Saproxylic Mycodiversity in the Future of Oak Forests Experiment

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Introduction

I present a preliminary study of the saproxylic mycoflora community in the future of Oak Forests Experiment.

Wood-decaying fungi are essential for forest ecosystem functioning through involvement with:

- Recycling ligno-cellulosic and mineral nutrients back into the ecosystem.
- Soil formation and the carbon budget of forest ecosystems.
- Providing habitat for many other organisms.

Coarse wood debris (CWD) and its associated wood-decomposition organisms have been drastically reduced in abundance and diversity by forestry and so these features often have the potential as conservation indicators (Lonsdale et al. 2007).
It has been shown that designing a management model that provides artificial accumulation of CWD by cutting tops and girdling or inoculating standing living trees with wood-decay fungi hastens the development of decay-based habitat . The presence of CWD in the forest has potential influences on tree health and a new strategy to control pathogens. There are inter-specific interactions between the vast diversity of saprothrophics and the few fungal pathogens inhabiting wood (which are potential controlled by other saprothrophic organisms) that reduce risk of diseases posed by CWD accumulation (Woods et al. 2006).

Methods

Sampling procedure
At each site, plots were established at randomly chosen points along transect lines. The sites were sampled between May and August 2010 and between September and October 2010.
Each treatment plot was sampled by using15 plots of a 5 m diameter, and not closer than 1 m from its nearest neighbor.
Decay class was described for each log according to the five-degree scale of Harmon (Harmon and Sexton 1996).

I measured diameters both at the base and the top of logs, allowing calculation of the dead wood volume using the formula:

$$V = \frac{\pi h}{3} \times \left(b^2 + bd + d^2\right)$$

where h is the height of the frustum, b the basal diameter and d the top diameter.

Identification:
Fruiting bodies were identified to species using morphological characters.
Each species record from the BRF receives the correct name, authorities, synonymy, distribution, frequency, and bibliographic references.

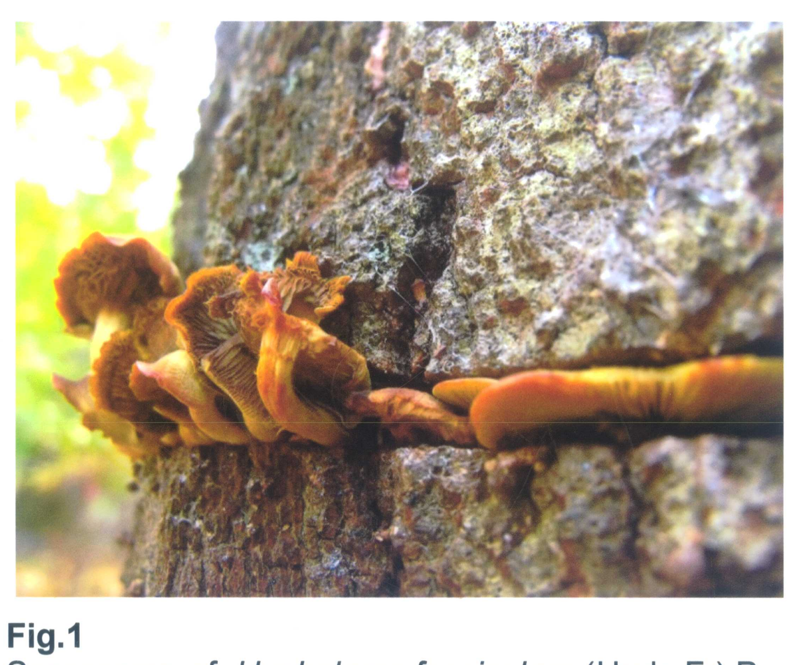

Fig.1
Sporocarps of *Hypholoma fasciculare* (Huds.Fr) P. Kumm from a girdlered oak.

