

BEECH BARK DISEASE: MORTALITY DUE TO INFECTION OF BEECH
TREES AND SUBSEQUENT FOREST SUCCESSION AT COLONIAL POINT
MEMORIAL FOREST, MICHIGAN

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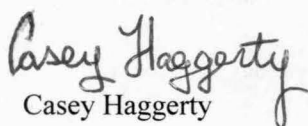
Abstract

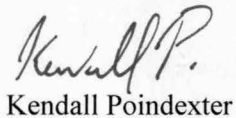
Among forest pathogens, Beech Bark Disease (BBD) is unique in having a two-part attack on the American beech (*Fagus grandifolia*) by the beech scale insect and an invasive fungus. Interactions between beech scale and fungus have led to widespread beech mortality as populations are increasingly infected. A previous study on Colonial Point Memorial Forest beech populations in 2012 by The University of Michigan Biological Station (UMBS) established two plots of beech trees to be monitored temporally for the effects of BBD. This study examined the percent mortality of this beech population with respect to level of BBD infection and the status of forest succession as beech are eradicated. High levels of mortality were found, with one plot exhibiting significantly greater mortality, perhaps related to higher levels of infection in 2012. Species richness of saplings was comparable between beech plots despite differing beech mortality, whereas species richness of seedlings was more diverse in the plot with higher mortality. Continued monitoring of beech trees infected with BBD is critical for the understanding and conservation of populations threatened with extirpation.

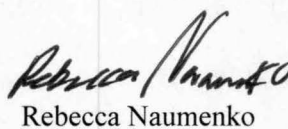
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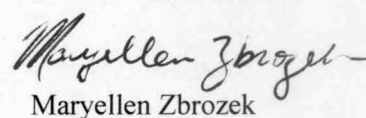
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1. Introduction

The spread of forest pathogens has been well-documented throughout the 20th and 21st centuries. These pathogens have disrupted countless ecosystems, including those in temperate climates in North America. Many are invasive species that are believed to have been harbored on materials in the hulls of ships. The spread of pathogens through international trade has caused significant amounts of ecological and economic damage (Work et al., 2005). For example, chestnut blight, a fungal pathogen, extirpated the American chestnut (*Castanea dentata*) from Eastern North America, potentially altering nutrient cycling in affected ecosystems (Smock & MacGregor, 1988). They found that the absence of chestnut leaves was correlated with a decrease in the growth rates of endemic macroinvertebrates, which rely on the rapid decomposition of chestnut leaves for nutrients. The invasion of exotic fauna has also been well documented, particularly in the case of the Emerald Ash Borer (*Agrilus planipennis fairmaire*), an Asian beetle that eats the phloem and cambium of ash trees (*Fraxinus americana*), and is ultimately fatal (Pugh, Liebhold & Morin, 2011). The death of ash trees was estimated to cost 10.7 billion U.S. dollars from 2009-2019 (Kovacs et al., 2009). Though these particular examples are well represented within the scientific literature, the emergence of Beech Bark Disease (BBD) is a topic requiring further research.

Beech Bark Disease is a two-part attack on beech trees (*Fagus grandifolia*) by the beech scale beetle (*Cryptococcus fagisuga*) and one or more fungi (*Nectria coccinea* or *Nectria galligena*; Houston, 1998). The insect itself is not devastating to the tree, though some damage is inflicted by the colonies. Beech scale is not native to North America. Although it has been historically recorded in Europe, its origin is believed to be in Central Asia, but has not been confirmed (Gwiazdowski, 2006). Beech scale was first observed in North America in a Nova

Scotian botanical garden in the late 19th century. The beech scale colonies themselves consist of only females, which are parthenogenic (Hale, 2006). The beetles expand their territory when they are carried throughout a forest by wind. The insect has three life stages: wingless larvae (also called crawlers or nymphs), second stage nymphs, and adults. Crawlers cause direct damage to beech trees by burrowing in with a needle-like mouth in search of nutrients, which makes the trees vulnerable to fungal exposure. The fungus follows the beetle, entering the small holes produced by the larvae. Since the scales themselves cannot survive on a tree that has been infected by the fungus, they must move on to another tree or die. The fungus is visible as a fruiting body in the fall (Houston, 1998).

