Community overlap between foliar fungal endophytes and leaf decay fungi associated *with Quercus chrysolepis* leaves

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INTRODUCTION

Fungi are important contributors of breaking down organic matter and helping recycle nutrients such as carbon dioxide into the atmosphere. Many act as decomposers and are essential for the growth of most plants. Species-rich assemblages of fungi and other microorganisms decompose fallen leaves that make up leaf litter. Endophytic fungi are found in all plants such as trees and grasses. These foliar fungal endophytes are highly diverse and are primarily composed of ascomycetous fungi that enter and thrive within the plant leaves to form mutual symbiotic interactions.[1] Research on these communities is important to fields of biochemistry and physiology due to their capacity to produce many bioactive metabolites and biotechnologically relevant enzymes that help the host to survive.[2] Despite their importance, the relationship between foliar fungal endophytes and leaf decay communities is not well understood.

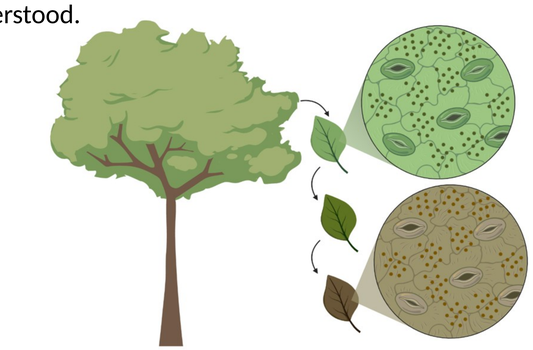


Figure 1. Process of leaves abscising to become leaf litter.

OBJECTIVE

Isolate and distinguish the extent of overlap between foliar endophytic fungi and leaf litter communities in the leaves of *Q. chrysolepis* (canyon live oak) from Big Chico Creek Ecological Reserve (BCCER) at four sites.

METHODS

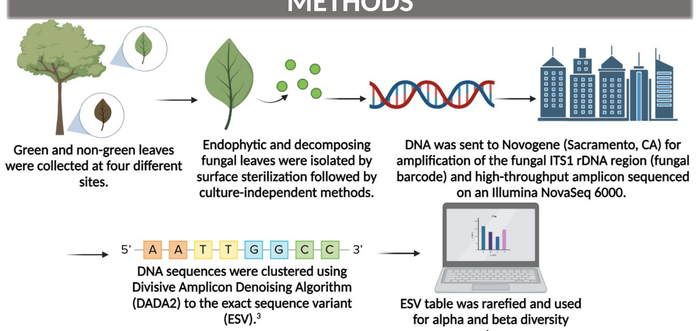


Figure 2. Schematic overview of methods used to isolate and extract fungal DNA from canyon live oak leaves and clustered sequences for analyses.

RESULTS



Figure 3. Venn diagram of fungal ESVs. Representing the number of fungal ESVs shared between the endophytic (green) and decay (orange) fungal communities.

Fungal Guild				
Community	*Undefined Saprotroph*	*Plant Pathogen*	*Unassigned*	*Other*
Decay	15.8	9.3	45.9	29.0
Endophyte	15.6	9.5	45.7	29.3
Overlap	16.4	10.8	42.9	29.8

Trophic Mode					
Community	*Symbiotroph*	*Saprotroph*	*Pathotroph*	*Unassigned*	*Other*
Decay	16.6	13.0	5.2	45.9	19.3
Endophyte	16.1	12.9	5.4	45.7	19.9
Overlap	17.4	13.9	4.4	42.9	21.3

Table 1. Composition of fungal functional groups and trophic modes based on FUNguild database.[4] Guilds and trophic modes are shown in percentages for each community. Guilds with less than 5% are under "Other."

