

Investigating spore dispersal and pathogen populations in UK arable crop systems

Seasonal airborne fungal communities across wheat, oilseed rape and oat field systems

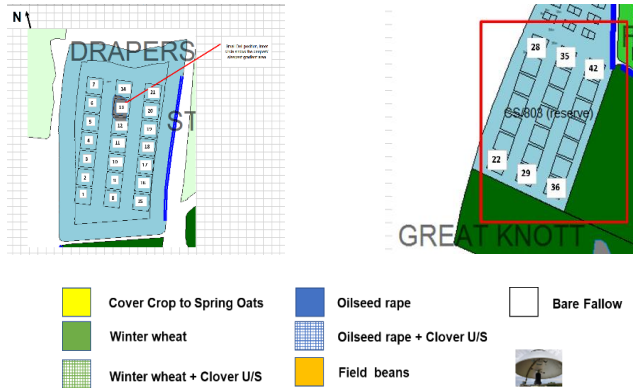
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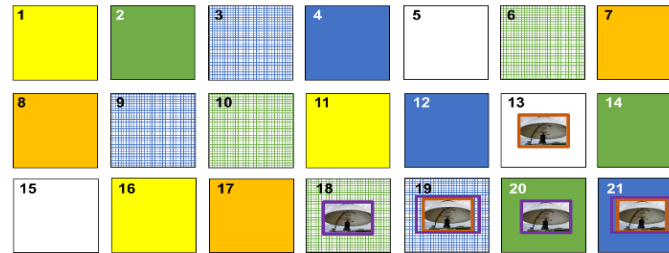
Experimental design and analytical workflow

Field sampling layout

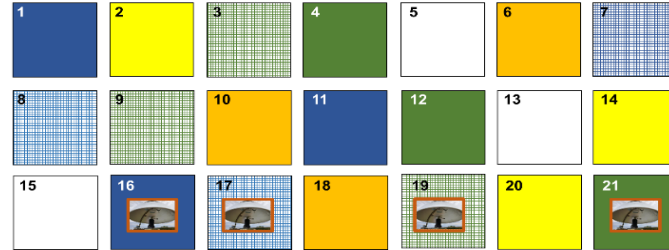


Two field sites and repeated seasonal deployments allowed comparison across crops, rotations and management combinations.

2023-24



2024-25



Sampling Procedure



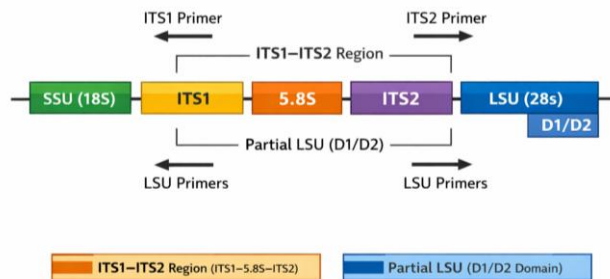
- Rotorod spore traps
- Weekly collections
- 7-week sampling period
- Spring and Autumn
- Placed at 0.5 & 2.5 meters

Experimental design and analytical workflow B

Fungal ITS

The **Internal Transcribed Spacer (ITS)** region of ribosomal DNA is the most widely used genetic marker for identifying fungi.

- **Highly variable between species** – allows accurate taxonomic identification
- **Conserved flanking regions** – universal primers can amplify a wide range of fungi
- **High copy number in fungal genomes** – improves detection sensitivity in environmental samples
- **Extensive reference databases** (e.g. UNITE) enable reliable sequence classification



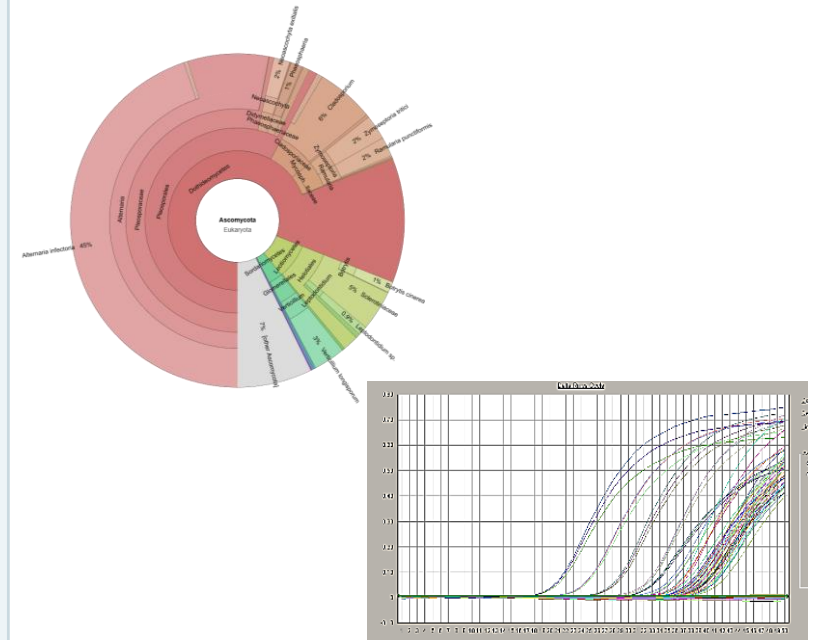
MinION sequencing & Metabarcoding

- Samples run through ONP MinION
- Added barcodes to label samples
- Pooled samples into one sequencing library
- Loaded library onto a MinION flow cell



