



Using spatial genomics to distinguish drivers of spruce budworm outbreak synchrony

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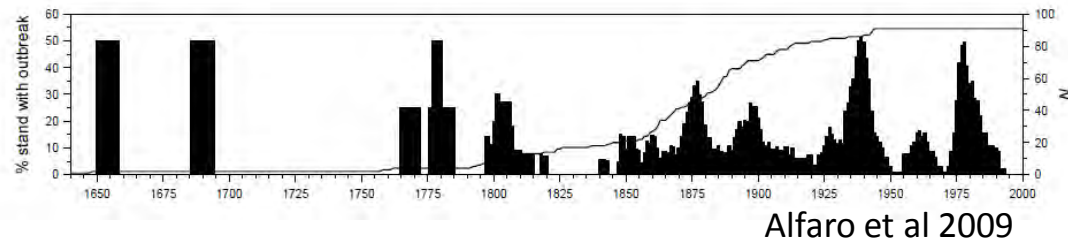


Collaborators :

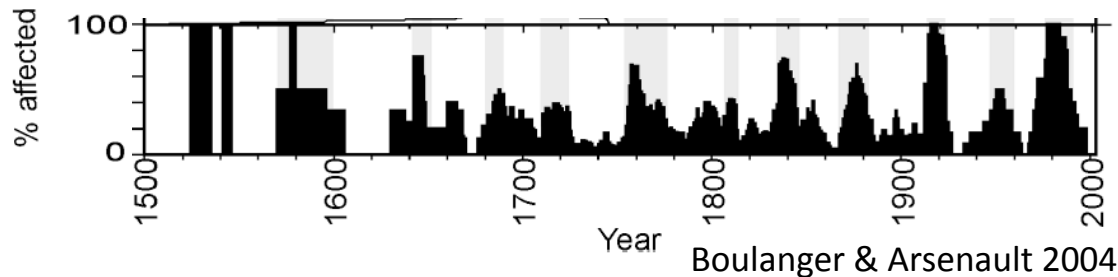
- Michel Cusson
- Rob Johns
- Felix Sperling
- Lisa Lumley
- Bryan Brunet
- Simon Legault
- Julian Wittische
- Jeremy Larroque
- Julie Marleau
- Brian Boyle

Population cycles are common in forest insect pests

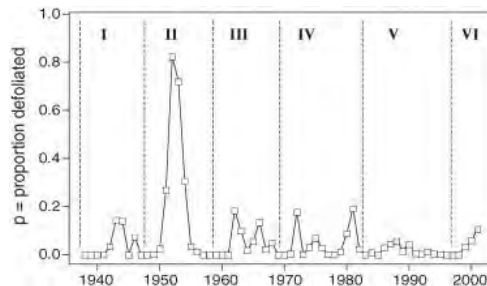
MPB (*Dendroctonus ponderosae*)



SBW (*Choristoneura fumiferana*)



FTC (*Malacasoma disstri*)



SBW

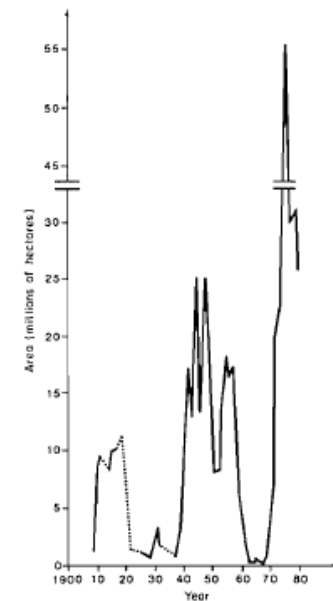
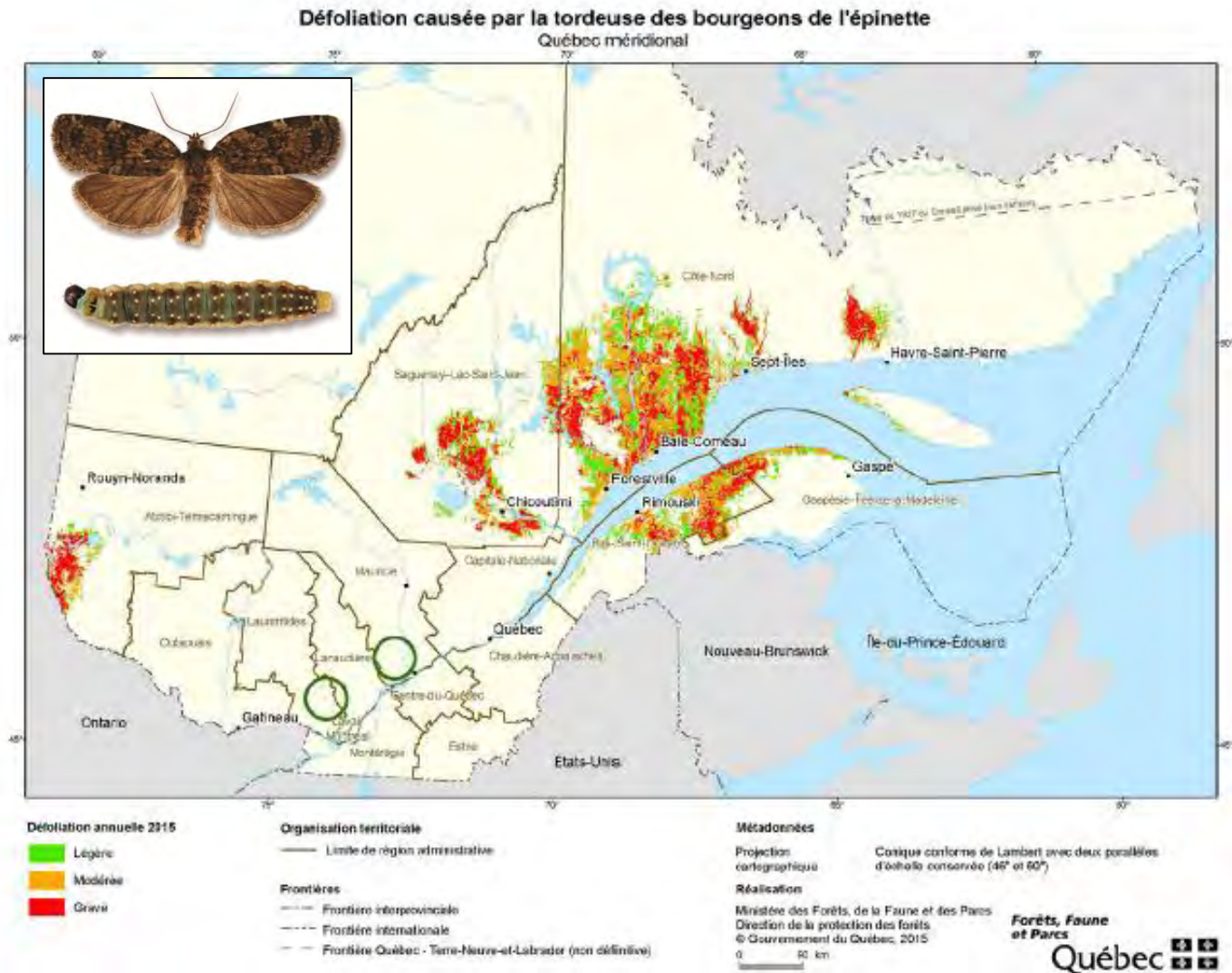


FIG. 2. The area moderately or severely infested by the spruce budworm 1909–1979.

