

Genetic study in giant evergreens reveals clues to pest resistance

July 13 2021, by Laura Oleniacz



Justin Whitehill photographs a Sitka spruce tree. Credit: North Carolina State University

Recent research into a group of giant evergreens is helping scientists better understand why some trees are able to survive in the face of insect pests, and could help foresters breed trees with the resistance necessary to survive in the face of new and emerging challenges to forest health.

At issue is a cluster of Sitka [spruce trees](#)—coastal giants that can live for hundreds of years and grow to be 300 feet tall on the West Coast from California into Alaska. Most Sitka [trees](#) are susceptible to a hungry pest called the [spruce](#) weevil that can stunt the trees' growth, cause deformities, and ultimately kill the trees.

However, foresters discovered a small group of Sitka trees with natural resistance to the pest. In a new analysis, a researcher from North Carolina State University led a study to identify patterns in how genes are expressed in resistant trees that might allow them to fight back against the spruce weevil. The findings, published in the journal *Plant-Environment Interactions*, could help researchers breed resistance.

The Abstract (TA) spoke with the study's lead author, Justin Whitehill, assistant professor in the Department of Forestry and Environmental Resources at NC State, about the findings. Whitehill also leads the NC State Christmas Tree Genetics Program, which is working to identify genes and traits that can be used to breed genetically improved Christmas trees in North Carolina.

TA: How common is natural resistance to this pest in the Sitka spruce?

Whitehill: Sitka spruce can live hundreds of years on the coast out West to become giant trees. Some of the largest spruce are over 300 feet tall and nearly 1,000 years old. Because they have such long generation times, it's hard for them to quickly develop resistance to pests and diseases.

In terms of resistance, forest geneticists working in British Columbia, Canada, noticed a small population of Sitka spruce that were growing pretty well, even if they were in areas with high levels of weevil

infestations. The geneticists worked to integrate those trees with their breeding program to develop resistant varieties. This work has been ongoing for decades. Only recently have we begun to understand how the trees are able to resist attack from this pest.

TA: What's already known about natural resistance in these trees?

Whitehill: In the early 2010s, a specialized cell type called stone cells were first recognized to be a contributing factor to resistance against spruce weevil. If you've ever eaten a pear, the gritty texture is due to the presence of stone cells. In Sitka spruce, they're highly lignified, meaning they are very similar to wood cells, making them rigid or hard. One of the first clues that some people noticed when trying to propagate the trees was that these trees were much harder to cut. As a result, their knives were worn down more quickly than on the susceptible trees. The areas people were cutting happened to be the same place where the weevil tends to hang out and complete its life cycle. Ultimately, that area was filled with stone cells.

TA: What did the genetic analysis show about resistance?

Whitehill: The big story is that the resistant tree is already well defended against the weevil long before an attack even takes place. It seems that the genes are already turned into the "on" position so the defenses are always present, and the primary defense is the presence of a lot of stone cells.

Another interesting finding was that we identified a set of genes belonging to fungi that were consistently present in resistant trees and susceptible trees actively being attacked by the weevil. We think this

means resistant trees and susceptible trees being attacked by weevil harbor a natural fungal community. This previously unexplored interaction could have negative impacts on the weevils' survival.

It's possible there are additional complex ecological interactions that need to be explored further. Thanks to the use of new molecular tools, we are now starting to paint a more complete picture of this complex system.

TA: Was there anything about the Sitka spruce genome that made these trees challenging to study?

Whitehill: One of the challenges of studying the genomes of spruce, or any conifer, is that their genome is about seven to eight times the size of the human genome, on average, with about 21 to 22 billion base pairs of genetic code. Not only do conifers have huge genomes, but they also have these extremely long pieces of genetic code that are repeated many times throughout the genome. That makes it difficult to sequence the gene segments.

The gene space is also not well evaluated and defined in conifers. If you think of the human genome, the Human Genome Project was initiated in 1990, and cost billions to complete before a finalized draft of the human genome was published in 2003. In the case of Sitka spruce, we had to base our findings on the next best studied organism to figure out what the genes were potentially doing. Most of the genes in plants that have been functionally validated are in a small mustard plant called Arabidopsis. We base conifer gene function on Arabidopsis genes.

TA: Why is it important to study this particular spruce?

Whitehill: Sitka spruce is a coastal species found mainly in the Pacific Northwest of Canada down through the northern part of California and throughout coastal Alaska. From an economic standpoint, it has been planted as a wood source throughout coastal British Columbia, but because of this pest, its use in planting has been reduced for the last 30 years or more.

The tree that I used in my study comes from a population of trees that are very susceptible to the weevil. However, those trees grow very quickly and have a very good wood quality. Because of their fast growth and good quality wood, those trees were taken back to England in the 1800s, and now form the foundation of England's forestry industry.

The ultimate goal of this project, and my plan for the NC State Christmas Tree Genetics program moving forward, is to apply advanced genomic techniques and tools to understand how trees tolerate stress, to identify the underlying mechanisms that support resistance, and ultimately use new genomic approaches to rapidly develop pest-resistant trees and ensure their long-term survival in the face of increasing forest health challenges.

More information: Justin G. A. Whitehill et al, Constitutive and insect-induced transcriptomes of weevil-resistant and susceptible Sitka spruce, *Plant-Environment Interactions* (2021). [DOI: 10.1002/pei3.10053](https://doi.org/10.1002/pei3.10053)

Provided by North Carolina State University

Citation: Genetic study in giant evergreens reveals clues to pest resistance (2021, July 13)
retrieved 3 May 2024 from
<https://phys.org/news/2021-07-genetic-giant-evergreens-reveals-clues.html>

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