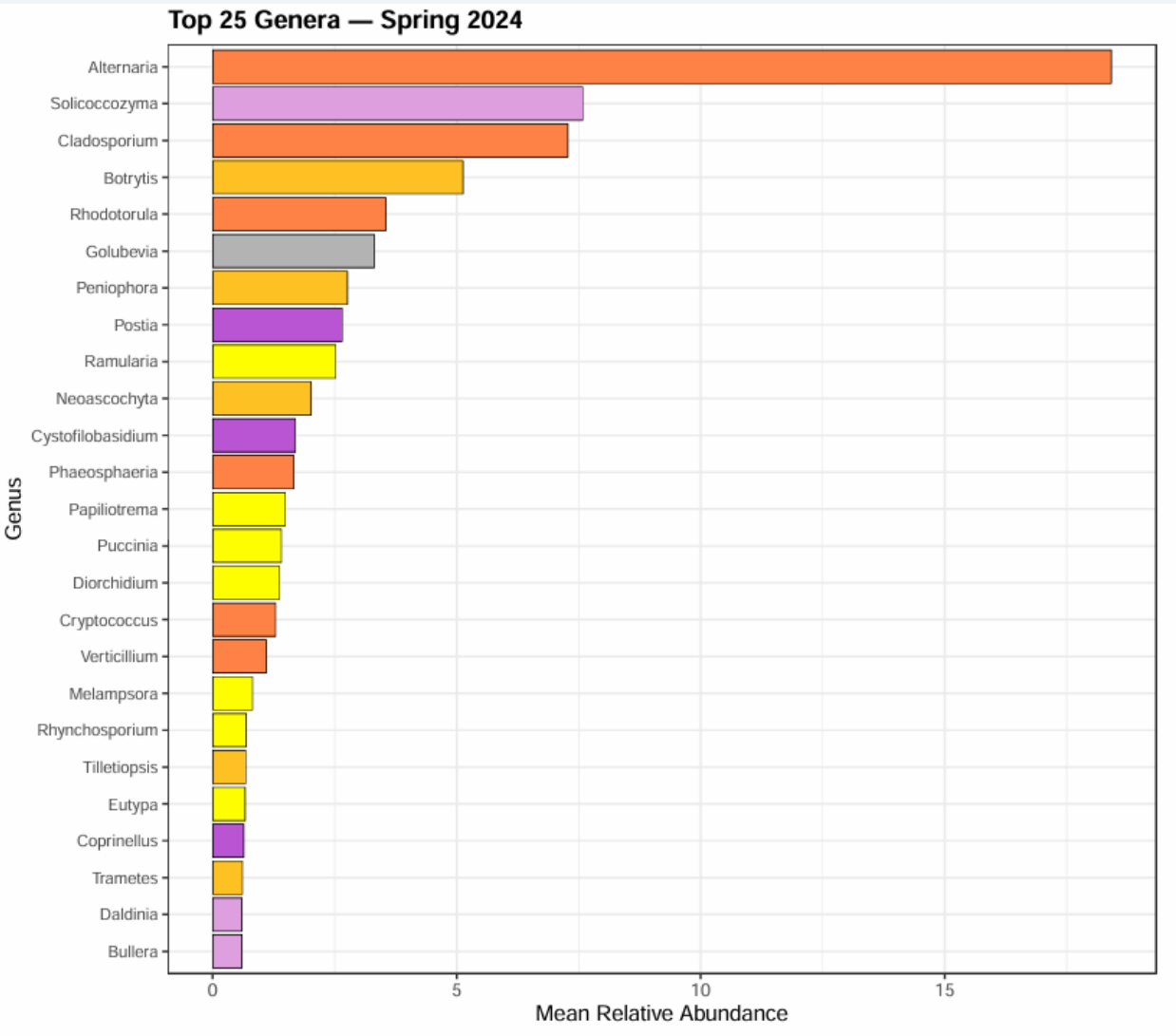
Molecular analysis

- GAIA output analysed in R for abundance and alpha/beta diversity.
- qPCR used to quantify major wheat and OSR pathogens.