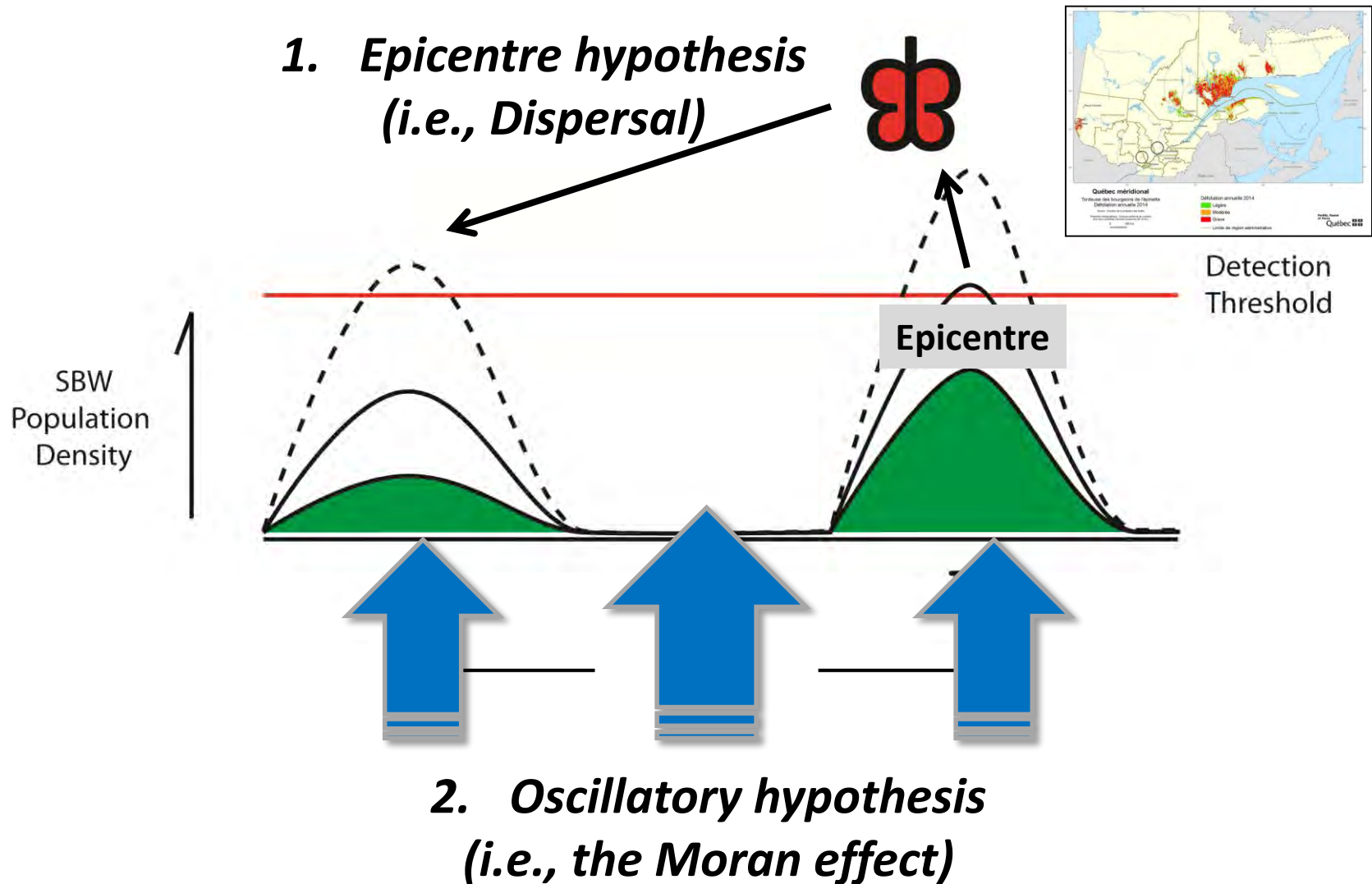
CAN. J. FOR. RES. VOL. 13, 1983

Blais 1983

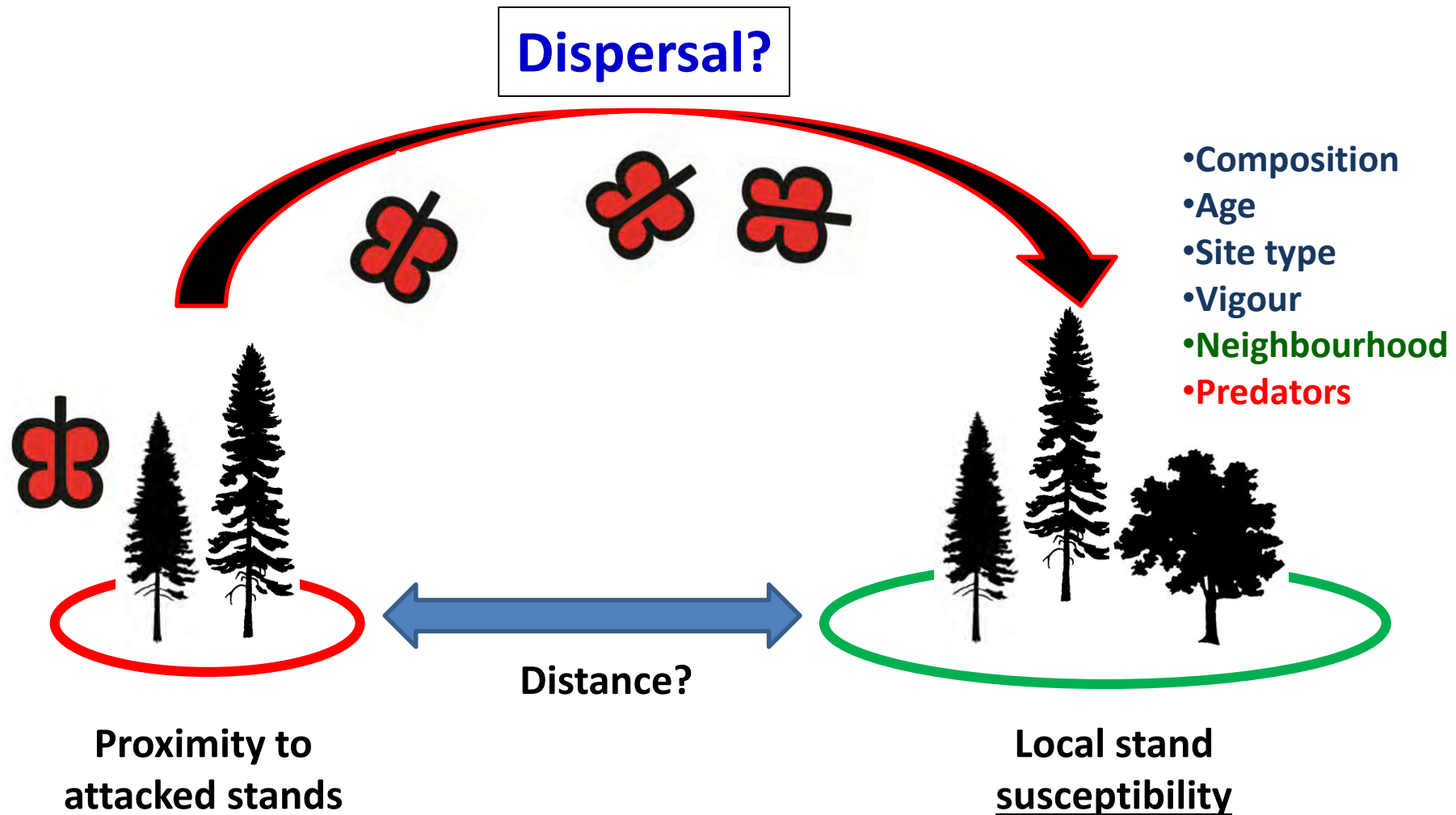
Outbreaks are often spatially synchronous



