



Use of Molecular Techniques to Identify Everglades' Aquatic Fungal Community Associated with Cattail Decomposition

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Greater Everglades
Ecosystem Restoration
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sfwmd.gov

Peat Accumulation is a CERP/CEPP Restoration Objective

- It is a direct result of decomposition processes.
- Fungi are essential in decomposition and therefore directly impact peat accumulation.
- Fungi are known to produce phenol oxidase – among the few enzymes able to fully degrade phenolic compounds for example lignin. It is thought to be a **latch enzyme** to decomposition.
- Peat accumulation is critical to wetland health.



Research Objectives

- Determine effects of nutrient conditions and active management on fungal community diversity.
- Establish a relationship between decomposition rates and fungal diversity.
- Use study results to explore community structure, function relationship.
- Potentially use data as indicator of ecosystem conditions in future work.

Project Objectives

1. Test whether creating openings within densely vegetated areas will sufficiently alter trophic dynamics such that wildlife diversity and abundance is increased and quality of habitat is improved.

2. Assess to what extent the structure and function of these created open areas compare to the natural Everglades

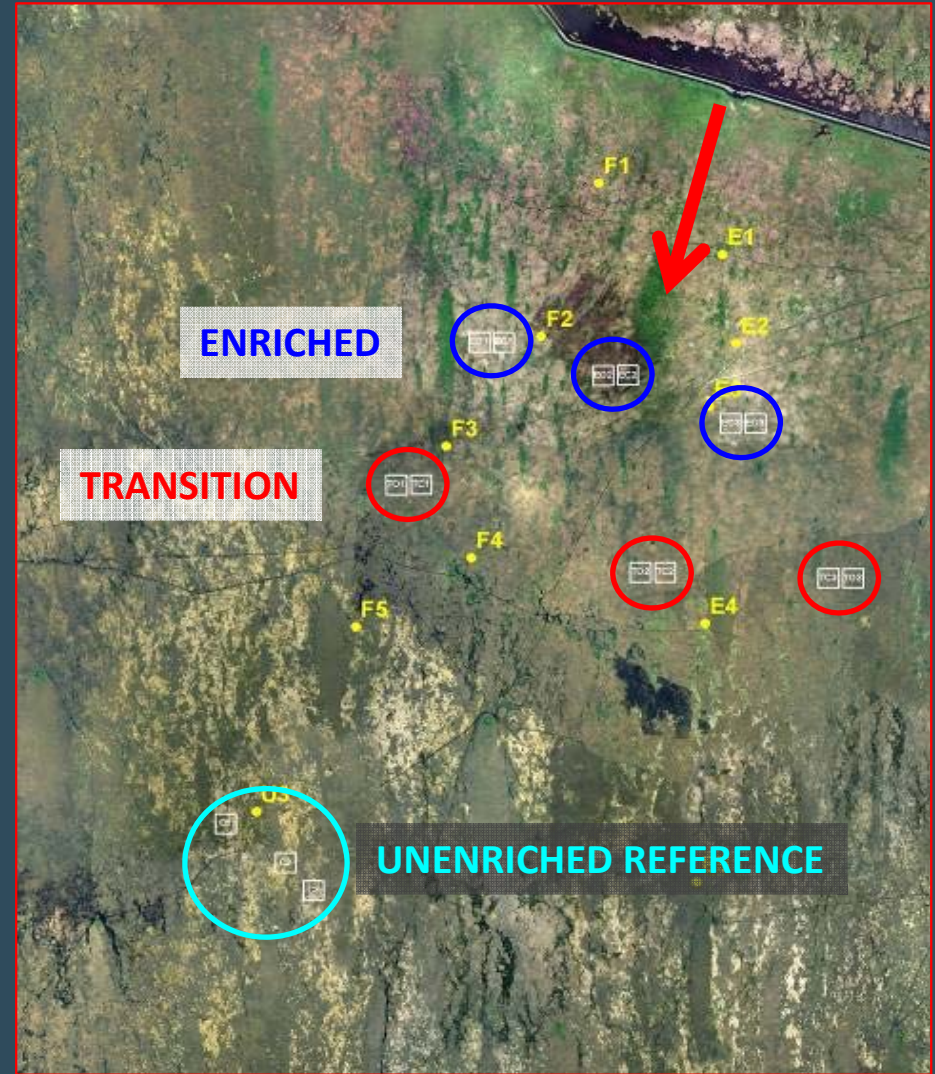


Cattail Habitat Improvement Project (CHIP)

Creating the “open” plots



Open & Control Pair



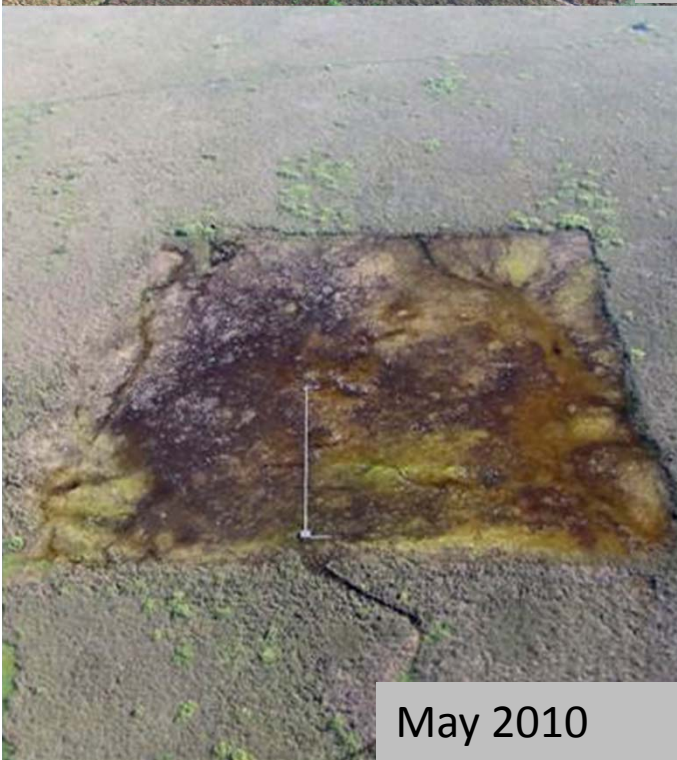
Succession of the Ecosystem (T01)



