



Sigrid Dassen (NIOO), George Kowalchuk (UU),
Wim van der Putten (NIOO), Gerlinde De Deyn (WUR)

Plant species richness enhances plant biomass productivity. Soil organisms may play a role here. With increasing plant richness the abundance of soil microbes increase. However, it is unknown how the soil microbial community structure changes with plant species richness.

Objectives

Analyse the soil microbial community structure along a plant community diversity gradient.

- Plant species richness
- Plant functional group identity
- (a)biotic environmental variables

*Operational Taxonomic Units ≈ 'species'



The Jena Experiment, established in 2002

Conclusions

- Soil microbial richness does not increase with plant species richness ($A_{1,2,3}$).
- Plant functional group identity affects AMF community composition, but not total fungal or bacterial community composition ($B_{1,2,3}$).
- Bacterial community composition is largely driven by soil structure and by phosphorus content of the plant (C_1).
- Fungal community composition is driven by soil structure, plant chemistry, and plant productivity (C_2).
- AMF community composition is correlated with soil structure and plant productivity (C_3).

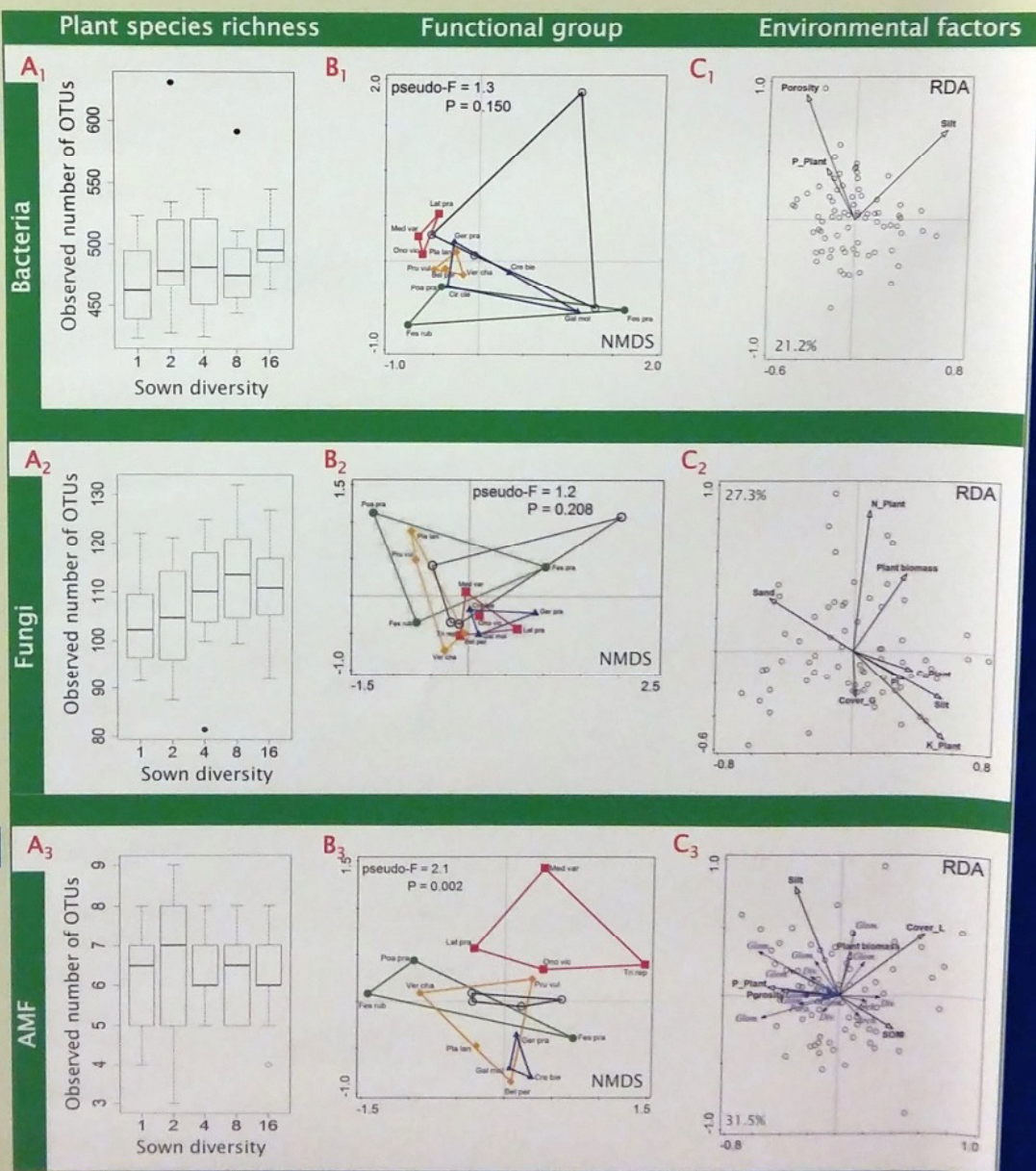
Results

$A_{1,2,3}$ OTU richness per sown plant species diversity level.

$B_{1,2,3}$ NMDS based on Bray-Curtis distance matrix.

Green: *Festuca pratensis*, *Festuca rubra*, *Poa pratensis*, Yellow: *Plantago lanceolata*, *Prunella vulgaris*, *Bellis perennis*, *Veronica chamaedrys*, Red: *Lathyrus pratensis*, *Medicago varia*, *Onobrychis viciifolia*, Blue: *Geranium pratense*, *Gallium mollugo*, *Crepis biennis*. Black: 60-species mixture.

$C_{1,2,3}$ Microbial community composition response to biotic and abiotic factors. The model was built by forward selection and significance of factors was tested with permutation tests ($P < 0.05$).



Experimental approach

- Soil samples were taken from monocultures, 2, 4, 8, 16 and 60 species plant mixtures.
- 454-pyrosequencing of 16S and 18S was used to analyse the soil microbial community composition.

