In-depth analysis of the origin of Primary Biological Aerosol Particles (PBAPs) in a temperate forest of Leipzig

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What are bioaerosols?

- **Primary Biological Aerosol Particles (PBAPs)** are airborne biological components which are directly emitted from the biosphere into the atmosphere.
- They include bacteria, fungi, viruses, spores, pollen, and plant or animal debris (Després et al., 2012).
- Their dispersion is influenced by physical, meteorological, and biological factors.

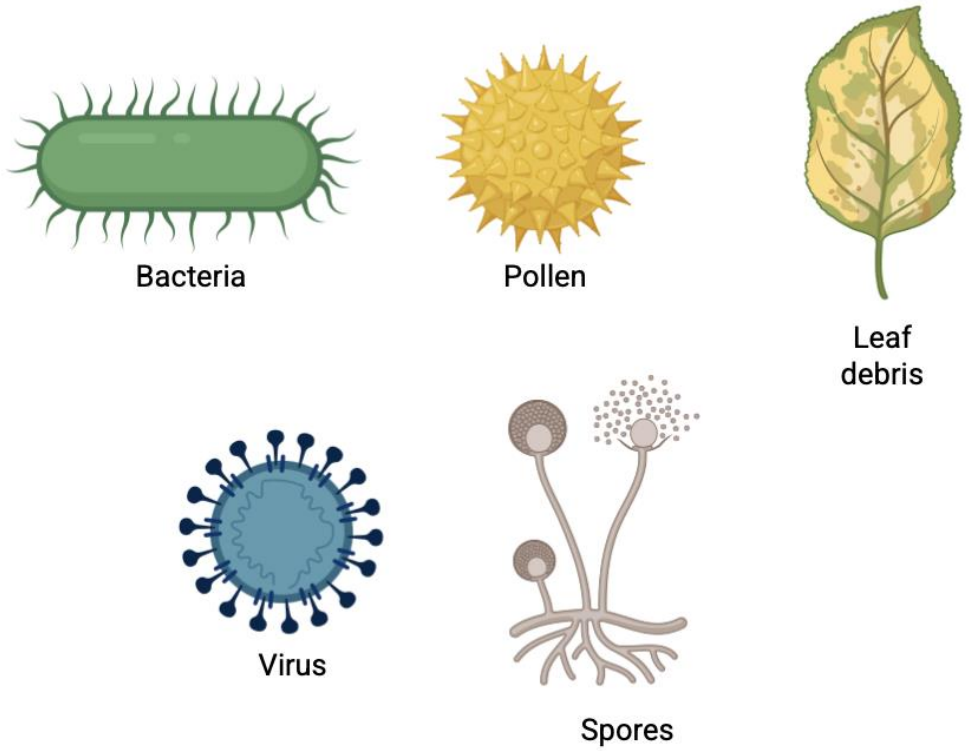


Fig 1: Different types of PBAPs (Made in BioRender)

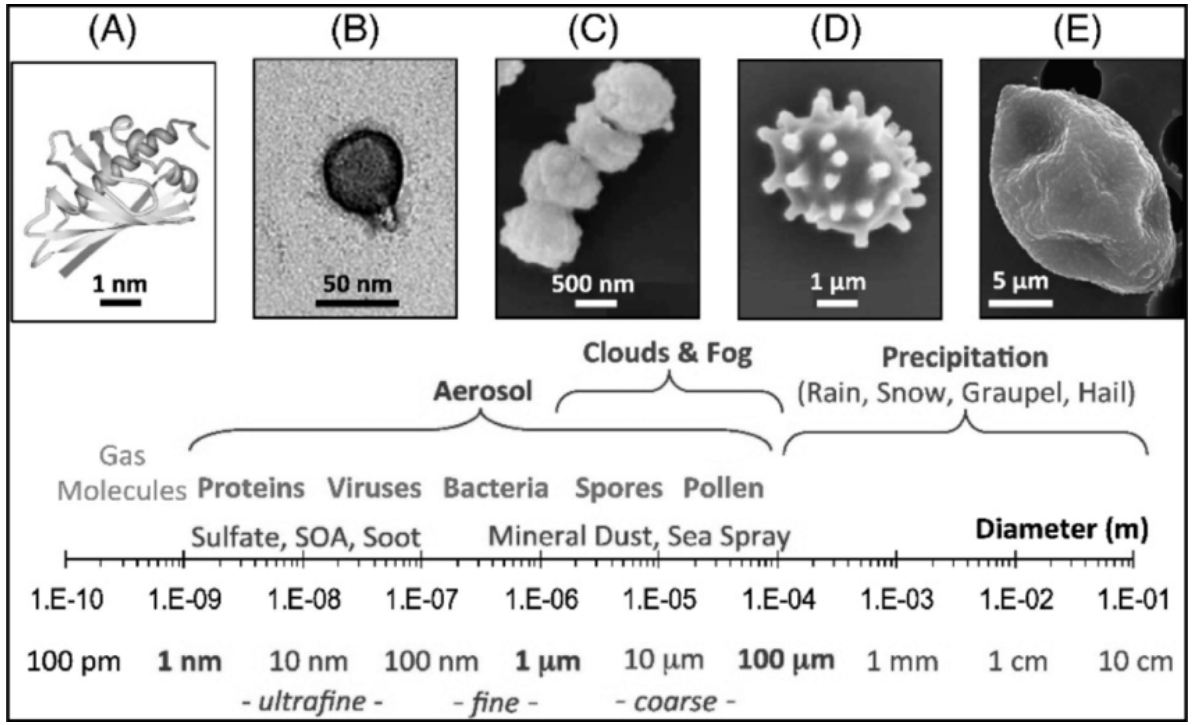


Fig 2: Characteristic size ranges of atmospheric particles and bioaerosols
(A) protein (B) virus, (C) bacteria, (D) fungal spore and (E) pollen grain
(Fröhlich-Nowoisky et al. 2016)

