Honey Fungus: A Silent Killer

Distribution of *Armillaria* and its effect on an old growth Douglas-fir/ Western Hemlock Forest

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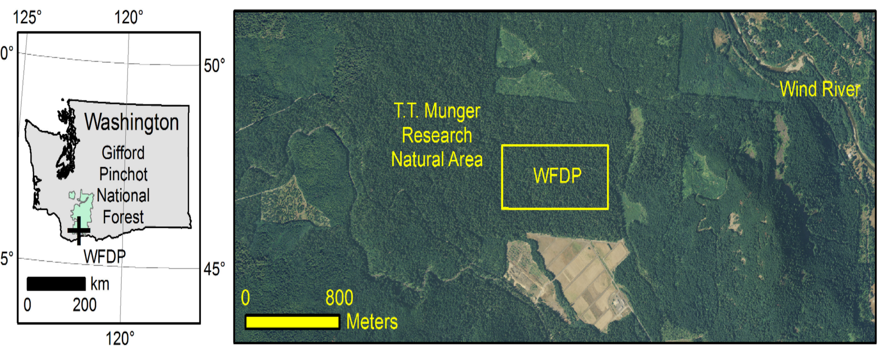


Introduction:

Armillaria root disease is found in many temperate and tropical forests throughout the world. It is responsible for on average 2-3 % of mortalities in infected forests. This root disease is caused by many species of fungus from the *Armillaria* genus. They are commonly referred to as Honey Fungus. This fungus spreads mainly through the interaction of tree roots.

The Wind River Forest Dynamics Plot shows evidence of an infection by *Armillaria*. However the Extent of the infection has not been studied or mapped.

Research Question :
How much of the WFDP is infected and what are the effects of *Armillaria* on the plots mortality?

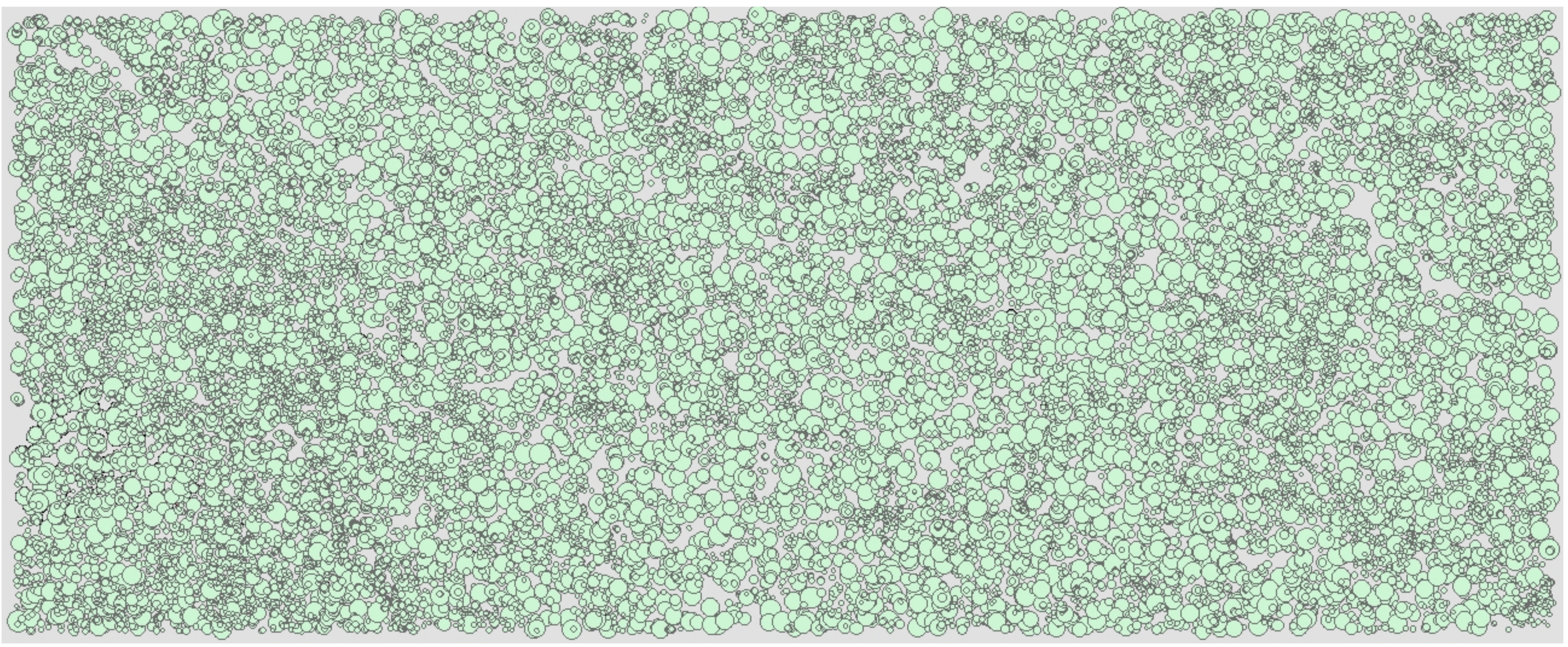
Methods:

