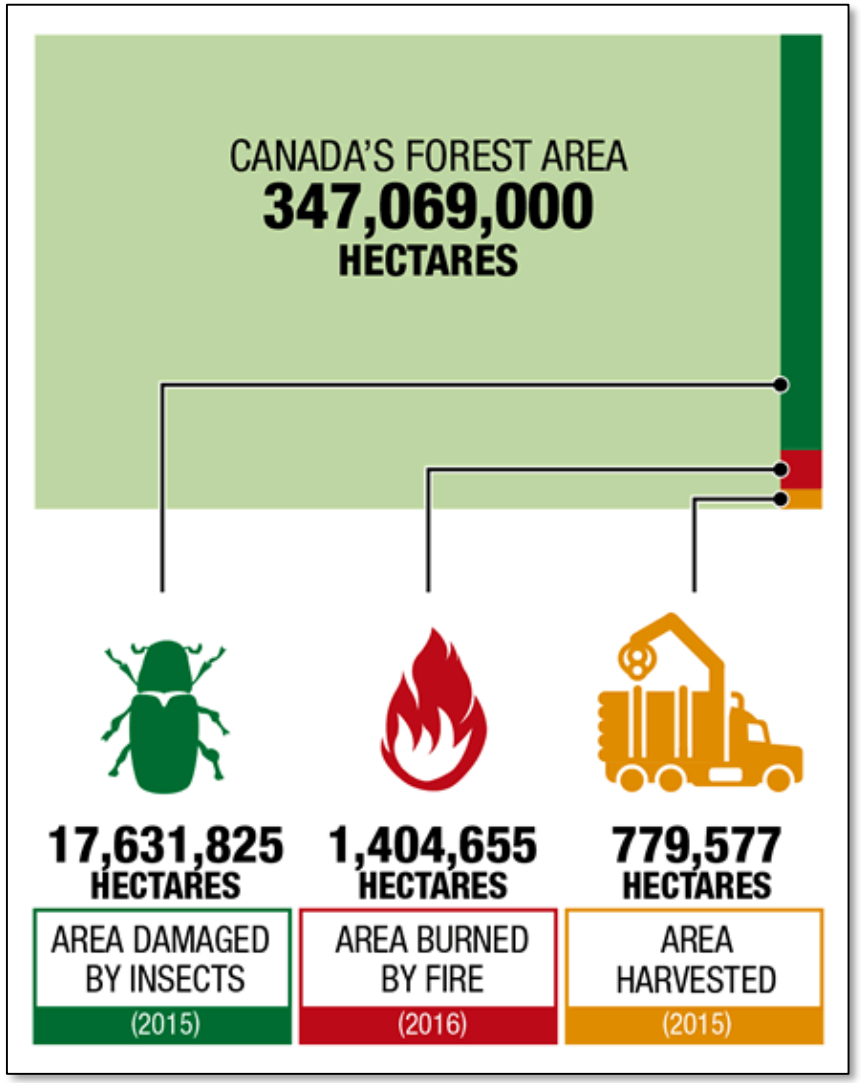
Causes and consequences of mountain pine beetle outbreaks: from genes to ecosystems

Patrick M. A. James

Université de Montréal

Forest health and disturbance

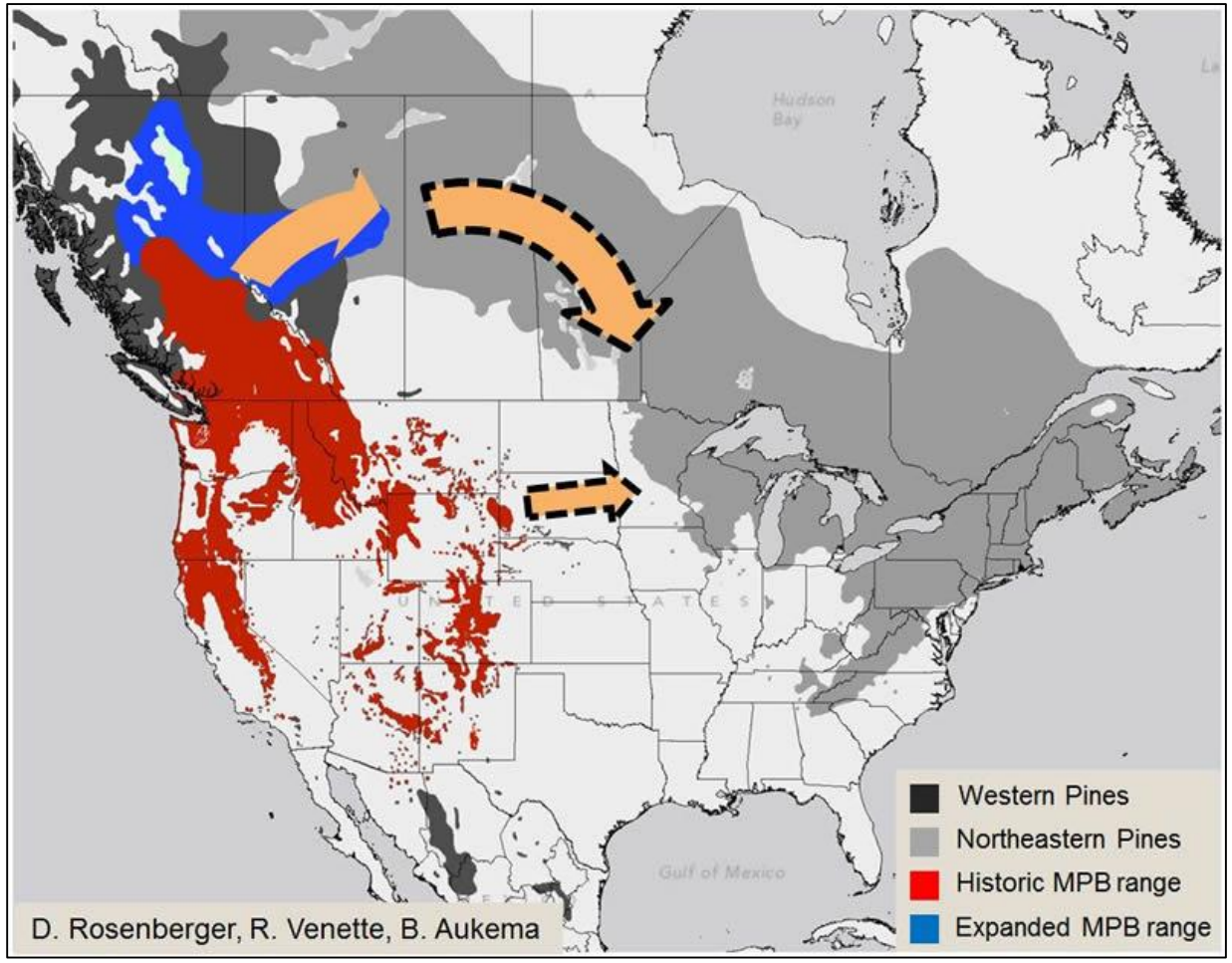


https://www.nrcan.gc.ca/forests/report/disturbance/16502

Mountain Pine Beetle

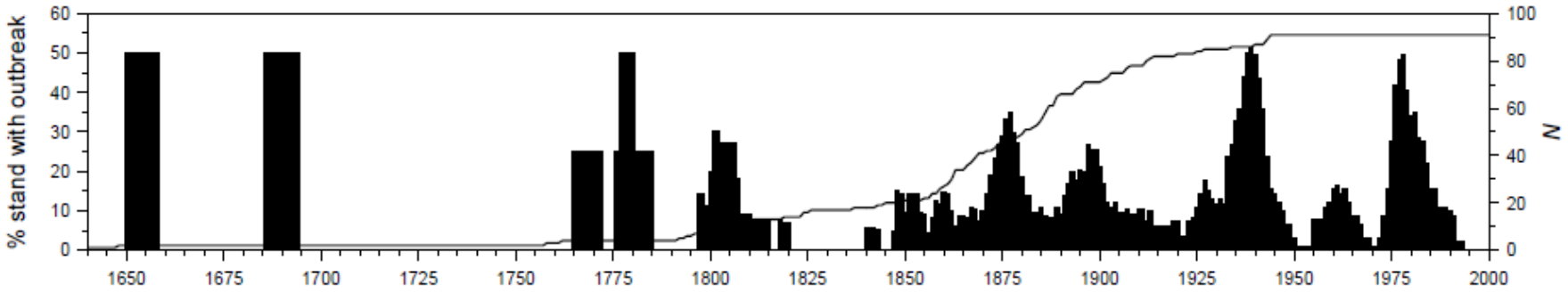
> 18 × 10^6 ha affected in Canada; > 6 × 10^6 ha in the USA

Lorraine Maclauchlan



D. Rosenberger, R. Venette, B. Aukema

Mountain pine beetle outbreaks are episodic and natural



Alfaro et al 2009

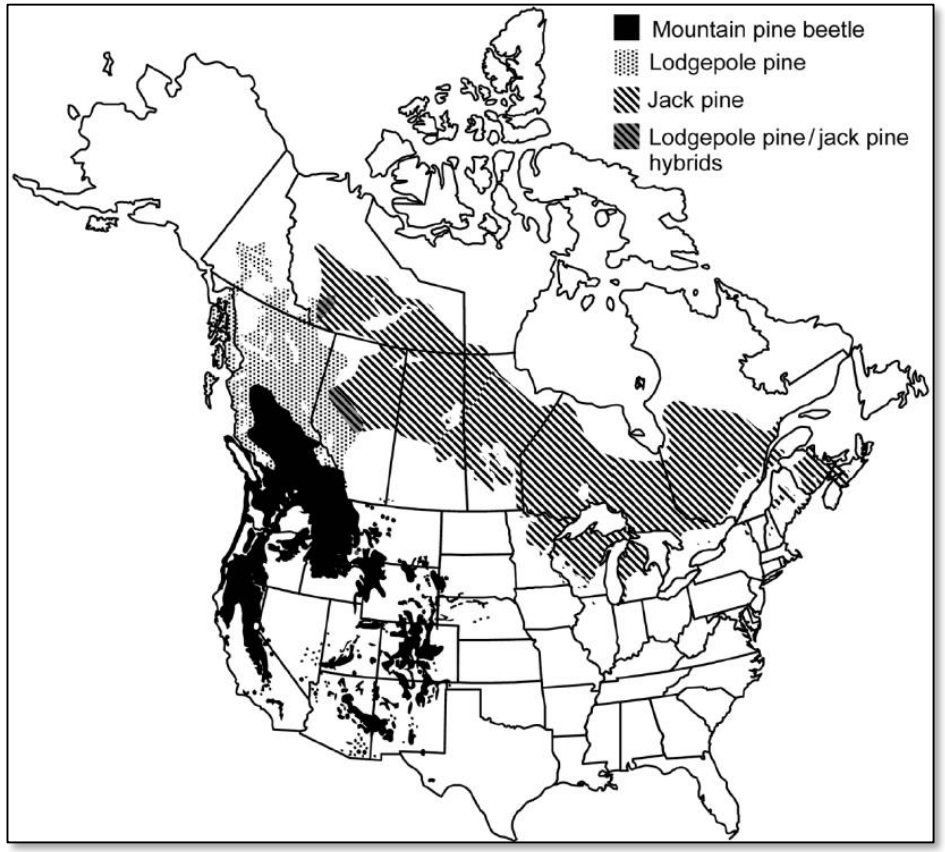
Dendroctonus ponderosae

Forest health and disturbance

- **Outbreaks of native forest insects are an important agent of disturbance in the boreal forest**

