

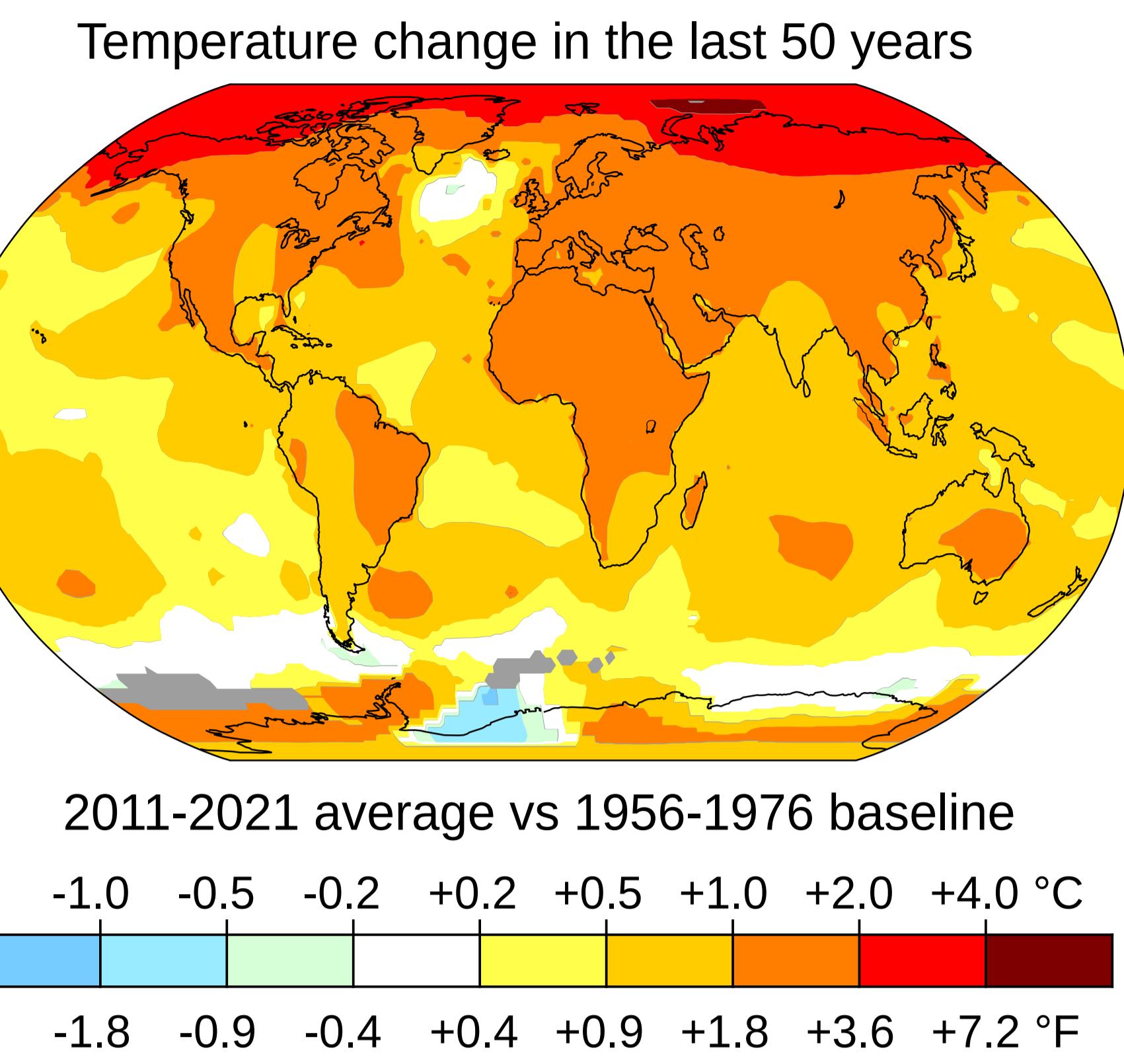
Effects of short-term warming on bacterial communities in Arctic soils

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INTRODUCTION Global warming affects all ecosystems worldwide but Arctic regions, and the life they sustain, are particularly sensitive. Here, microbes play a fundamental role in decomposing an increasingly available quantity of organic matter which byproducts, i.e. CO₂, may lead to positive climate feedback. Therefore, understanding the potential effects of warmer temperatures on Arctic soil microbial communities is important.