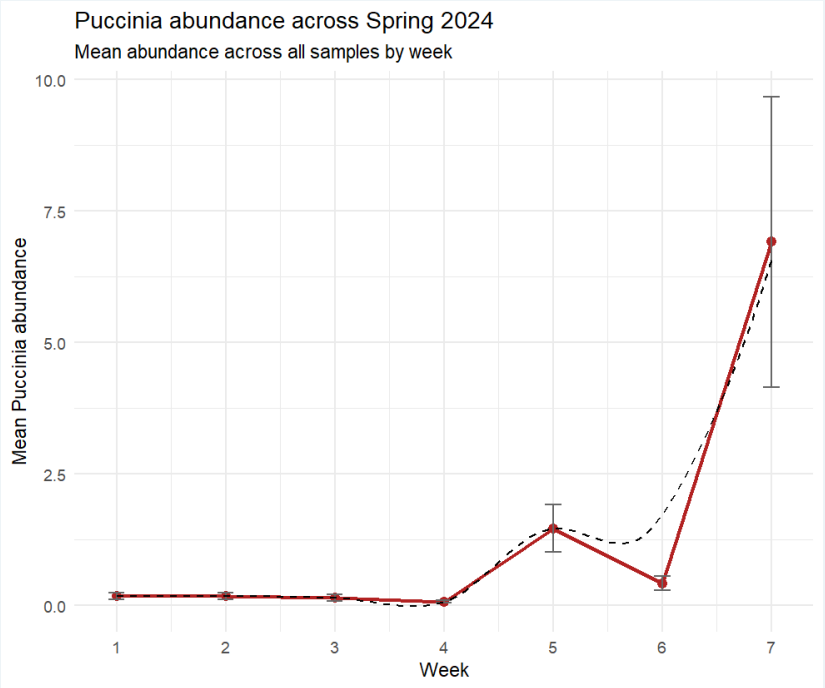
Seasonal sampling overview

Analysis of Abundance



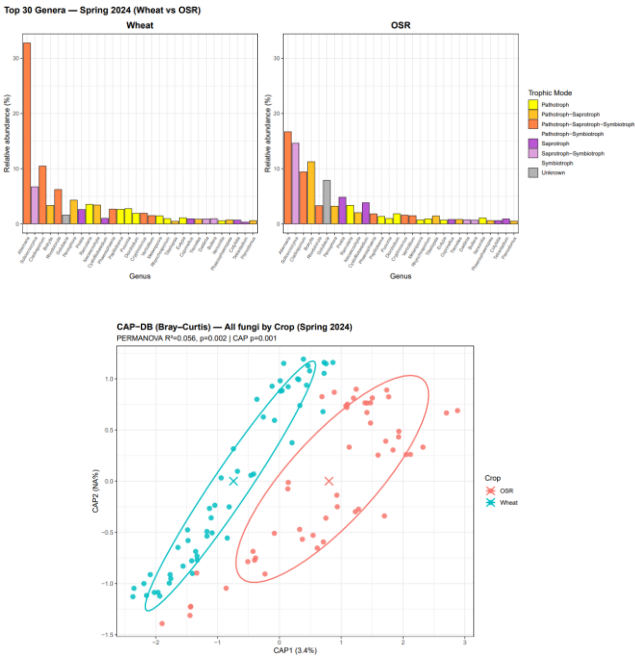
Spring 2024

Spring 2024 communities again showed strong dominance of crop-associated and phyllosphere taxa. *Alternaria* (21.53%), *Solicoccozyma* (8.87%) and *Cladosporium* (8.51%). *Botrytis* (5.99%) was also prominent, with all species-level assignments corresponding to *Botrytis cinerea*. Additional recurrent taxa included *Golubevia* (3.87%), *Ramularia* (2.95%), and *Neoascochyta* (2.36%).



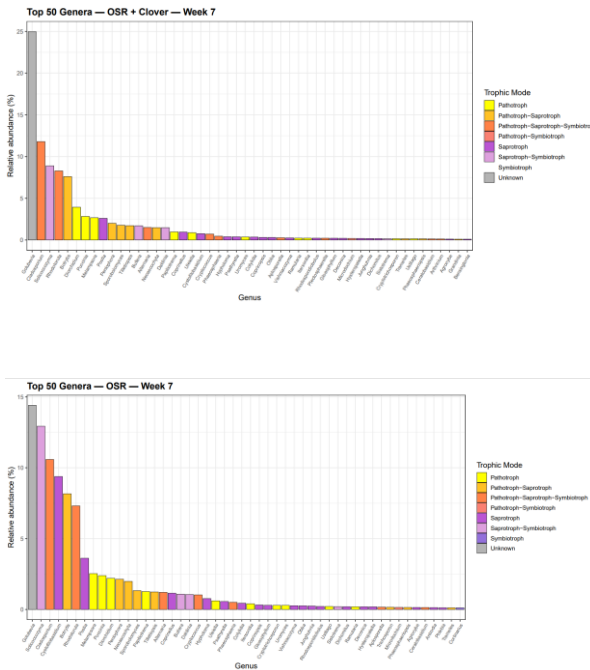
Crop, cover crop and weather effects

Crop effects



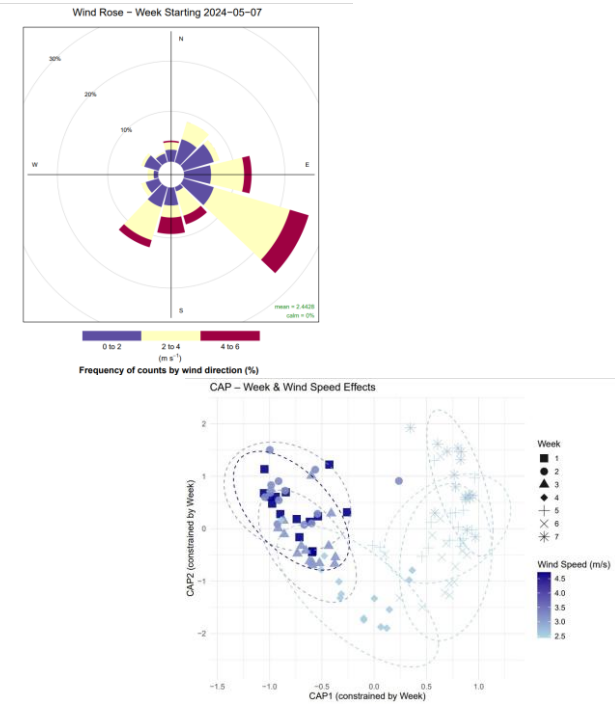
Crop identity separated communities and shifted the abundance of key genera.

Cover crop effects



Clover management also reorganised community structure, especially within Spring 2024 comparisons.

