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Microaggregates as habitat for microorganisms

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Soils represent a major habitat for microorganisms and harbor the most diverse microbial communities on Earth. This is explained by spatial and compositional heterogeneity of the soil, which supports a broad range of spatially separated microniches for microorganisms. To get more insight concerning the question whether and to what extent soil microaggregates serve as bacterial habitat, we applied microscopic as well as molecular biological methods to analyze the bacterial colonization of microaggregates.

To visualize bacterial colonialization we applied life dead staining to soil particles using epifluorescence microscopy and the LIVE/DEAD BacLight Bacterial Viability Kit. A monochrome camera was used to image fluorescently labeled living as well as dead bacterial cells, while a color camera in combination with bright field microscopy was used to visualize soil particles in true colors. Pictures were taken in Z-stacks allowing to image the localization of bacterial cells linked to the topography of the different soil particles. To illustrate those Z-stacks, images were presented in advanced depth of focus, which means that all optical sections are merged into one focused picture. We observed a heterogeneous colonization of soil particles. Cells occurred frequently isolated, but seldom in micro-colonies or in larger aggregates. This applied to living as well as dead cells, both occurred mostly in a scattered manner on microaggregate surfaces.

Furthermore, we analyzed the bacterial community composition in dependence of soil size fraction and soil clay content to answer the questions if the spatial variability is reflected by soil aggregate structure, and how this variability is affected by clay content. Therefore, we analyzed the bacterial community composition in samples from a clay catena ranging from 19 to 35 % clay content. The soil samples were size fractionated by wet sieving resulting in 10 size categories between <8000 μm for the largest and <20 μm for the smallest fraction. For the analysis of the bacterial community composition, DNA was extracted, the 16S rRNA gene amplified, and the PCR products were sequenced using Illumina technology. First results suggest that soil aggregate size does affect microbial communities.