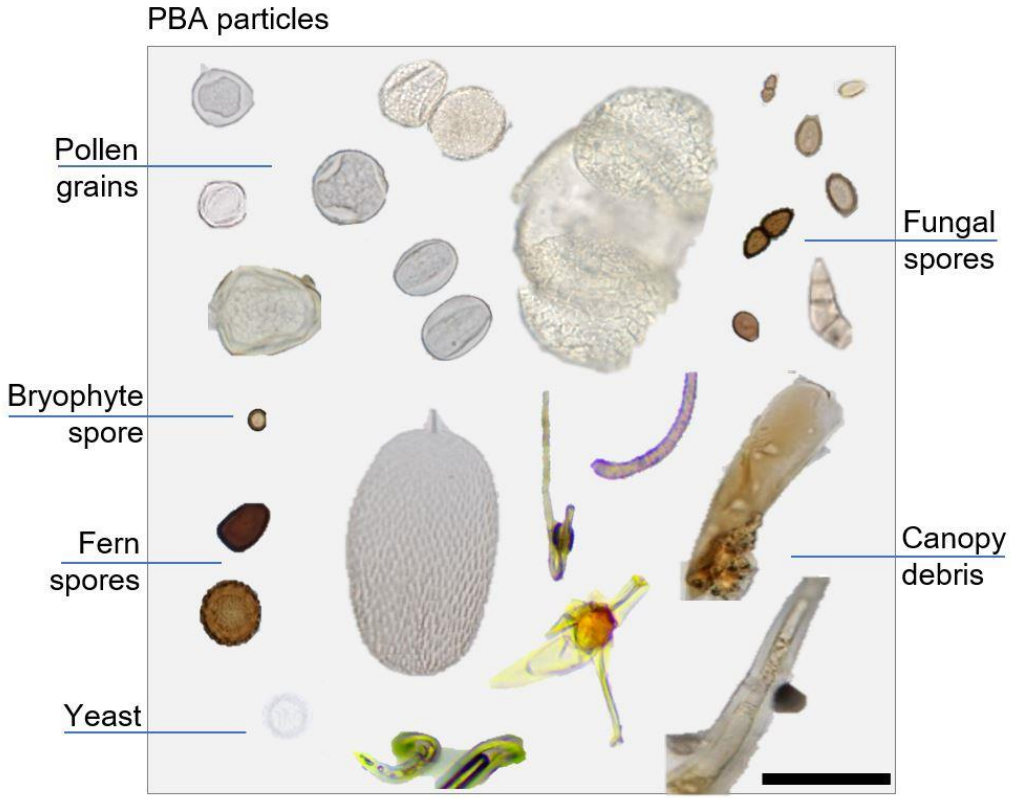
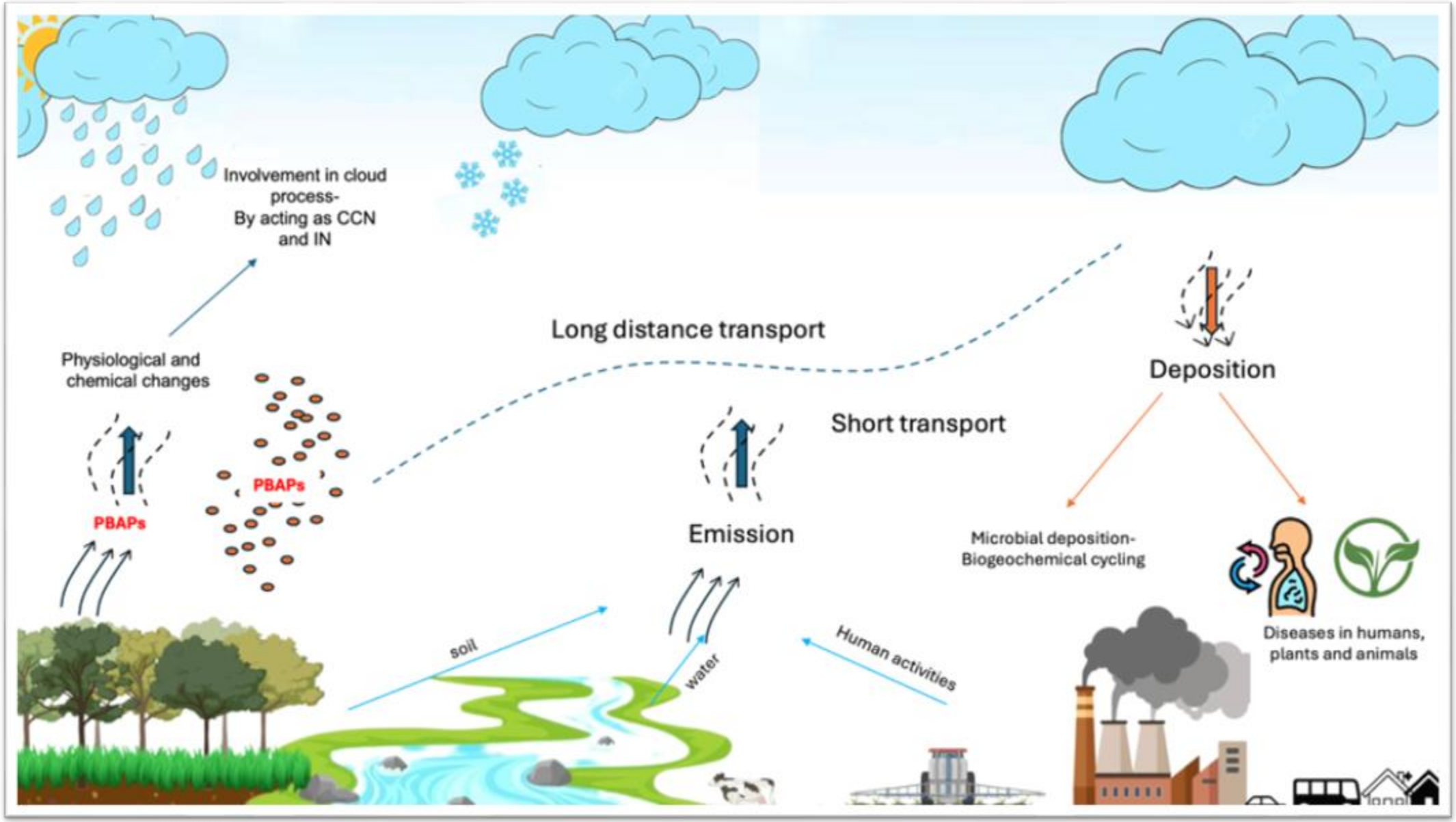
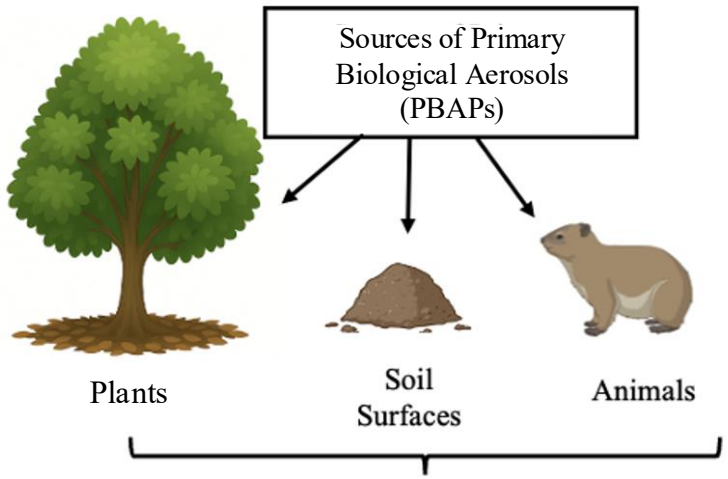


Fig 3: Microscopic images of giant aerosol particles found at ATTO
(Barbosa et al., 2022)

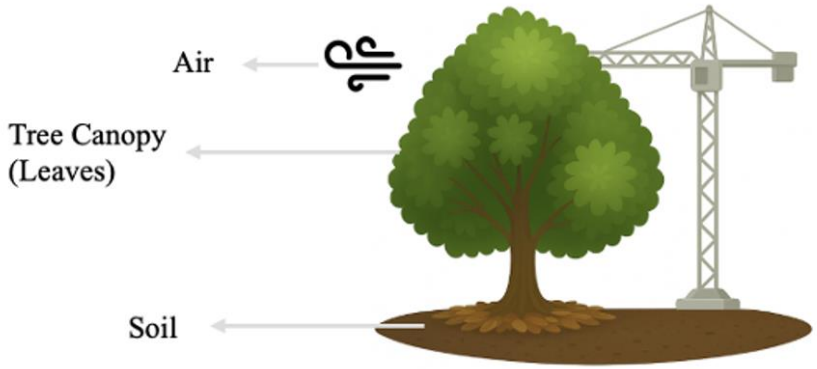
Why to study them?



RESEARCH OBJECTIVE-



STUDY SITE- Leipzig Canopy Crane (LCC)



STUDY MICROORGANISMS-

SEASONAL COMPARISON-

CHALLENGE-

PBAPs travel short as well as long distances making it difficult to trace their exact sources.