EXPERIMENTAL DESIGN to study seasonal variations in bacterial communities, Arctic tundra topsoil samples were collected from six plots. The experimental site was located in western Greenland (Disko Island). Soil samples were collected from warming and control plots after one year of warming treatment, simulated through open-top chambers, in June, July, and August 2013. DNA and RNA were extracted from soil samples and used to characterise i) bacterial communities by 16S amplicon sequencing and ii) bacterial functional genes involved in methane and nitrogen cycle.



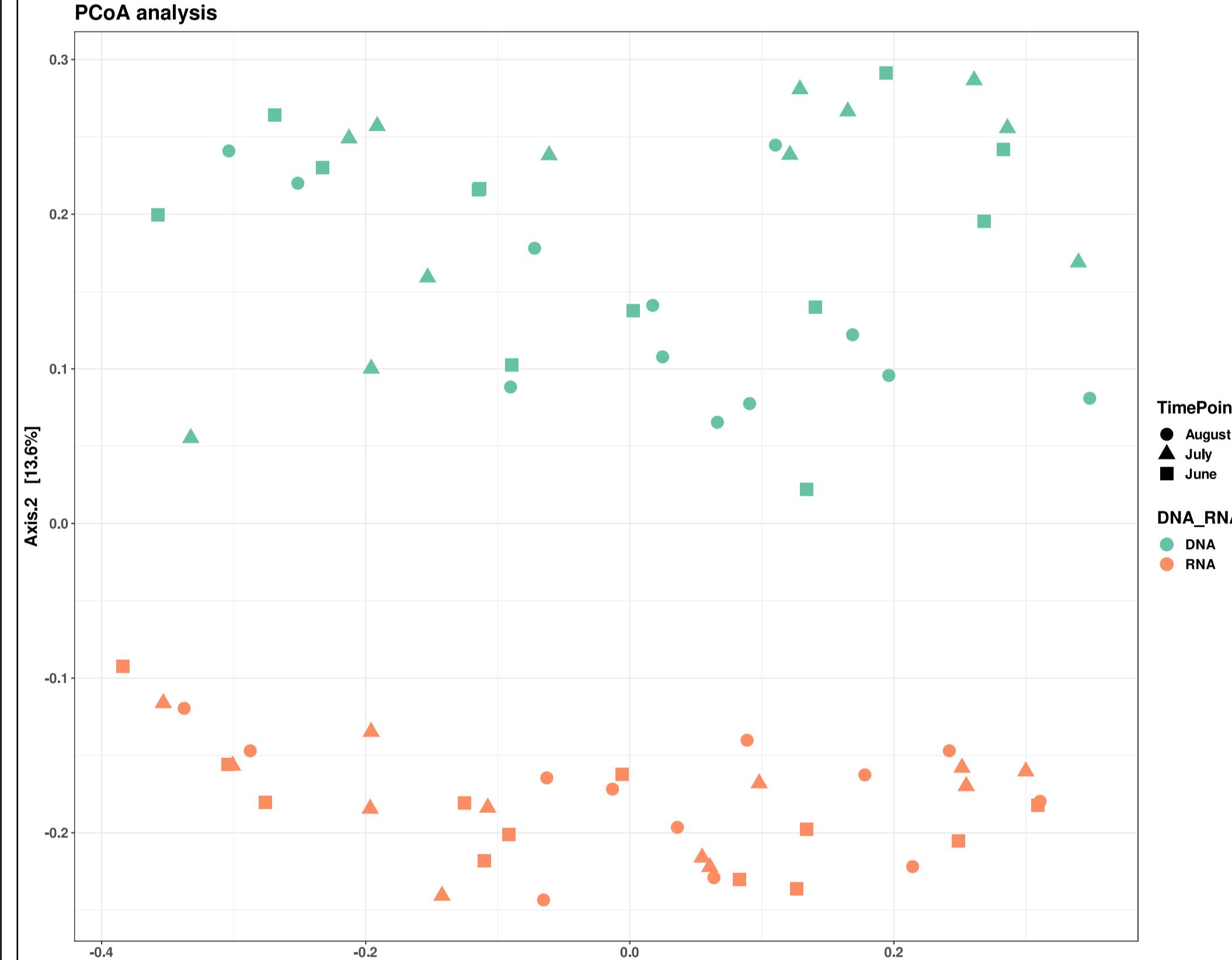
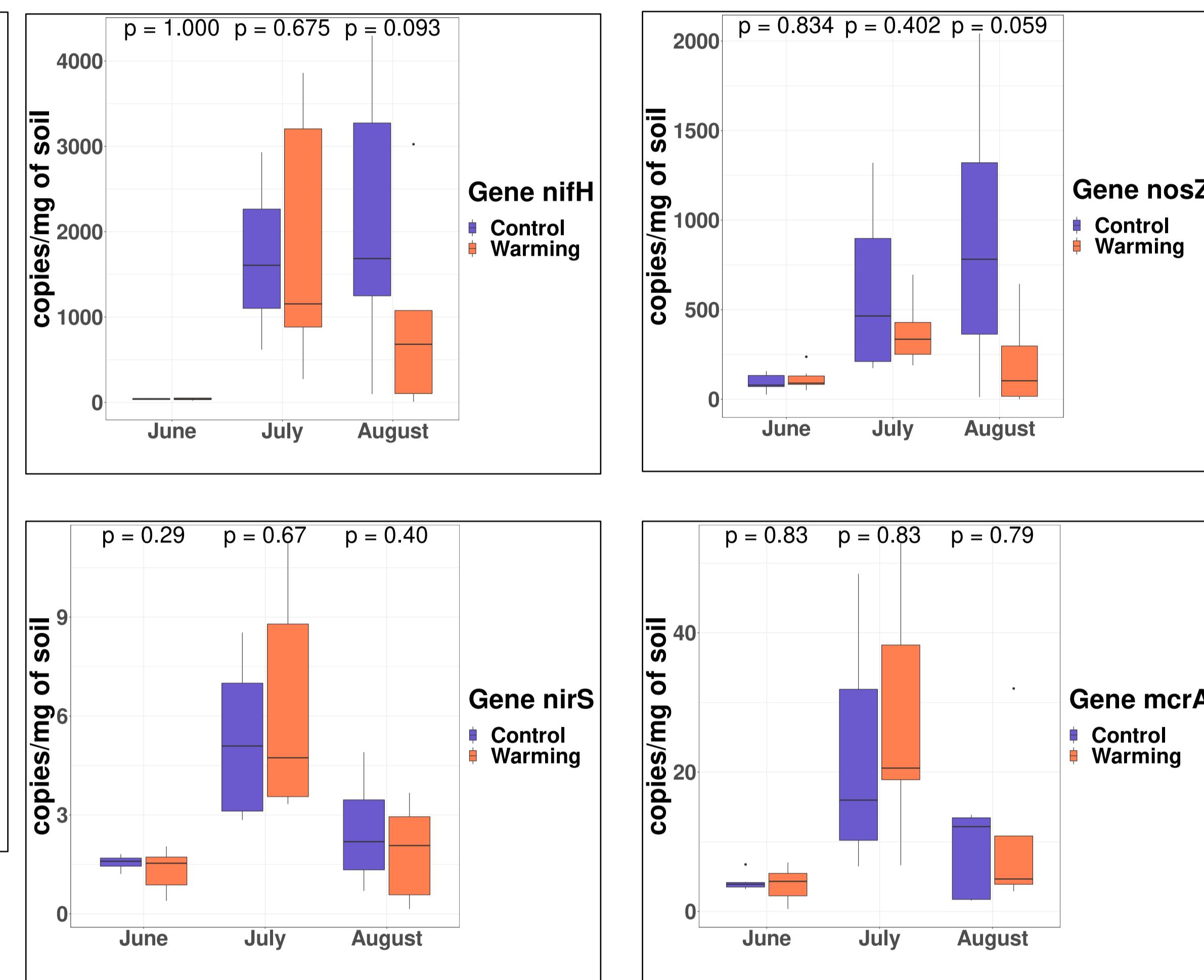
NASA's Scientific Visualization Studio, Key and Title by Eric Fisk https://data.giss.nasa.gov/gistemp/maps/index_v4.html
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RESULTS