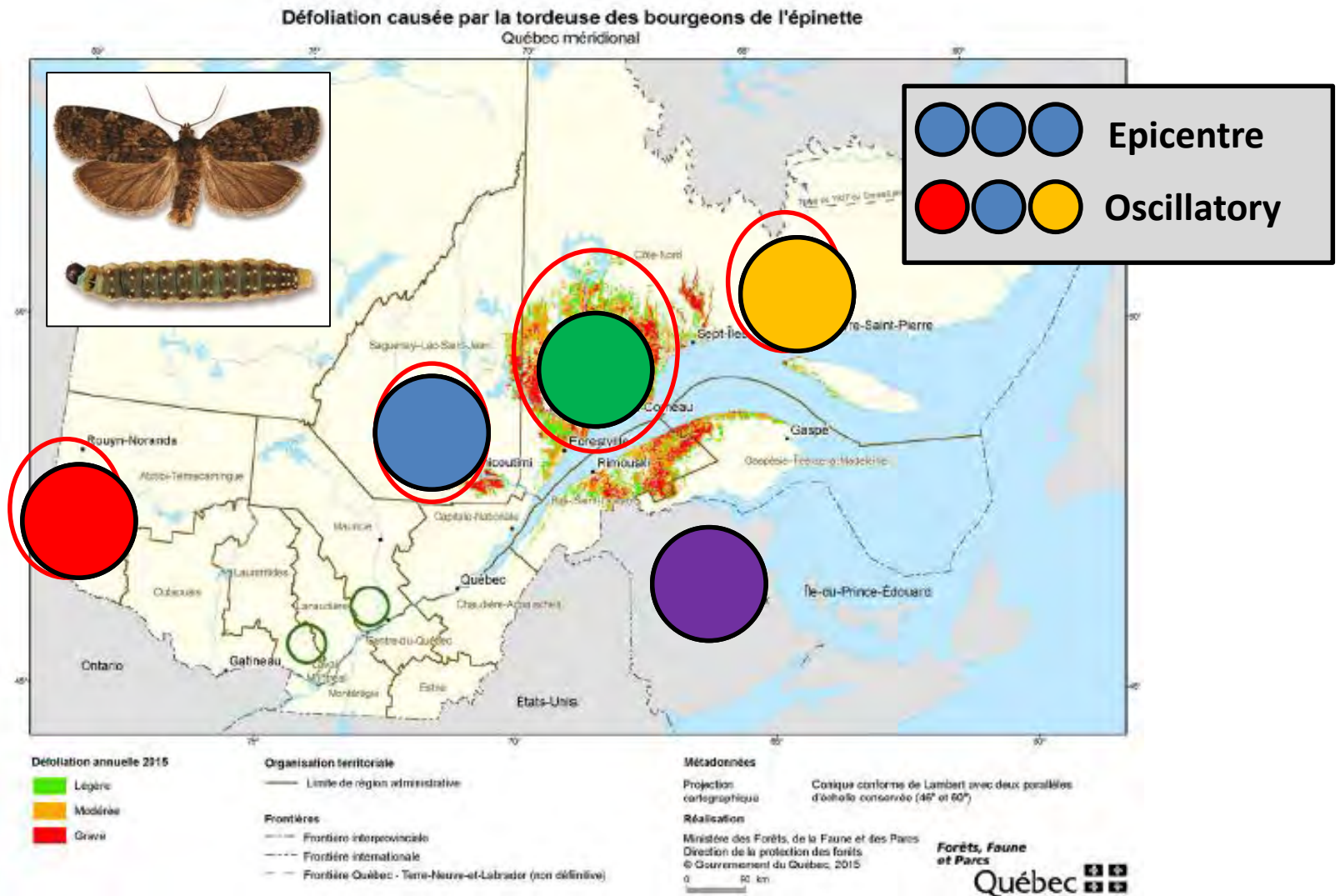
Two contrasting outbreak hypotheses



Factors contributing to **risk** and outbreak spread

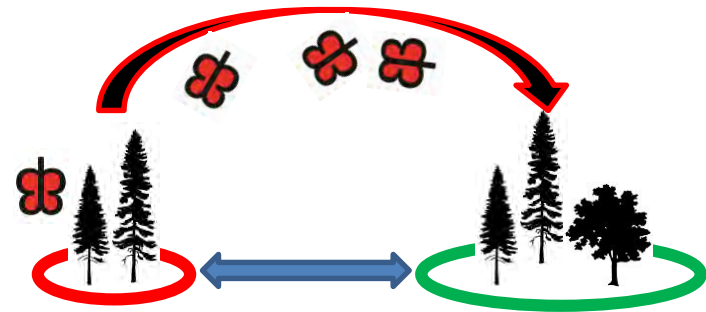
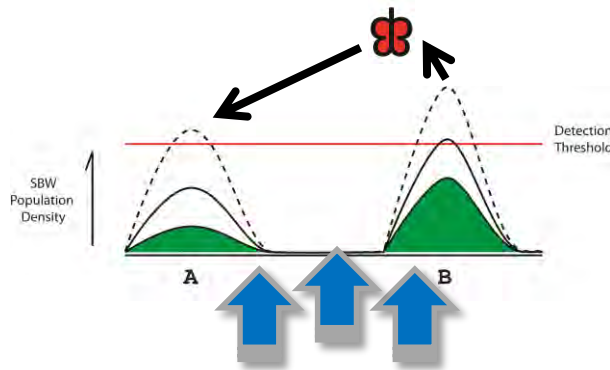


Two competing hypotheses...



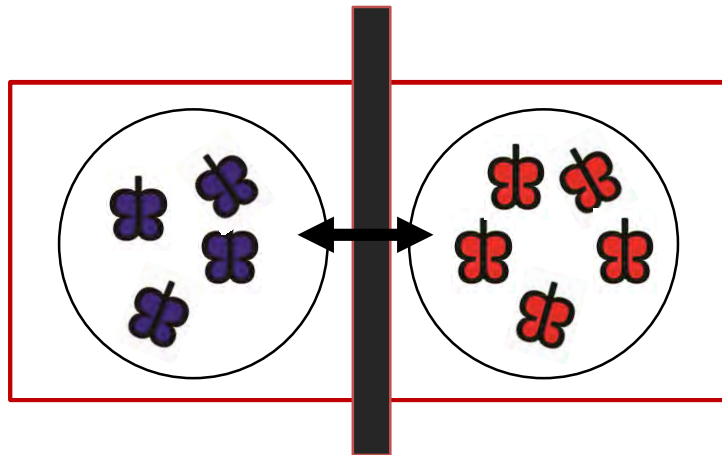
Objectives

1. Assess genetic connectivity (i.e., *effective dispersal*) among populations of SBW in the current outbreak.
2. Evaluate the relative support for the **epicentre** and **oscillatory** hypotheses.
3. *Inform early intervention management strategies.*



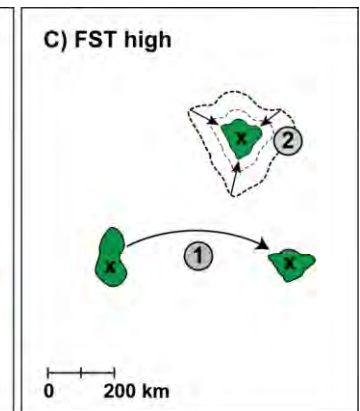
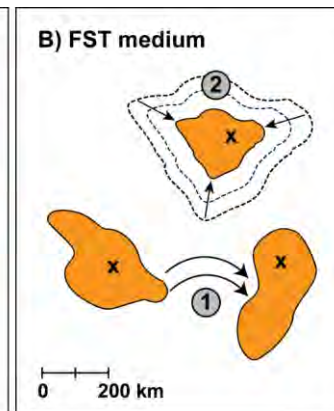
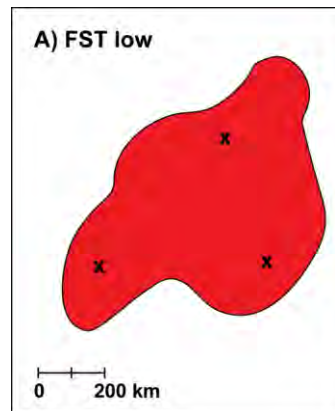
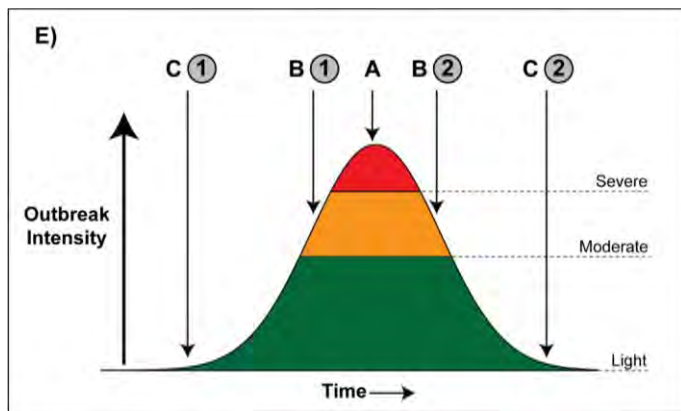
Inferring dispersal from genetic connectivity

