# Characterization of Soil Bacterial Communities in Different Forest Soils

Mélody Rousseau[1], Arjen de Groot[2], Andjin Siegenthaler[1] & Andrew Skidmore[1]

[1]University of Twente, The Netherlands & [2]Wageningen UR, The Netherlands

Email: m.s.d.rousseau@utwente.nl
@melo_rousseau

## Aims

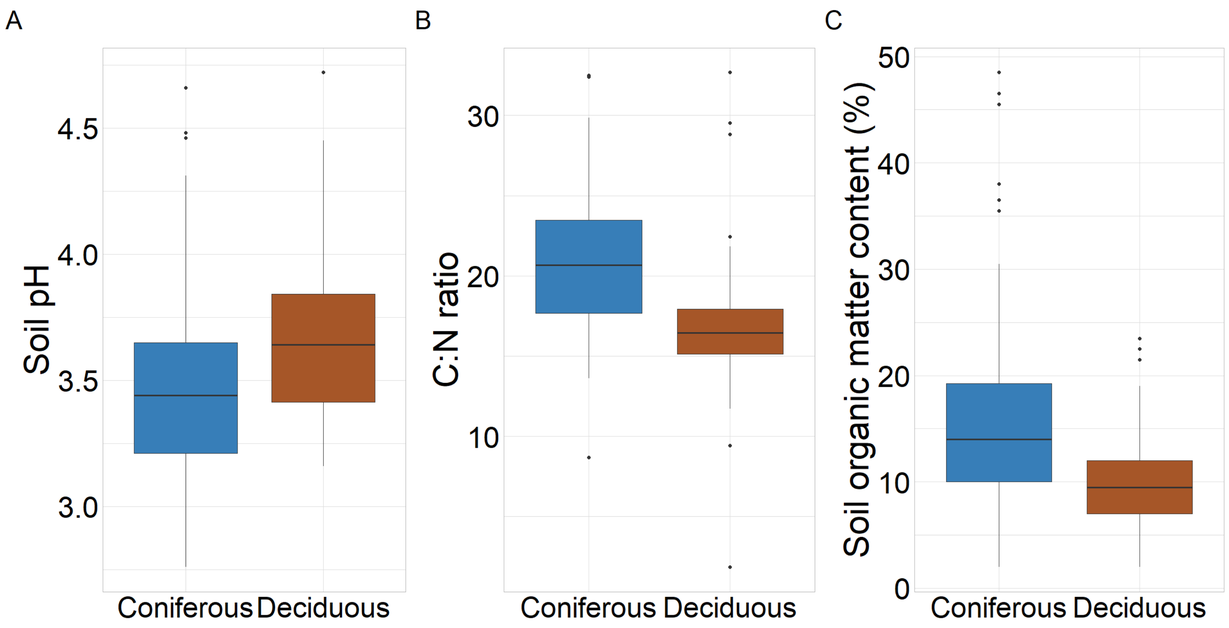
- Characterizing and comparing **bacterial community profiles** among different soil forest profiles using the **DNA metabarcoding** technique
- Determining if the "mull-mor" **humus-type concept** still applies to **narrow and acidic soil pH ranges (2.7 – 4.7)**

## Conclusion

By providing valuable information on the **community composition** (taxonomic diversity) and **species populations** (species distribution), **eDNA metabarcoding profiles** allow us to understand the soil microbiome better. In the **context of acidification**, we demonstrated that the **humus-type concept remains pertinent**. Although bacterial communities in mull and mor soils are acidic-tolerant, distinct bacterial profiles were observed with mull soils more diverse and richer than mor soils.

