

# Succession of soil and moss bacterial communities in the Fláajökull forefield

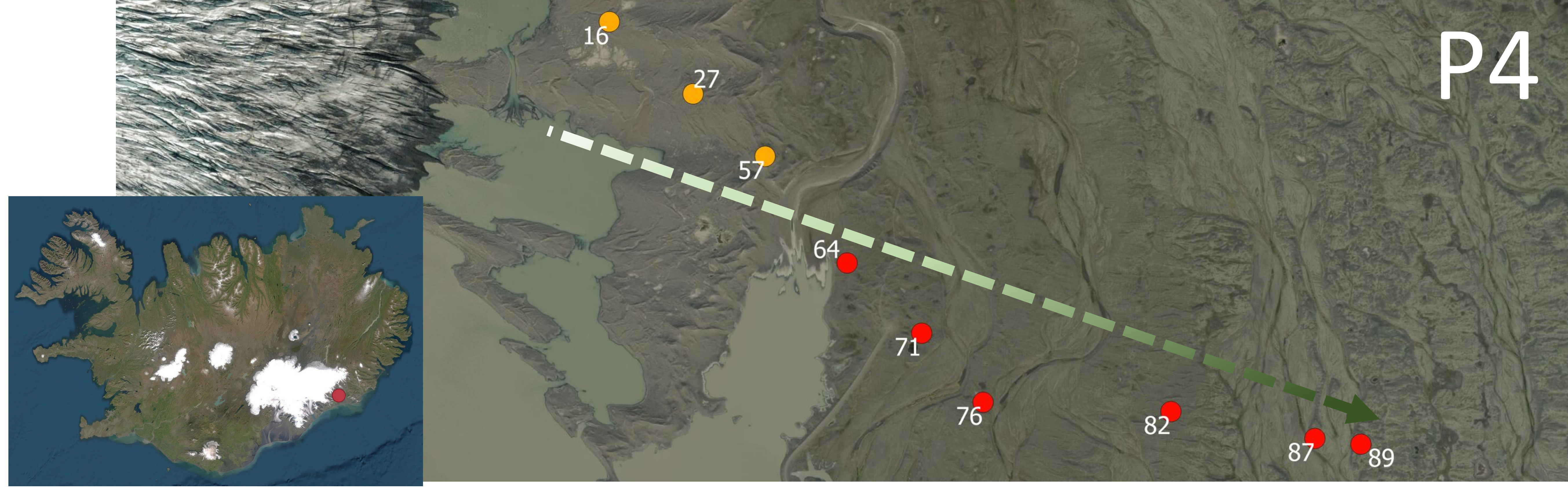
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## Introduction

Mosses can develop into thick moss mats during primary succession in glacier forefields. They enhance soil development by contributing to nitrogen accumulation, by retaining moisture and contributing to soil organic matter build-up, partly via their microbiome. These processes can in turn influence the microbial communities of the moss-covered substrates. We have a very limited understanding of the dynamics between mosses and their microbiome, nitrogen fixation and their effect on the soil microbiome during ecosystem development in glacier forefields.

We hypothesised that: (i) moss functional traits will change with soil age with total nitrogen (TN) and total carbon (TC) increasing with soil age; (ii) changes in moss functional traits and soil age will lead to shifts in moss-associated bacterial communities and the underlying soil bacterial community; and (iii) that moss-associated N<sub>2</sub>-fixation rates and *nifH* gene abundance will depend on soil age, moisture content, TN and/or bacterial community composition.

## Methods

We used a chronosequence in the glacier forefield of Fláajökull, in which we collected moss and underlying substrate along a transect covering nine moraine ridges. Three moss and soil samples were taken on each of the nine moraines. The satellite image in the right upper corner shows the sampling sites with the soil age and the colour indicates moss species (*Racomitrium ericoides* in the three youngest successional stages and *Racomitrium lanuginosum* in the older successional stages).