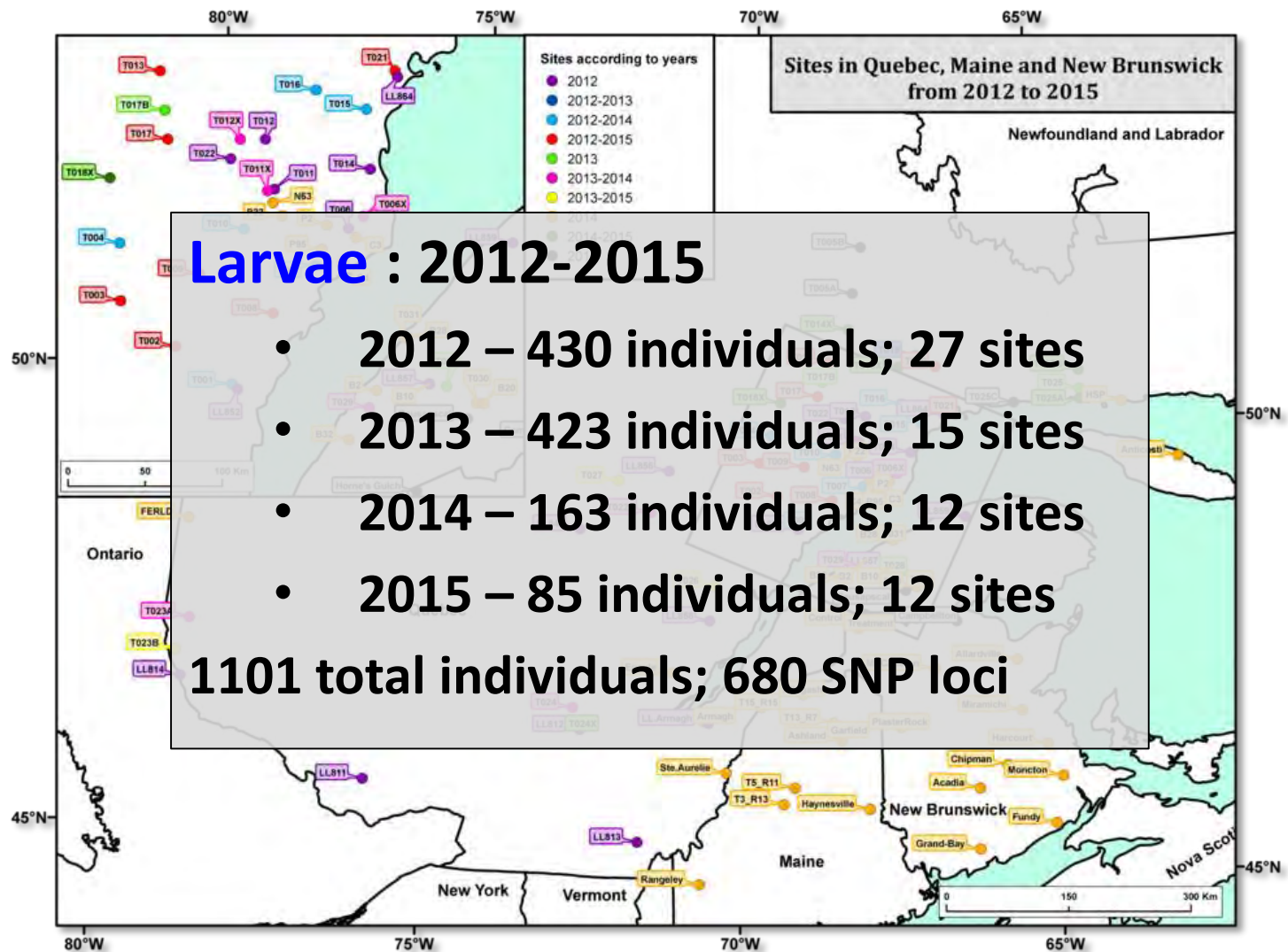
- **Gene flow** can be used as a proxy to estimate effective dispersal.
- Estimated using spatial variation in genetic markers and derived genetic distances (e.g., *F_{st}*).
 - Ratio of variance within vs. among sites.
 - We generally expect a decline in genetic similarity with increasing distance (IBD).



Challenge

- Our ability to use genetics to understand the role of dispersal in outbreaking systems may depend on “outbreak context”.
- Indicators of provenance may decay as outbreaks progress.





2012-2015

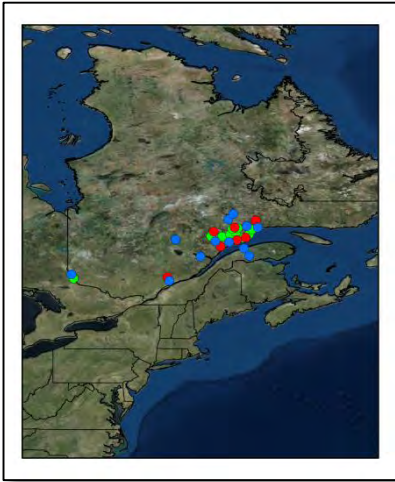
All sites sampled between 2012 and 2015. Many sites were sampled each year, whereas others were sampled for a single year. Each site can contain larvae, moths, or a combination of both.

Analysis pipeline

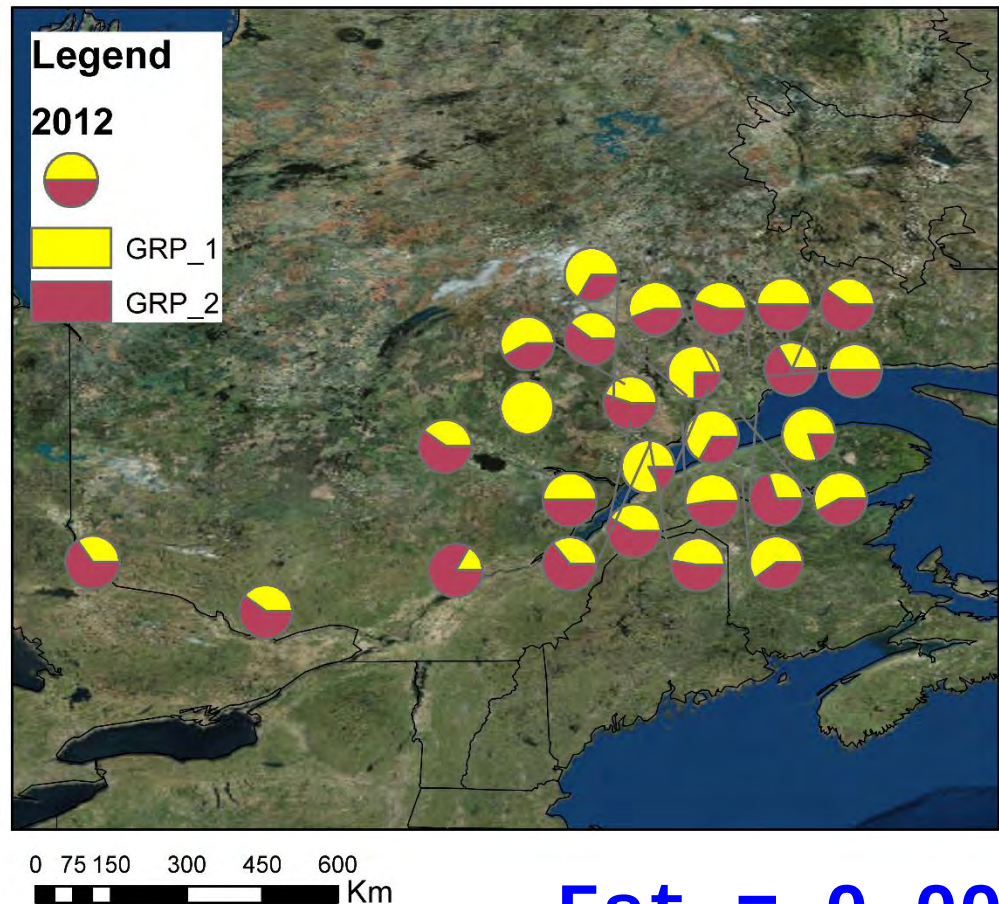
- **SNP identification** using “genotyping by sequencing” (GBS; Elshire *et al.* 2011)
- Data processing :
 - UdeM – DNA extraction
 - IBIS / U. Laval) – Library preparation
 - McGill Genome Centre – Illumina sequencing
 - UdeM – Bioinformatics (*UNEAK* + *TASSEL*)

Ind.	Site	SEQUENCE
1	BSL	AA A TCGTAC T CAAT C CTATA C TT
2	BSL	AA A TCGTAG T CAAT T CTATAC A T
3	BSL	AA T TCGTAC T CAAT C CTATAC A T
...	...	...
<i>n</i>	<i>p</i>	...
		...
		