April 2006



October 2008

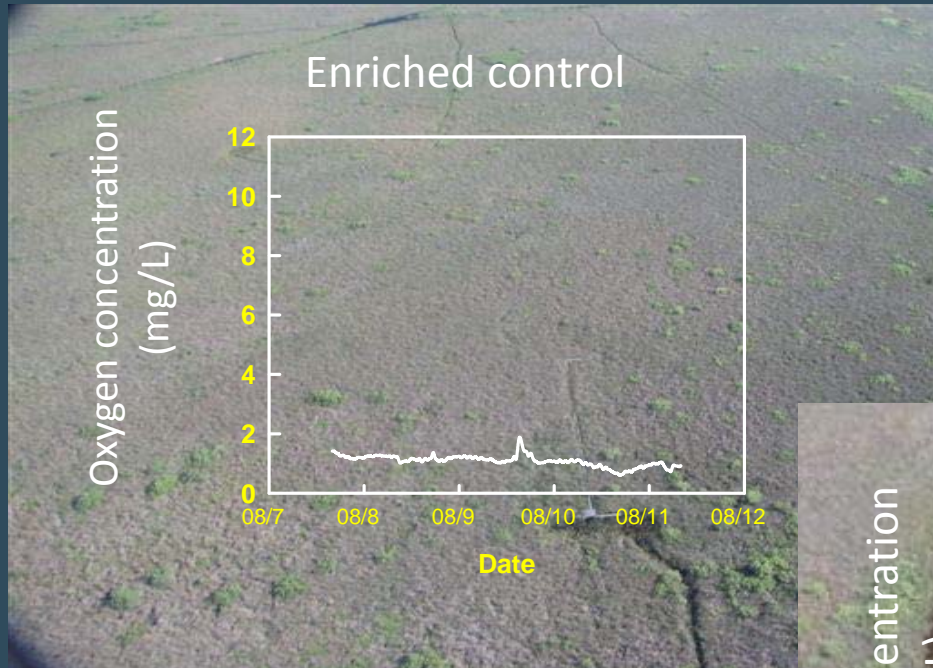


May 2010

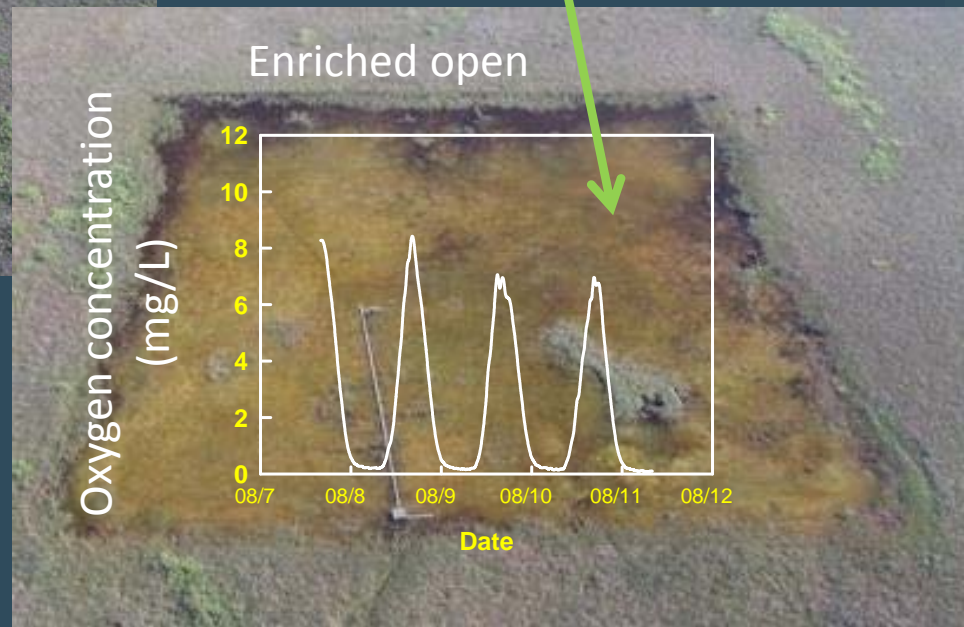


May 2012

Rapid Increase Daily Oxygen Concentrations in Open Plots



Algae and submerged vegetation



Hypotheses

- **1. Open vs. control:** Fungal consortia in these plots will have the ability to diversify improving function and ecosystem quality.
- **2. Nutrient gradient:** We will see greater species diversity in the areas of lesser nutrient impact.

Decomposition is captured by numerous parameters...

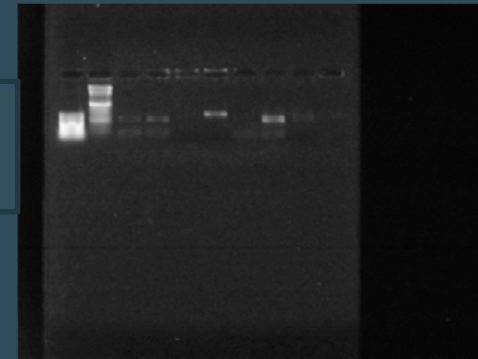
- Mass loss
- Litter nutrients
- Enzyme Activity
- Microbial biomass C,N,P and Respiration
- PLFA
- Primary production
- Water quality
- Hydrolabs
- Ergosterol
- **Molecular Ecology**



28S Gene Sequencing

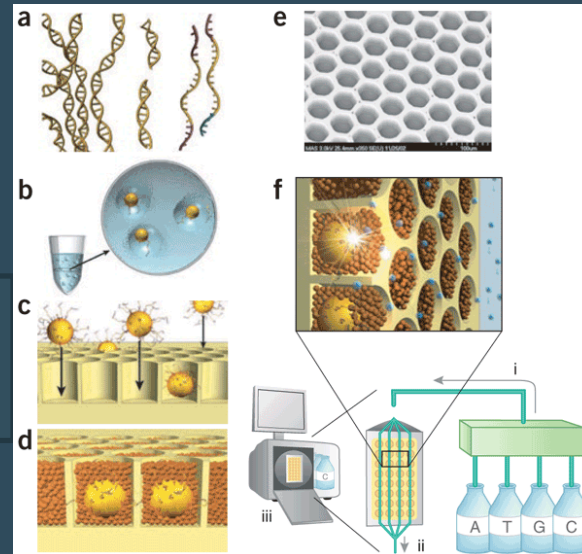
- DNA – Several iterations before arriving at the method we used.

