

Metaproteogenomics reveals the soil microbial communities active in nutrient cycling processes under different tree species

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Tree species exert strong effects on microbial communities in litter and soil and may alter rates of soil processes fundamental to nutrient cycling and carbon fluxes (Prescott and Grayston 2013). However, the influence of tree species on decomposition processes are still contradictory and poorly understood. An understanding of the mechanisms underlying plant influences on soil processes is important for our ability to predict ecosystem response to altered global/environmental conditions.

In order to link microbial community structure and function to forest-floor nutrient cycling processes, we sampled forest floors under western redcedar (*Thuja plicata*), Douglas-fir (*Pseudotsuga menziesii*) and Sitka spruce (*Picea sitchensis*) grown in nutrient-poor sites in common garden experiments on Vancouver island (Canada). We measured forest-floor total N, total C, initial NH_4^+ and NO_3^- concentrations, DOC, C_{mic} and N_{mic} . Gross rates of ammonification and NH_4^+ consumption were measured using the ^{15}N pool-dilution method. Organic carbon quality was assessed through FTIR analyses. Microbial community structure was analysed by a metaproteogenomic approach using 16S and ITS amplification and sequencing with MiSeq platform. Proteins were extracted and peptides characterized via LC-MS/MS on a Velos Orbitrap to assess the active microbial community.

Different microbial communities were active under the three tree species and variation in process rates were observed and will be discussed. This research provides new insights on microbial processes during organic matter decomposition. The metaproteogenomic approach enables us to investigate these changes with respect to possible effects on soil C-storage at even finer taxonomic resolution.