The Effect of Coarse Woody Debris on the Ectomycorrhizal Community in Subalpine Clearcuts in Interior BC

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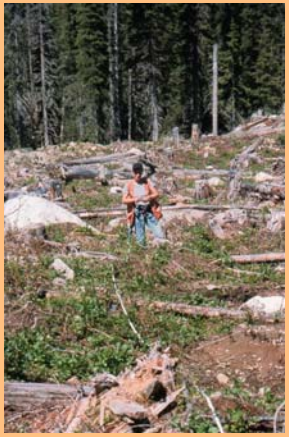
Background

Coarse woody debris (CWD) or downed wood is widely recognized as an important component of forest ecosystems. Therefore, forest certification criteria often include a requirement that coarse woody debris be retained on site after harvesting (e.g., Forest Stewardship Council 2005). The argument for retaining coarse woody debris typically focuses on the maintenance of animal biodiversity; however, major questions remain about the effectiveness of coarse woody debris in achieving these goals (Jonsson et al. 2006). Furthermore, there is rarely any attention paid to the importance of CWD in influencing soil biodiversity, and yet soil factors and associated ecosystem functions are always highly ranked in sustainability criteria.

Objective

To determine whether retention of coarse woody debris at the time of harvest influences the species composition of the ectomycorrhizal fungal community on planted spruce, 10 years after planting.

Planted spruce in September 2006



Normal coarse woody debris plots in 2000

Amount of coarse woody debris left on plots in 1996

Cutblock	Treatment	Volume (m^3/ha)
A	*Low*	57.0
A	*High*	453.3
B	*Low*	112.9
B	*High*	347.9
C	*Low*	60.4
C	*High*	416.9

Experimental approach

- Initial harvest took place over the winter of 1994-95 to create three blocks.
- In 1996-97, two 1-ha plots were established in each 10-ha clearcut with:
  - complete removal of downed wood, or
  - no removal of downed wood after harvest.
- Engelmann spruce seedlings were planted in 1996.
- In September 2006, we harvested one long lateral root from 10 trees on each plot.
- 100 randomly selected ectomycorrhizas per root sample were carefully separated into those colonized by different fungi.
- The fungal ITS region of nuclear rDNA was amplified and sequenced using the methods of Twieg (2006).
- Each sequence was BLAST-searched through NCBI-linked and UNITE databases.
- A functional species-level match criterion was set at 98% sequence similarity for double-pass and 97% for single-pass sequences.
- Sequences that could not be matched to one unique sequence type without ambiguity were not used for analyses.

Summary of results

- **We found 28 unique ITS sequence types, with *Thelephora americana* and *Amphinema* sp. dominating the community.**
- **We could detect no difference in species composition amongst plots, using mycorrhizas that could be identified with confidence,**

BUT, we could not fully analyze the data set because *Alloclavaria purpurea* DNA was amplified from mycorrhizal types representing 41 % of sampled root tips. These tips therefore had to be left out of the analyses.

What do we know about *Alloclavaria purpurea*, the mystery fungus present on many of the root tips?

- It is not a known mycorrhizal fungus.
- It has recently been renamed from *Clavaria purpurea* and placed in the Hymenochaetales.
- Many non-xanthochroic hymenochaetoids are wood decomposers. There have been reports of only one or two genera within the Hymenochaetaceae being mycorrhizal, but these reports were not definitive.
- Fruitbodies of *A. purpurea* are always found in spruce-fir forests.

Next steps

We cannot interpret our results until we determine whether *Alloclavaria purpurea* is mycorrhizal or is a saprotrophic fungus that is common on the rhizoplane.

We will take two approaches:

1. Culture *A. purpurea* from fruit bodies and run an inoculation trial on spruce to determine whether the fungus forms mycorrhizas under lab conditions.
2. We will clone DNA from last year's samples and sequence the clones separately to determine whether *A. purpurea* and a known mycorrhizal fungus co-occurred on the same root tips.

References

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