

Distribution and severity of beech bark disease on American beech (*fagus grandifolia*) in the
Wells Plot in northern lower Michigan

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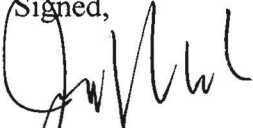
University of Michigan Biological Station
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Prof. Robert Pillsbury

American beech trees (*fagus grandifolia*) are commonly infested by a beech scale insect (*Cryptococcus fagisuga*) and then infected by a fungus (either *Nectria coccinea* var. *Faginata* or *Nectria galligena*). This phenomenon is called beech bark disease and affects forest stands of trees in the eastern and midwestern United States. The Wells Plot is located in Pellston, Michigan and is a one hectare plot that has not been studied since beech bark disease became prevalent in the area. This study examines the distribution and severity of beech bark disease in the Wells Plot through the relationships between the disease and diameter-at-breast-height of trees, growth rate of trees, and clustering of beech trees. Correlation between severity and increasing size of trees was observed as well as slowed growth rate and increase severity. However, no significant relationship between clustering and spread of disease was observed.

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Abstract

American beech trees (*fagus grandifolia*) are commonly infested by a beech scale insect (*Cryptococcus fagisuga*) and then infected by a fungus (either *Nectria coccinea* var. *Faginata* or *Nectria galligena*). This phenomenon is called beech bark disease and affects forest stands of trees in the eastern and midwestern United States. The Wells Plot is located in Pellston, Michigan and is a one hectare plot that has not been studied since beech bark disease became prevalent in the area. This study examines the distribution and severity of beech bark disease in the Wells Plot through the relationships between the disease and diameter-at-breast-height of trees, growth rate of trees, and clustering of beech trees. Correlation between severity and increasing size of trees was observed as well as slowed growth rate and increase severity. However, no significant relationship between clustering and spread of disease was observed.

Introduction

Beech bark disease (BBD) is a common disease among American beech trees (*fagus grandifolia*). The beech scale insect (*Cryptococcus fagisuga*) feeds on the beech tree for nutrients which makes the tree vulnerable to fungi in the *Nectria* genus (mainly *Nectria coccinea* var. *Faginata* or *Nectria galligena*, the native fungus species) (Latty *et al.*, 2002). The scale insect invades the inner living bark of the tree, which allows the fungi to infect deep into the bark

afterwards (Morin *et al.*, 2007). *N. Faginata* specifically attacks beech trees while the native species, *N. galligena*, can infect various types of hardwood trees in Europe and North America (2006). The infection can lead to death, although in some trees it is gradual and they can still survive for decades (Morin *et al.*, 2007). The first report of the beech scale insect in North America was in Nova Scotia around 1920 and believed to be brought from Europe (Ehrlich, 1934). The first infestation of the fungus was discovered in 1929, although it is assumed that infestations were present about 10 years prior (Houston, 1994). The first report of Beech Bark Disease in Michigan was in 2001 in Oceana, Mason and Muskegon counties (O'brien, Ostry, Mielke, Mech, Heyd, & McCullough, 2001). As of 2015, the presence of the beech scale insect is prevalent mainly in the northwestern lower peninsula of Michigan and the eastern half of the Upper Peninsula (Wieferich & McCullough, 2015).

When beech bark disease is monitored in an area, there are three defined phases of the disease. The first is the introduction of the invasion of the beech scale insect and the beginning of the spread of the infection of the majority of the trees in the area. The second phase is when the majority of the trees in the area are infected and the fungus is likely to have infected many of the trees in the area. The third is when BBD has prevailed in the area and has led to mortality of many trees and the composition of future growth of beech trees in the area will be affected (Houston, 1994). The three phases are referred to as the “advancing front,” the “killing front,” and the “aftermath forest,” respectively (Morin *et al.*, 2007). Within this study, the “advancing front” is the phase the study is currently experiencing.

This study observes the spread and severity of beech bark disease in Lower Northern Michigan, specifically, in the University of Michigan Biological Station's (UMBS) Wells Plot.