Wind effects

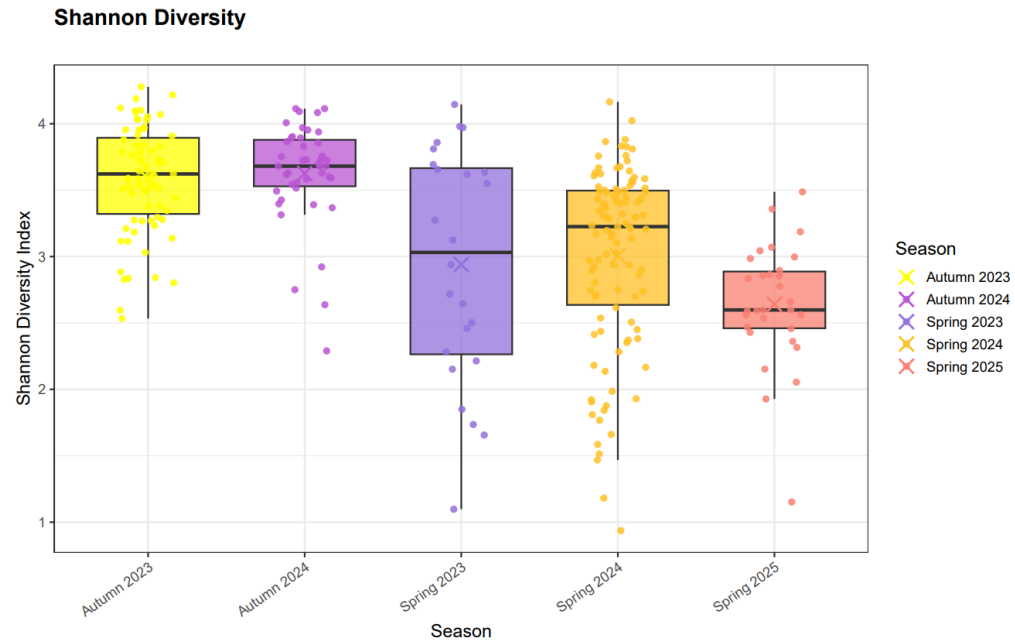


Wind speed and direction helped explain short-term variation in airborne assemblages.

Diversity and community structure

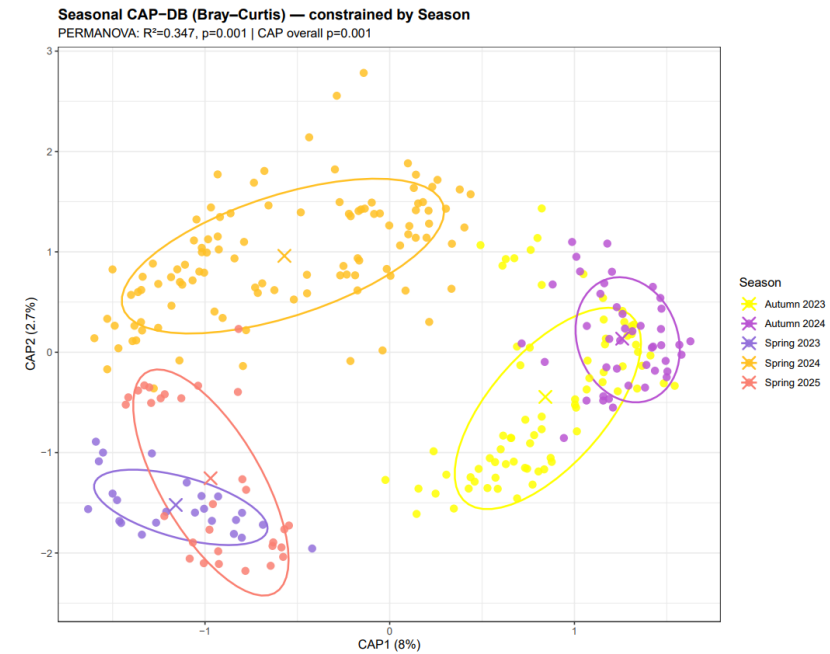
Alpha diversity

Shannon diversity was highest and most consistent in autumn, while spring communities were lower in diversity and more variable.



Beta diversity

Season explained a significant share of community composition, with distinct clustering and greater dispersion among spring samples.





FUNGAL COMMUNITY ANALYSIS & PATHOGEN POPULATIONS IN UK ARABLE CROP SYSTEMS

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Background

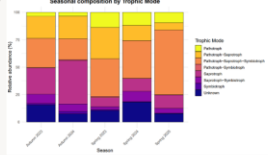
- Airborne fungal communities are highly diverse and dynamic, composed of spores capable of long-distance wind dispersal and originating from plant surfaces, soils, crop residues, and surrounding habitats.
- Plant pathogens are dispersed through the atmosphere, enabling rapid spread of disease and making airborne fungi directly relevant to disease forecasting.
- Seasonal dynamics of airborne fungi above wheat and OSR remain poorly understood, particularly the roles of crop identity, transitions, and management.

