

Beech Bark Disease: A study on the effects of disease and demise of The American beech (*Fagus grandifolia*) in the Wells Plot.

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Abstract

The American beech (*Fagus grandifolia*) has experienced major decline due to the presence of beech bark disease (BBD) in the United States since 1929. We studied how the radial size and growth related to the disease of the beech tree and its severity. We also looked at the spatial aspect of the disease and if this had any correlation with how the BBD was dispersed throughout the forest. To do this we used the Wells plot near Pellston, MI to conduct our study since there have been recordings of the diameter at breast height (DBH) of all trees in a one-hectare piece of land since 1927. We recorded DBH and severity of the disease on all 287 trees within the Wells plot and ran statistical analysis to see how radial growth was related to severity of disease and how distance effected the spread of the disease. We collected data that suggested there was correlation with the size and growth of the trees and the severity of the infection. We also collected data that suggested that the larger the DBH the more likely that there will be clustering of the disease. Beech may survive for long periods of infection from beech bark disease. However, our results demonstrate that the radial growth is reduced as the infection enters an area of uninfected beech trees.

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The American beech (*Fagus grandifolia*) has experienced major decline due to the presence of beech bark disease (BBD) in the United States since 1929. We studied how the radial size and growth related to the disease of the beech tree and its severity. We also looked at the spatial aspect of the disease and if this had any correlation with how the BBD was dispersed throughout the forest. To do this we used the Wells plot near Pellston, MI to conduct our study since there have been recordings of the diameter at breast height (DBH) of all trees in a one-hectare piece of land since 1927. We recorded DBH and severity of the disease on all 287 trees within the Wells plot and ran statistical analysis to see how radial growth was related to severity of disease and how distance effected the spread of the disease. We collected data that suggested there was correlation with the size and growth of the trees and the severity of the infection. We also collected data that suggested that the larger the DBH the more likely that there will be clustering of the disease. Beech may survive for long periods of infection from beech bark disease. However, our results demonstrate that the radial growth is reduced as the infection enters an area of uninfected beech trees.

Introduction:

Beech bark disease (BBD) can be considered a conglomerate of three pandemics, the first is the introduced insect originator, the second, the introduced pathogen, (*Nectria coccinea*), and the third, is the native pathogen (*N. galligena*), on the host, scale infested beech (Loman & Watson 1943, Houston 1994). In 1890, the woolly beech scale insect (*Cryptococcus fagi* Baer.)

was first recognized on the European beech trees (*Fagus sylvatica*) by researchers in Halifax, Nova Scotia (Ehrlich, 1934; Houston, 1994). In 1929, the United States observed its first scale infestations on American beeches in the Arnold Arboretum near Boston (Ehrlich, 1934). Since then, the American beech has experienced a major decline due to the disease all throughout the eastern United States. A West Virginia outbreak began at a well-trafficked scenic area and Ohio observed the infestation at a popular arboretum. These results suggest that humans are inadvertently spreading the disease (Houston, 1994). In 2000, Luce and Mason county of the upper and lower peninsulas of Michigan were the first sites that encountered beech scale (Witter *et al.*, 2005). The scale insects persisted throughout the state and spread to six counties in the lower peninsula and five counties in the upper peninsula. By 2005, there were eight counties throughout Michigan with beech plots infected with BBD (Witter *et al.*, 2005).

Previous studies investigated the physical and chemical characteristics of infected tree communities including the diameter at breast height (DBH) and severity of the infection (Latty *et al.*, 2003; Houston, 1994; Lonsdale, 1980; Gavin & Peart, 1993). Larger trees seem to have a higher probability of having high severity of BBD because they are able to provide more habitat to the scale insects. According to Latty *et al.* (2003) it is likely that the more nutritious bark of larger trees results in a greater number of scaled insects, which promotes higher infestation densities, and greater fungal and disease development. Another detriment to the beech trees according to Gavin & Peart (1993) is that growth reduction could be caused with infection of the disease and the effects of growth on trees with the infection should be analyzed.

In this study, we addressed the following research questions for the Wells plot affected by BBD: (i) How was the severity of the disease spread amongst older and younger trees? (ii)

Did the severity of the disease affect the growth of the trees? (iii) Is there a pattern of severity of disease or DBH throughout the Wells plot?

Materials and Methods:

Location:

Our location was the Wells Plot in Pellston, Michigan on Bryant Road at 45°33'08.3" N and 84°42'48.5" W. (Fig. 1). This location has been studied sporadically from 1927 to 2000. All trees have been identified and tagged in this location and DBH of every tree has been recorded. This location hadn't been studied since BBD was first observed in the lower peninsula in 2004.