Being a well-studied area, there are records of all tree species and the diameter-at-breast-height (DBH) of each adult tree since 1974. Since the plot was last studied in 2000 prior to the infestation of BBD in the area, we expect changes in the beech tree community which may indicate patterns in the spread of the disease within the area and its effect on individual trees. This study investigates the effect that clustering of beech trees have on the severity of the disease on individual trees and the relationship between the size and growth rate of the trees and the severity of beech bark disease.

Methods

Study Site

The Wells Plot is located in Pellston, Michigan on Bryant Road at 45°33'08.3"N and 84°42'48.5"W (Fig. 1). It is a one hectare plot divided into one hundred 10x10 meter plots. Although the trees have all been identified in the Wells Plot, no true marker or tagging system has been implemented in the specific plot of this study apart from metal posts that signify the four corners of each of the plots. The individual tree locations were recorded with their X, Y distances from the northeast corner of every plot. A transect was used to locate the beech trees based on the previous data. Another group of researchers are developing a different study within a grid that overlaps this study grid in the Wells Plot and have tagged a majority of beech trees within the study. New tags for beech trees in the study grid have been added to the original data set for future reference.

Data collection

In order to track BBD distribution in the study site, the DBH of each tree was taken. A five-step rubric was formulated to visually determine the severity of the disease (Fig. 2). Severity

1 being the lowest infection and severity 4 being dead due to the spread of the disease. Severity 5 was added for any tree that was dead due to causes other than BBD. The visual examination of the disease was based on the spread of the white, wooly accumulation on the tree itself, which is a result of the infestation of the scale insect. The assumption was made that this accumulation is indicative of the disease and that the fungus that follows after scale insect infestation may also be attacking the tree, although not visible on the tree. The severity levels on the rubric are based on the white, wooly secretions of the scale insect when infesting the beech tree.

Spatial Analysis

ArcGIS was used in spatial analysis of the plot and BBD severity. The original dataset was used to project the beech trees onto a map of the plot. Severity of the disease for each tree was then projected onto the trees in the plot in ArcGIS (Fig. 1). A nearest neighbor test was run in order to see if clustering occurs within various subsets of the population. The test was run to determine clustering for all of the beech trees in the plot, for small, medium and large beech trees. Any trees below 4.5 cm DBH were classified under small, trees between 4.5 and 8 cm DBH were considered medium-sized trees and any tree over 8 cm DBH was considered a large tree. The nearest neighbor test was also run to determine clustering for beech trees with severity 1, severity 2, and severity 3 of the disease.

Statistical Analysis

A chi-squared test of independence was initially run to look at the sizes of trees between each category of severity. An ANOVA test was run to determine if there is a relationship between the size of the tree and the severity of the disease. The test compared the average DBH within each severity category. A linear regression was run to examine the effect of severity of the

disease had with the growth rate of the tree. The growth rate was calculated by the comparison of growth between the last two years of study (1987 - 2000) and between the last year and this study (2000-2018).

Results

Spatial Analysis

The nearest neighbor analysis explored the clustering of trees and severity. A total of seven nearest neighbor analyses were conducted. The first test, which we ran to analyze all of the trees and their locations and did not specifically look at severity, showed statistically significant clustering of all the trees in the area (Fig. 3). When looking at whether size affected the clustering of trees, nearest neighbor tests on small and large trees suggested that there is significant clustering of trees of small and large trees (Fig. 3). However, medium sized trees showed a random distribution and no significant clustering (Fig. 3). The nearest neighbor analysis was also run for the first three severities of the trees. The test resulted in trees of severity 1 of BBD were significantly clustered (Fig. 4). Tests on severity 2 and severity 3 infected trees were not significantly clustered and therefore, had a random distribution (Fig. 4).

