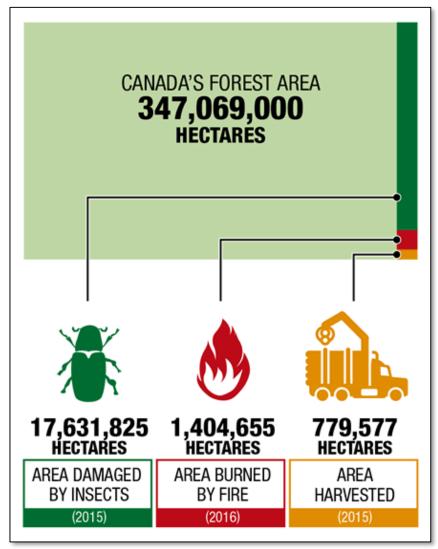
Causes and consequences of mountain pine beetle outbreaks: from genes to ecosystems

Patrick M. A. James

Université de Montréal

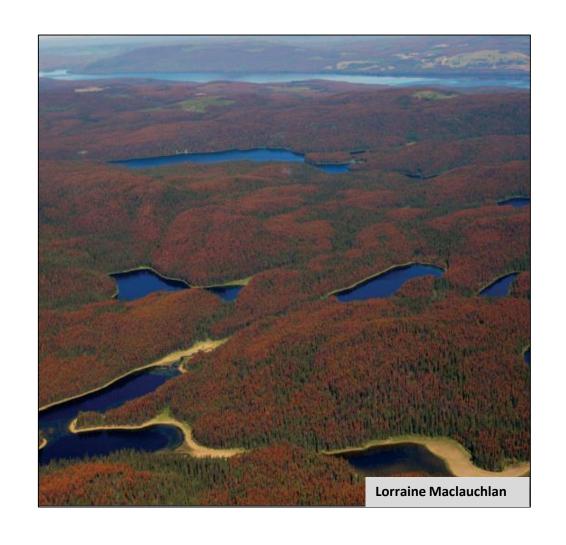


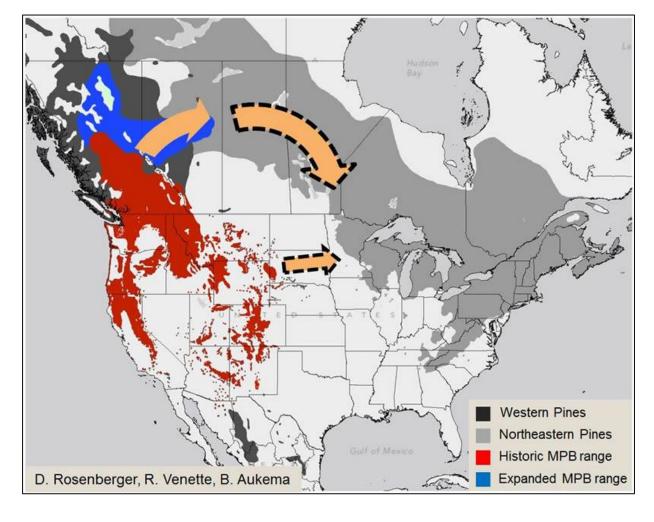


https://www.nrcan.gc.ca/forests/report/disturbance/16502

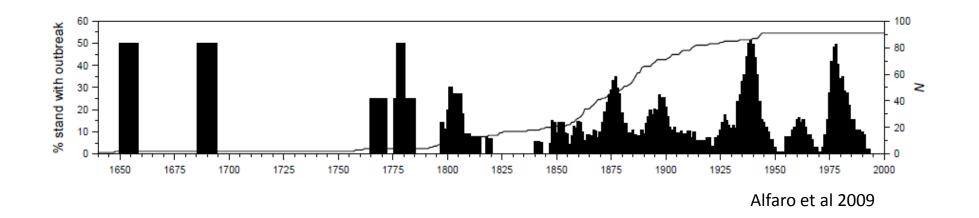
Mountain Pine Beetle

 $> 18 \times 10^6$ ha affected in Canada; $> 6 \times 10^6$ ha in the USA





Mountain pine beetle outbreaks are episodic and natural







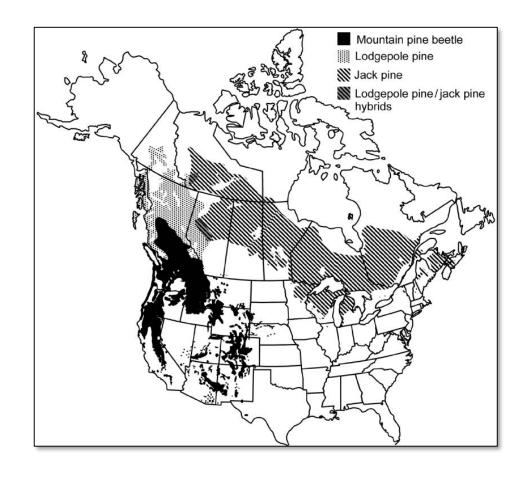


Dendroctonus ponderosae

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



- 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)



- 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 ...