In 2012, research was conducted by Dr. Joel Heinen and associate Marshall McMunn on two plots of beech trees located at Colonial Point Memorial Forest, a property of the University of Michigan Biological Station (45°29'31.14"N, 84°41'10.81"W; Heinen & Vande Kopple, 2003). Colonial Point is located on a peninsula in Burt Lake, Michigan. The site and its ecosystem were influenced by glacial activity after the Wisconsin Glacier retreated roughly 13,000 years ago (Nadelhoffer, Hogg & Hazlett, 2010; Michigan DNR, 2017). The ecosystem within the study site is a transition zone of mixed hardwood and boreal forests (Curtis et al., 2005). Beech (*Fagus grandifolia*), sugar maple (*Acer saccharum*), hophornbeam (*Ostrya virginiana*), and hemlock (*Tsuga canadensis*) are species present within the site. In 2012, the beech-dominated forest showed signs of widespread BBD infection. Heinen and McMunn recorded information about the size and infection level of beech trees, as well as the prevailing succession of the forest's seedlings and saplings. These data were collected with the intention of observing the site over time to determine the effects of BBD progression in the two plots.

The primary objective of this study was to measure the percent mortality of all marked beech trees that were studied in 2012 and to determine if this percent differs between the two plots sampled. In addition, we sought to investigate which species of tree will succeed in the forest following the extirpation of the beech population. Given that Plot 1 had three dead beech trees and Plot 2 had none in 2012, we hypothesized that there would be a significant difference in percent mortality between the two plots in 2017, with Plot 1 exhibiting greater mortality than Plot 2. Given our initial observations of the understory at Colonial Point, we also hypothesized that sugar maple would be the primary species to succeed as the beech trees die. Although this study will likely not provide any definite conclusions or solutions for preventing BBD, we hope that our research will lend to the ongoing investigation of its devastating impacts on beech tree populations.

2. Materials and Methods

Two plots were studied following the protocol established by Heinen and McMunn in 2012. Plot 1 was located on the western side of the main trail bisecting Colonial Point Forest, while Plot 2 was located on the eastern side of the same trail (*Figure 1*). The previously-studied adult beech trees were remeasured for diameter at breast height (DBH) and infection status. Seedling and sapling species and frequency were recorded within each plot.

The DBH of each adult beech tree was recorded in centimeters at the height used in previous data collection (1.9 m). The infection status was determined by placing a 10 cm string transect 1.9 m high on each beech trunk and counting the number of points at which the transect intersected the white scales left by the beech scale. This was repeated four times on each tree in all cardinal directions. The average infection status of each tree was determined by averaging the

white scale intersection counts from all faces of the trunk. To reduce inconsistencies, all infection status measurements were collected by the same observer. Dead trees were catalogued as such, and they also were measured for DBH and infection status when possible. Some trees were too decomposed for accurate measuring. Each measurement was recorded with the tree's tag number so individuals could be compared to past data.

