

Microbial community structure is distinct across the Holocene-Pleistocene boundary in ancient Beringian permafrost

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Purpose of the Research

The response of soil microbes to climate change is not well understood, and they might contribute more to release of greenhouse gases.

The fingerprints of past climate change since ice age have been preserved in permafrost sediments.

By tracing taxonomic and key metabolic changes in the ancient microbial community entrapped in permafrost, we might be able to reconstruct the past, assess the present and predict the future of these microorganisms and the key direct and indirect parameters that might cause them to rapidly respond to climate change as a consequence of increased temperatures.

Big Questions ?

1. How quickly do microbes change their taxonomic role in response to climate change?

2. What environmental parameters drive these changes?

3. Is the effect of climate change on microbes direct or indirect?

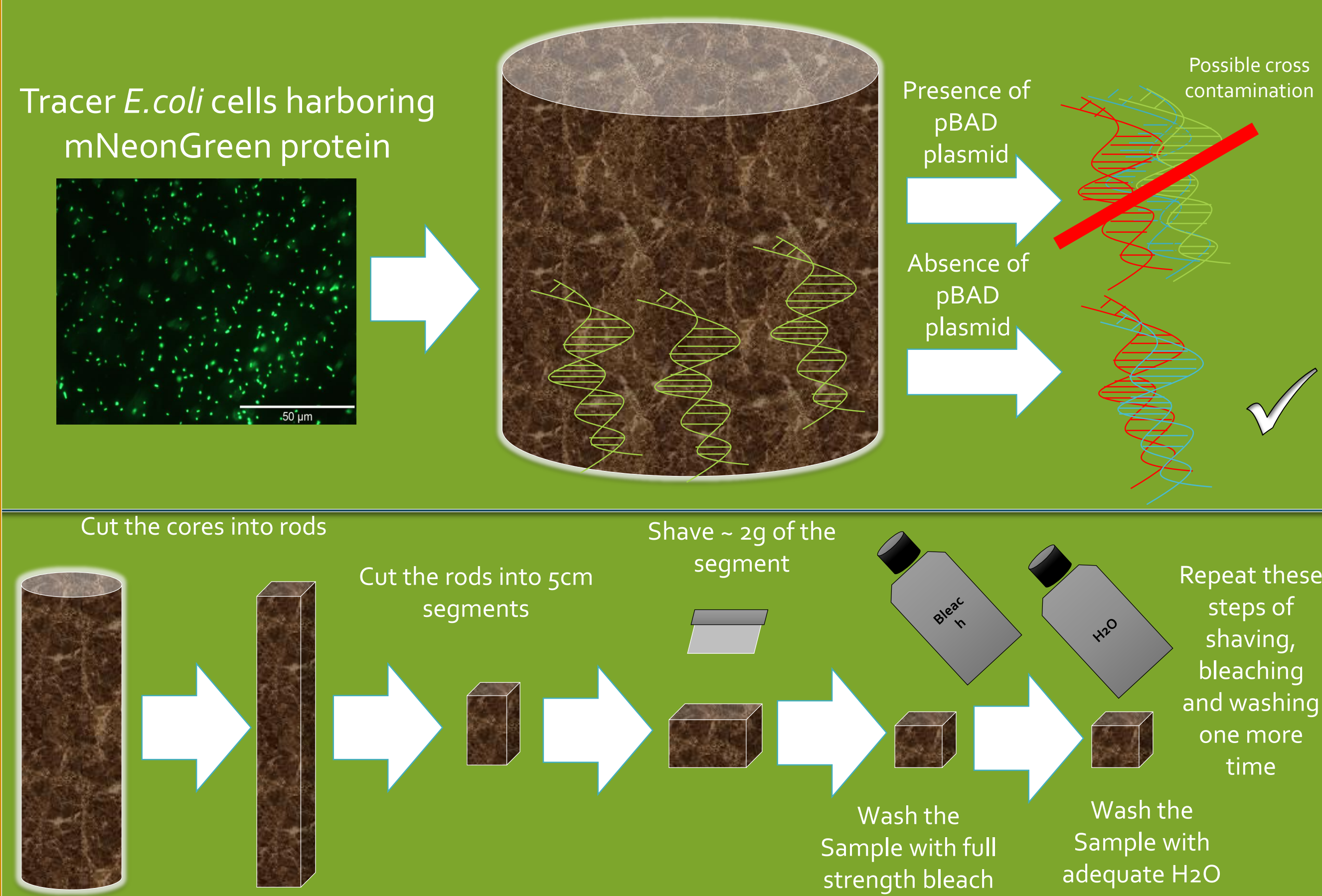
4. At what scale does climate change influence core microbial metabolic processes and nutrient cycling?



