Utiliser la génétique des populations afin de mieux comprendre les épidémies d'insectes forestiers

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Fonds de recherche
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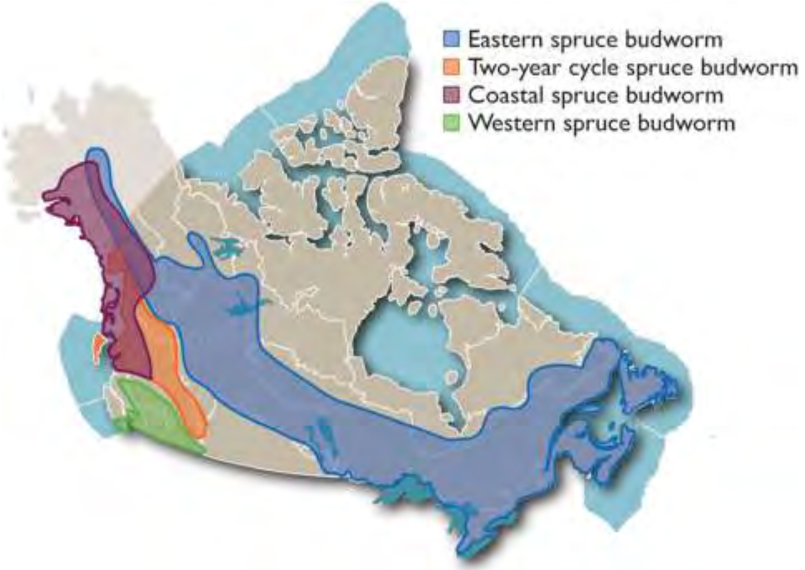
Spruce budworm (*Choristoneura fumiferana*)

- Native defoliator of fir (*Abies*) and spruce (*Picea*)
- Periodic outbreaks every ~35 years
- Broad geographic range
- Kills host trees after 5-6 years of severe defoliation
- Creates widespread patterns of tree mortality
- Population dynamics driven by complex spatial trophic interactions that include dispersal and interactions with climate and weather



Spatio-temporal dynamics of the SBW system

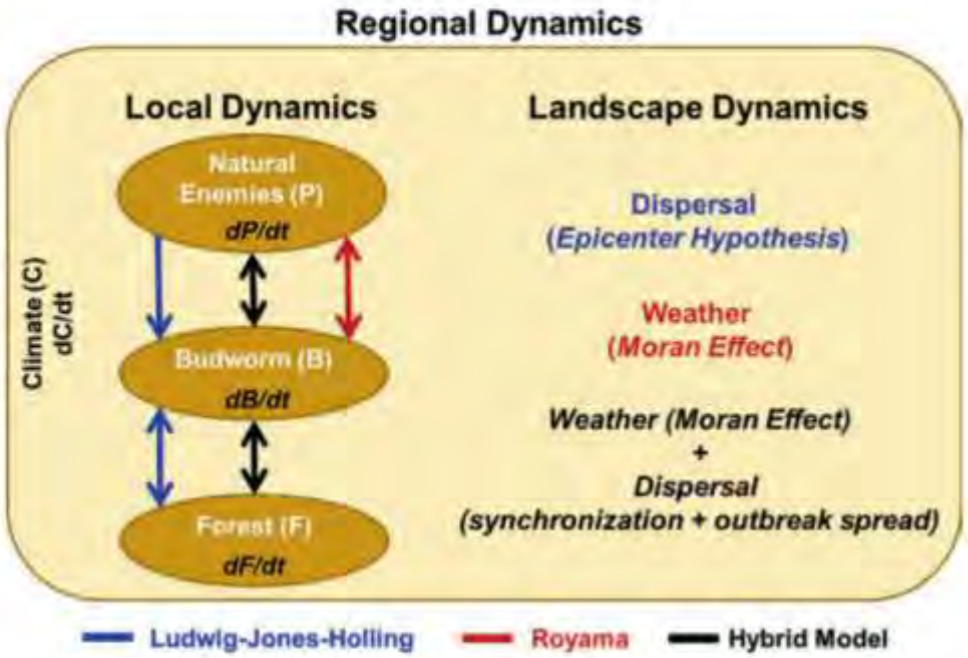


Fig. 5.8 Multiple equilibrium models championed by Holling and colleagues (Ludwig et al. 1978; *blue*) included predation; however, strong reciprocal feedback centers on the budworm–forest interaction. In contrast, the harmonic oscillation model championed by Royama (1992; *red*) emphasized strong reciprocal feedback in the higher trophic levels, with budworm–forest interactions as a secondary consideration. A modern synthesis (*black*) would consider both levels jointly, including the potential for eruptive and cyclic behavior, as well as the broader-scale context of climate

Sturtevant *et al.* 2015.

Non-Trivial Economic Consequences

3.6M
hectares of defoliation in 1975 outbreak

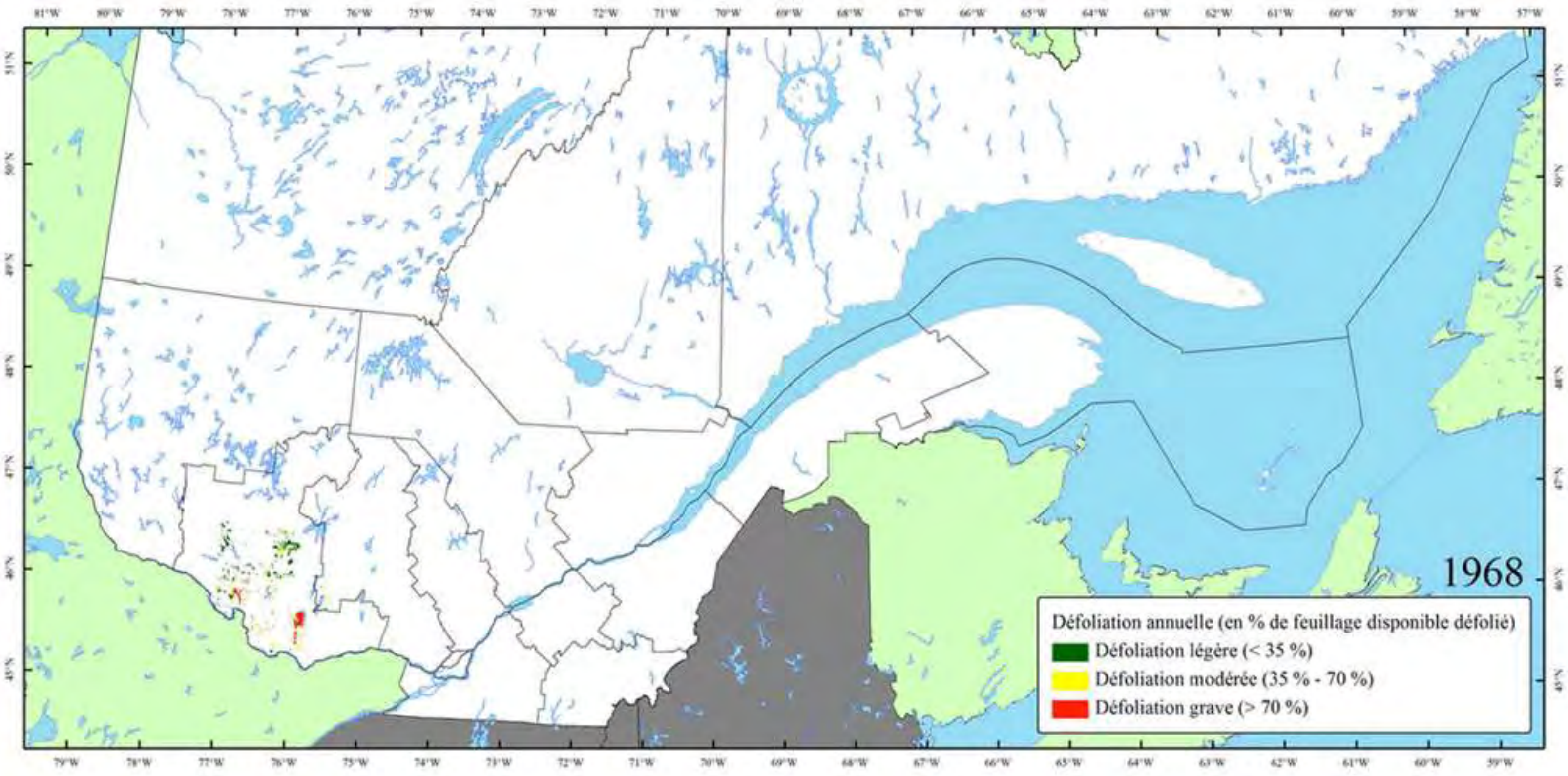
\$4.7B-\$6.7B
potential losses to the NB economy over 40 years

1,500-1,900
person year decrease in jobs, yearly for 30 years

1M-1.4M m^3
yearly decrease in NB wood supply for 40 years

Healthy Forest Partnership

- Same scale of results expected in Quebec over the next 30 years (Chang et al 2012)

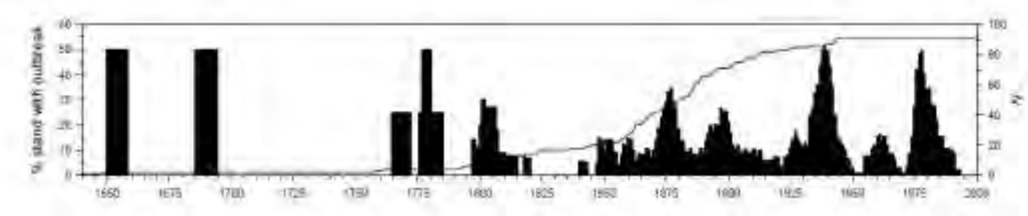


2017 : 7 x 10^6 ha. affected

https://www.reddit.com/r/MapPorn/comments/4sox8e/gif_animated_map_of_southern_quebec_canada/

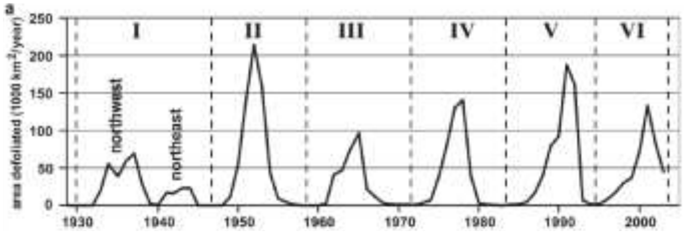
Population cycles are a regular phenomenon in forest insects (Berryman 1996, Myers and Cory 2013)

- **Mountain pine beetle** (*Dendroctonus ponderosae)*



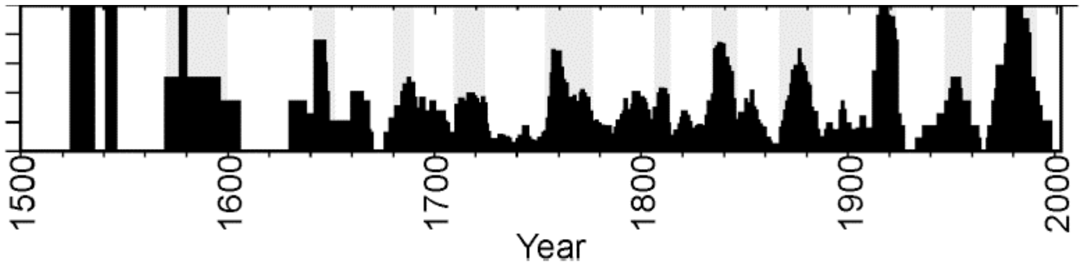
Alfaro et al 2009

- **Forest tent caterpillar** (*Malacasoma disstri*)

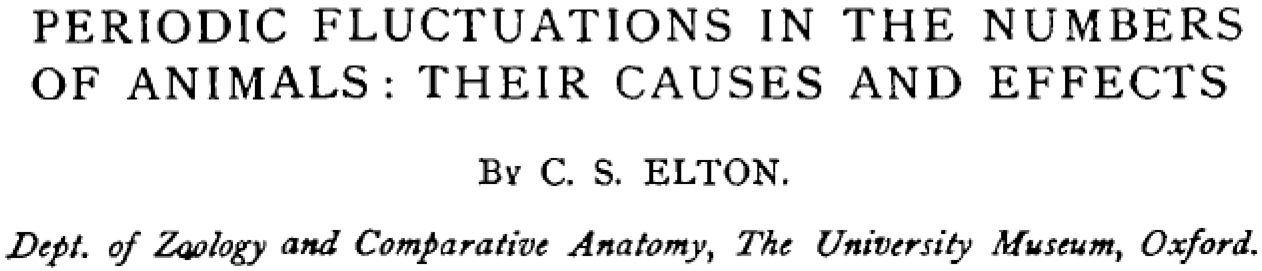


Cooke & Roland 2007

- **Spruce budworm** (*Choristoneura fumiferana*)



Boulanger & Arsenault 2004



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.

