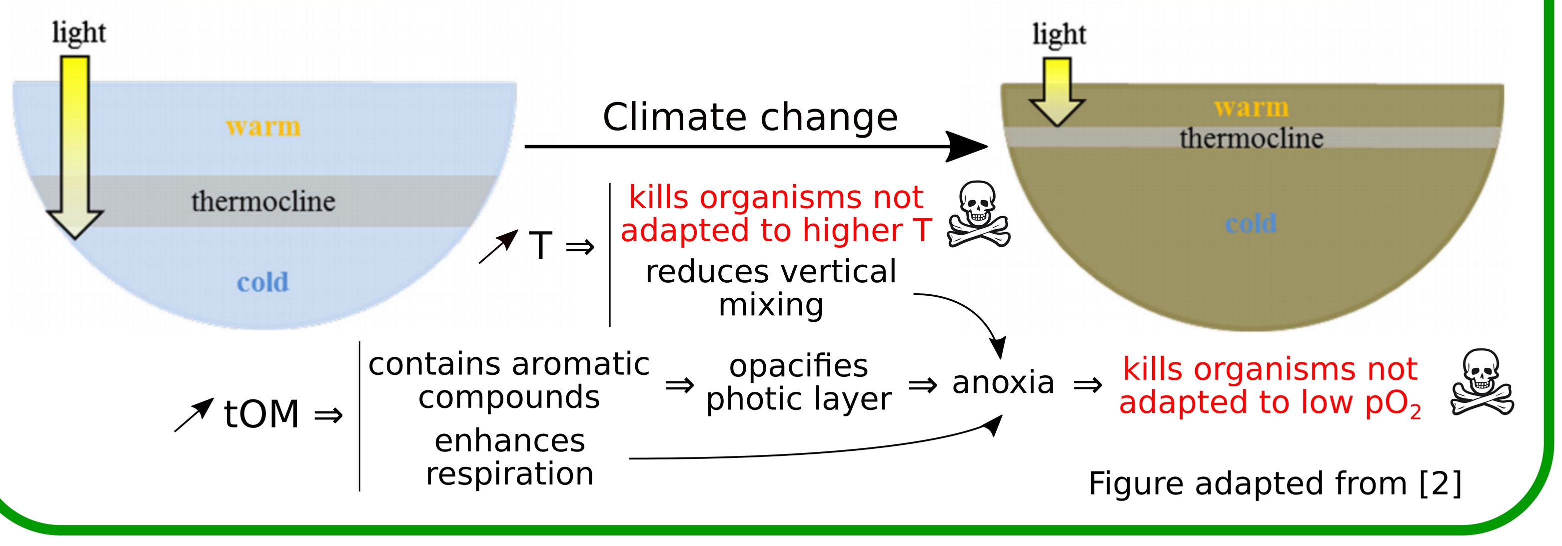


Figure adapted from [2]

