



## Experimental evidence of the role of pores on movement and distribution of bacteria in soil

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It has been generally recognized that micro-scale heterogeneity in soil environments can have a substantial effect on movement, fate, and survival of soil microorganisms. However, only recently the development of tools for micro-scale soil analyses, including X-ray computed micro-tomography ( $\mu$ -CT), enabled quantitative analyses of these effects. The long-term goal of our work is to explore how differences in micro-scale characteristics of pore structures influence movement, spatial distribution patterns, and activities of soil microorganisms. Using X-ray  $\mu$ -CT we found that differences in land use and management practices lead to development of contrasting patterns in pore size-distributions within intact soil aggregates. Then our experiments with *Escherichia coli* added to intact soil aggregates demonstrated that the differences in pore structures can lead to substantial differences in bacteria redistribution and movement within the aggregates. Specifically, we observed more uniform *E.coli* redistribution in aggregates with homogeneously spread pores, while heterogeneous pore structures resulted in heterogeneous *E.coli* patterns. Water flow driven by capillary forces through intact aggregate pores appeared to be the main contributor to the movement patterns of the introduced bacteria. Influence of pore structure on *E.coli* distribution within the aggregates further continued after the aggregates were subjected to saturated water flow. *E. coli*'s resumed movement with saturated water flow and subsequent redistribution within the soil matrix was influenced by porosity, abundance of medium and large pores, pore tortuosity, and flow rates, indicating that greater flow accompanied by less convoluted pores facilitated *E. coli* transport within the intra-aggregate space. We also found that intra-aggregate heterogeneity of pore structures can have an effect on spatial distribution patterns of indigenous microbial populations. Preliminary analysis showed that in aggregates from an organic agricultural system with cover crops, characterized by greater intra-aggregate pore heterogeneity, bacteria of Actinobacteria and Firmicutes groups were more abundant in presence of large as compared to small pores. In contrast, no differences were observed in the aggregates from conventionally managed soil, overall characterized by homogeneous intra-aggregate pore patterns. Further research efforts are being directed towards quantification of the pore structure effects on activities and community composition of soil microorganisms.