



Molecular microbial indicators of land use change and their functional role in soil ecosystems

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Land use is known to alter soil physical and chemical properties as well as impact on microbial communities in soils, which in combination can change soil ecosystem services. To optimise soil management for enhanced ecosystem services, we need to determine the explicit relevance of management driven diversity change for the resilience of soil functionality. Furthermore, from a regulatory and monitoring perspective, we need to better identify functionally relevant molecular indicators of land use change in order to evaluate the progress of land restoration.

In this presentation, I assess the responses of a variety of soil, microbial and functional metrics to land management across a geographically distributed range of calcareous soil systems in the South of England. Their high levels of above and belowground diversity and the capacity to store large amounts of carbon are typical characteristics of calcareous grassland soils. In a landscape scale survey of old undisturbed grasslands, nearby croplands and a corresponding chronosequence of restored ex-arable grasslands, the recovery of soil was compared with microbial and plant community structures along a time gradient.

DNA amplicon sequencing, microbial biomass and soil extracellular enzymatic activities are used to detect changes in the ecosystems with re-conversion of arable fields. All grasslands show higher organic matter contents than the arable fields, with a clear trend in increase with restoration time.

Between treatments, land use specific differences in microbial communities are detected and significant bacterial and fungal indicators were determined on the species (OTU) level. Hydrolytic enzyme activity did not follow that classification as clearly, but interacted with soil chemistry and each other, indicating the complexity of these ecosystem functions that impact soil nutrient cycling and fertility.