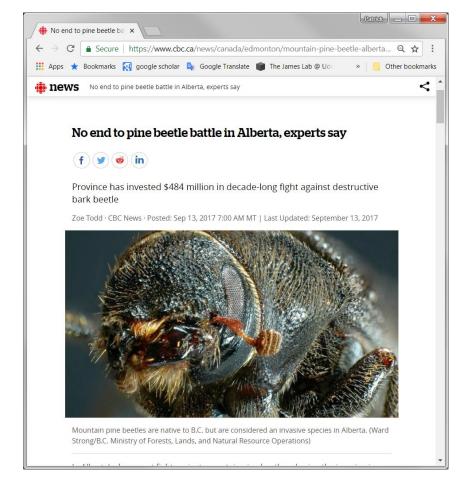




Forest insect outbreaks are costly

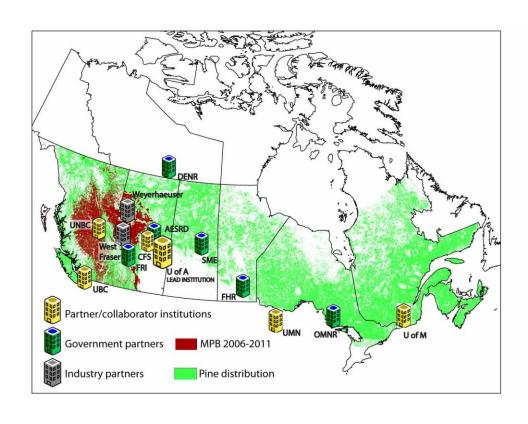
- ~ \$500 million invested so far in Alberta to combat the MPB
- Estimated cumulative loss equal to ~\$57 billion from 2009 to 2054 in British Columbia
 - Corbett et al 2015; Forestry
- Current spruce budworm outbreak in NB is expected to result in losses between \$5 and \$7 billion over the next 40 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