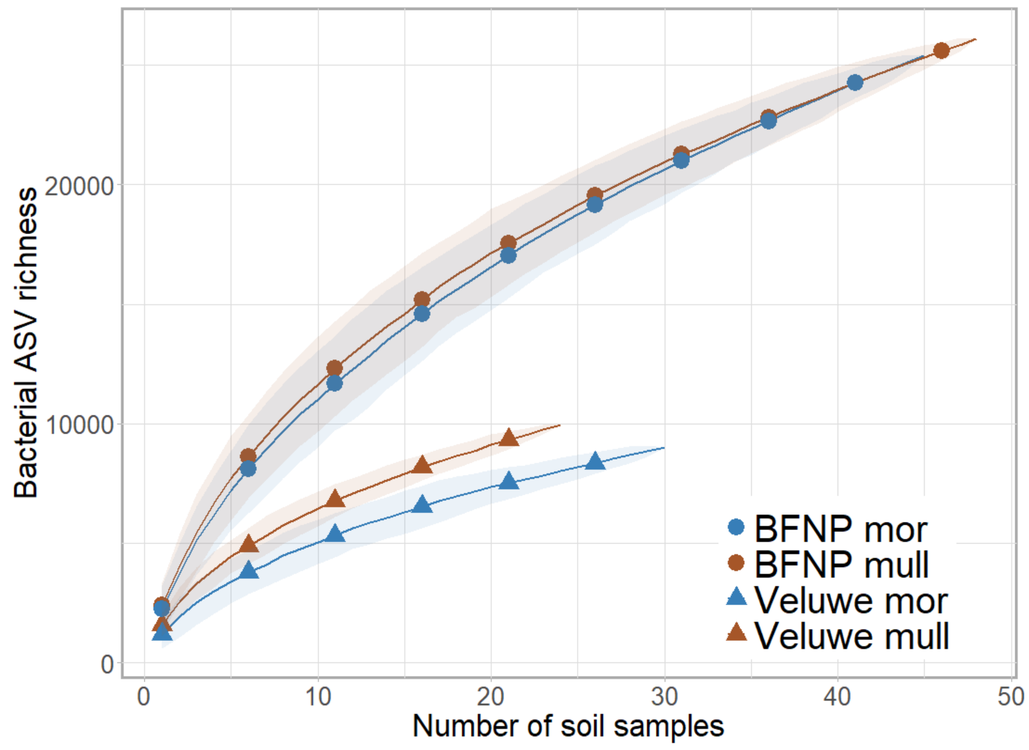
## Results

### 1. Forest types have different but consistent soil profiles, which can be translated into mull (nutrient-rich) and mor (nutrient-poor) humus.



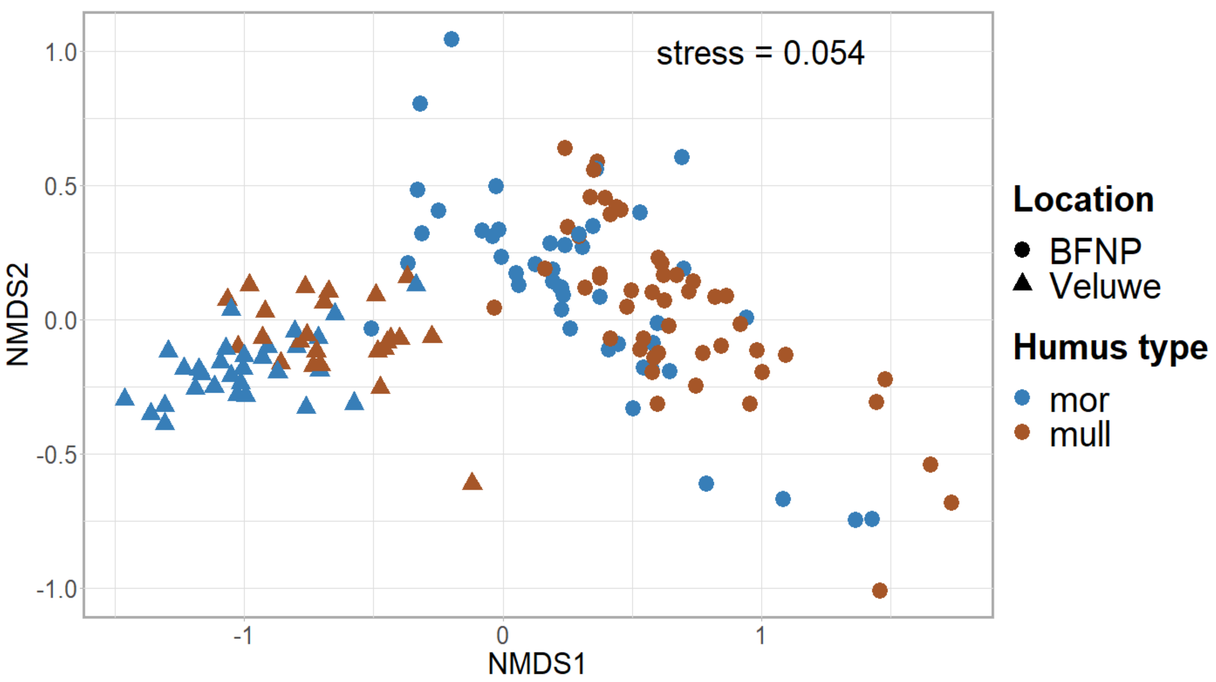

Boxplots show the variation in soil pH (A), C:N ratio (B), and soil organic matter content (C) for each forest type.