Objectives: Tracing the origins of PBAPs

- To compare air vs. soil microbial diversity and composition.
- To determine the extent to which soil acts as a source of airborne microbes.
- To evaluate the influence of seasonality and tree type on PBAPs diversity.
- To advance the understanding of ecological role of the PBAPs contributing to broader insights into biodiversity dynamics and ecosystem functioning.

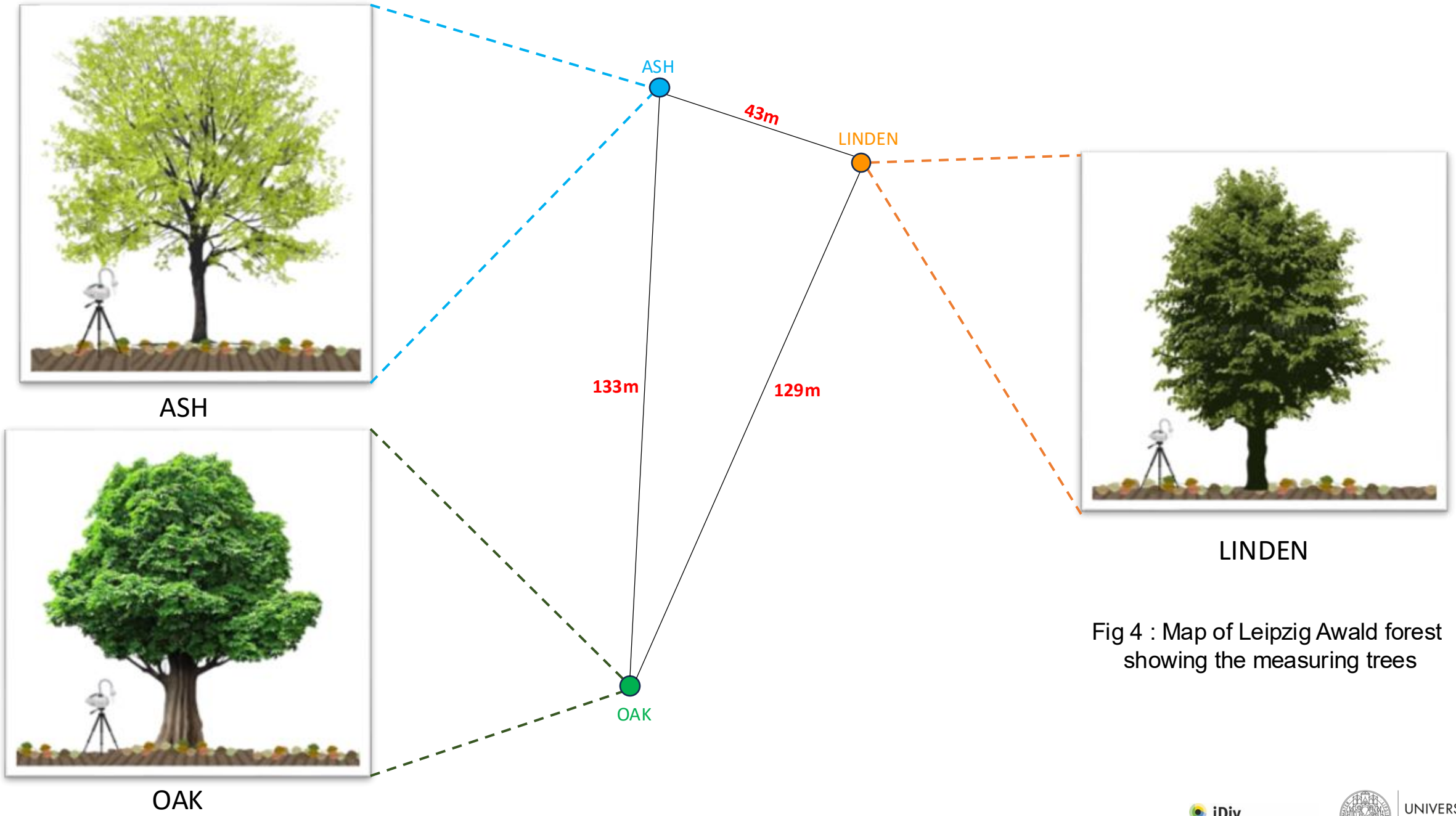
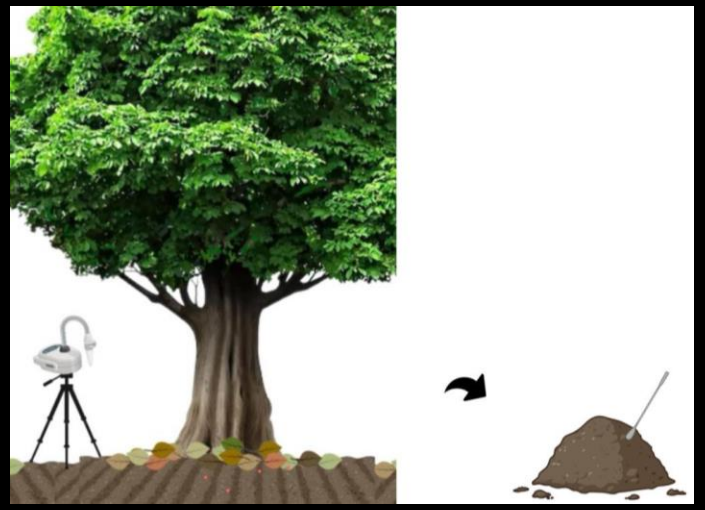