Statistical Analysis

A chi-squared test of independence was run to compare the abundance of trees with each severity level in the small, medium, and large size tree categories (Fig. 5). All small trees were infected by the disease with a severity 1 (d.f.=4, $p \leq 0.05$). The majority of heavily infected trees reside among the larger tree category (d.f.=4, $p \leq 0.05$). The ANOVA test suggested a higher average DBH for severity 3 trees and a lowest average DBH for severity 1 trees (Fig. 6). The regression trend suggests that trees with a severity 3 of the disease began growing slower once

BBD was introduced than those only moderately or lightly infected (Fig. 7). Old growth refers to tree growth between 1987-2000 and new growth refers to growth between 2000-2018.

Discussion

The large trees of the study in the Wells Plot were significantly more affected by beech bark disease than the medium and small sized trees. The smallest trees were the least infected. This is characteristic of the distribution of BBD because larger and more mature trees are more susceptible to the disease (Twery and Patterson, 1984). This is due to larger trees having more characteristics desirable to the scale insect like branch scars and cankers (Gavin and Peart, 1993). Gavin and Peart (1993) also suggest that areas with a high density of large sized trees will suffer from higher severity of the disease. This is evidenced in the Wells Plot. All of the trees that were heavily infected were large trees in the study and 100% of the small trees were a slightly infected or not infected. The regression conducted looked at tree characteristics further and examined the growth of the trees compared to the severity of the trees. Gavin and Peart (1993) concluded that there was a significant decrease in the growth rate of beech trees that were infected by BBD. Trees that were more heavily infected also had slower growth rates than those that were only lightly infected (Gavin and Peart 1993). The analysis on the Wells Plot followed these same trends. The linear regression resulted in a trend that the infected trees were growing at a slower rate between 2000-2018 than from 1987-2000. The severity 3 trees showed the largest difference between the two growth rates, where the more recent growth tended to be slower than the older growth.

The spatial analysis looked at the clustering of both trees and severity. The analysis on clustering of tree size was taken in order to determine whether clustering severity results were

due to the actual disease or just the trees themselves. There was significant clustering of the small trees in the plot as well as those with severity 1. Although there was significant clustering of severity 1 trees, this may be coincidental due to the fact that all small trees were a severity 1 and not due to any actual clustering of the disease itself. Griffin *et al.* (2003) also concluded that there was not significant correlation between the distances of beech trees and BBD infection. They suggest that other factors more significantly cause the distribution of BBD among small scale areas. Stress was one factor that may make the tree more susceptible to BBD and therefore, areas that put beech trees under high stress may result in a larger amount of trees in that specific area to exhibit signs of infection (Lonsdale, 1980). More significant conclusions about the effect of clustering on BBD distribution may be seen on larger scale studies that more than one hectare like the Wells Plot.

As beech bark disease is a multi-step infection of the beech tree, much of the literature has inconsistent definitions of every step of the infection. In this study, the woolly white secretions of the scale insect left on the tree as it infests was used as the basis of determining whether BBD was present on the tree and to what scale. The fungus was not evaluated and not observed in this study. Gavin and Peart (1993) suggest that although external evaluation of the disease is useful, especially in looking at distribution, methods for looking into the internal parts of the tree may be more valuable for studying the growth of the infection within individual trees. Much of the literature on BBD is through external methods of identifying the disease on beech trees but consistency in these methods would be beneficial to the study overall. Gavin and Peart (1993) also determined differences in forests stands in old-growth and second-growth forests. As

the study of the Wells Plot continues, the changes in BBD distribution that occur due to forest succession or disturbances within the forest may be topics of future studies.

