

Temporal Dynamics of Microbial Communities Associated with Ectomycorrhizal *Piloderma* Mat and Non-mat Soils



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Introduction

Mats formed by ectomycorrhizal (EcM) fungi are prominent features in Douglas-fir forest ecosystems. They can cover up to 25% of the forest floor and contribute up to 40% of the forest soil microbial biomass. Through their activities, EcM mats create a unique soil environment and likely result in the establishment of distinct microbial communities and activities.



The distinctive rhizomorphic mats formed by *Piloderma* in the organic horizon

Results of a phylogenetic survey showed 28 species of EcM mat formers, yet nearly half of all mats found were *Piloderma* species. The abundance of fungal material, and thus chitin, found in these distinct rhizomorphic mats may provide a valuable C and N source to the microbial communities associated with mats.

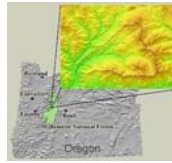
Previous research has shown that EcM mats vary in active fungal biomass throughout the year. This variation combined with the phenological allocation of carbon from host trees creates a unique temporal research opportunity.

Objective

- Examine the seasonal dynamics of ectomycorrhizal *Piloderma* mats and their associated microbial communities

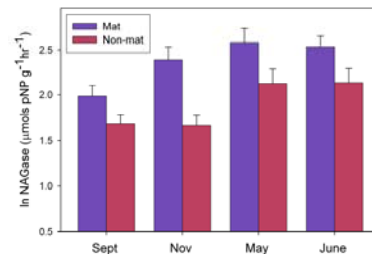
Study Design

- 5 sites throughout H.J. Andrews Experimental Forest
- 2 *Piloderma* mats and 2 non-mats per site
 - All mats phylotyped prior to sampling
- Repeated sampling of mat and non-mat plots
 - Sept 9, 2006 (hot and dry)
 - Nov 5, 2006 (cool and wet)
 - May 5, 2007 (post snowmelt)
 - June 23, 2007 (warm and moist)



Temporal Dynamics of Chitin Degradation

- The potential for chitin degradation was determined using N-acetylglucosaminidase (NAGase) activity



- NAGase activity is significantly higher in *Piloderma* mats than non-mats at all time points
- Lowest activity seen in the dry, summer sampling
- Mat activity had a greater response to the fall moisture than non-mats
- No significant changes in activity between May and June for either mat or non-mat samples

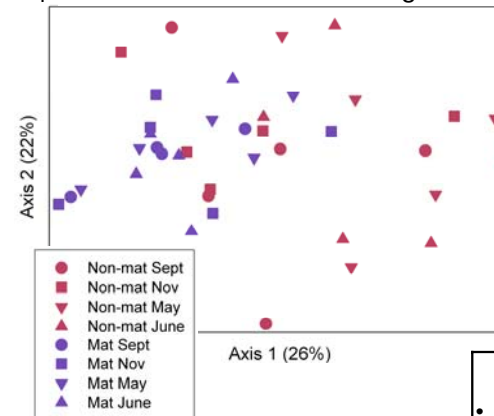
Fungal Community Analysis

- Fungal ITS region was amplified from soil DNA and submitted for fragment analysis
- Total of 70 peaks identified
 - Average of 11 peaks per sample for both mat and non-mats
- Distribution of fungal taxa varies with sample type and date
- LH669 is the dominant fragment in mats and the primary indicator for mat samples
 - Fragment analysis of a phylotype confirmed LH669 to be *Piloderma*

Indicator Species Analysis

Mat	Non-mat
LH669 (84.3, $p < 0.01$)	LH587 (79.1, $p < 0.01$)
LH661 (62.4, $p = 0.01$)	LH653 (66.6, $p = 0.03$)
LH567 (59.7, $p = 0.04$)	LH701 (38.9, $p = 0.05$)

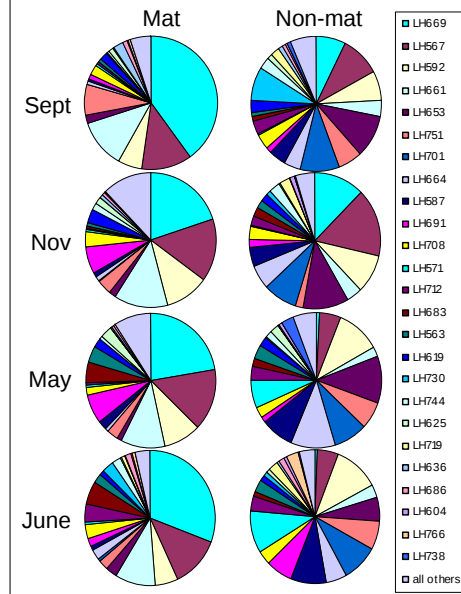
NMS Ordination of ITS Fragments



Acknowledgements

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Distribution of Fungal Taxa



- NMS ordination shows grouping of mat and non-mat samples
- MRBP confirms significant grouping of mats after accounting for site differences ($A = 0.187$, $p = 0.07$)
- No significant grouping by date

Future Work

- TRFLP of fungal communities for greater resolution of community
- 16S TRFLP of bacterial community
- Quantitative PCR to determine fungal and bacterial biomass
- Cloning and sequencing to identify key LH and TRF fragments