

# Genomics of the Mountain Pine Beetle System



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 mountain pine beetle (MPB) epidemic, currently affecting 16.3M ha of forest in western Canada (over twice New Brunswick).

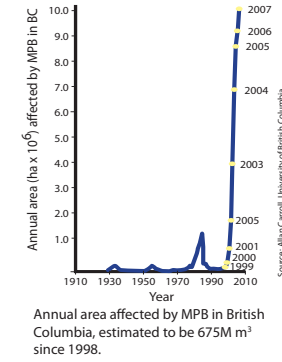
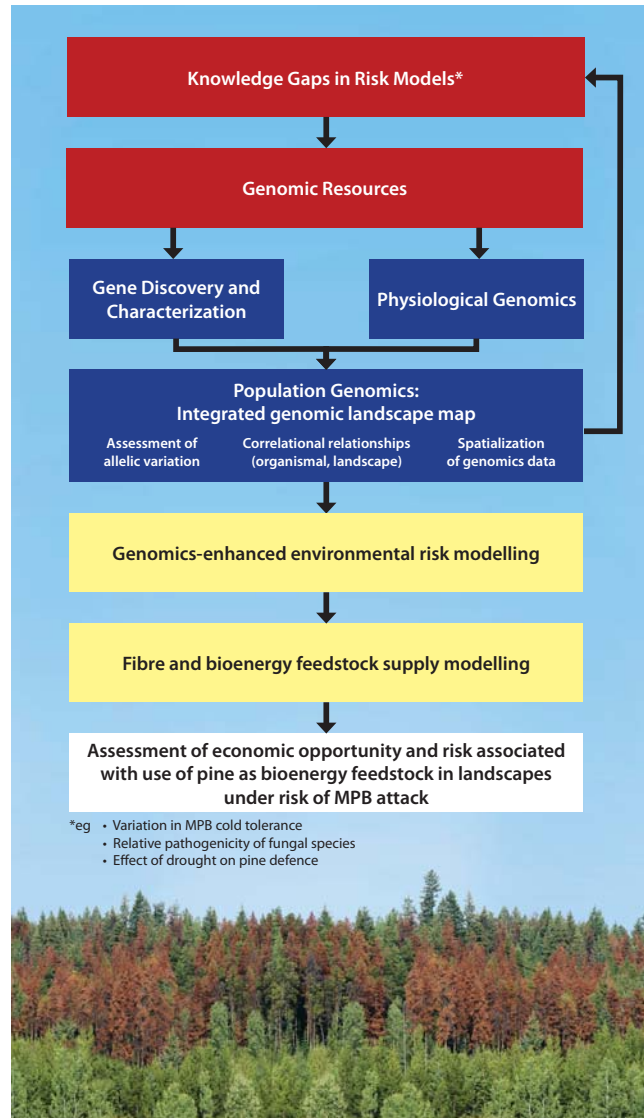
Having spent two years adding genomics resources to the existing foundation of biology, chemical ecology and population genetics, the Tria Project now has a means for examining some of the MPB system interactions more closely. Critical information generated at the organismal and population levels is being incorporated into ecological risk models to improve forest resource (feedstock) prediction tools.

These improved tools can be used to better predict, analyze and address the challenges of pest outbreaks, including more accurate prediction of feedstock availability from renewable forest inventory for possible industry such as bioenergy production.

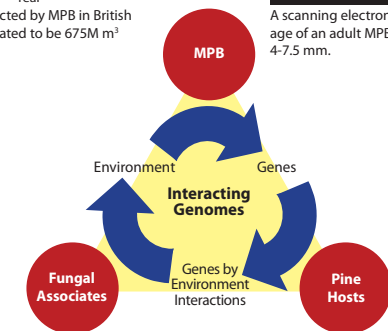
The project supports a key priority of Genome Canada's program: "ensure that the right bioenergy feedstock is available at the right time and in the right place".

The Tria Project Consortium includes:

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A scanning electron microscope image of an adult MPB, average size 4-7.5 mm.



A scanning electron microscope image of *G. clavigera*, a MPB fungal associate.



Blue-stain fungus: the fungus plays an important role in the epidemic by facilitating beetle colonization.



Genomics-enhanced forecasting tools to secure Canada's near-term lignocellulosic feedstock supply for bioenergy using the mountain pine beetle system