

What is a healthy soil microbiome? The search for baselines and indicators as revealed by PCR-amplicon analyses

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INTRODUCTION

Soil microbiomes are highly diverse communities of bacteria, archaea, protists, fungi and viruses, which together provide important ecosystem functions, i.e. the biogeochemical cycling of carbon and nitrogen. In agroecosystems they provide the foundation to a sustainable use of soils for food and feed production. However, along with an agricultural intensification during the last 50 years, the sustainable use of soils is increasingly threatened, mainly due to chemical pollution with excessive loads of fertilizers and pesticides and soil erosion as a consequence of deep ploughing and increasing field sizes. In order to counteract these trends with more sophisticated and intelligent management practices it is important to evaluate responses of the microbiome and promote stabilisation of their beneficial ecosystem services. But what distinguishes a good, healthy or valuable microbiome from a poor one? In order to answer this question, patterns along which soil microbial diversity evolves and responds to external physical, chemical or biological forces must be revealed and mechanisms promoting microbial adaptation and resilience identified.

METHODOLOGY

The composition and potential functionality of the soil microbiome is characterised here by amplifying structural and functional marker genes using highly conserved primers with PCR. This yields specific DNA from the majority of soil microorganisms, even if their identity is unknown. Total DNA is extracted and purified from soil samples, usually from 0.5 g, but, for specific questions preferably from as little as 1 mg. Real-time qPCR then serves to quantify the number of target genes in a sample and thereby estimate their abundance. Furthermore, the same gene targets are subjected to massively parallel amplicon sequencing, e.g. on an Illumina MiSeq platform, for determining their identity. Target genes or sequences include the prokaryotic 16S rRNA genes for bacteria and archaea, 18S rRNA genes for protists, ITS sequences for fungi, and, depending on the objective, also functional genes responsible for specific ecosystem services, e.g. for denitrification.

RESULTS

By evaluating the microbial community composition of different soil particle size fractions (clays, silt, sand, organic particles) we could demonstrate that a majority of soil bacteria and fungi exhibit specific preferences. In the future, this may allow for predictions regarding the presence of specific microbial taxa depending on soil texture. A comparison of different land use sites across Europe revealed the importance of readily available soil organic carbon fractions for structuring the microbiome. Analysing rhizosphere and non-rhizospheric soils in the presence and absence of added straw material revealed that both soil microhabitats exhibited contrasting responses of the microbiome to salinity stress, emphasising that ecological niches must be considered when interpreting microbiome data. For an environmental risk assessment, we compared the structural and functional diversity of rhizosphere inhabiting microbiomes of genetically modified and non-modified maize and potatoes both cultivated at different sites in Europe. In an ongoing project on monitoring biodiversity in German agroecosystems (<https://agrarmonitoring-monvia.de/en/>) we evaluate the importance of soil storage conditions and season

DISCUSSION

At higher phylogenetic ranks, the composition of soil microbiomes is similar, but microhabitat conditions and the presence of energy rich nutrients have a dramatic effect on their constituting taxa and diversity. This is indicated e.g. by seasonal community dynamics on arable fields, or contrasting compositions in rhizosphere and non-rhizospheric soils. Thus, the change of a microbiome cannot per se act as an indicator of vulnerability or damage. Based on our own research results we propose to consider specific members of the microbiome as indicators, e.g. those that are less abundant and oligotrophic, and/or arbuscular mycorrhizal fungi. Additional information on the functionality of the microbiome and their response to stressors can be gained from multivariate statistics and network analyses, including taxa compositional but also environmental data. – Overall, our studies emphasise the strength of amplicon-based microbiome analyses for developing tools to assess the diversity, functionality and vulnerability of the soil microbiome. Including such information can be highly instructive to develop and evaluate the environmental friendliness of future agricultural management options.