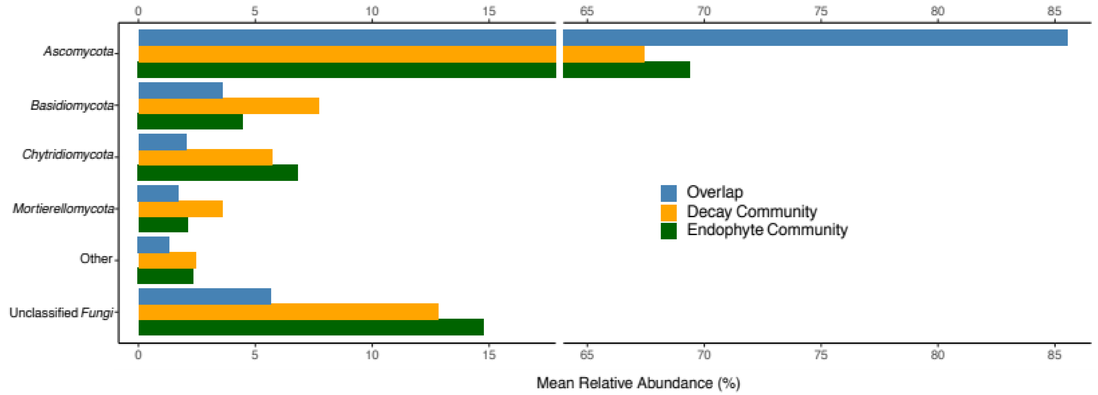


Figure 4. Fungal mean relative abundances at phylum level. All communities are highly abundant under phylum Ascomycota, while phylum Basidiomycota predominates in decay community. Phyla with less than 3% are identified as "Other".

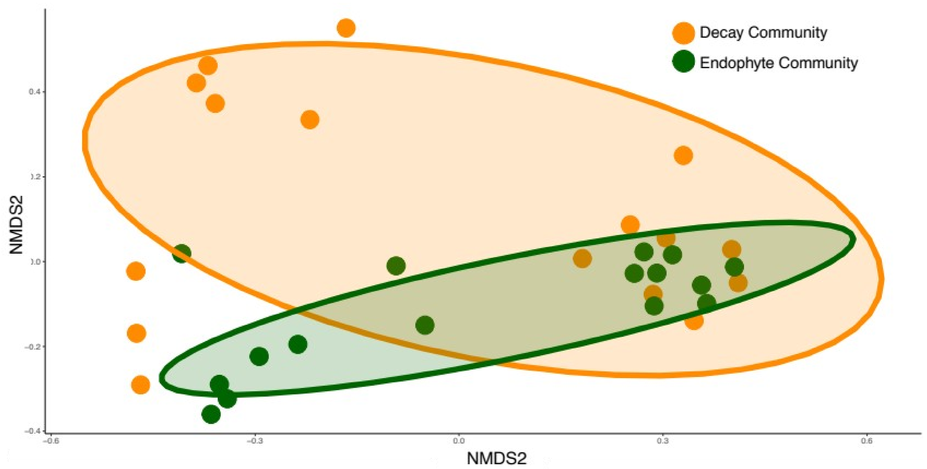


Figure 5. Non-metric Multi-dimensional Scaling (NMDS) plot of fungal ESV-based clustering data. The clustering of samples in NMDS ordination indicates that the composition of fungal endophyte and fungal decay communities are significantly different (PERMANOVA test, $p \leq 0.05$).

STATISTICAL ANALYSES

Alpha diversity:

- Species richness (ESVs between communities).
- Relative abundances for each community.
- FUNguild

Beta diversity:

- Bray-Curtis dissimilarity[5]
- NMDS plot
- Permutational multivariate analysis of variance (PERMANOVA) (*adonis* function from Vegan package)[6]

CONCLUSION

- Less than 25% of endophytic and leaf decay communities overlapped (Figure. 3), indicating that some foliar fungal endophytes may be early colonizers of leaf decay community.
- Fungal guilds and trophic modes for all communities are similar and dominated by unassigned taxa (Table 1).
- All three communities were dominated by phylum Ascomycota. Whereas phylum Basidiomycota was more abundant in the decay community (Figure 4).
- Most fungal endophyte samples are similar while fungal decay samples are more diverse (Figure 5).

FUTURE RESEARCH

- Examine the priority effect of endophytes as early colonizers of leaf decay communities.
- Determine how the assembly order of leaf decay communities influences decay rates which can have implications for global carbon flux.



Figure 6. *Collybiopsis quercophila* on *Quercus* leaf.

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