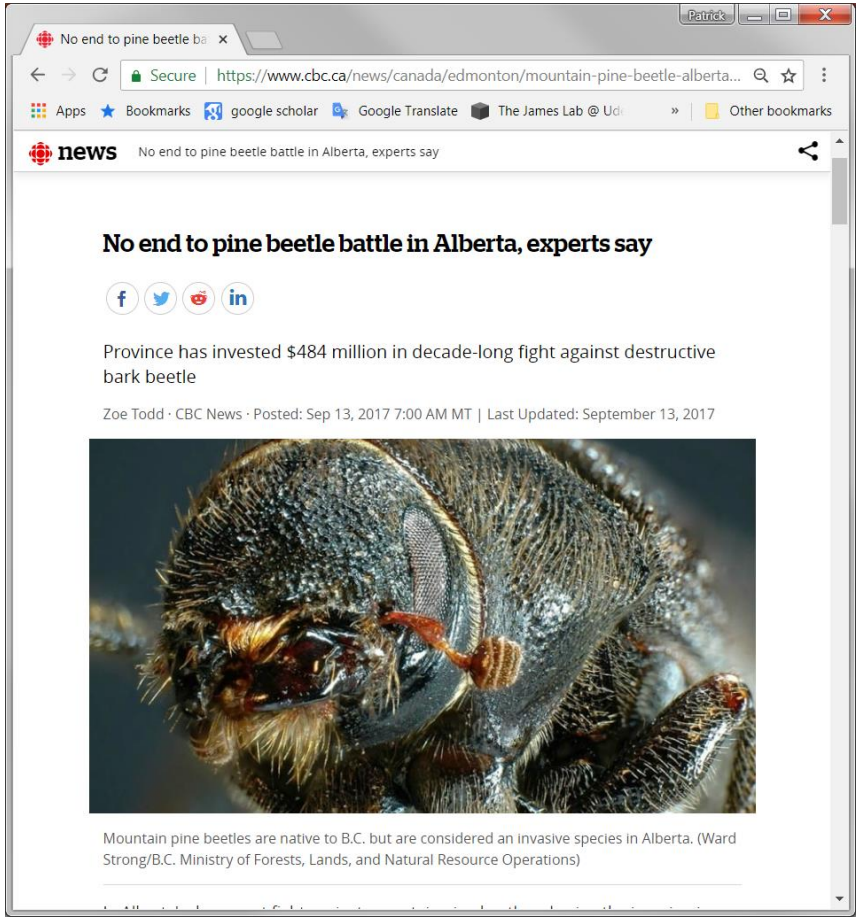
Forest health and disturbance

- **Outbreaks of native forest insects are an important agent of disturbance in the boreal forest**
- However… the current MPB outbreak is larger than ever observed and the species appears to be undergoing a range expansion
- Climate change and the legacies of forest management are the likely cause (Raffa et al 2008; Bioscience)
- Downstream effects on timber, forest succession, carbon, fire risk, water quality, and biodiversity …



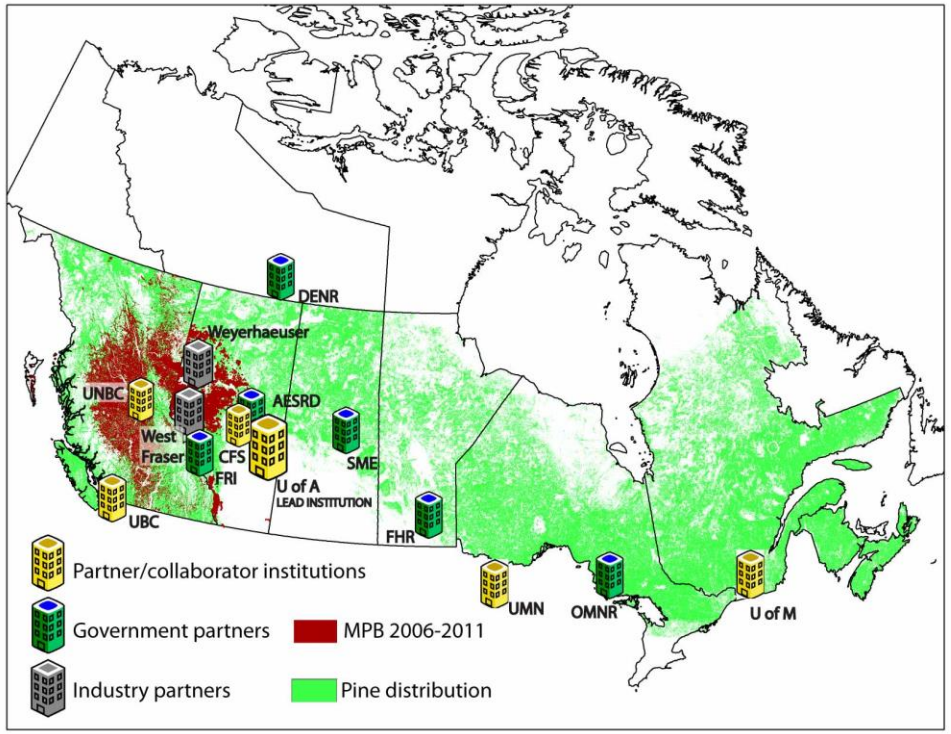
Forest insect outbreaks are costly

- ~ $500 million invested so far in Alberta to combat the MPB
- Estimated cumulative loss equal to ~$57 billion from 2009 to 2054 in British Columbia
  - Corbett et al 2015; *Forestry*
- Current spruce budworm outbreak in NB is expected to result in losses between **$5 and $7 billion** over the next 40 years
  - Healthy Forest Partnership, NB. 2017
- Similar losses expected in Quebec
  - Chang et al 2012; *CJFR*



TRIA-Net

Turning Risk Into Action for the Mountain Pine Beetle Epidemic



NSERC
CRSNG

Alberta Agriculture and Forestry

Natural Resources Canada
Ressources naturelles Canada
Canadian Forest Service
Service canadien des forêts

fRI foothills RESEARCH INSTITUTE
Research Growing Into Practice

Manitoba

Northwest Territories Environment and Natural Resources

Ontario
Ontario Ministry of Natural Resources
Ministère des Richesses naturelles de l'Ontario

Saskatchewan Ministry of Environment

Weyerhaeuser

West Fraser

UNIVERSITY OF ALBERTA

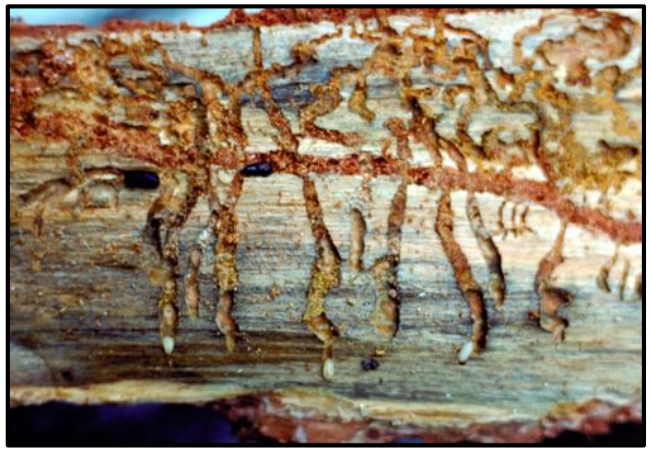
UNBC UNIVERSITY OF NORTHERN BRITISH COLUMBIA