Natural Resources

Canadian Forest Service

Ressources naturelles Canada

Service canadien des forêts























a place of mind THE UNIVERSITY OF BRITISH COLUMBIA

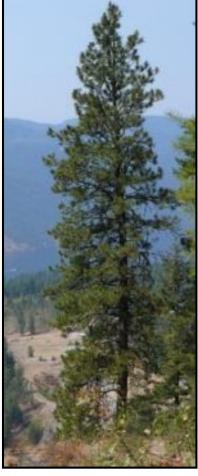




Mountain Pine Beetle Outbreak System





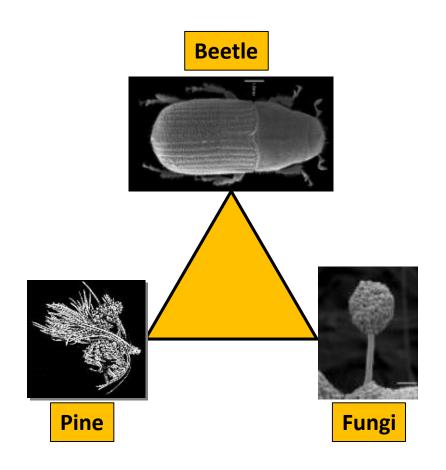


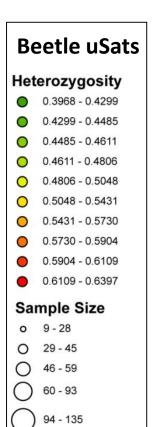


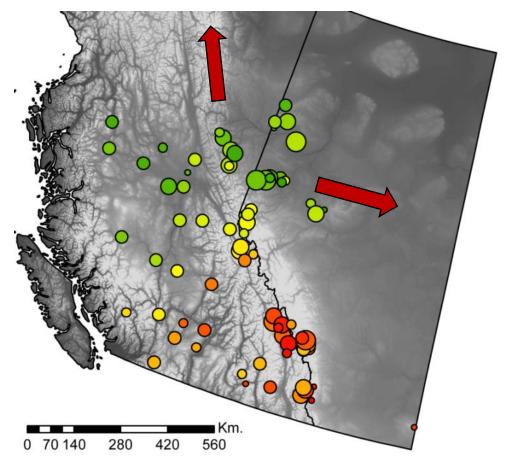




Ongoing Range Expansion

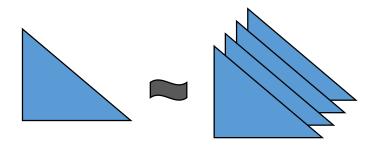




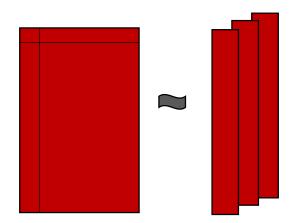


Landscape Genetics / Genomics

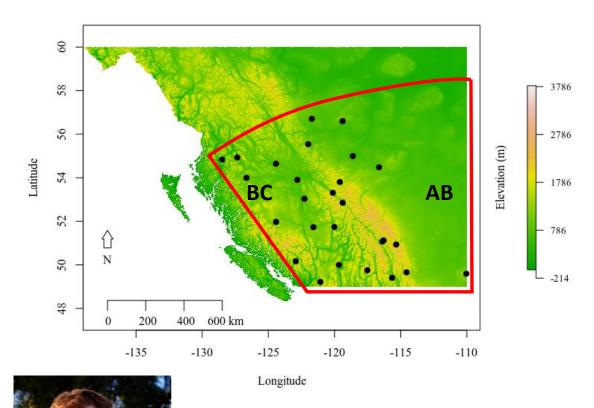
• Landscape Genetics: Combination of landscape ecology, spatial statistics, and population genetics to examine how spatial heterogeneity affects gene flow and dispersal (Manel et al. 2003).



• 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

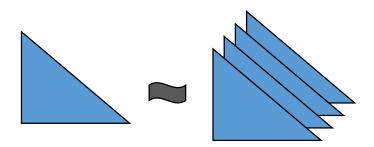


Why do we care about MPB movement?

- 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**.

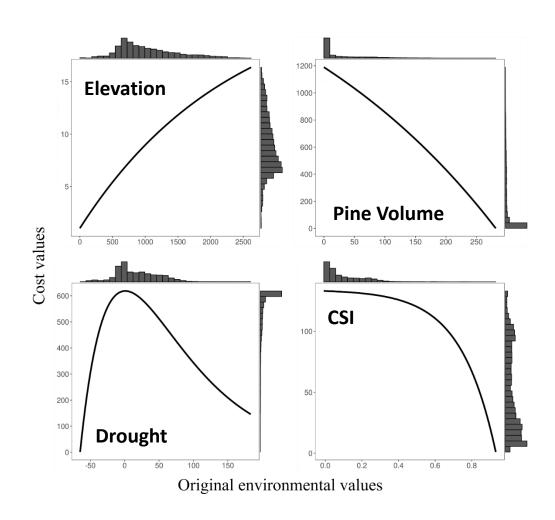
Specifying resistance surfaces is challenging

