

Do bacteria shape the soil structure by EPS production?

Antje Bettermann¹, Jeroen Zethof², Cordula Vogel², Broder Rühmann³, Volker Sieber³, Karsten Kalbitz² and Kornelia Smalla¹

¹ Julius Kühn Institute, Institute for Epidemiology and Pathogen Diagnostics, Braunschweig

² Technische Universität Dresden, Institute of Soil Science and Site Ecology, Tharandt

³ Technical University of Munich, Straubing

E-mail of corresponding author: antje.bettermann@julius-kuehn.de

Erosion is considered to be one of the most important processes contributing to soil degradation. Soil microbial communities are shaped by vegetation and plant exudates are known as major drivers of the development of the microbial community composition in the vicinity of the roots. Microorganisms produce diverse extracellular polymeric substances (EPS) that are assumed to contribute to soil aggregation and thus may have important implications for soil erosion. We hypothesize that the amount and diversity of microbially produced EPS is plant- and soil type dependent.

Soil samples were taken at two semi-arid field sites in Almería Province, Spain. Both sites were located on moderately steep slopes, with a micaceous substrate that was either rich or poor in carbonates. Soils at both sites are particularly prone to erosion as under the semi-arid climate conditions plant density is low. At each of the sites, five hydrological disconnected plots were defined. Within each plot, one *Anthyllis cytisoides* individual and one *Macrochloa tenacissima* tussock was chosen which are abundant plants at both field sites. Around the plants, a gradient in distance to the stem/outer border of the tussock perpendicular to the hillslope was sampled to a depth of 5 cm, avoiding the sieving crust. The samples were subjected to extraction and characterization of EPS as

well as to extraction of total microbial community – DNA and plated onto R2A medium in order to determine colony forming units as well as to isolate randomly picked bacterial colonies. The 400 bacterial isolates were transferred to a biofilm inducing medium. Obviously well growing strains were then screened for the composition of produced exopolysaccharides – an important part of EPS. The isolates were identified by sequencing of the 16S rRNA gene. The composition of the total soil bacterial communities was assessed by PCR-DGGE (denaturing gradient gel electrophoresis) of 16S rRNA gene fragments amplified from total community DNA. DGGE revealed changes in the bacterial communities depending on the distance to the plant as well as depending on the soil type of the respective sites. Among the 225 isolates, 67 were able to synthesize exopolysaccharides, 45 of which could be identified. These exopolysaccharide producers were affiliated to the four major phyla detected in soil: Actinobacteria, Firmicutes, Bacteroidetes and Proteobacteria. Their occurrence was linked stronger to the plant species than to the respective soil.

Linking soil properties to bacterial communities, total EPS and particularly exopolysaccharide production will provide a better understanding of processes leading to soil aggregation and erosion.