UBC a place of mind THE UNIVERSITY OF BRITISH COLUMBIA

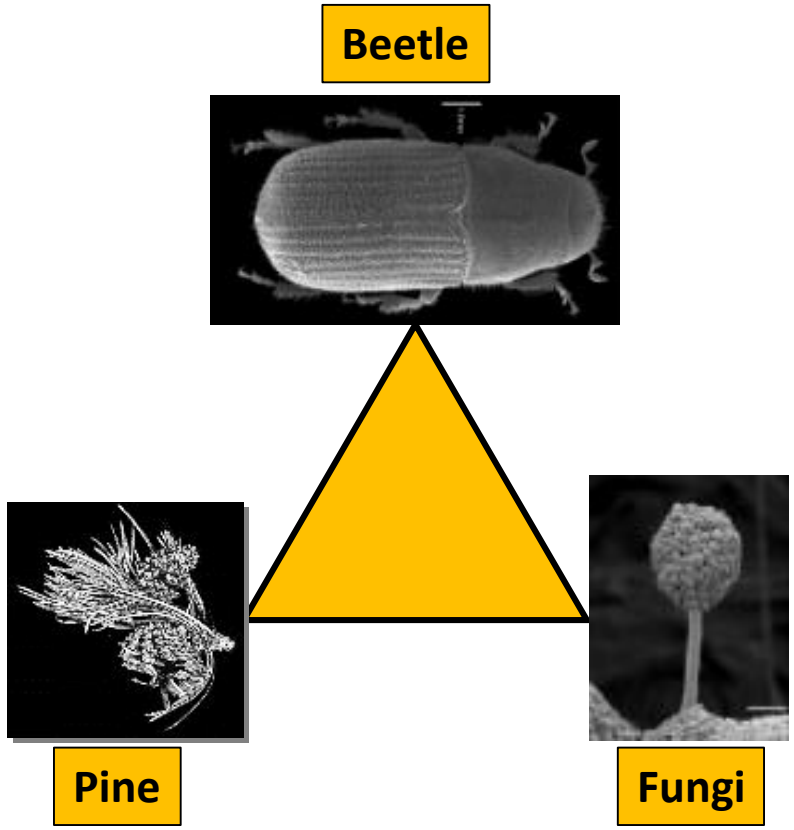
Université de Montréal

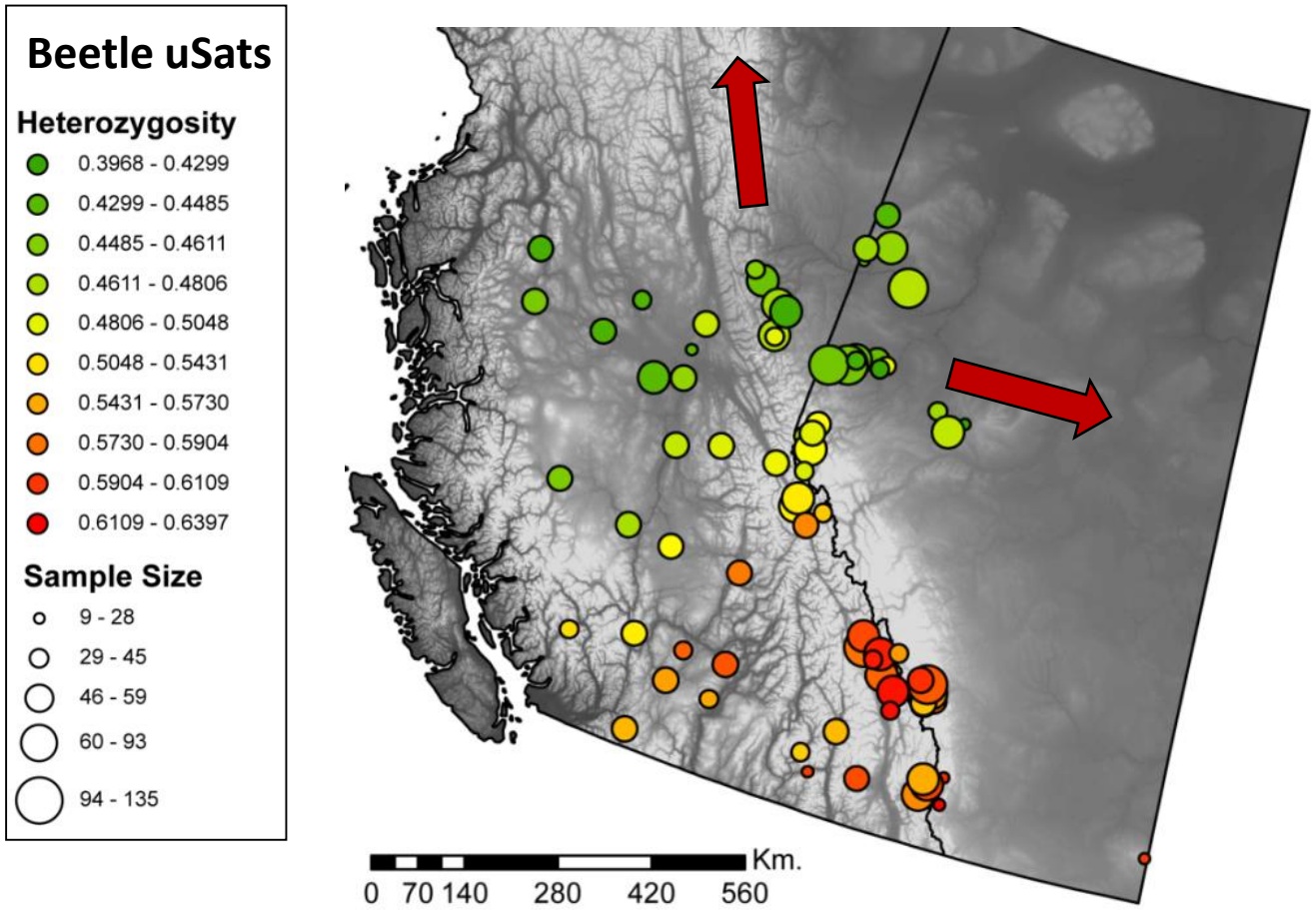
UNIVERSITÉ LAVAL

Mountain Pine Beetle Outbreak System



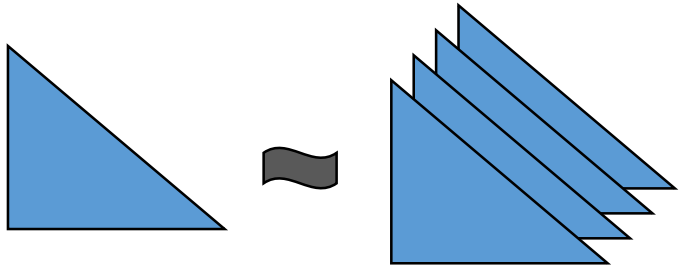
Ongoing Range Expansion



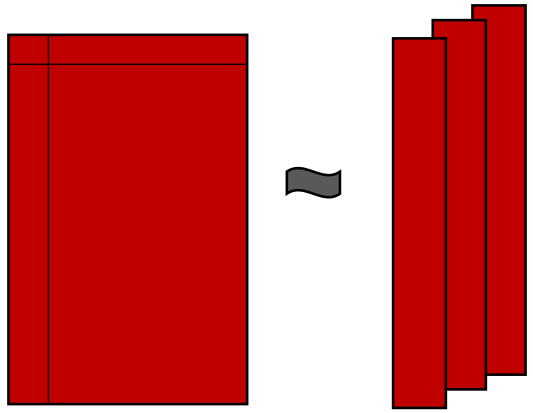


Landscape Genetics / Genomics

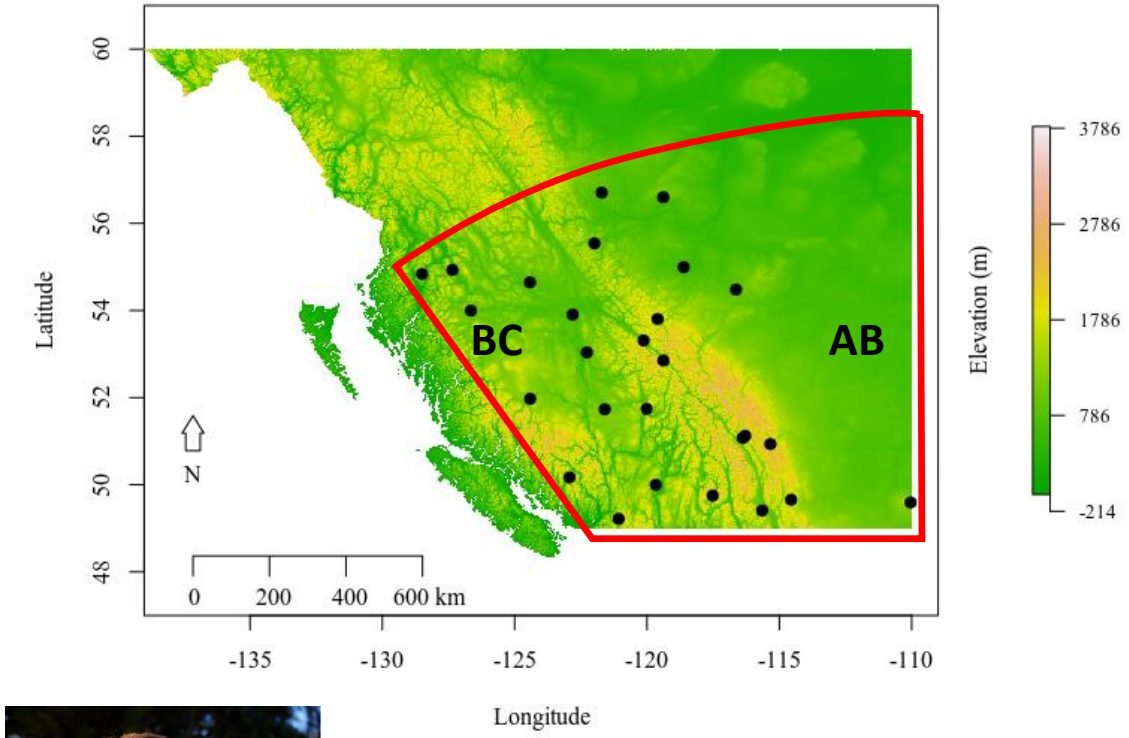
- **Landscape Genetics**: Combination of landscape ecology, spatial statistics, and population genetics to examine how **spatial heterogeneity** affects **gene flow and dispersal** (Manel *et al.* 2003).



- **Landscape Genomics**: Combination of landscape ecology, spatial statistics, and population genomics to examine how **spatial heterogeneity** affects spatial patterns in **adaptive genetic variation**.



MPB Landscape Genetics



- **Question : What environmental features influence MPB genetic connectivity and gene flow?**
- Addressed using **532** beetles sequenced at **764** SNP loci (*Illumina GoldenGate*) collected from **27** sites across AB and BC.
- Predictors examined : elevation, pine volume, drought, and climate suitability

Julian Wittische

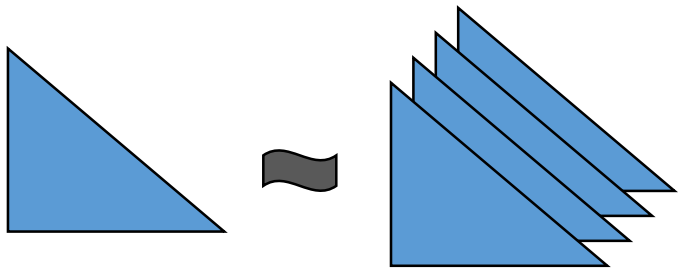
Wittische J, Janes J, James PMA. Using machine learning to model landscape genetic connectivity of the mountain pine beetle in western Canada. *Canadian Journal of Forest Research. In review.*

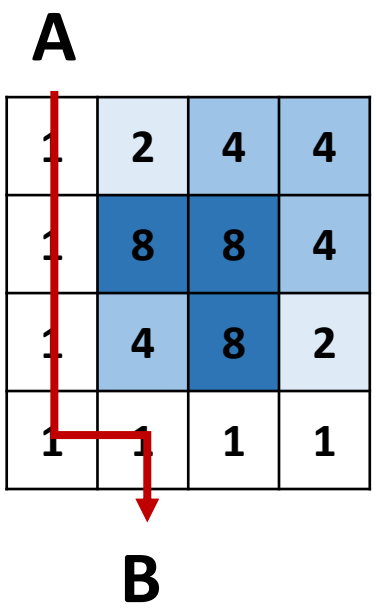
Why do we care about MPB movement?