- 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



A				
1		2	4	4
1		8	8	4
1		4	8	2
1		4	1	1
В				

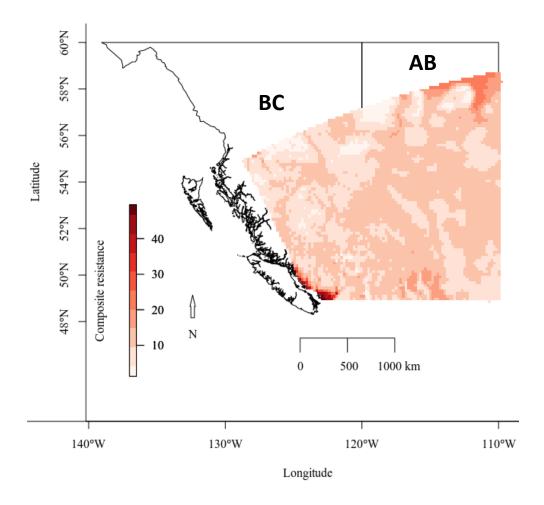
Single surface optimizations



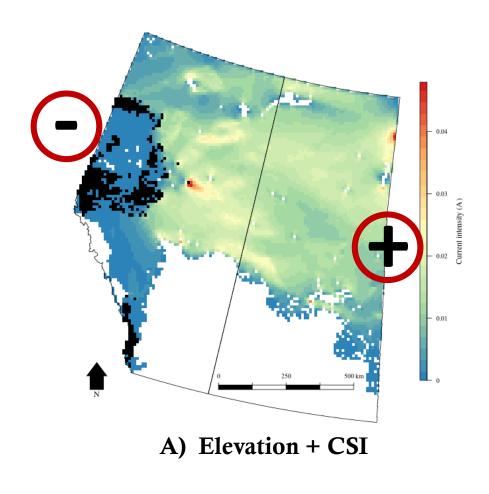
 These curves represent the optimized functional relationships between each spatial variable and resistance to gene flow (movement) based on our SNP data set

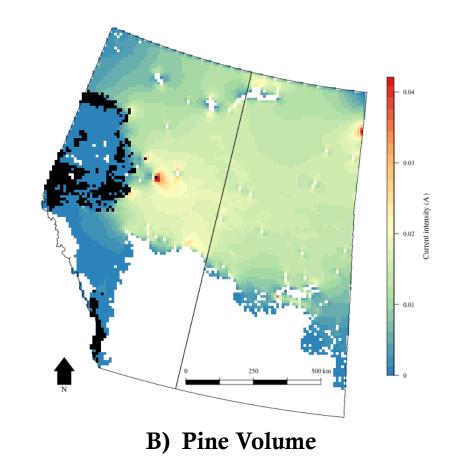
Optimized "best" composite surface

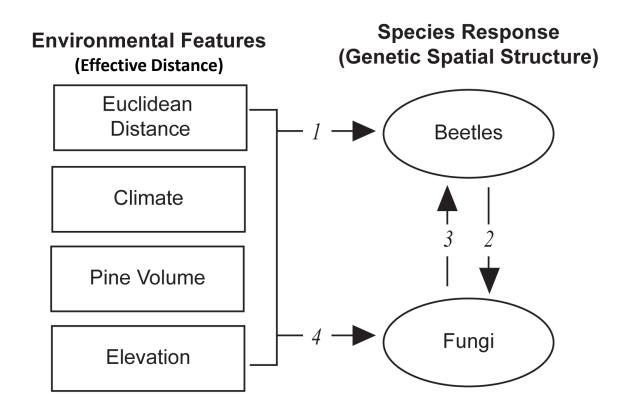
- Elevation + Climate Suitability
- Weighting: 69% climate; 31% elevation
- Large islands of less resistance
- Cost heterogeneity decreases eastward: consequences for expansion?

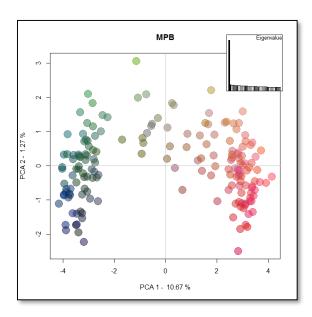


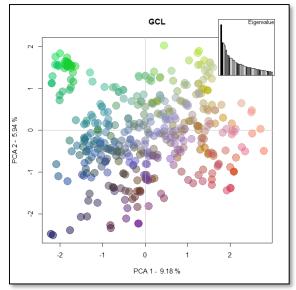
Forecasting future spread risk using circuit theory...

