

EGU2020-9707

<https://doi.org/10.5194/egusphere-egu2020-9707>

EGU General Assembly 2020

© Author(s) 2021. This work is distributed under the Creative Commons Attribution 4.0 License.



Spatial sampling approach to unravel the impact of soil texture and root genotype on maize root gene expression profiles

Minh Ganther¹, Marie-Lara Bouffaud¹, Lucie Gebauer¹, François Buscot¹, Doris Vetterlein¹, Anna Heintz-Buschart^{1,2}, and Mika Tarkka¹

¹Helmholtz-Centre for Environmental Research – UFZ, Halle, Germany

²German Centre for Integrative Biodiversity Research (iDiv) Halle–Jena–Leipzig, Leipzig, Germany

The complex interactions between plant roots and soil microbes enable a range of beneficial functions such as nutrient acquisition, defense against pathogens and production of plant growth hormones. The role of soil type and plant genotype in shaping rhizosphere communities has been explored in the past, but often without spatial context. The spatial resolution of rhizosphere processes enables us to observe pattern formation in the rhizosphere and investigate how spatial soil organization is shaped through soil–plant–microbiome interactions.

We applied spatial sampling in a standardized soil column experiment with two maize genotypes (wildtype vs. *roothairless3*) and two different soil textures (loam vs. sand) in order to investigate how in particular functions of the maize roots relating to nutrient/water uptake, immunity/defense, stress and exudation are affected. RNA sequencing and differential gene expression analysis were used to dissect impact of soil texture, root genotype and sampling depth. Our results indicate that variance in gene expression is predominantly explained by soil texture as well as sampling depth, whereas genotype appears to play a less pronounced role at the analyzed depths. Gene Ontology enrichment analysis of differentially expressed genes between soil textures revealed several functional categories and pathways relating to phytohormone-mediated signaling, cell growth, secondary metabolism, and water homeostasis. Community analysis of rhizosphere derived ACC deaminase active (*acdS* gene including) plant beneficial bacteria, which suppress the phytohormone ethylene production, suggests that soil texture and column depth are the major factors that affect *acdS* community composition.

From the comprehensive gene expression analyses we aim to identify maize marker genes from the relevant core functional groups. These marker genes will be potentially useful for future experiments; such as field plot experiments for investigation of later-emerging plant properties.

This research was conducted within the research program “Rhizosphere Spatiotemporal Organisation – a Key to Rhizosphere Functions” of the German Science Foundation (TA 290/5-1).