

Microbial response to future climate characteristics in the Greenland Arctic



Tosadori G (1), Haskell MJ (1), Algora C (1), Novotná A (1), Hindborg Mortensen L (2), Maccario L (3), Elberling B (2), Priemé A (2, 3), Baldrian P (1), Voříšková J (1)

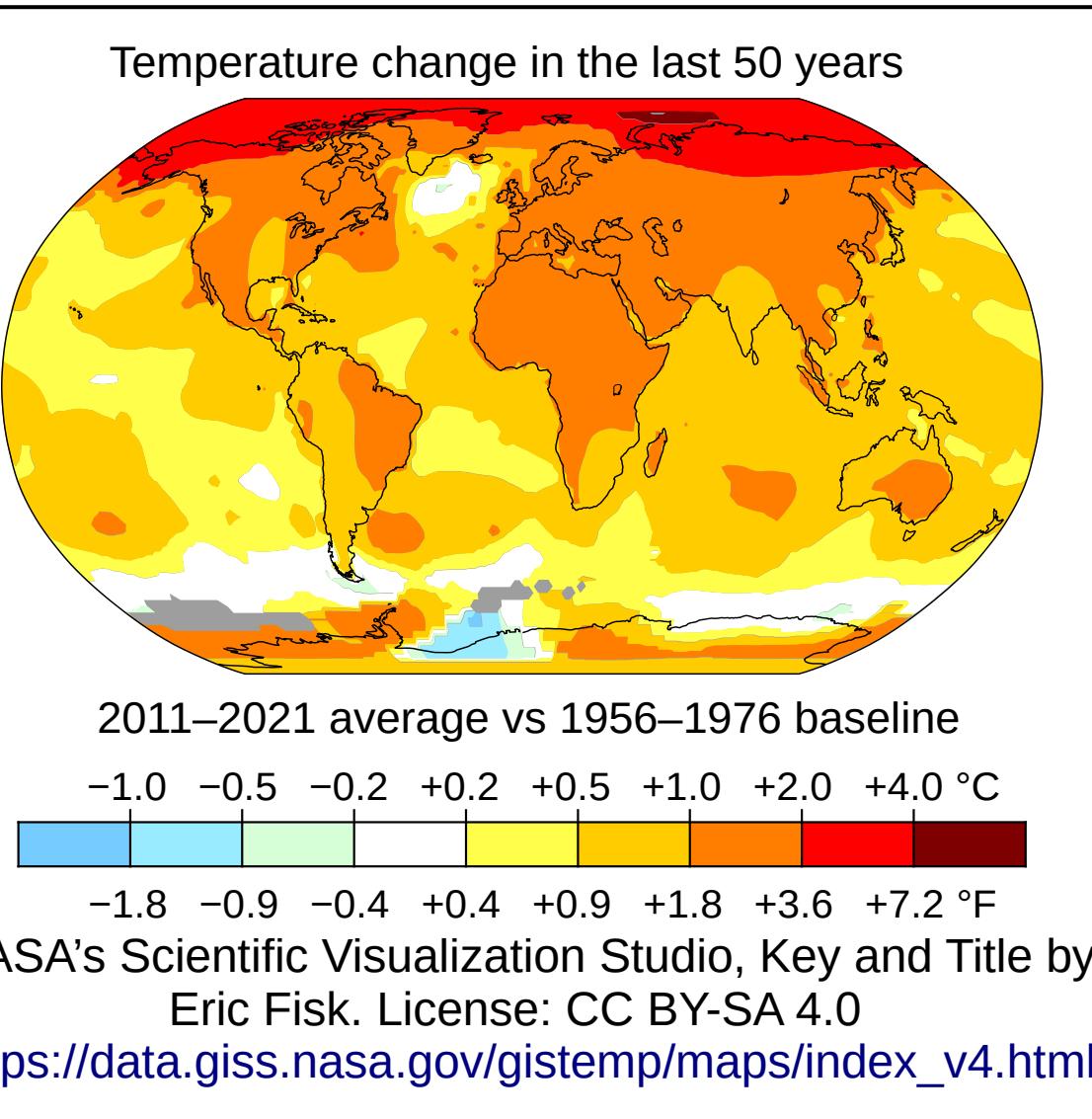
[1] Laboratory of Environmental Microbiology, Institute of Microbiology, Czech Academy of Sciences, Vídeňská 1083, 142 20 Prague 4, Czechia

