

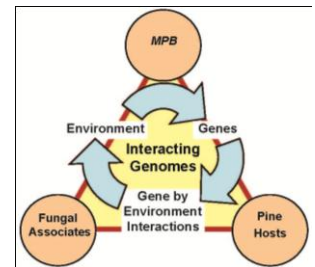
## GENOMICS-ENHANCED FORECASTING TOOLS TO SECURE CANADA'S NEAR-TERM LIGNOCELLULOSIC FEEDSTOCK SUPPLY FOR BIOENERGY USING THE MOUNTAIN PINE BEETLE SYSTEM

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[www.thetriaproject.ca](http://www.thetriaproject.ca)

**Overview:** Canada is home to ten percent of the world's forests and is a leader in sustainable forest management. Canada's forests could potentially provide a large volume of renewable biological materials for energy production (i.e. bioenergy). One of the most devastating factors to long-term forest resource management is loss due to large-scale disturbances such as the mountain pine beetle (MPB) epidemic. Having crossed the Rocky Mountains into Alberta, there is concern that boreal forests across Canada might be affected by MPB, putting at risk national industry, tourism and forest-dependent communities.

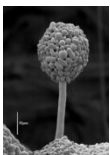
Prior to the Tria Project, very little was known about the genomic and molecular mechanisms of the interacting bark beetles, fungi and pine trees of the MPB system. Having spent two years adding genomics resources to the existing foundation of biology, chemical ecology and population genetics, the Tria Project now has a means for examining some of the MPB system interactions more closely. Critical information generated at the organismal and population levels will be incorporated into ecological risk models to improve forest resource prediction tools.



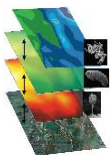
**Pine Tree Hosts:** Pine trees rely primarily on constitutive and induced oleoresin terpenoid defenses for their protection against insects and insect-associated pathogens. We will use a combination of biochemical genomics and metabolite profiling to identify essential pine defense mechanisms in MPB hosts. Physiological genomics will also be used to assess the impact of environmental factors on the capacity of pines to support stable versus eruptive populations of MPB. This is an emerging field that seeks to explain the function of gene products within an organism in the context of its environment. *(Photo: a group of MPB-attacked pine trees. Source: Alberta Sustainable Resource Development)*



**Mountain Pine Beetle:** Warmer winters – an indicator of climate change – and other factors have enabled MPB invasion into regions where it has not been previously recorded. A genome-based understanding of the molecular physiology of olfaction, detoxification, pheromone biosynthesis, and over-wintering physiology will provide the foundation for a better understanding of beetle population diversity and spread, for incorporation into better-informed models for predicting the risk of MPB infestations. *(Photo: a scanning electron microscope image of an adult MPB, average size 4-7.5 mm. Source: Jack Scott, University of Alberta)*



**Fungal Associates:** By comparing differences in genome sequence, gene function and gene expression between a pathogenic sapstaining fungus that kills pine (*Grosmannia clavigera*) and a saprophytic sapstaining fungus (like *Ophiostoma piceae*) that only discolours processed softwood but is unable to grow in living trees, we will gain further insights as to how epidemic dynamics relate to genomic and phenotypic differences (e.g. pathogenicity and host specificity). *(Photo: a scanning electron microscope image of Grosmannia clavigera, an MPB fungal associate). Source: Adrienne Rice, George Braybrook, University of Alberta)*



**Population Genomics:** Population genomics can be used to answer critical questions about MPB population structure and beetle dispersal. We propose to use genomic technologies and landscape genetic analyses to determine population structures for organisms in the MPB system. Having recently identified patterns of spatial genetic structure at each taxonomic level, we are now determining what genetic interactions exist between the partners of this complex relationship. This information is critical to informing any regionally-specific risk assessment strategy. *(Source: Amanda Roe, University of Alberta)*



**Ecological and Economic Modeling:** Although dead timber from the MPB epidemic has created an unexpected surplus of potential bioenergy feedstock, the supply is not necessarily sustainable over the long-term. For strategic investments to be made in the sector, current feedstock prediction tools need to be significantly enhanced. Opportunity now exists in ecological risk modeling to additionally incorporate genomics information from the insect, associated microorganisms, or tree components of the MPB epidemic. By improving model parameters and structure, and characterizing population-level variation, we will create a platform to better estimate MPB spread. This, in turn, allows more accurate prediction of pine feedstock supplies for various possible industrial uses, including bioenergy production. *(Photo: pine forest affected by the current MPB outbreak in the Quesnel Forest District. Source: Leo Rankin, BC Ministry of Forests and Range)*

### Funding provided by:



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