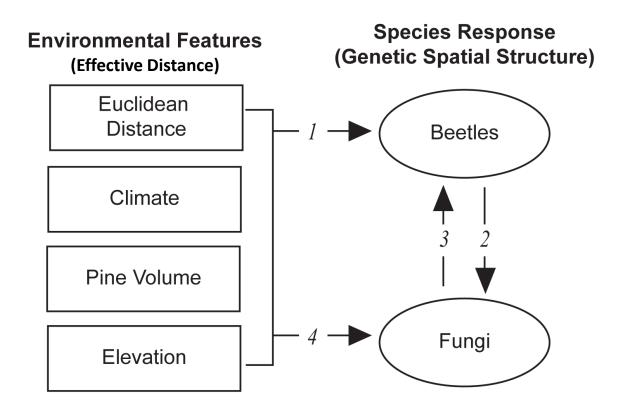


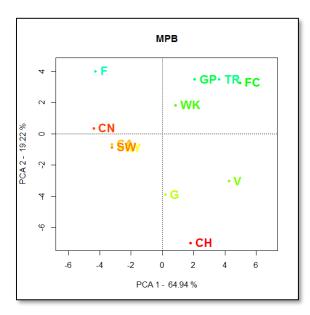


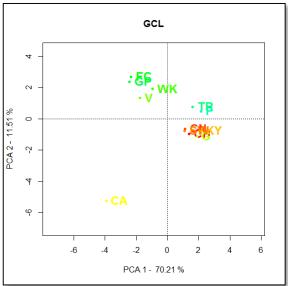


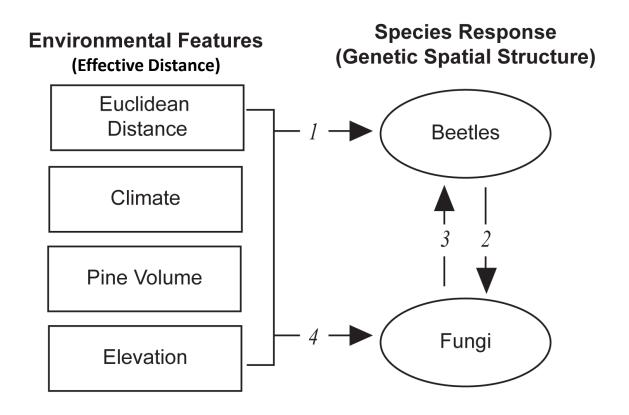


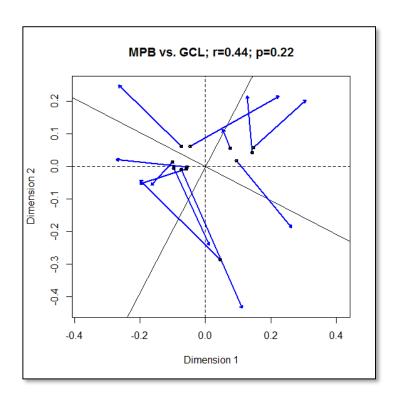


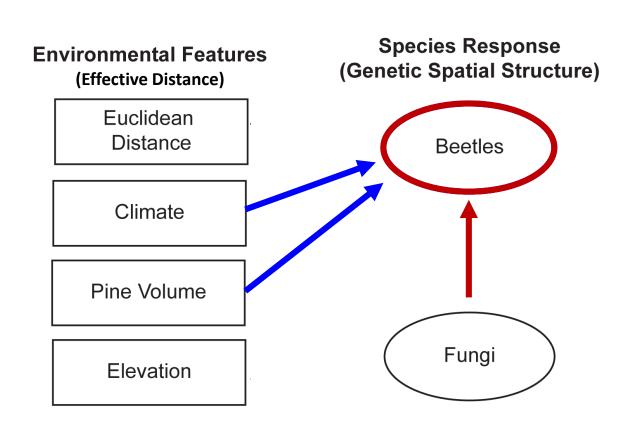


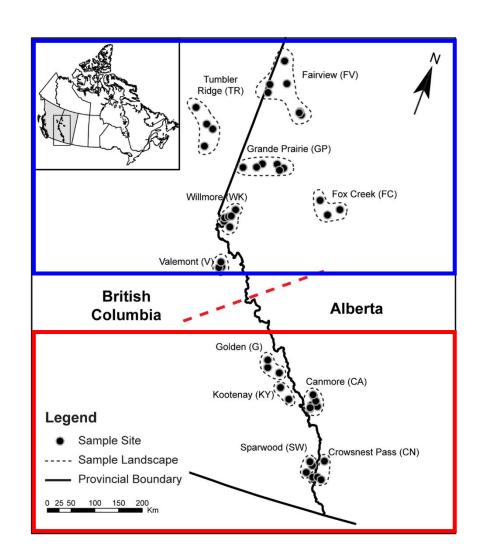












Landscape Community Genomics

Ecology, 84(3), 2003, pp. 559-573 © 2003 by the Ecological Society of America

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, Scott Woolbright, 1,3 and Cheryl R. Kuske⁵

OPEN @ ACCESS Freely available online



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

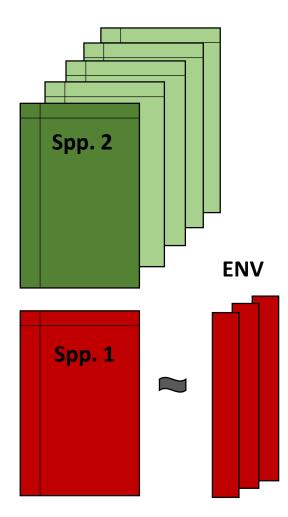
Patrick M. A. James¹∗¤, Dave W. Coltman¹, Brent W. Murray², Richard C. Hamelin³,⁴, Felix A. H. Sperling¹