Fig 4 : Map of Leipzig Awald forest showing the measuring trees

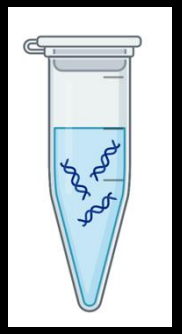
METHODOLOGY

1



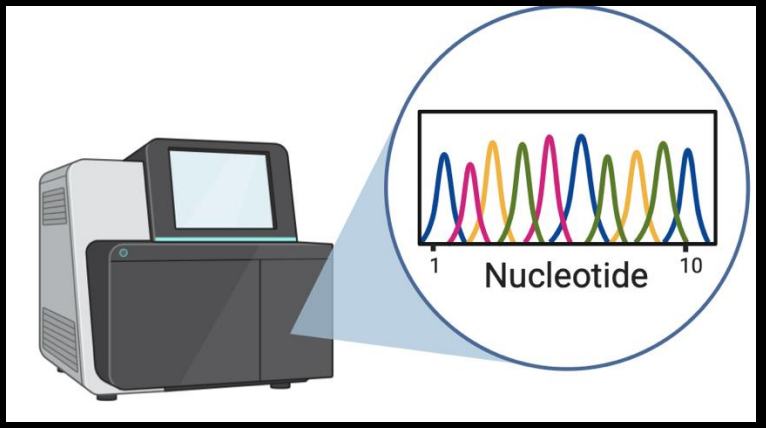
Air and Soil sampling

2



DNA extraction

3

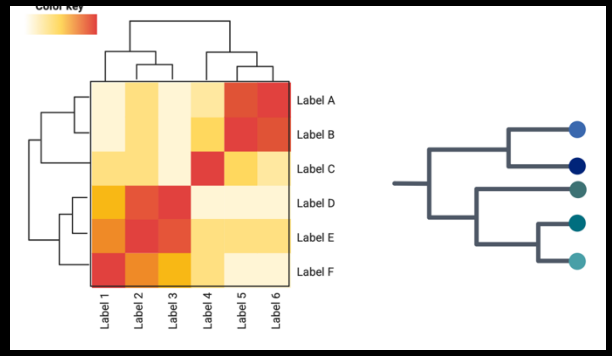


Next Generation Sequencing (NGS)

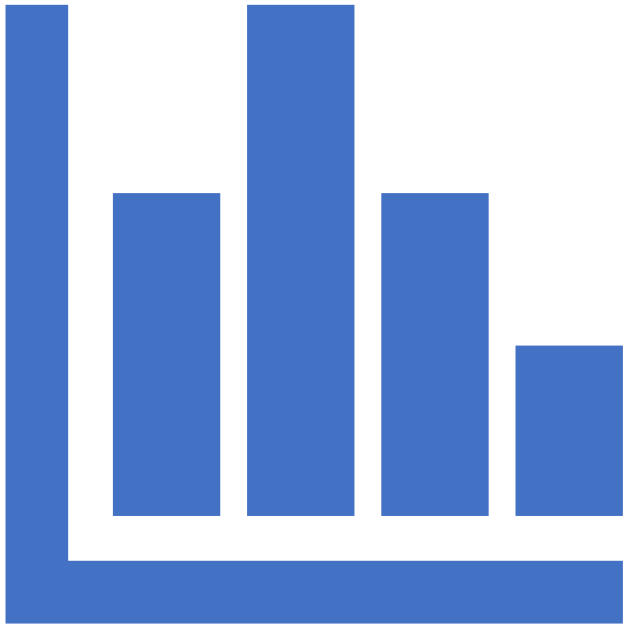
qPCR

Flow cytometry

Organic matter analysis



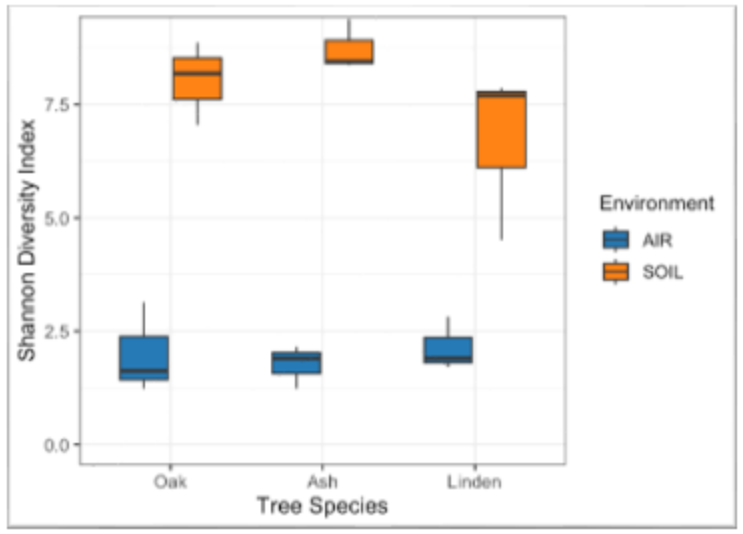
Amplicon Sequence Variance (ASV) analysis



Results

1. Alpha Diversity
2. Beta Diversity
3. Taxonomic classification

BACTERIA



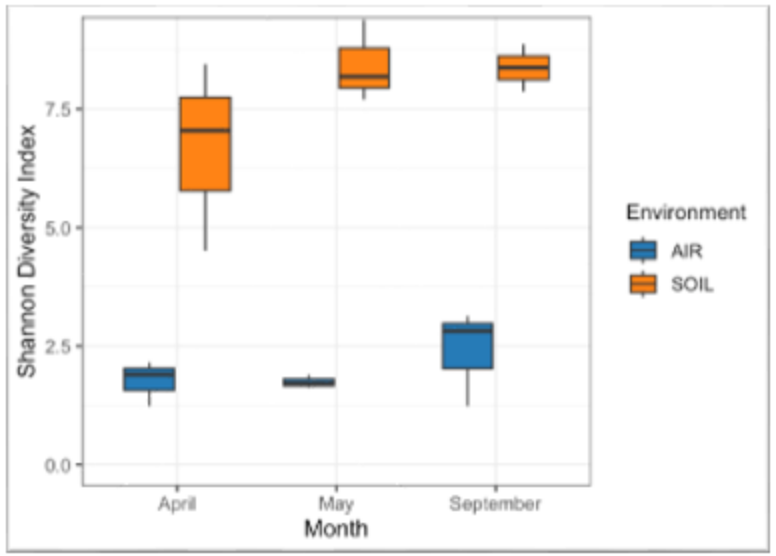
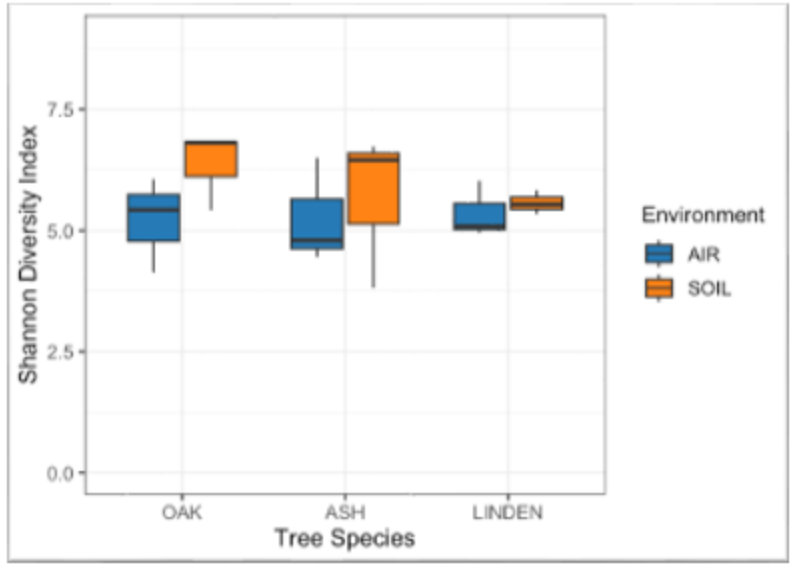