Moss TN, TC and  $\delta^{13}\text{C}$ : element analyzer

Nitrogen fixation rates: acetylene reduction assays

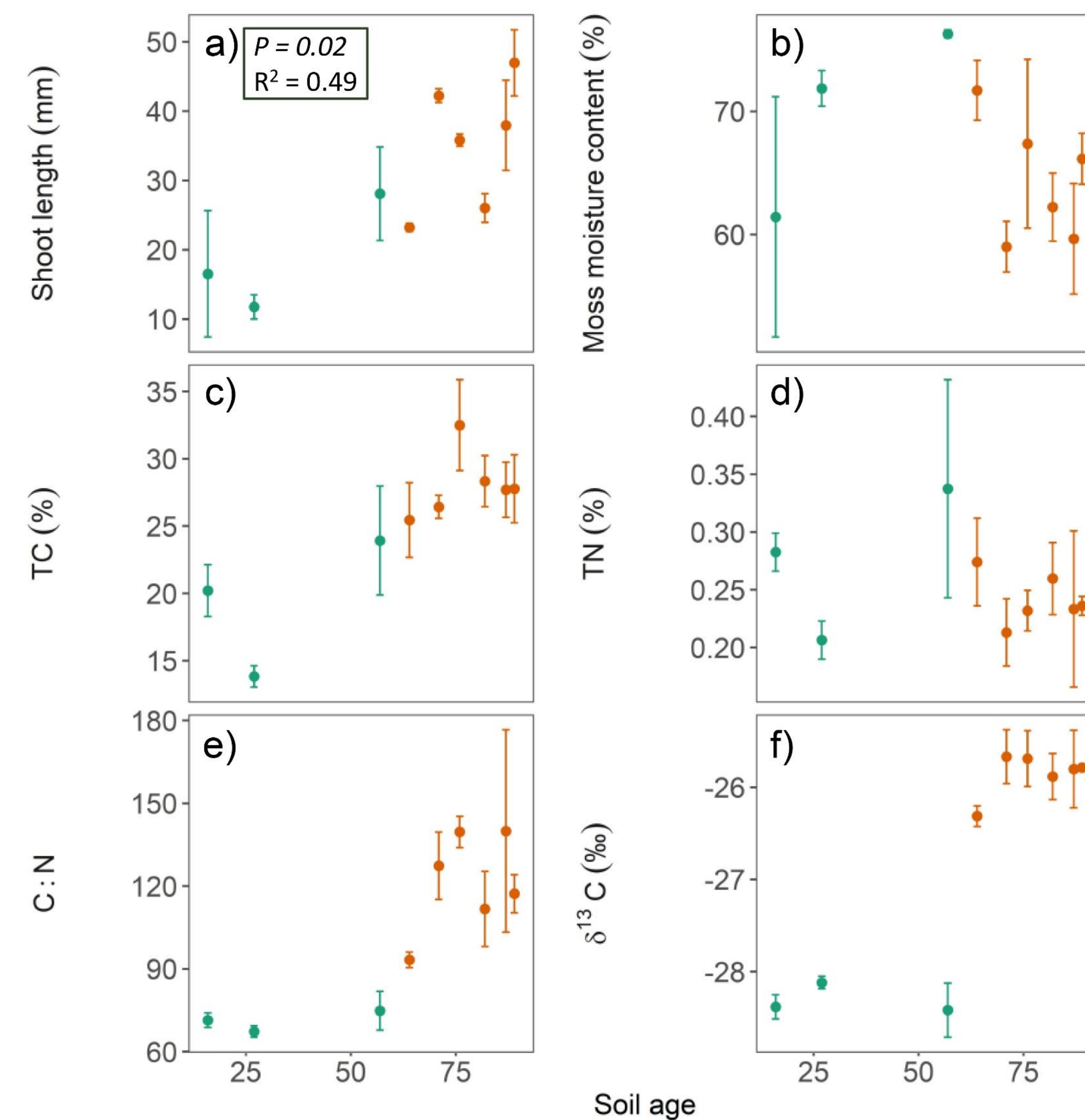
*nifH* gene abundance: qPCR

Bacterial communities: 16S rRNA gene amplicon sequencing on a HiSeq and the sequences were processed with DADA2

Statistical analysis included linear models, a structural equation model and PERMANOVAs.

## Moss functional traits

Only shoot length significantly increased with soil age. Moss TC and C:N ratio showed increasing trends with soil age when ignoring moss species. And  $\delta^{13}\text{C}$  was higher in *R. lanuginosum* than in *R. ericoides*.