		
		
		
		SNP SNP SNP SNP

Clusters through space and time

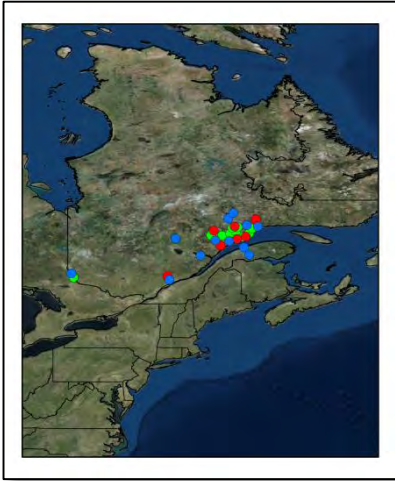


- Clusters identified using **DAPC**
- **2** groups : 2012-2014
- **1** group : 2015
- Weak overall SGS (mean $F_{st} < 0.05$)
- No spatial pattern in groups
- $N \rightarrow 3 - 36$; mean = 18

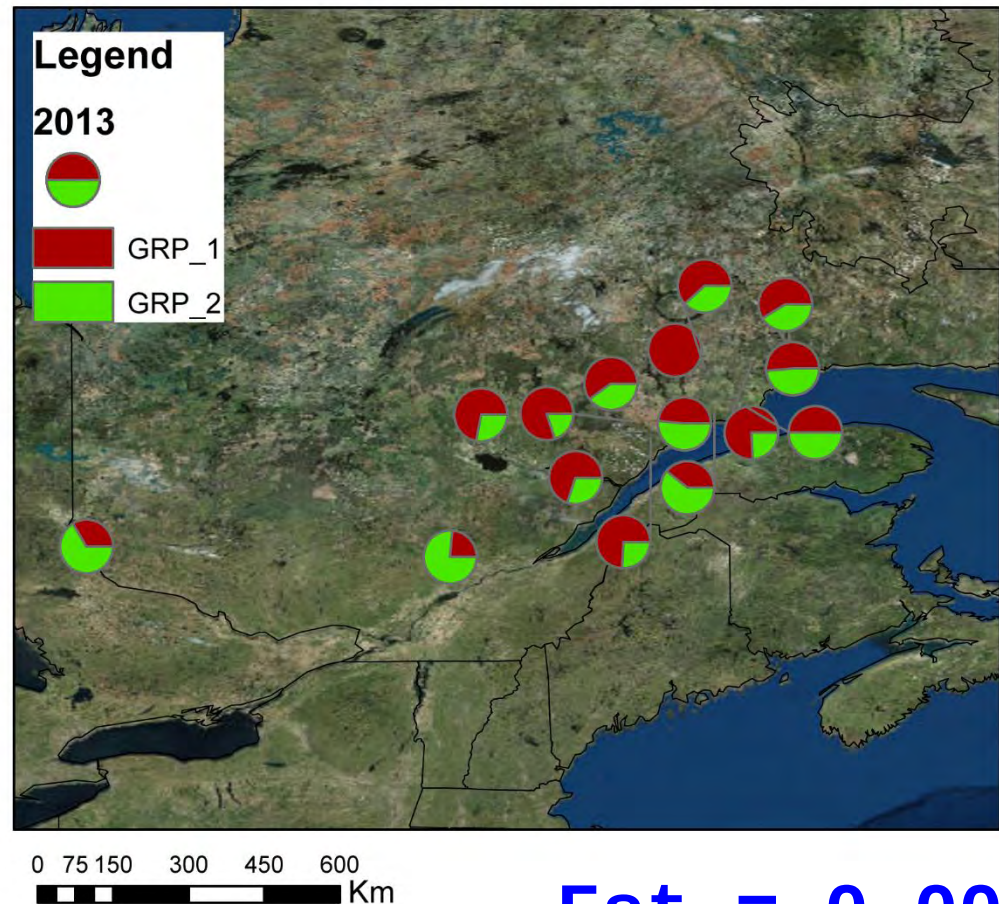


$F_{st} = 0.006$

Clusters through space and time

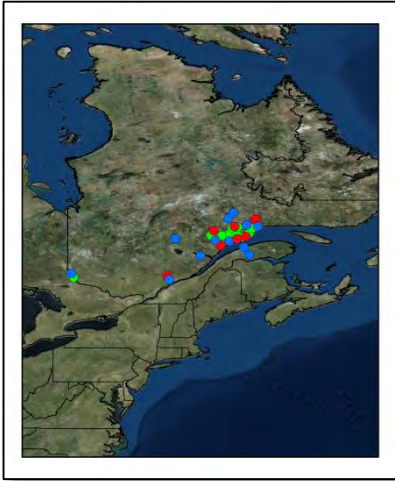


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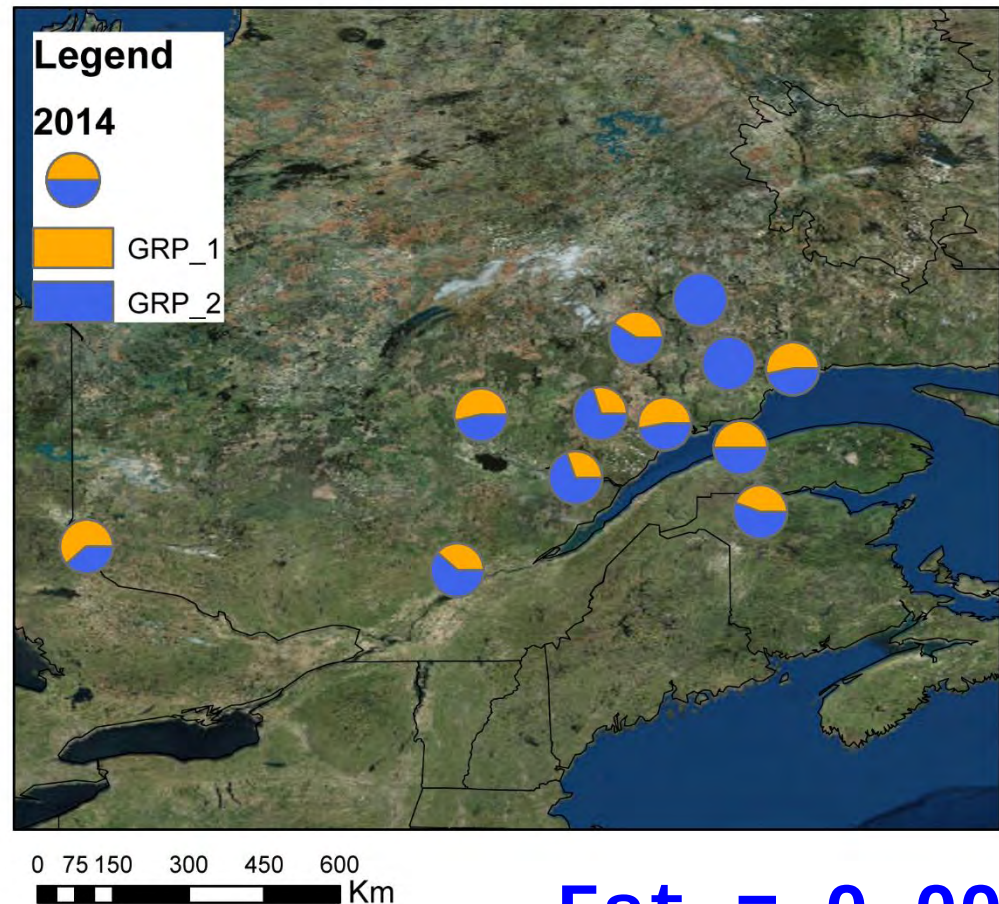


