Neonectria faginata **System:** Terrestrial

Kingdom	Phylum	Class	Order	Family
Fungi	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae

Common name beech bark canker (English), beech bark disease (English), BBD (English)

Synonym *Nectria coccinea* , var. *faginata* M.L. Lohman, A.M.J. Watson & Ayers 1943

Similar species *Neonectria coccinea, Neonectria ditissima*

Summary Ascomycete *Neonectria* fungi along with beech scale (*Cryptococcus fagisuga*) form the disease-complex responsible for beech bark disease (BBD) of American and European beech. In North America *N. faginata* and *N. ditissima* are responsible for the disease on American beech, whereas in Europe *N. ditissima* and *N. coccinea* affect European beech. *N. faginata* has only been recorded to infect American beech and has not been recorded outside North America, although genetic analysis suggests *N. faginata* is native to Europe. Beech scale infests mainly larger sized beech trees, feeding on host tissues and causing small fissures on the bark. This initial damage to the tree allows *Neonectria* to enter the tree, which kills host tissue and eventually girdles the tree causing it to die. BBD can dramatically alter forest stand composition and structure, through loss of large trees and proliferation of smaller trees that originate from root sprouting. Reduction of beech nut production and loss of large trees in infected stands may affect mammals and birds that use beech nuts as important food source and old trees as habitat. Around 1% of American beech is estimated to be resistant to BBD. Research is currently focused on modes of inheritance and propagation methods.

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Species Description

Neonectria faginata (= *Nectria coccinea* var. *faginata*) is an ascomyete fungi. It produces fruiting bodies (ascomata) called perithecia. Perithecia are tiny (200-300 µm diameter; 250-400µm high), lemon shaped, bright red and occur in clusters of 7-15 on reddish-orange stroma in cracks of living or dead bark. Each perithecium contains sacs (asci) that are filled with sexual ascospores. Asci are narrowly clavate with ascospores arranged uniseriately within. Ascospores are ellipsoid to broadly ellipsoid, measuring 10.5-12.5 x 5-6 µm and are ornamented with regularly scattered warts. On some trees perithecia are abundant, causing large areas of the bark to appear red.
The imperfect (anamorphic) asexual state of *N. faginata* is *Cylindrocarpon faginatum*. *C. faginatum* produces both micro- and macroconidia. Microconidiophores form as simple lateral branches 11-15 x 3 µm. Microconidia are transparent, cylindrical, usually non-septate, 11-14 x 3 µm. Microconidia are produced during saprophytic growth on infested bark and are spread by water films. Macroconidiophores initially formed sparsely from simple conidiophores, but later become restricted to sporodochia developing as stromatic cushions, 15-20 x 3-4 µm. Macroconidia are very long, up to 120 µm, strongly curved and cylindrical, and are produced on dead bark (Lonsdale & Sherriff, 1983 in Houston, 1994a; McCullough *et al*., 2003; Castlebury *et al*., 2006; MycoBank, 2007).
A full, detailed description and images of *N. faginata* are available in Castlebury *et al*. (2006).

Lifecycle Stages

The imperfect (anamorphic) state of *Neonectria faginata* is *Cylindrocarpon faginatum* C. Booth 1966 (Mycobank, 2007). *C. faginatum* produces both micro- and macroconidia. Microconidia which can spread in water films are produced during saprophytic growth on infested bark. Macroconidia are produced on dead bark in sporodochial pustules which erupt through the thin outer bark.*Neonectria faginata*produces ascospores within perithecia that usually occur in clusters, often where sporodochia had occurred. Both macroconidia and ascospores are dispersed by wind and water, and are the agents responsible for infecting new trees (Houston, 1994a).

Habitat Description

American beech (*Fagus sylvatica*) appears to be the sole host of *Neonectria faginata* (Plante et al. 2002). While its native range is thought to be Europe, it has not actually been recorded outside North America (Mahoney *et al*., 1999; Castlebury *et al*., 2006).