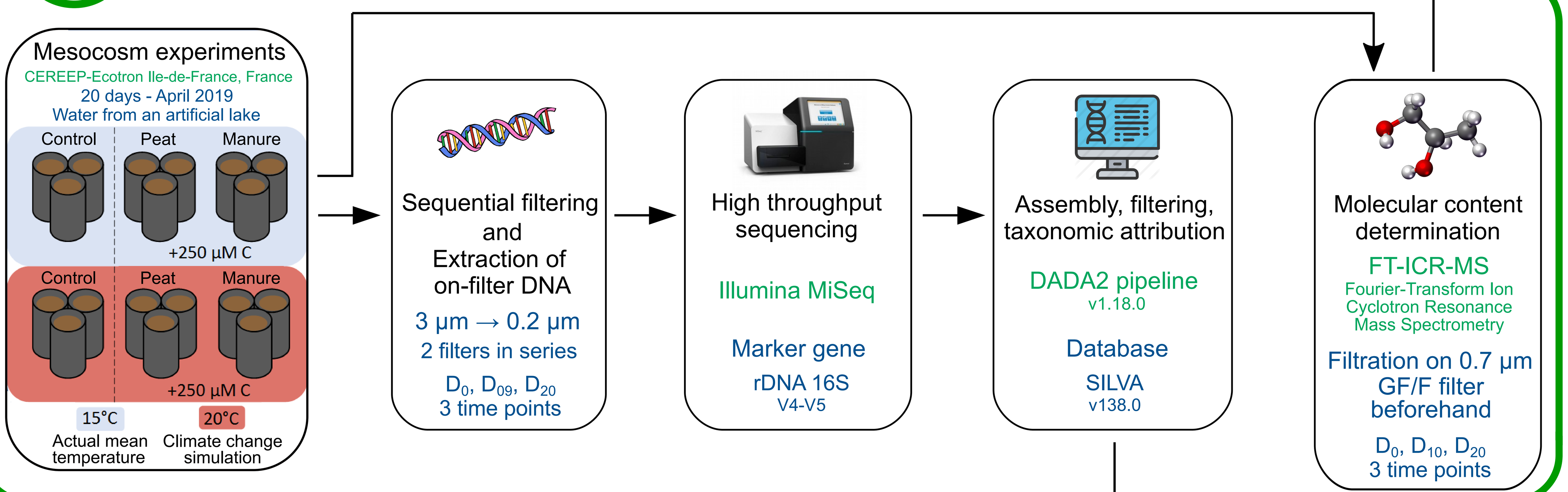
2 Objectives

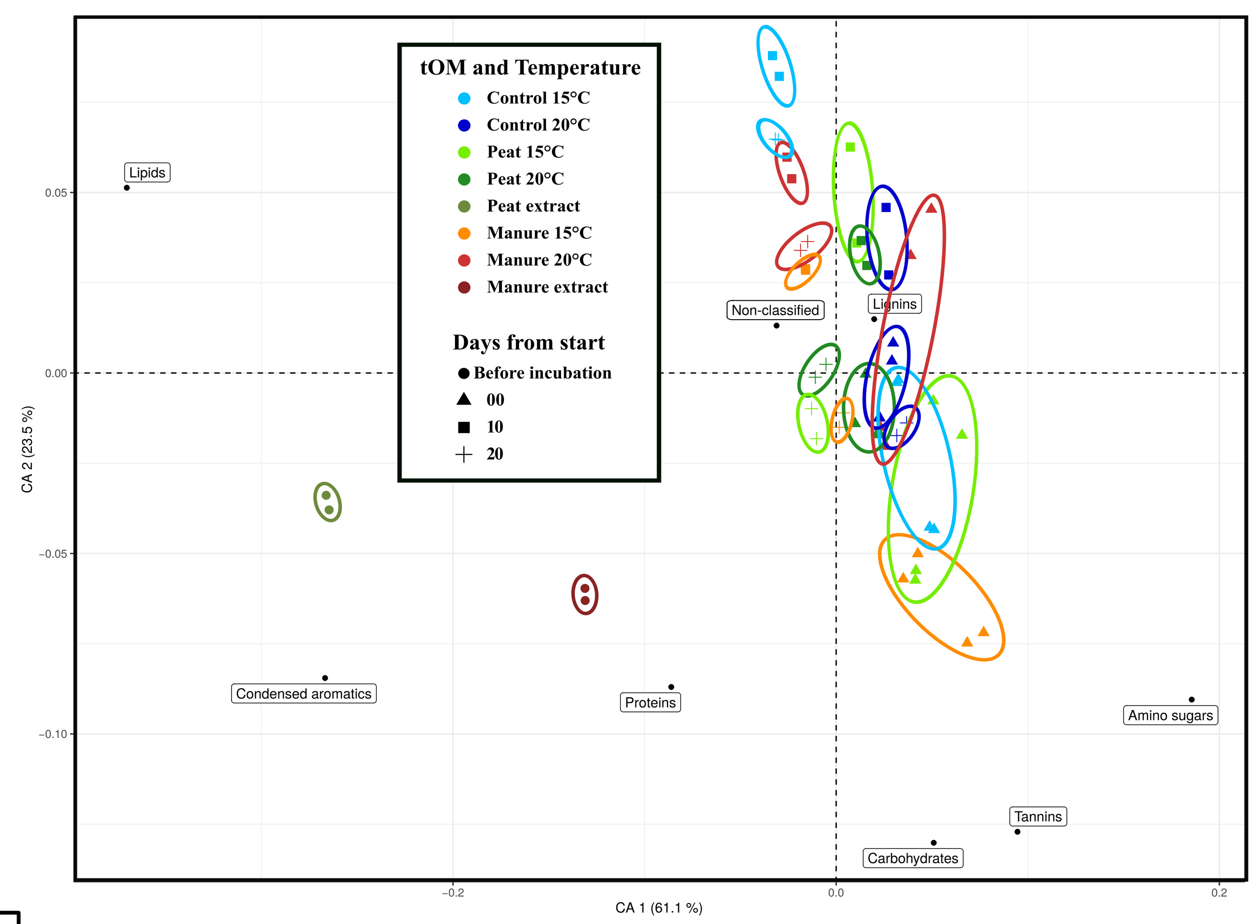
Heterotrophic bacteria are key remineralizers of tOM in aquatic ecosystems [3]. Evidence suggest that while the ability to use low molecular weigth compounds is a widespread trait among bacteria, the capacity to use specific higher molecular weight compounds is restricted to some bacterial groups. It is then unclear whether or not heterotrophic bacteria may be able to cope with increased amounts of potentially different-from-usual compounds, under higher temperatures, without affecting the efficiency of their functions in their ecosystems. As bacterial communities are at the basis of trophic webs, a change in their composition can have critical effects on upper trophic levels and on services aquatic ecosystems provide to human societies. We hence raise the questions:

A **Would higher temperatures and inputs of tOM due to climate change significantly modify the taxonomy and functions within the aquatic heterotrophic bacterial communities?**