October 2011 | Volume 6 | Issue 10 | e25359

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

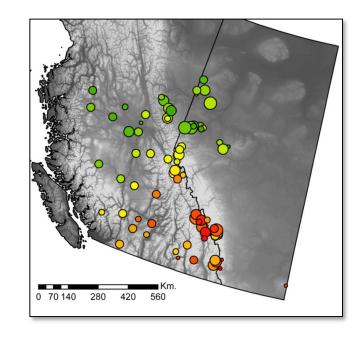
Brian K. Hand^{1*}, Winsor H. Lowe^{2*}, Ryan P. Kovach^{1,3}, Clint C. Muhlfeld³, and Gordon Luikart¹

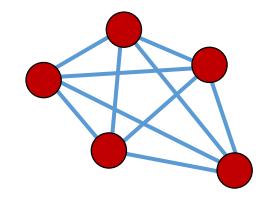
Trends in Ecology & Evolution March 2015, Vol. 30, No. 3



Landscape Community Genomics

- Can we identify groups of potentially adaptive loci *among* species that cluster together?
- Search for <u>OUTBREAK SYNDROMES</u>
 - → spatially structured, inter-species associations of putatively adaptive alleles.



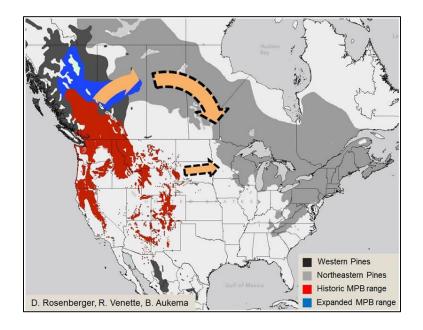


ADAPTIVE* VARIATION

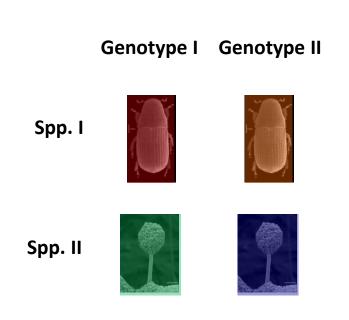
Landscape Community Genomics

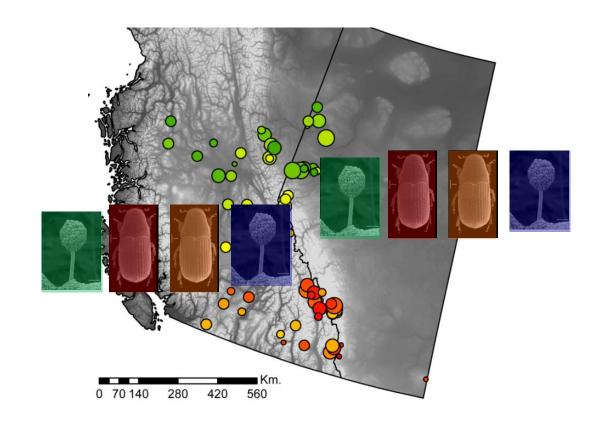
Why do we care?

- 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?

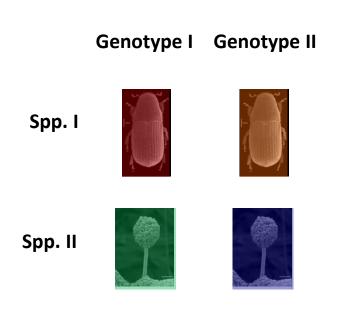


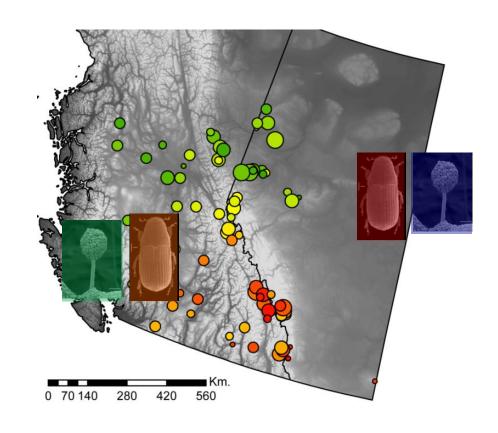
MPB Landscape Community Genomics



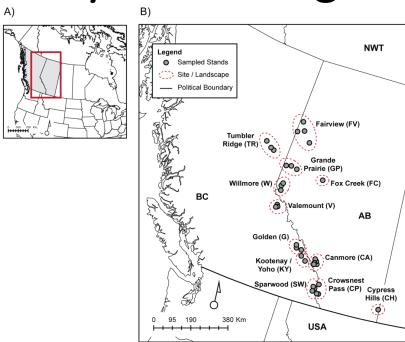


MPB Landscape Community Genomics





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

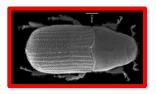
- *D. ponderosae* (MPB)
 - 175 individuals; 1532 loci