At establishment, The Wind River Forest Dynamics Plot was a 25.6 ha permanent plot in which 30,973 woody stems ≥ 1 cm dbh where tagged and mapped. The plot contains 26 different tree, shrub and liana species. After establishment each woody stem ≥ 1 cm dbh was measured and mortality data, including factors associated with death, was collected on all trees that died from establishment until the 2016 field season.

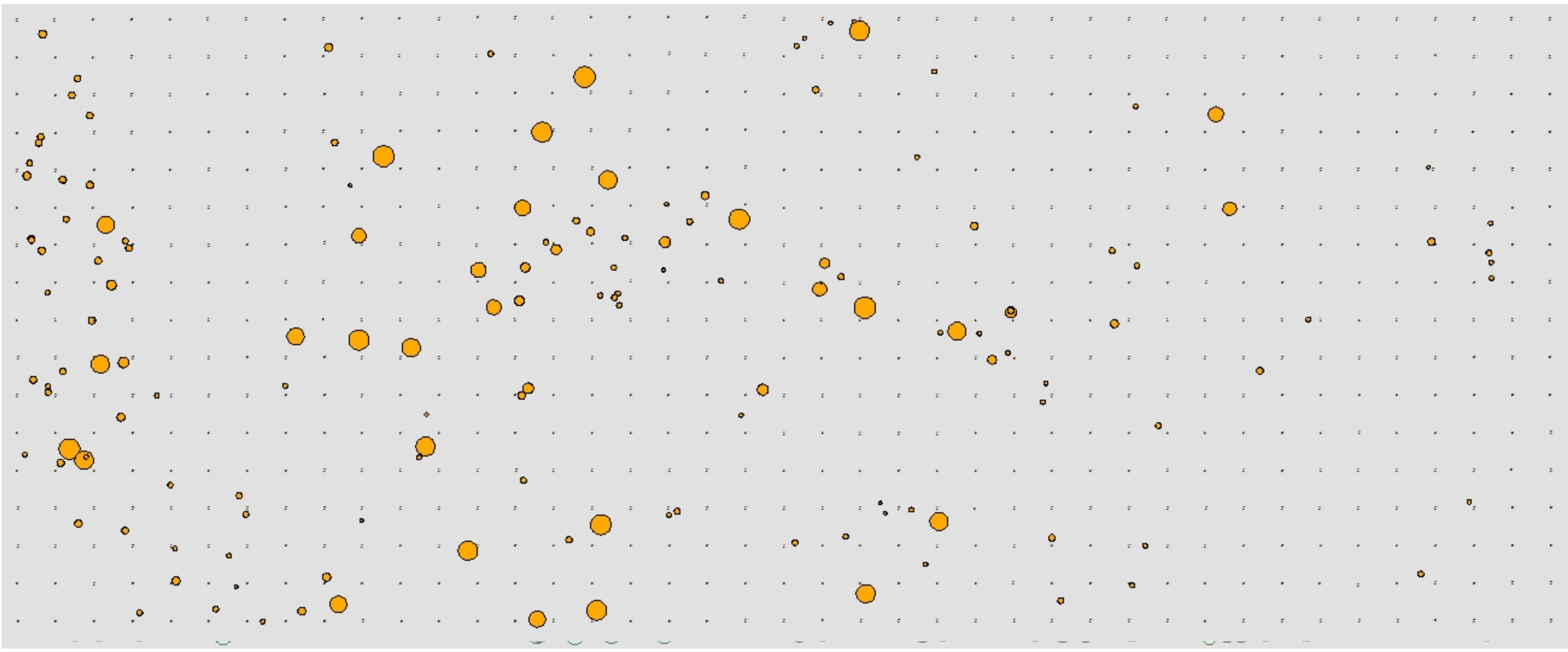
Using the mortality data we determined all tree species which have mortalities that where associated with armillaria root disease (Figure 3) and determined the relationship mortality had with the size of the tree.(Figure 2) Once these species where determined we calculated and mapped the crown radius of each trees based off their dbh using the equation and parameters of table 3 in Betchtold. If a species was not in the table we substituted the parameters from a similar species. We set the estimated coarse root radius equal to the radius of the crown. After mapping the root radius of each tree we then mapped trees whose mortality data showed an association with *Armillaria* and mapped any root systems that where touching an infected tree and expanded out from all infected trees in 5 meter groups to show the probability of the area being infected (Figure 1).The area for The total root system, known infected area and the predicted total infected area where calculated.