Fig 5: Alpha diversity-Shannon index for bacterial samples
i) based on tree type ii) based on month

FUNGI



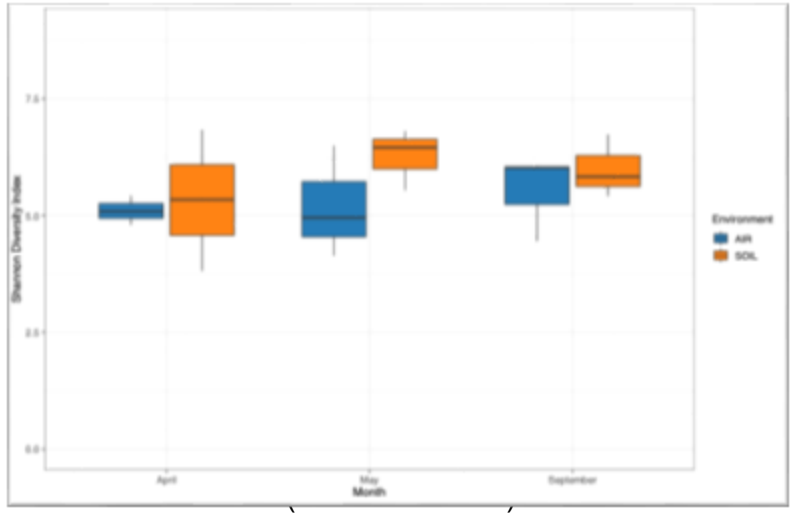


Fig 6: Alpha diversity-Shannon index for Fungal samples
i) based on tree type ii) based on month

BACTERIA

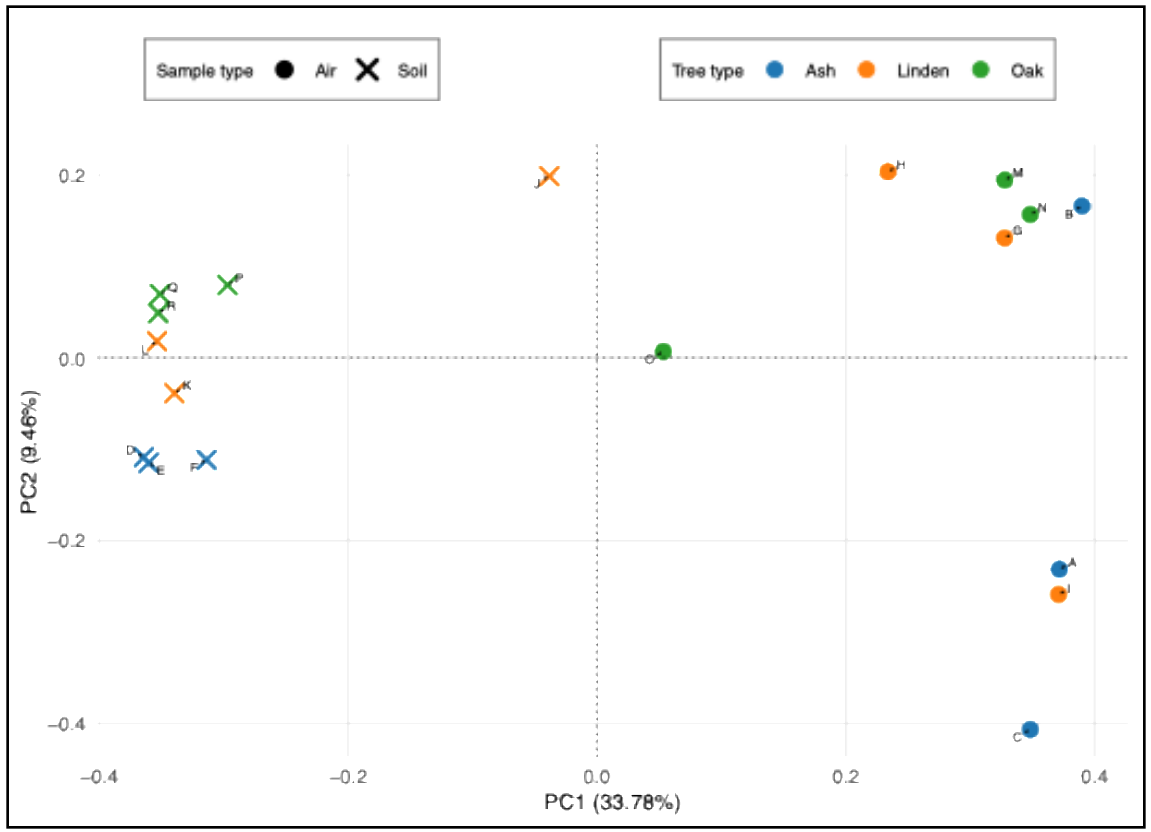


Fig 7: Beta diversity-Unweighted UniFrac for bacteria (based on tree type and month)

FUNGI

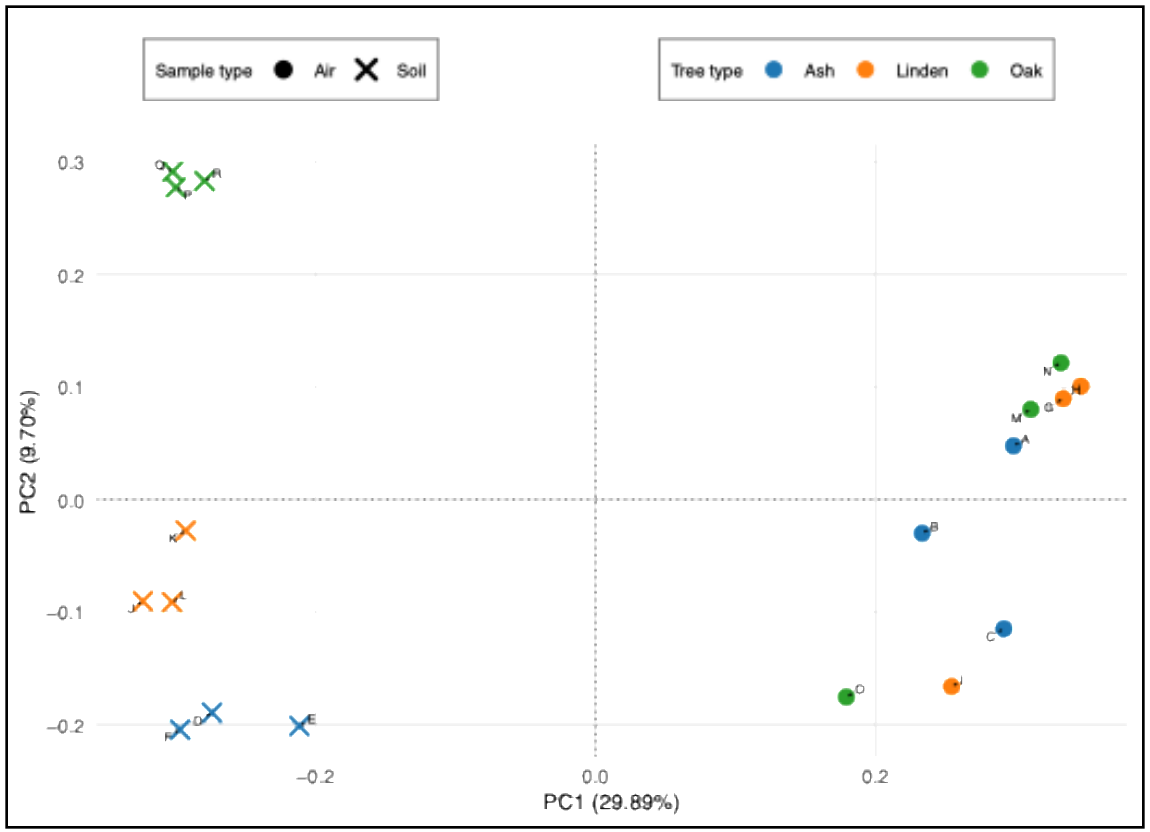
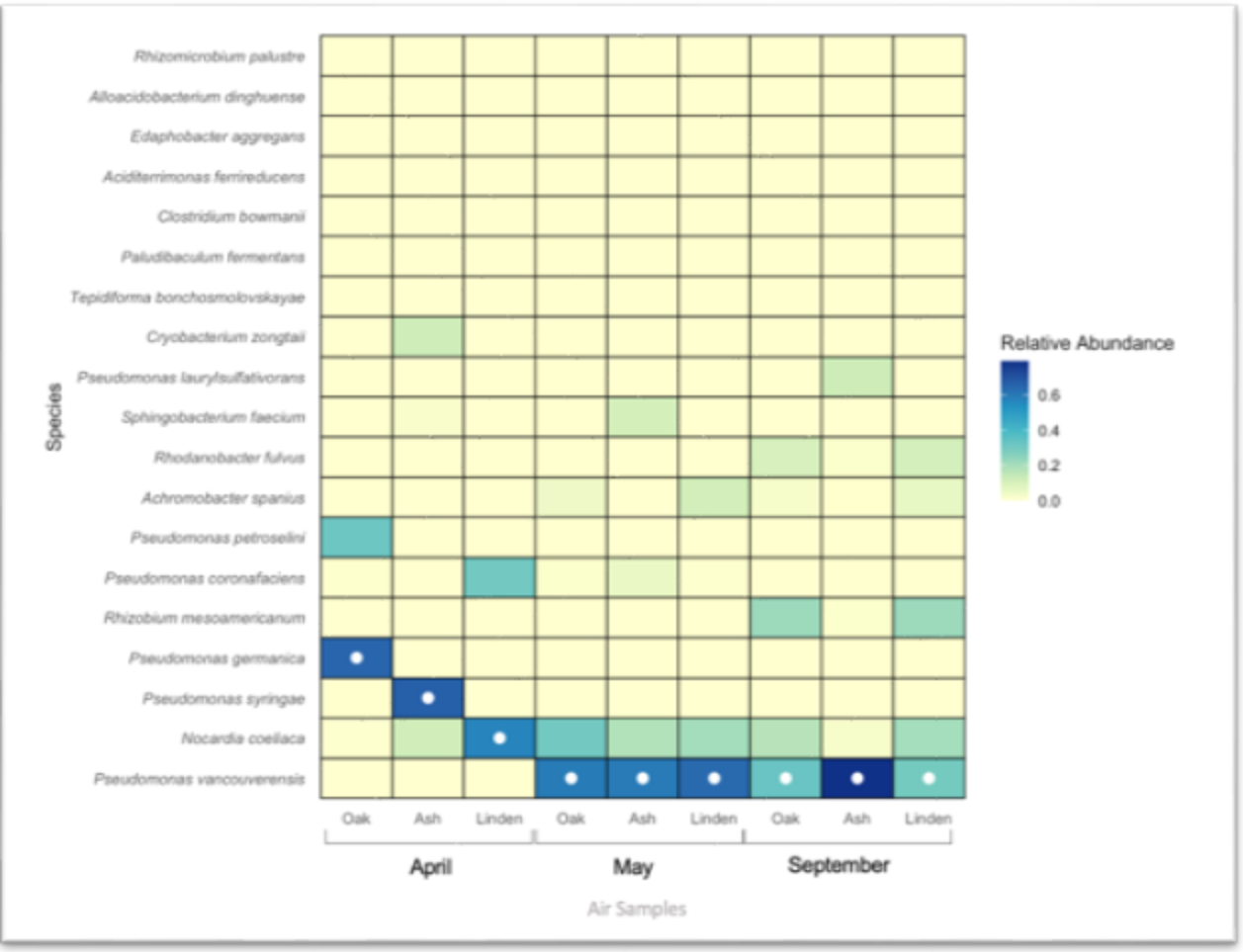