Maps and Figures

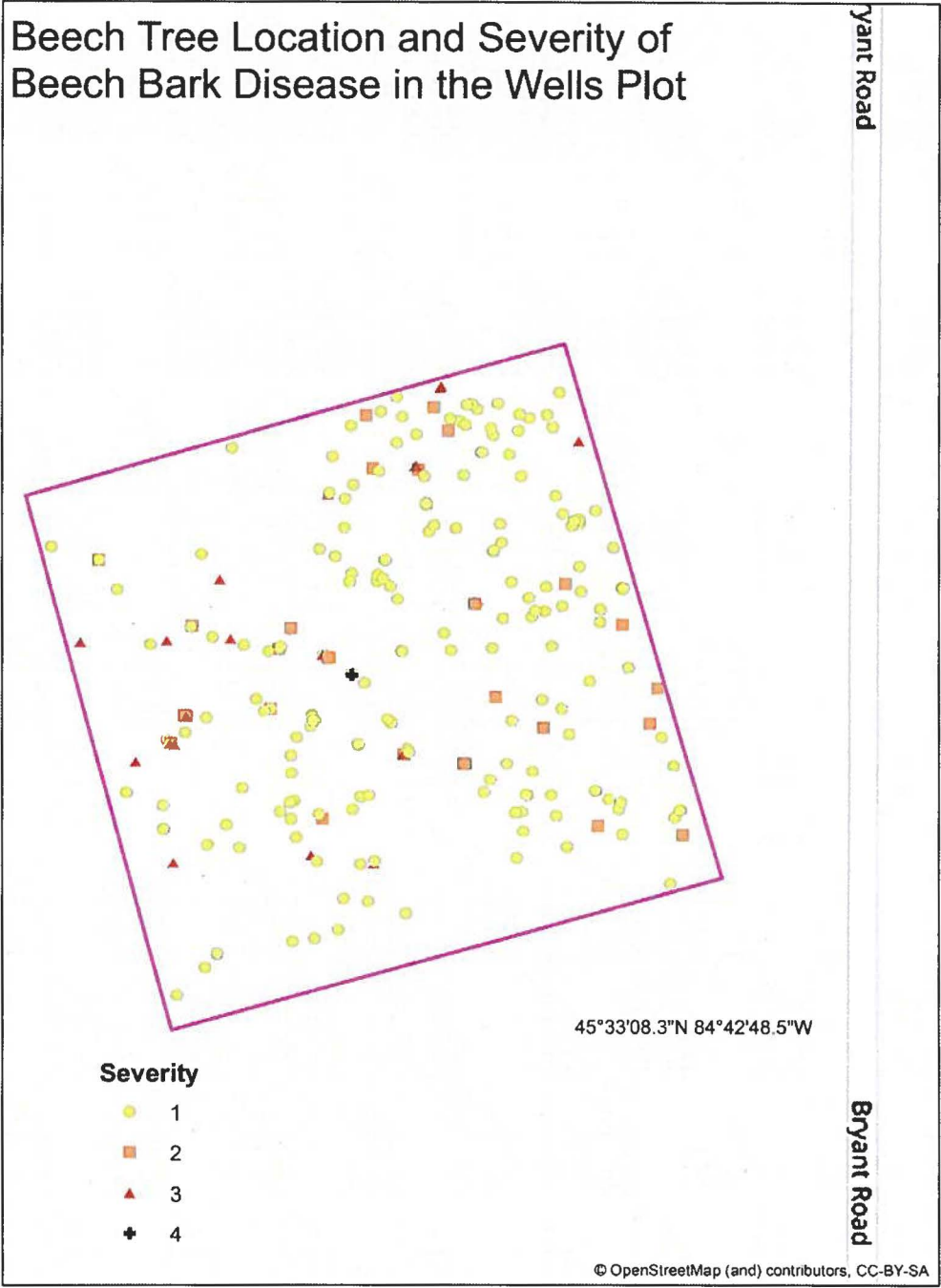


Figure 1. Map of Wells Plot with beech trees identified with severities

Beech Bark Disease Severity Rubric



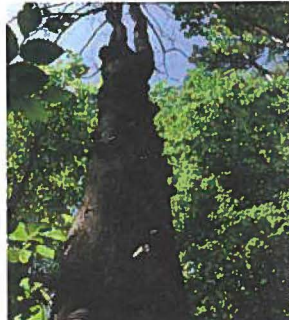
Severity 1: none to little disease
Either no sign of disease or small, sparse spots dispersed around random areas of the tree.