PCR using fungi specific primers

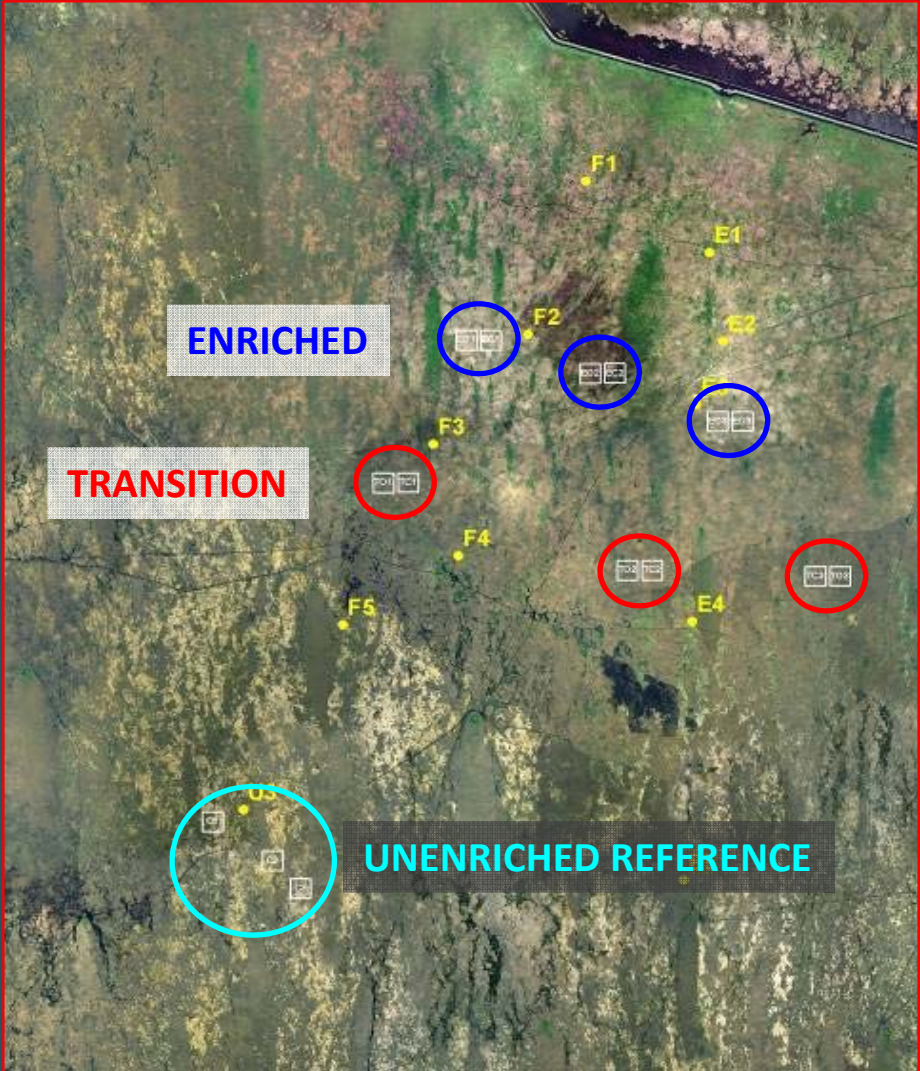


Cloning

Pyrosequencing



RESULTS



36 Months