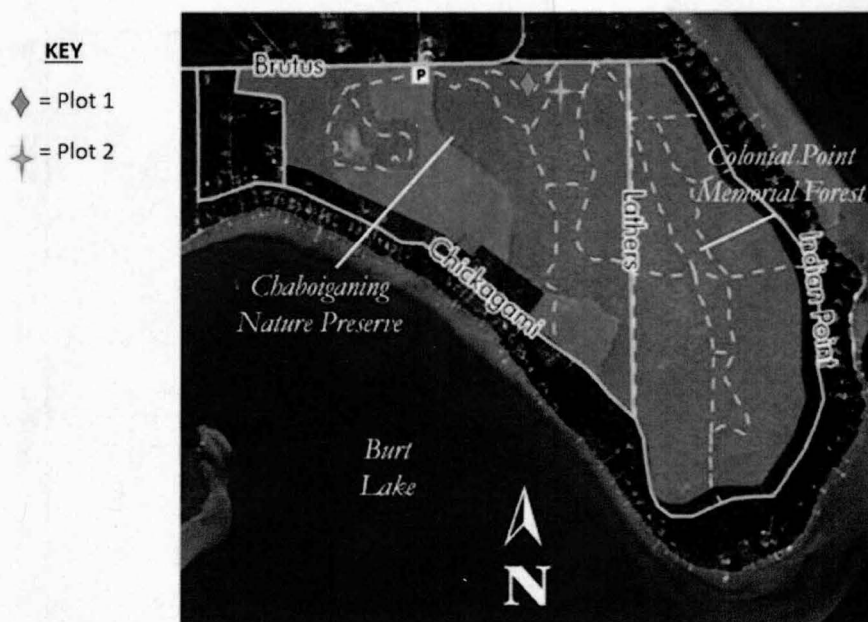


Figure 1. Map of Colonial Point Memorial Forest depicting the locations of Plot 1 and Plot 2. Source: Little Traverse Conservancy.

The species and frequencies of saplings and seedlings were recorded in Plot 1 by laying a 40 m baseline from the southeastern to southwestern corner of the plot. A transect tape was then run 100 m north perpendicular to the baseline's 20 m mark. Along this central transect, 40 m lines running east to west were drawn every 20 m for a total of six lateral transects. We replicated this protocol on Plot 2, with the baseline running from the northeastern to northwestern corner and the central transect running south. Data were then recorded along these

lateral transects at 10 m and 20 m to either side of the central transect, where 5x5 m plots were marked north of the lateral transects on the side facing the central transect (*Figure 2*).

Within these plots, all saplings measuring more than 1 m in height and less than 5 cm in DBH were counted, and their species and infection status were recorded. Seedling species and frequency were also recorded within 1x1 m plots that were randomly selected within the 5x5 m sapling plots.