### 2. Mull soils have a greater bacterial richness and diversity.



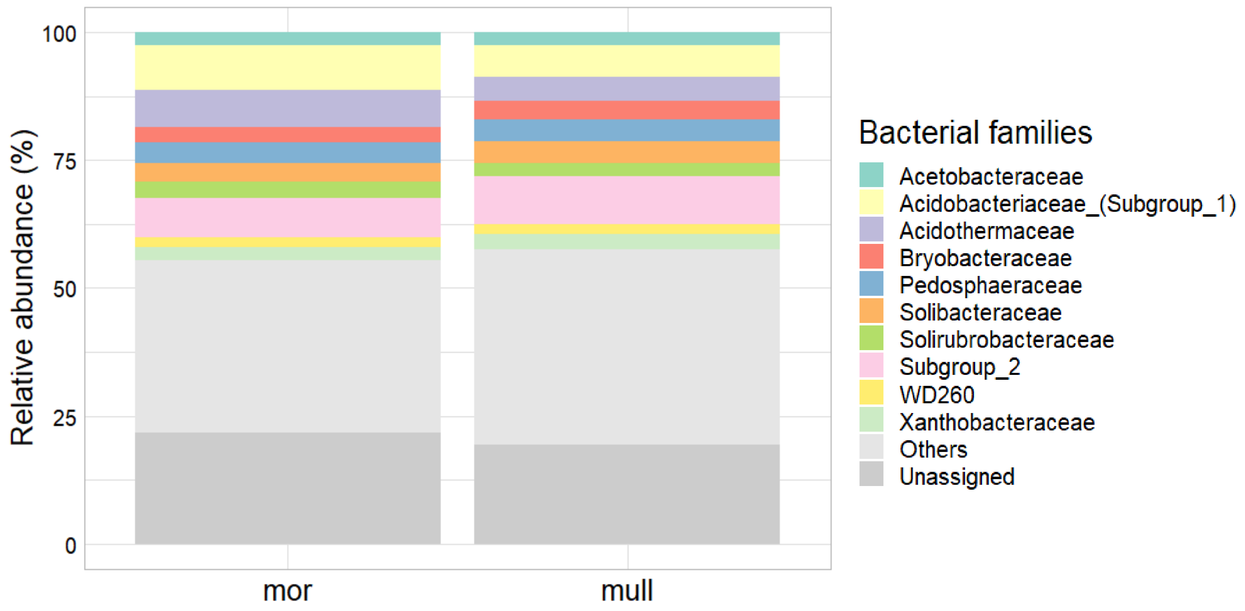

Accumulation curves of the number of bacterial ASVs detected per location x humus type. 95% confidence intervals are represented.

### 3. Mull and mor soils have distinct soil bacterial profiles.




Variation in bacterial community composition between mull and mor soils (Bray-Curtis dissimilarity).

### 4. Bacterial community composition reflects acidic-stress environments.




Stacked barplot of the mean relative abundance in mull and mor soils of the 10 most abundant bacterial families, unassigned families, and remaining families (Others).

## Background

Soil bacterial communities provide **essential ecosystem services**, and are influenced by both forest types and biogeochemical properties of the soil[1]. The **humus-type concept**[2] acknowledges and captures these abiotic factors along a **gradient of soil nutrient availability, quality, and pH**. This concept was initially developed by Müller[3] who observed differences in decomposition rate and organic matter incorporation under different forest types. In other words, mull soils are found in deciduous stands which are nutrient-richer, less acidic, and with a higher decomposition rate than mor soils. As soil pH is an important environmental filter, **specific bacterial communities under acidic conditions are expected**. While soil biodiversity should be higher and more diverse in mull soils, it is still unknown if forest soils host different bacterial community profiles under extreme acidification.

## References

1. Prescott, C. & Grayston, S. (2013). *Forest Ecology and Management*, **309**.
2. Ponge, J. (2013). *Soil Biology & Biochemistry*, **57**.
3. Handley, W.R.C. (1954). *Forestry Commission*, Bulletin No.**23.**

## Discussion

- Even under extreme acidification, coniferous and deciduous stands have distinct soil biochemical properties which can be translated into "mull" and "mor" humus type.
- **Distinct bacterial profiles between mull and mor soils** were observed, with more diverse and richer bacterial communities in mull soils.
- BFNP and Veluwe are **environments under acidic stress**, which is reflected in bacterial communities **dominated by acidic-tolerant families** such as *Subgroup 1, Acidothermaceae*, and *Subgroup 2*.
- The humus-type concept still applies to acidic-stress environments.