

Clip #2 Transcript: Explanation of Dr. Lu's Research Process

There are a couple ways in which foresters can plant trees that are better adapted to new climates. Foresters can collect seed from local native species, but from warmer adapted populations. Or they can plant species farther north or higher in elevation than their current species range, **assisting their migration**. Additionally, foresters can select and breed trees that can withstand increasing climatic stresses or disease.

To gain the knowledge to support these strategies, we can use genomics tools to speed up the **breeding** process. Using conventional breeding methods, people **hybridize** tree populations with extreme **phenotypes** to locate the candidate genes in the genome. But this method takes at least tens of years to get results because conifer trees have a long generation time. For the current climate change scenario, we don't have time to conduct conventional breeding. Genomics tools can help us accelerate the breeding process, including locating the candidate genes and **selecting** the appropriate markers.

In doing all this “omics” research—including **genomics**, **transcriptomics**, **proteomics**, **epidemics**—we need to analyze **next-generation sequencing** data. By analyzing the patterns using this data, we can have ideas of the past, present, and future situations of the studied population. In the past millions of years, some tree species migrated from other places to their current habitat. We can **model** the decline and growth of the population size of the studied species in history and correlate this knowledge to historical climate change to understand the factors that drive adaptation and migration. We can associate the gene patterns with adaptation phenotypes in a specific population to figure out the **genetic architecture** and the link to adaptation phenotypes.

If no genes relating to adaptation can be found in one species, we may consider introducing genes from other species to improve adaptation. We can also use the current **association model** between gene patterns and climate variables to project the adaptation scenario in future climates and locate the vulnerable populations in the face of climate change.