[2] Center for Permafrost (CENPERM), University of Copenhagen Øster Voldgade 10, DK-1350 Copenhagen K, Denmark

[3] Section of Microbiology, Copenhagen University, Universitetsparken 15 DK-2100 Copenhagen Ø

Introduction: it has been 70 years since the first newspaper article [1], mentioning global warming as a side effect of human activities was published. To these days, and despite huge efforts to study this phenomena, we still know very little. However, global warming is affecting every place on Earth but some, such as the Arctic, are more affected than others and the effects are hard to predict. Arctic soils are huge carbon sinks and understanding whether their carbon stocks may be released in the atmosphere as greenhouse gases by microbial organisms adapting to new climate conditions, is fundamental.

Materials and Methods: the experimental site was established in 2015 and located in south Greenland (Narsarsuaq). Samples were collected in summer 2020, after five years of warming treatment. The site comprised climate manipulation treatments including summer warming (W), increased snow cover (S), their combination (SW), and untreated controls (C) set up in six replicates. Increased snow cover was induced through snow fences allowing increased snow accumulation while summer warming was induced through open-top chambers (OTCs). Soil samples were collected at three different depths and used for microbial community analysis via amplicon sequencing of 16S rDNA and ITS region, enzyme assays and quantitative PCR.



Narsarsuaq experimental site: snow fences and open top chambers. Pictures by Louise Hindborg Mortensen.

Table 1: all depths, bacteria - Model: *taxa ~ Treatment + Depth*

Treatment	Df	SumOfSqs	R2	F	Pr(> F)
Treatment	3	1753	0.03357	0.8483	0.728
Depth	2	5008	0.09591	3.6358	0.001
Residual	66	45457	0.87052		
Total	71	52218	1.00000		

Table 2: all depths, fungi - Model: *taxa ~ Treatment + Depth*

Treatment	Df	SumOfSqs	R2	F	Pr(> F)
Treatment	3	1063.0	0.04039	0.9737	0.147
Depth	2	1238.8	0.04707	1.7021	0.001
Residual	66	24017.6	0.91254		
Total	71	26319.4	1.00000		

