Honey Fungus: Death from Underneath
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 2-4% 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 2017 field season.

Using the mortality data we determined all of the tree species which have mortalities that were associated with Armillaria root disease (Figure 3) and determined the relationship mortality has with the size of each tree. (Figure 2) Once these species where determined, we calculated and mapped the crown radius of each tree based on 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. Then we set the estimated coarse root radius equal to the radius of the crown and adjusted the infected radius according to tree susceptibility. 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 were 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 can then be calculated and mapped.

Results:

Figure 1
Map of the estimated area of coarse roots for all trees whose mortalities show Armillaria as a factor associated with death.

Susceptibility to Armillaria

Figure 2
Snag DBH vs Mortality

Figure 3
Percent mortality by species

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 Armillaria because a tree may still be infected and has yet to die. Using the estimated coarse root systems we determined that the infected area is a lot greater than previously 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.

REFERENCES: