

# Mapping Susceptibility and Spread Associated with Beech Bark Disease

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## Abstract

Also known as beech scale *Nectria* canker, beech bark disease is an insect-fungus complex composed of the European 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*) (Houston 1994). The disease results when a *Nectria* fungus infects the bark through feeding wounds caused by beech scale insects. Around the turn of the century, the beech scale insect was introduced into Nova Scotia from Europe. It has since spread southwestward into New England, New York, Pennsylvania, and West Virginia (Manion 1991). Fungal invasion occurs about 3 to 5 years after the scale insects appear. Extensive mortality often occurs in the years following the appearance of *Nectria*; some trees may survive for several years.

Invasions by exotic insects and diseases are one of the most important threats to the stability and productivity of forest ecosystems around the world (Liebhold et al. 1995; Vitoušek et al. 1996). The forests of the eastern US seem to be particularly vulnerable to these invasions; over the last century they have suffered devastating effects by notorious forest pests such as chestnut blight, gypsy moth, and beech bark disease (Mattson 1997). One of the most important steps in the development of effective strategies for management of alien species is to evaluate the risk of future impacts from specific exotic organisms (Byers et al. 2002). The generic activity, "risk assessment" is considered an important component to management of exotics both before and after their arrival in new habitats (Liebhold et al. 1995). Our research focuses on estimating the expected geographical extent of beech bark disease through 2025 and which areas within that extent will be the most at risk. We used USDA Forest Service Forest Inventory and Analysis (FIA) data to create an estimated surface of American beech basal area and historical survey data to model beech bark disease spread.

## Introduction

Beech bark disease is an alien pest species complex consisting of the scale insect, *Cryptococcus fagisuga* (Fig. 1) and at least two species of *Nectria* fungi (Fig. 2), *N. coccinea* var. *faginata*, and *N. galligena*. The scales typically achieve large numbers feeding on sap in the inner bark and allow the pathogenic *Nectria* fungi to invade the xylem, often resulting in dieback or tree mortality. The disease was apparently introduced to North America near Halifax around 1890 and has been slowly expanding its range. As this disease invades new areas, large proportions of American beech, *Fagus grandifolia*, are often killed. In order to plan for the management of the beech bark disease in the future, there is a need to delimit the distribution of susceptible stands in areas that are currently uninfested. American beech has a very large range and beech bark disease has only invaded a fraction of that area. While the greatest concentrations of this tree species occur in northeastern North America, this species exists through much of the southeast as well. We expect that the impacts of this disease are likely to increase in the future.



Figure 1. Beech scale nymph, about 0.3 mm long.



Figure 2. Sexual fruiting bodies of *Nectria coccinea* var. *faginata*.

## Methods

### FOREST SUSCEPTIBILITY

The geographical distribution of the suitable habitat for beech bark disease was mapped by interpolation of host species basal area ( $m^2/ha$ ) estimated from 93,611 forest inventory plots located throughout the eastern U.S. These data represented the most recent available USDA Forest Service Forest Inventory and Analysis data sampled in each of the thirty-seven states in the Eastwide Database. Host abundance for beech bark disease was measured as basal area/ha of American beech.

The ordinary kriging procedure described by Deutsch and Journel (1998) was performed to interpolate a surface of basal area/ha of American beech. Kriging is a geostatistical method that provides unbiased estimates at unsampled locations as weighted averages of values from nearby locations (Issaks and Srivastava 1989; Liebhold et al. 1993). In this analysis we generated a map from the plot data by calculating kriged estimates on a grid of 1- by 1-km cells. Variography and kriging were performed using the GSLIB software library (Deutsch and Journel 1998). One percent of the plots were excluded to use in validating the estimated surface.

The forest susceptibility map was then adjusted for forest density. FIA plots are located randomly but restricted only to forest land area. Therefore, it was necessary to adjust estimates in each 1- by 1-km cell for forest density. This was accomplished using land cover data (National Land Cover Data) which was acquired from the Multi-Resolution Land Characteristics Consortium as a raster matrix of 30- by 30-m cells coded for land use. These data were aggregated to 1- by 1-km cells to estimate percent forest cover for each cell. Next, the forest susceptibility map was multiplied by the forest density map to generate a forest susceptibility map adjusted for percent forest cover.