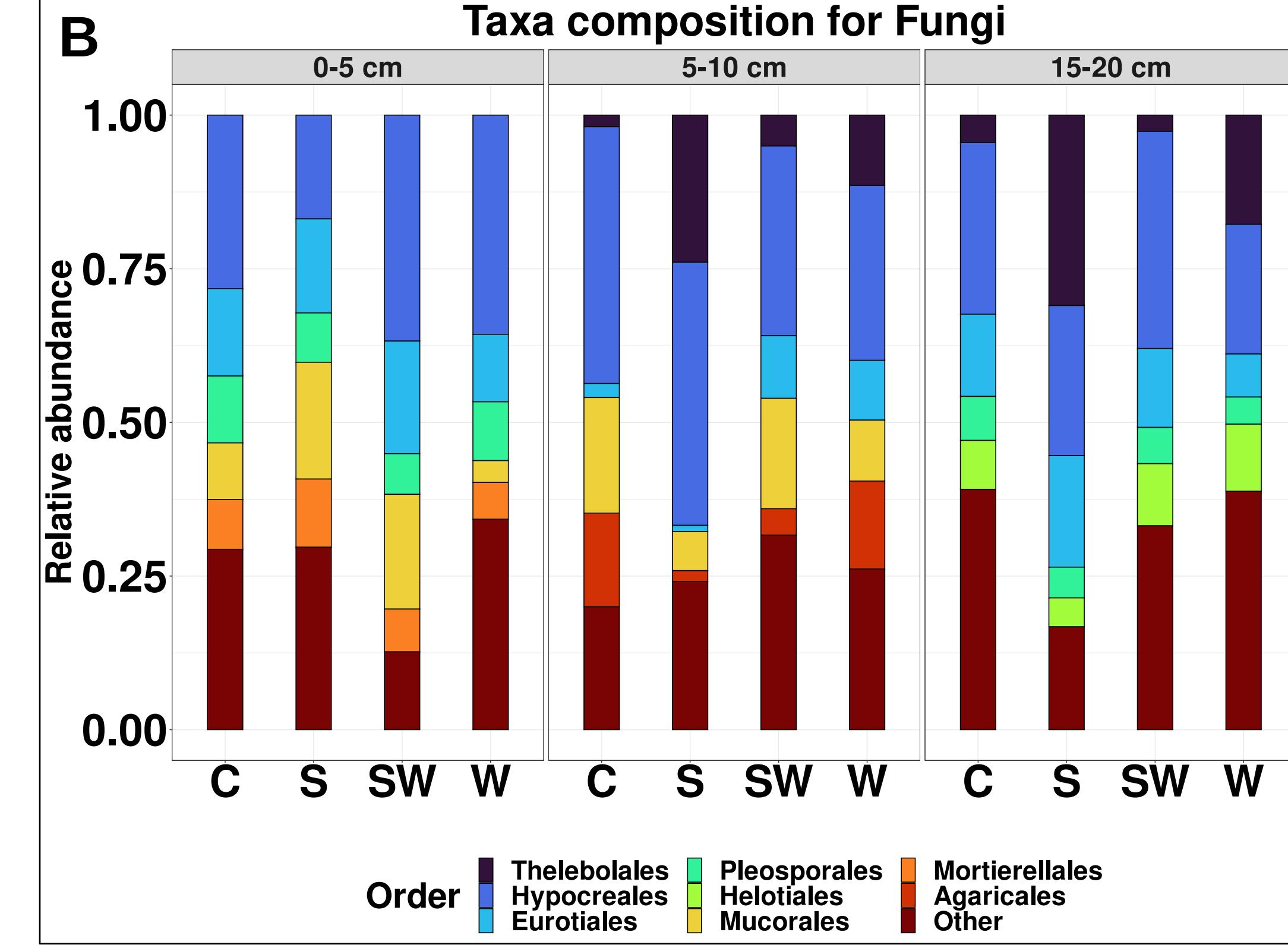
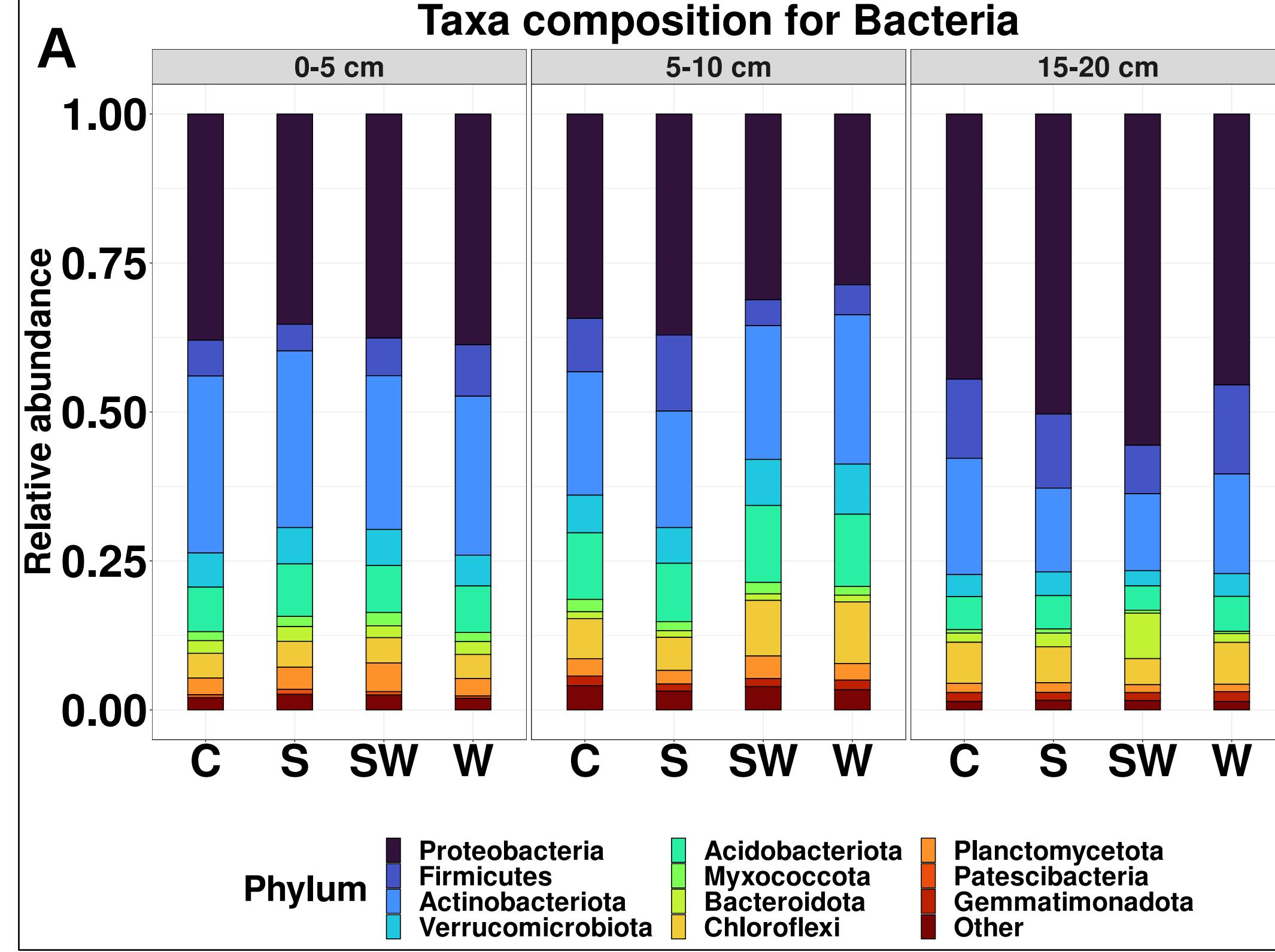
Tables 1 and 2 report the results of PERMANOVA test.