- Movement is a fundamental but poorly understood aspect of MPB biology
- Understanding which landscape features **hinder** or **facilitate** MPB movement can help us develop and inform better spatial tools to **forecast** outbreak dynamics.
- Forecasting can help managers to **reduce risk** and limit the impacts of the outbreak on the economy and **ecosystem services**.

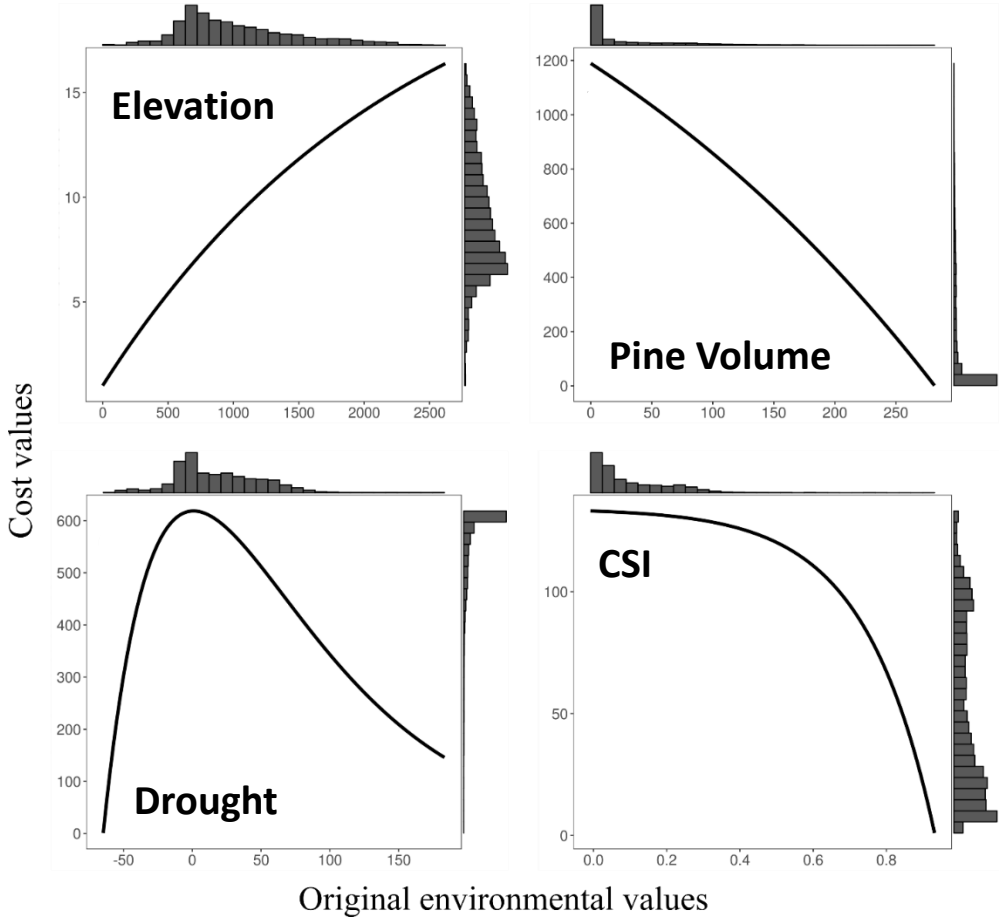
Specifying resistance surfaces is challenging

- **Modelling spatial environmental effects on gene flow requires specification of genetic and GEOGRAPHIC ecological distance matrices**
- Forms of relationships between landscape values of resistance to movement is typically unknown (Spear et al 2010)
- How to choose costs appropriately without *a priori* knowledge?
  - *Linear mixed effects model with a maximum likelihood population effects (**MLPE**)*
  - *Machine Learning / Genetic Algorithms*





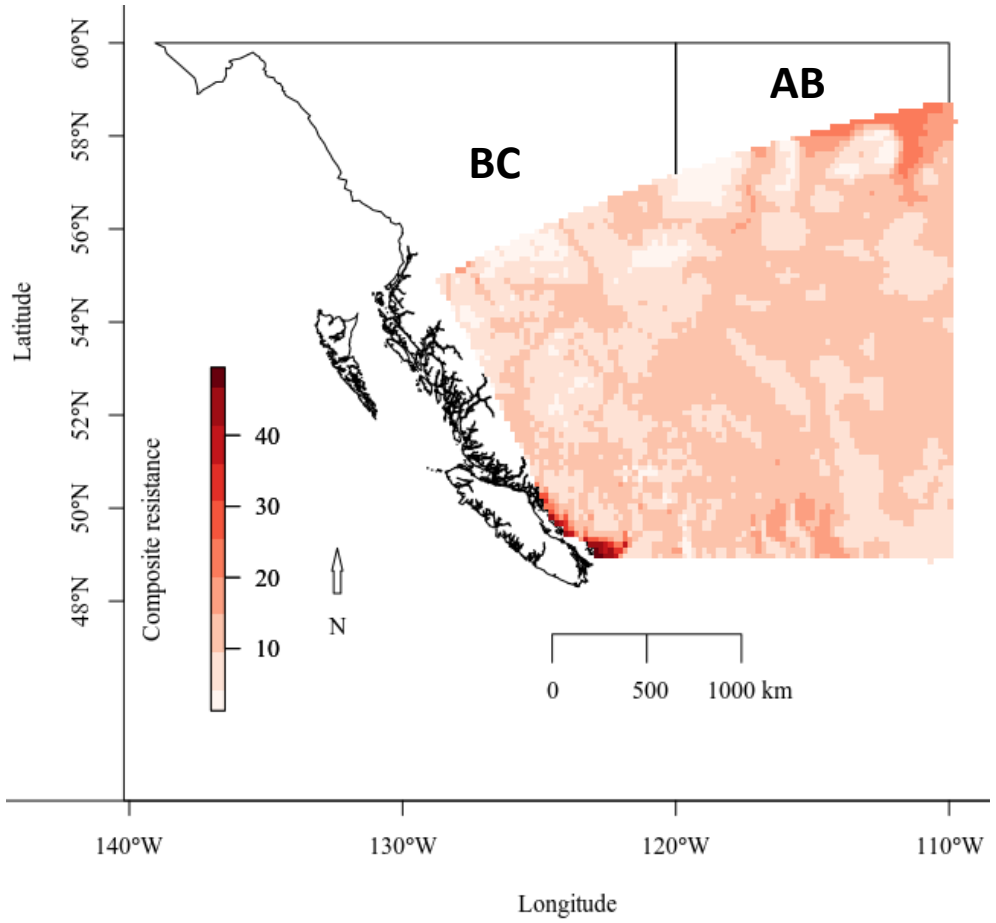
Single surface optimizations



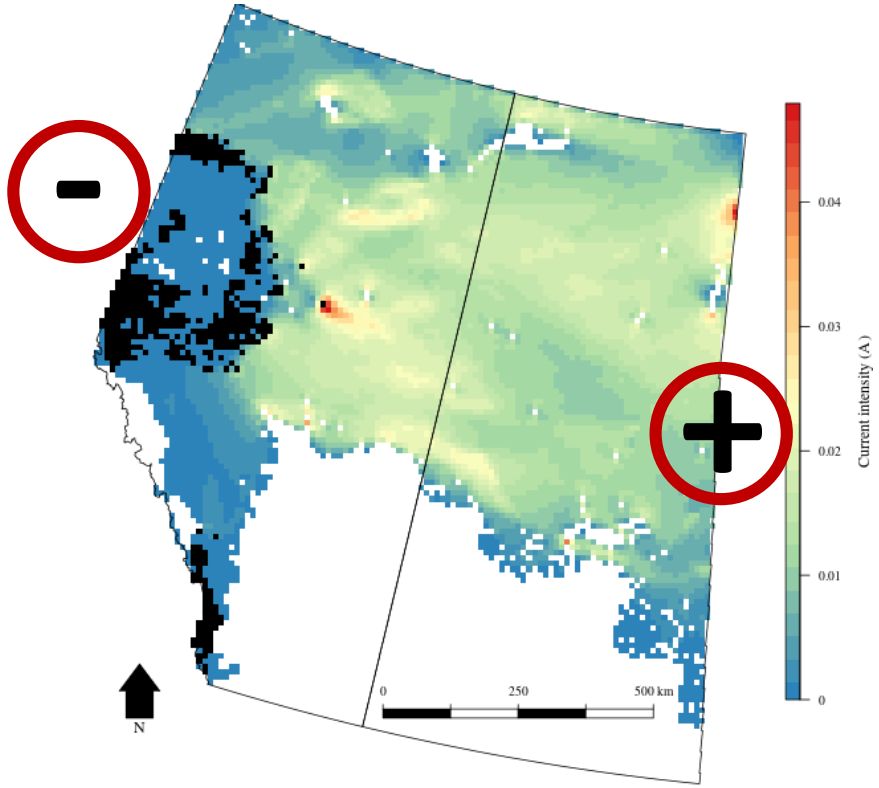
- These curves represent the optimized functional relationships between each spatial variable and resistance to gene flow (movement) based on our SNP data set

Optimized “best” composite surface

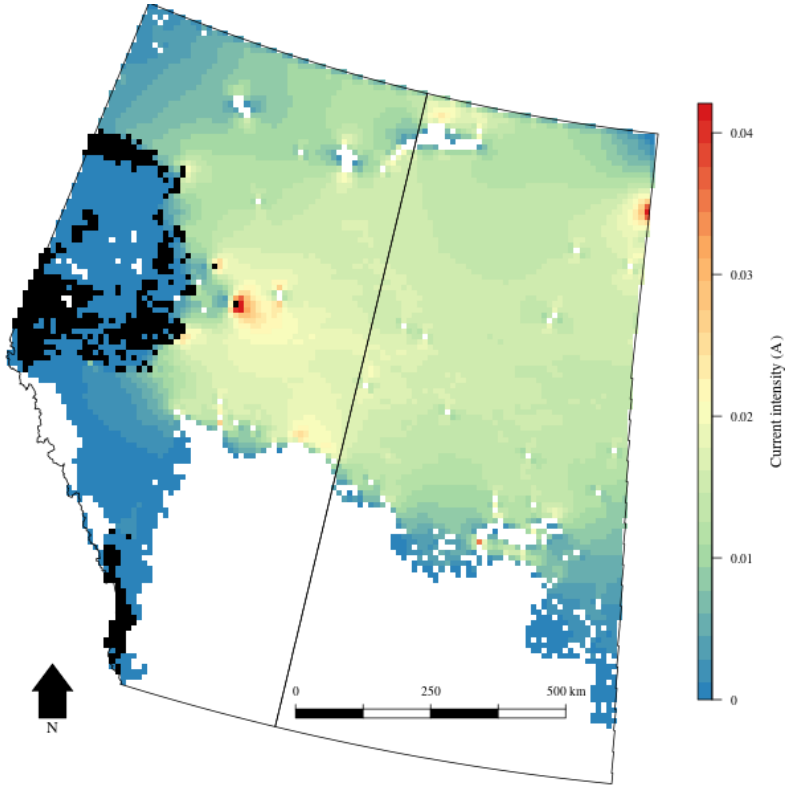
- **Elevation** + **Climate Suitability**
- Weighting: 69% climate; 31% elevation
- Large islands of less resistance
- Cost heterogeneity decreases eastward: consequences for expansion?