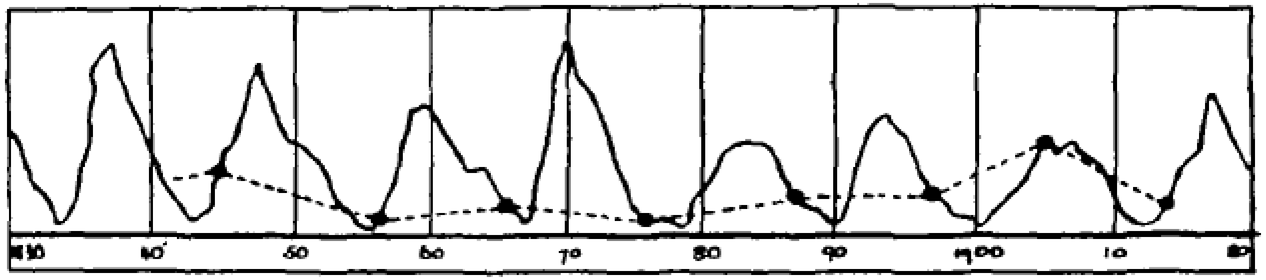
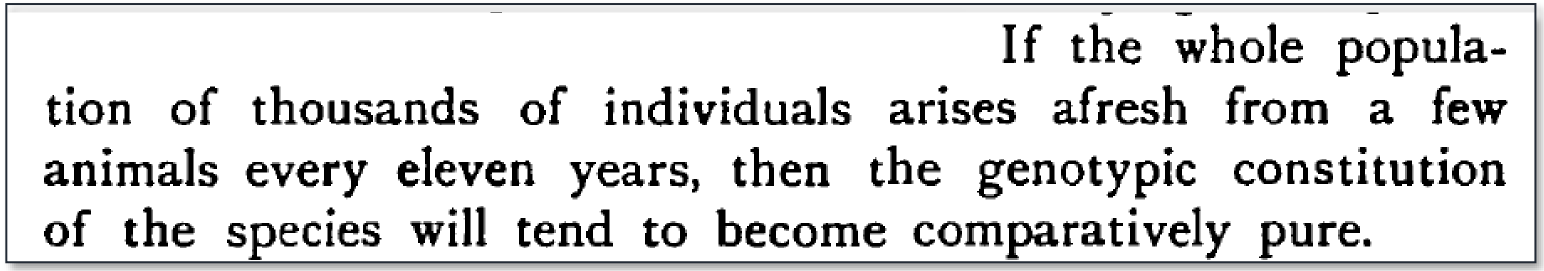


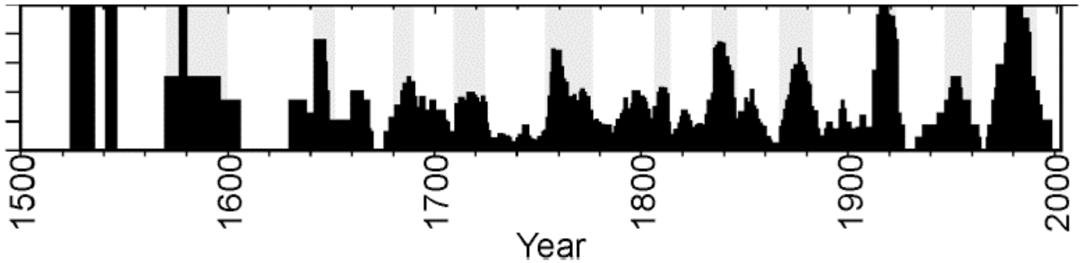
FIG 6.—Years of maxima of the Canadian rabbit (varying hare), from fig. 5, marked on the sunspot curve. (Latter from Huntington, 1923.)



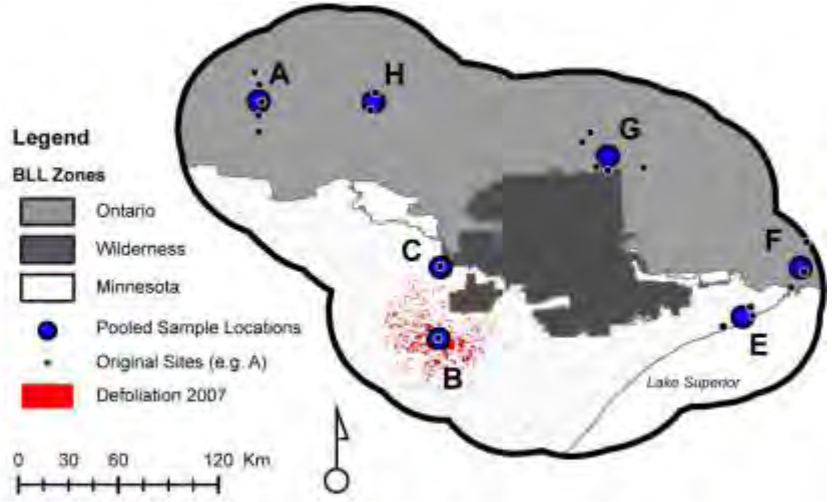
If the whole population of thousands of individuals arises afresh from a few animals every eleven years, then the genotypic constitution of the species will tend to become comparatively pure.

p. 159

What is driving spatially synchronous outbreaks in cyclic irruptive forest insect systems?



SBW Spatial Connectivity



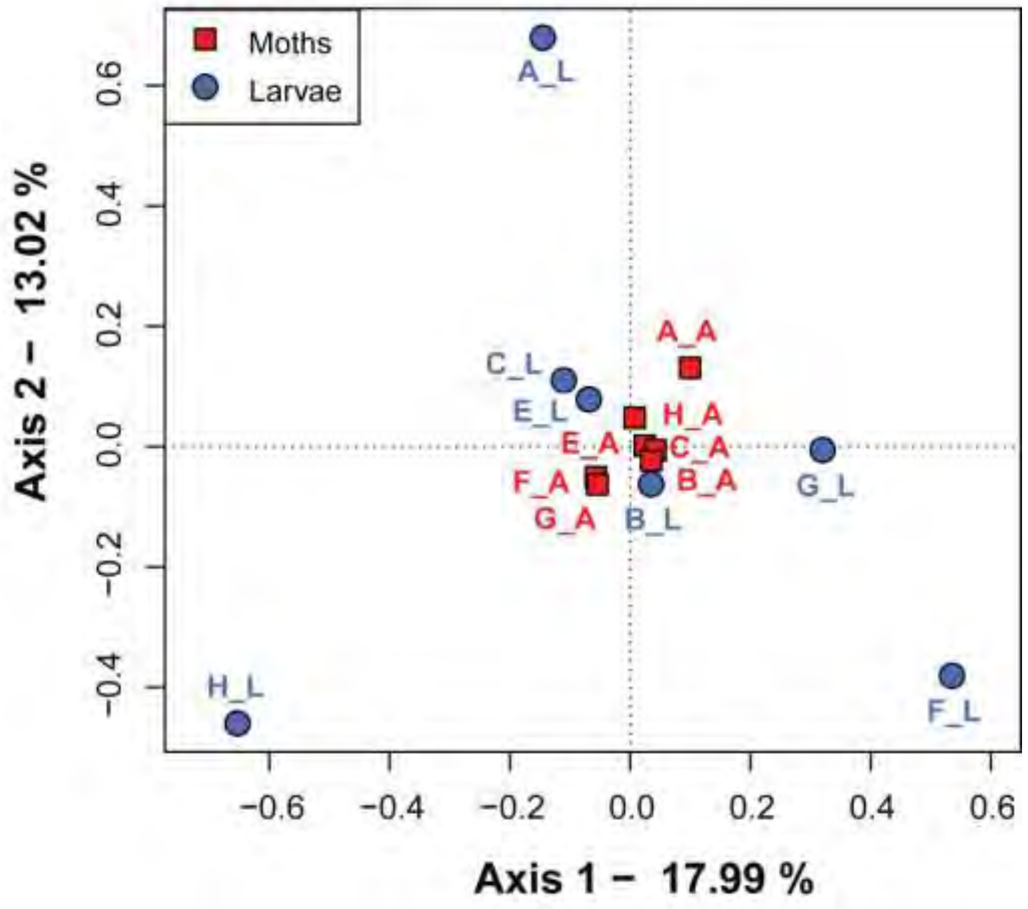
James et al. 2015 - Molecular Ecology

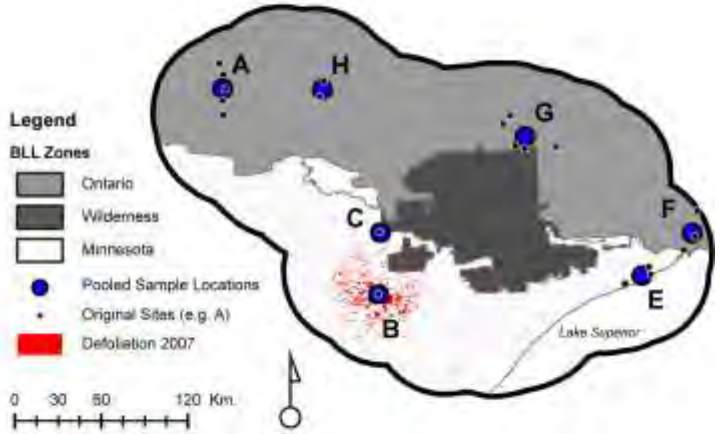
- 231 individuals (moths and larvae)
- 16 microsatellite loci; 7 sites
- **1 ongoing outbreak**
- Larvae collected and reared to moths (« residents »).
- Moths captured from pheromone traps (« possible migrants »).
- **Are residents and migrants genetically similar?**
- **What is the role of dispersal?**

Brian Sturtevant; USFS

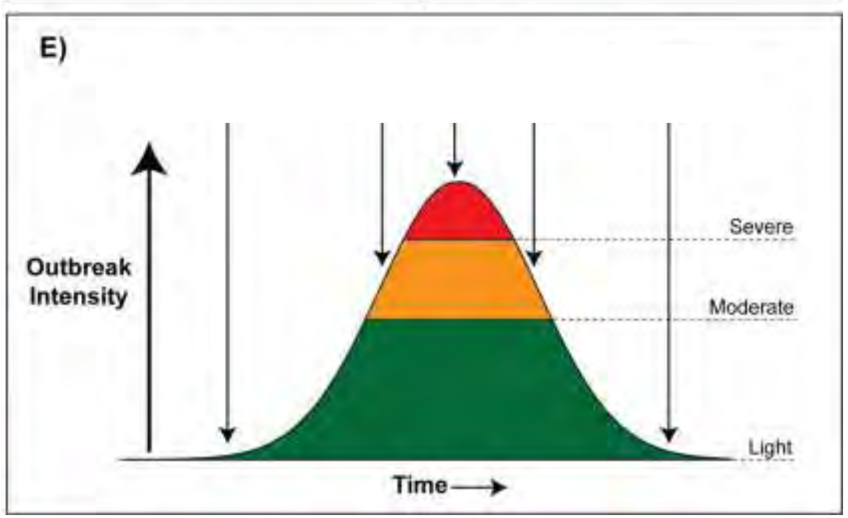
SBW Spatial Connectivity

PCoA - *Fst*





Ecological context influences what spatial genetic patterns we can detect

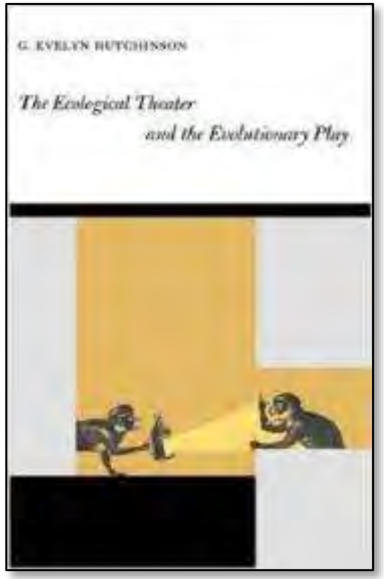


So what?

- When trying to understand **SGS** in systems with complex population dynamics, ecological context and scale are going to influence your inference.
- With cyclic irruptive populations, **the ecological theatre changes.**
- Functional connectivity is dynamic over the course of an outbreak.
- Non-stationary population dynamics (in **space*** and **time***) requires new approaches.