$F_{st} = 0.003$

Clusters through space and time

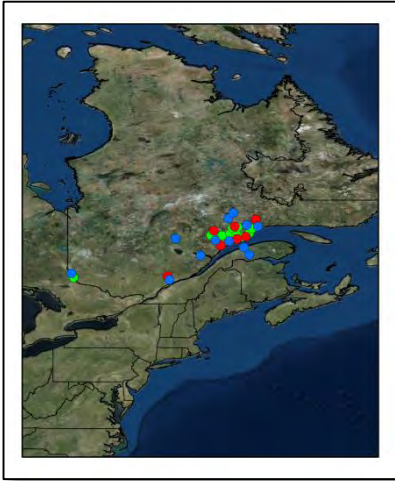


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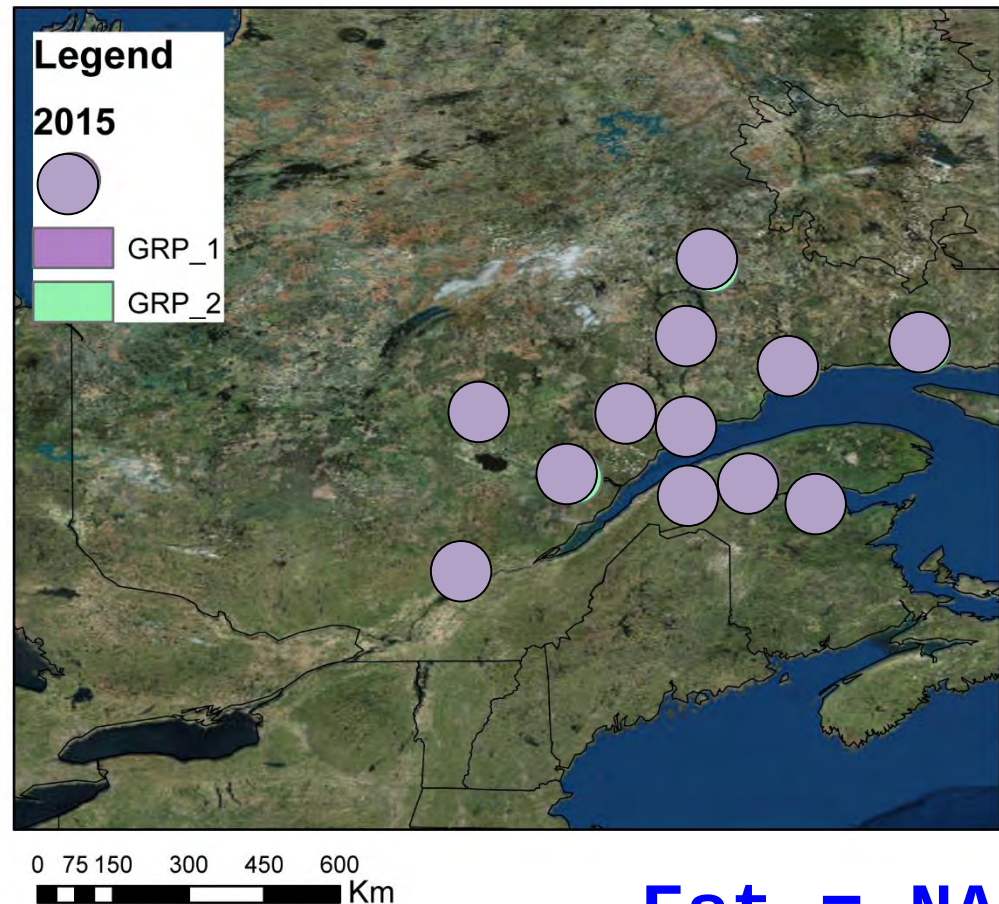


$F_{st} = 0.002$

Clusters through space and time

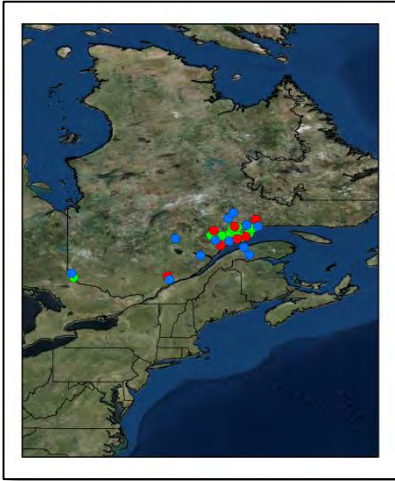


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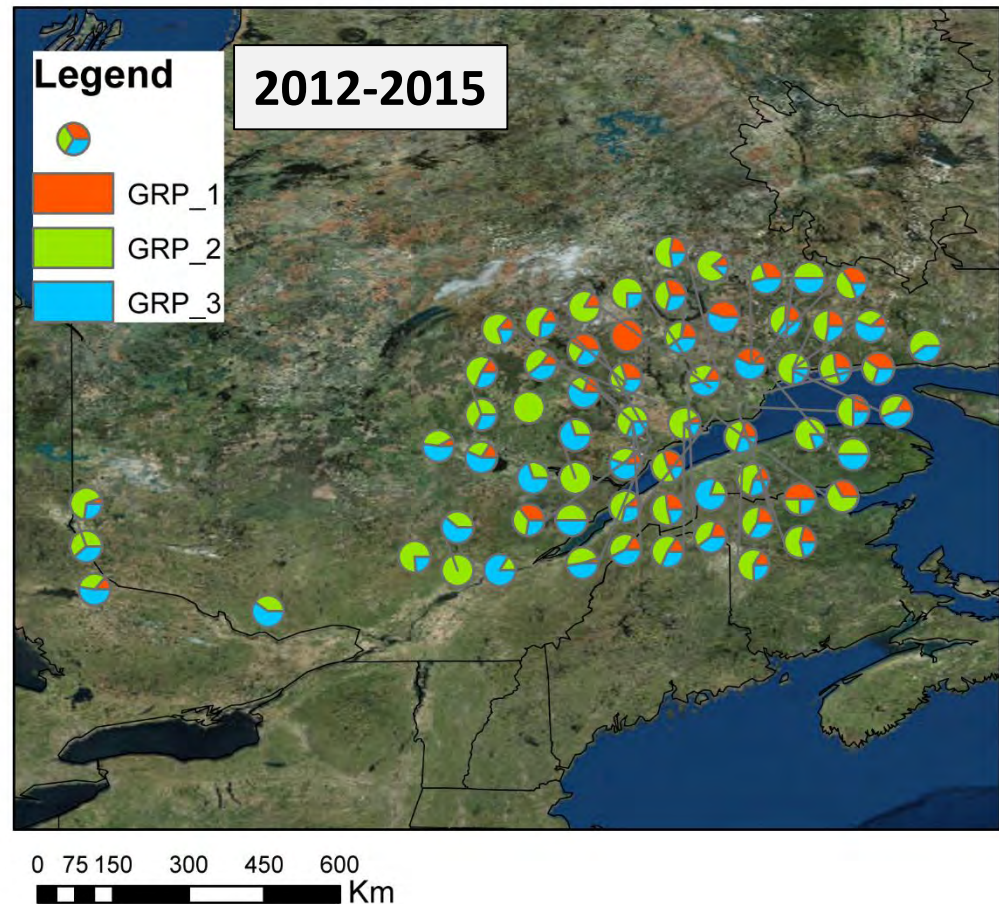


$F_{st} = NA$

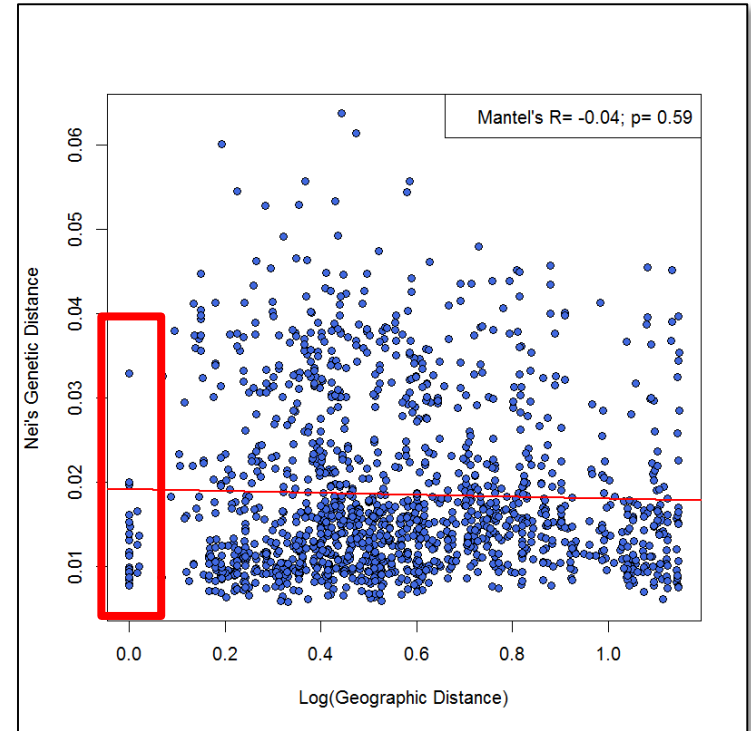
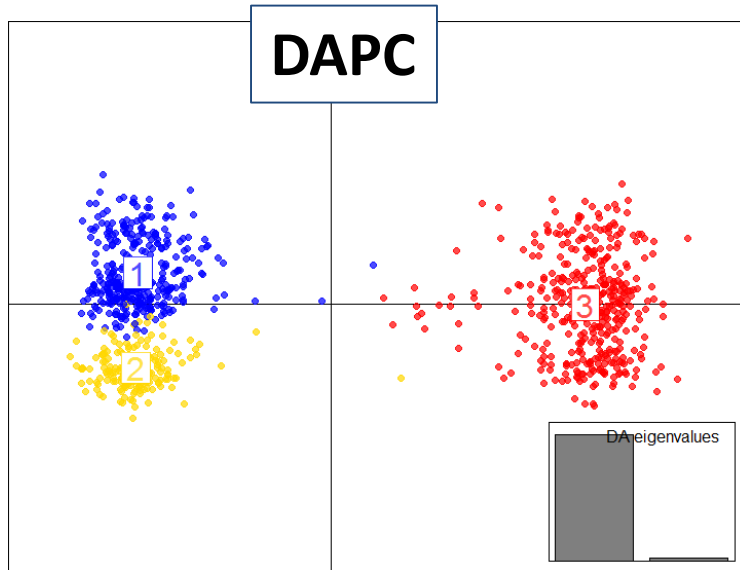
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Temporal Genetic Variation: 2012-2015