Forecasting future spread risk using circuit theory…



A) Elevation + CSI



B) Pine Volume


Canada
MANITOB
ALBERTA
SASKATCHEWAN
BRITISH
COLUMBIA
Google

Landscape Community Genomics

Ecology, 84(3), 2003, pp. 559–573

COMMUNITY AND ECOSYSTEM GENETICS: A CONSEQUENCE OF THE EXTENDED PHENOTYPE

Thomas G. Whitham,[1,3,6] William P. Young,[1,3] Gregory D. Martinsen,[1,3] Catherine A. Gehring,[1,3] Jennifer A. Schweitzer,[1,3] Stephen M. Shuster,[1,3] Gina M. Wimp,[1,3] Dylan G. Fischer,[2,3] Joseph K. Bailey,[1,3] Richard L. Lindroth,[4] Scott Woolbright,[1,3] and Cheryl R. Kuske[5]

OPEN ACCESS Freely available online PLoS one

Spatial Genetic Structure of a Symbiotic Beetle-Fungal System: Toward Multi-Taxa Integrated Landscape Genetics

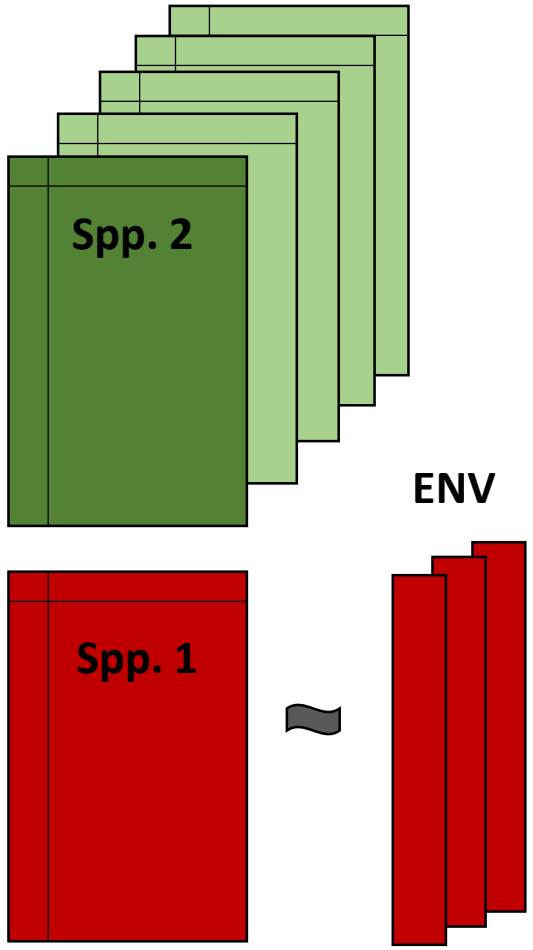
Patrick M. A. James[1*¤], Dave W. Coltman[1], Brent W. Murray[2], Richard C. Hamelin[3,4], Felix A. H. Sperling[1]

October 2011 | Volume 6 | Issue 10 | e25359

Landscape community genomics: understanding eco-evolutionary processes in complex environments

Brian K. Hand[1*], Winsor H. Lowe[2*], Ryan P. Kovach[1,3], Clint C. Muhlfeld[3], and Gordon Luikart[1]

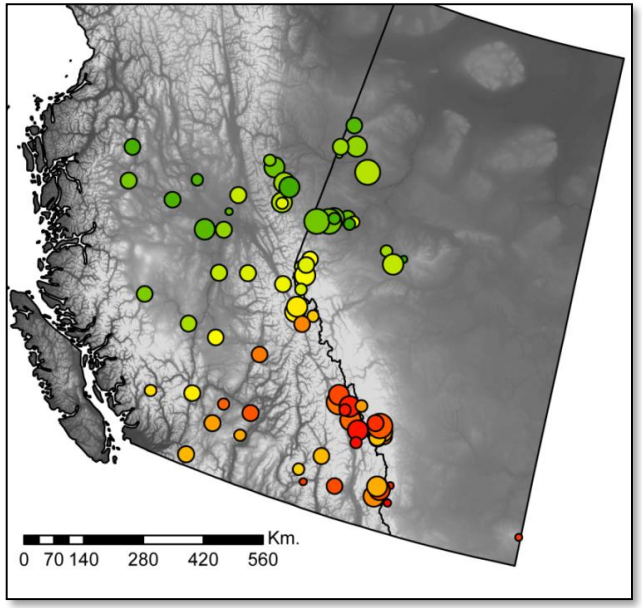
Trends in Ecology & Evolution March 2015, Vol. 30, No. 3

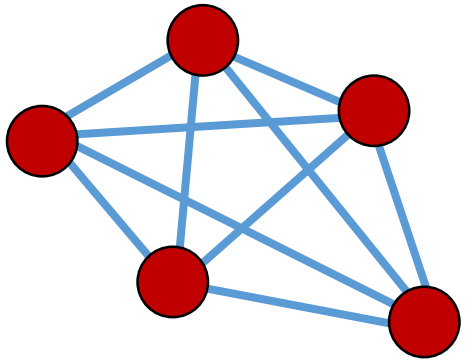


Landscape Community Genomics

- Can we identify groups of potentially adaptive loci ***among species*** that cluster together?
- Search for **OUTBREAK SYNDROMES**

  → **spatially structured**, inter-species associations of putatively adaptive alleles.



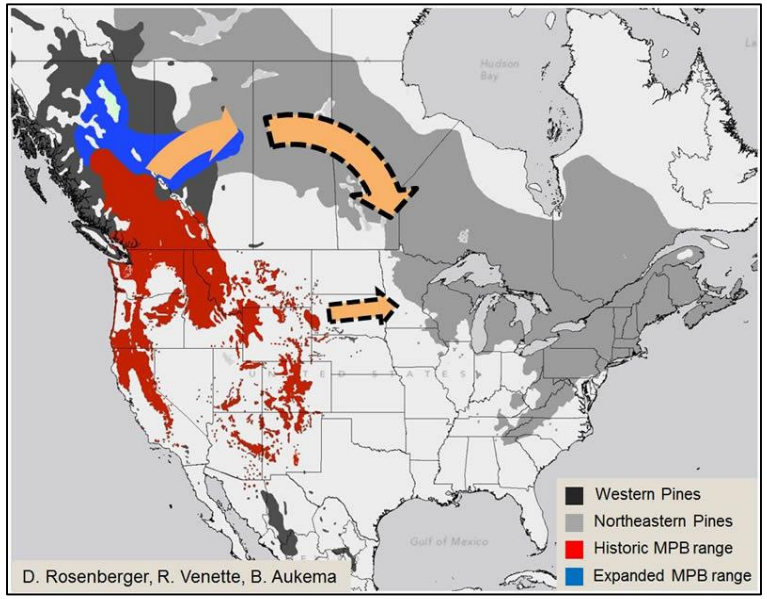


ADAPTIVE* VARIATION

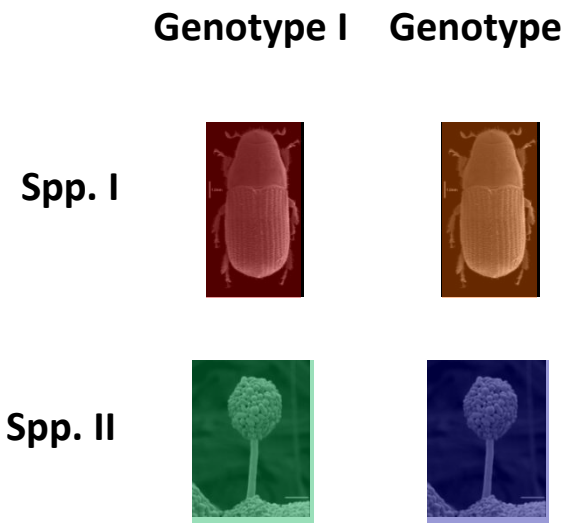
Landscape Community Genomics

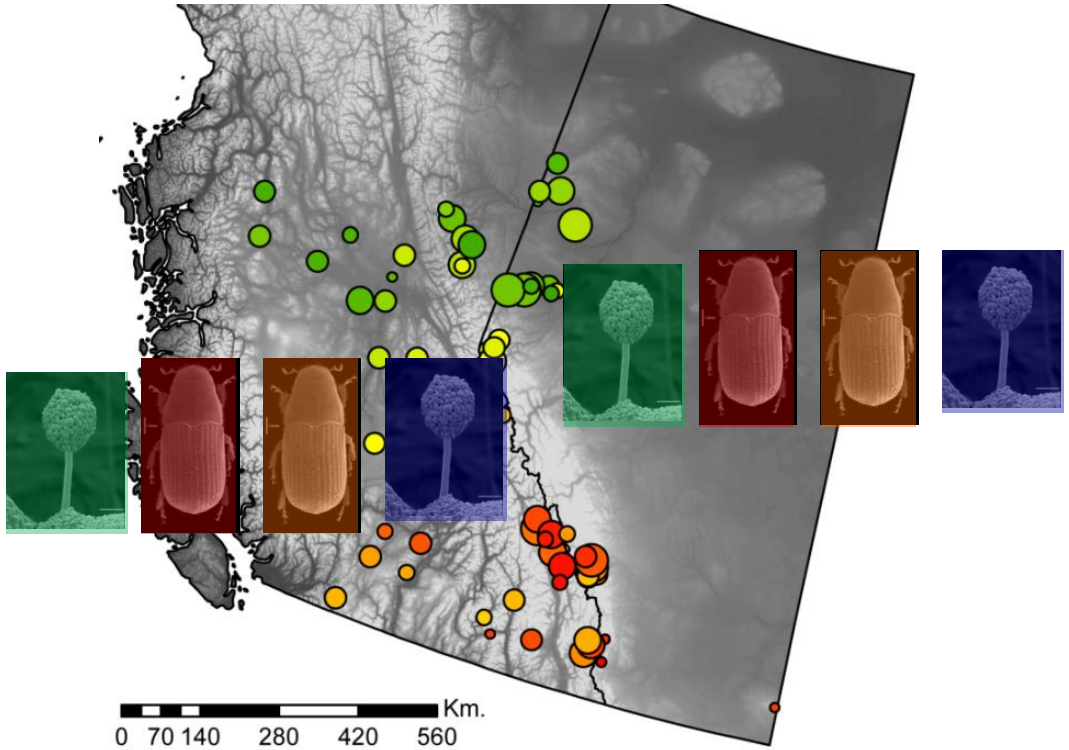
Why do we care?