*** Habitat suitability**

*** Outbreak status**



G. EVELYN HUTCHINSON

The Ecological Theater and the Evolutionary Play

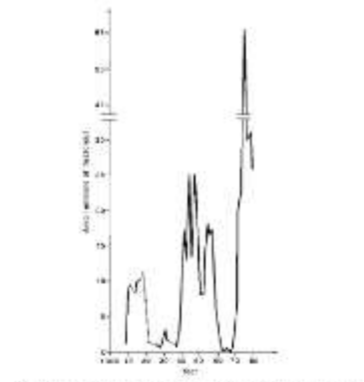


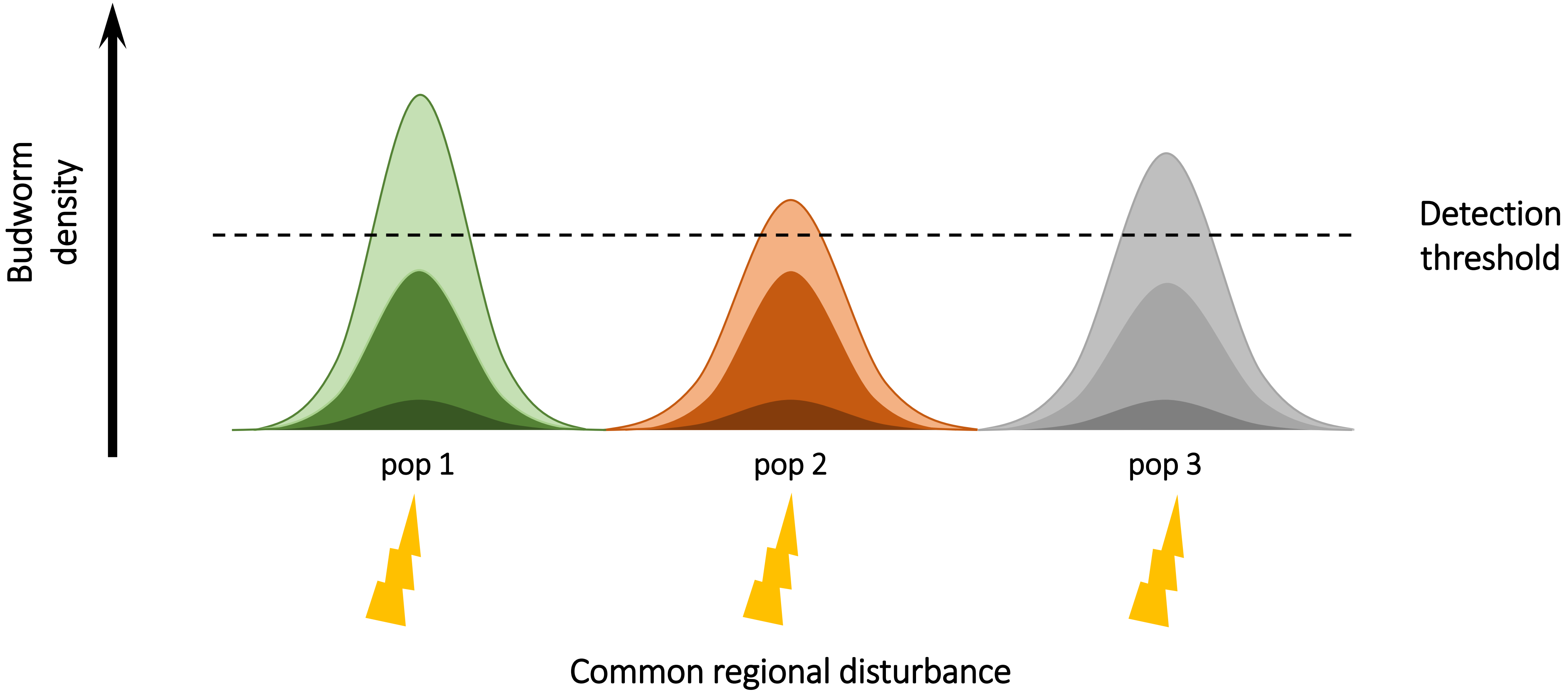
Fig. 2. The area moderately or severely infested by the spruce budworm 1909–1959.

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

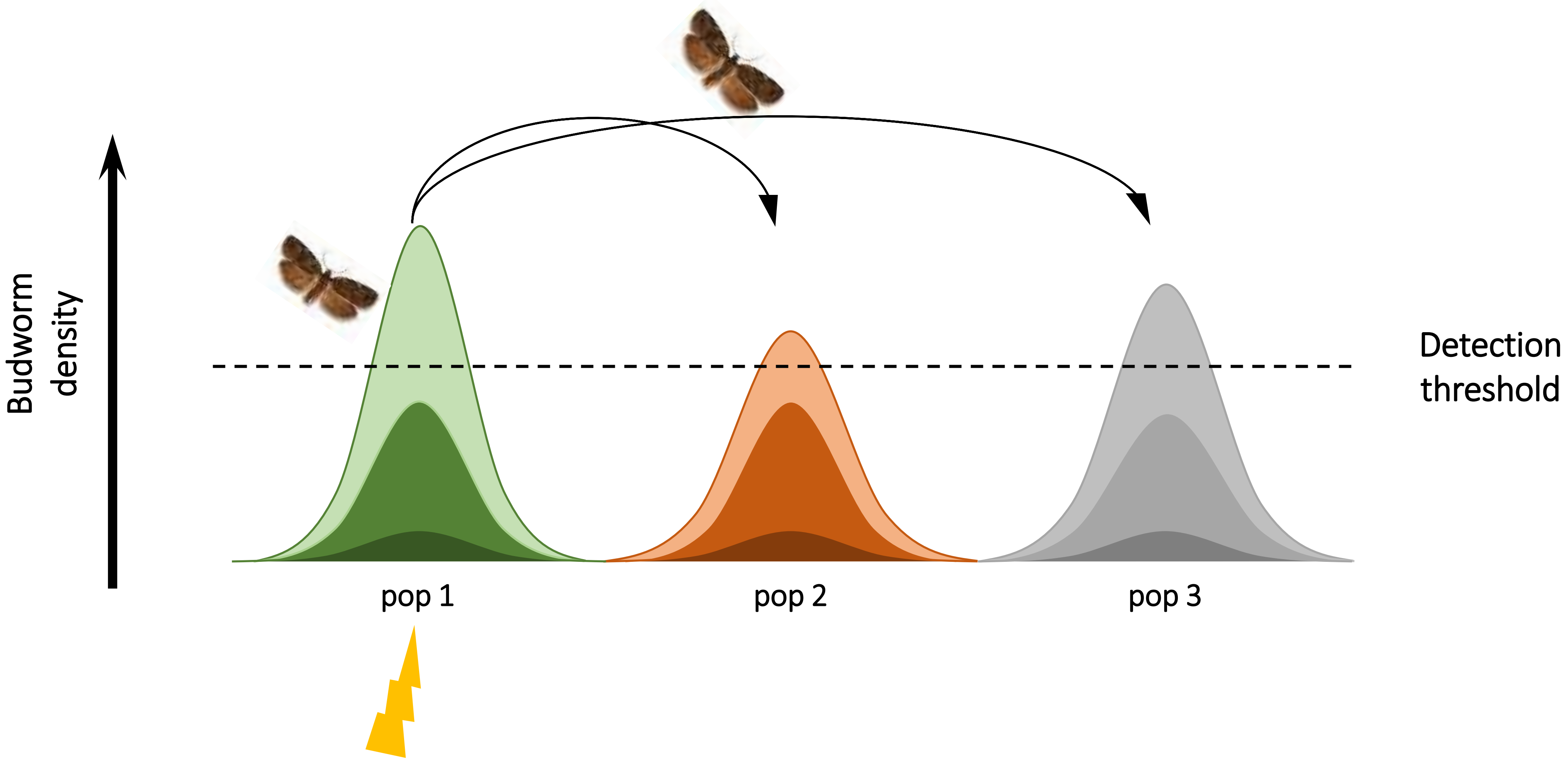
What drives synchronous outbreak dynamics?

- **Two** (*main*) **hypotheses**:
  1. **Oscillatory hypothesis** (weather; The "Moran effect")
  2. **Epicentre Hypothesis** (dispersal)
- Distinguishing between these two possibilities has consequences for how we approach management of outbreaks.

Oscillatory hypothesis (Moran effect)

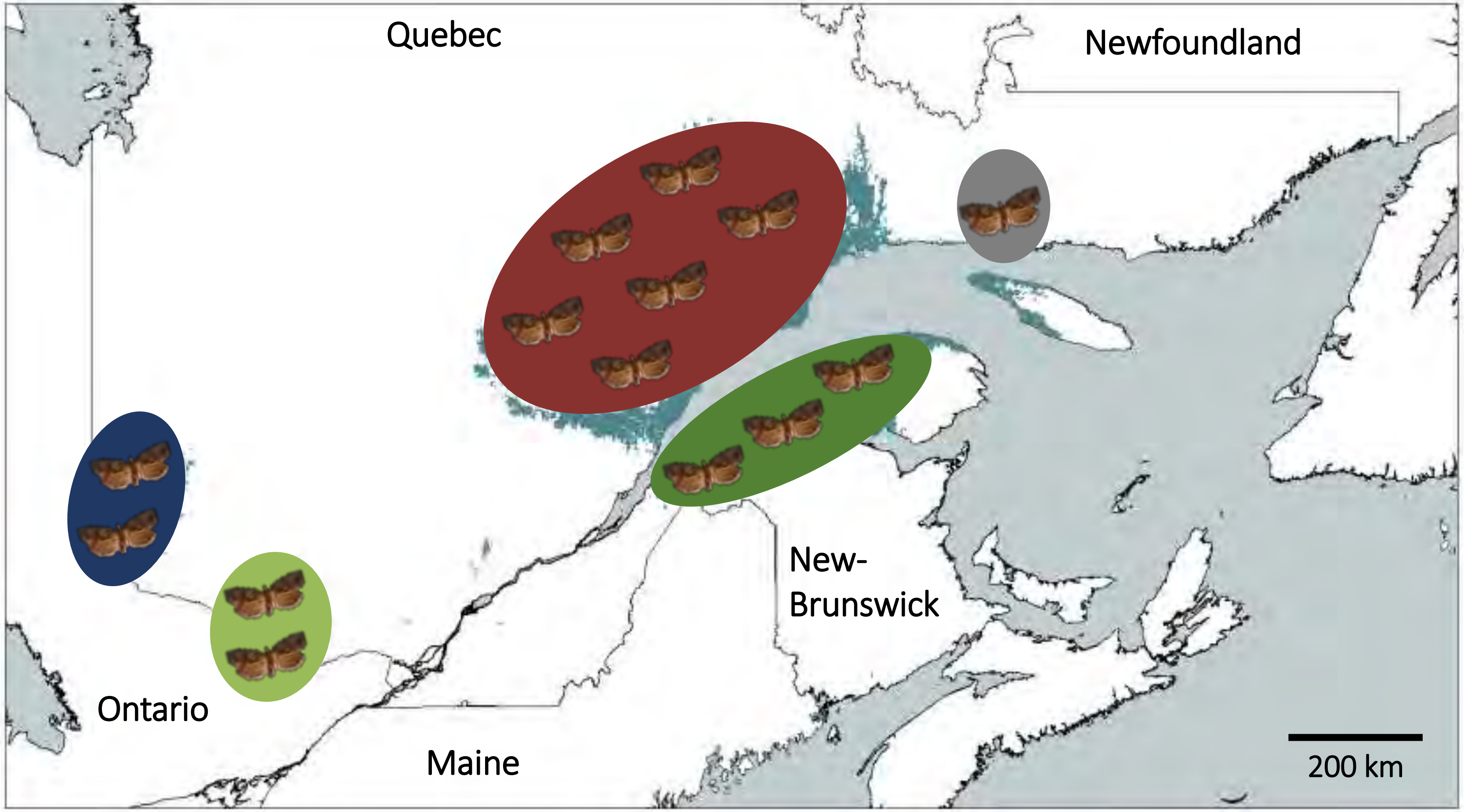


Epicenter hypothesis (*i.e.*, dispersal)



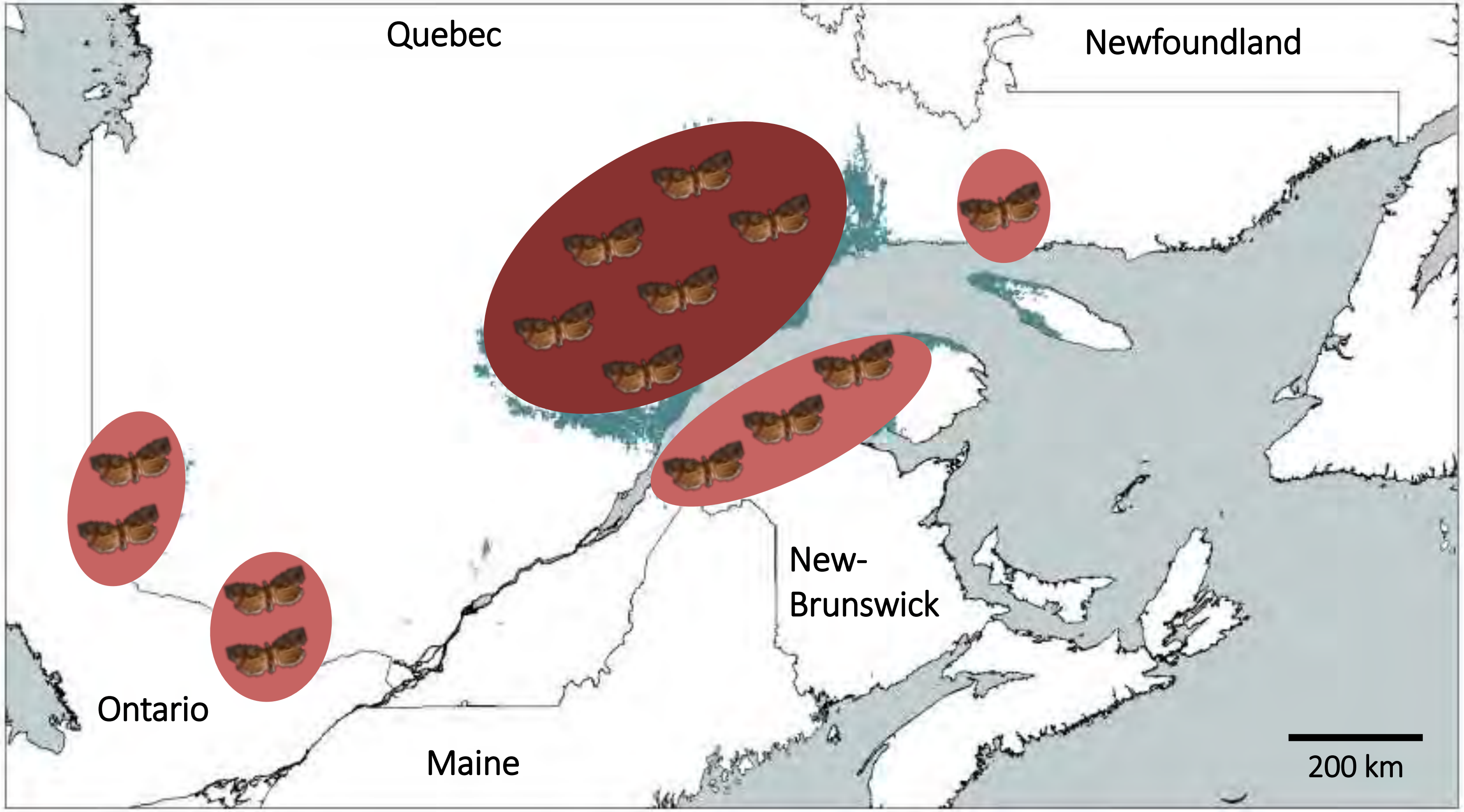
Common regional disturbance

Oscillatory hypothesis (Moran effect)