The fungus requires prior infestation of American beech by the scale insect *Cryptococcus fagisuga*. The scale insect causes damage to host cells and results in small fissures on the bark that allows *N. faginata* to enter the tree. Indeed the most important factor determining the course of infection by *N. faginata* and other *Neonectria* species is the level of scale infestation. Heavy infestations allow *Neonectria* to spread rapidly within the bark (Houston, 1994a). High rainfall is thought to be detrimental to beech scale and *N. faginata*, as it may wash crawlers from trees and affect *Neonectria* spore production and dissemination; particularly the wind dispersed *Cylindrocarpon faginatum* stage (Houston, 1988). Cold temperatures also reduce the overwintering second-instar beech scale populations in the winter (Houston, 1988). There appears to be a direct connection between climate and beech scale insect populations. In northern latitudes beech scale is limited by low winter temperature; minimum daily temperatures of -34 °C or below correlate with scale population dieback (Houston & Valentine, 1988 in Dukes *et al*., 2009).

Neonectria appear to only be limited geographically by the current distribution of beech scale, suggesting that they are not constrained by climate. In fact, perithecium production may be highest in winter as host dormancy reduces the capacity of trees to resist infection (Gove & Houston, 1996 in Dukes *et al*., 2009). The effect of future climate change scenarios of disease dynamics is unknown, but increased CO_2 may enhance tree growth and thus increase susceptibility. Alternatively, increases in CO_2 tend to decrease tissue nitrogen concentration, possibly decreasing bark nitrogen and thus susceptibility to scale attack. Increases in the frequency and severity of storms may influence the longevity of infected trees which are highly vulnerable to windthrow (Dukes *et al*., 2009).

General Impacts
Beech bark disease (BBD) is caused by the combined impacts of beech scale insect (*Cryptococcus fagisuga*) and several species of ascomycete fungi in the genus *Neonectria*. BBD affects American (*Fagus grandifolia*) and European beech (*F. sylvatica*). Two principal species of *Neonectria fungi* are associated with BBD in North America. The probably introduced *Neonectria faginata* only infects F. grandifolia and is the main species involved with the disease. Native *N. ditissima* (*N. galligena*) affects a range of tree species, including beech (Houston, 1994a). In many cases *N. faginata* spreads to stands infected with *N. ditissima* and replaces this species as the dominant pathogen (Houston, 1994b; Kasson *et al*., 2009). A third species *N. ochroleuca* (now named *Bionectria ochroleuca*) has been found in association with BBD in some regions of the United States (Houston, 2005). In Europe the fungi associated with BBD are *N. ditissima* and *N. coccinea* (Twery & Patterson, 1984; Castlebury *et al*., 2006).
The beech scale insect feeds on host parenchyma cells which collapse and die, resulting in small fissures on the bark that allow *Neonectria* to enter the tree. Heavy infestations of scale allow *Neonectria* to spread rapidly within the bark (Houston, 1994a). As the fungal mycelia grow, large areas of tissues become weakened and die, sometimes causing cankers on the trunk and branches. Sometimes red-brown liquid oozes from the bark tissues killed by the fungi, and the foliage of severely affected trees may become sparse and turn yellow (LeGuerrier *et al*., 2003). If enough tissue is killed the tree will be girdled and die (Koch *et al*., 2010). The course of the disease may take as little as two years, but other trees may linger for several years.
Much research has suggested that BBD mainly affects large, older trees, and may cause up to 80% mortality of beech within a stand (Houston, 1994a). Death of older trees leads to gradual gaps in the canopy. This gives the opportunity for other tree species to take over, sometimes leading to drastic changes in the composition and structure of stands (Twery & Patterson, 1984; Runkle, 1990; Wiggins *et al*., 2004). Particularly in stands dominated by BBD-tolerant species such as eastern hemlock (*Tsuga canadensis*) and sugar maple (*Acer saccharum*); these species dominate and American beech may become a minor component of the stand (Twery & Patterson, 1984).
However in most forest stands BBD favours the development of dense beech thickets that interfere with the regeneration of other trees (Houston, 1994a; Garnas *et al*., 2011), due to beech’s propensity to reproduce vegetatively via adventitious root sprouts, especially from damaged root sprouts (Garnas *et al*., 2011). Thus in many forests there is actually an increase in beech volume accumulation, particularly 10-20 years after BBD invasion (Morin *et al*., 2007).
Beech is a highly important tree for many birds and mammals due to the habitat large old trees provide and for the beechnuts produced during mast years. Loss of larger trees may reduce food and habitat and have negative impacts for animals, which may ramify through the ecosystem (Lovett *et al*., 2006; Wiggins *et al*., 2004).
Diseased trees are more prone to “beech snap” during high wind events. This poses a threat to people and personal property where trees occur in campgrounds, recreation areas or near homes (McCullough *et al*., 2003; Heyd, 2005). Alteration to beech composition may also have economic impacts, both negative and positive (Garnas *et al*., 2011).
For a detailed account of the impacts of beech bark disease please read Impacts of Beech Bark Disease

