



Soil warming leads to an up-regulation of genes involved in the decomposition of organic N in a subarctic grassland

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Soil microorganisms control the breakdown (depolymerization) of high molecular weight organic matter in soil and its mineralization and release as CO₂ to the atmosphere. The enzymatic reactions involved in these steps are known to be temperature sensitive. Therefore, increasing global temperatures are expected to accelerate microbial activity and ecosystem processes and stimulate further CO₂ emissions, potentially causing a positive feedback to climate change. On the other hand, higher turnover rates demand an increased amount of energy allocated for growth, enzyme production and maintenance, which can progressively deplete soils from substrate, forcing a reduction of microbial biomass and/or activity and a higher metabolic investment in resource acquisition.

The response of ecosystems to warming has been shown to be related with its duration and magnitude. In this study, we analyzed soils from long-term (>50 years) and short-term (8 years) warmed plots at the natural geothermal warming experiment ForHot (<https://forhot.is>), located in a sub-arctic grassland in Iceland. Previous studies at this warming experiment have shown an accelerated C cycle in response to warming, with decreased soil carbon stocks, and higher rates of decomposition of labile and recalcitrant organic matter, regardless of the warming duration. In addition to carbon losses, increased N losses from soils were found, but no change in the N content of the vegetation along the temperature gradient. Additionally, both ammonification and nitrification rates were shown to increase under warming, pointing to higher N losses from warmed soils.

In this study, we tested the hypothesis that under warming microorganisms become progressively limited in organic substrates, leading to a higher microbial investment in organic N decomposing

enzymes to mine the existing organic N sources present in their surroundings. This hypothesis is based on previous data, that showed that microbial turnover was increased in the warmed plots. Under this assumption, we expected to observe higher expression levels of genes coding for organic N mining extracellular enzymes in warmed plots.

We analyzed the metatranscriptome from a total of 16 soil samples representative of ambient (n=4) and +6°C warmed (n=4) soils, for both grassland types. Additionally, we sequenced the metagenomes of 4 soil samples, representative of each condition, to allow for transcript mapping and differential gene expression analysis.

We used Hidden Markov models to screen the assembled metatranscriptomes for genes involved in the degradation of chitin, proteinaceous compounds, nucleic acids and microbial cell walls. The subcellular location and presence/absence of signal peptides was assessed with Psort and SignalP to discriminate transcripts involved in internal recycling from those targeted for secretion. First results show a general up-regulation of all transcripts involved in organic N degradation in the grassland subjected to long-term warming, whereas this trend is less clear in the short-term warmed grassland. Further work includes cross-referencing gene expression patterns with potential changes in active community composition.

We conclude that an acceleration in microbial turnover rates in response to warming is coupled to a higher investment in N acquisition enzymes, as indicated by an up-regulation of genes involved in upstream processes of organic N degradation.