↳ Demographically independent populations

Epicenter hypothesis (*i.e.*, dispersal)

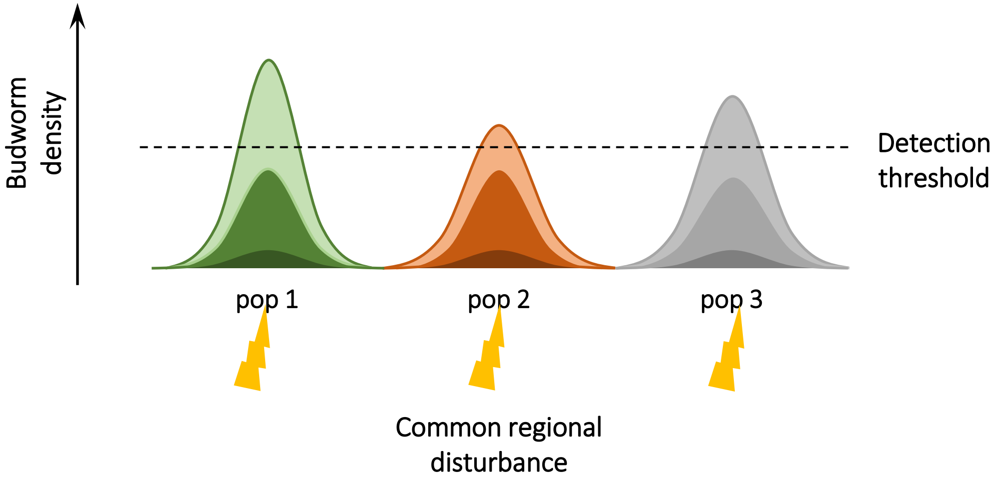


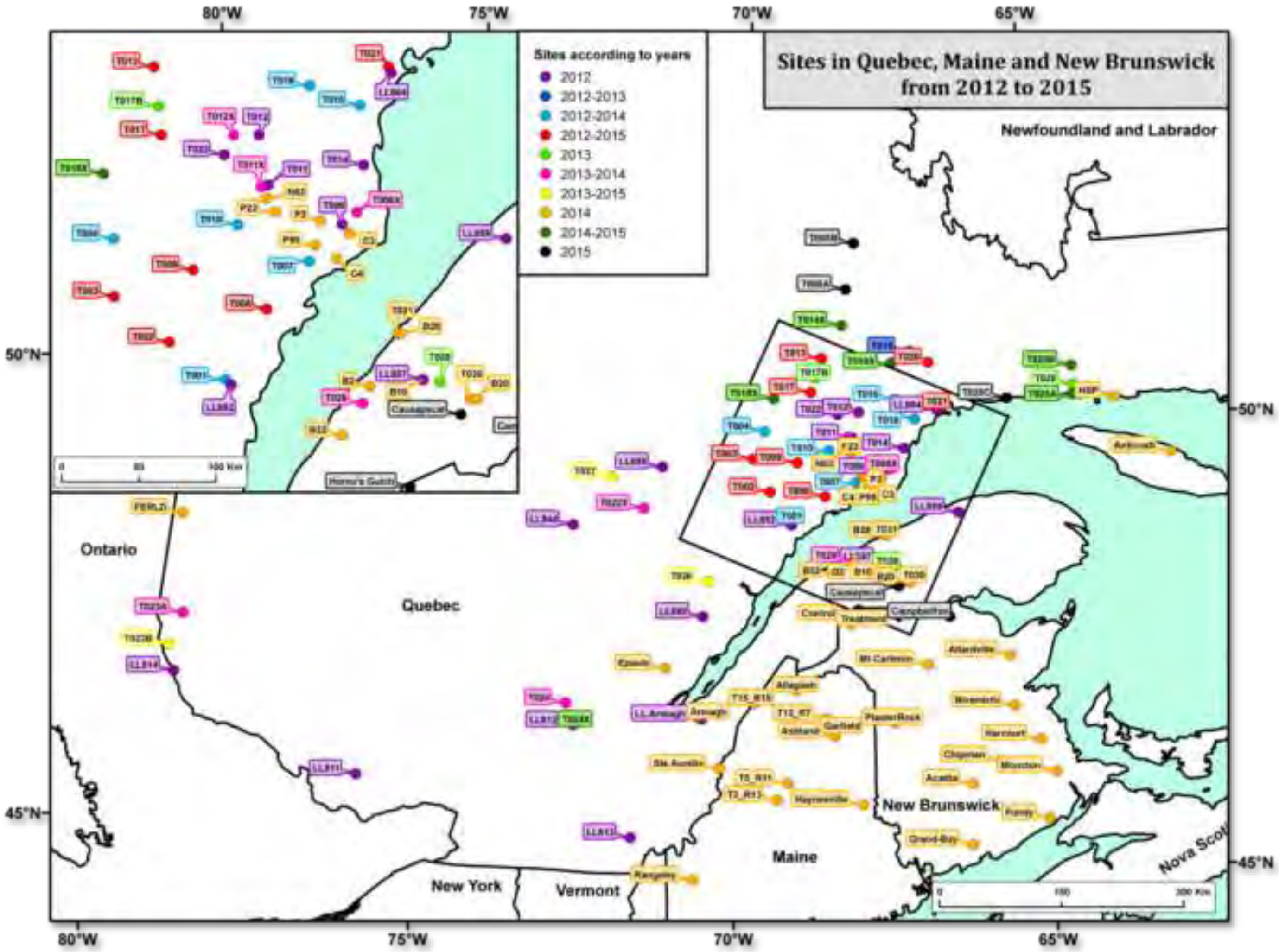
↳ Demographically connected populations

Research Objectives

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

Jeremy Larroque





[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.

Year	n_{site}	n_{ind}
2012	27	527
2013	14	420
2014	17	260
2015	10	163

↳ 1370 larval individuals

↓ Genotyping (GBS)

188 908 SNPs

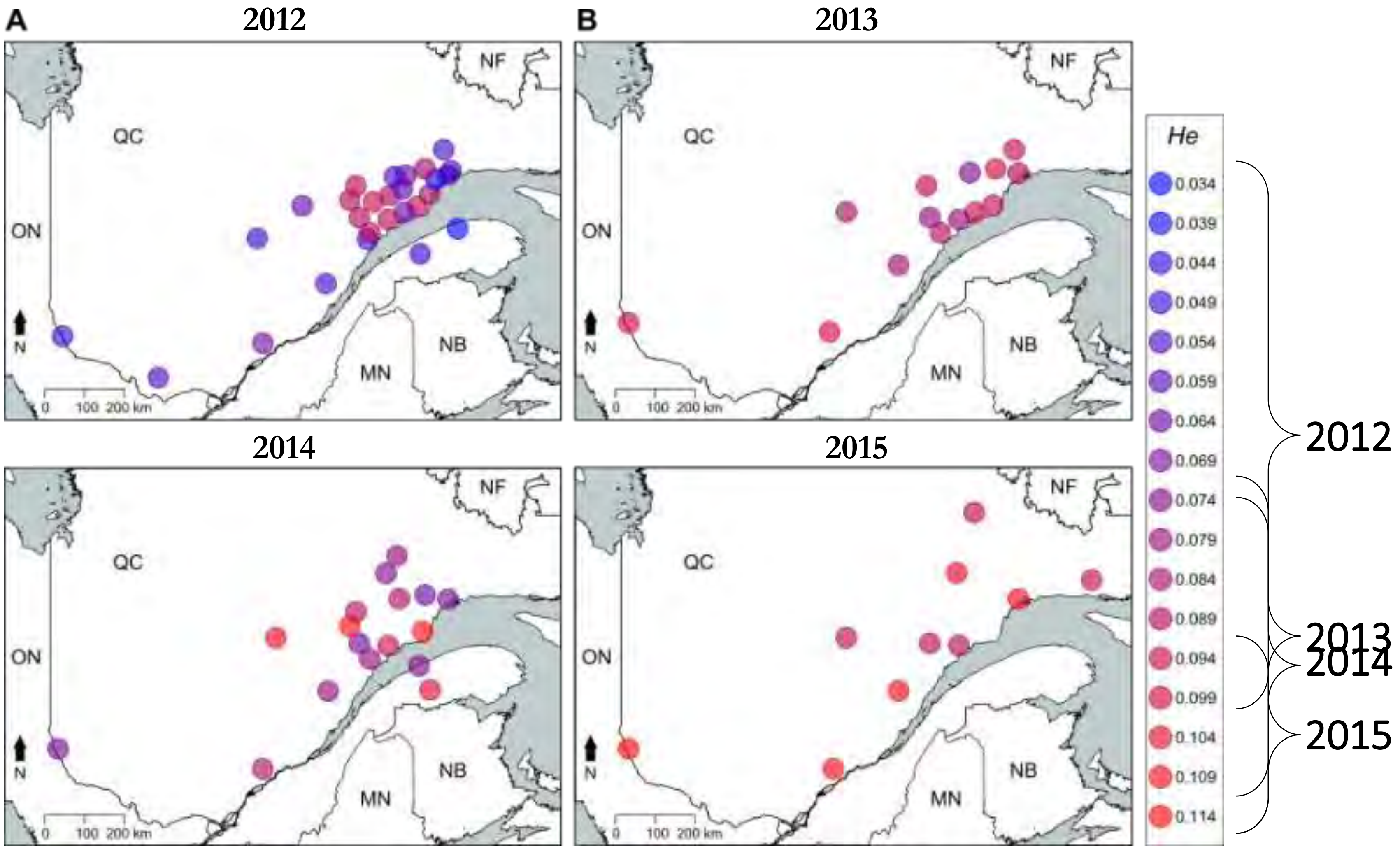
↓ Filtering (MAF, LD, HWE, Selection)

23 577 SNPs

AMOVA: site x year ($F_{25, 1302} = 1.208$, $p < 10^{-3}$)

