Project Database of ICP Forests
PROJECT DESCRIPTION

PROJECT INFORMATION

Project title:	**Longitudinal investigation of microbial interactions between bacteriovores eukaryotes and bacteria in forest soils**
Project ID:	305
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PROJECT DESCRIPTION

Our research group studies microbial interactions in the top layer of forest soils (~2cm below the leaf litter). We are in particular interested in studying the interactions between bacteriovores eukaryotes, also known as protozoans, and bacteria. Protozoan predation can strongly impact microbial soil communities1 and is thought to be a major driver for remineralization of soil nutrients. Although there is a wealth of meta-genomic data characterizing microbial soil communities2, there is a general lack of longitudinal studies that simultaneously investigate the abundance of both protozoan and bacterial species in the soil3. In our project, we therefore propose to address this knowledge gap by performing such a longitudinal study.
We will obtain soil samples at our sampling sites around EMBL (Heidelberg, Germany) at regulator time intervals (monthly) for a period of 8 years. For each sample, we will determine the community composition using meta-genomic sequencing. To this end, we will combine both short-read Illumina sequencing and long-read nanopore sequencing, which allows us to (a) determine the abundance of each protozoan and bacterial species in our soil samples and (b) assemble their genomes to perform gene enrichment analyses. We expect that changes in the soil community will strongly depend on soil properties, so besides performing meta-genomic sequencing, we will also characterize a range of soil properties (e.g., particle size, temperature, pH, volumetric water content, osmolarity, C/N ratio). We believe that this data can best be evaluated against an extensive reference dataset, to determine whether microbial communities in other forest habitats might be exposed to similar biotic and abiotic conditions. More broadly, we would also like to determine how the forest around Heidelberg compares to other forest in Germany and Europe. For these reasons, we think that the ICP Forest dataset could be of invaluable importance for our research.

Since our research group (van Gestel group, https://www.embl.org/groups/van-gestel/) has a background in microbiology and molecular biology, and not forestry, we would be strongly interested in connecting to the broader research community of the ICP Forest network. I can image that the diverse research backgrounds could foster some existing collaborations. Finally, I would like to point out that we will share all data generated during our project publicly available, using standard public repositories (e.g., European Nucleotide Archive and Github).

1. Rosenberg, K. *et al.* Soil amoebae rapidly change bacterial community composition in the rhizosphere of *Arabidopsis thaliana*. *ISME J* **3**, 675–684 (2009).
2. Bahram, M. *et al.* Structure and function of the global topsoil microbiome. *Nature* **560**, 233 (2018).
3. Geisen, S. & Bonkowski, M. Methodological advances to study the diversity of soil protists and their functioning in soil food webs. *Applied Soil Ecology* **123**, 328–333 (2018).