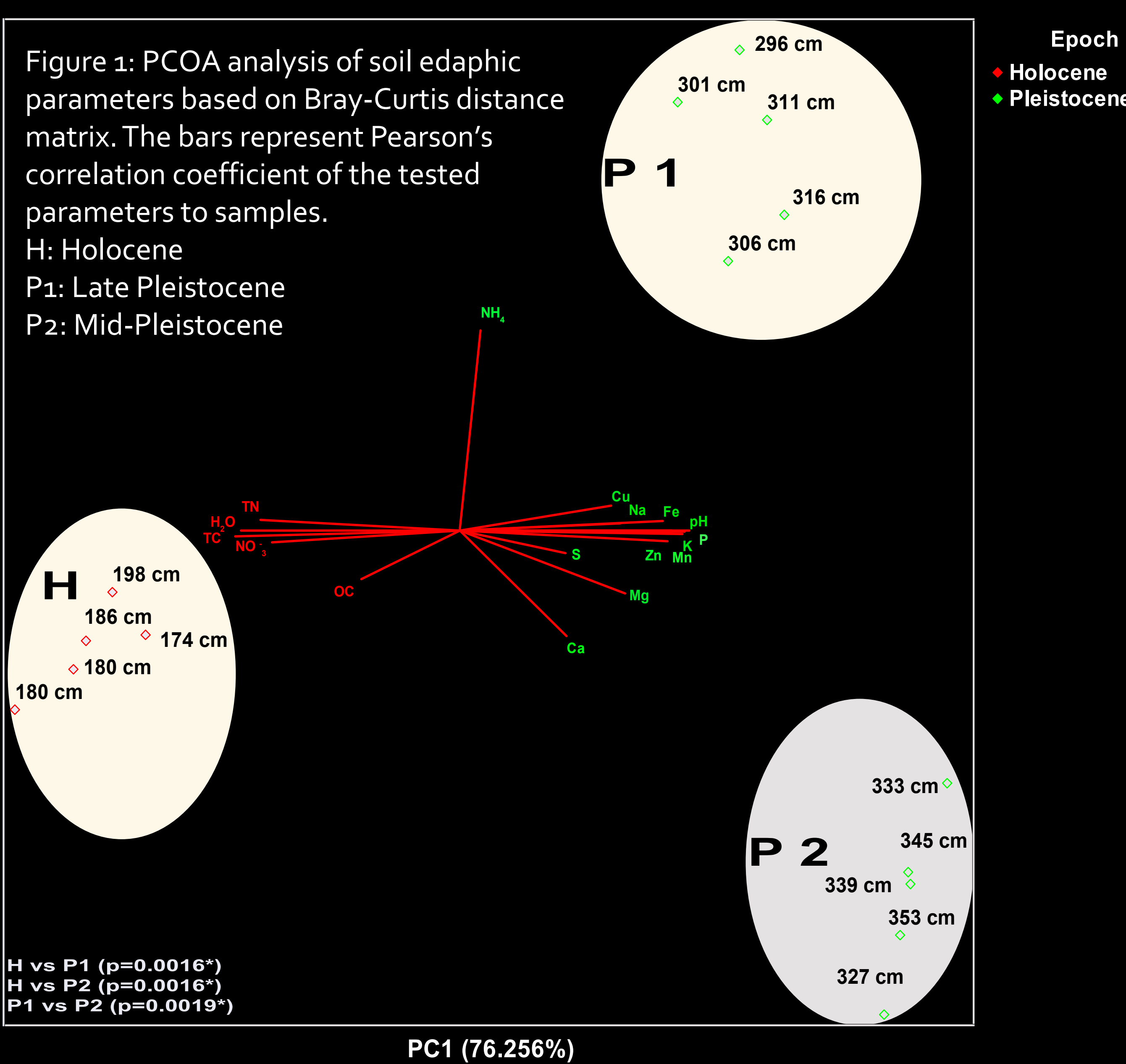
