

Enhancement of soil microbial activity by silviculture management practices

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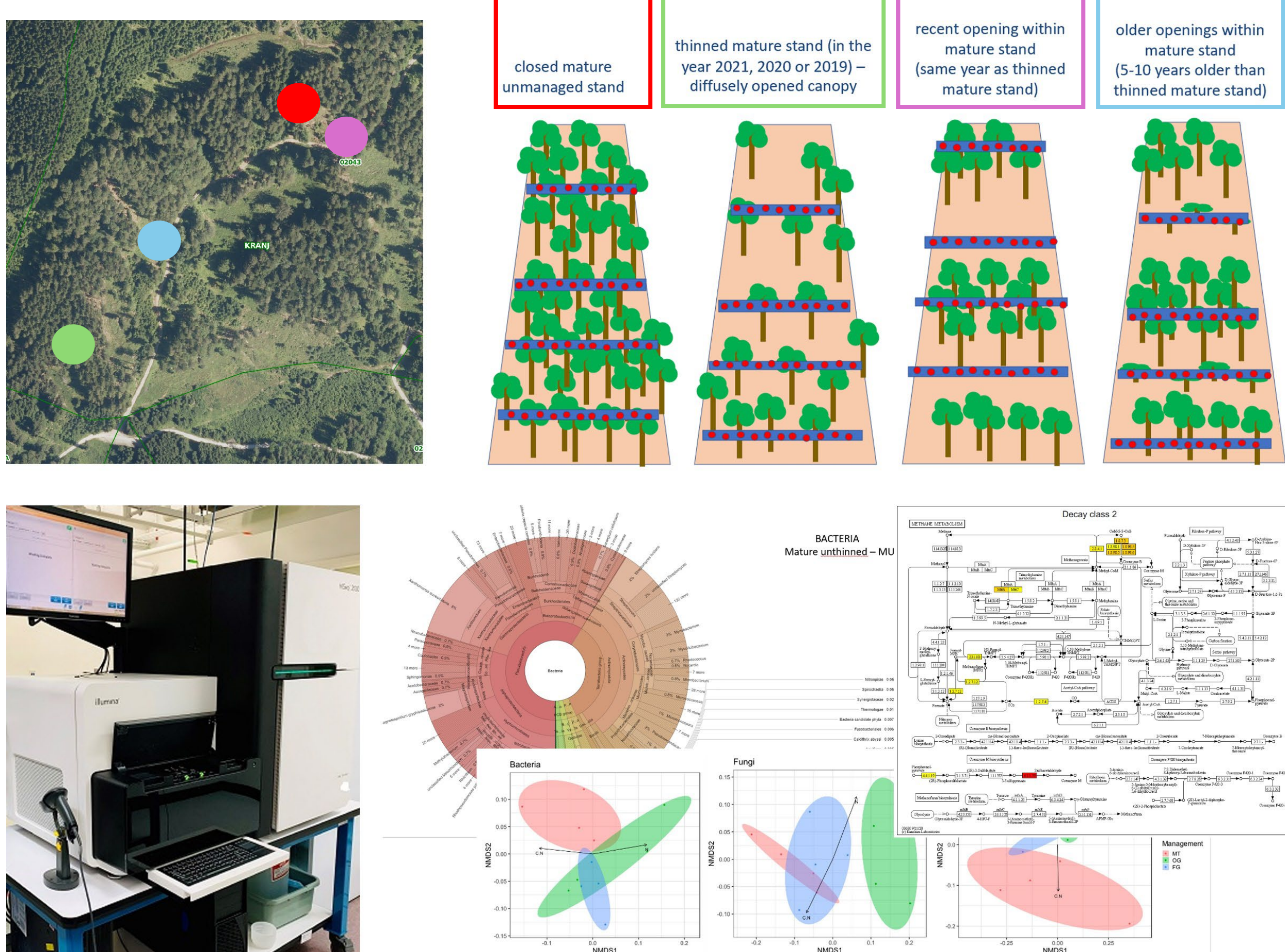
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Introduction

