Spread of Beech Bark Disease and its Relationship to Regional Forest Composition

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Abstract

Beech bark disease is an insect-fungus complex involving the beech scale insect (*Cryptococcus fagisuga*) and the exotic canker fungus *Nectria coccinea* var. *faginata* or the native *Nectria galligena* that kills or injures American beech (*Fagus grandifolia*). Beech scale was introduced to Nova Scotia around 1900 and the disease has subsequently expanded its range through a large portion of the range of American beech. In this study we used historical maps of the extent of the disease in the USA to estimate the historical spread rate of this disease as 19.3 km/year ± 0.82 km/year. This spread rate was applied to the current distribution of the disease to predict the future geographical extent beech bark disease through 2025. Maps of past and future spread of the disease were overlayed with a maps of estimated American beech density (basal area / ha) estimated from recently measured forest inventory plots located through out the eastern USA. This analysis indicated that beech bark disease has already invaded most of the regions where American beech is a dominant component of stands and that despite the impacts of the disease, considerable amounts of beech remains in invaded areas. In the future, the disease is expected to invade a large region where beech represents a relatively minor component of forest composition. Recent plot data also indicate the accumulation of large numbers of standing dead beech trees in invaded areas. Analysis of historical forest inventory data indicate that in most of the area invaded by the disease, the volume of American beech has actually increased, though generally at lower rates than that observed in associated tree species (sugar maple and eastern hemlock).

Introduction

The long-term effect of beech bark disease on forest composition is not clear. It appears that in some stands, the advent of beech bark disease results in significant decreases in the proportional representation by beech but in other stands, beech is able to persist due to its often prolific regeneration via sprouts and seedlings.

In this study we used historical information to reconstruct historical spread of beech bark disease in the eastern USA. We then make use of regionally sampled forest inventory data to draw some inferences about the condition of forests following the invasion by this disease. Finally, we use our estimate of the rate beech bark disease range expansion to predict future spread and characterize the composition of forests where the disease will spread in the future.

Methods

ESTIMATION OF SPREAD

The historical rate of beech bark disease spread was estimated from maps depicting the distribution of the disease (Figure 1). The progression of disease range expansion was thus compiled in a geographical information system (GIS) that recorded the year that the disease was first observed in a county.

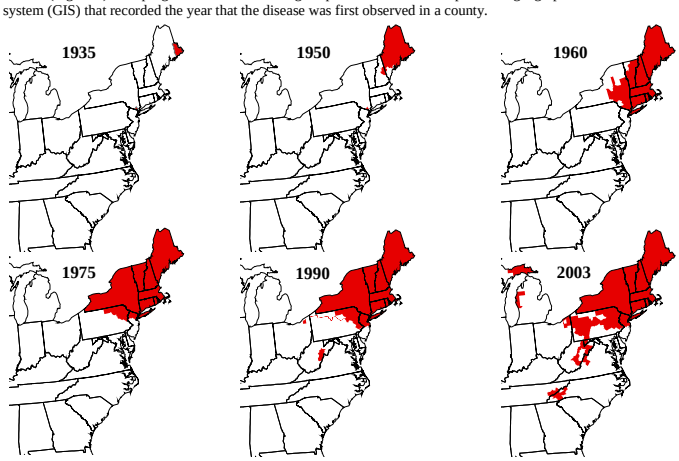

Figure 1. Maps of beech bark disease spread (1935-2003)

FOREST COMPOSITION DATA

The USDA Forest Service has conducted surveys of overstory forest composition in the eastern USA as part of the "Forest Inventory and Analysis" (FIA) program since the 1940's. By extracting volume of American Beech from successive surveys, we were able to characterize temporal trends in beech volume. In order to elucidate the role of beech bark disease on these trends, we also estimated similar time series of the volume of sugar maple, *Acer sachrum* and eastern hemlock, *Tsuga canadensis*.

We used data from the "Eastwide database" (consisted of data from 93,611 plots located in 37 states) to provide more detailed information about forest composition. We also used FIA plot data to estimate the percentage of standing beech basal area that was dead in each county.

Estimates of beech basal area per ha by county were plotted vs. the year that each county was first infested with beech bark disease or vs. the year that it was predicted to become infested through 2025. The year of predicted infestation was obtained from applying the historical spread rate as described above. This analysis provided a representation of the amount of beech in historically infested areas as well as information about the amount of beech in areas yet to be infested. Similarly, we plotted the percentage of beech that was dead in each county vs. the year it was first infested or predicted to become infested. This provided information about the accumulation of standing dead beech in aftermath stands.

Results

A linear model, which included an intercept term was fit to the data in Figure 2 and yielded a slope of 19.3 km/year ± 0.82 km/year (a =-636.58 ± 67.67, r2=0.75) and this was used as the best estimate of the radial rate of spread in subsequent analysis (Fig. 3).