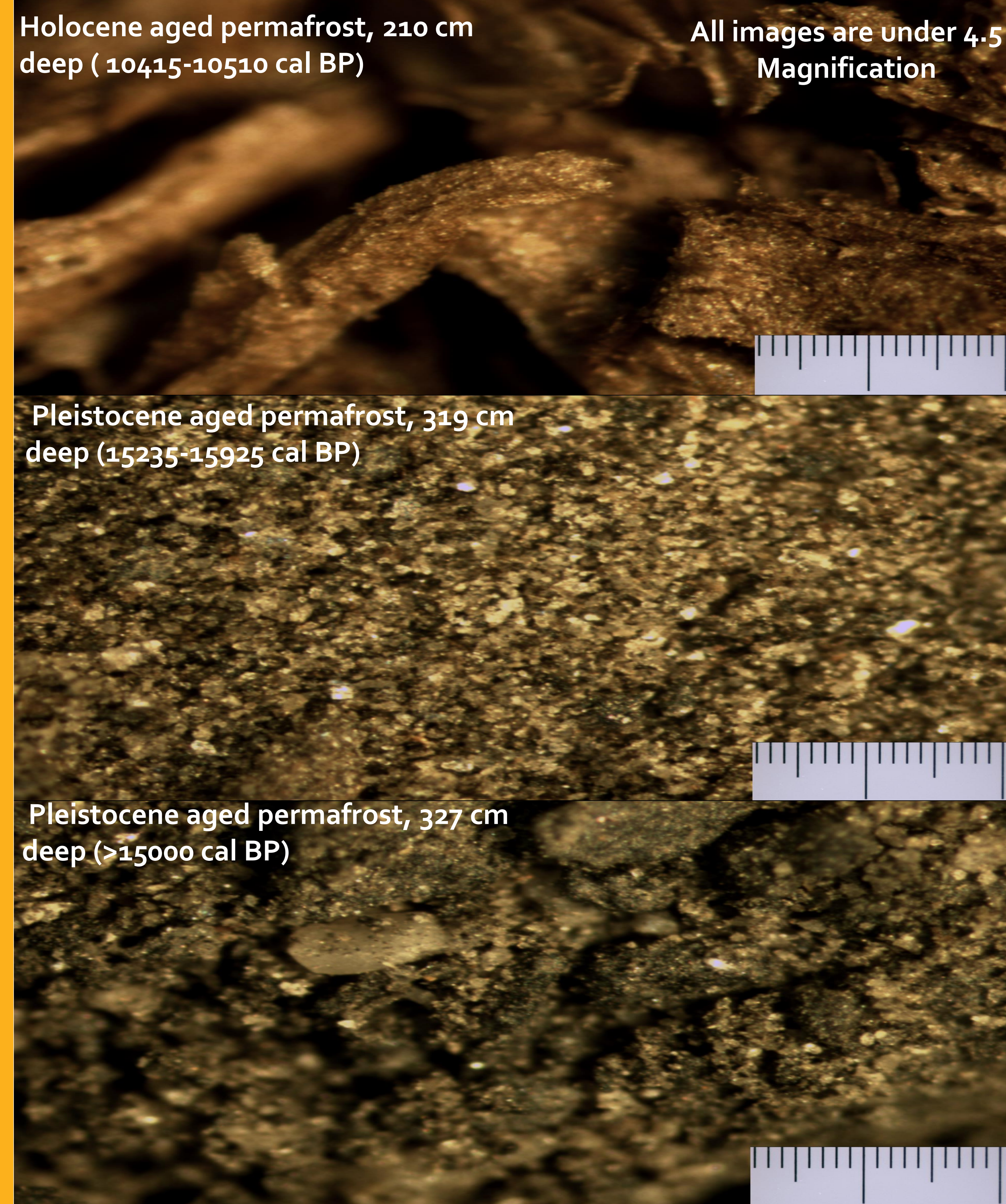
Hypothesis