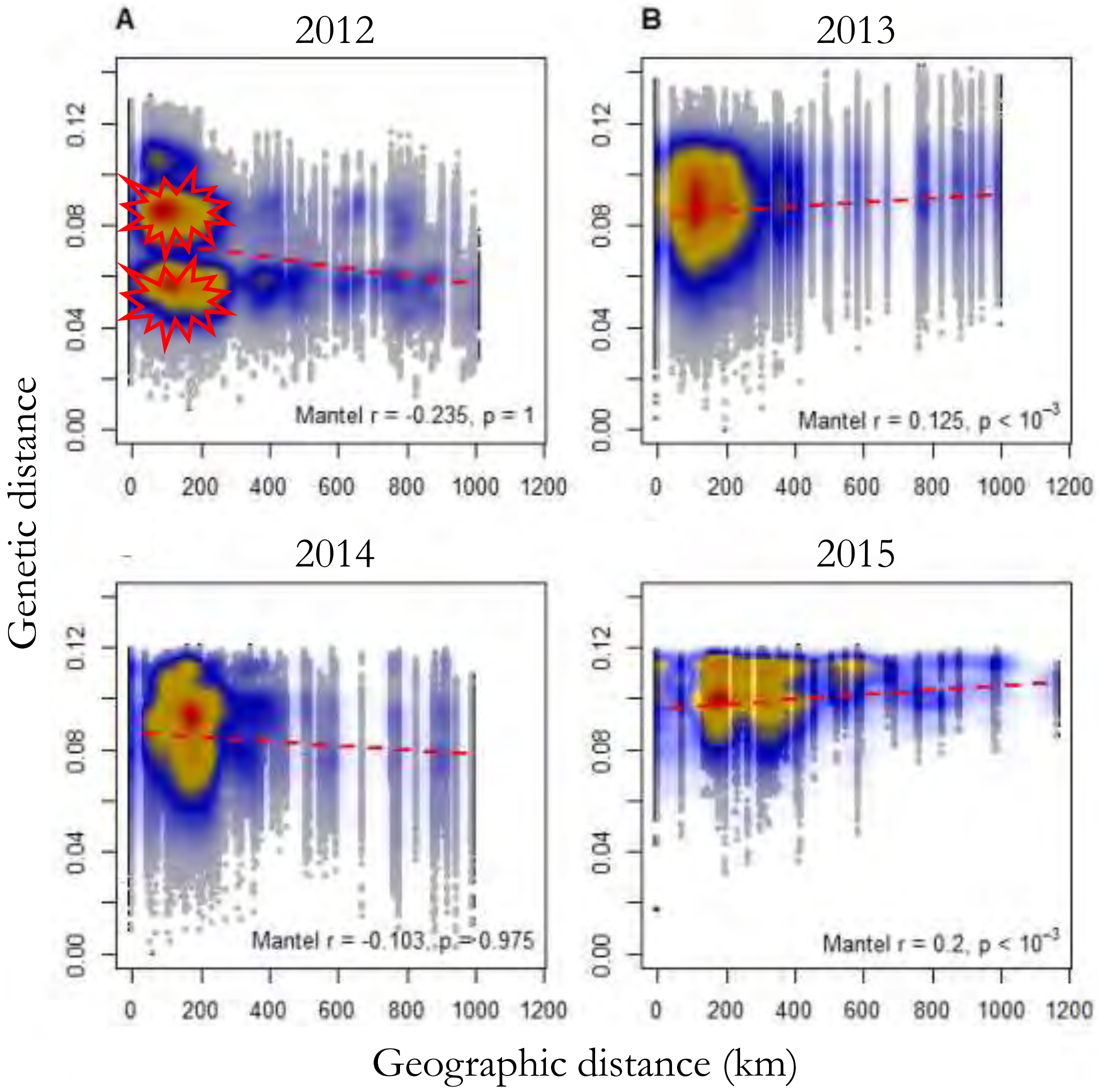
↳ Analyses for each year separately

Heterozygosity



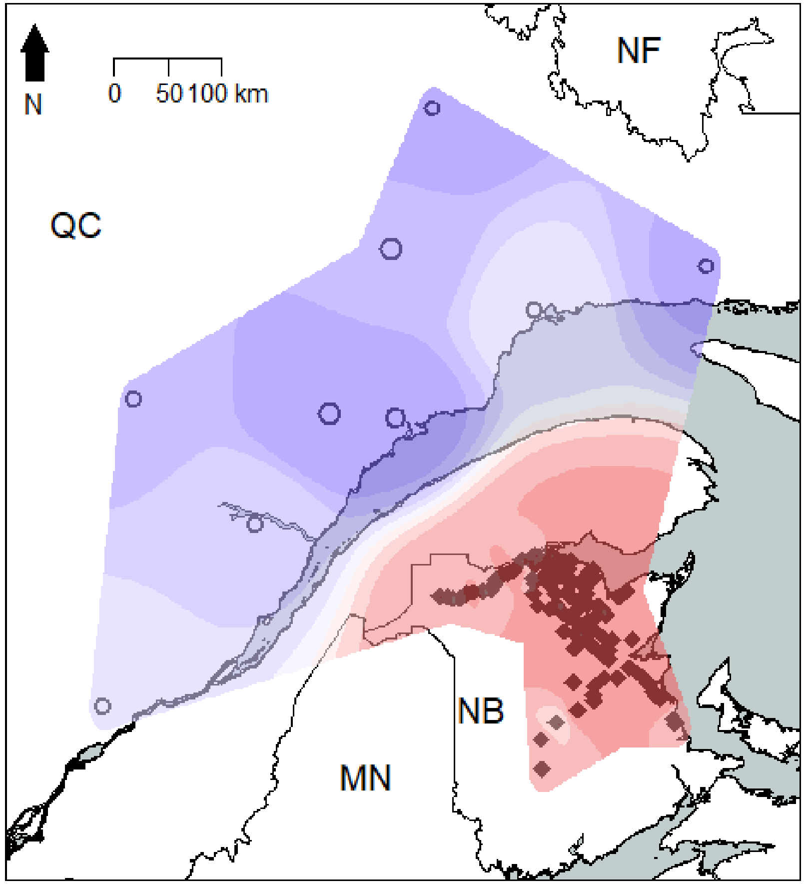
↳ Fast genetic homogenization = high rate of dispersal

Isolation By Distance & Clustering



- 2012 : Two clusters of individuals with the same level of genetic differentiation
  - 2 genetic groups
- 2013, 2014, 2015 : One cluster – 1 group
  - Fast genetic homogenization = high rate of dispersal
- Clusters supported by DAPC

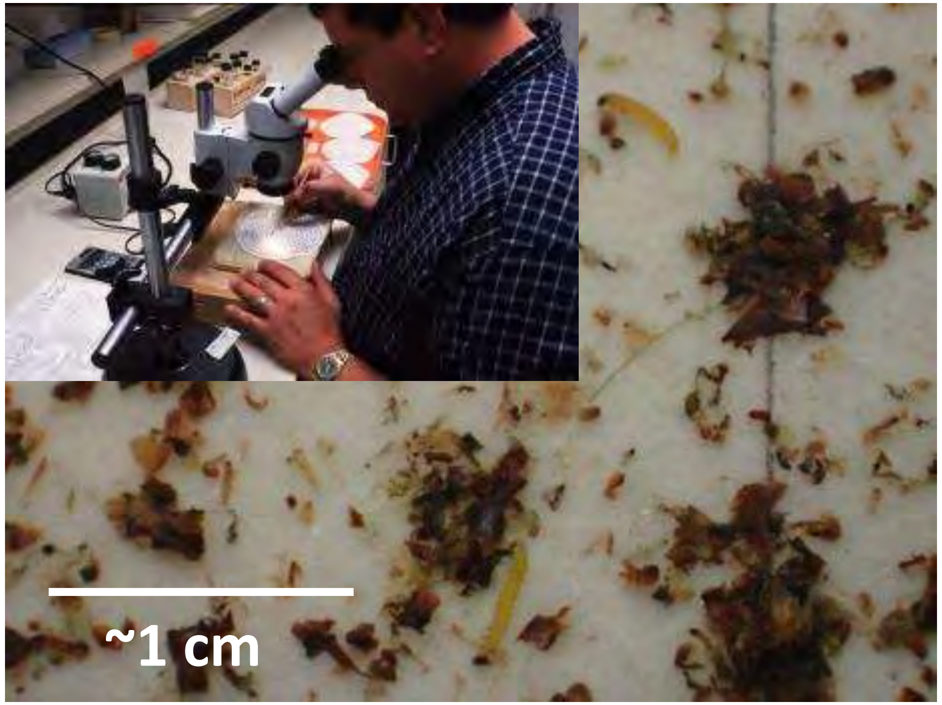
NB – not yet attacked reference zone



sPCA

- Population in QC is now synchronized.
- Difficult to detect legacies of previous outbreak collapse - was 2012 early enough?
- Opportunities (and challenges) remain to examine and protect areas not yet affected – e.g., ON, NB, ME
- Initial results (NB; 2014) indicate important differences in genetic structure between regions

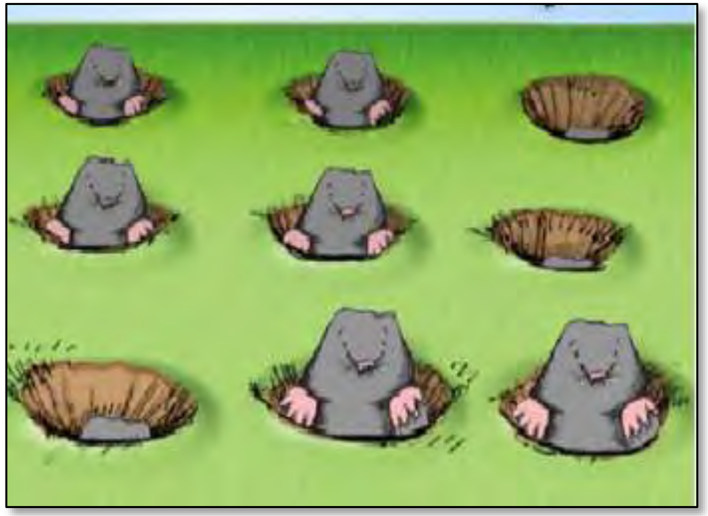
Second Instar Larvae (L2)



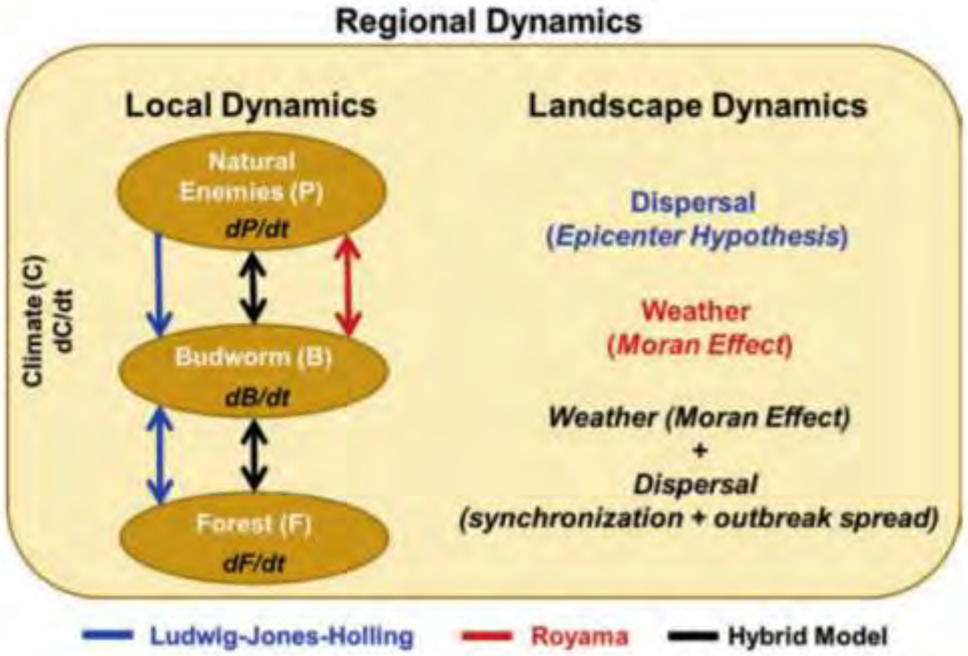
Too many moths

Application

- H0 = no connectivity among sites
  - (Only weather matters; Moran effect)
- H1 = some sites are connected
  - (Dispersal matters; Epicentre)



The Influence of Natural Enemies



Regional Dynamics

Local Dynamics

Landscape Dynamics

Natural Enemies (P)
dP/dt

Budworm (B)
dB/dt

Forest (F)
dF/dt

Climate (C)
dC/dt

Dispersal
(*Epicenter Hypothesis*)

Weather
(*Moran Effect*)

Weather (Moran Effect)
+
Dispersal
(synchronization + outbreak spread)