Fig 8: Beta diversity-Unweighted UniFrac for fungi (based on tree type and month)

BACTERIA

Air



Soil

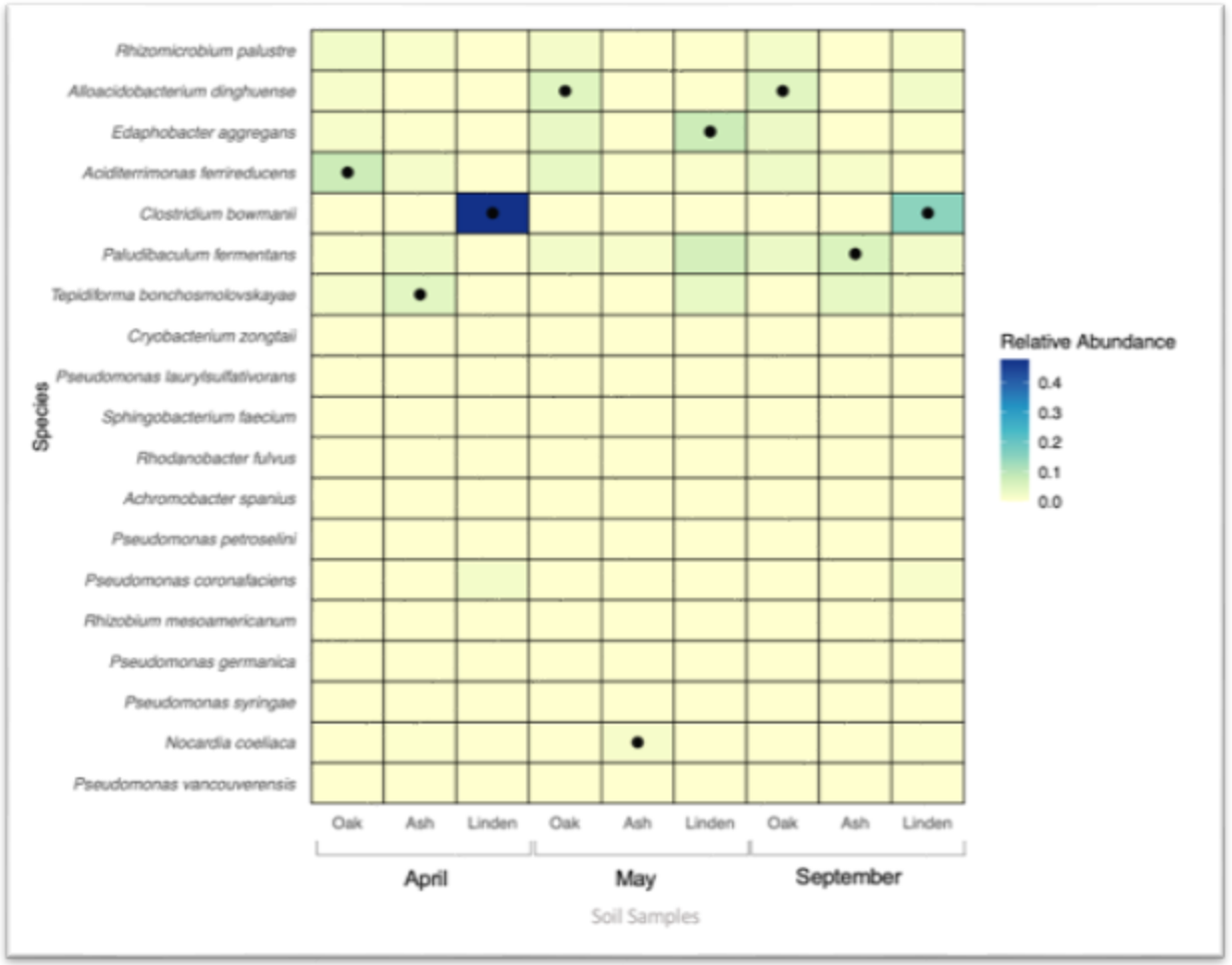


Fig 9: Heat Map comparing most dominant bacterial species

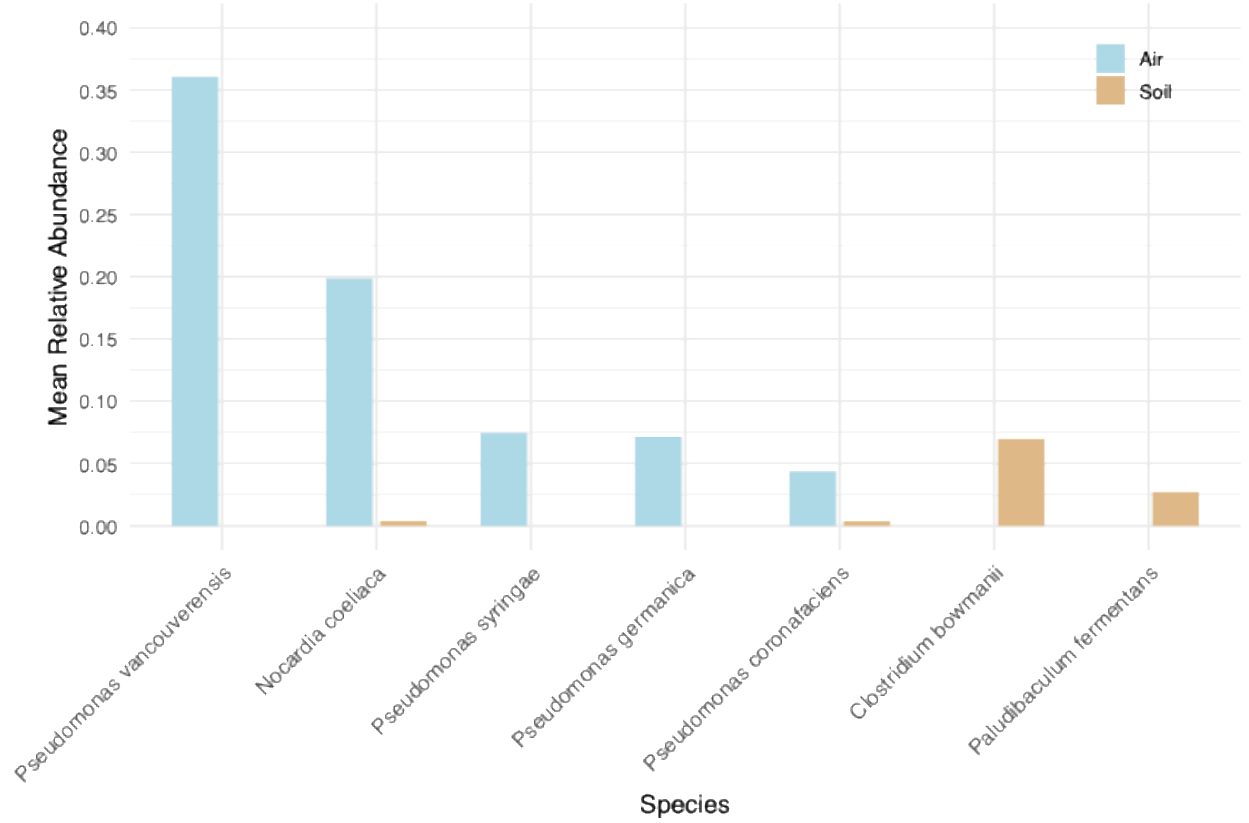
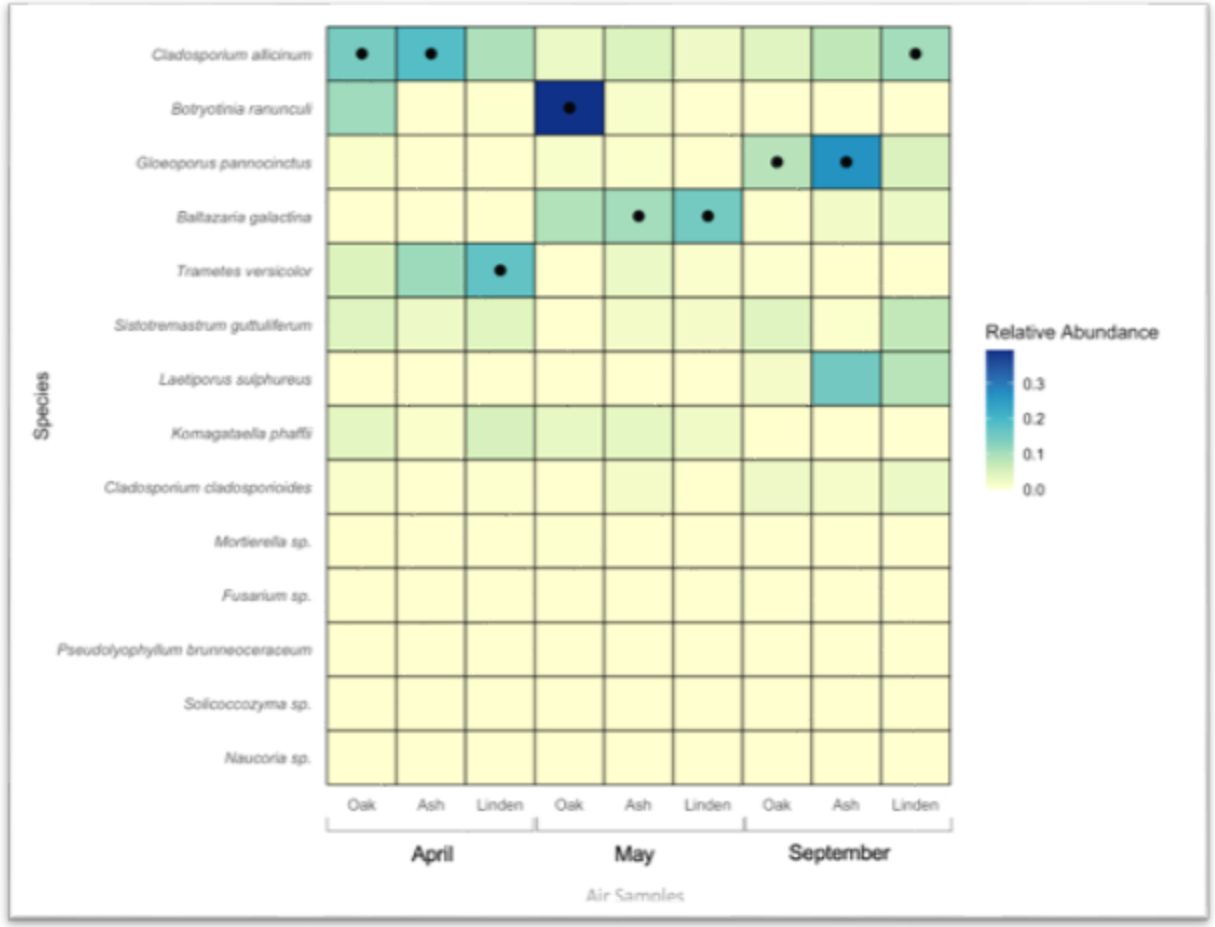


Fig 10: Comparison of mean relative abundance of the most dominant bacterial species in the air samples

