

Microbial community structure is stratified at the millimeter-scale across the soil-water interface

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The interface of terrestrial and aquatic ecosystems, such as the soil-water interface, are biogeochemical hotspots characterized by millimeter-scale redox gradients[1]. It is hypothesized that parallel changes are also present in microbial community structure and activity[3]. However, soil-based analyses of microbial community structure rarely consider variation at a scale relevant to environmental heterogeneities due to sampling approaches and analytical methods used[2,3]. In many cases, the interface is sliced into about 1cm layer to obtain sufficient material for microbiome analysis that may obscure the microbial community change[2]. Here we applied a 2mm soil sectioning method in a lab flooded soil incubation experiment and profiled the transcriptionally active members of the microbial community using the analysis of rRNA content [3]. At this fine-scale resolution, the active microbial community structure was consistent with the stratification of the biogeochemical properties (e.g. redox potential, nitrate)[3]. Also, the clear shifts in the relative abundance of transcriptionally active microbial populations are associated with the changing redox conditions[3]. Our results demonstrate that spatial scale should be carefully considered when investigating ecological mechanisms underlying the microbiome and identifying novel contributors to the cryptic biogeochemical process.

[1] McClain, Boyer, Dent, Gergel, Grimm, Groffman, et al (2003), *Ecosystems* 6, 301-312.

[2] Meyer, Memiaghe, Korte, Kenfack, Alonso, Bohannon (2018), *ISME Journal* 12, 1404-1413.

[3] Cai, Liu, Zhang, Liu, Nicol & Chen (2022), *ISME Communications* 2, 53.