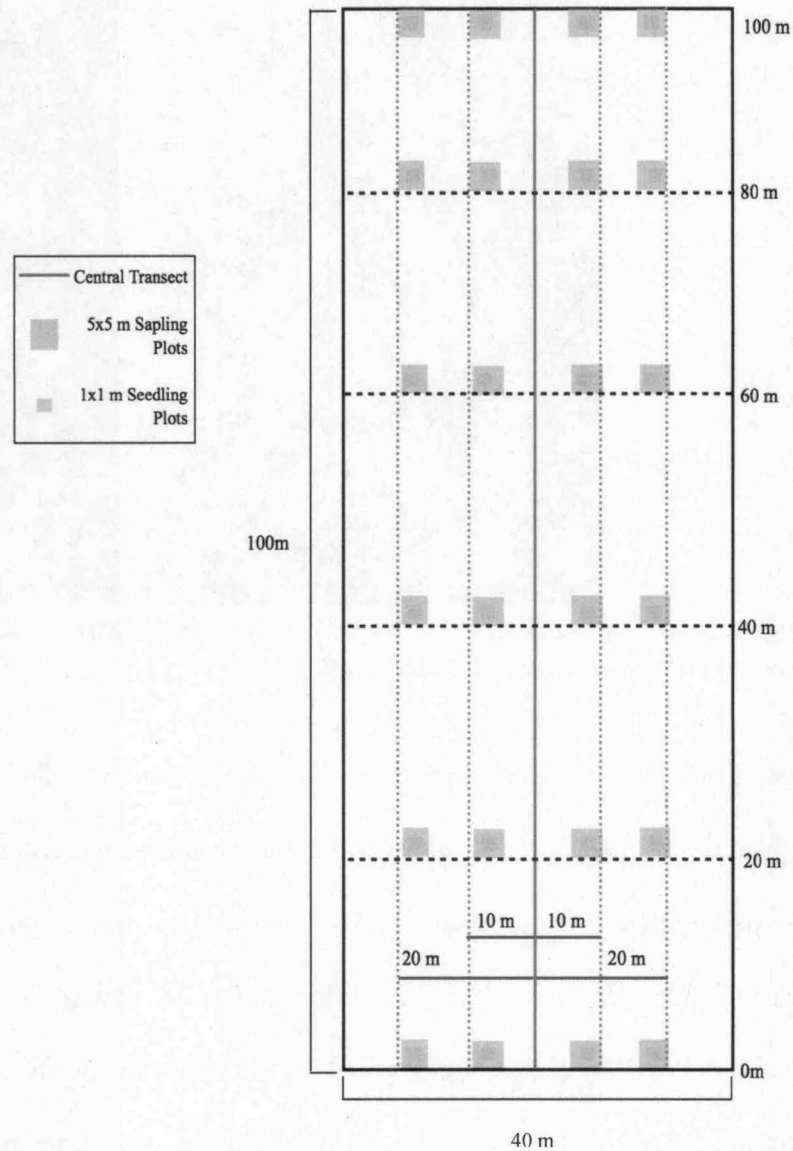


Figure 2. Overhead view of Plot 1 and Plot 2 in Colonial Point Memorial Forest. Twenty-four subplots were measured along six transects.

3. Results

We used a Mann-Whitney U Test to determine whether average infection status of beech trees in Plot 1 and Plot 2 had significantly changed from 2012 to 2017. The results for Plot 1 average infection status were non-significant at the $\alpha = 0.05$ confidence level. Conversely, the test indicated a significant difference in Plot 2 average infection status. A Mann-Whitney U Test to determine whether infection was more prevalent on one side of the tree trunk revealed no significant difference between north and south or east and west (*Table 1*). Observations in Plot 1 revealed that 88.1% of beech saplings exhibited signs of beech scale presence, while saplings in Plot 2 exhibited 84.3% scale presence.

Table 1. The table indicates that there are no significant differences in infection rates of tree trunks based on cardinal direction.

Infection of Adult Beech by Cardinal Direction	
Direction	P-Value
North	0.416
South	0.231
East	0.547
West	0.064

In 2012, Plot 1 exhibited 6% mortality and Plot 2 exhibited 0% mortality. Measurement of tree mortality in 2017 revealed that, of the trees that were alive in 2012, Plot 1 had 66% mortality and Plot 2 had 17% mortality. According to a linear regression, there was a significant relationship between plot and mortality (p-value < 0.001). A binomial logistic regression comparing 2012 DBH to 2017 beech mortality revealed no association between age of infected beech and likelihood of death within a five-year interval (Nagelkerke R-Square = 0.003, p-value = 0.691).

To measure the diversity and abundance of seedling species within each plot, we used a Simpson Diversity Index (Table 2; Simpson, 1949). This is calculated using the equation $D = \frac{(\sum_{i=1}^N n_i(n_i-1))}{N(N-1)}$, in which N is the total number of individuals and n_i is the number of individuals of species i . The results are represented on an index ranging from 0 to 1, with 0 being high diversity and 1 being low. In 2012, Plot 1 had an index value of 0.32 and Plot 2 had an index value of 0.66. In 2017, Plot 1 had an index value of 0.86, while Plot 2 had an index value of 0.92. Species similarity between plots was measured using a Sørensen Similarity Index, which uses the equation $QS = \frac{2C}{A+B}$ (Table 3; Magurran, 2004). The variable C represents the number of species the two plots share in common, A is the number of species in in Plot 1, and B is the number of species in Plot 2. This index ranges from 0 to 1, with 0 being no similarity between plots and 1 being complete similarity. In 2012, Plot 1 and Plot 2 had a similarity of 0.66, while the plots had a similarity of 0.88 in 2017. Between 2012 and 2017, Plot 1 had a similarity of 0.73, while Plot 2 had a similarity of 0.85.

Table 2. This index describes species diversity and abundance between plots for seedlings and saplings, with 0 indicating high diversity and 1 indicating low diversity.

Simpson Diversity Index: Seedlings	
Plots	Index Value
2012 Plot 1	0.32
2017 Plot 1	0.86
2012 Plot 2	0.68
2017 Plot 2	0.92

Simpson Diversity Index: Saplings	
Plots	Index Value
2012 Plot 1	0.66
2017 Plot 1	0.92
2012 Plot 2	0.7
2017 Plot 2	0.96

Table 3. This index describes species similarity between plots for seedlings and saplings, with 0 indicating no similarity and 1 indicating complete similarity.