Ludwig-Jones-Holling

Royama

Hybrid Model

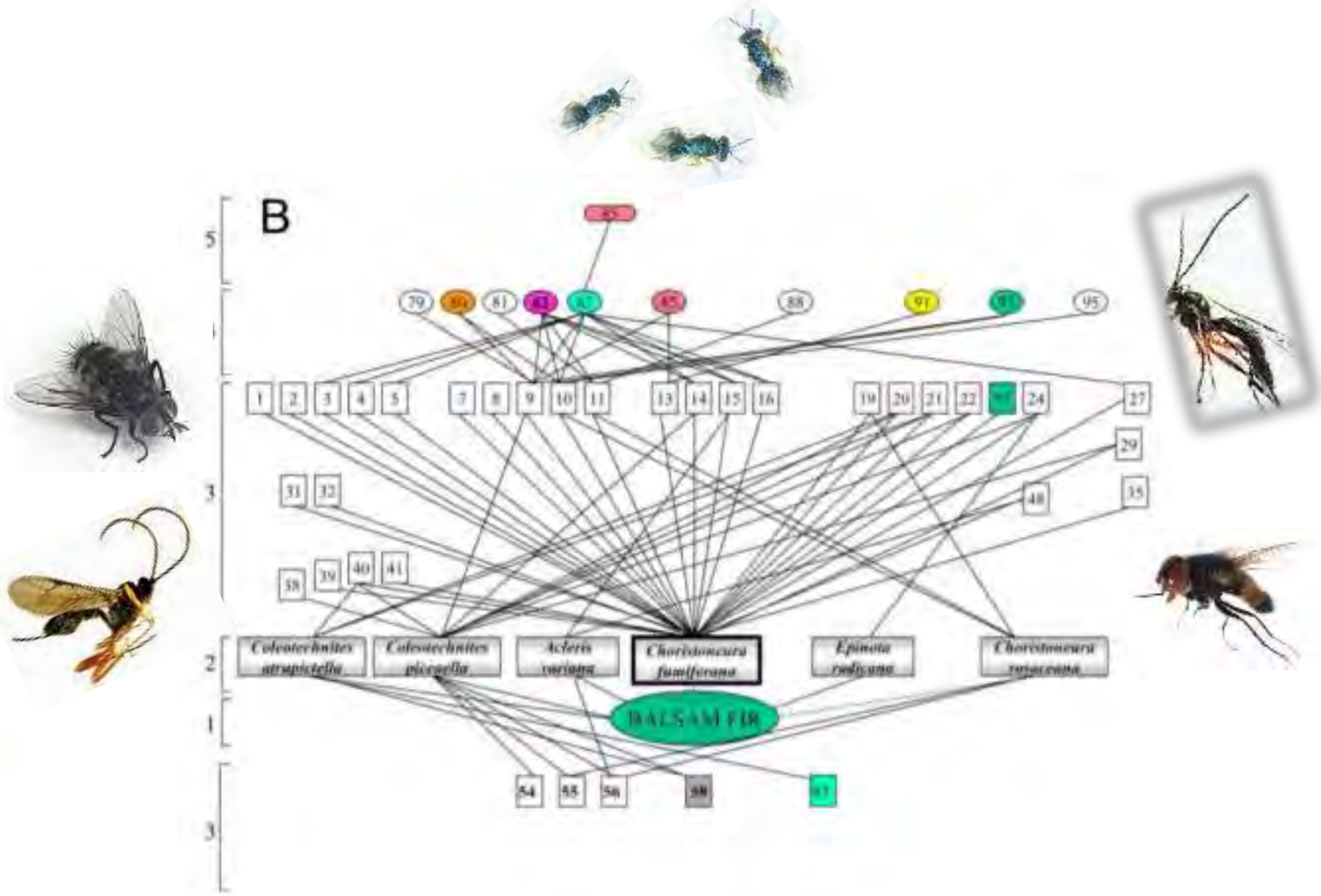


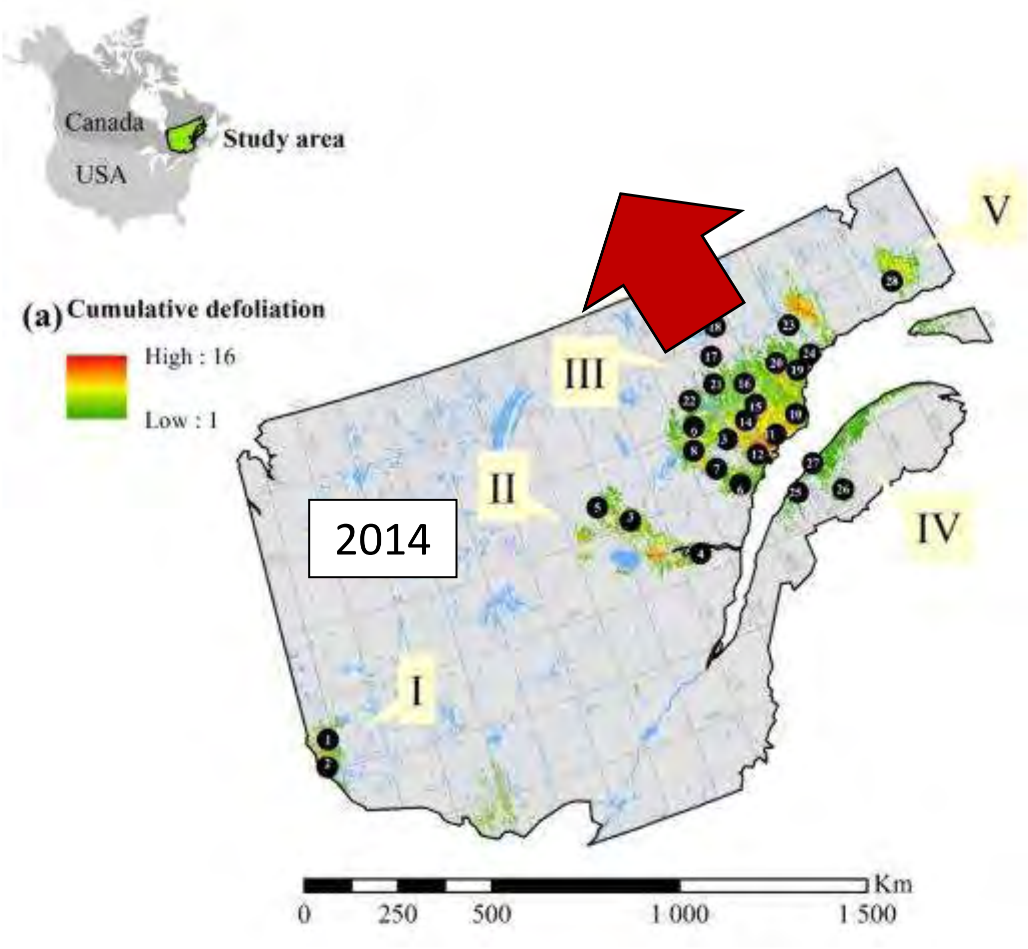
Fig 1. Eveleigh et al, 2007

The Influence of Natural Enemies

- Prey switching by mobile parasitoid natural enemies is another potential synchronizing / stabilizing mechanism
- Little is known about the spatial ecology of parasitoids (Cronin and Reeve 2005)
- **Questions**:
    - What is the spatial scale of genetic structure in two species of hymenopteran parasitoid? (DISPERSAL)
    - How does it compare to that of the SBW?
    - Can we detect a signature of expansion?

Simon Legault

Spatial Patterns in Parasitism



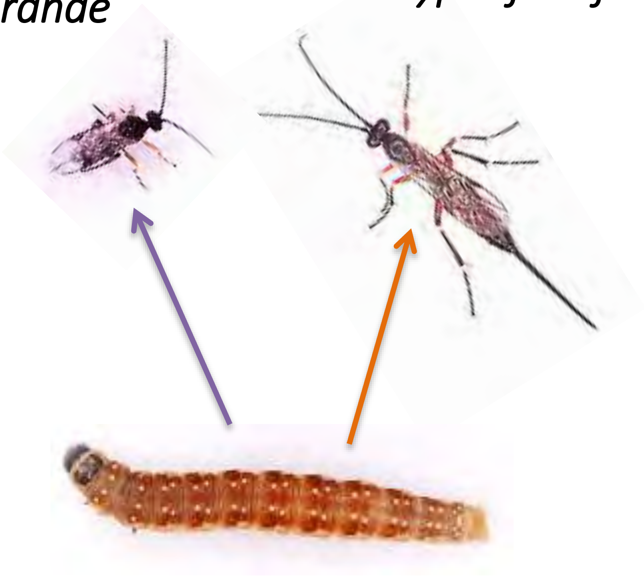
2014

6.2 %

Apanteles fumiferanae

7.3 %

Glypta fumiferanae

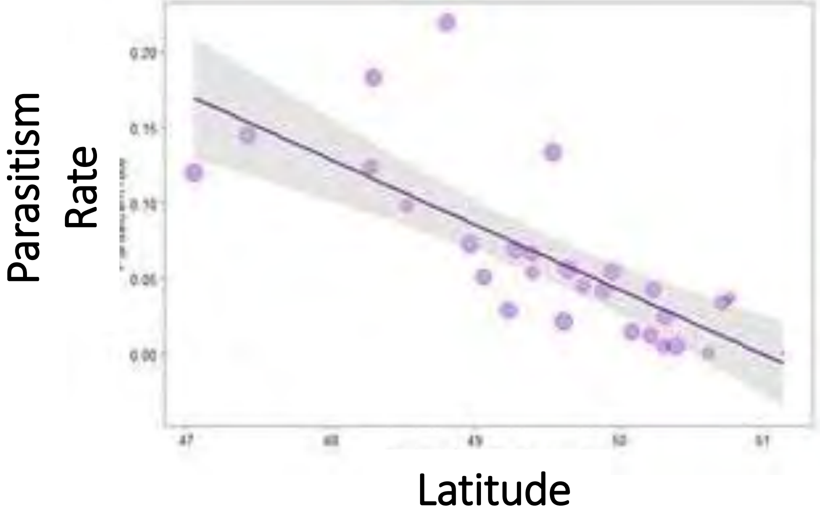


N = 5300

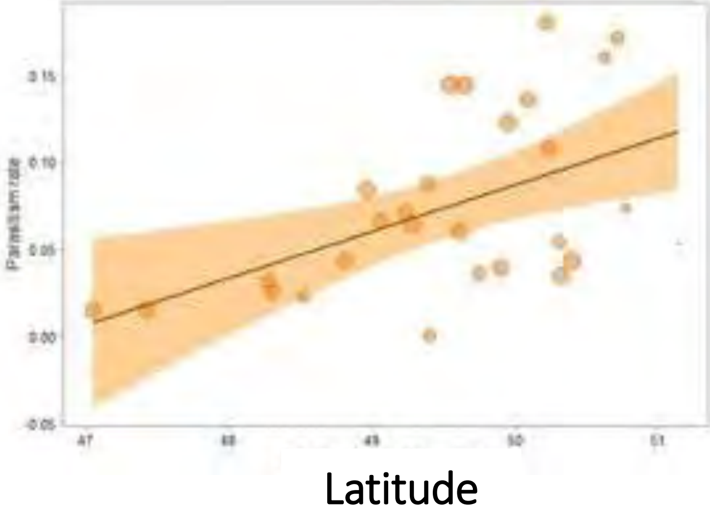
(≈265/site)

