

Modelling the colonization of the decay fungus *Heterobasidion annosum* in Scots pine (*Pinus sylvestris* L.) root system

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Highlights: We have constructed a three dimensional model that gives us structural information about the Scots pine root systems in a forest stand and the spatial distribution of roots in that stand. The model allows us to make predictions how fast *Heterobasidion annosum sensu stricto* colonises the pine roots, transmits from one root system to another and to recreate the distribution patterns of the pathogen in time and space.

Keywords: boreal forest, root architecture, *Pinus sylvestris*, *Heterobasidion annosum*

Heterobasidion species are economically the most destructive forest pathogens of conifers in Finland. It is estimated that annual losses caused by *H. parviporum* and *H. annosum s. str.* are about 50 million euros of which 90% are damages on Norway spruce (*Picea abies* L. Karst.) and 10% on Scots pine. The primary infection happens in summer, when the basidiospores of *Heterobasidion spp.* are released. The airborne spores infect freshly cut stumps when falling on them. The fungal mycelium then colonises the stump and spreads into root system. In pine roots, the fungus may spread up to 2.0 m per year. The fungus cannot grow freely in soil. Instead, it relies on root contacts and grafts to infect adjacent trees. Spreading of the fungus in pine stands results first in infection of individual trees and later groups of trees. Severe infection leads to the death of the trees (Risbeth 1950, 1951).

In this work we utilize a three dimensional structural model for woody root system for Scots pine (Kalliokoski et.al. 2010). This model describes the root system as a branching structure and it has been implemented as a part of the LIGNUM model (Fig. 1.). The model needs as input the characteristics of the main roots connected to the stump: diameter, length to the first branching point and spatial orientation. We have added geometrical algorithms to calculate the distance between any two root segments (Fig. 2.) and the existence of root contacts. In addition, the root model has a new module that describes the spread of the fungus in an infected root system. Furthermore the new module implements the transfer of the fungus to another root system in case of root contacts or if two root segments are close enough. With these new modelling components it is possible assess the colonization dynamics of *H. annosum* both in a single Scots pine root system and in a forest stand.

LITERATURE CITED

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Fig. 1. Schematic presentation of the bifurcating root system: RS=root segment, RBP=root branching point, B=bud, α =branching angle. Shades of grey denote branching orders.

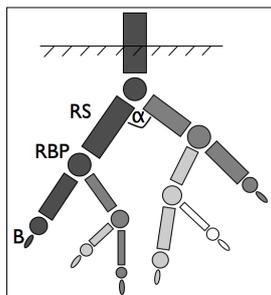


Fig. 2. Distance between two root segments in a set of two root systems. The transfer of *H. annosum* between them is possible but unlikely: segments must be connected or no more than few millimetres apart.

