



Clay mineral contents shape the bacterial community composition and the production of extracellular polymeric substances

Antje Bettermann (1), Doreen Babin (1), Karsten Kalbitz (2), Kornelia Smalla (1), and Cordula Vogel (2)

(1) Julius-Kuehn-Institut, Institut für Epidemiologie und Pathogendiagnostik, Braunschweig, Germany (antje.bettermann@julius-kuehn.de), (2) Institute of Soil Science and Site Ecology, Technical University of Dresden, Tharandt, Germany

Extracellular polymeric substances (EPS) are the most important constituents of bacterial biofilms. EPS impart several functions for microbial life, e.g. promoting microbial adhesion to surfaces and increasing the tolerance to harsh environmental conditions. Together with the respective soil properties, EPS produced by soil bacteria are also supposed to contribute to soil aggregation. However, there is little knowledge about the relations among the composition of the soil and the residing bacterial community, the amount of bacterial EPS produced and the extent of its influence on soil aggregation. Therefore, the interrelationships between the amount of fine-sized particles (clay content), the decomposability of organic matter and the bacterial community composition were studied. It was hypothesized that an increased microbial activity, induced by organic matter input (starch or cellulose) will stimulate EPS production depending on the clay content in the soil. We conducted an incubation experiment (20°C and 50% WHC) with a sandy arable topsoil spiked with either starch or cellulose as substrate source over 80 days. Different amounts of montmorillonite were added to the soils to build a gradient of clay contents (+0, 0.1, 1, 10%). The CO₂ respiration, microbial biomass, EPS content and soil aggregation were measured over the incubation time. In addition, the composition of the bacterial communities was assessed by denaturing gradient gel electrophoresis (DGGE) and Illumina high-throughput sequencing of bacterial 16S rRNA genes amplified from total community DNA. DGGE fingerprinting showed that the bacterial community changed over the incubation time. Pronounced shifts in the microbial community composition have been found for the soil with highest clay mineral addition after 10 and 20 days of incubation compared to soils without clay addition. In contrast, the different organic matter substrates had no strong influence on microbial community composition. 16S rRNA gene sequencing revealed that the relative abundance of the phylum Firmicutes was enhanced by spiking of starch to the soil. However, this effect was depending on the amount of clay added. On lower taxonomic rank, a number of different bacterial genera enriched in response to the different treatments were identified. The EPS contents were shaped by the clay mineral contents with distinct dynamics in EPS concentrations over time. These results will especially provide insights into how shifts in the soil bacterial community composition may affect EPS production and their consequences for soil aggregation.