Methodology

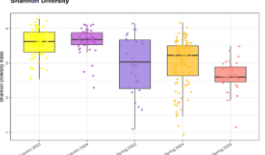
- Airborne fungi were sampled above arable crops at two experimental field sites as part of the Growing Health Institute Strategic Programme.
- Spores were collected using **roto-rod samplers** deployed within wheat and oilseed rape plots.
- Extracted DNA was amplified (ITS1-ITS2). Amplicons were sequenced on an Oxford Nanopore MinION platform, quality filtered, and taxonomically assigned using the GAIA metagenomics pipeline.



Results 1: Seasonal Effect



Clear seasonal shifts were observed in the trophic composition of airborne fungal communities. Saprotrophs dominated in autumn, while spring communities showed a greater contribution from mixed pathotrophic modes.



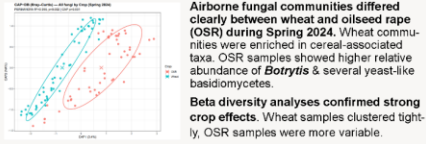
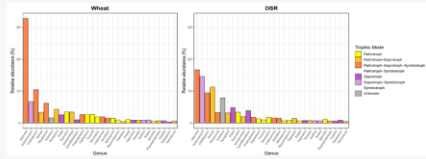
Shannon diversity varied strongly among seasons. Diversity was highest and most consistent in Autumn 2023–2024, whereas spring samples showed lower diversity and greater variability, with the lowest values in Spring 2025. Seasonal differences were significant (Kruskal–Wallis $\chi^2 = 86.16$, $p < 0.001$), with both autumn seasons differing from all spring periods ($p < 0.01$).



Beta diversity analysis revealed pronounced seasonal structuring. Canonical Analysis of Principal Coordinates showed clear separation between spring and autumn samples. Autumn samples displayed relatively consistent community composition.

Spring communities displayed greater dispersion, with Spring 2024 exhibiting the highest within-season variability. Spring 2023 and Spring 2025 formed distinct but partially overlapping clusters. **Season explained a significant proportion of the observed variation in community composition (PERMANOVA, $p = 0.001$).**

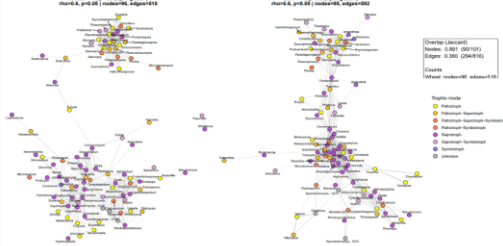
Results 2: Crop Effect



Airborne fungal communities differed clearly between wheat and oilseed rape (OSR) during Spring 2024. Wheat communities were enriched in cereal-associated taxa. OSR samples showed higher relative abundance of *Botrytis* & several yeast-like basidiomycetes.

Beta diversity analyses confirmed strong crop effects. Wheat samples clustered tightly, OSR samples were more variable.

Spring 2024 Co-occurrence Networks — Wheat vs OSR (Top 100)



Spring 2024 co-occurrence networks revealed marked differences in network structure between wheat and OSR. The OSR network had a comparable number of nodes but a higher number of edges than the wheat network indicating denser connectivity above OSR canopies. Node overlap between crops was high, while edge overlap was substantially lower demonstrating crop-specific differences.

Conclusion

Airborne fungal communities above arable crops were primarily **structured by season**, with pronounced differences between spring and autumn in diversity, functional composition, and network organisation. **Crop identity** further influenced spring communities, with wheat and oilseed rape showing distinct co-occurrence patterns despite high taxonomic overlap. Ongoing work is extending these findings by examining the effects of **clover cover cropping**, **meteorological drivers**, and **qPCR detection** of key pathogens, providing insight into short-term aerobiome dynamics and disease-relevant inoculum dispersal.

Questions?

Thank you