Results:

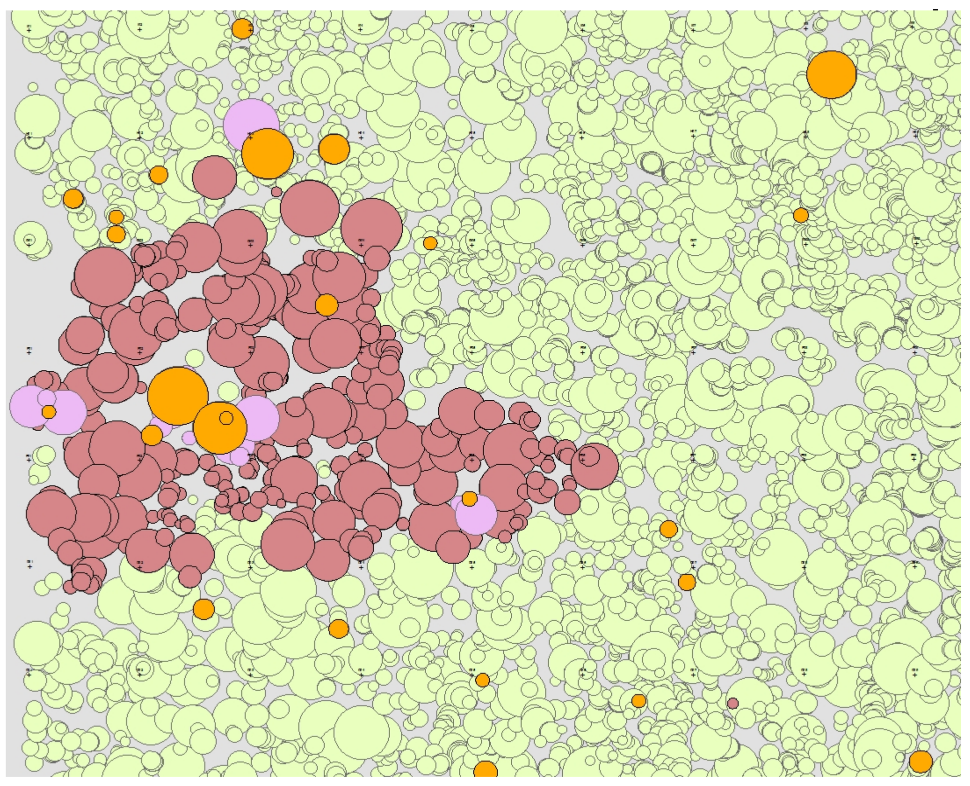
Figure 3



Map of the estimated area of coarse roots for all susceptible species. Each circle is the coarse root area of a single tree.