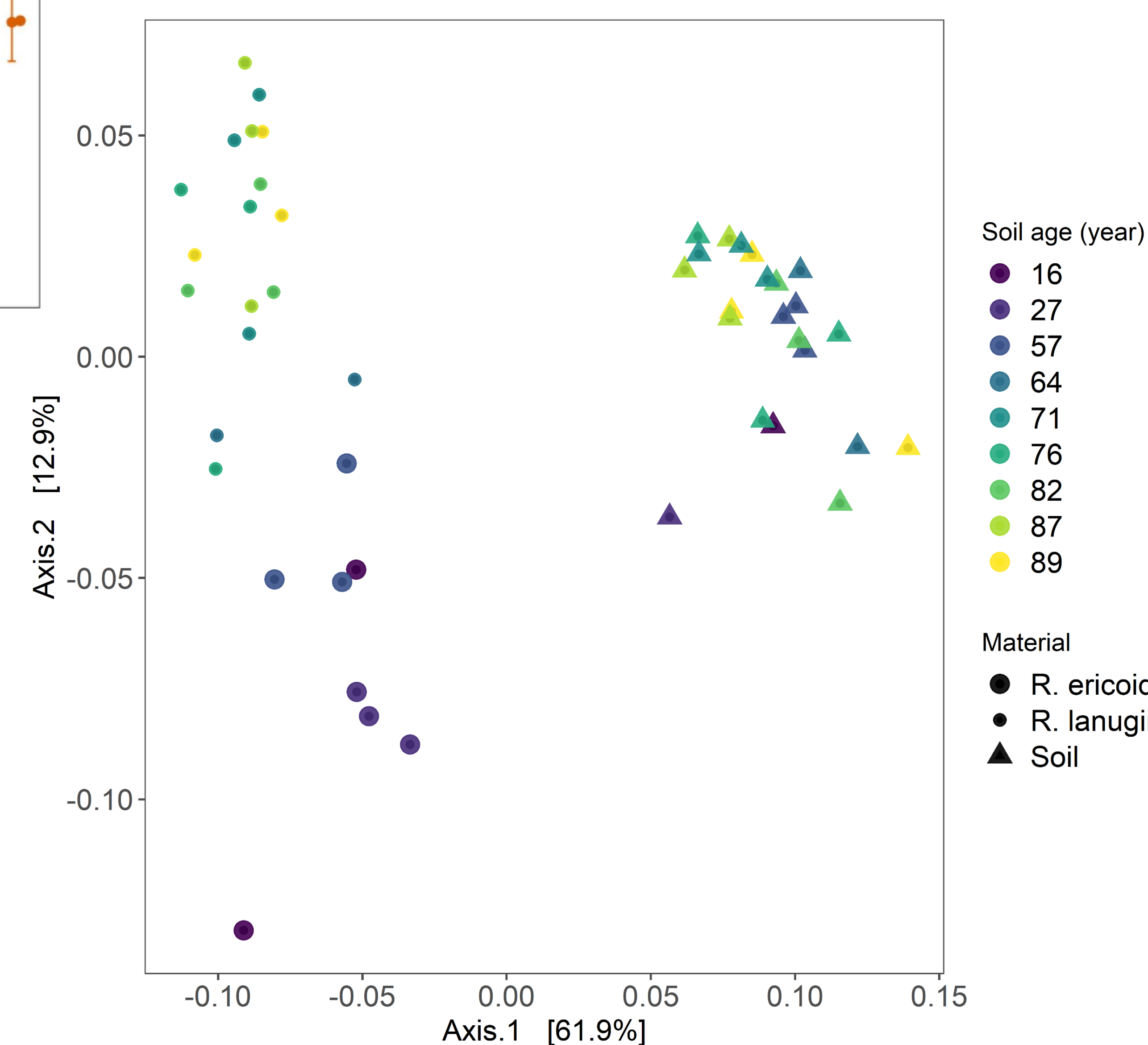
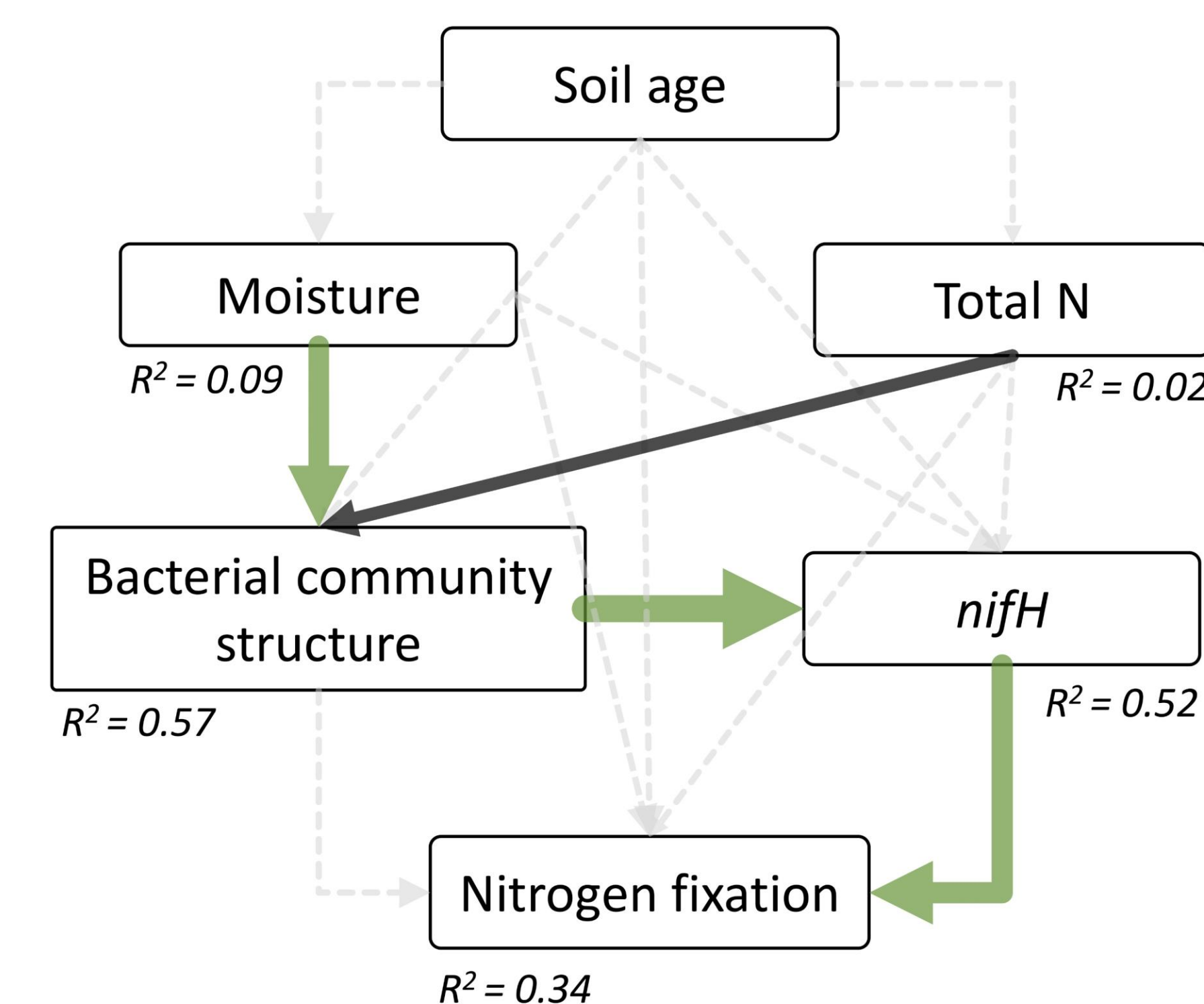
## Conclusions

