



Genome Alberta

THE TRIA PROJECT



Mountain Pine Beetle System Genomics

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INTRODUCTION

- The Mountain Pine Beetle (MPB) has devastated over 15 million hectares of forest in Western Canada and there is potential for a continued spread (Fig. 1)
- At least three interacting biological components are involved—the MPB, beetle-associated tree killing fungi, and their pine tree hosts
- MPB and fungal-associate attack overwhelms tree defenses, interrupts water and nutrient transport, and can lead to the death of the tree
- Genetic information is vital to understanding eruption and spread of MPB as molecular interactions between these organisms play an important role

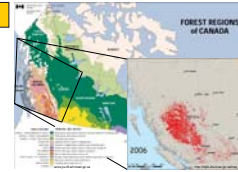


Figure 1. Location of the current MPB epidemic in Western Canada. Having crossed into Alberta, MPB may spread eastwards through the boreal regions. Images: Natural Resources Canada



Figure 2. A pine forest affected by the current MPB outbreak in Alberta, Canada. Photo: Alberta Sustainable Resource Development

OBJECTIVES

- Provide new, state of the art knowledge about MPB, their fungal associates, the host pine trees, interactions between these organisms, and how these interactions impact MPB population dynamics
- Use this information to equip forest managers and policy makers with better tools and management options to guide more effective management decisions (Fig. 2)

APPROACH

- A multidisciplinary, highly collaborative project involving researchers in genomics, population genetics, molecular biology, ecology, systematics, and mathematics
- Combine gene expression profiling with ecological assays

BUILDING GENOMICS RESOURCES

- Genomic resources provide the foundation for investigating the molecular interactions between organisms (Fig. 3)

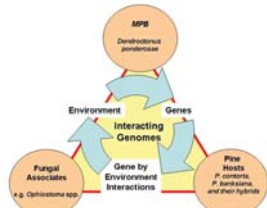
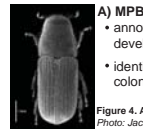


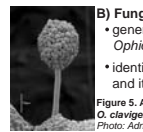
Figure 3. MPB interactions. Genomic resources allow detailed examination of the link between environmental influences, physiological responses, and underlying genomic control.

- These resources will be developed directly from samples linked to the current epidemic and include:
 - Whole genome and/or expressed gene sequences
 - Molecular marker development (neutral and gene-based)



- A) MPB**
- annotate expressed sequences from various developmental stages and tissues of MPB
 - identify functional genes involved in host colonization and reproductive success

Figure 4. An scanning electron microscope image of an adult MPB. Photo: Jack Scott



- B) Fungi**
- generate a complete genome sequence for *Ophiostoma clavigerum*
 - identify genes related to fungal pathogenicity and its interaction with pine

Figure 5. An scanning electron microscope image of an *O. clavigerum* conidiophore with conidia (spores). Photo: Adrienne Rice and George Braybrook



- C) Pine trees**
- annotate expressed sequences of genes involved in tree defense responses
 - compare gene expression in wounded versus unwounded treatments and between pine species

Figure 6. A group of MPB attacked pine trees. Photo: Alberta Sustainable Resource Development

POPULATION GENOMICS: Assessing Population Dynamics

- Understanding population structures within the existing outbreak provides the basis to examine potential spread
- An extensive sampling of landscapes in Alberta and British Columbia was conducted, generating over 10,000 MPB, fungal-associate, and pine tree samples (Figure 8)
- These samples will allow us to assess:



Figure 7. Field sampling of an MPB infested tree in Alberta. Photo: Matt Bryman

- genetic substructure of each interacting system
- relatedness of MPB populations in western Canada
- fungal-associate species composition and distribution
- delineation of pine tree populations (lodgepole pine, jack pine, and hybrids)
- adaptive variation using the genomics resources developed for each species (e.g. are beetles becoming more cold adapted?)

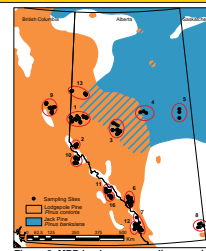


Figure 8. MPB landscape sampling map including pine species distribution. Pine tree samples were also obtained from Saskatchewan and Ontario. Image: Amanda Roe

FUNCTIONAL GENOMICS: Investigating environmental influences on pine tree responses

- Alberta presents a different growth environment for pine trees compared to British Columbia
- Environmental conditions may influence pine tree defense to MPB/fungal-associate attack
- To analyse effects on molecular interactions between the organisms in the epidemic we will:
 - examine pine tree genomic responses to water limitation and nutritional status
 - equate genomic responses to alterations in chemical defense responses, metabolite profiles, and tree volatile emissions
 - examine effects of environmental variables on MPB reproductive and behavioural traits
- This will link environmental conditions pine tree's capacity to sustain low versus high MPB levels



Figure 9. An olfactometer for testing MPB responses to pine tree volatile emissions. Environmental conditions may alter pine tree volatile emissions and influence MPB behaviour. Photo: Matt Bryman

MAINTAINING HEALTHY FORESTS

- The MPB epidemic represents a serious economic and ecological threat to Canadian forests
- Forest management strategies rely on the ability to predict MPB spread
- This project is generating detailed information on the complex biological interactions (physiology and population genomics) between organisms in the MPB epidemic
- Providing this information to forest management individuals will allow development of better strategies and management options
- This novel research approach can be applied to the study of other insect/fungal pests
- By enhancing strategies to respond to, predict, and/or prevent future epidemics, this project will maintain Canada's status as a leader in forest health research



Figure 10. A helicopter removing an MPB infested tree. Photo: Barry Cooke

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Partner Institutions