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





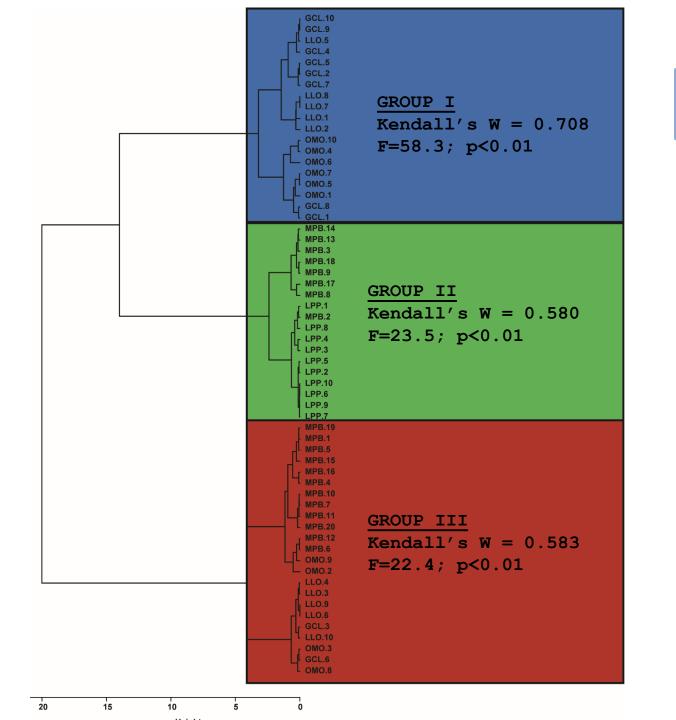






Analysis pipeline

- 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*
 - Ks (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.



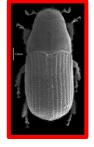










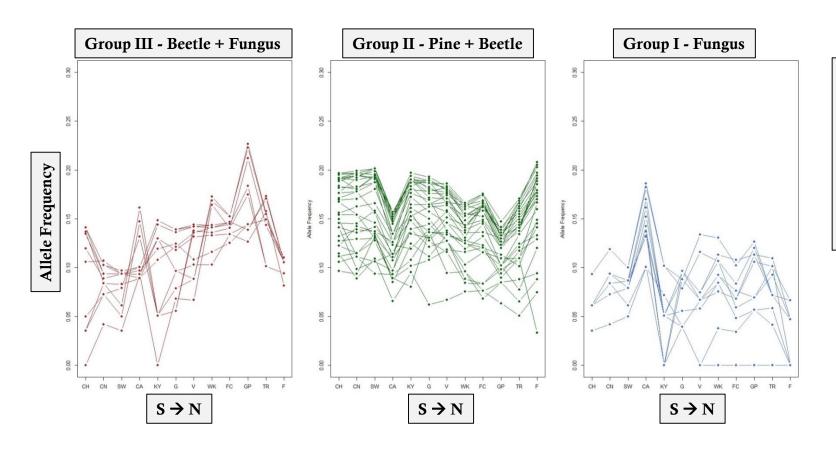






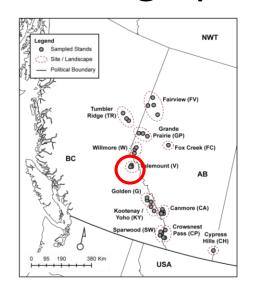


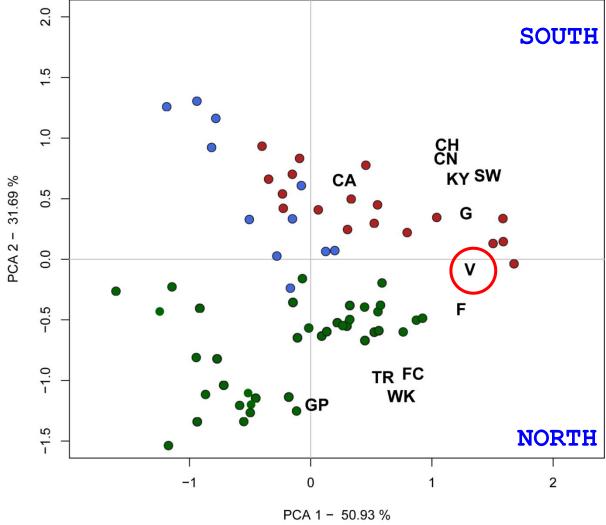
Cluster behaviours (latitude)

