

Microbial quantitative PCR data

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Introduction

This data sheet contains the mean qPCR measurements aggregated from triplicates measured on the 16S rRNA gene for prokaryotes and the ITS gene for fungi. The ratio is from ITS over 16S copy numbers. The sheet contains the columns plot id, X16s, ITS and ratio.

Table 1: General information.

project_name	ETH+ Arctic Greening
creation_date	2024-11-10
last_modification_date	2024-11-10
creator	Lena Bakker
contact_1	lena.bakker@eaps.ethz.ch
contact_2	cara.magnabosco@eaps.ethz.ch
number_samples	122
sampling_period	2022-07-09 – 2023-08-09
X16s	copy numbers/g of soil
ITS	copy numbers/g of soil
ratio	No unit; ITS/X16s
processing_status	incomplete = more data will be uploaded
upload_status	structured

Table 2: Variable overview.

variable	explanation	unit
X16s	Measurement of total abundance with qPCR of the prokaryotic soil microbial community using the 16S rRNA gene	copy numbers/g of soil
ITS	Measurement of total abundance with qPCR of the eukaryotic soil microbial community using the ITS gene	copy numbers/g of soil
ratio	Ratio of the 16S abundance over the ITS abundance	No unit

Methods

Soil sampling

Each of the samples were homogenized by mixing the bags, if the soil was loose enough, if it was not loose, by mixing in a bag using a mortar and pestle. The homogenized soil was then subsampled into cryovials in triplicates and shock frozen in liquid nitrogen. The remaining soil was kept for soil analysis. The molecular samples were kept in -80 °C and transported back in liquid nitrogen (one of the triplicates for potential RNA analysis) or frozen in a cooler (two of the triplicates for DNA analysis).

DNA Extraction

DNA was extracted from 0.25 g of sample material using the commercial soil DNA extraction kit DNeasy PowerSoil Pro Kit (Qiagen®, Germany) with a bead beater, FastPrep 24 (MP Biomedicals, Germany) for mechanical lysis. DNA concentrations were determined using Qubit fluorometric quantification using the high sensitivity kit (Invitrogen™, USA). All DNA extracts were normalized to 2 ng/μl for further processing.

Quantitative PCR

Prokaryotes (16S rRNA region V4 and V5, primers 515F (GTGYCAGCMGCCGCGGTAA, (Caporaso et al., 2012)) and 926R (CCGYCAATTYMTTTRAGTTT, (Quince et al., 2011)) and fungi (region ITS2, primers ITS3: (GCATCGATGAAGAACGCAGC) and ITS4: (TCCTCCGCTTATTGATATGC)) were quantified with a LightCycler® 480 II (Roche, Switzerland). Normalized DNA extracts were quantified as triplicates following the protocols shown in the work by Han et al. 2023 and that were adapted to our needs (for details see Bakker et al. 2025 (in prep)).

Sample processing

DNA extract from flash frozen soils stored at -80°C, sequencing on an Illumina NextSeq.

References

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