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Microbial life in soil – from aggregates to biomes

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Abstract:

Aqueous habitats in unsaturated soil are highly fragmented thus imposing constraints on bacterial dispersion and shaping interactions among spatially confined microbial species. We developed a hierarchy of modeling tools to represent key biophysical processes within soil pores and to study cell-level interactions and assembly of microbial communities. We show how species trophic dependencies in patchy diffusion fields give rise to collective spatial self-organization in pore networks (soil aggregates) where "hot spots" inhabited by aerobic and anaerobic bacterial communities support important biogeochemical fluxes. Experiments with tagged aerobic and anaerobic bacteria in glass-etched pore networks under oxygen and carbon cross-gradients confirm salient features of life in soil aggregates including new insights from detailed metabolic network models of metabolite exchanges among the populations. Results are upscaled to consider assemblies of aggregates and "hot spots" towards predicting fluxes of methane and NO_x from soil profiles and landscapes. The size distribution of aqueous habitats in unsaturated soils (and their connectivity) affects cell level interactions and exerts strong influence on soil diversity under different climatic conditions (biomes). A heuristic model for linking biome NPP and climatic water content towards predicting soil bacterial carrying capacity and richness provides a means for global mapping of bacterial diversity in good agreement with global observations. We identify sensitive regions with large diversity (across climatic transition zones) susceptible to climate and land use changes.