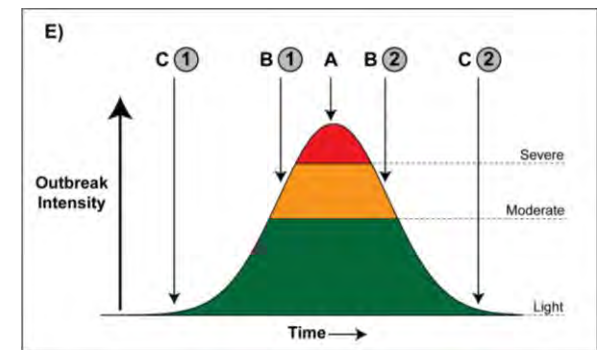
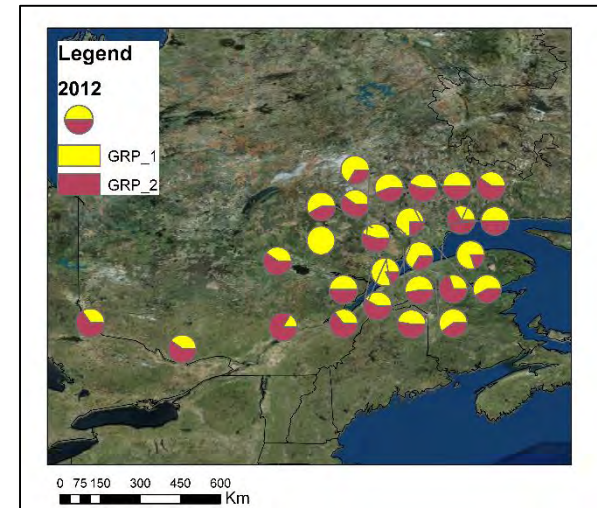


AMOVA

	Df	SumsOfSqs	MeanSqs	F	R2	Pr(>F)
YEAR	1	995	994.68	2.74	0.00246	0.001
SITE	43	19042	442.85	1.22	0.04712	0.001
YEAR : SITE	12	4984	415.3	1.14	0.01233	0.001
Residuals	1044	379115	363.14	0.94		
Total	1100	404136	1			

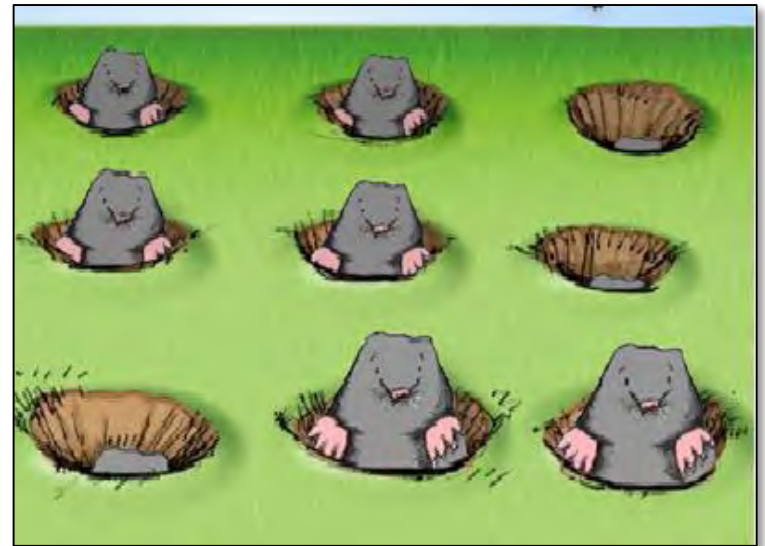
Interpretations

- Lack of strong spatial structure and IBD is confusing.
- Potential legacies of previous outbreak mixed with current epicentric outbreak?
- Results suggest that dispersal may be driving synchrony.
 - BUT It may also depend on timing!
 - Genetics **may** not be able to discern the details at this point in time.
 - Has the signature of epicentric dynamics already been lost ...?



Interpretations +

- H_0 = no connectivity among sites
 - (i.e., oscillatory hypothesis)
- H_1 = some sites are connected
 - (i.e., epicentre)



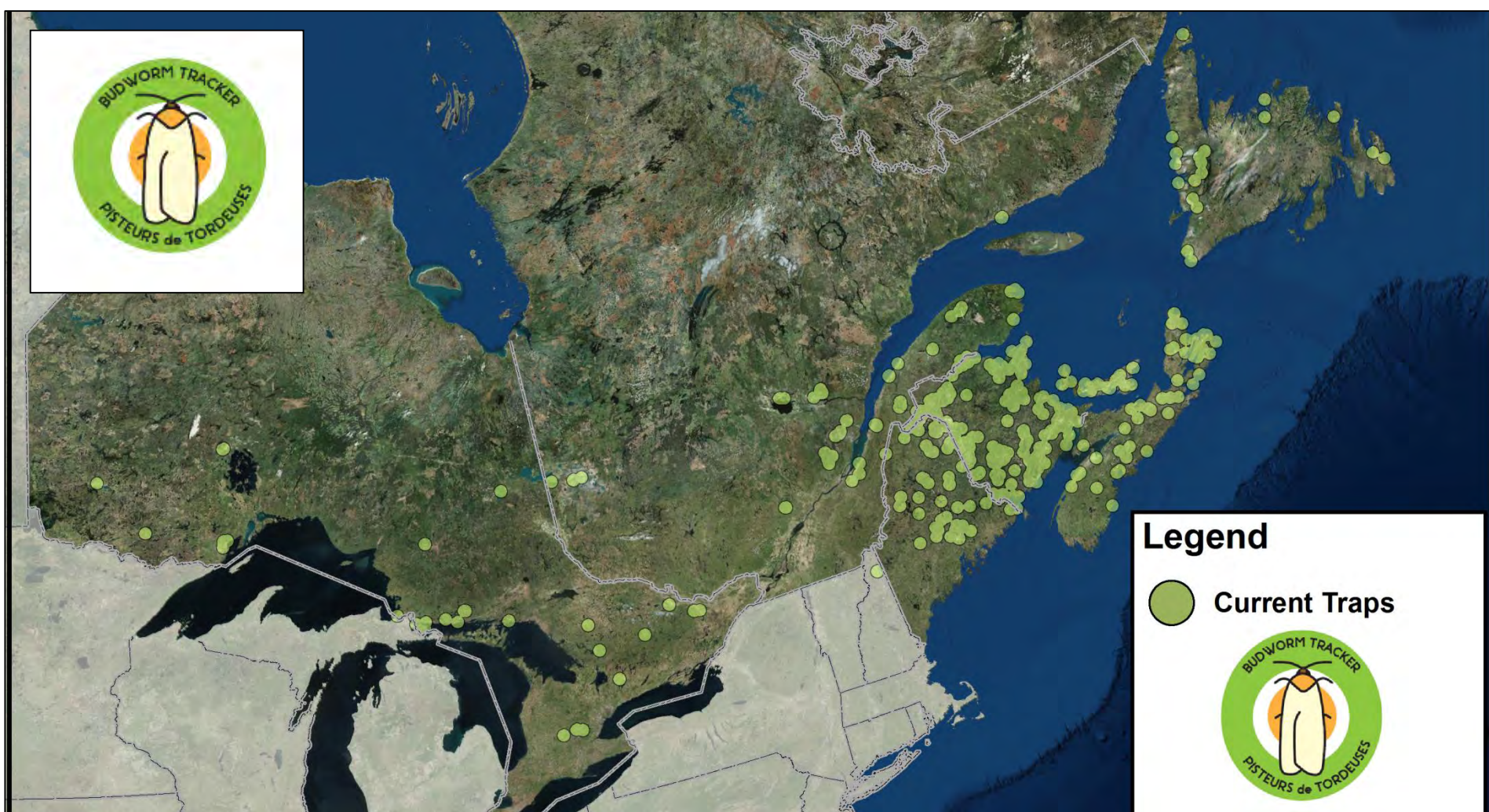
Next Steps

- **Analysis of moths : 2012-2016**
(n=~1500).
 - Budworm tracker moths
 - Focused analysis of moths not in local phenological synchrony (putative migrants).
 - **How does outbreak development affect our ability to distinguish residents from migrants?**