- Our goal is to improve understanding of spatial eco-evolutionary community and population dynamics of **outbreaks** and **range expansions**.
- **Is rapid co-evolution driving system dynamics and outbreak expansion?**

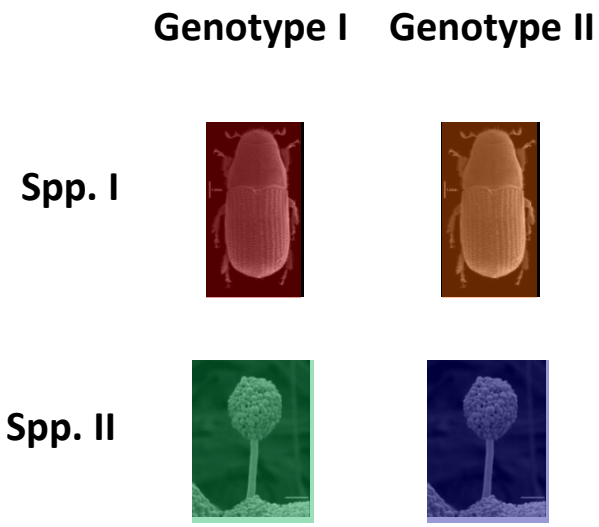


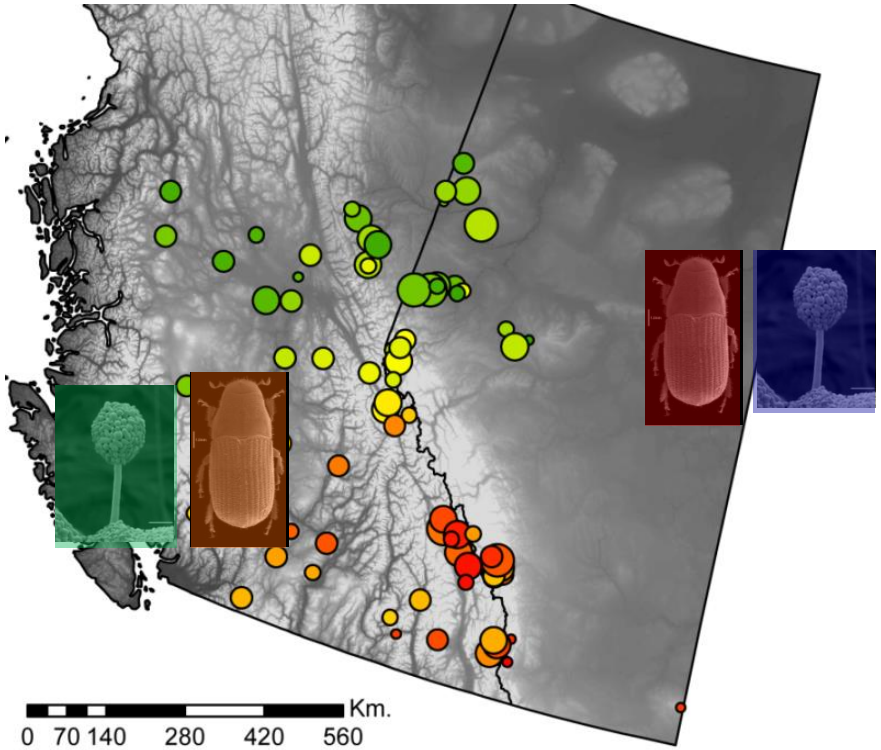
MPB Landscape Community Genomics



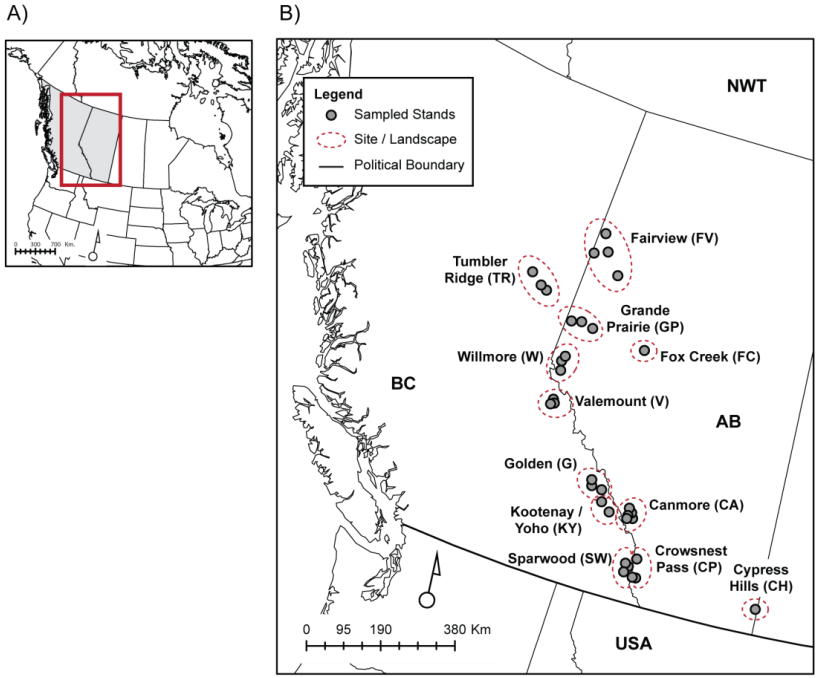


MPB Landscape Community Genomics





Study area and genomic data



- Samples collected in **2007/2008**
- Sequenced using Illumina (MPB) / Sequenome (fungi)
- For beetle data, see Janes et al 2014. MBE

BEETLE

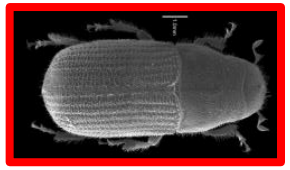
- *D. ponderosae* (MPB)
  - 175 individuals; 1532 loci

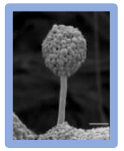
FUNGI

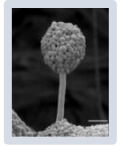
- *G. clavigera* (GCL)
  - 142 individuals; 242 loci
- *L. longiclavatum* (LLO)
  - 140 individuals; 254 loci
- *O. montium* (OMO)
  - 88 individuals; 112 loci