Management Info
Most control methods focus on reducing populations of the beech scale, as *Neonectria* are unable to colonise trees that have not been previously infested with the scale. Thus control of *Cryptococcus fagisuga* is likely to slow the spread of BBD (Wiggins *et al*., 2004).
Cultural: Thinning and removal of infected or susceptible trees, while retaining resistant trees is a commonly used management strategy. This is important for decreasing long-term susceptibility and vulnerability of forests to beech bark disease. Potentially resistant trees can be identified by smooth bark and vigour. In contrast, large overmature trees, trees with rough bark, and trees with wounds, broken tops or other obvious problems are most likely to be infested by beech scale and most vulnerable to *Neonectria* infection (McCullough *et al*., 2003). However such practices not feasible in large areas of natural forest due to labour, financial and practical constraints (Wiggins *et al*., 2004).
Physical: Physical removal of scale insects by scrubbing trees, high pressure water, or use of petroleum-based oils, which cover and suffocate scale insects may be used on individual high-value ornamental or yard trees (McCullough *et al*., 2003).
Chemical: There is no practical chemical control for beech scale (Pond, 2008), although insecticides may be used for individual high-value ornamental or yard trees (McCullough *et al*., 2003). Herbicides may be used in some cases to control beech regeneration, in order to minimise root sprouting and the creation of dense beech thickets (McCullough *et al*., 2003). Pesticides are not acceptable control options in large natural areas because of labour, financial, environmental and practical constraints (Wiggins *et al*., 2004).
Biological: The most desirable option for control of BBD is a biological control agent of *C. fagisuga* (Wiggins *et al*., 2004). A number of natural predators and pathogens of *C. fagisuga* have been identified including coccinellids, mites, gall gnats and a fungus (Shingo, 1964 in Houston, 1994a; Wiggins *et al*., 2004; Dukes *et al*., 2009). However none are effective in stopping its spread to date (Pond, 2008), and much further research is required (Wiggins *et al*., 2004).
Genetic: An estimated 1% of American beech trees are resistant to scale insect infestation, and thus BBD. The cause of resistance to BBD remains unidentified (Koch *et al*., 2007), although in European beech resistance appears to be due to anatomical features that act as barriers to infestation (Lonsdale, 1983a in Houston, 2005), whereas in American beech resistance may be associated with less total and amino nitrogen concentration (Wargo, 1988 in Houston, 2005). Recent findings suggest that resistance to BBD ranges from partial to total resistance (Ramirez *et al*., 2007).
Currently the only known method to identify resistant trees is the artificial infestation method developed by Houston (1982). Drawbacks to this method include the minimum 1-year wait for results and the reliance on live scale eggs which could result in spread of the insect. Thus much research is focused on identification of genetic markers for resistance, trials to clarify modes of inheritance via cross-breeding resistant and susceptible individuals, and methods of propagation via somatic embryogenesis (Koch & Carey, 2005; Loo *et al*. 2005; Pond, 2008).
For a detailed account of management options for beech bark disease please read Management of Beech Bark Disease

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