FUNGI

Air



Soil

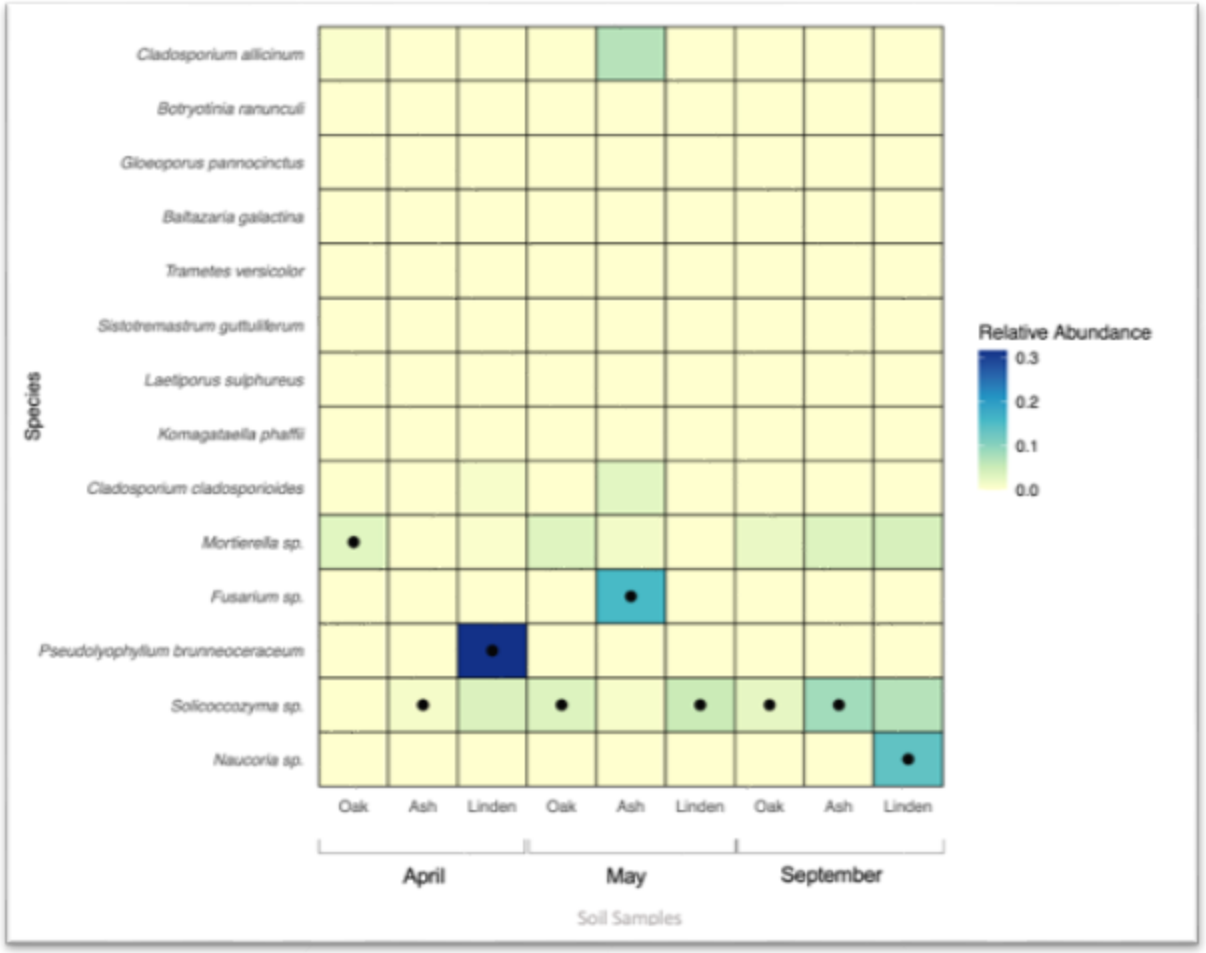


Fig 11: Heat Map comparing most dominant fungal species

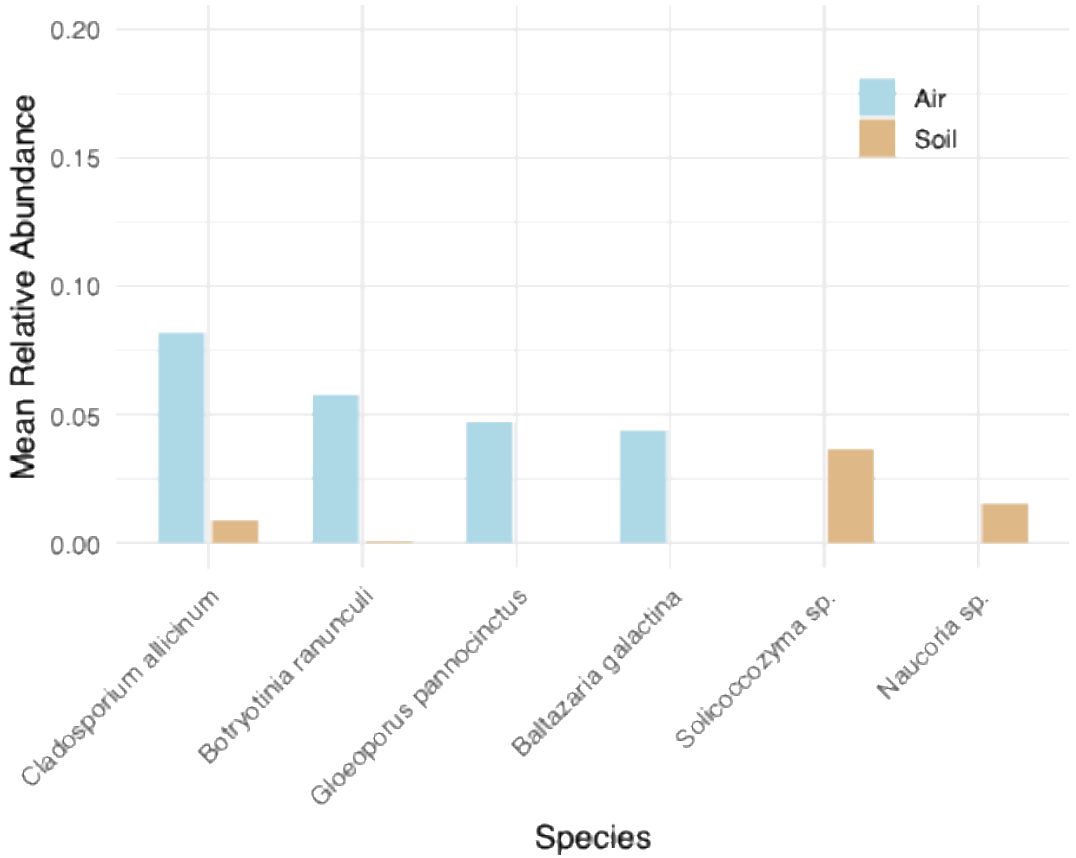


Fig 11: Comparison of mean relative abundance of the most dominant Fungal species in the air samples

FUNGuild based classification

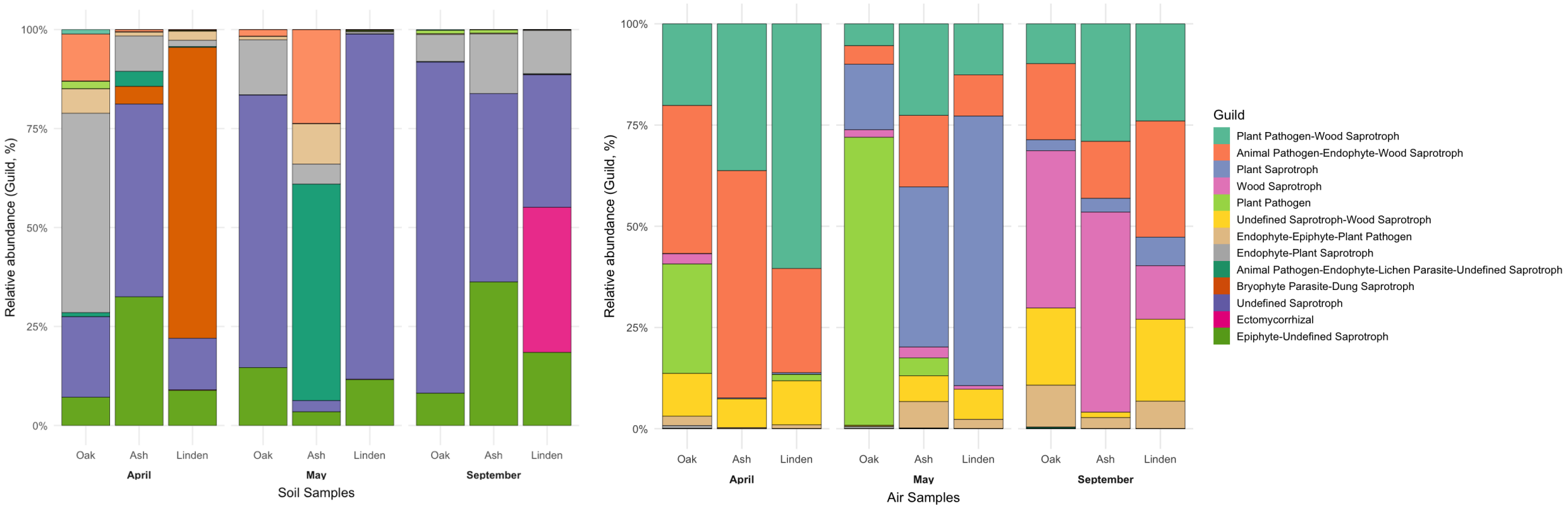


Fig 13: Comparison of to most dominant guilds in air a) Soil and b) air samples

Conclusions:

- For Bacteria, air samples showed *lower diversity*, mostly dominated by a few similar species like *Pseudomonas* spp. while soil samples were *more diverse and even*.
- For Fungi, air samples showed relatively higher diversity, similar to the corresponding soil samples.
- Microbial communities in soil and air were distinctly separated in composition.
- Seasonality and tree type did not seem to influence the composition and diversity of PBAPs in our dataset.
- Soil does not appear to be the original source of the dominant airborne microbes, suggesting the need for further exploration of other sources like phyllosphere and surrounding water bodies.

- For the ecological role analysis of Fungi, the soil samples showed dominance of saprotrophs and epiphytes while the air samples showed dominance of wood saprotrophs and plant/animal-pathogens.
- The presence of potential plant as well as animal pathogens in the air reinforces the importance of air monitoring.