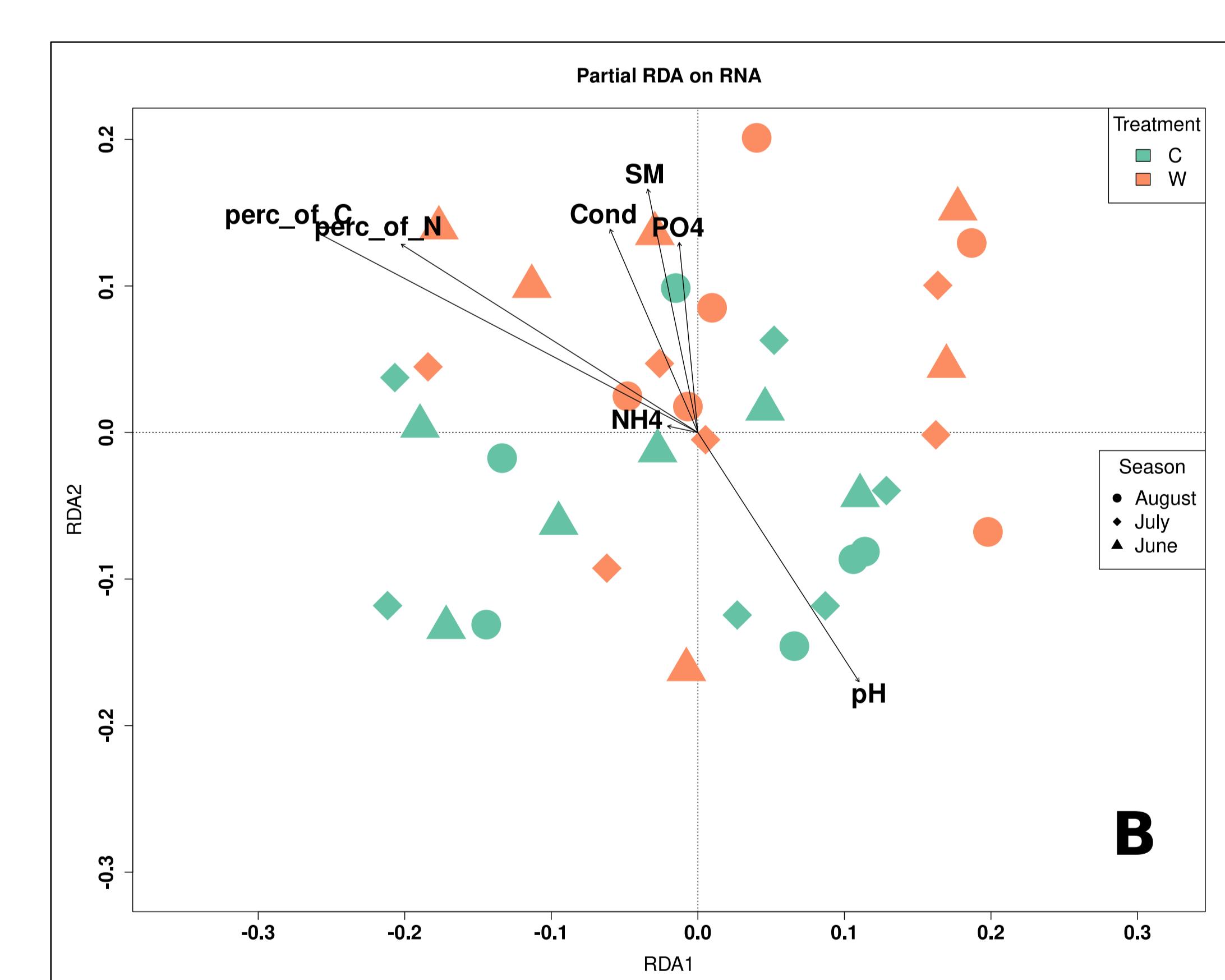