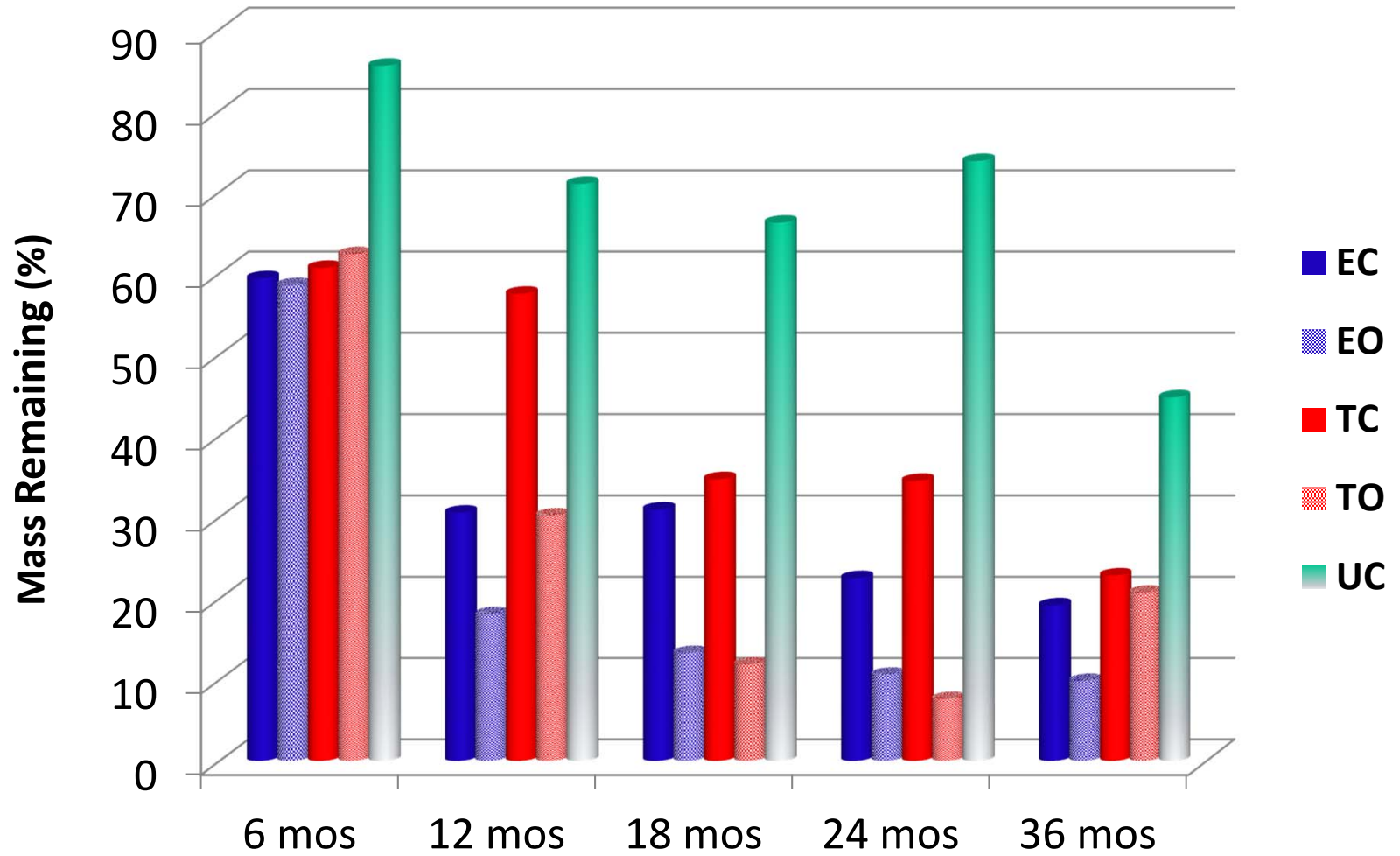


Unenriched Plot

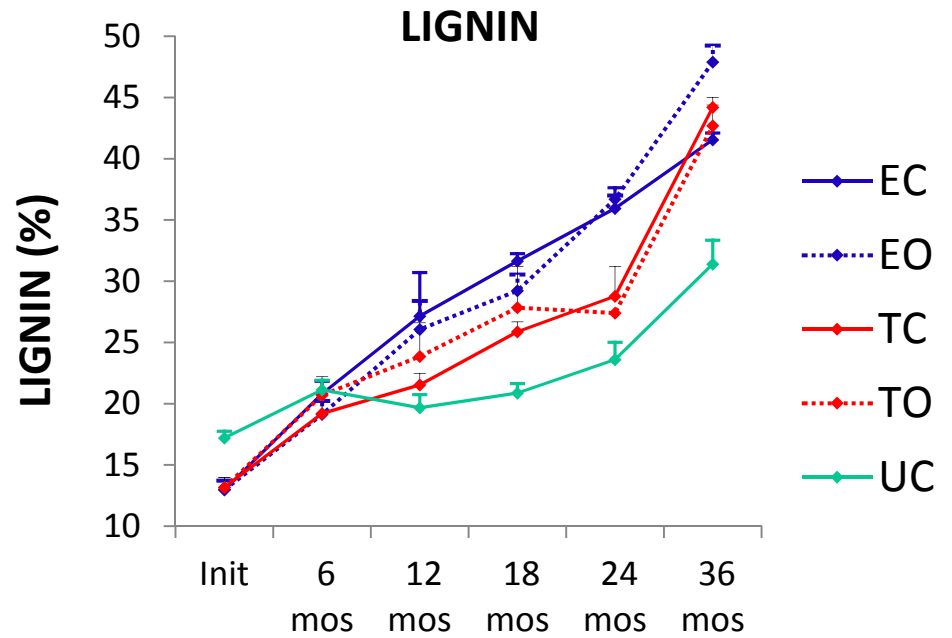
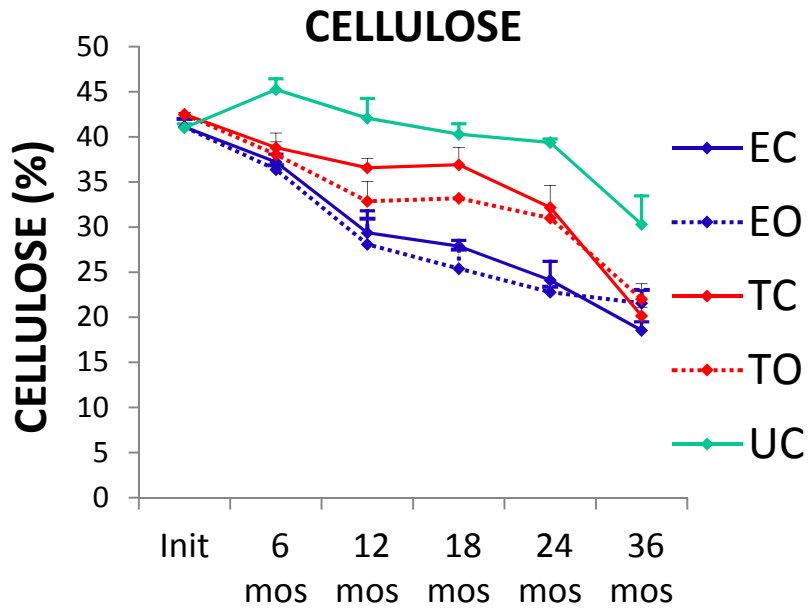


