

Impact of long-term agricultural management practices on the rhizosphere microbiome and plant health

Doreen Babin (1), Soumitra Paul Chowdhury (2), Martin Sandmann (3), Loreen Sommermann (4), Johanna Nelkner (5), Saskia Windisch (6), Andreas Fließbach (7), Paul Mäder (7), Andreas Schlüter (5), Günter Neumann (6), Jörg Geistlinger (4), Michael Rothballer (2), Kornelia Smalla (1), and Rita Grosch (3)

(1) Julius Kühn-Institut, Federal Research Centre for Cultivated Plants (JKI), Institute for Epidemiology and Pathogen Diagnostics, Braunschweig, Germany, (2) Institute of Network Biology, Helmholtz Zentrum München, German Research Center for Environmental Health, Germany, (3) Leibniz Institute of Vegetable and Ornamental Crops (IGZ), Großbeeren, Germany, (4) Institute of Bioanalytical Sciences (IBAS), Anhalt University of Applied Sciences, Bernburg, Germany, (5) Center for Biotechnology (CeBiTec), Bielefeld University, Germany, (6) Institute of Crop Science (340h), University of Hohenheim, Stuttgart, Germany, (7) Research Institute of Organic Agriculture (FiBL), Frick, Switzerland

Increasing food and energy demands have resulted in a considerable intensification of farming practices, which brought about severe consequences for agricultural soils during last decades. In order to maintain soil quality and health for the future, the development of more extensive and sustainable farming strategies is urgently needed. The soil and rhizosphere microbiome play an integral role in virtually all soil processes and are intimately linked to plant performance. Various studies indicated that agricultural management practices affect soil microbiomes. We therefore hypothesized that this external impact is conveyed by the microbial communities to the current crops at the time of their establishment. We used twelve differently managed soils from three long-term field trials established in 1978 (Therwil, Switzerland), 1992 (Bernburg, Germany), and 2006 (Thyrow, Germany) to analyze the impact of various management strategies (crop rotation, fertilization, tillage) on soil and its associated rhizosphere microbiomes under consideration of plant productivity, plant health, and the ability of the soils to suppress soil-borne phytopathogens. The model plant lettuce (Lactuca sativa L.) was cultivated for ten weeks under growth-chamber conditions in these soils. High-throughput sequencing of bacterial 16S rRNA genes or fungal ITS fragments, respectively, PCR- amplified from total community DNA of rhizosphere and soil samples showed significant differences in microbial community compositions between soils that originated from the different field sites and long-term farming practices. Moreover, differences depending on long-term agricultural management in plant productivity and health as measured by RT-qPCR of stress-related plant genes were observed. Localized analysis of rhizosphere soil solution was performed using non-invasive sampling techniques with sorption filters placed onto the surface of soil-grown roots along the root observation windows with subsequent HPLC-MS profiling. Amino acids, sugars and antifungal organic acids such as benzoic acid detected in the rhizosphere soil solutions confirmed variations in concentrations depending on the site and management practice indicating different stress potentials of farming practices for plants. Agricultural management also affected soil suppressiveness to the soil-borne model pathogen Rhizoctonia solani.

Under controlled growth chamber conditions, we could show the legacy of long-term agricultural management practices on the establishment and performance of a subsequent plant generation and its associated rhizosphere microbiome.