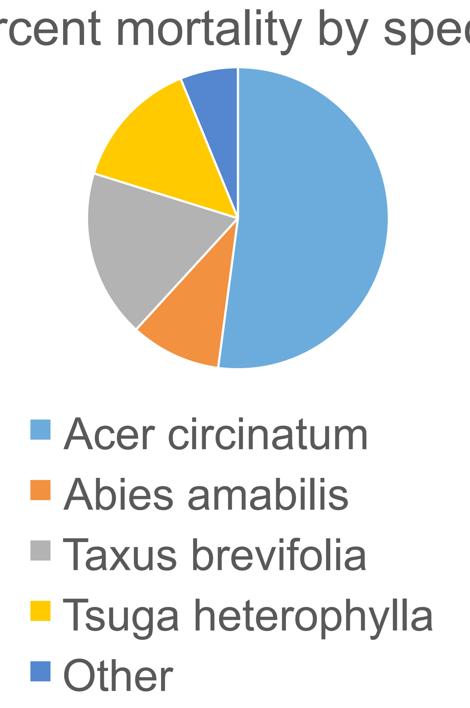


Map of the estimated area of coarse roots for all trees whose mortalities show *Armillaria* as a factor associated with death.



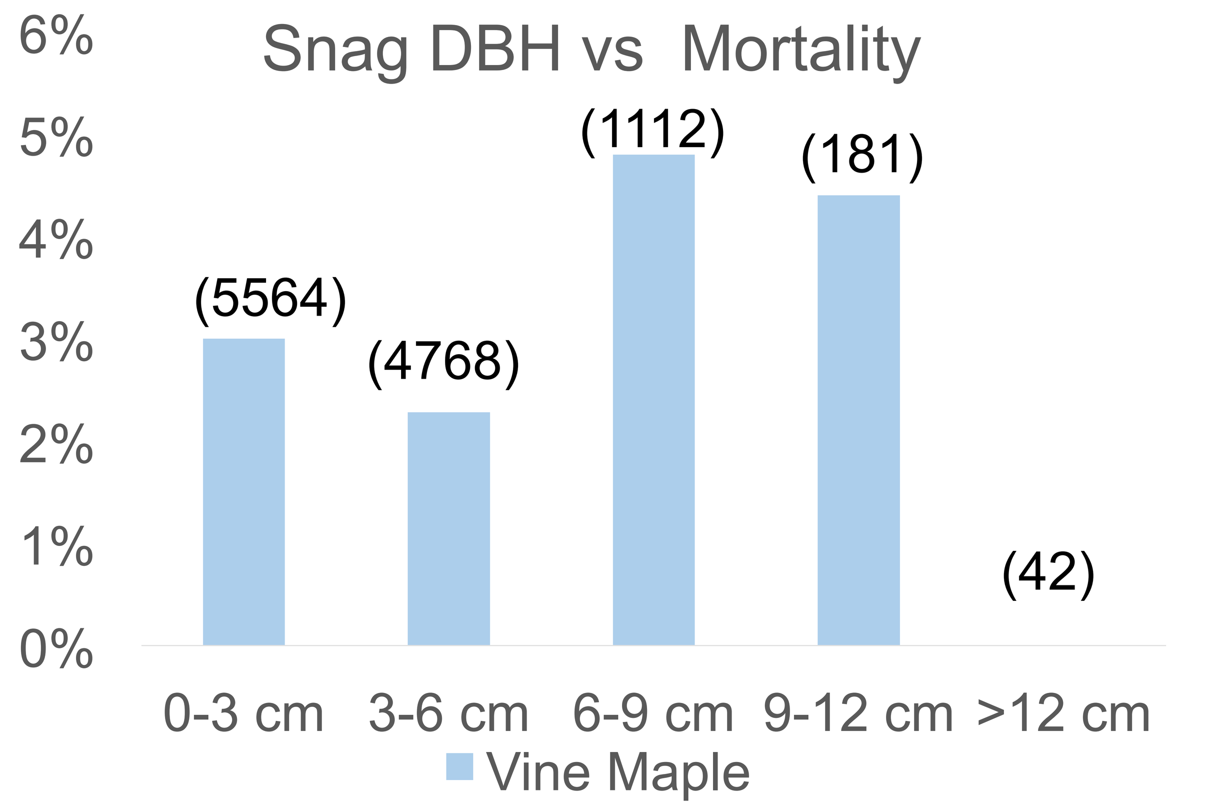
Map of the estimated infected area based on root interactions with trees known to be infected. The probability of infection decreases with distance from the infected tree. Orange Circles represent known infected trees, Purple represents high probability of infection, red is a lower possibility of infection and green circles represent no infection.