Severity 2: moderate disease
Clustered areas or patches of disease along most of the tree. Typically in weaker areas of the tree and around bases of branches.



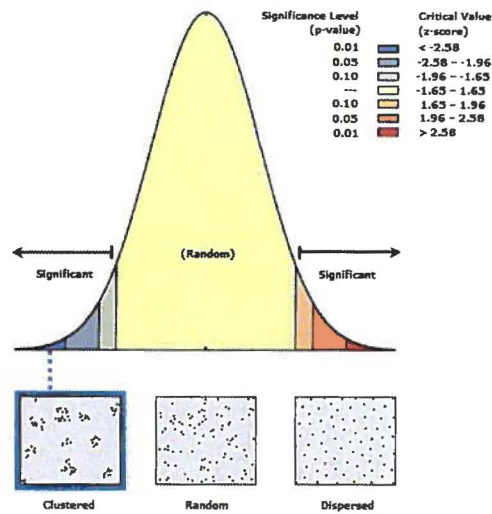
Severity 3: heavy disease
Disease has spread to the whole tree. More uniform dispersal around the tree. The scale insect is more commonly found on more heavily infected trees.



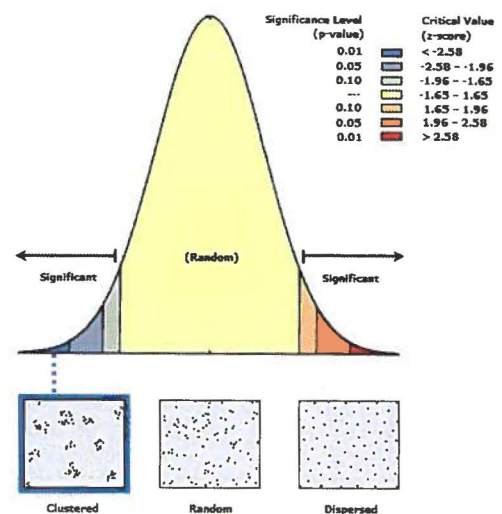
Severity 4: death by disease
Sign of disease is still apparent on the tree. Detritivorous fungi attach to the tree.

Figure 2. Rubric describing identification methods of BBD severity

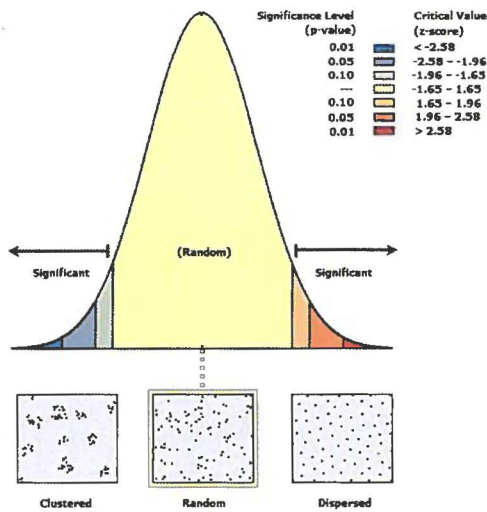
Nearest Neighbor Results for Tree Clustering



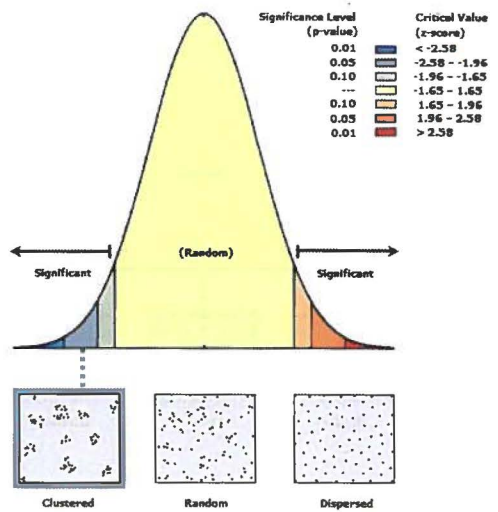
1. Significant clustering of all trees ($p \leq 0.05$)