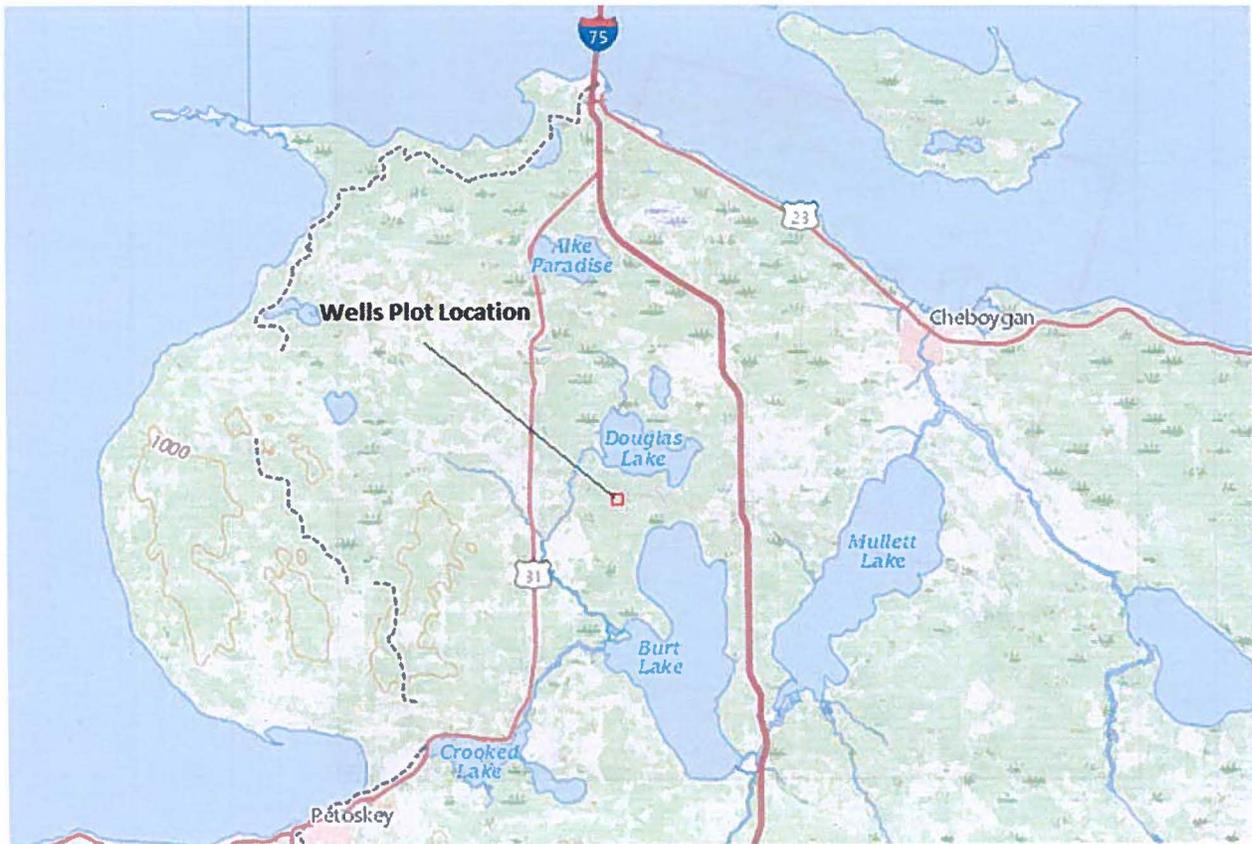


Figure 1: Map of the Wells plot location in relation to the State of Michigan.

Plots:

Wells Plot is a one-hectare plot that is defined by metal post in the ground at each corner (Fig. 2). The plot is then divided into one-hundred 10m x 10m subplots marked by orange rebar

protruding from the ground by a meter. There were measurements where each American beech tree was located starting from the north-east corner of each subplot that gave us X Y coordinates. We would measure these by using the data provided and a transect tape to get accurate measurements to each beech location.