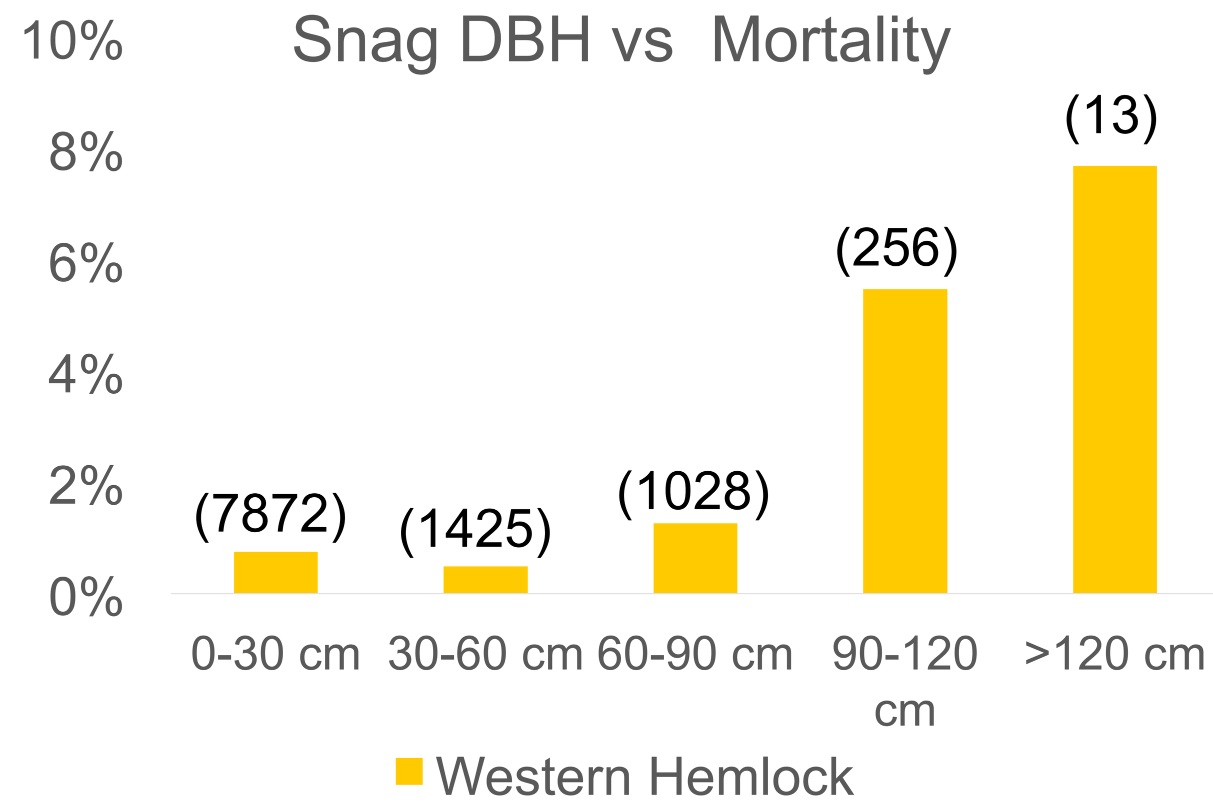
Figure 1

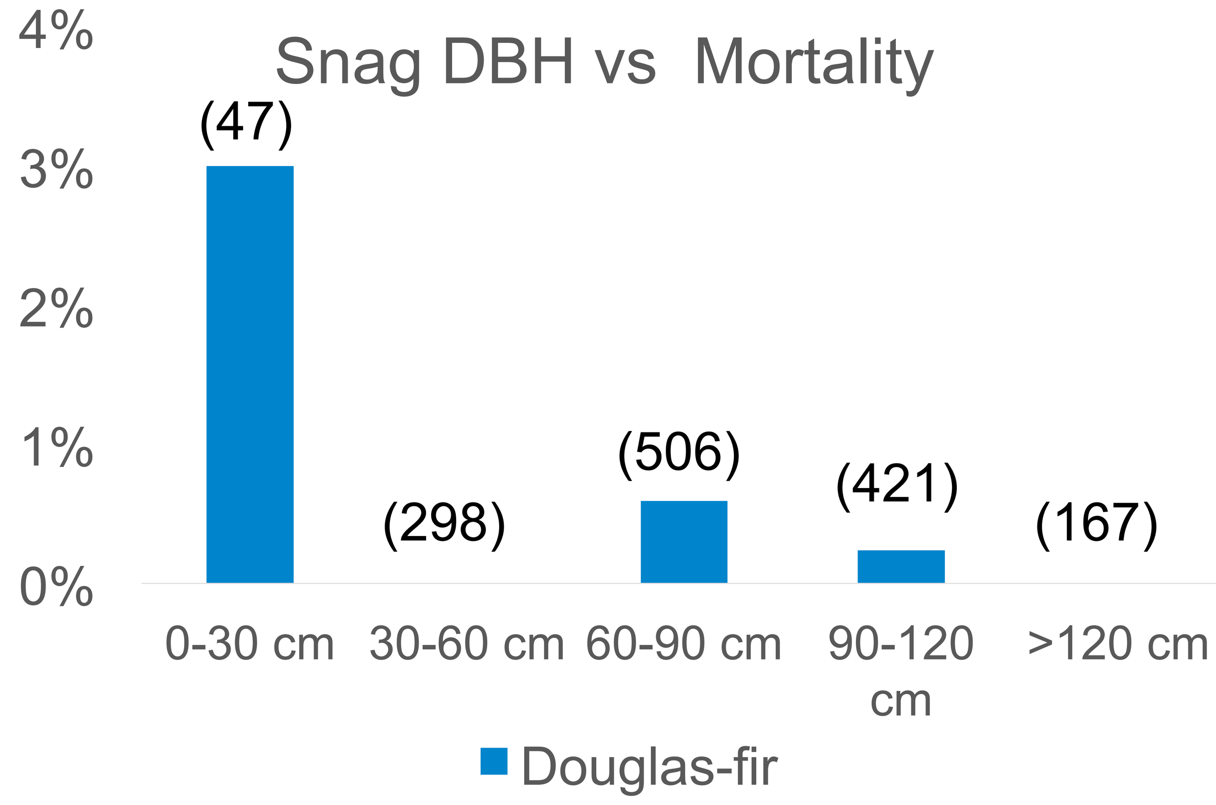


996 tree mortalities are associated with *Armillaria*. This graph shows the distribution of mortality by tree species.

Figure 2







The percent mortality based off of the woody stem size. The numbers above the graph in parentheses shows the total number of trees in that size class.

Conclusion:

Determining the total infected area in the plot for *Armillaria* is very difficult. The total infected area cannot be determined solely from mortalities associated with *Armilliaria* because a tree may still be infected and has yet to die. Using the estimated coarse root we determined that the infected area is a lot greater than thought in the Wind river forest dynamics plot. This new information will help us develop a model to predict the growth of the infection. An accurate model of the disease and its spread will allow conservation efforts to be made more effectively and also can help in many industries such as lumber and farming.

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