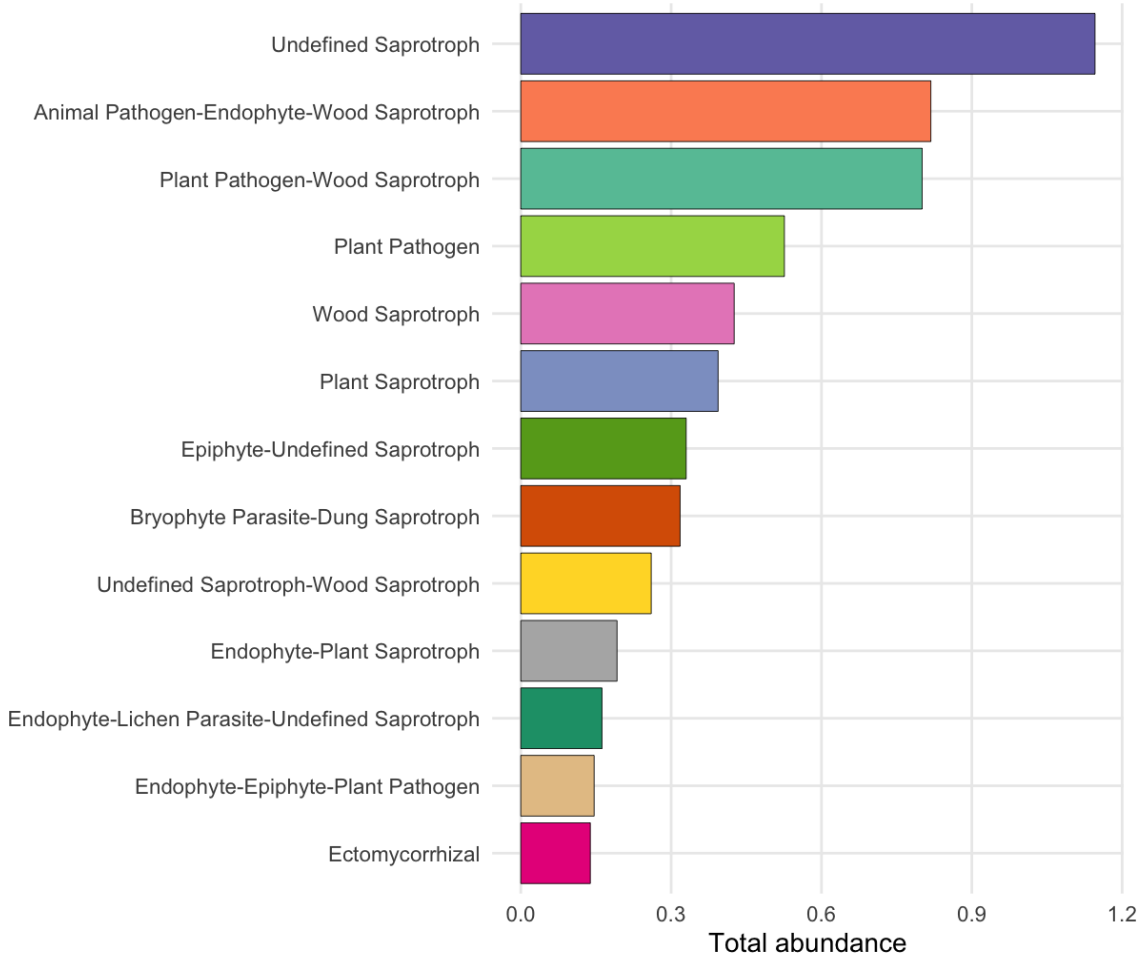
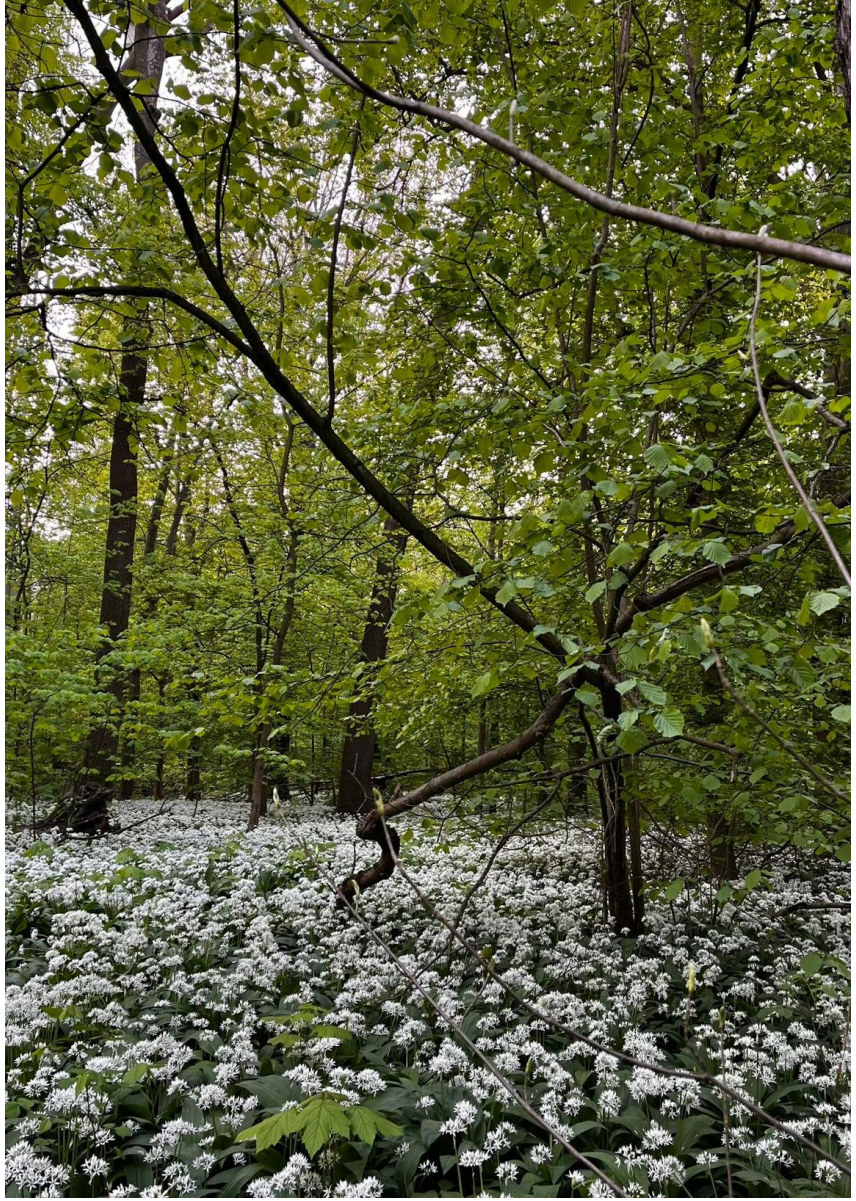


Fig 14: Most dominant guilds in soil and air samples



THANK YOU!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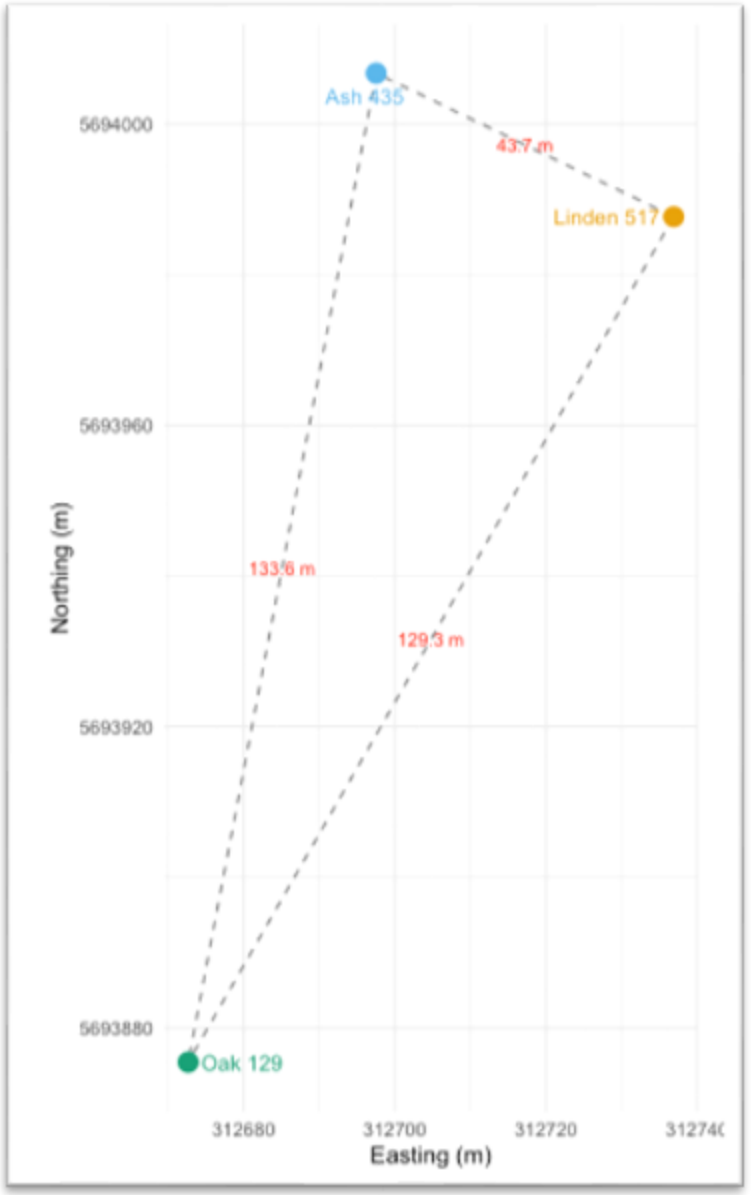
Supplementary material-



	Tree	Sample type	Month
A	Ash	Air	April
B	Ash	Air	May
C	Ash	Air	September
D	Ash	Soil	April
E	Ash	Soil	May
F	Ash	Soil	September

	Tree	Sample type	Month
G	Linden	Air	April
H	Linden	Air	May
I	Linden	Air	September
J	Linden	Soil	April
K	Linden	Soil	May
L	Linden	Soil	September

	Tree	Sample type	Month
M	Oak	Air	April
N	Oak	Air	May
O	Oak	Air	September
P	Oak	Soil	April
Q	Oak	Soil	May
R	Oak	Soil	September

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For 16S

- **Primers-** 16S V3-V5 region (459 bp approx)

341F: CCTACGGGNGGCWGCAG

799R: CYAACGAGCGCAACCC

- **Sequencing depth**: Between ~100k–120k usable reads per sample (after QC).
- **Amplicon size**: ~460 bp (16S V3–V5 region, 341F, 799R).
- **Primers**: Standard 341F/799R primer set, removed during preprocessing.
- Bacteria (16S V3–V5, 341F–799R primers)
- Databases: NCBI NT + RDP
- **Reads per sample** (raw to non-chimeric):

Raw data (initial reads): ~**125,099**
Non-chimeric reads (after removing chimeras): ~**36,837**
ASVs after length filtering (final usable reads): ~**35,067**

For ITSFngs

- The fungal sequencing targeted the ITS region (Internal Transcribed Spacer).
- **Primers-** ITS1F (forward) and ITS2R (reverse).
  - ITS1F: CTTGGTCATTTAGAGGAAGTAA
  - ITS2 R: GCTGCGTTCTTCATCGATGC
- **Amplicon size**: 250–600 bp (variable across fungal taxa).
- **Databases**: UNITE Fungi + NCBI NT + UNITE INSD All eukaryotes.
- Analysis: ASV (DADA2) pipeline
- **Reads per sample** (raw to non-chimeric):

  Raw: 102,544 – 151,989 (median 134,596)
  Non-chimeric: 84,494 – 118,802 (median 110,264,
  mean ~107,930)
  Overall retained (final vs. raw): ~82.7%

Month	Mean temperature (average)	RH% (average)	Wind speed (average)
April 2024	≈ 11.3 °C	72 %	14.3 km/h
May 2024	≈ 15.9°C	75 %	15 km/h
September 2024	≈ 13°C	69 %	21.1 km/h