Conclusions - Depth was a major driver of both fungal and bacterial communities.

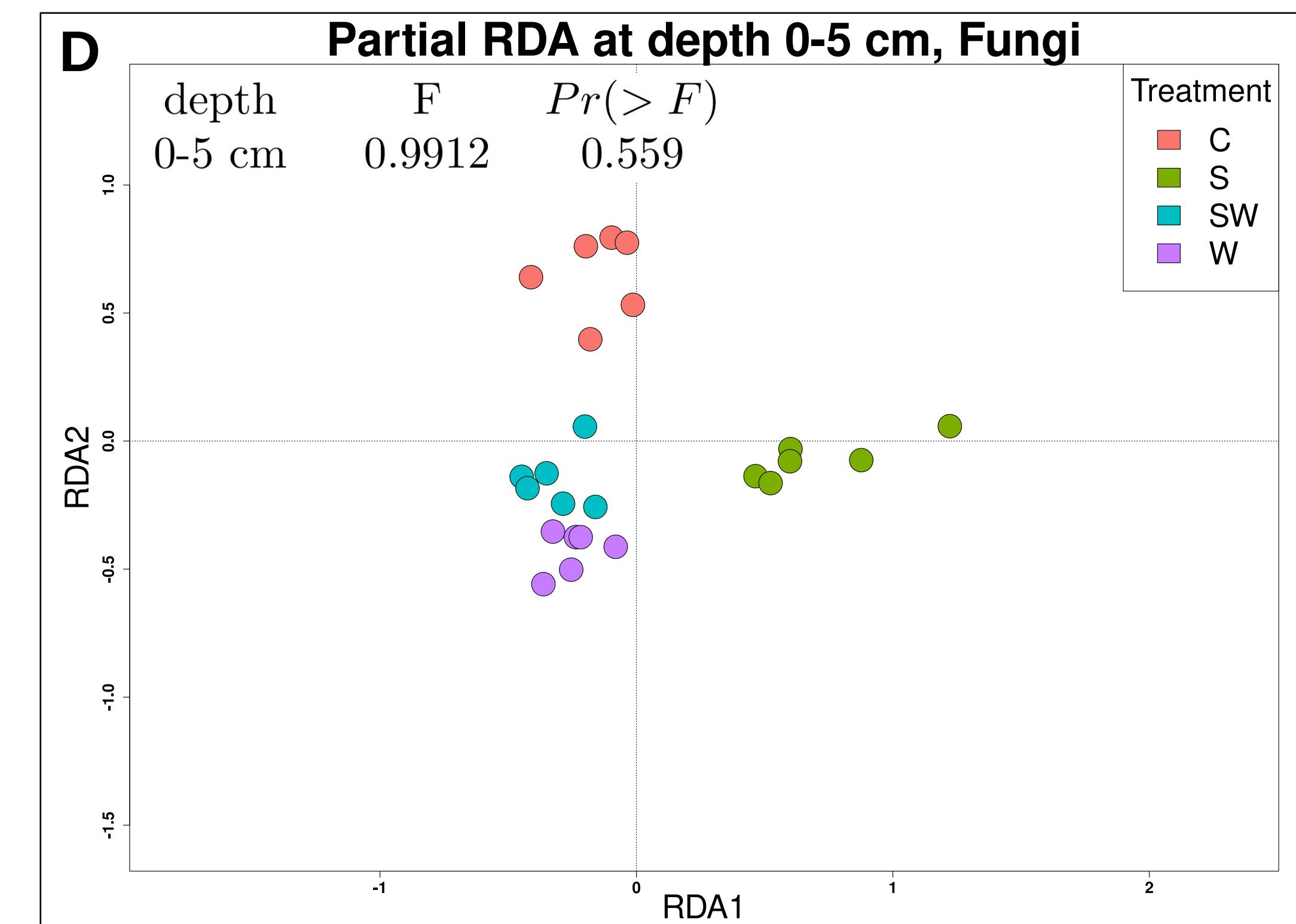