2. Significant clustering of small trees ($p \leq 0.05$)



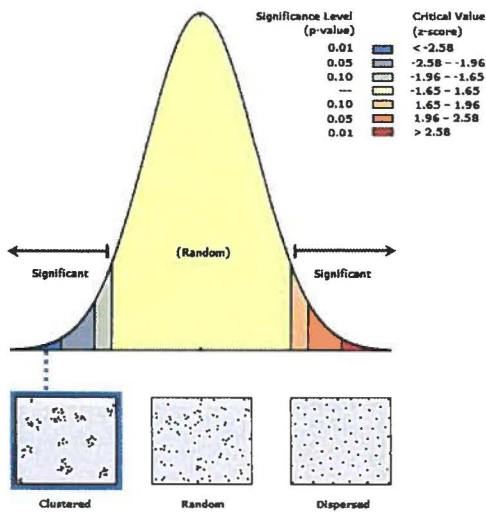
3. Not significant clustering of medium trees ($p \leq 0.05$)



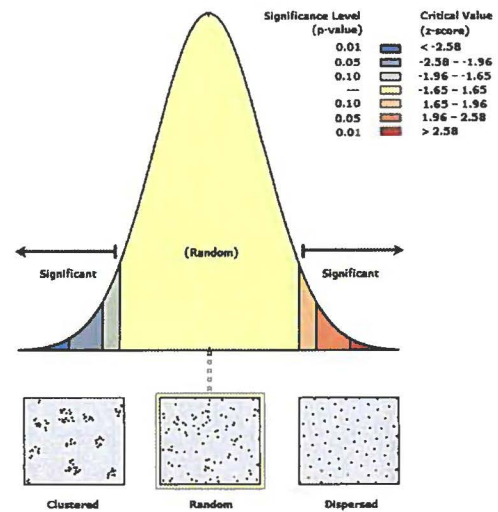
4. Significant clustering of large trees resulting in a random distribution ($p \leq 0.05$)

Figure 3. Nearest neighbor test to examine clustering of all, small, medium, and large trees.

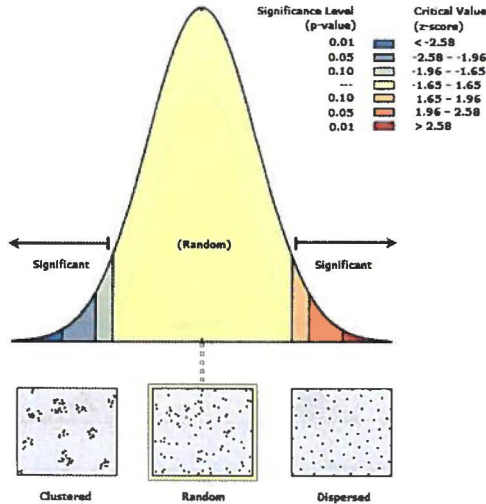
Nearest Neighbor Results for BBD Severity Clustering



1. Significant clustering of trees with severity 1 ($p \leq 0.05$)



2. Not significant clustering of trees with severity 2 ($p \leq 0.05$)



3. Not significant clustering of trees with severity 3 ($p \leq 0.05$)

Figure 4. Nearest neighbor test examining the clustering of severity 1, severity 2, and severity 3 trees.

