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Genomics-Enhanced Forecasting Tools to Secure Canada's Near-Term Lignocellulosic Feedstock Supply for Bioenergy using the Mountain Pine Beetle System

Status	Approved
Competition	Applied Genomics in Bioproducts or Crops
Sector	Environment
Genome Centre	Genome British Columbia
Project Leaders	Jorg Bohlmann, UBC / Janice Cooke, U. of Alberta

Project Description

The recent mountain pine beetle outbreak in British Columbia, now spreading into Alberta, has caused unprecedented damage to the Canadian forest industry. The current infestation has affected more than 14 million hectares of pine forests and is the largest such epidemic in recorded history. Conifer forests are Canada's largest renewable source of ligno-cellulose, used for energy production, paper and wood products. Understanding the biology of the mountain pine beetle in order to use that knowledge for anticipating and helping to control future outbreaks is an important contribution to Canadian forest economics, particularly related to energy production. Although massive amounts of dead timber from the mountain pine beetle epidemic have created an unexpected surplus of potential energy feedstock, this will not necessarily provide a sustainable feedstock supply in the future. Before strategic investments are made in the forest industry, current methods of predicting feedstock need to be improved.

The mountain pine beetle infestation has three interacting components: the host trees, lodge-pole pine and jack pine, the beetle itself and multiple beetle-associated tree-killing fungal species. Our study has four parts. First, we will carry out extensive genomic studies of all three organisms, with an emphasis on genes that are important in their interaction. Second, we will use this information to build a map that shows the inter-relationships of populations of these organisms in relation to geographic location, time, environment and climate. Third, we will use the above information to create models that could forecast the likelihood of a mountain pine beetle outbreak in any location at a particular time. Finally, we will use all of this information to make an analysis of the economics of forest use for energy production. A unique aspect of this project is our ability to combine all the genetic and genomic data with geographic and economic information to provide a detailed picture of the threat of a mountain pine beetle outbreak.

The overall goal of our applied genomics project is to generate new genomics-based information and tools for improved prediction of renewable energy feedstock supply from conifer forests, using the current mountain pine beetle epidemic as an example of an important host-pest-pathogen system.