Black Rock Forest
Future of Oak Forests Experiment 2006-2013

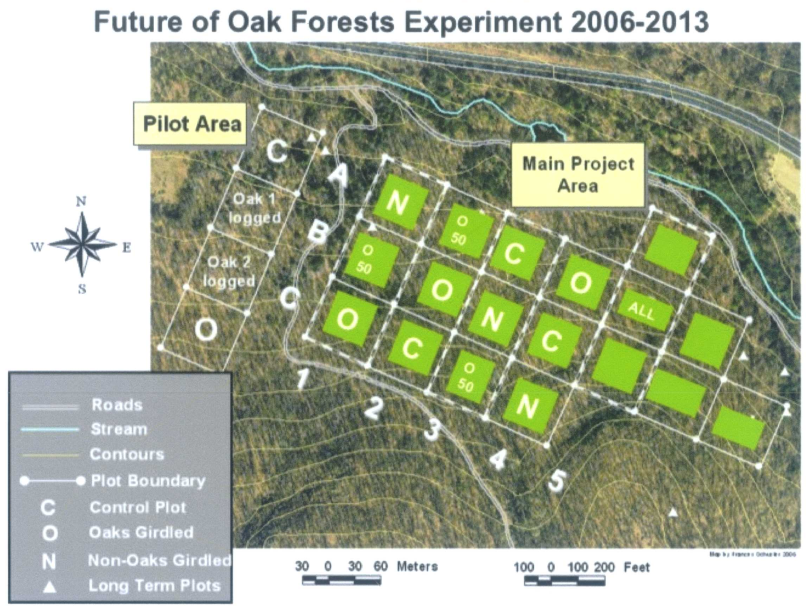

Fig.2
Plot Origination. Diagram courtesy by Bill Schuster.
1.O= girdling of all oak trees on a plot around their circumference at breast height, into the xylem tissue.
2.H= girdling of half of the oak tree on a set of plots.
3.N= girdling of all non-oak trees on a set of plots.
4.C= a fourth set of plots were left unmanipulated to represent controls.
5.A= All trees girdled

Fig.3
Trametes versicolor (L.) Lloyd: common wood decay basiomycete.

Results

A total of 119 records representing 33 species of wood-inhabiting fungi were identified in this study.

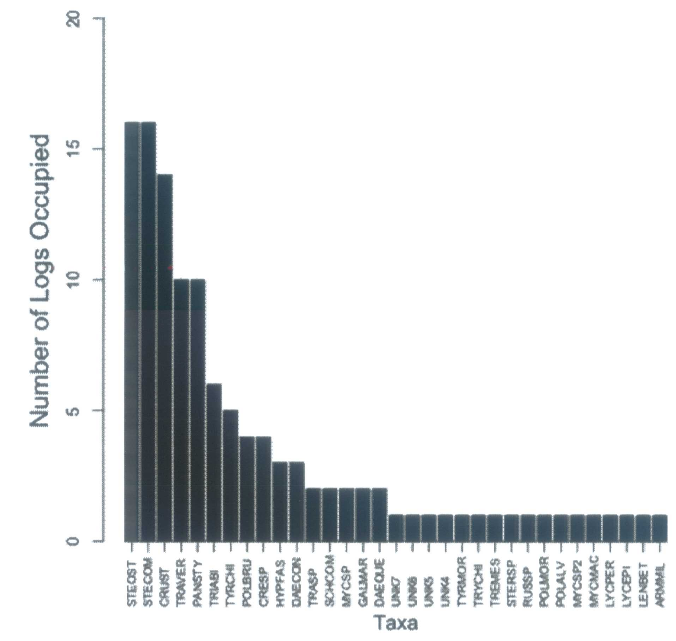

Fig.4
The rank abundance graph shows that the most abundant species are the unspecialized opportunistic species and the early stage decomposer. The 50% of the species recorded were found in only one log.

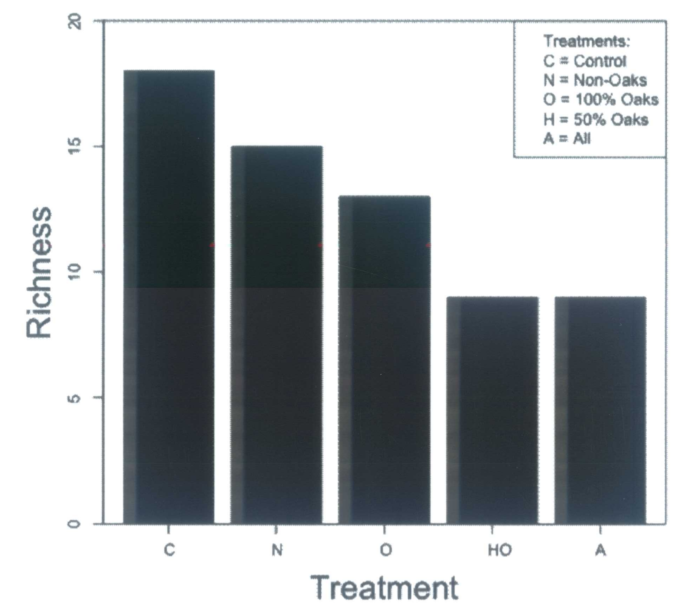

Fig.5
The control plots show the highest species richness.