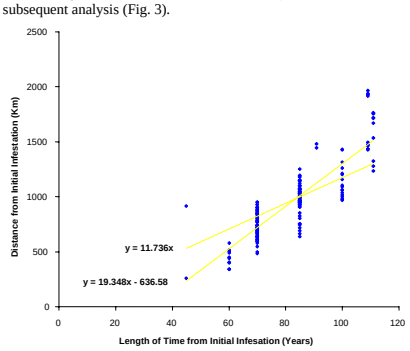

Figure 2. Linear model for the beech bark disease spread rate

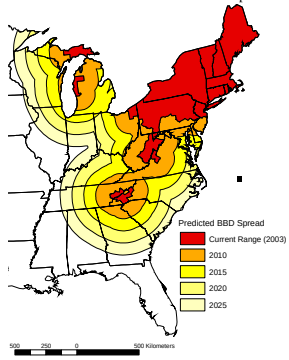

Figure 3. Predicted spread of beech bark disease through 2025

Results continued

Visual comparison of the distribution of beech (Fig. 4) with the current distribution of beech bark disease (Fig. 1) suggests that the disease has already invaded most of the areas with the greatest host abundance. Calculations shown in Table 1 confirm that > 50% of the total beech basal area in the USA occurs in the area where beech bark disease is present; however the disease only occupies a relatively small fraction (< 30%) of its potential range.

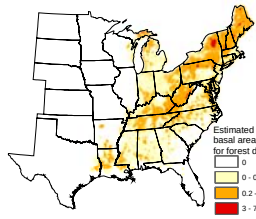

Figure 4. Map of beech basal area per ha interpolated from Forest Inventory and Analysis data

Table 1. Total land area and beech basal area estimated for the potential range and current range of beech bark disease

Item	Eastern USA	Currently infested area	Percent
Land area (km²) of stands with beech present	1,589,744	434,548	27.3
American beech basal area (m²/ha)	606,734	348,311	57.4

Figure 5 depicts the current (1990 – 2002) geographical distribution of American beech basal area. By combining these county-level beech basal area estimates with historical (Fig. 1) and predicted (Fig. 3) spread data we described the current distribution of beech basal area in relationship to historical and future spread of the disease. There was considerable variation in beech basal area but the trend of beech basal area over time was generally concave, indicating the historical spread of beech bark disease into areas of increasing beech density, followed by spread into decreasing beech abundance in the future.

Figure 6 depicts the geographical distribution of standing dead American beech. While the proportion of standing beech that was dead was generally higher within the range of beech bark disease, there were several areas outside the range of the disease that have apparently also experienced relatively high levels of mortality. Comparison of current standing beech mortality with historical and future spread suggested that the proportion of standing beech that was dead was proportional to the numbers of years of disease presence.

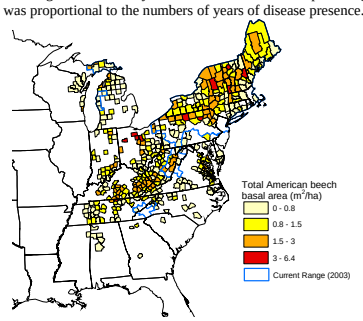

Figure 5. Total standing American beech basal area in m²/ha (estimates are only provided from counties with at least 10 FIA plots)

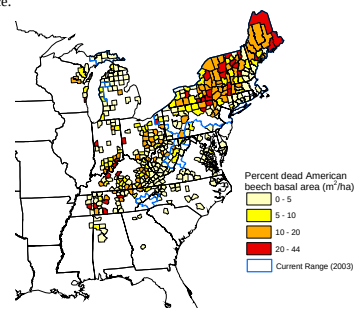

Figure 6. Percentage of standing beech that was dead (estimates are only provided from counties with 10 beech stems > 12.7 cm in diameter)

While it was not possible to reconstruct precise regional trends in beech abundance during the time course of historical invasion by beech bark disease, inference of these trends could be derived from historical reports of American beech volume reported by state in periodic forest inventories (Fig. 7).

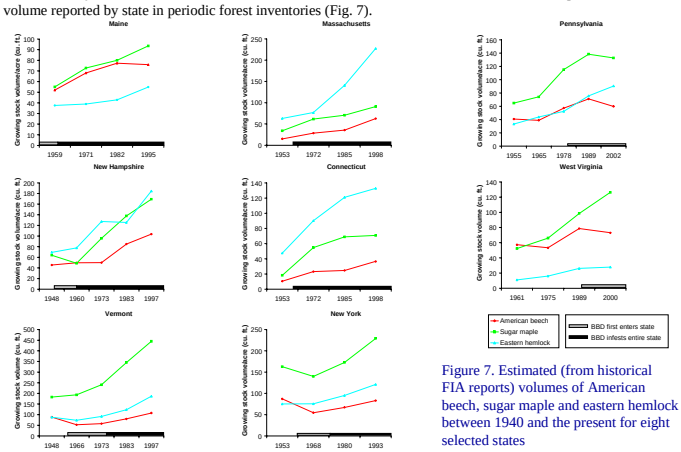

Figure 7. Estimated (from historical FIA reports) volumes of American beech, sugar maple and eastern hemlock between 1940 and the present for eight selected states

Conclusions

- Over the next 50 years it is likely that beech bark disease will continue to expand its range in the USA.
- Analyses of current inventory data suggest that beech bark disease has already invaded most of the areas with relatively high densities of beech; most of the range, where beech occurs at low densities, has yet to be invaded.
- Invasion by BBD may have caused a slight decrease temporarily in the relative dominance of American beech on a regional scale, but the disease has not caused the elimination of the species and in most cases, it appears to have not caused a substantial decrease in regional levels of beech. Although others have shown that post-BBD beech stems are both smaller and reduced in quality.