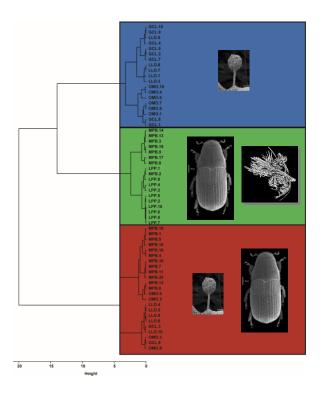


- Tendencies in allele frequencies of the three adaptive groupings plotted against sites sorted from South to North
- Different patterns are what the clustering algorithm is picking up

Geographic association of clusters?

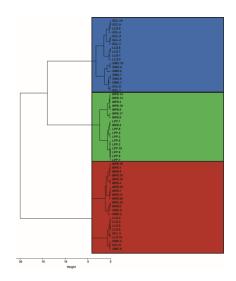


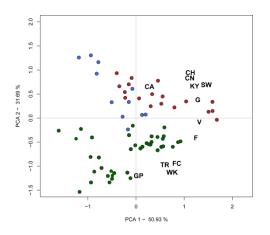




Interpretations

- 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.
- 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.

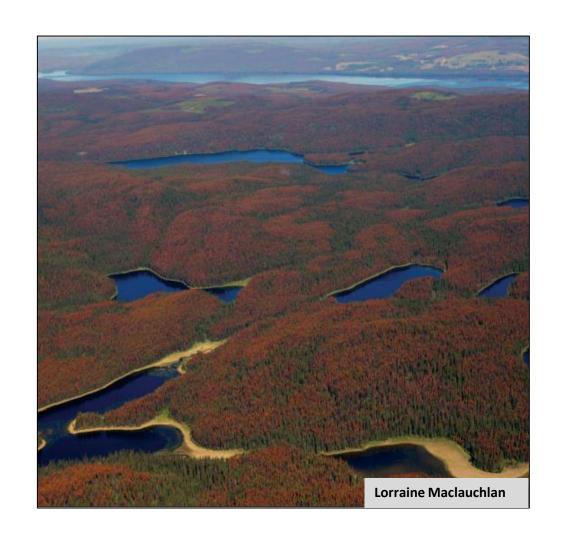


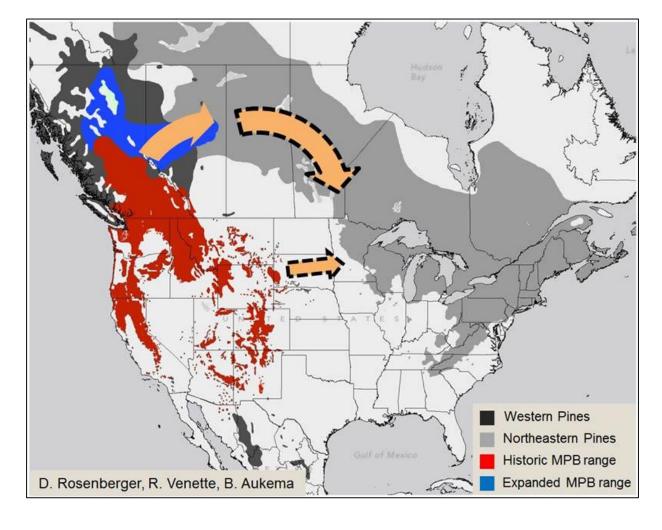


Caveats

- 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...

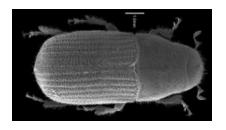
Mountain Pine Beetle in Canada





Acknowledgements

- TRIA Net team
- Cathy Cullingham (UofA)
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- Dave Coltman (UofA)
- Richard Hamelin (UBC)
- Janice Cooke (UofA)
- Jasmine Janes (UofA)
- Julian Wittische (UdeM)











jameslab.ca