Jeremy Larroque, PDF





- From ~450 traps: 15,464 moths in 2016.
- 75% return rate (...more incoming).
- ~\$60 per kit (mailed out and samples returned).
- <http://budwormtracker.ca>

Next Steps

- Analysis of L2s from NB, N.S., and Nfld.
 - Are they independent populations, or are they functionally connected to the QC outbreak patch?
 - Paradox of low density populations...
 - ~~Difficult to extract high quality DNA~~

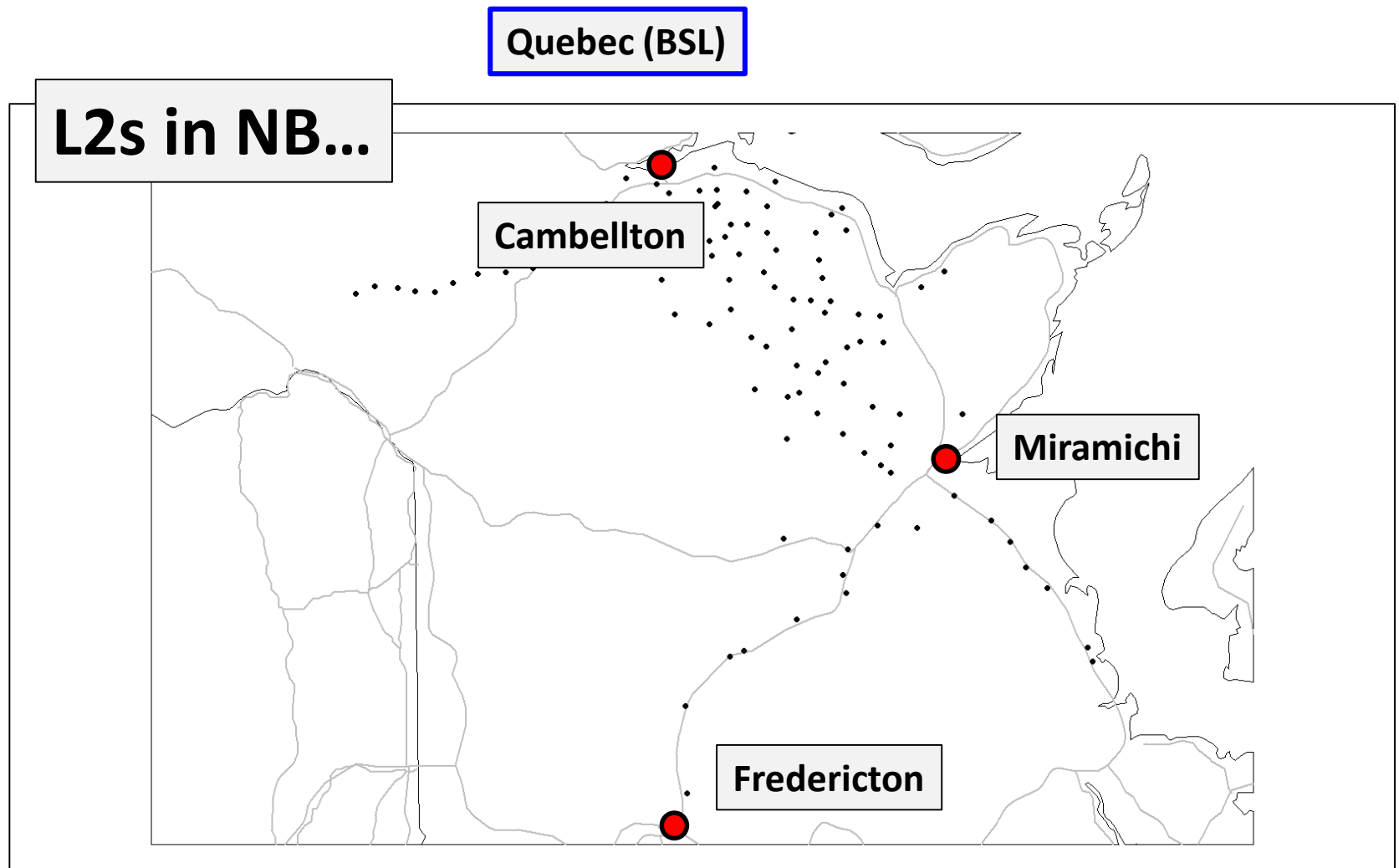


Jeremy Larroque, PDF



Simon Legault, PhD student

Next Steps



PERIODIC FLUCTUATIONS IN THE NUMBERS OF ANIMALS: THEIR CAUSES AND EFFECTS

By C. S. ELTON.

Dept. of Zoology and Comparative Anatomy, The University Museum, Oxford.

Elton CS, 1924. Journal of Experimental Biology.

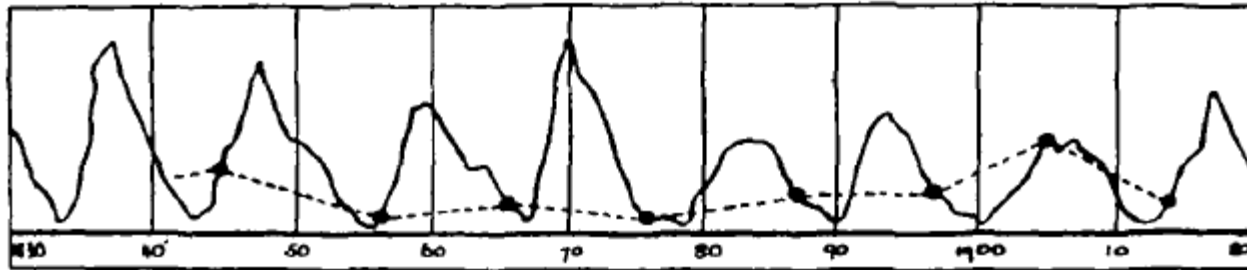


FIG 6.—Years of maxima of the Canadian rabbit (varying hare), from fig. 5, marked on the sunspot curve. (Latter from Huntington, 1923.)



If the whole population of thousands of individuals arises afresh from a few animals every eleven years, then the genotypic constitution of the species will tend to become comparatively pure.



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What are the consequences of periodic population dynamics on spatial genetic structure?

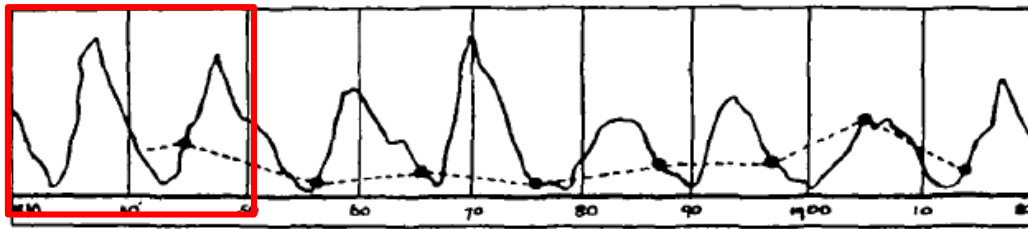
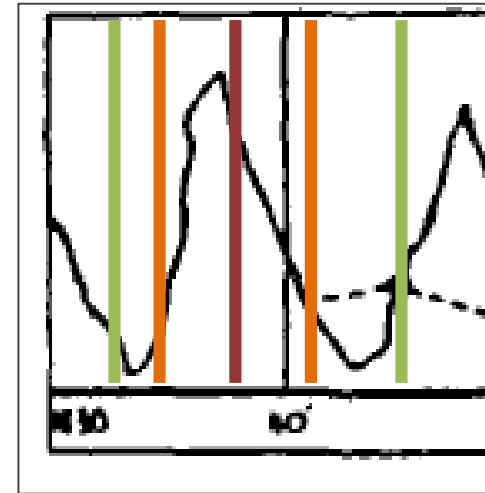


FIG 6.—Years of maxima of the Canadian rabbit (varying hare), from fig. 5, marked on the sunspot curve. (Latter from Huntington, 1923.)



Outbreak dynamics and genetic differentiation will also vary with landscape context, effective population size, and dispersal