Networks of soil biota in a secondary succession gradient: Is it biodiversity or network structure that determines soil function?

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Land abandonment is considered an effective tool for restoring biodiversity and ecosystem functions. However, thus far little attention is given to the role of soil biodiversity. Here, we present results of a soil biodiversity development and ecosystem functioning from a chonosequence of ex-arable fields in The Netherlands. These fields are typically managed by low-intensive grazing while undergoing a transition from an arable system into a species-rich grassland. We manipulated soil biodiversity to be able to couple biodiversity loss to loss of soil functions. We hypothesized that biodiversity loss would lead to less N uptake by plants and slower C transfer to microbes. A greenhouse mesocosm experiment was performed in which sterilized soils from the chronosequence were re-inoculated with a dilution series of soil suspensions (filtered to include only bacteria, fungi and protozoa) to manipulate soil diversity. These mesocosms were planted with a community of plants that naturally occur in all of the grasslands along the chronosequence. We measured microbial community development with TRFLP and sequencing, plant C, N and biomass and using dual labelled 15N ammonium nitrate ($15NH_415NO_3$) and 13C in the form of $13CO_2$ fed to the plants to assess the short term fate, turnover and retention of recent plant assimilated carbon and nitrogen in soil. The faith of the C and N were followed by sequential sampling of aboveground and belowground plant tissues and soil bacterial and fungal PLFA and NLFA biomarkers. With the first method the role of microbial diversity and soil on plant carbon assimilation and nitrogen uptake was evaluated. This was further related to the amount of recently photosynthesized carbon plants allocated to different microbial groups in soils. Microbial end-communities were pyrosequenced to evaluate the end diversity. In this study we showed the effects of the loss of soil biodiversity to C and N cycling in plants and microbes.

Next to this manipulative experiment we did a field sampling of intact soil cores within the same chronosequence of ex-arable fields. We identified bacteria and fungi by pyrosequencing, while archaea were identified using TRFLP. The protists, micro-fauna, nematodes, enchytraeids and earthworms were extracted and morphologically identified until high taxonomic levels, often species level. In total, around 15 000 species were identified from the soils. We created a Spearman-rank correlation matrix based on abundance data of species which we visualized in a network categorized as recent, mid-term and long-term abandoned fields as an overview of the soil community present. After stable isotope probing using similar methods the soil food web structure was resolved by identifying the microbes using phospholipid markers and identifying soil fauna by morphology into similar groups as for the network analysis, both combined with isotopic measurements. We show that structural changes in the food web topology also leads to functional changes in the soil food web which can act as a driving force during land use change after human disturbance.