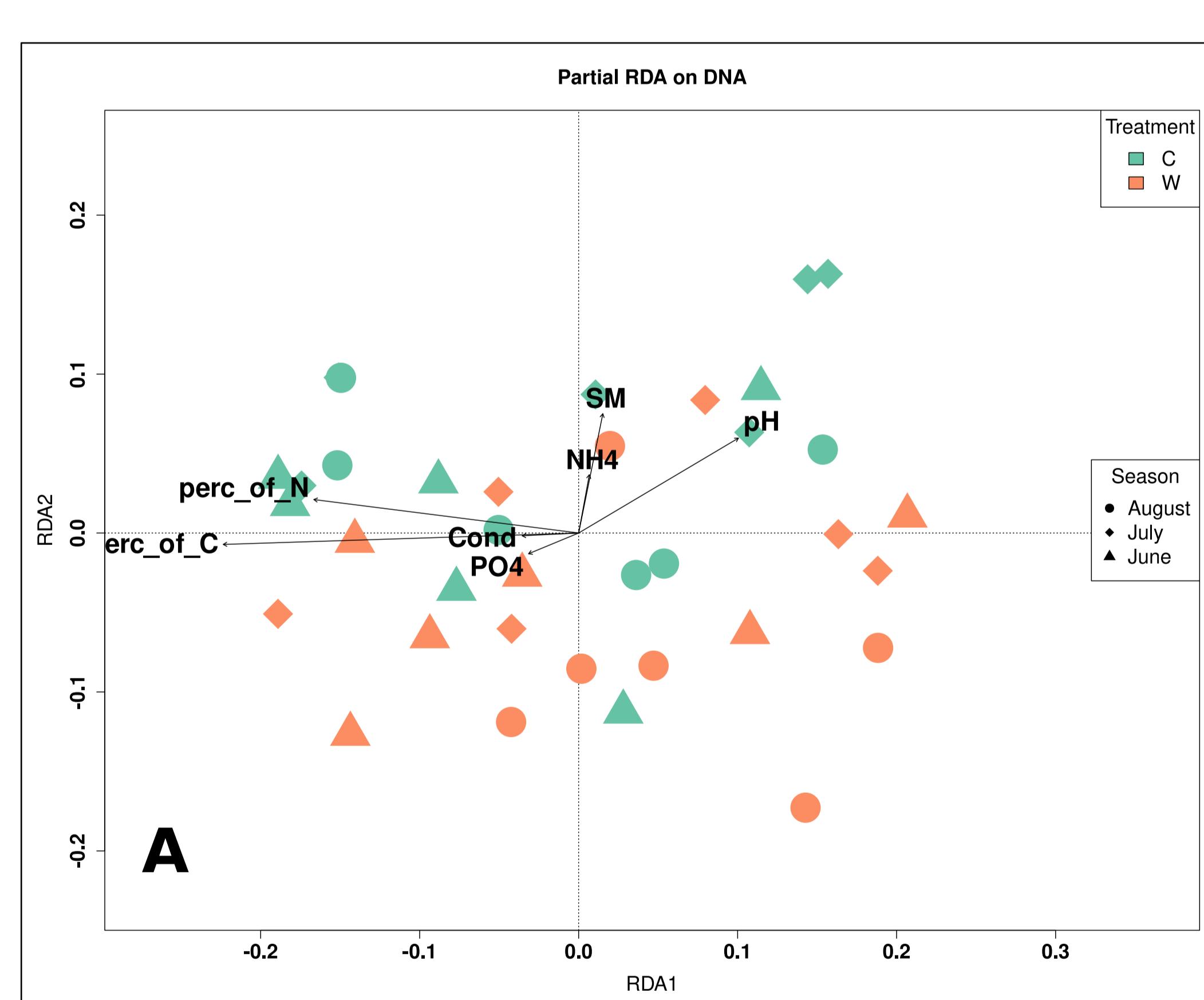
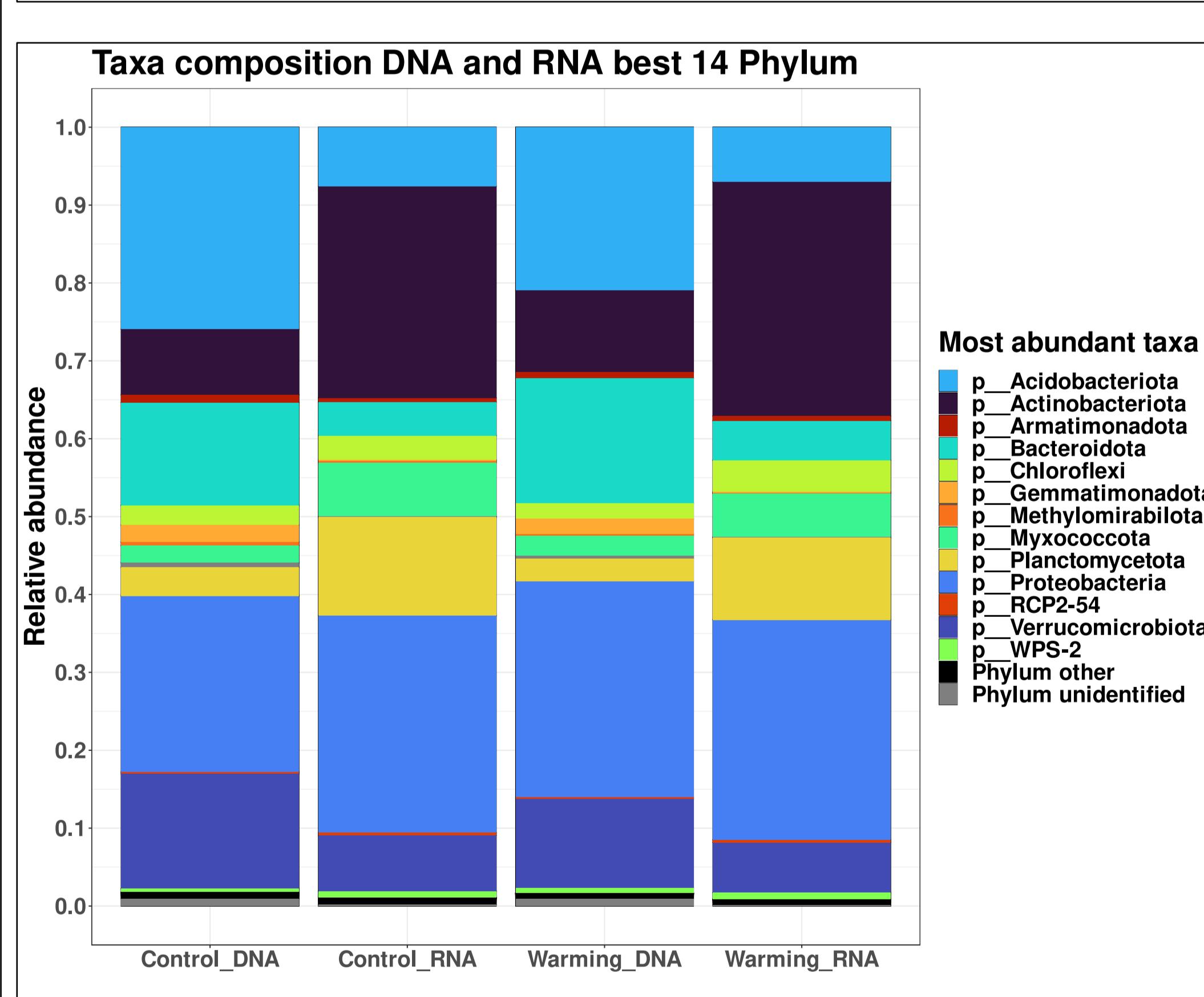