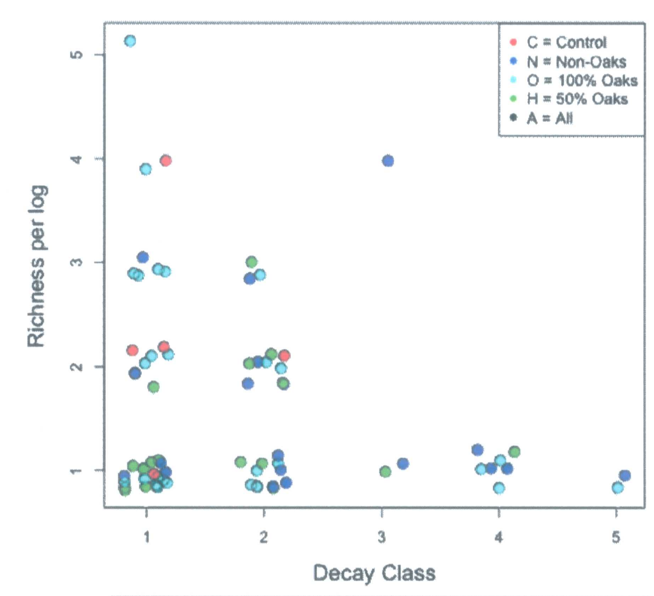

Fig.6
The relationship between decay class and species richness per log shows that most of logs sampled were in decay class 1. Community structure continually changes during wood decomposition until the resources has completely decomposed. (Boddy 2001) Fungi associated with decay class 5 are more rare and have specific nutritional requirements.

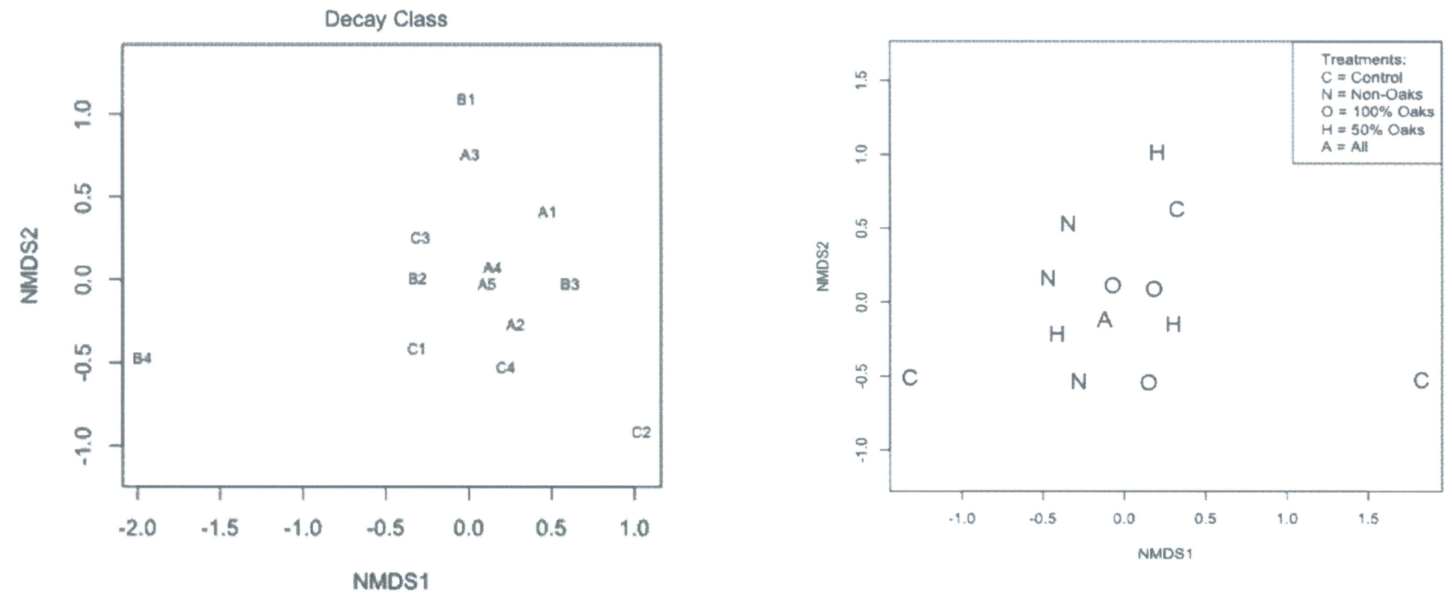

Fig.7 Non-metric Multidimensional Scaling of species in treatment plots.
Control plots are spread out and treatment plots appear to be more clustered.

Conclusions

- Saproxylic myco-communities comprising an unspecialized opportunistic species (*Stereum* spp.) and an early stage decomposer (*T. versicolor* ,fig.3) appear to be related to the 3 treatments O, H, N (fig.4).
- The decomposition stage of the substrate appears to be more important than the species of tree substrate.
- The treatments seem to have a similar effects on the saproxylic fungal community (fig.7).
- The number of species of wood-decay seems to depend more on a range of decay classes of substrata than type of wood from different species. The treatments generate a large amount of CWD.

Further Questions:

- How will the treatment communities change over time, and what factors drive the assembly of fungal communities?
- How decomposition (and carbon dioxin release) is affected by different communities?

Is there a method to detect taxa in the field without relying on fruiting ?

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