- Moss functional traits are not necessarily related to soil age.
- Moss functional traits can affect the bacterial community structure of the moss and the underlying soil.
- Moss-associated nitrogen fixation takes place along the whole chronosequence and thereby likely contributes to N availability. Further, Nitrogen fixation rates are not linked to soil age or moss TN, but rather to the bacterial community structure.

## Nitrogen fixation

*NifH* gene abundance decreased with soil age, while nitrogen fixation did not show any trend with succession.

The structural equation model showed that, at least for *R. lanuginosum*, nitrogen fixation was not affected by moss TN, moisture content nor soil age. However, nitrogen fixation negatively linked to *nifH* gene abundance, and *nifH* gene abundance to bacterial community structure. This implies that with soil age, a shift in nitrogen fixing taxa takes place with different nitrogen fixing efficiencies. We for instance found a decrease in the relative abundance of Cyanobacteria in the moss.



## Bacterial communities

The moss and soil bacterial communities were significantly different from each other. Both were affected by soil age, but the moss bacterial communities more strongly. Moss moisture content was found to be a driver of the moss bacterial communities regardless of moss species and both moss species separately.

We also found that moss C:N ratio affected the soil bacterial community structure. Our soil samples did not contain any visible moss parts, so moss C:N ratio potentially directly affects the soil bacteria via leaching of nutrients.