### SPREAD PREDICTION

Future range expansion of beech bark disease was predicted by applying estimates of past spread rates derived from historical records (Figure 3). These records consisted of the year that each county first became infested. A GIS was used to calculate the distance of each county from the area initially infested. The rate of spread was estimated as the slope of the estimated linear model of the distance of the county as a function of its time of first infestation. Least-squares regression was used to estimate linear models and the intercepts were forced through the origin. A predicted spread map representing years of expected presence (2001-2025) was generated on a 1- by 1-km grid using the estimated spread rate. Then the number of years of expected presence was divided by 25 (years of possible infestation) to produce a proportion of expected years of presence between 2001 and 2025. The proportion map was multiplied by the adjusted forest susceptibility map to create a map of beech bark disease risk through 2025.

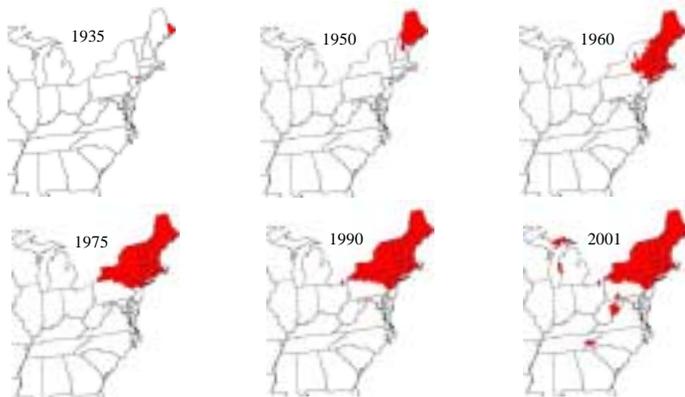


Figure 3. Maps of beech bark disease spread (1935-2001)

## Results

American beech basal area ( $m^2/ha$ ) was estimated using ordinary kriging (Figure 4) and then multiplied by the forest density map (Figure 5) to create a beech abundance map adjusted for forest density (Figure 6). A least-squares regression was run to validate the kriged estimates. The linear model explained 11% of the variation. Historical spread of beech bark disease was estimated at  $24.3 \text{ km/year} \pm \text{SEM}$  ( $r\text{-square}=0.5323$ ,  $\text{RMSE}=167.92$ ) (Figure 7). A predicted beech bark disease spread map was generated using this historical rate (Figure 8). Finally, the spread map and adjusted beech basal area map were multiplied to create a map of beech bark disease risk for the next 25 years (Figure 9).

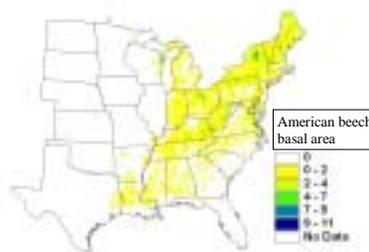


Figure 4. Estimated American beech basal area ( $m^2/ha$ ).

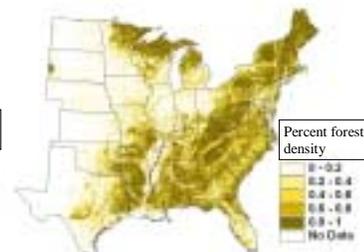


Figure 5. Percent forest density from NLCD data

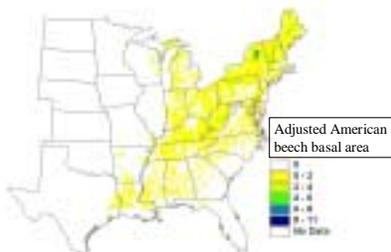


Figure 6. American beech basal area ( $m^2/ha$ ) adjusted for forest density.

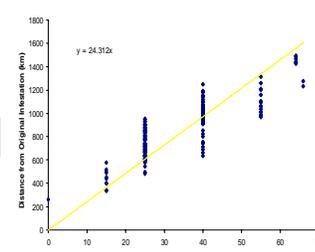


Figure 7. Linear model for beech bark disease spread rate.

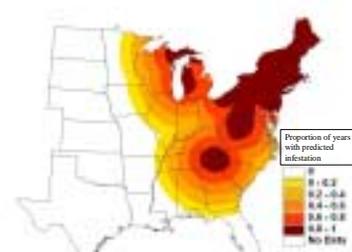


Figure 8. Proportion of years with predicted beech bark disease infestation (2001-2025).

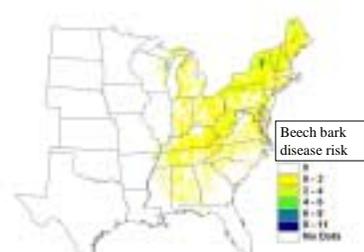


Figure 9. Beech bark disease risk (2001-2025)

## Conclusions

- Beech bark disease has already spread into much of the range of American beech.
- American beech is most abundant in the Adirondack and Appalachian Mountains.
- Eastern Kentucky is the highest risk area that is currently uninfested.

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