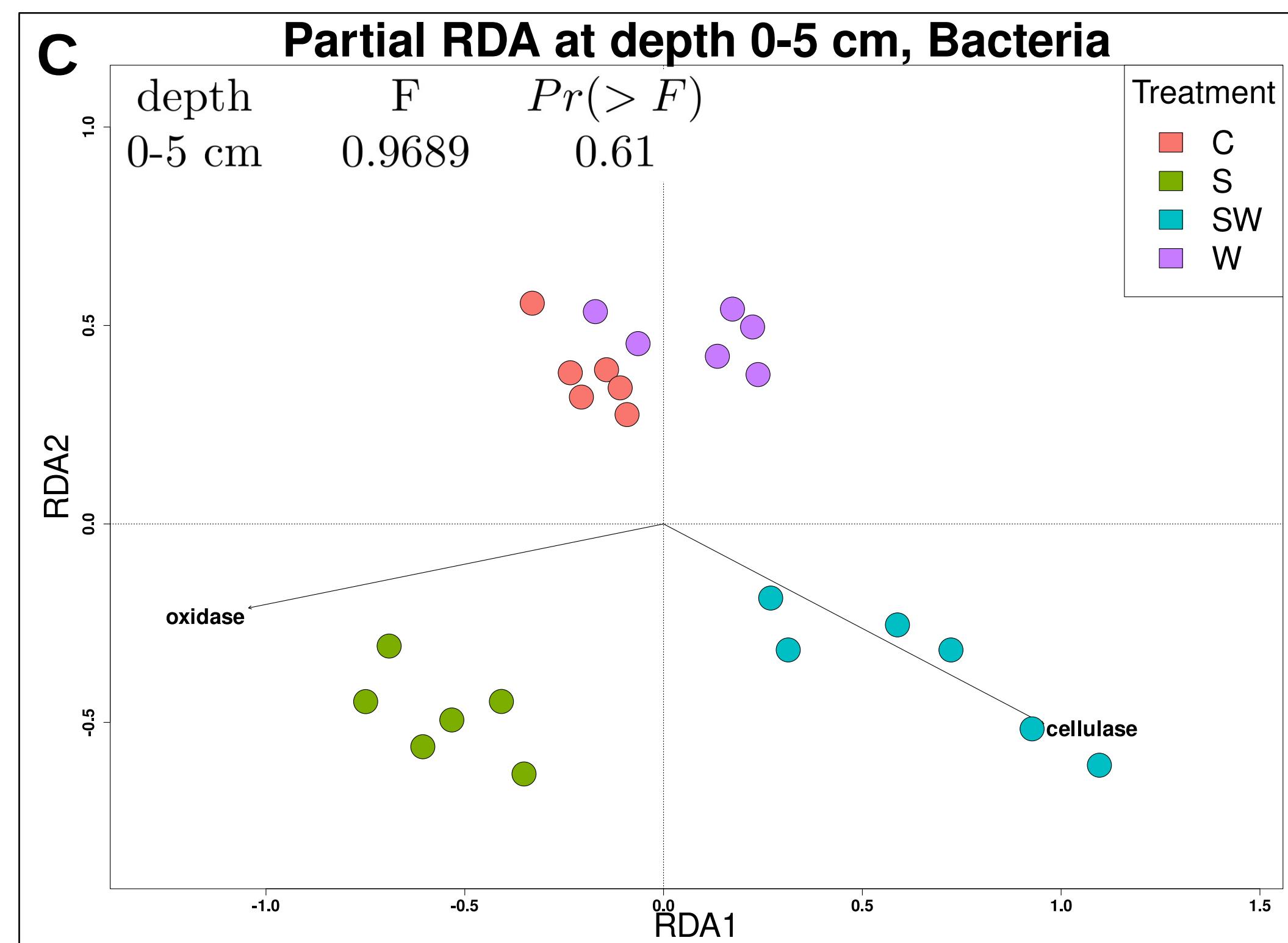
Partial RDA showed separation between different treatments, but no statistically significant difference was found.