Sørensen Similarity Index: Seedlings	
Plots	Index Value
2012 Plot 1/2012 Plot 2	0.66
2017 Plot 1/2017 Plot 2	0.88
2012 Plot 1/2017 Plot 1	0.73
2012 Plot 2/2017 Plot 2	0.85

Sørensen Similarity Index: Saplings	
Plots	Index Value
2012 Plot 1/2012 Plot 2	0.57
2017 Plot 1/2017 Plot 2	0.8
2012 Plot 1/2017 Plot 1	0.85
2012 Plot 2/2017 Plot 2	0.8

Sapling data was analyzed similarly to that of seedlings. The Simpson Diversity Index showed that in 2012, Plot 1 had a diversity of 0.66 and Plot 2 had a diversity of 0.70. In 2017, Plot 1 had a diversity of 0.92 and Plot 2 had a diversity of 0.96. The Sørensen Similarity Index showed that Plot 1 compared to Plot 2 had a similarity of 0.57 in 2012. Plot 1 compared to Plot 2 had a similarity of 0.80 in 2017. Between 2012 and 2017, Plot 1 had a similarity of 0.85, while Plot 2 had a similarity of 0.80 (*Table 3*). In both 2012 and 2017, both plots were dominated by sugar maple seedlings, while the dominant sapling species was beech. Sugar maple saplings decreased in frequency between 2012 and 2017 (*Table 4 & 5*).

A Chi-squared test for homogeneity revealed no significant difference in sapling counts between Plots 1 and 2 at the $\alpha = 0.05$ confidence level. We conducted an additional Chi-squared test for homogeneity to determine if there was a significant difference in seedling counts between plots. Again, no significant difference in seedling counts between plots was found.

Table 4. This table describes the proportion of each seedling species within Plots 1 and 2.

Seedling Species	Plot	Proportion within Plot (2012)	Proportion within Plot (2017)
Ash	1	0.017	0.008
Beech	1	0.167	0.014
Ostrya	1	0.033	0.005
Red Maple	1	0.317	0.035
Hemlock	1	0.017	0
Sugar Maple	1	0.450	0.938
Ash	2	0.031	0.007
Beech	2	0.165	0.030
Stripe Maple	2	0	0.007
Red Maple	2	0	0.002
Sugar Maple	2	0.803	0.954

Table 5. This table describes the proportion of each sapling species within Plots 1 and 2.

Sapling Species	Plot	Proportion within Plot (2012)	Proportion within Plot (2017)
Beech	1	0.808	0.865
Ostrya	1	0.058	0.056
Sugar Maple	1	0.135	0.079
Beech	2	0.832	0.981
Ostrya	2	0	0
Ash	2	0.004	0
Sugar Maple	2	0.163	0.019

4. Discussion

The average infection status in Plot 1 did not significantly change between 2012 and 2017, but the average infection status in Plot 2 increased significantly from 2012 to 2017. This is likely because Plot 1 was already heavily infected with BBD in 2012. Plot 2 also exhibited signs of infection in 2012, though to a lesser extent than Plot 1. Our findings therefore suggest that beech plots already strongly infected with BBD will not exhibit a significant change in average infection status over a five-year interval, while beech plots with a low average infection status

will likely show a strong increase in average infection status within the same time frame.

Interestingly, we found that the majority of beech saplings sampled within the plots showed signs of beech scale presence. Stephanson (2017) also noted that it is common to see the scale on saplings in Northeastern America. We do not currently know if the saplings are infected with both the scale and the fungus, which prevents us from drawing conclusions regarding infection status of saplings or potential future mortality.

Additionally, there was no significant difference between which sides of the trees were most infected. Between the north and south sides of the trees and the east and west sides of the trees, infection status was relatively evenly distributed. This suggests that the beech scale does not preferentially infect one cardinal direction over another. These findings are consistent with the literature, since it is known that the larvae expand their territory to the entirety of the accessible bark when a clutch of scale eggs hatch (Houston, 1998).