Latitudinal gradients in parasitism

Apanteles fumiferanae

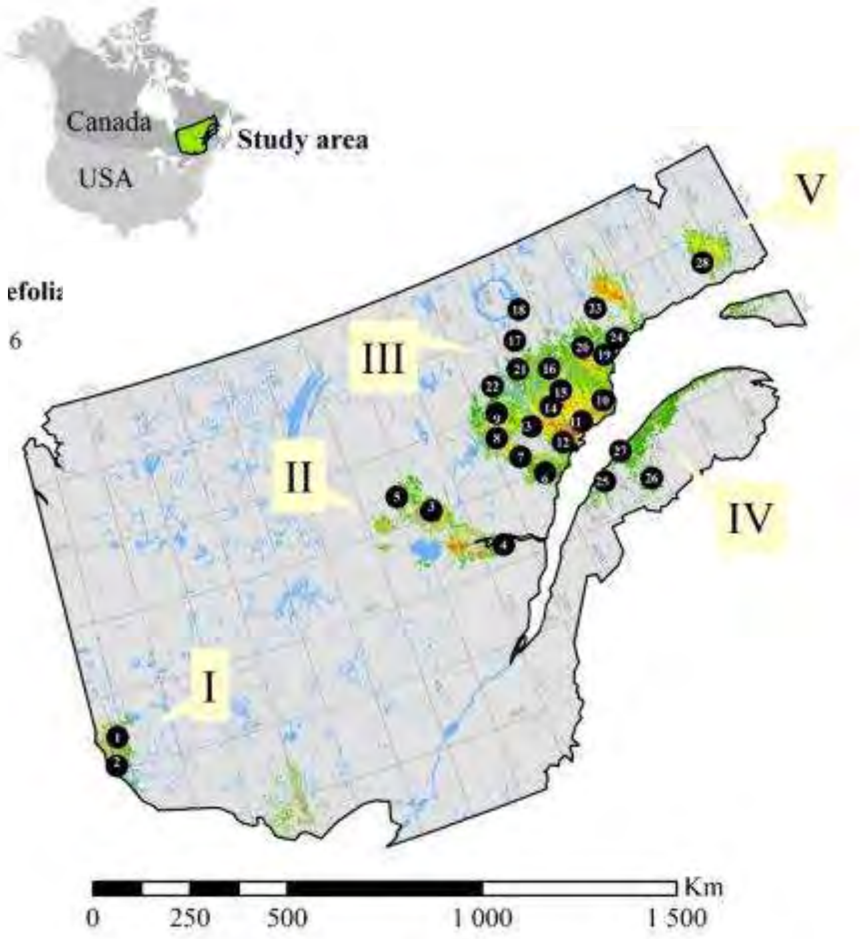


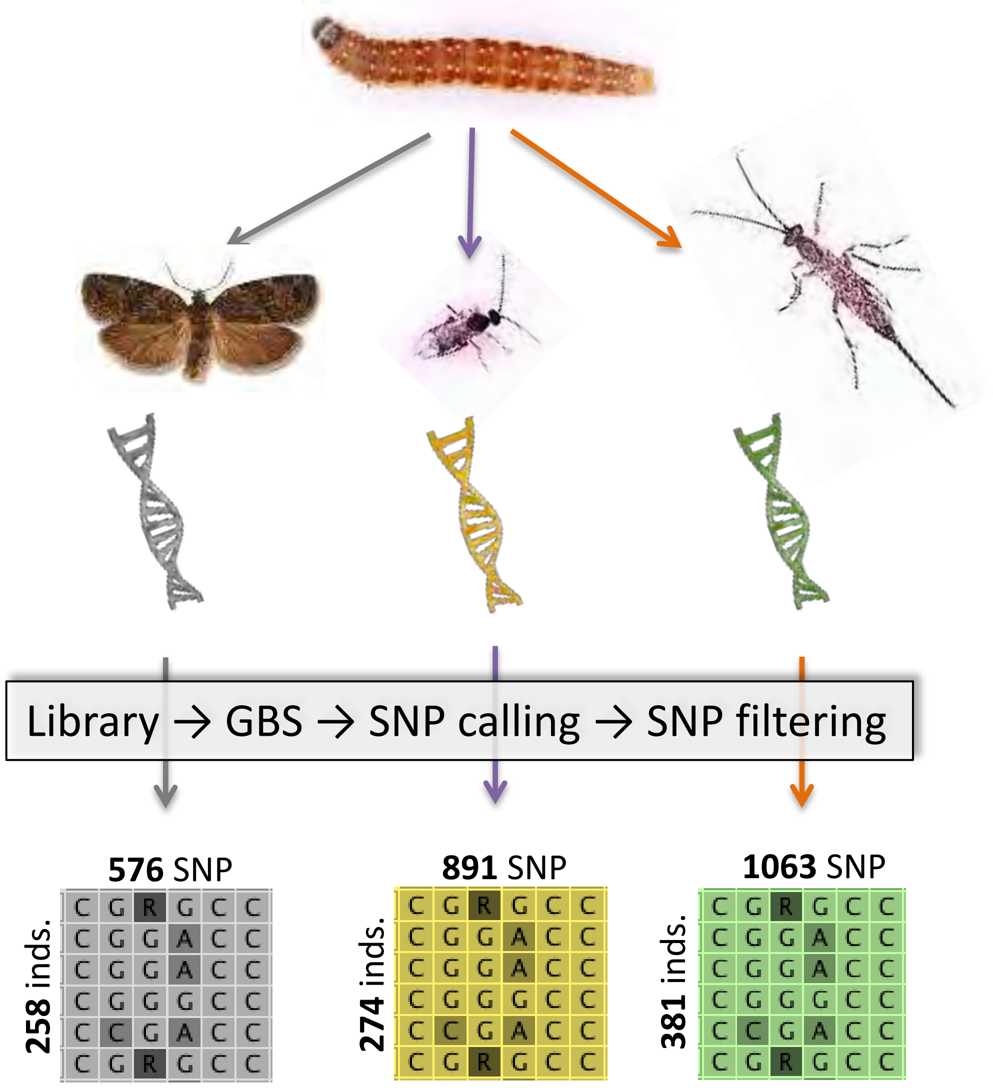
Glypta fumiferanae



- Is genetic structure is influenced by latitude?
- Is genetic diversity is influenced by latitude?

Study area and genotyping by sequencing





Library → GBS → SNP calling → SNP filtering

576 SNP

258 inds.

C	G	R	G	C	C
C	G	G	A	C	C
C	G	G	A	C	C
C	G	G	G	C	C
C	C	G	A	C	C
C	G	R	G	C	C

891 SNP

274 inds.

C	G	R	G	C	C
C	G	G	A	C	C
C	G	G	A	C	C
C	G	G	G	C	C
C	C	G	A	C	C
C	G	R	G	C	C

1063 SNP

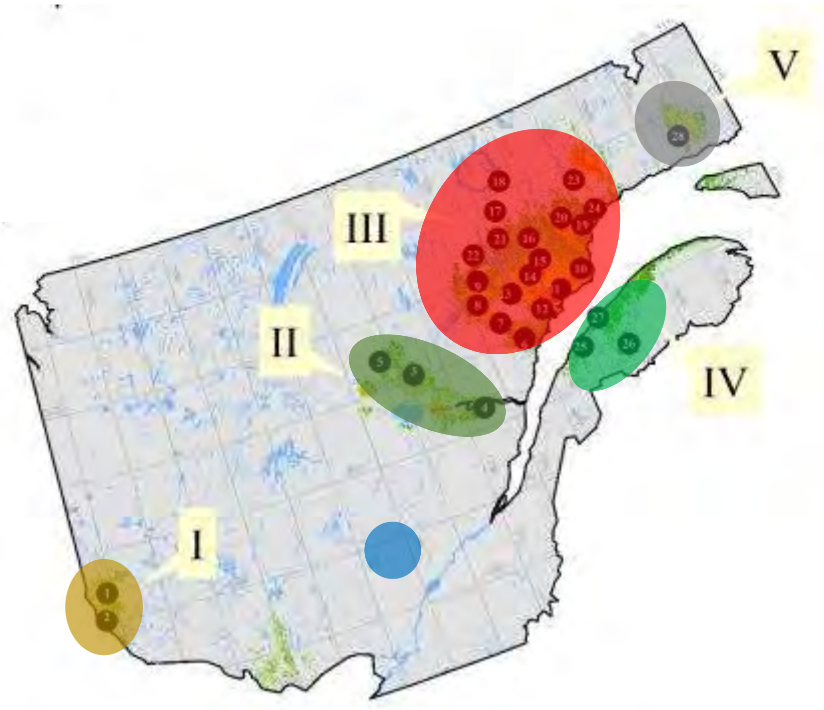
381 inds.

C	G	R	G	C	C
C	G	G	A	C	C
C	G	G	A	C	C
C	G	G	G	C	C
C	C	G	A	C	C
C	G	R	G	C	C

Analyses

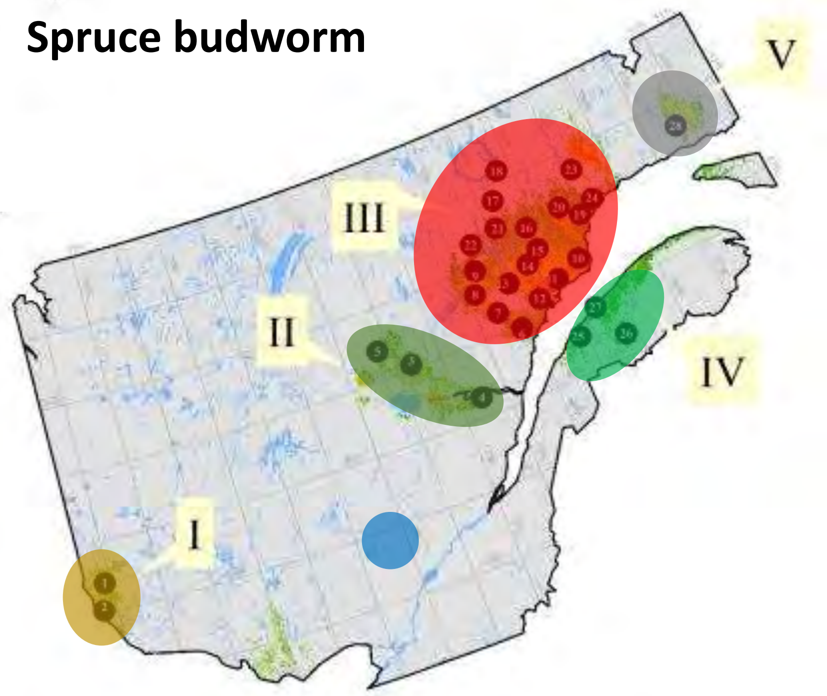
- Describe the **genetic structure** of two species of spruce budworm parasitoid.
  - AMOVA (Outbreak areas/Sites); PCA

- Is there a signature of expansion?
  - Model H_e~latitude



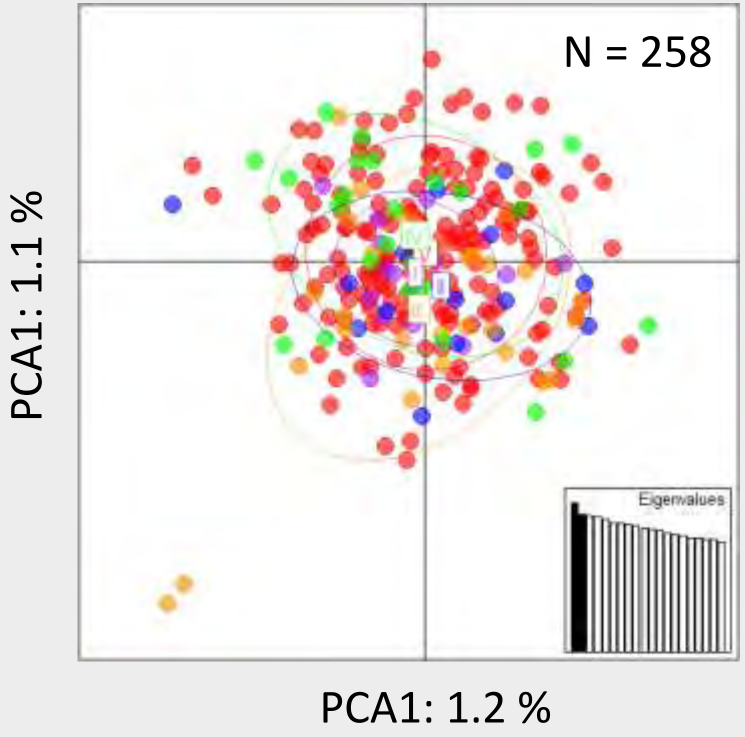
Results – AMOVA & PCA

Spruce budworm



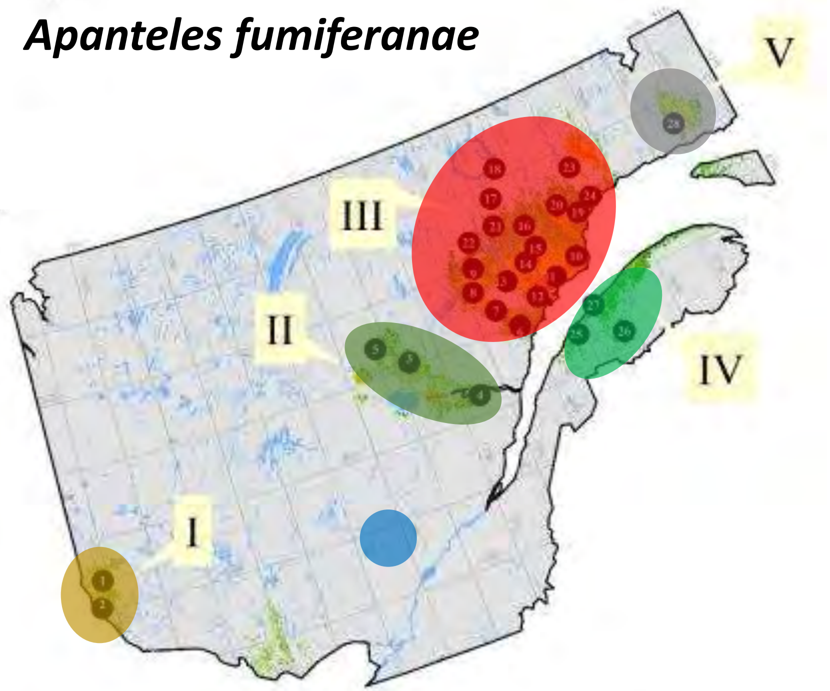
Component	σ^2	%	P^1
Outbreak Area	0.66	0.22	0.060
Site	0.30	0.10	0.653
Error	300.77	99.68	

