Depth or type of cultivation? Which has bigger impact on diversities of bacterial and fungal metacommunities in the soil?

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INTRODUCTION

Conventional, intensive mono-crop agricultural practices, aimed at meeting the needs of the growing world population and ensuring sufficient food production, have already resulted in the loss of microbial biodiversity. In the context of an ever-growing population, it is necessary to provide people with sufficient food supply, which can be challenging with the current level of soil exploitation. Fortunately, **intercropping** systems can produce higher yields with the same or lower input of fertilizers. The ability of intercropping to enhance agricultural productivity is based on the concept of ecological intensification. In this approach, different organisms within the community are specialized in ways that complement each other, resulting in the optimal utilization of resources within the niche (in this case, the soil).

Intercropping, which has been known and used since ancient times, is based on the principle of growing at least two species simultaneously in the field. The plant genera are selected to best fulfill their characteristics, allowing for the optimum use of the soil—for example, legume-cereal pairs. These pairs do not compete for nitrogen (N) and share resources through mycorrhizal networks, allowing increased alpha-diversity of microbiomes.

While the depth of soil can have an effect on the microbiome diversity, we tesed which of these—type of cultivation or soil depth have an impact on alpha diversity of bacterial and fungal communities.

METHODS

1) The samples of bulk soil from 0-10 cm and 10-20 cm depths from long term experiments in Noreikiskes, Lithuania were collected (in triplicates). The samples consisted of 4 variants: no tillage with NPK + cath crop + straw leftover; no tillage with NPK + straw leftover; tillage with NPK (control) and tillage with NPK + straw leftover

2) The total DNA was isolated with GeneMATRIX Soil DNA Purification Kit (EURx, PL)

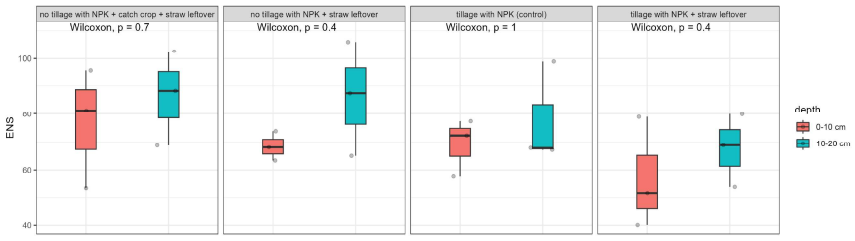
3) The 16S and ITS regions were amplified and sequenced on Illumina MiSeq platform (2x300)

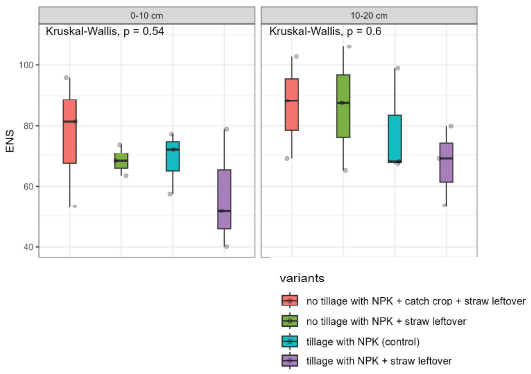
5) The data was processed with DADA2 (Bolyen et al. 2019) environment in Linux shell (Ubuntu ver. 20.04.3 LTS) with taxonomy based on Silva and UNITE databases

4) The ASV table, metadata and taxonomy tables were analyzed in R

RESULTS

fungi





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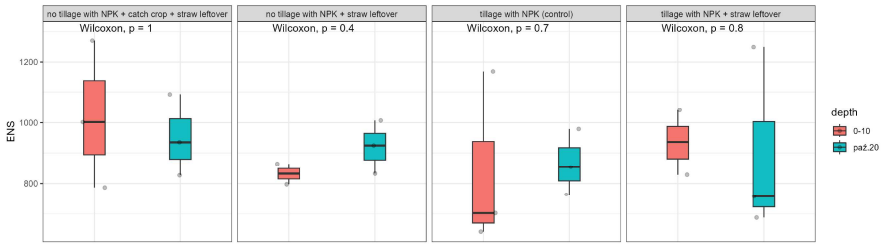

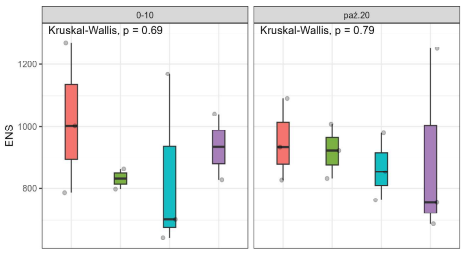

CONCLUSION

The analysis revealed no significant differences of bacterial and fungal alpha diversity (ENS) between the groups between neither, soil depth nor cultivation variant. Futher analyses are needed (such as beta-diversity, differential abundance and network analyses) to reveal significant differences between the combinantions.

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