Leaf litter and deadwood have important roles in the forest ecosystems, providing shelter for several organisms, preventing erosion and microclimate fluctuations. Their decomposition is a key process of biogeochemical cycles in forest. Microorganisms are the primary agents of decomposition. Particularly, fungi are considered the major contributors due to their ability to produce specific enzymes and the possibility to access new substrates through hyphae. However, we must also highlight the role of fungi in litter and deadwood decomposition and reconsider the role of bacteria, neglected in the past, identifying key research needs and knowledge. Particular attention must be given to the succession of different taxa and of different functional genes with different ecological role that are able to use a substrate that undergoes to chemical and structural modifications. The quality of substrates is a critical factor that influences the microbial community together with environmental variables, such as temperature and moisture. However, the microbial community is also able to influence the substrate characteristics. Litter nitrogen content is influenced by the uptake of exogenous N by decomposers to meet their metabolic requirements. The complex interactions among microbial communities, ecosystem attributes and chemical composition of fine litter and woody debris remain unclear. Here we wanted to investigate how different forest management can contribute to the overall ecological diversity and functionality of the forest microbiome.

Methodology



Case study is located in Northern Slovenia. Four type of managed forest has been investigated for soil and deadwood microbiome. Illumina shotgun metagenome plus qPCR and SEM analysis allowed a multiphasic approach to the microbiological studies, including fungi, bacteria and archaea. Final data included ecological indices on the taxonomy and on the functional genes; N/C-cycle gene quantification and pathway reconstruction. Multivariate statistical analysis to correlate genomic data with environmental and soil chemical data.

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Results

SOIL CHEMICAL ANALYSES

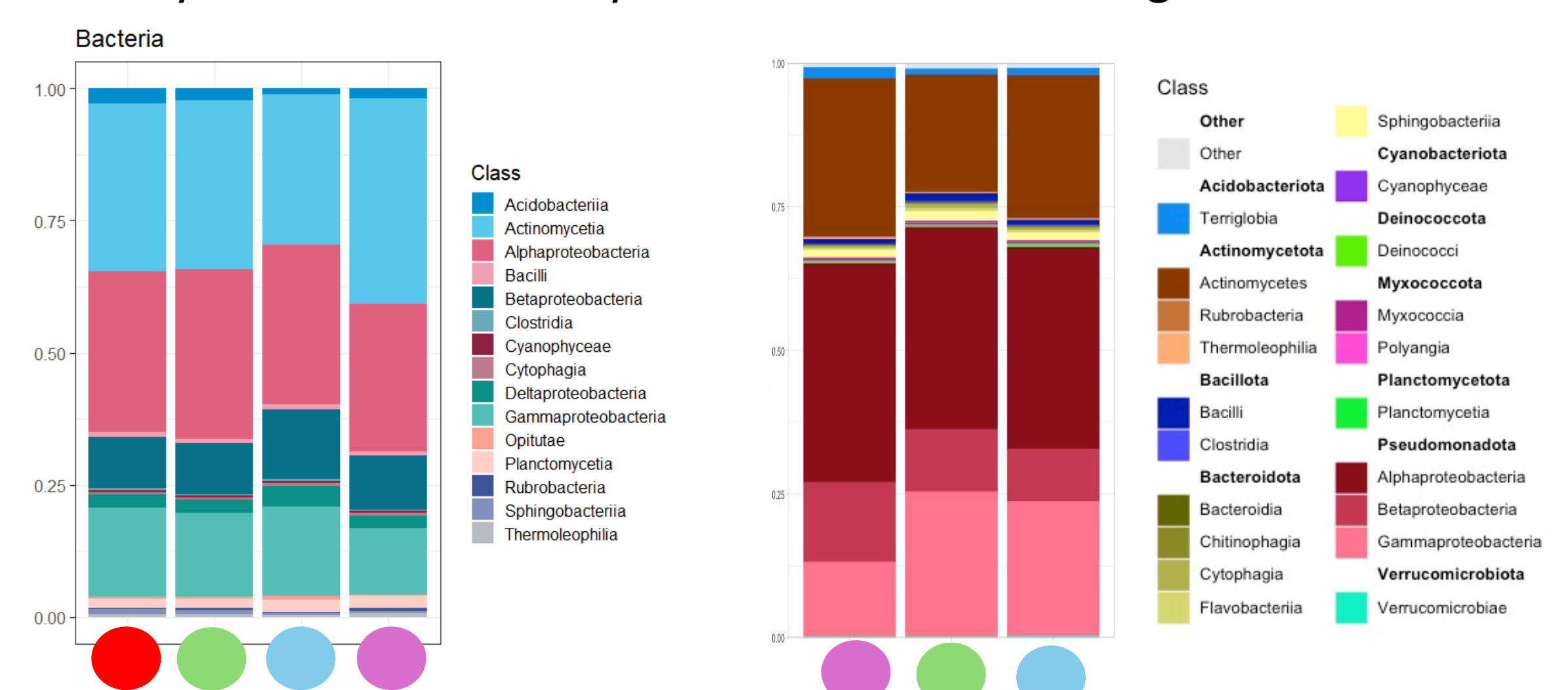
- C/N ratio was maximum in mature forest stands, than decreasing to old gap stands and even lower in the more recent gaps.