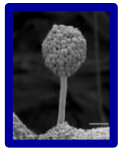
PINE

- *P. contorta* (LPP)
  - 278 individuals; 367 loci



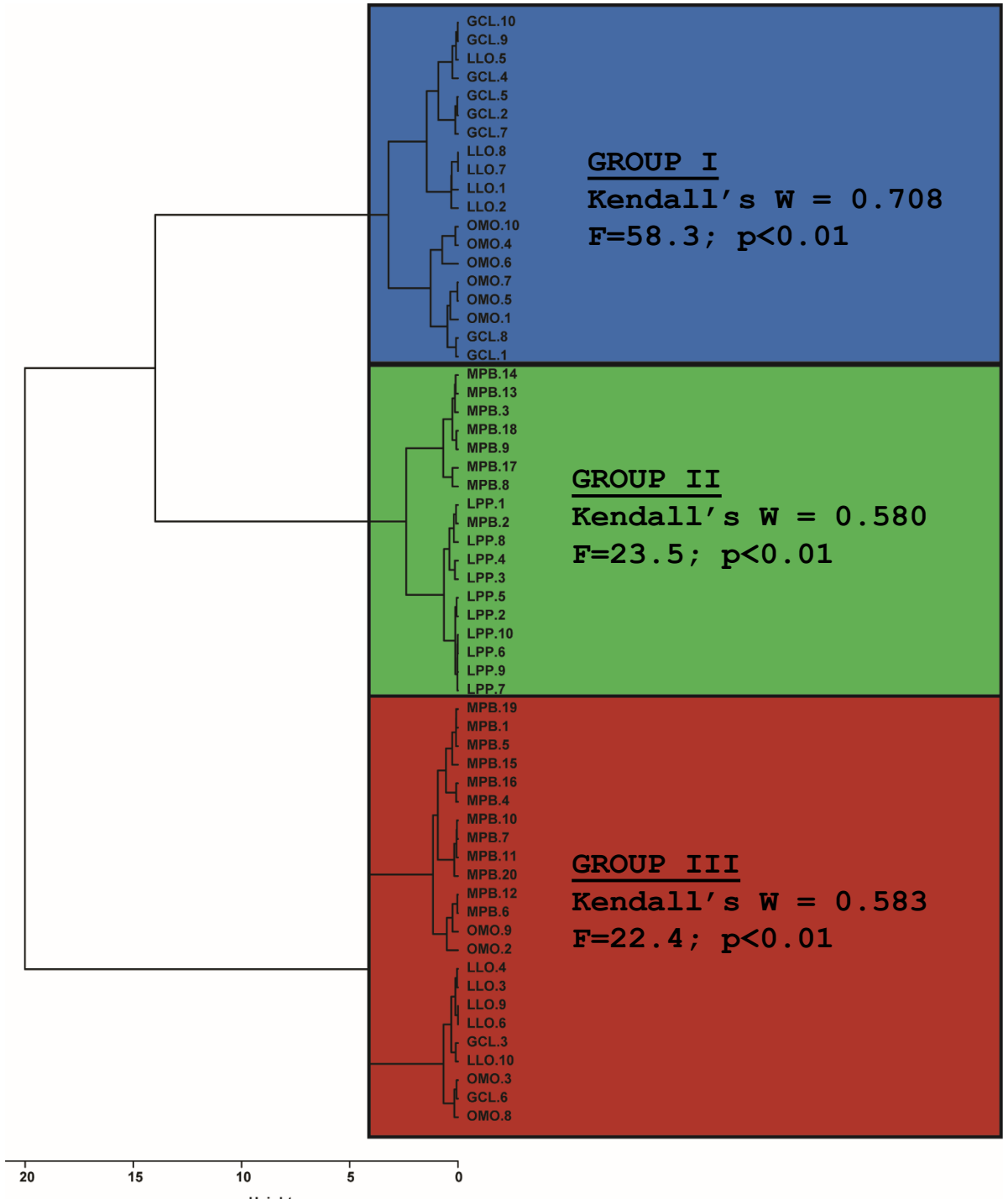


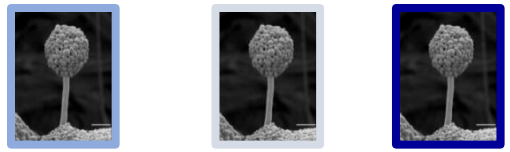


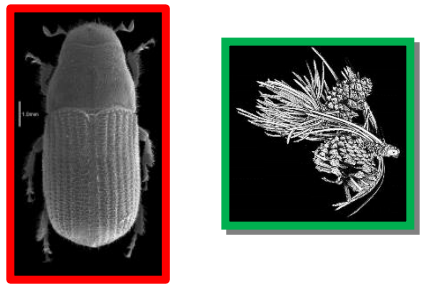


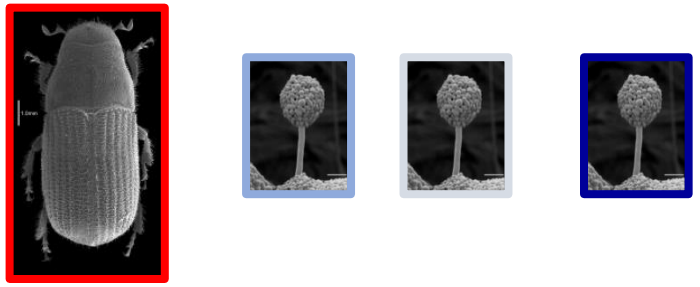
Analysis pipeline

1. Start with community genotypic data (SNPs).
2. Identify outlier loci using **Latent Factor Mixed Models** (Frichot et al 2015).
   - **Response**: top 10 putatively adaptive loci for each species (MPB = 20)
   - **Predictor**: Latitude*
   - *K*s (latent factors) selected on the basis on min. cross-entropy (**LEA**).
3. Merge individual species tables into a to single **genomic community** table
4. Cluster outlier loci based on frequency of co-occurrence among sites.
5. Assess significance of co-occurring loci clusters using ***Kendall's W***.
   - Legendre 2005. Species Associations: The Kendall coefficient of Concordance Revisited. Journal of Agricultural, Biological, and Environmental Statistics. 10(2): 226-245.
6. Assess geographical distribution of clusters using PCA.

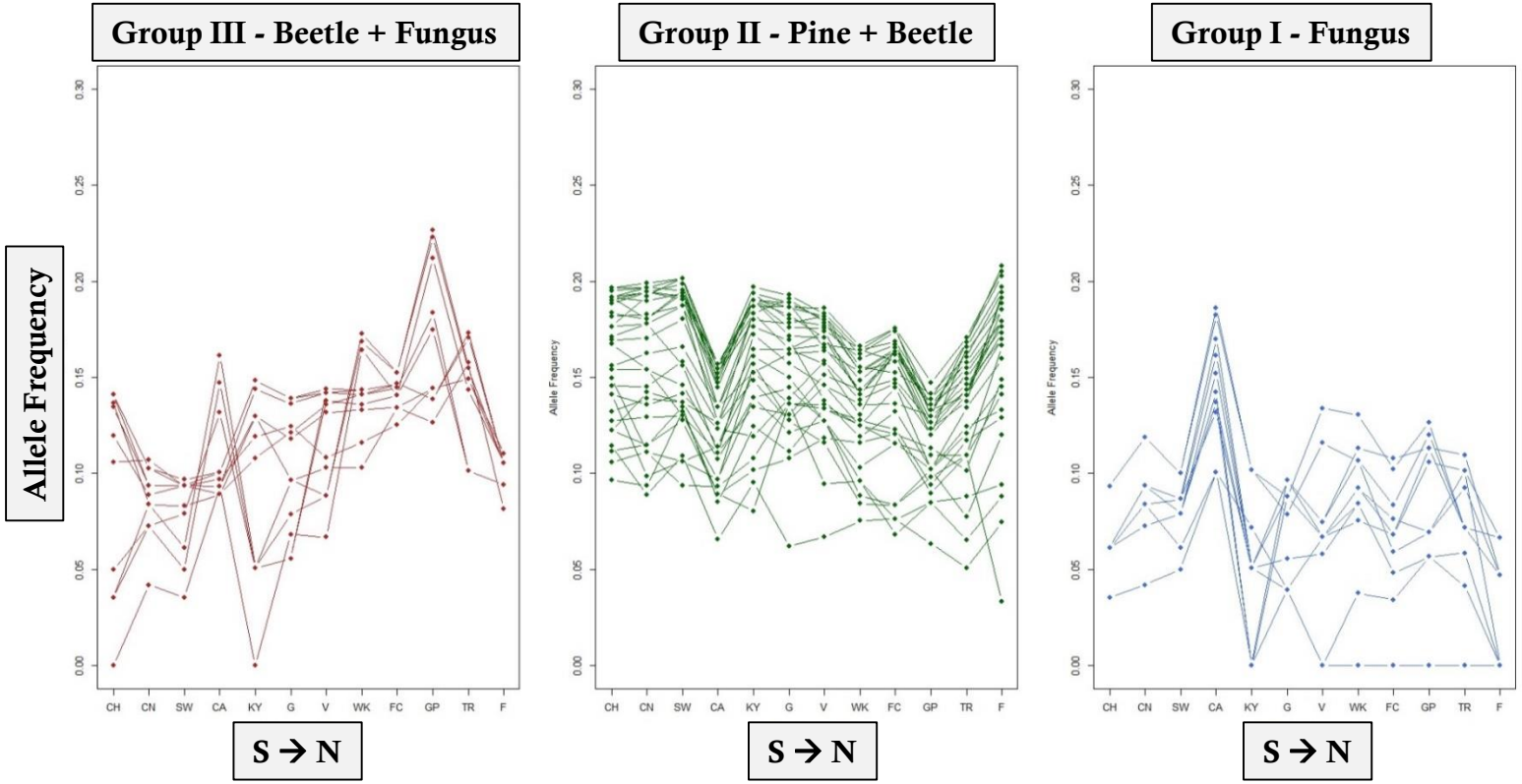

GCL.10
GCL.9
LLO.5
GCL.4
GCL.5
GCL.2
GCL.7
LLO.8
LLO.7
LLO.1
LLO.2
OMO.10
OMO.4
OMO.6
OMO.7
OMO.5
OMO.1
GCL.8
GCL.1
GROUP I
Kendall's W = 0.708
F=58.3; p<0.01
MPB.14
MPB.13
MPB.3
MPB.18
MPB.9
MPB.17
MPB.8
LPP.1
MPB.2
LPP.8
LPP.4
LPP.3
LPP.5
LPP.2
LPP.10
LPP.6
LPP.9
LPP.7
GROUP II
Kendall's W = 0.580
F=23.5; p<0.01
MPB.19
MPB.1
MPB.5
MPB.15
MPB.16
MPB.4
MPB.10
MPB.7
MPB.11
MPB.20
MPB.12
MPB.6
OMO.9
OMO.2
LLO.4
LLO.3
LLO.9
LLO.6
GCL.3
LLO.10
OMO.3
GCL.6
OMO.8
GROUP III
Kendall's W = 0.583
F=22.4; p<0.01
20
15
10
5
0