The strong correlation between mortality and plot found through a linear regression supports the observed difference that Plot 1 had a higher percent mortality than Plot 2. From this, it is possible that there may be a factor not captured in this study that is impacting the survival of the beech scale or the fungus. Beech in Plot 1 may exhibit qualities that cause BBD to preferentially infect them. These preferences, or lack thereof, cannot be attributed to tree age, as DBH in 2012 had no significant impact on tree mortality in 2017. Furthermore, they cannot be contributed to temperature, humidity, or elevation, since the two sites are in such close proximity. There could be different nutrients taken in by the trees, though this is unlikely. However, wind patterns may vary between the plots, which could influence the dispersal of beech scale. Genetic factors may also be impacting these relationships, as some trees may have stronger resistance against BBD.

Following our analysis of beech mortality, we examined succession within the two plots. It is common for beech dominated forests to have minimal understory other than beech and shade tolerant species. Presence of any other species is indication of the impact of beech tree mortality and the subsequent light gaps this creates (Stephanson, 2017). Light gaps in the forest canopy promote greater understory growth than would naturally occur in forests with limited light (Dai, 1996). Therefore, we expected the plot with higher mortality to have more light gaps, resulting in a higher sapling and seedling count. However, there was no difference between seedling or sapling count between plots, despite Plot 1 having greater beech mortality. This may have been due to light gaps having been newly formed in the canopy, resulting in insufficient time for the presence of light to affect the understory. Additionally, it may be possible that insufficient light reached the forest floor even after beech tree death, as a study conducted by Emborg (1998) found that seedlings within a temperate forest were not successful when relative light intensity (RLI) was under 10%. Though we did not measure RLI, this variable may explain the understory trends we observed in our study.

The Simpson Diversity Index showed that in 2012, seedling variety of both plots was shown to be more diverse than their 2017 counterparts. Sapling diversity was found to be comparable between beech plots despite differing beech mortality, whereas seedling diversity was found to be more prominent in the plot with higher mortality. This could be due to the timing of light gap availability. If there was less light to allow for growth in the time that the saplings were first germinating, only those species that were better competitors in shady environments would persist, leading to lower diversity. Now, in 2017, plentiful light gaps due to the death of beech trees in Plot 1 may be allowing more species to compete for this space than was previously possible (*Tables 2 & 3*).

Despite light gaps allowing a wider diversity of seedling species to compete within Plot 1, the most prevalent seedling species in both plots was sugar maple. This is likely because sugar maple seedlings are extremely shade-tolerant and can withstand suppression for several years (Goodman, Yawny & Tubbs, 2017). However, there was a decrease in sugar maple sapling frequency from 2012 to 2017, despite sugar maple seedlings dominating the understory in 2012. This suggests that there may be a mechanism by which the seedlings are prevented from maturing into saplings. Based on these findings, we cannot accept our hypothesis that sugar maple will be the primary successional species in Colonial Point.

Although we replicated Heinen and McMunn's data collection, methodology from 2012 was challenging to interpret. This may have altered the accuracy of method replication. One complication that arose due to this was that the rebar marking the northeast corner of Plot 2 had either been misplaced or moved since 2012, causing the plot's location to need remeasurement in 2017. As this was an estimation of the original area measured, it is possible that the 2017 seedling and sapling plots are not the same plots that were measured in 2012. However, we do not believe that this would have caused a significant change in our results. Additionally, Heinen and McMunn's methods required random sampling of seedlings. Since this random sampling was conducted by humans, it may not have been truly randomized as we may have been more likely to select an area based on its accessibility. In the future, it would be useful to divide the plots into grids from which randomized cells could be selected for sampling.

Colonial Point should continue to be studied in five year intervals in order to monitor infection, mortality, and succession of the beech plots. This may lead to a more comprehensive understanding of the effects of BBD over time beyond the scope of the current study. In future studies, genetic analysis of the beech scale and fungi that infect beech trees may lead to insights

regarding the mechanism of infection, which trees are preferred, or which fungus is most commonly present. Further study of beech bark disease and its effects on forests is vital for understanding the future of beech populations and for the future conservation efforts that may be necessary to maintain them.

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