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Enabling detection of ecological patterns in 10.000 samples representing the Danish soil microbiome

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MICROFLORA DANICA – THE MICROBIOME OF DENMARK

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Introduction

By sampling soil, sediment, and water across both natural and cultural habitats and by applying novel DNA-based sequencing technologies, the aim of Microflora Danica is to generate an almost complete reference database of the microbiome of Denmark. The purpose of Microflora Danica is to establish a common reference database and to link the identified microbes to their functions and distributions across different habitats.

Project Progress



Samples 10.000/10.000

DNA 9.570/10.000

Library 9.396/10.000

Sequencing 8.874/10.000

Types of Data

10 000 samples

Shallow Metagenomics [Illumina 5 gbp; 17 mill. Reads]

Small subunitLarge subunit16S rRNAITS Region23S rRNA5S rRNA

Comparison of reads to databases. **Abundance** of 16S/18S rRNA genes across all samples. **1000 samples** rRNA amplicon [Nanopore/PacBio]

Large subunit

2490R

Small subunit

ERSIT

- 10.000 samples covering natural and cultural habitats
- **EMP500** samples included

Developed Methods

- Barcoding and automated registration of samples
- High throughput DNA extraction **276 samples a day**
- **10x down-scaling** of sequencing library preparation through nanoliter dispensing
- Automated workflows using liquid handlers
- Automated sequence processing pipeline

100 samples Deep Metagenomics [Illumina + Nanopore]

Retrieval of **genomes** from novel bacteria selected from samples of interest.

Phylogenetic

marker genes

(ex. rRNA genes)

Database of high-quality reference 16S/18S rRNA sequences to build the tree-of-life.

16S rRNA - ITS Region - 23S rRNA - 5S rRNA

Interesting samples FISH and FISH-Raman microspectroscopy



Visualization of **novel** and **uncultured** bacteria

Research Questions



• Assessment of novelty and

Database

- Based on latest release of SILVA
- Addition of new full length 16S sequences
- De novo name generation when needed
- Expectation: final version based on < 15 million sequences

diversity

- Importance for habitat function
- Prediction of habitat
 - preferences
- Naming of novel organisms









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