

AN INVESTIGATION OF NUTRITIONAL EFFECTS ON CAUSAL ORGANISMS OF BEECH BARK DISEASE IN AFTERMATH FORESTS



Lasser, G.A.¹, Johnston, M.T.², Mahoney, M.J.¹, Leimanis, V.A., Stoodley, J.R.³

¹Department of Forest and Natural Resources Management, SUNY-ESF, Syracuse, NY 13210

²Department of Forest and Natural Resources Management, The Ranger School, Wanakena, NY 13695

³Department of Environmental and Forest Biology, SUNY-ESF, Syracuse, NY 13210



INTRODUCTION

- Beech bark disease (BBD) invaded North America over a century ago, but the pathosystem is still not well understood
- BBD occurs when beech scale insects, *Cryptococcus fagisuga* (invasive) and *Xylococcus betulae* (native), attack American beech (*Fagus grandifolia*) and feed on the inner bark making the tree susceptible to fungal infections, primarily by *Neonectria ditissima* and *N. faginata*, which cause cankers that kill the tree
- Three stages of BBD: the Advancing Front, the Killing Front, and the Aftermath Forest.
- I am conducting research in the White Mountain National Forest in New Hampshire, USA, at Hubbard Brook and Bartlett Experimental Forest, taking advantage of an existing study of Multiple Element Limitation in Northern Hardwood Ecosystems with treatment plots of N, P, N+P, Ca, and untreated controls across three forest stand age classes (young, mid-aged, old)

OBJECTIVES

- Identify *Neonectria* species in our forest stands
- Assess the density of native and invasive beech scale
- Assess if older stands will have higher lesion densities than younger stands
- Challenge findings by Cale et al. (2015) that high bark N:P predicted *Neonectria* canker development. If correct, N and N+P plots would have higher lesion densities than P and control plots.

DISCUSSION

- This work was started in July 2017 with an anticipated completion date of January 2018 and currently there are no results
- Establishing baseline measurements of disease severity allows for future comparisons
- Fungal identification will allow us to examine potential impacts of nutrient additions to *Neonectria* species
- Nutrient application may show direct or indirect correlations to aftermath forest biodiversity, particularly with *X. betulae*; most studies of BBD focus on European beech scale
- Creating a *Neonectria* library will more easily allow for future nutrient manipulation trials

FUNGAL
COLLECTION

METHODS

PHOTOGRAPHIC
ANALYSIS

Neonectria
identification

DNA
Analysis

agar media
Neonectria
library

Neonectria
lesion
density

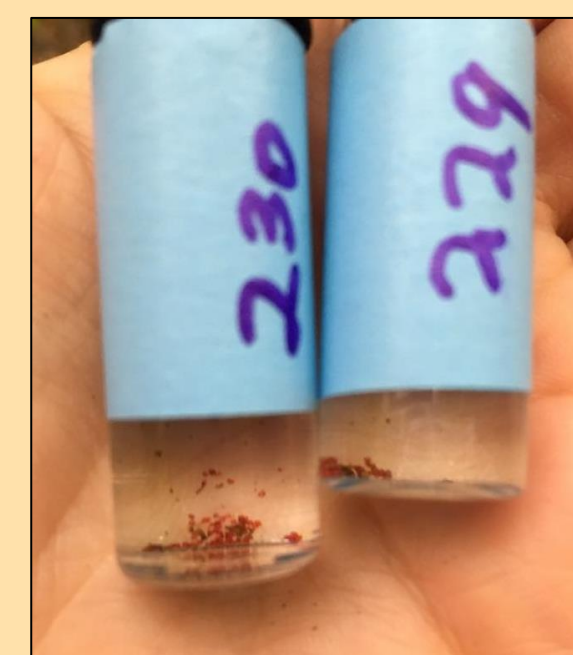
Beech scale
feeding
wounds

Using microscopy, the mean length of at least 25 ascospores from 2-3 perithecia per lesion will be measured (Cotter and Blanchard, 1981). *Neonectria* species can co-occur on a tree.



Ascospores of *N. faginata* (11) and *N. ditissima* (9) from Castlebury et al. 2006.

Samples collected in CTAB solution will undergo DNA extraction and polymerase chain replication (PCR), and identified to species using restriction fragment length polymorphisms (RFPLs) and direct sequencing.



Culturing a *Neonectria* library on potato dextrose agar for future nutritional comparisons of growth rates, and to determine key fungi food sources.



Five trees per treatment plot were selected for photographing at 2 heights (0.5 and 1.5m) in the 4 cardinal directions resulting in 8 pictures per tree. Images will be analyzed using ImageJ.



C. fagisuga is easily identified by its white masses and *X. betulae* is easily identified by its characteristic excretory tube (pictured below). Images will be analyzed using Image J.



REFERENCES

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