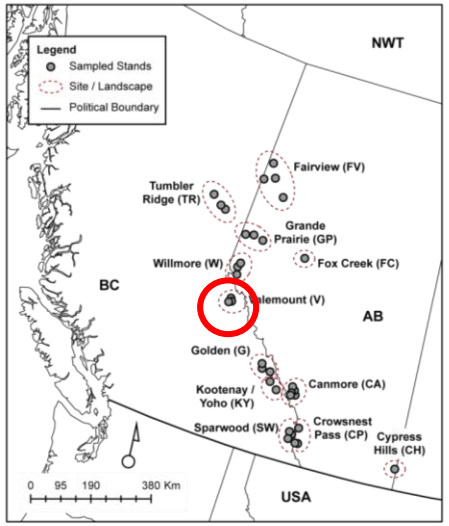


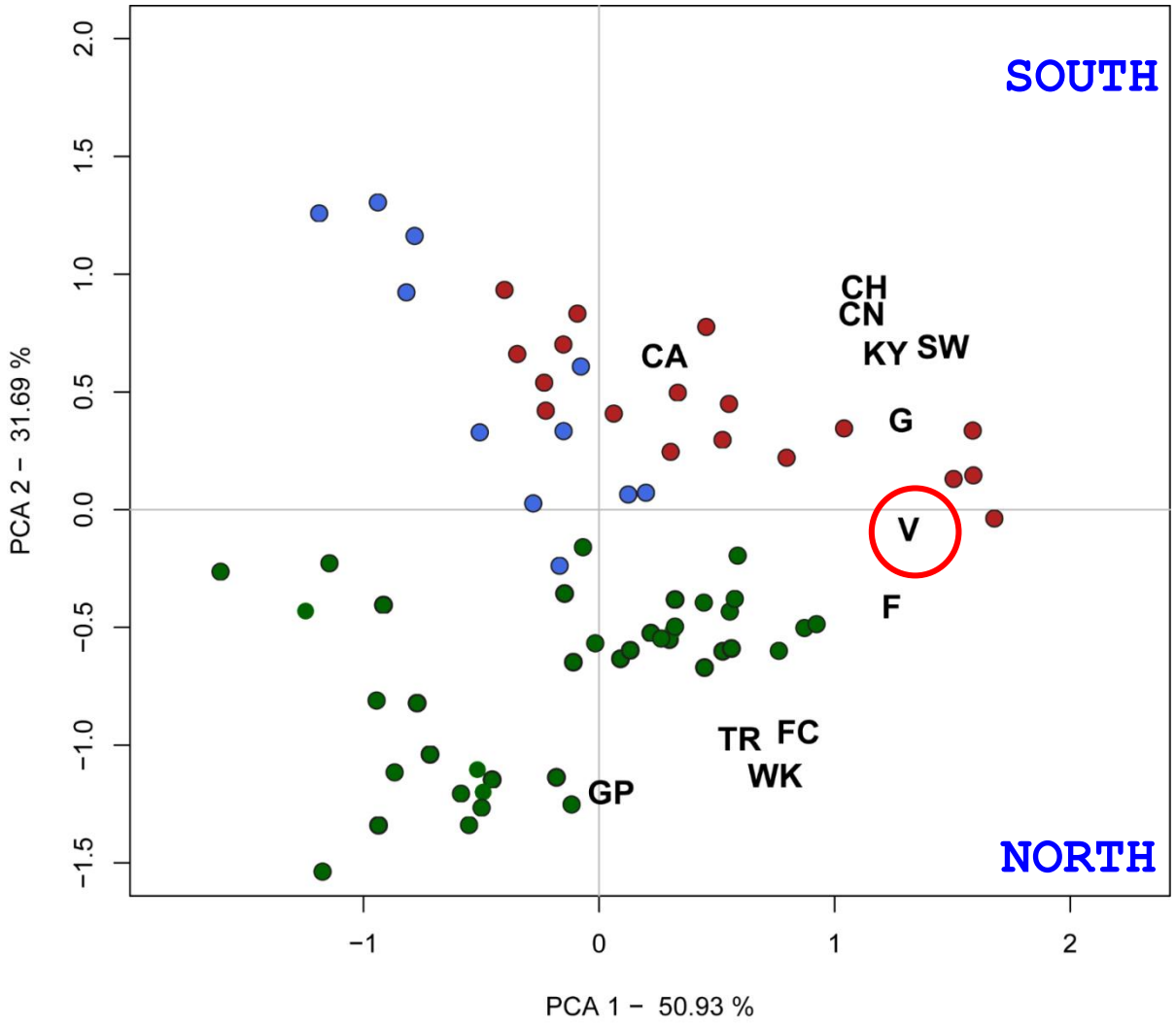
Cluster behaviours (latitude)

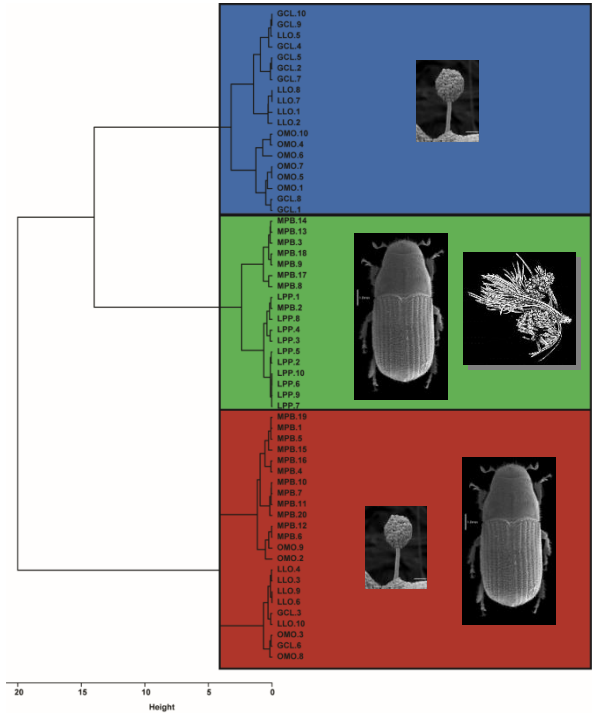


- Tendencies in allele frequencies of the three adaptive groupings plotted against sites sorted from South to North
- Different patterns are what the clustering algorithm is picking up

Geographic association of clusters?

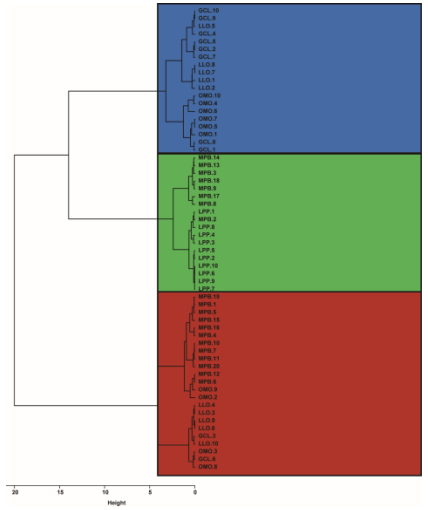


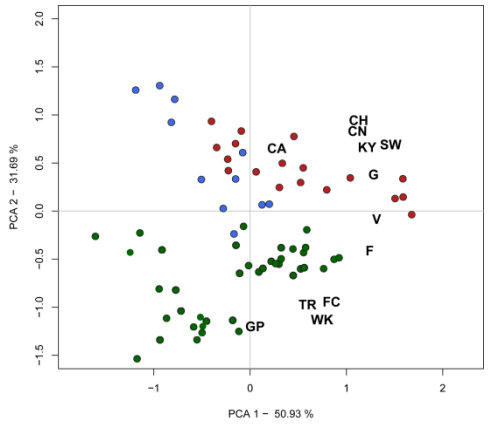




Interpretations

1. We identified significant **inter** and **intra**-specific clusters of outlier loci at the community level.
2. These clusters show some fidelity to known expansion axes.
3. **Outbreak expansion *may* be in part due to spatial evolutionary dynamics among species.**
4. This community-genomics framework can be applied to other multi-taxa systems to better understand adaptive dynamics during outbreaks and range expansions.



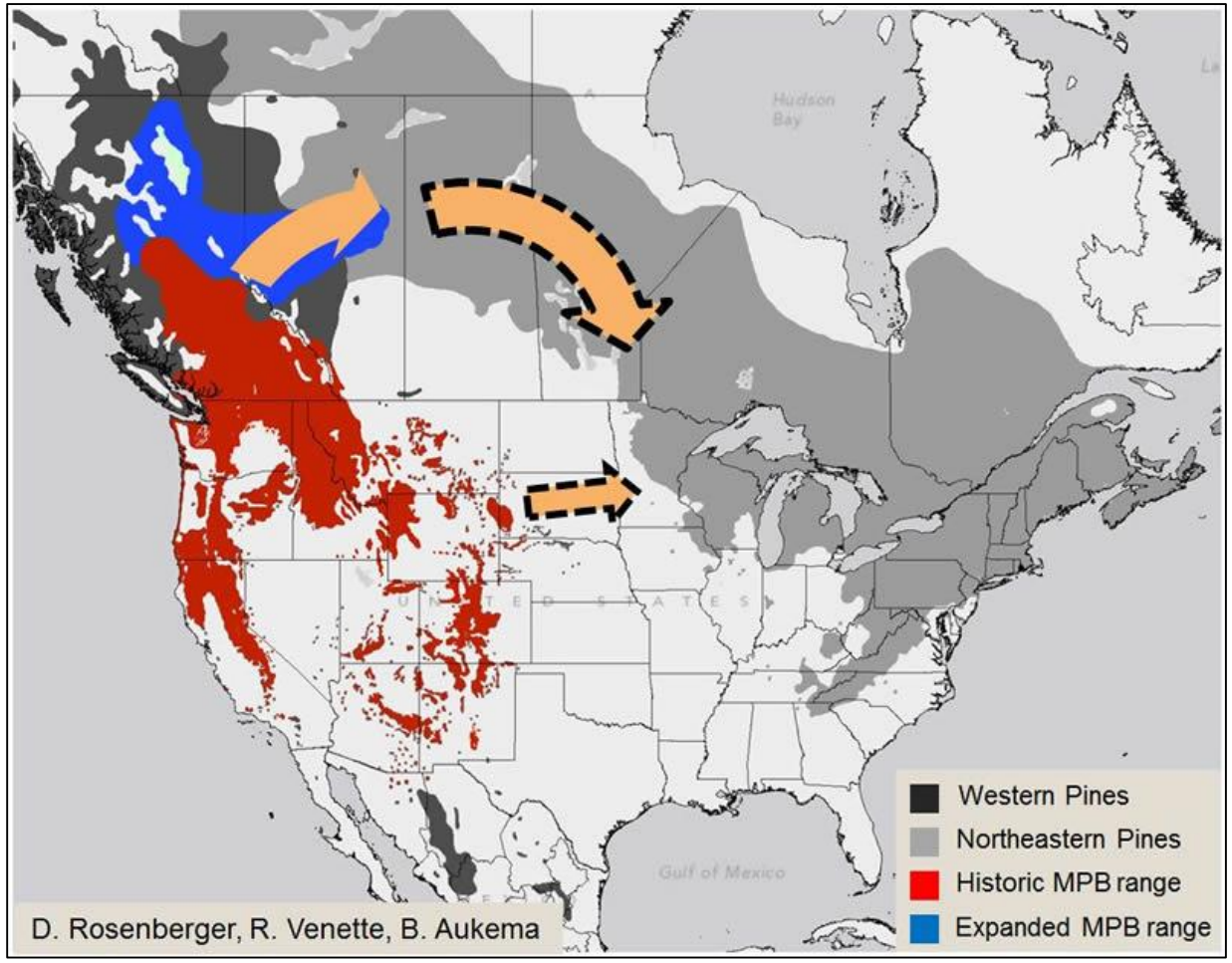


Caveats

- We don’t know if the loci we used are really “**adaptive**”.
  - Further functional characterization is still required to identify specific roles.
- Identifying loci under selection during range expansions can be biased due to allele surfing.
- Correlative results; we don’t yet know the eco-evolutionary mechanisms connecting allele frequencies among species.
- We have not distinguished yet between simple induced spatial dependence vs species interactions…

Mountain Pine Beetle in Canada

Lorraine Maclauchlan



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Turning Risk Into Action for the Mountain Pine Beetle Epidemic

Université de Montréal

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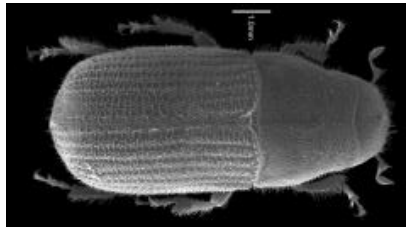

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