B **To what extent the molecular composition of dissolved organic matter in aquatic habitats may change as a consequence of climate-change-induced inputs of tOM? How would this additional tOM be transformed along time by aquatic micro-organisms?**

3 Methods





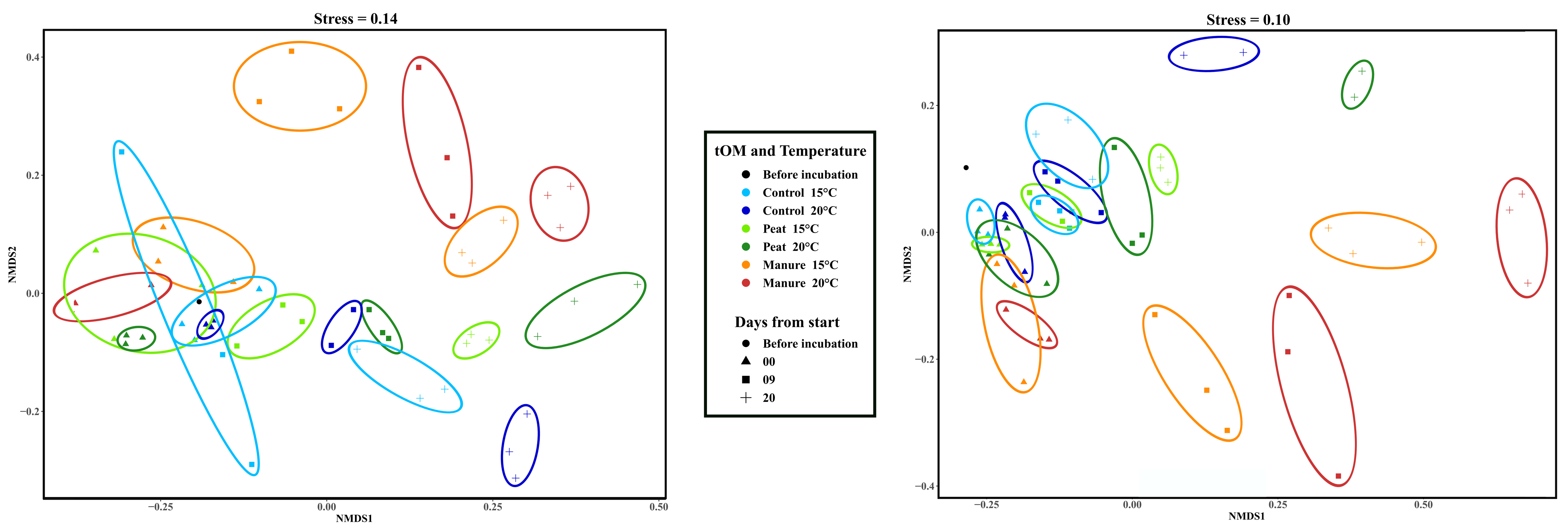
Evolution of the molecular composition of dissolved organic matter along a 20-days incubation as a function of temperature and input tOM

- Evaluated using a Correspondance Analysis (CA).
- Binning into categories according to the classification by Wu et al. [4].
- "Peat extract" and "Manure extract" are the molecular compositions of the peat and manure extracts that were added to samples at D_0.
- Each sample was passed twice to the mass spectrometer, hence each sample has two dots on the plot.
- Two replicates of each sample from D_0 were measured.
- Displayed ellipses are meant to improve readability, and must not be interpreted as convidence intervals.

4 Results

0.2 - 3 µm	Free-living Bacteria	3318 ASVs

> 3 µm	Particle-attached Bacteria	3493 ASVs



Evolution of the bacterial community composition along a 20-days incubation as a function of temperature and input tOM

- Evaluated using Non-Metric Multidimensional Scaling (NMDS) at the ASV level using Bray-Curtis dissimilarity on data normalized to relative abundances within a sample.
- "Before incubation" corresponds to water from the artificial lake sampled before incubating the mesocosms.
- Displayed ellipses are meant to improve readability, and must not be interpreted as convidence intervals.

5 Conclusions

A ↗ tOM and ↗ T seem to **enhance taxonomic changes** for free-living and particle-attached Bacteria.

⚠ However

Control drifts ⇒ **no steady state.**

Community composition **differs significantly** at D_0 between groups.

Next: Focus on functional groups as the ability to use specific complex molecules is reported as poorly linked to phylogenetic proximity [3].

B The molecular composition of samples is dominated by **lignin** and **non-classified** compounds.

Stochastic effects seem to have more influence on this composition than tOM and T.

However, there seems to be a **pattern** of increasing lignin/non-classified molecules at $\mathbf{D_{10}}$ and an increase of Carbohydrates/Amino sugars/ Tannins/Proteins at $\mathbf{D_{20}}$.

Next: Link bacterial functional groups and variations of the molecular content.

6 References

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