Enriched Plot

Mass Remaining

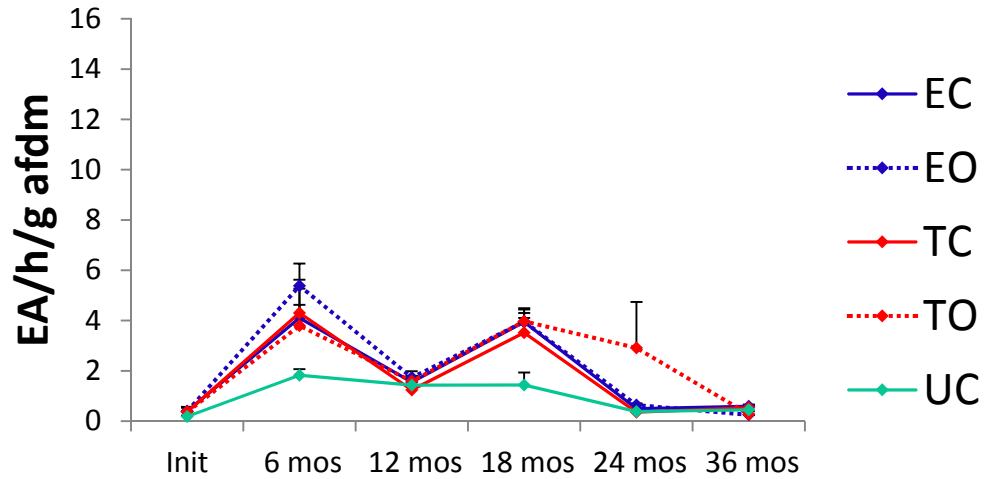


Carbon

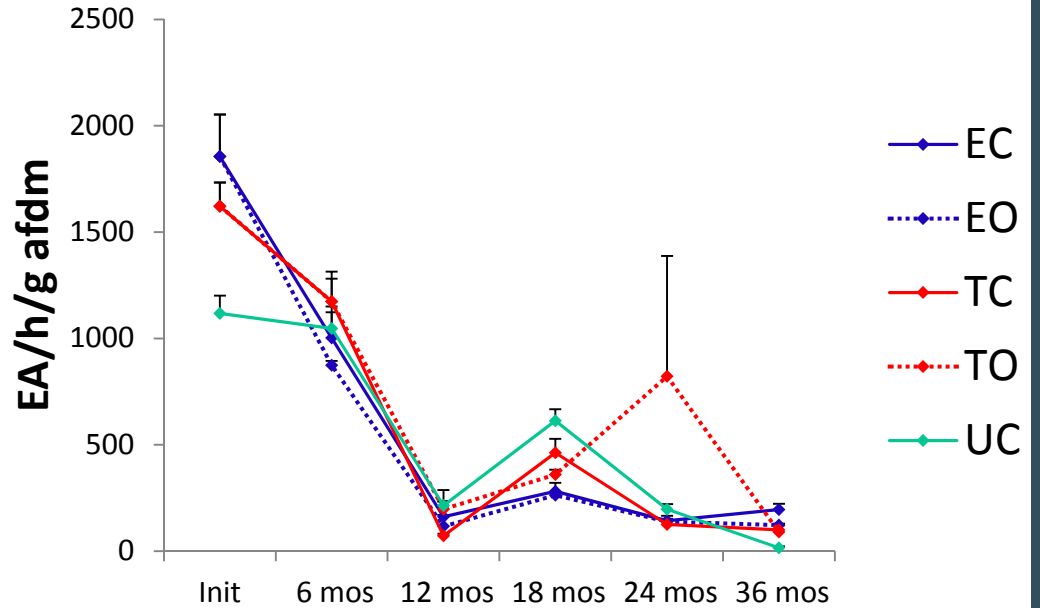


Enzyme Activity

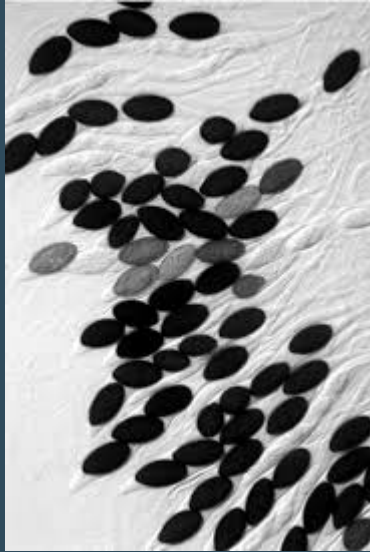
β -glucosidase



Phenol Oxidase



So Who's Responsible?