SOIL MICROBIAL RICHNESS INDICES

- Bacterial species richness was higher in mature forest compared to gaps, but negatively related to slope.
- Fungal richness was negatively correlated with slope, but not across managements.
- Archaeal richness was affected by forest management: higher in managed unthinned forest compared to the managed thinned.

SOIL MICROBIAL TAXA INDICES

- Bacterial beta diversity correlated to exposition and management.
- Actinomycetia, Alphaproteobacteria, Deltaproteobacteria and Gammaproteobacteria were the dominant classes in all the soils, with a major presence of Actinomycetia in the fresh gaps forest. Regarding genera, Bradyrhizobium, Pseudomonas and Streptomyces were the most abundant, with functions related to N-fixation and complex C-turnover.
- Fungal community were affected by exposition, slope, C, N, management.
- Dominant genera were the saprotrophs Podila/Mortierella, while occasional Fusarium has been found in mature unmanaged forest.
- For archaea, correlation has been found only for exposition. The effect of management was meaningful only when comparing mature vs gaps.
- They were dominated by Halobacteria. Methanogens were rarer.



DEADWOOD CHEMICAL ANALYSES

- Only C/N was found to be higher in mature forests than in the gaps.

DEADWOOD MICROBIAL RICHNESS INDICES

- Bacterial and fungal diversity indices did not vary significantly across the management types, except archaea evenness negatively correlated to C.

DEADWOOD MICROBIAL TAXA INDICES

- Beta diversity was significantly different across management for bacteria and fungi.
- All taxonomic groups were influenced by the C/N ratio.
- Dominated by bacteria belonging to Sphingomonas, Pseudomonas, Streptomyces and Rhizobium with a higher genus richness than soil.
- Also fungi exhibited higher richness and major genera were Pochinia, Psilocybe, Colletotrichum.
- For archaea, Halobacteria dominated all the deadwoods.

Conclusions

We have investigated diversity indices and beta diversity of microbiota in both soils and deadwood substrates within forest patches differing in their management. We found that on both substrates, composition and structure of forest microbiota changed across management types, although no consistent effect was observed for diversity indices. In general, the microbiota seems to be susceptible to changing environmental conditions determined by forest development stage, however, is not clear which type of management enhance the microbiome. Further evidence can be provided by results on microbial functional pathways which will better explain the effect of varying management intensity on nutrient cycling and carbon dynamics in forest ecosystems.

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