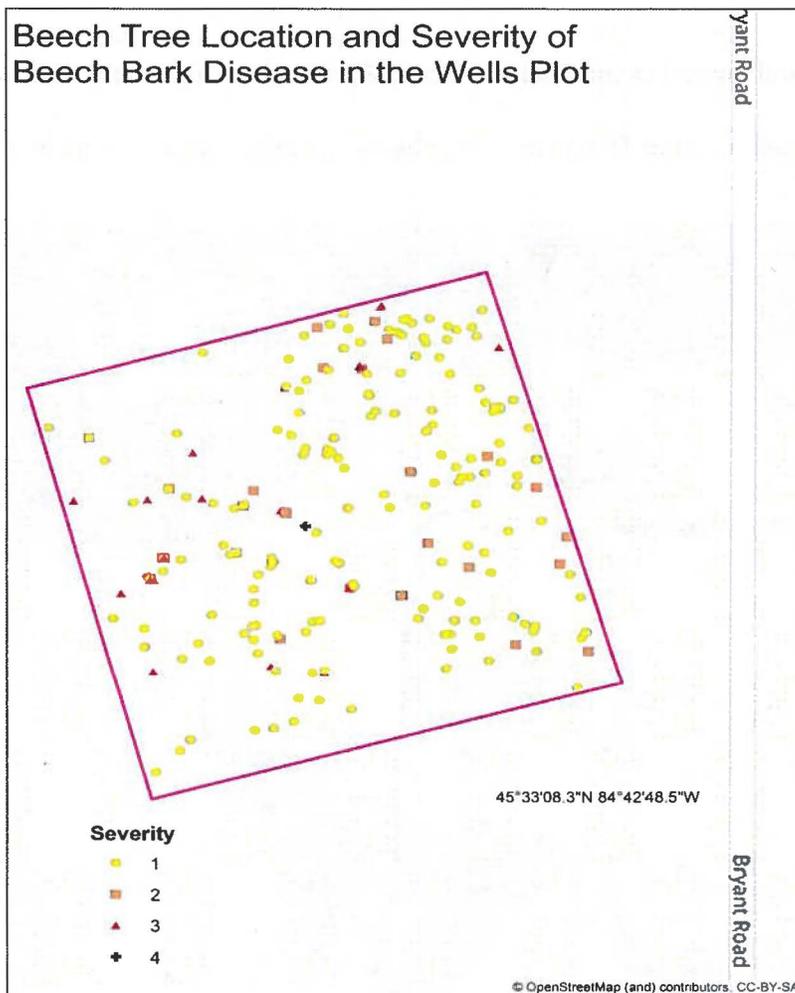


Figure 2: ArcGIS Wells plot map showing the beech tree locations and severity of the disease within the plot.

Measuring DBH:

We measured from the ground to 1.3 meters on our bodies and used this height to measure DBH throughout the study. We took the DBH of each tree in each subplot used a rubric for the severity of the BBD (App. A). For the severity of the disease, we assumed that the white scale that grows on the trees is the major sign of BBD. We recorded the tag IDs from each tree for further research use. This process was continued throughout the entire plot and all DBH, severity and tag IDs were recorded.

Data:

We used a Chi-squared test of independence to see if there was a correlation between the size of the trees and the severity of the disease. The sizes were split into three groups of small (0-4.5cm), medium (4.5-8cm) and large (>8cm). Trees that had died because of tree fall or other natural disturbances were removed from the data analysis because they were not necessary for the hypotheses that were proposed.

The analysis on old versus new growth by severity was analyzed using linear regression. This was done by taking the DBH from the 1987-2000 data, and comparing it to the newly collected data from 2000-2018. This growth data was observed and broken down into a ratio between tree growth percentages of old growth to new growth.

To determine if there was clustering among the beech trees that were infected throughout the plot we used geographic information system technology. This was used to see if the severity was clustered, random or dispersed throughout the plot.

Results:

Statistical analysis:

There was a total of 241 trees that were analyzed using a Chi-squared test of independence. There was a large amount of American beeches observed: 75 small trees, 86 medium, and 80 large (Fig. 3). ANOVA further suggests that the average DBH of severity 3 trees is higher than severity 1 (Fig.4).