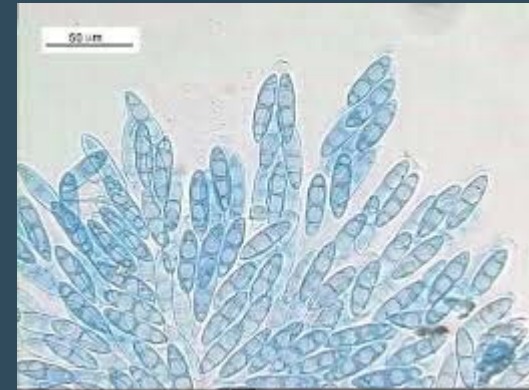


Podospora



Alternaria

Aniptodera

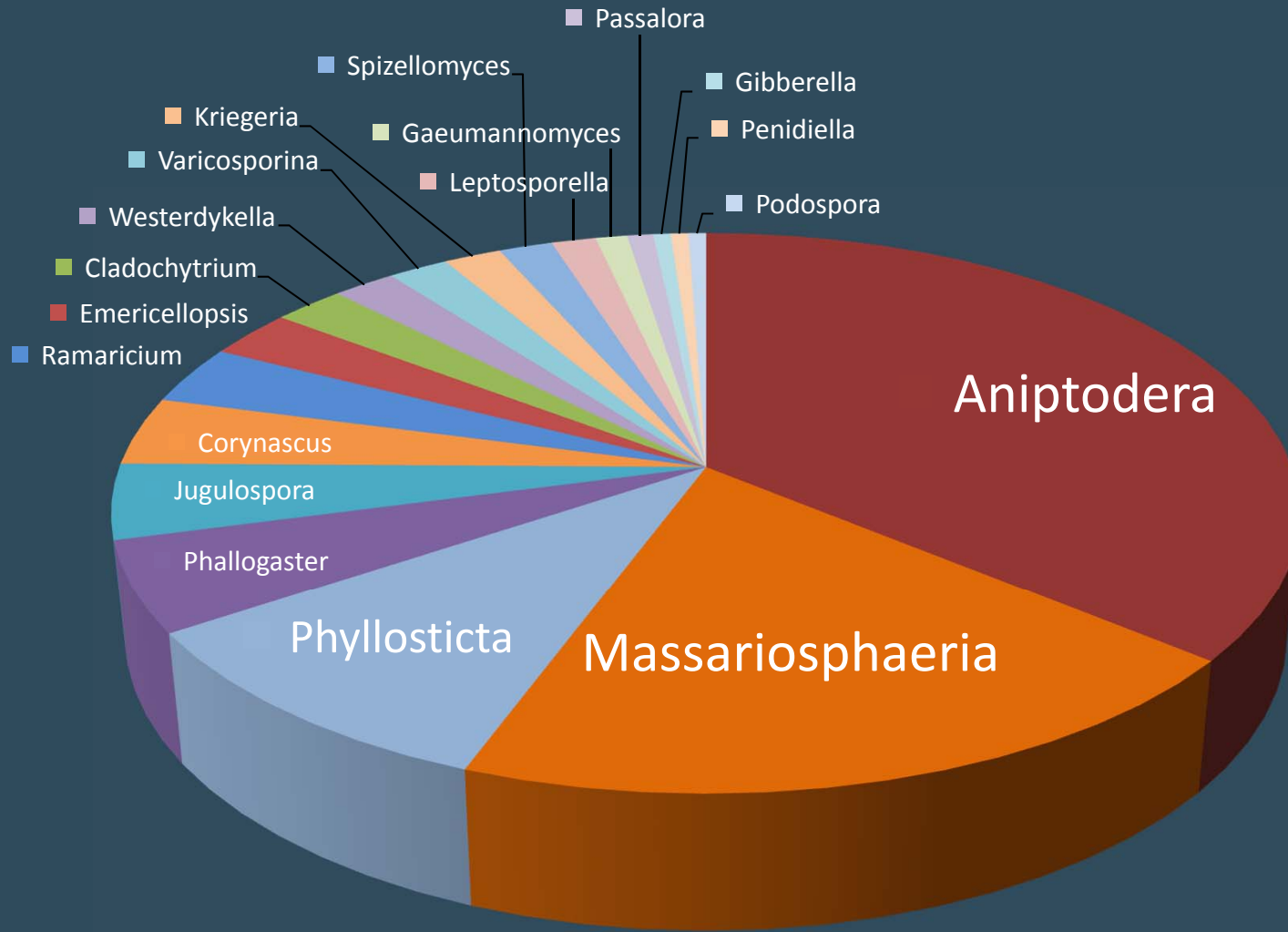


Gibberella

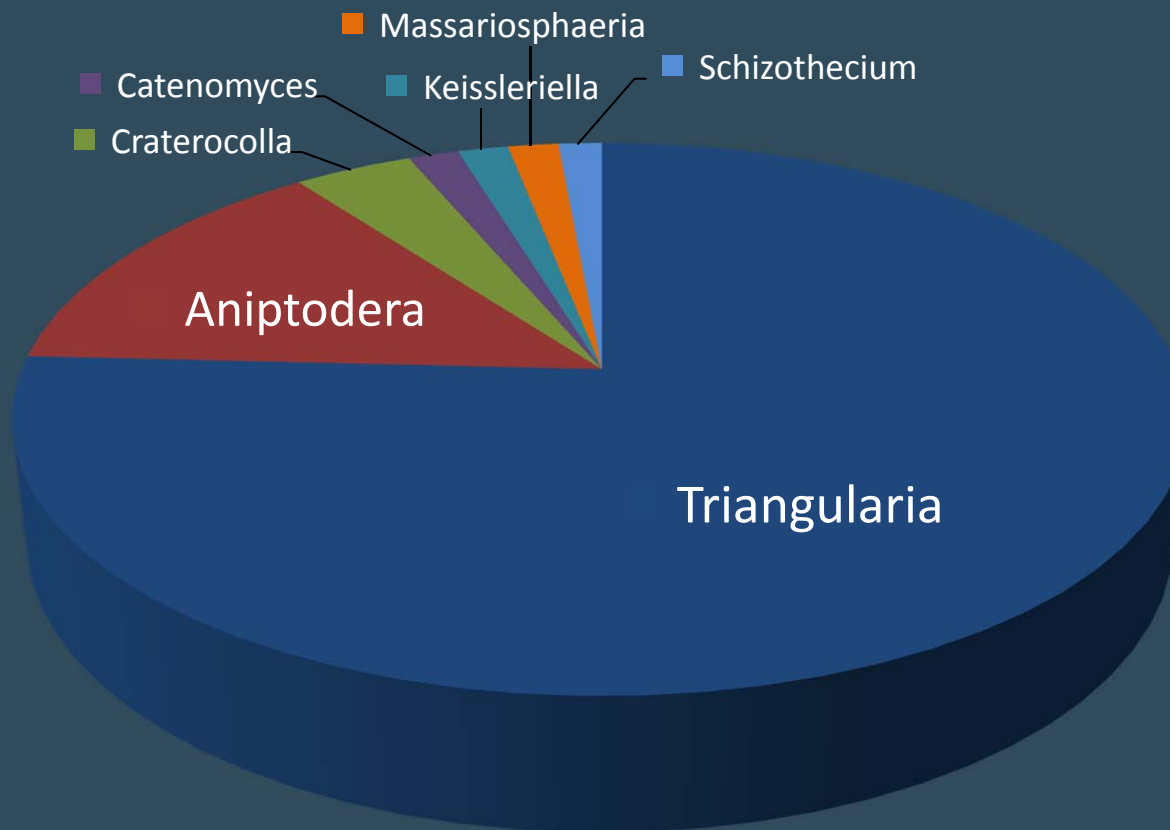
Unknowns?