The microbial community composition is different in Pleistocene aged (≥ 15 kya) permafrost in comparison to Holocene aged (~ 10 kya) permafrost.

Methods and Experimental Design



Results (Permafrost Physiochemical Parameters)



Results (Microbial Community Dynamics)

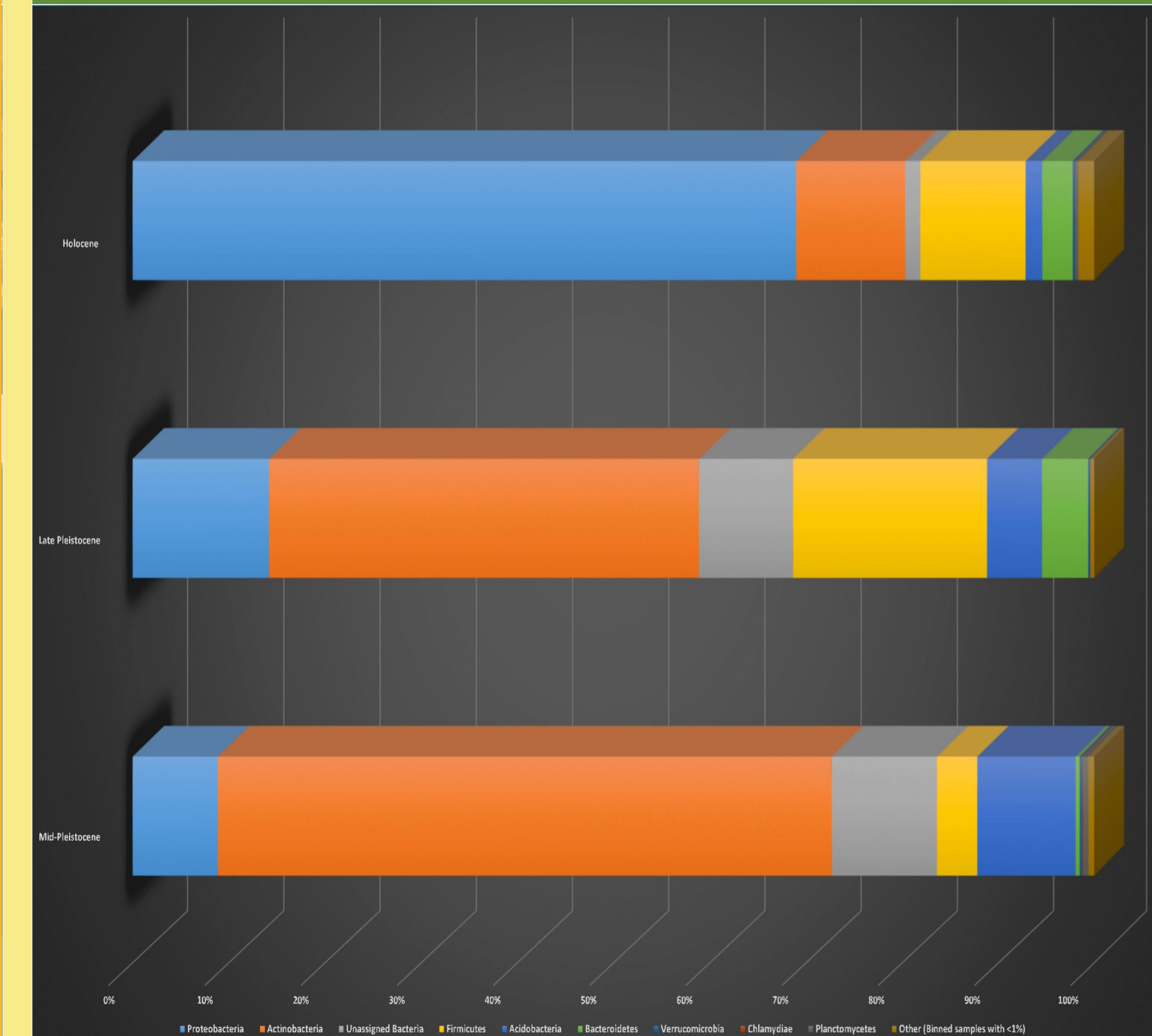
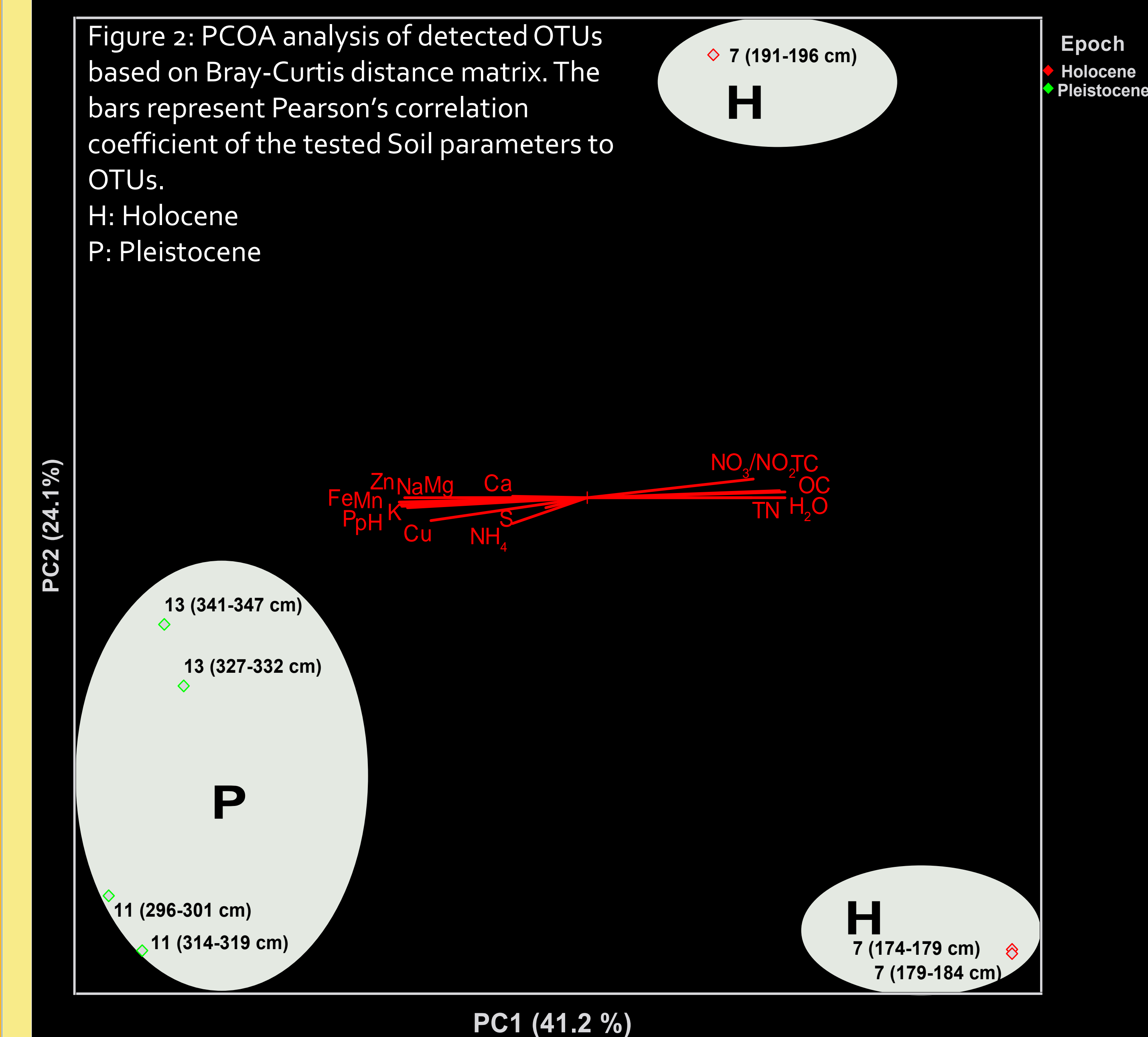


Figure 2: PCOA analysis of detected OTUs based on Bray-Curtis distance matrix. The bars represent Pearson's correlation coefficient of the tested Soil parameters to OTUs.



Acknowledgment

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Conclusion

- Soil physical and chemical (edaphic) parameters group samples by epoch (Holocene (H) vs. Pleistocene (P); surprisingly, Pleistocene aged samples also are separated into late Pleistocene (P₁) and mid-Pleistocene (P₂) (Figure 1). Based on these results, we predicted that microbial communities would be similarly separated.
- One measured environmental parameter that seemed to separate the P₁ and P₂ samples was NH₄ (Figure 1).
- While the microbial community separated into three groups (Figure 2), these were not the same three groups as observed for the edaphic parameters (Figure 1), but that they do separate by epoch (and that it is unclear what is driving the separation between the Holocene aged samples) (Figure 2).
- Based on this data, we predict that, in a changing modern climate, we are unlikely to see shifts in the microbial community structure unless there is a climate driven shift in the soil edaphic parameters. Such a shift could result in changes in the cryosphere, leading to local and global ecosystem change.