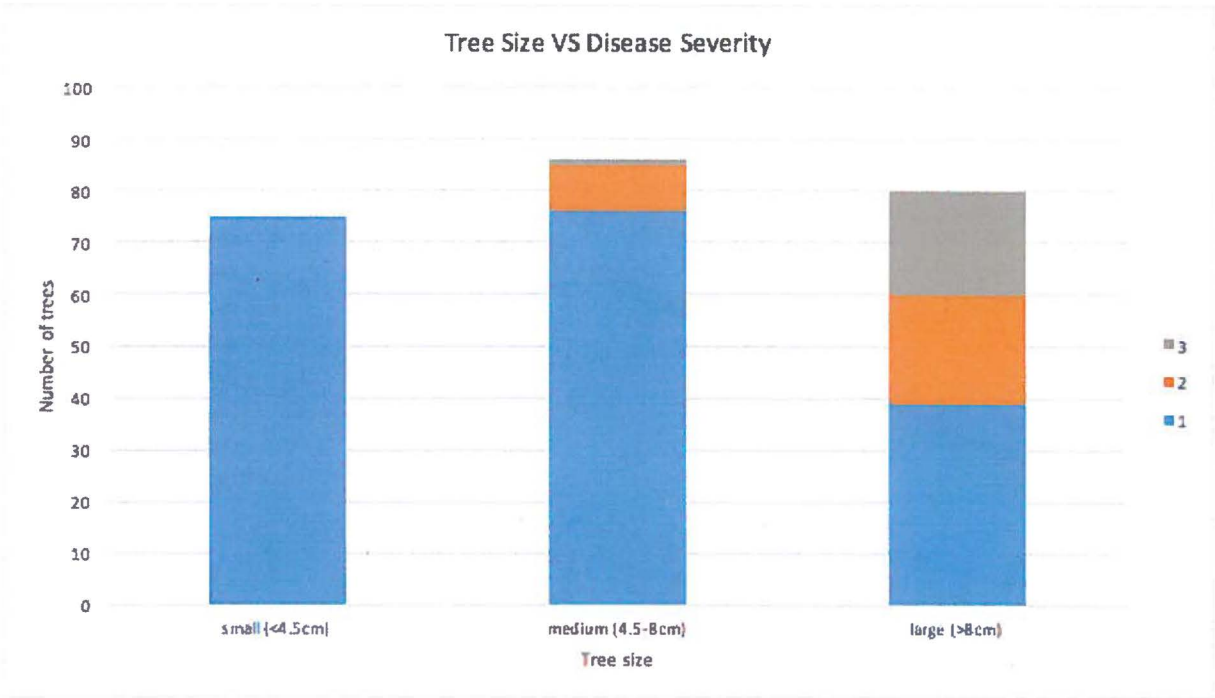


Figure 5. Chi-Squared Test of Independence results for small, medium, and large trees.

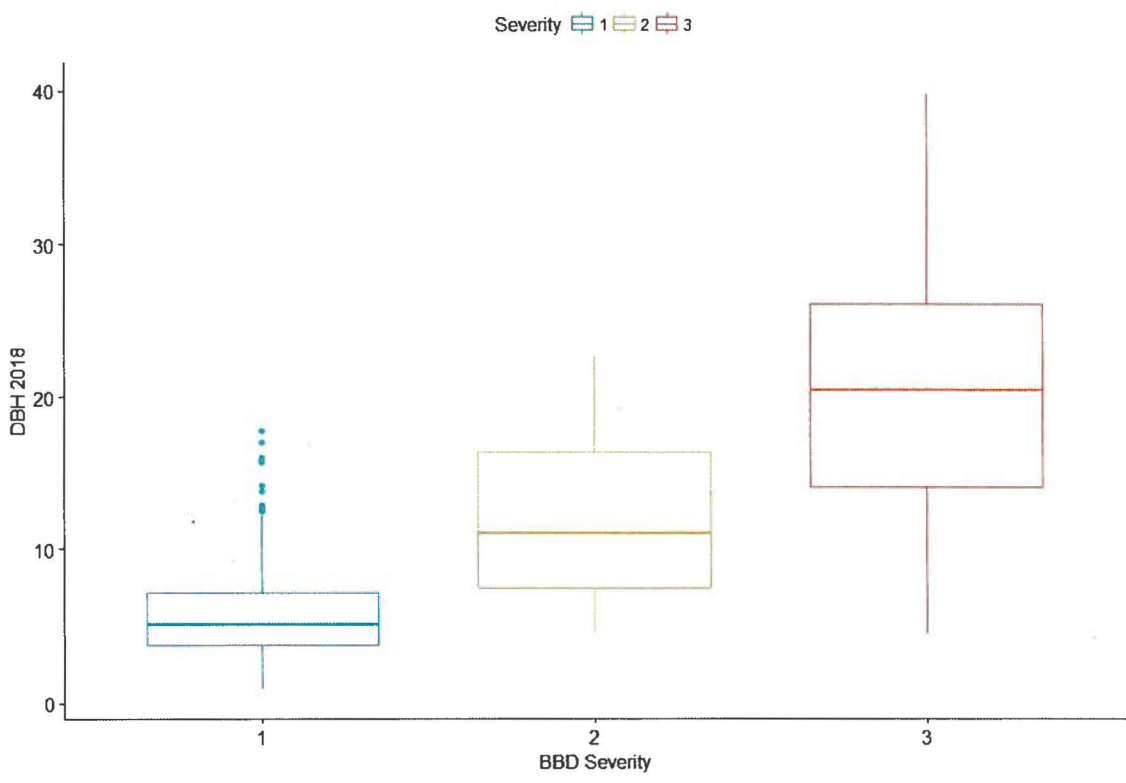


Figure 6. ANOVA test comparing average DBH of severities 1, 2, and 3.

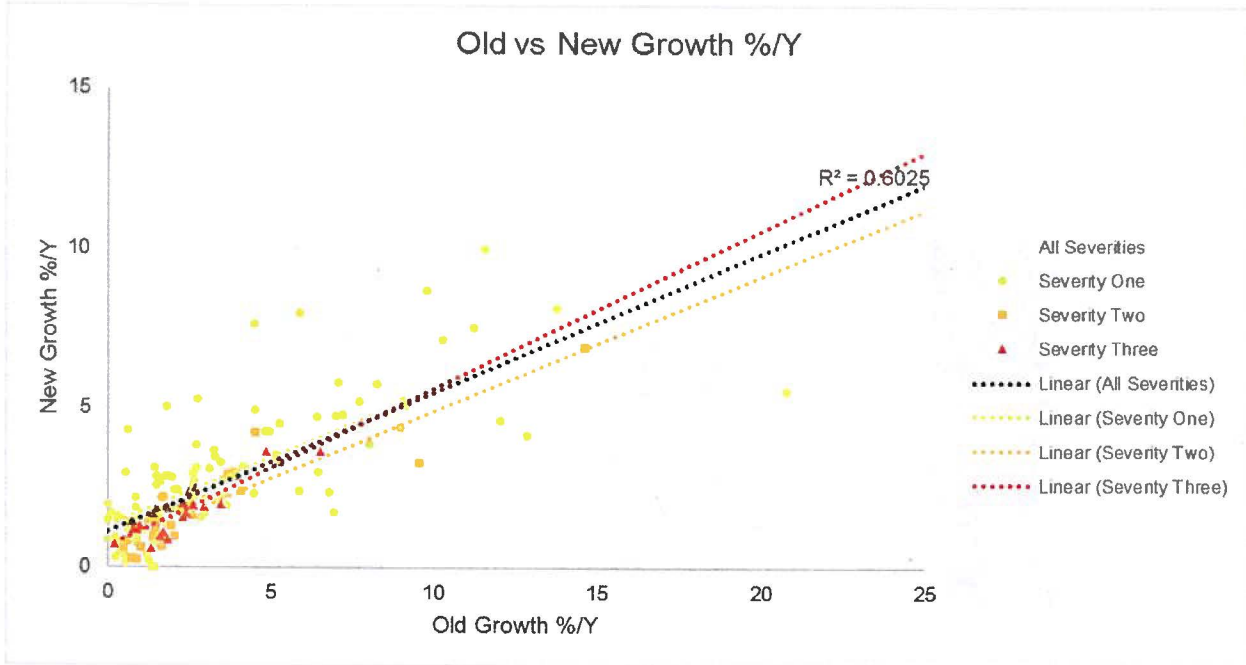


Figure 7. Regression of new growth and old growth for severity categories 1, 2, and 3.

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