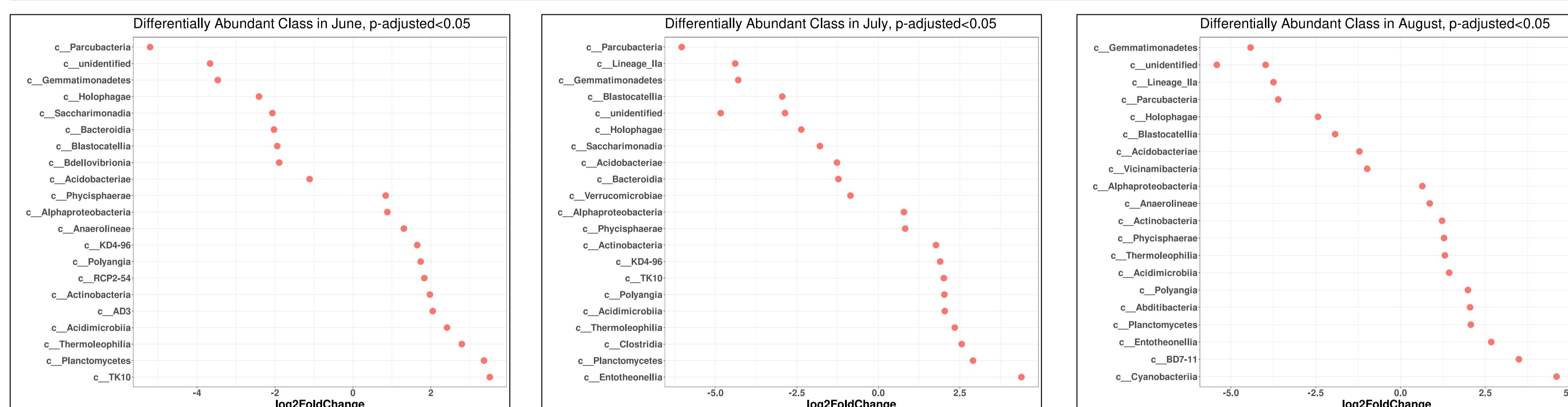


