Effects of land use change on soil microbial functioning in a long-term agroforestry system

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Introduction

Agroforestry is an agricultural land use management practice that can be described as the integration of trees with livestock and/or crops and has been demonstrated to provide multiple ecosystem service benefits such as improvements to soil, water, and air quality, as well as benefits to agronomic and livestock production. However, it is uncertain how historical changes in land use and land management within these systems can affect wider soil microbial community composition, abundance and functioning and therefore the potential impact on regulating processes such as soil nutrient cycling and carbon sequestration. This study tested the hypothesis that a change in land management will fundamentally alter soil processes and the ability of the ecosystem to deliver specific biological functions.

Methods

Shotgun metagenomic characterisation of soil samples from a long-term agroforestry site in the United Kingdom, that had experienced transitional management over time, were compared to i) permanent grassland and ii) woodland control plots to assess both variation in microbial taxa and potential functionality of microorganisms with a view to assessing ecosystem sustainability and resilience. The taxonomic and functional profiling as well as the relative abundance in each experimental plot were quantified at the phylum level. DNA data quality was evaluated using Nanodrop, Qubit and Gel electrophoresis. Minimum read length was 20bp. Microbiome functional capacity was then profiled across soil samples using KEGG Orthology (KO) modules and EC (Enzyme Commission) numbers for "carbon metabolism" and "nitrogen metabolism", grouped by type of compound they metabolise.

Preliminary Results and Discussion

5500 unique species were detected in total across the different land uses: 160 Archaea, 5259 Bacteria, 75 Eukaryota and 8 viruses. Of these 3967 have a mean relative abundance of less than 1%. Proteobacteria and Actinobacteria can be considered dominant species in all land uses.

Figure 1. Relative abundance of enzymes associated with carbon cycling functions in agroforestry relative to grassland and woodland control plots, Loughgall, UK

Initial results show clear differences between the abundance of enzyme functions associated with the macronutrient cycle in agroforestry plots relative to grassland and woodland plots. For enzymes related to carbon cycling functioning, enzymes related to the breakdown of hemi-cellulose (beta-glucosidases) are most abundant; and have significantly higher abundance in grassland and forest plots relative to agroforestry (P<0.01; Figure 1). In general, it is to be noted that there is a greater abundance of functional enzymes in the grassland system relative to the other habitat plots. This may be due to differences in management activities and practices such as inorganic fertiliser, grazing livestock excretal returns and liming additions.

Enzyme functions associated with nitrogen cycling functions including nitrate reduction and denitrification (NosZ, NirS, NirK) appeared to be most abundant, with a trend of greater abundance in monocrop grassland habitat plots relative to the other land uses. However, the greatest range of total abundance reads were found in the agroforestry plots. Nitrogen fixation (NifH) was highest in the grassland and woodland habitats relative to agroforestry.

Overall, it appears that management practices, such as higher inputs of nutrients in the monocrop grassland system have influenced the soil microbiome community composition, abundance and function and therefore potentially macronutrient cycling rates. Drivers of enzyme functional abundance is still being explored in the context of soil biogeophysical and chemical parameters and ecosystem vegetation to ascertain how land use change affects long-term ecosystem sustainability and resilience in these agricultural systems.

Keywords

Land Use, biodiversity, soil microbiome, climate change, Agroforestry

Aditional Attachment II.