Genomics in Society
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Clip #4 Transcript: Research Novelty and Importance

What we know already is quite a strong amount of **genetic variation** that is **locally adapted**—so it means that we do see differences in populations of a species that live in different environments, so it's locally adapted in this locality or that locality. And this is really important because you need genetic variation for adaptation and natural selection. So what's really great so far is that we do see signatures of local adaptation in the species that we're working on, but what's also cool is that we're seeing convergence—so, the same regions in the genome playing a role in adaptation to let's say cold tolerance in larch and in Douglas-fir and in pine, for example. And this is cool because the downstream technologies that we use—so the people who get our results—the regions of the genome that we identify as important go on to a thing called a SNP array. And that allows let's say people involved in forestry, they can very quickly genotype, so they can check if the good DNA (we call it a SNP—so allele) is in the trees or the populations that they are interested in, and then they will be able to predict whether these populations might be able to withstand environmental change or not.

The novelty with these projects is firstly conifers are really, really very difficult to work with. Their genome sizes, so the amount of DNA you have in one cell of these conifers is huge. Their genome sizes are around 20-30 gigabytes in size which is massive. So you can see that just dealing with the amount of data or trying to understand the amount of genetic information that these conifers possess is a challenge on its own.

Another novel aspect is that the phenotypes, the traits that we're looking at, are very complex—it's not like a simple trait like eye colour where one gene codes for white and one codes for brown or something—it's not a simple trait, the traits we are looking at are very complex, so there are lots of genes that are involved.

So one of the really cool innovative things is that we are able to show that adaptation in a trait can occur across different species—so convergently—and you can have lots of genes that are **convergently adapting** even though these species haven't been related for 150 million years. While most studies up until now have been able to show that 'this species uses this one gene to cause this one effect and this one uses this other gene'.

So it's usually been simpler adaptive scenarios, while here we're looking at more complex adaptive scenarios. There is very little known about the genetic basis of for example resistance or tolerance to Swiss needle cast in Douglas-fir, there is very, very little literature or research that has been done on it—especially at the genomic level. This will be a massive step in trying to understand the genetic basis of disease, resistance, and tolerance in these species. It will be really innovative and great for forestry.