Sampling site with a **snow fence** (the green net in the left picture) and an **Open Top Chamber** (OTC) that simulates summer warming.

qPCR analysis showed that nitrogenase reductase (*nifH*) and N₂O reductase (*nosZ*) genes seemed to have a positive trend with respect to the timepoints. In contrast, nitrite reductase (*nirS*) and methyl coenzyme-M reductase (*mcrA*) were found more active in July.



Differential abundance analysis performed with DESeq2 showed that, at each timepoint, several Classes were significantly different when DNA and RNA were compared.



Principal Component Analysis, (top) shows that DNA and RNA are well separated while Treatment and Controls at different timepoint are not.

Barplots (bottom) shows the Phyla found in the samples.

Table 1: Adonis (Permanova) tests			
Test	R2	F	Pr(>F)
~Treatment, DNA-June	0.09155	1.0078	0.09375
~Treatment, DNA-July	0.06018	0.6404	0.9688
~Treatment, DNA-August	0.08703	0.9533	0.1562
~Treatment, RNA-June	0.06417	0.6857	0.6562
~Treatment, RNA-July	0.06204	0.6615	0.8125
~Treatment, RNA-August	0.07174	0.7729	0.4375
~TimePoint, DNA	0.06739	1.1924	0.013
~TimePoint, RNA	0.04657	0.8059	0.268
DNA_RNA, DNA + RNA	0.12467	9.9696	0.001

Partial RDAs show, for DNA (A) RNA (B) how samples tend to be separated according to treatment. **Table 1** (left) shows all the tests that were performed to evaluate if any significant difference was found, for Treatment, DNA_RNA, and Timepoint.

CONCLUSIONS

- Microbial communities were significantly different when DNA and RNA samples composition was compared. Also, differential abundance analysis showed many significant Classes of bacteria, for each timepoint;
- Partial RDA suggested that there may be differences between timepoints;
- Permanova tests showed that differences between Controls and Warming, at all timepoints, were not significant. Differences between DNA and RNA were highly significant. DNA was found significantly different between timepoints;
- qPCR genes were not found different between Controls and Warming, but showed a trend that follows seasonality.

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