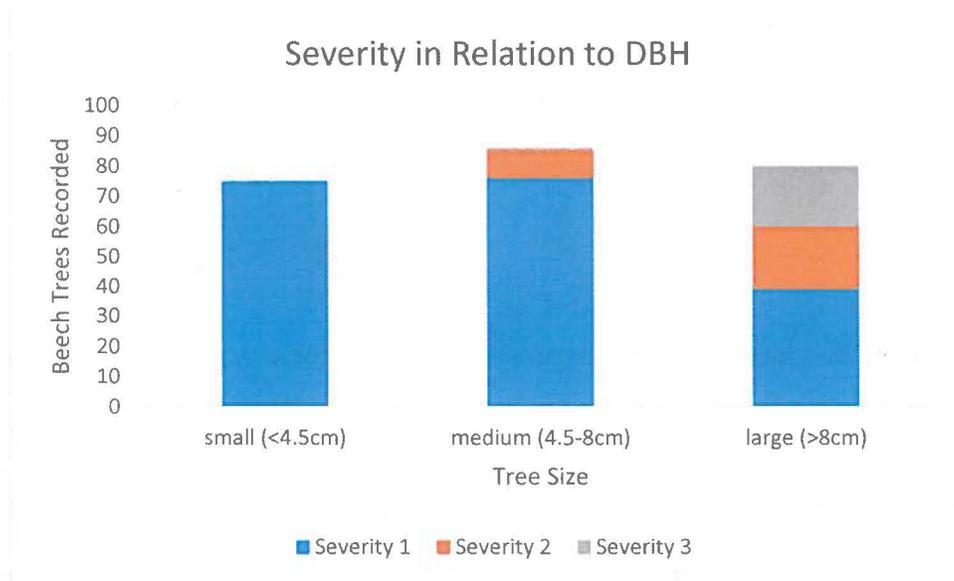


Figure 3: Tree size in relation to severity of disease (n=241). Chi-square test of independence showed significant values. (df=4, $X^2=72.8$, $p<0.001$)

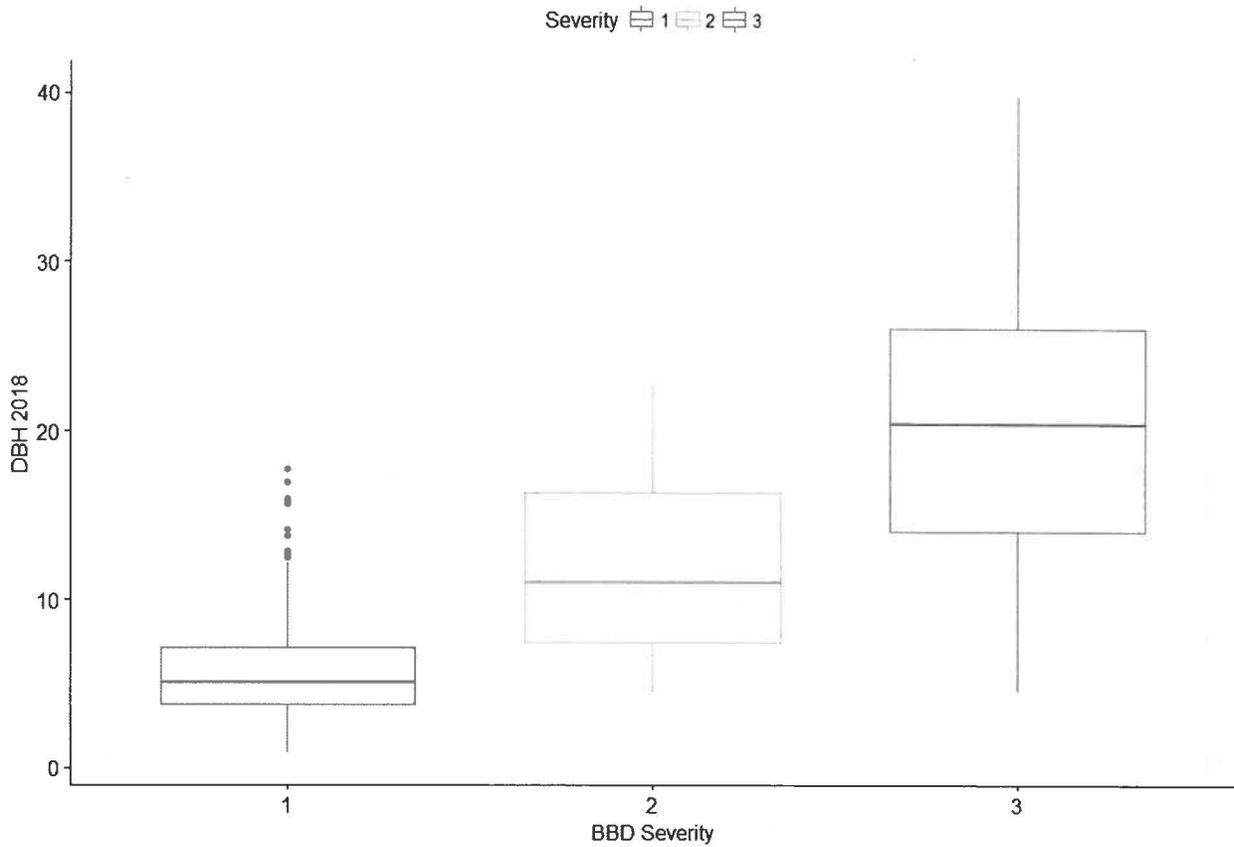


Figure 4: ANOVA comparing the average DBH within each severity level.