- Triangularia
- Massariosphaeria
- Jugulospora
- Spizellomyctes

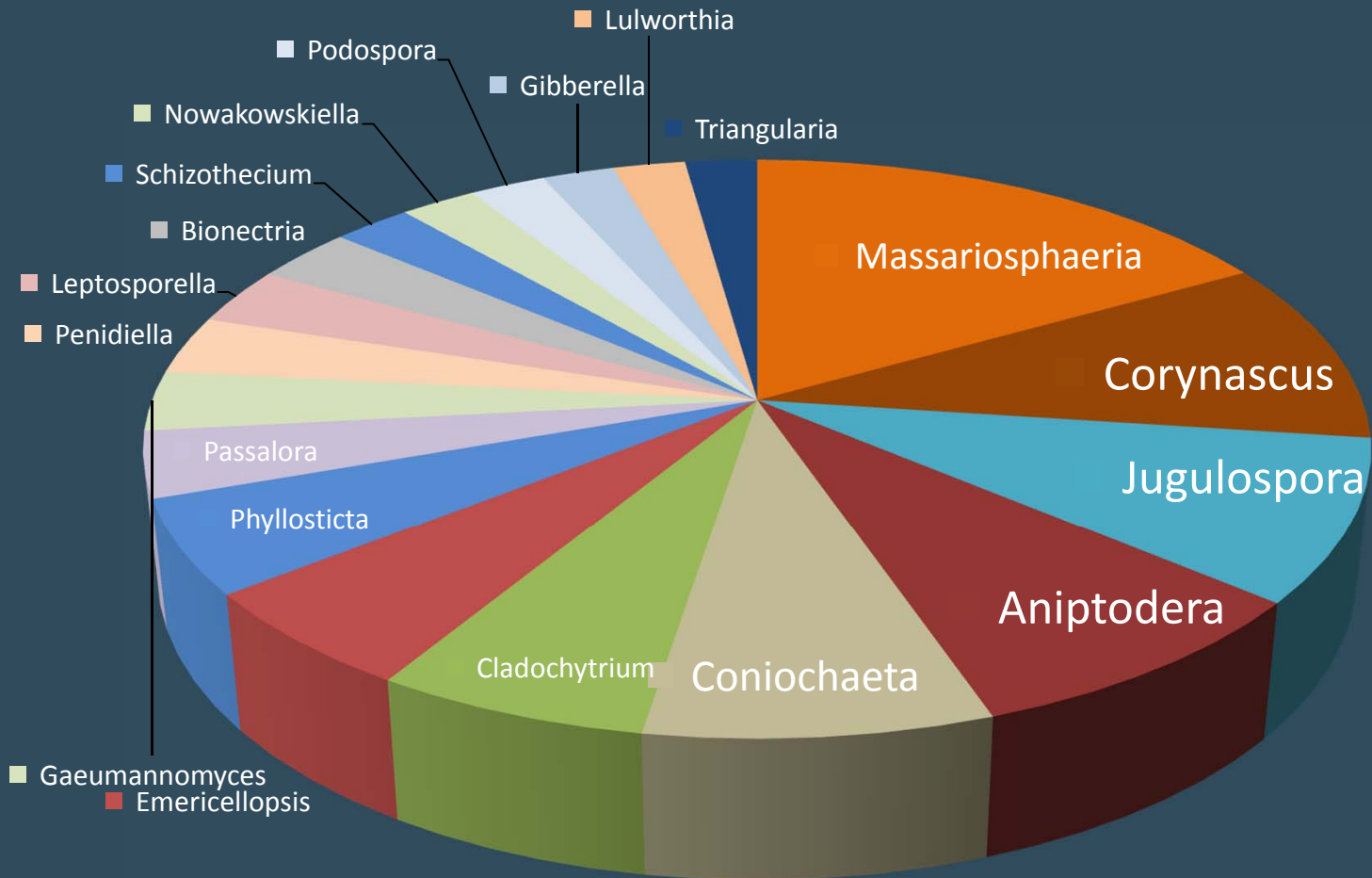
Enriched Control



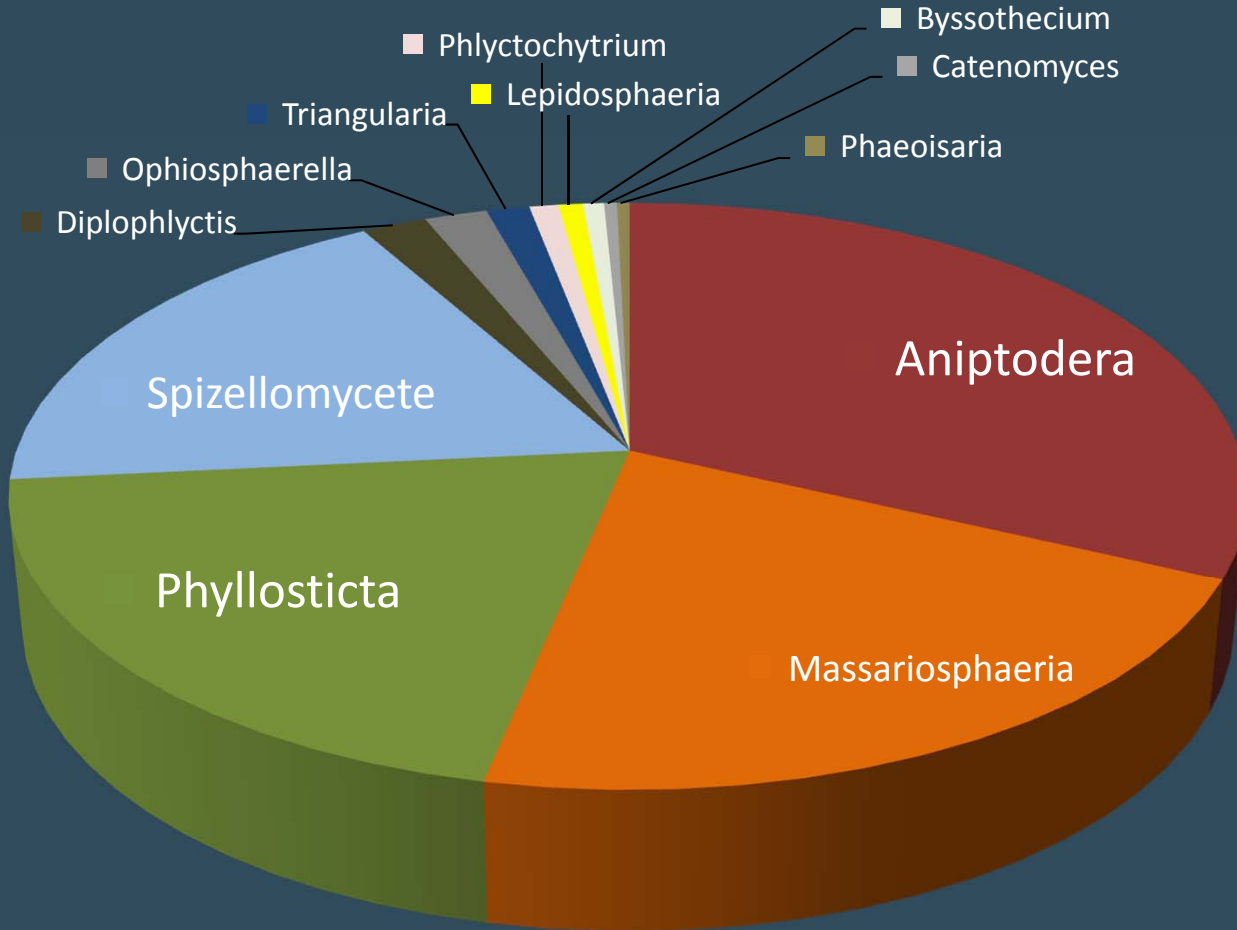
Enriched Open



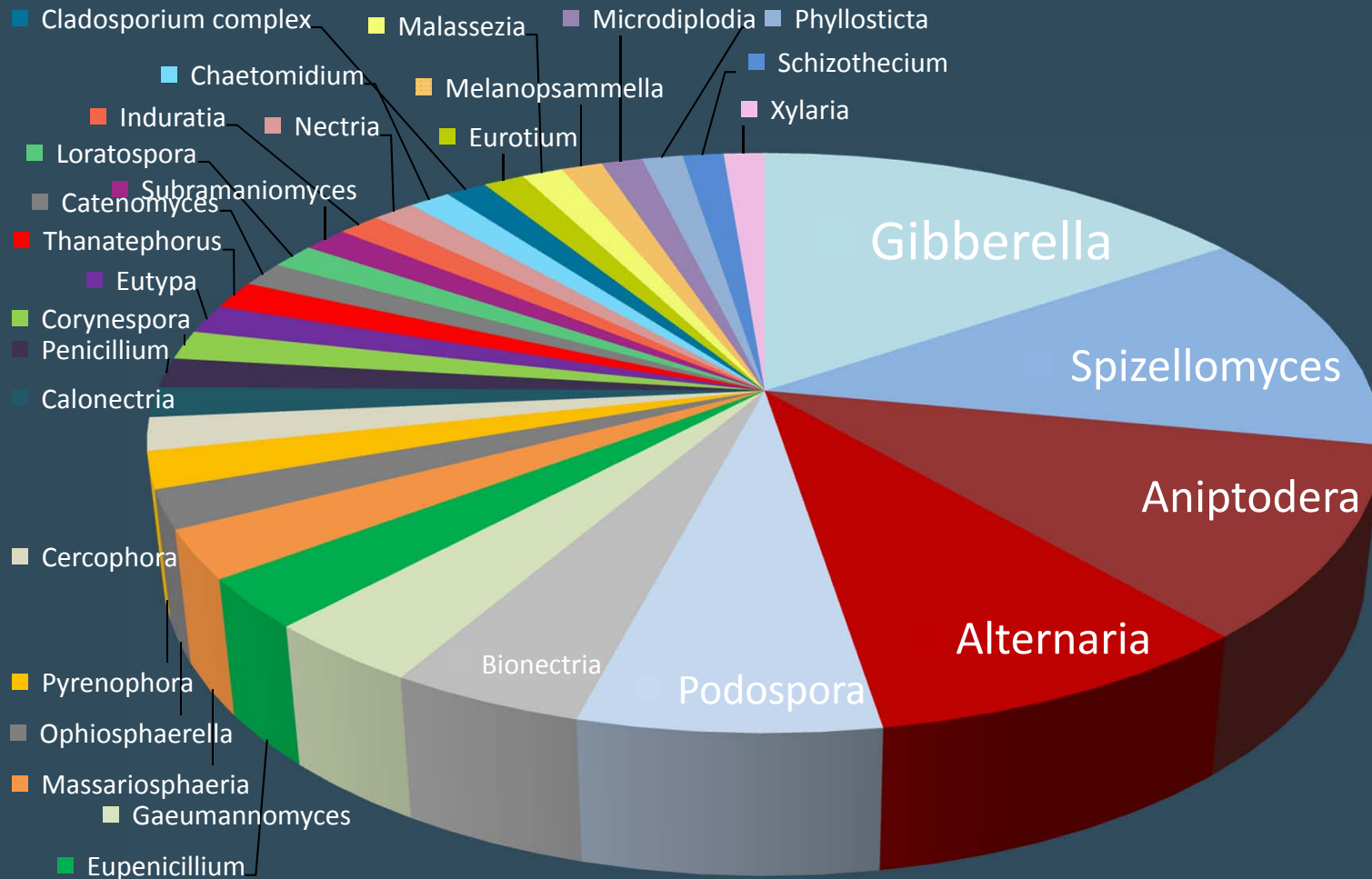
Transition Control



Transition Open



Unenriched Reference



What did we learn?

Open vs. control:

- We did see differences in diversity across treatments.
- At 24 months less diversity in open than control.

Nutrient gradient:

- We did see greater diversity in the areas of lesser nutrient impact.

What else did we learn?

Value of emerging technologies

- Cost effective
- Greatly improves our ability to identify microorganisms from 10% using traditional methods to 90% using new technology.
- Ability to link community structure to function of the ecosystem.
- Potential to use this as an indicator of ecosystem health.



Acknowledgements

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