Cellulase and oxidase were found significantly correlated with bacterial community. Specifically, cellulase was found correlated with bacterial community that underwent SW treatment while oxidase was found correlated with bacterial community that underwent S treatment. None of the tested enzymes was correlated with fungal community.

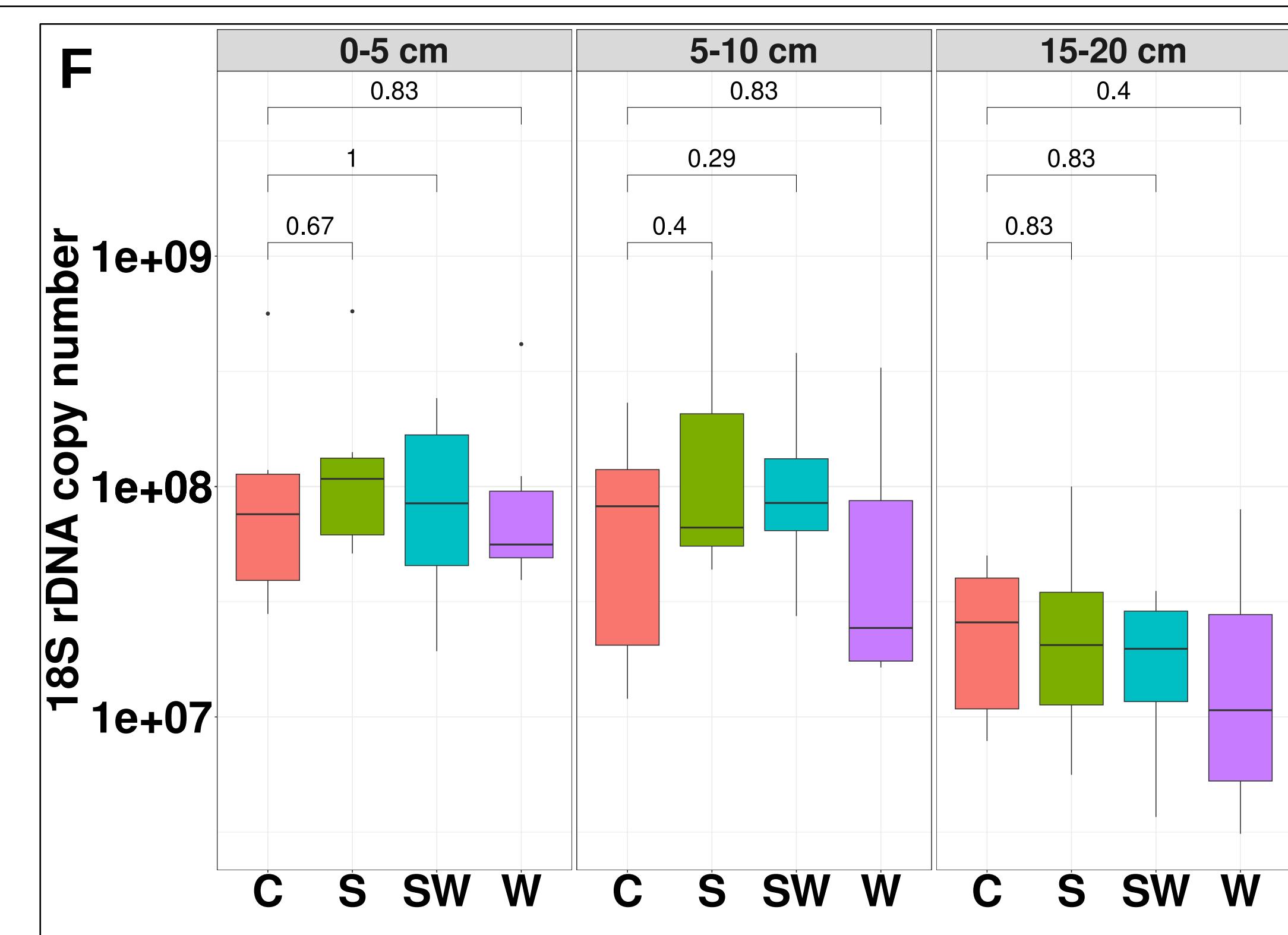
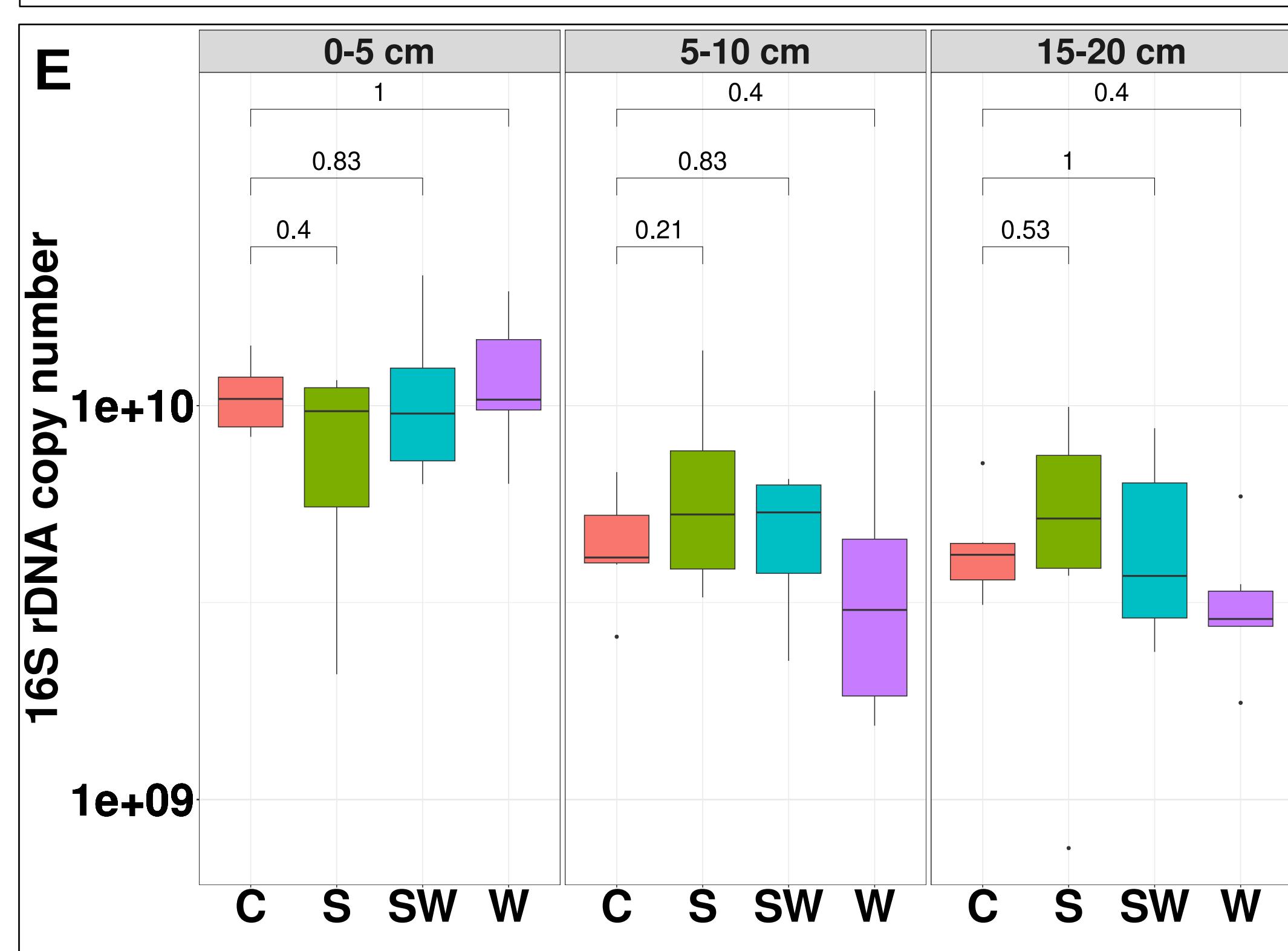
Copy numbers of 16S and 18S rDNA were higher in top layer and decreased with increasing depth. Treatment had no significant effect, at all depths.



Figures A and B show relative abundances and taxa composition for bacteria (Phylum level) and fungi (Order level), divided by treatment and depth. C = control, S = increased snow cover, SW = increased snow cover + summer warming, W = summer warming.



Figures C and D show partial redundancy analysis (RDA) performed on centered log ratio transformed abundances. The model used for this test included Treatment and Depth as fixed effects and sampling site as random effect. Environmental parameters were fitted on the partial RDA model. Those that were found statistically significant ($P\text{-value} \leq 0.1$) are shown in the plot as arrows. C = control, S = increased snow cover, SW = increased snow cover + summer warming, W = summer warming.



Figures E and F show the results from quantitative PCR analysis of 16S and 18S rDNA copy numbers. Plots are divided by treatment and depth. C = control, S = increased snow cover, SW = increased snow cover + summer warming, W = summer warming.

Acknowledgments - This work was supported by a grant to Center for Permafrost (CENPERM), from the Danish National Research Foundation (CENPERM DNRF100), and by Czech Science Foundation (21-19209M).

[1] The New York Times, 1953 <https://www.nytimes.com/1953/05/24/archives/how-industry-may-change-climate.html>