Growth analysis:

Categories using small, medium and large trees were also used when running our analysis on old and new growth. For this test, 163 trees were taken into consideration because they had to be growing from 1987-2018. Linear regression lines were formed based on the average growth percent per year (Fig. 5 and Appendix A).



Figure 5: Linear regression of old growth compared to new growth with consideration of severity. (n=163) ($R^2=0.6025$)

Spatial analysis:

ArcGIS was used in a variety of ways to determine if there were groupings throughout the Wells plot (Fig.6). The first analysis was to see if the trees in the plot were grouped together or spread apart. Classifications for the spatial analysis were clustered, random or dispersed. The second analysis was on if the different stages of severity, one, two, or three, were in certain classifications. Finally, DBH was taken into account for the three variables and analyzed to see if they were classified in certain groups.

Subset	All	Severity 1	Severity 2	Severity 3	<4.5 cm DBH	4.5≤ to ≤8 cm DBH	>8 cm DBH
Pattern	Clustered	Clustered	Random	Random	Clustered	Random	Clustered
P value	0.000000	0.000000	0.824627	0.223206	0.000000	0.357987	0.024986
Z score	-10.2771	-5.46731	-0.22159	1.218047	-5.99355	-0.91920	-2.24162
Observed. <i>M</i> Dist(m)	1.984217	2.823453	7.871490	10.11518	3.039892	4.684867	4.869850
Expected <i>M</i> Dist(m)	2.900903	3.561984	8.041538	8.881231	4.271985	4.931938	5.626028
Ratio	0.683995	0.792668	0.978852	1.138939	0.711589	0.949906	0.865592

Figure 6: ArcGIS spatial analysis of all trees alive in the Wells plot. (n=242)

Discussion:

The hypothesis that all sizes of trees in the Wells plot had the same amount of severity in regards to BBD was rejected. The Chi-squared test of independence showed that trees with a DBH higher than 8cm had high severity of the disease within the Wells plot. The severity of the disease symptoms increases as the diameter of the tree increases, because, as trees grow they are more likely to develop a suitable habitat for the scale insects, such as branch scars, bark fissures and cankers (Houston, 1975, Gavin & Peart, 1993). Next, looking at the data from the regression, the old growth (1987-2000) of the beech trees was greater than the new growth (2000-2018) in the Wells plot. This suggests that there is a decline in growth as the trees are infected with the BBD, for the trees are potentially putting more effort into fighting off the disease rather than growing larger to gain more nutrients. According to Gavin & Peart (1993), there is clear evidence that suggests that there is growth reduction that correlates with infection of the beech trees. Finally, when looking at the spatial analysis of all beech trees that were in the plot. The result was clustered which is something that needed to be identified before going any further with our analysis. Our data showed that there was clustering effects in trees with a severity of one and less than 4.5cm DBH. These two categories were very similar since we found that trees

with lower DBH mostly had a severity of one. The one cluster that stood out were trees with an 8cm DBH, this suggests that the trees could be spread to its nearest neighbor once it reaches a certain DBH. As mentioned earlier the scale insect could be more concentrated on trees with larger DBH, making their chances of being transferred to another tree within the region higher. The rest of the categories for testing nearest neighbor were not significant.

Throughout this study there have been many misunderstandings on the identification of the BBD. Some think that the scale is not an indicator of the BBD and that it is only a sign that it is coming. This should be investigated for better understanding of the disease presence in Michigan forest near the Wells plot. The presence of the disease and the progression within forested stands have been linked to a number of factors, including scale insect population densities, genetic resistance of the host and the nutritional quality of the beech bark (Houston, 1994; Houston and Houston, 2000). However, very little study has been focused on how these factors change with the disturbance history of the forest to show broad patterns of disease. If beech trees in a forest that is far from large populations of people have the disease, then there are implications that other trees around Michigan have the disease. There should be more efforts to try and combat the scale insects that first infect the trees. If we don't find a cure for the BBD in the American beech there is a chance that this iconic tree could be decimated throughout Michigan. The Wells plot should further be studied throughout time to track patterns of the disease and its effects on the beech trees.

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Appendix A:

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.

Severity 5: Death do to outside influences, such as, tree fall or nutrient loss.