[1] *999 permutations*



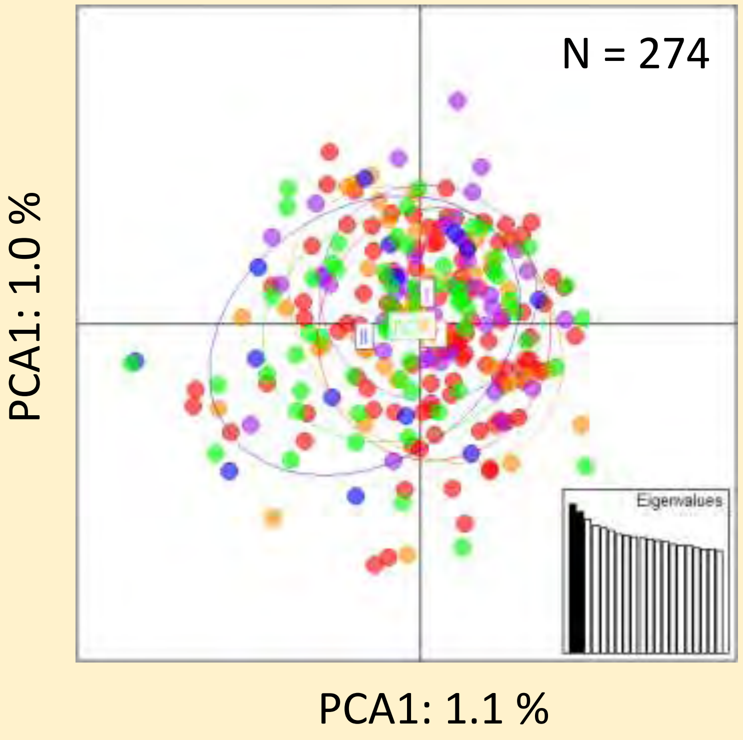
Results – AMOVA & PCA

Apanteles fumiferanae



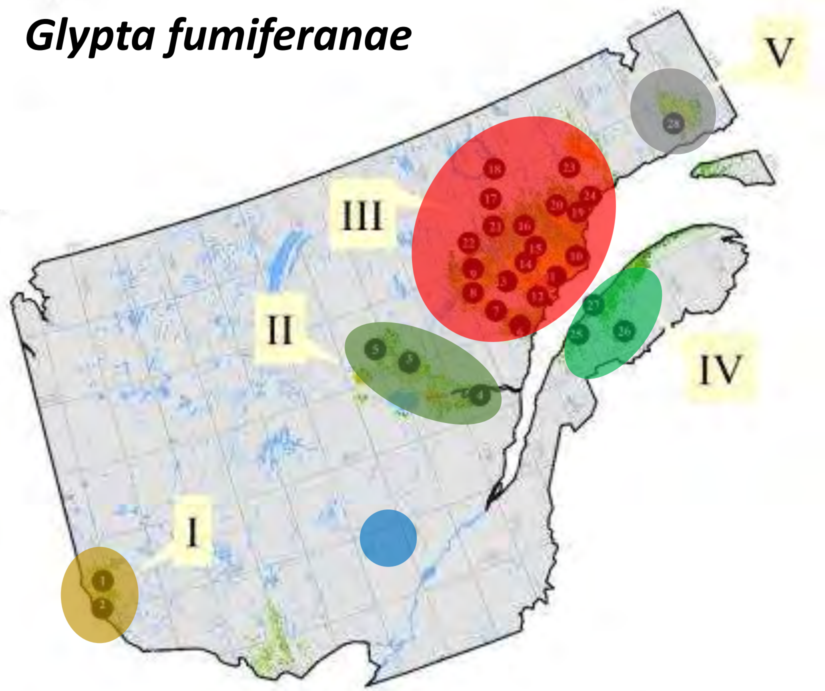
Component	**σ^2**	**%**	**P^1**
Outbreak Area	0.12	0.00	0.654
Site	1.07	0.22	0.063
Error	487.30	99.78	

^{1} 999 permutations



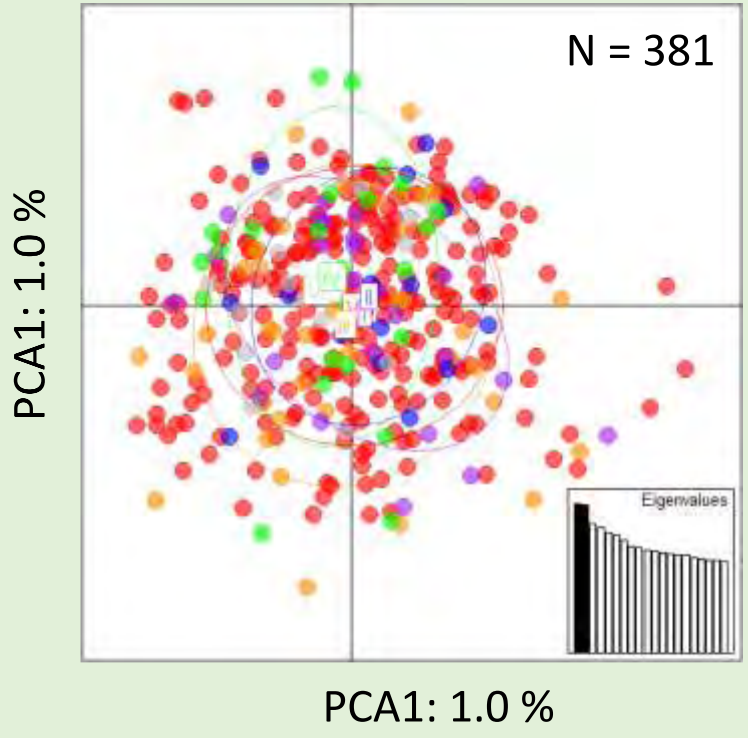
Results – AMOVA & PCA

Glypta fumiferanae

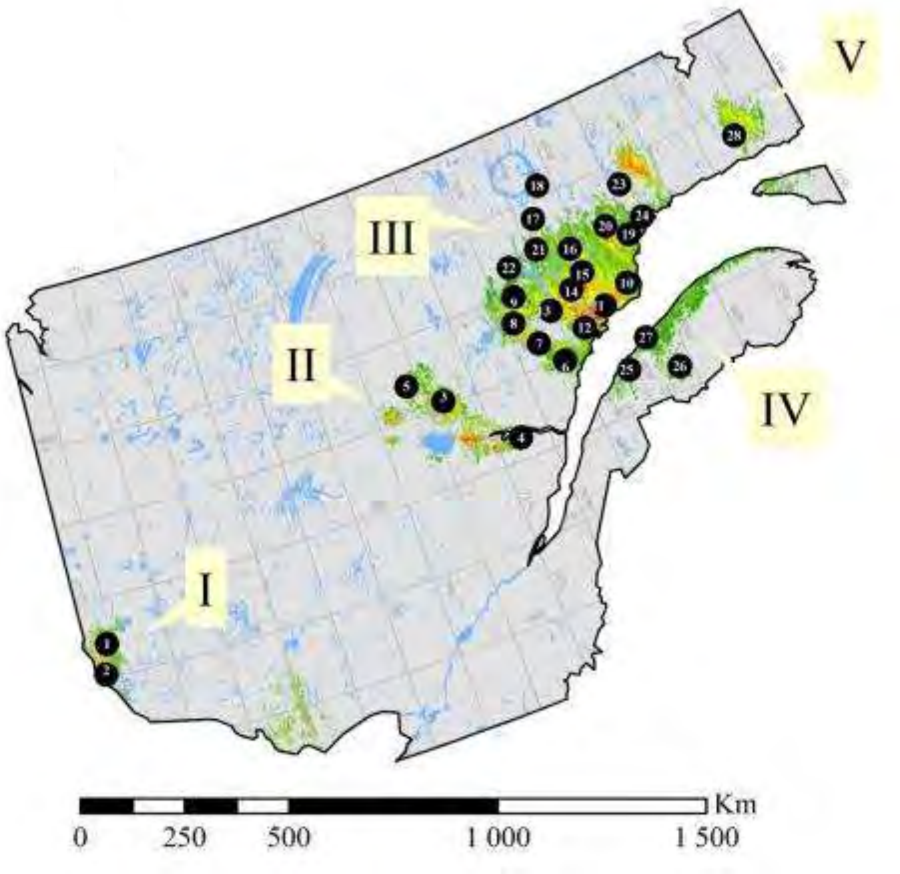


Component	**σ^2**	**%**	**P^1**
Outbreak Area	**0.38**	**0.00**	**0.880**
Site	**1.28**	**0.27**	**0.003 ***
Error	**472.55**	**99.73**	

^{1} 999 permutations



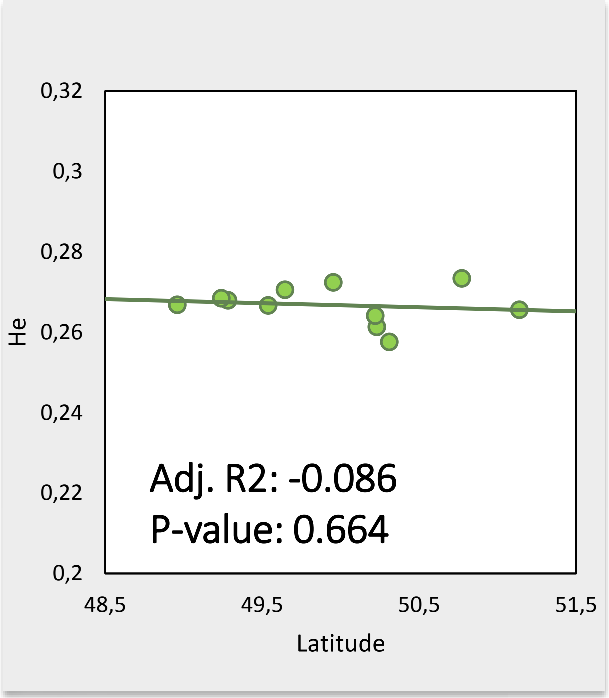
Consistently low genetic structure



- High parasitoid dispersal / connectivity?
- Confounding influence of population size and outbreak timing?
- Alternative hosts?
  - Are parasitoids “always there”?
- Downstream modelling applications.

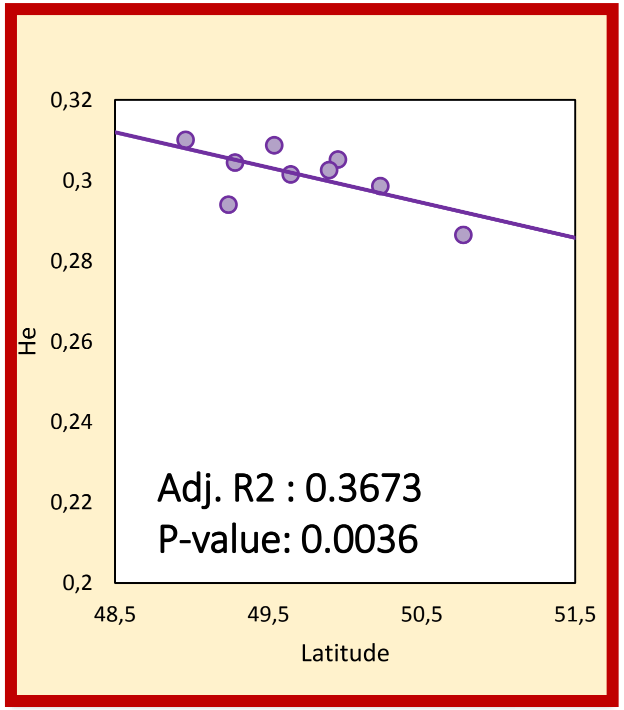
He ~ Latitude?

Spruce budworm



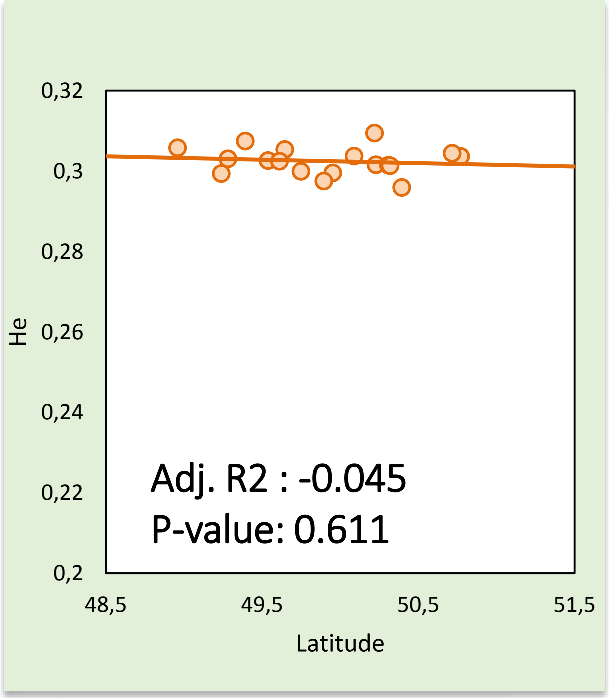
Adj. R2: -0.086
P-value: 0.664

Apanteles fumiferanae



Adj. R2 : 0.3673
P-value: 0.0036

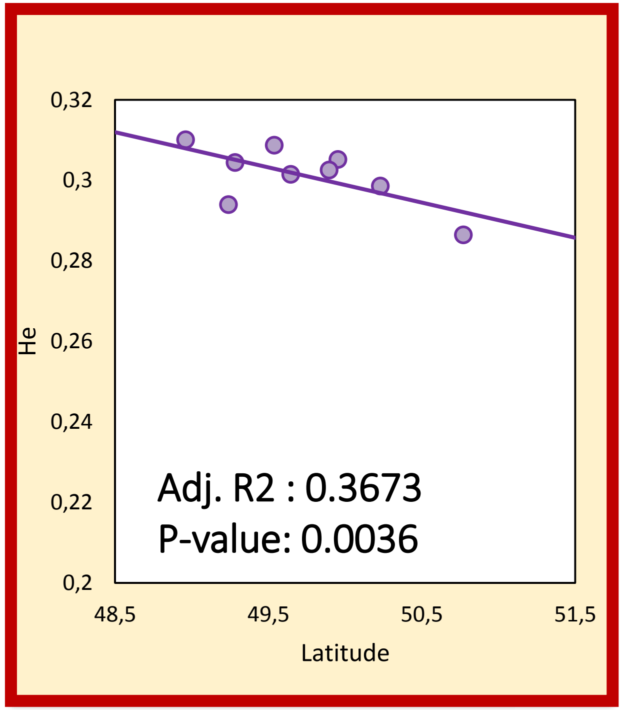
Glypta fumiferanae

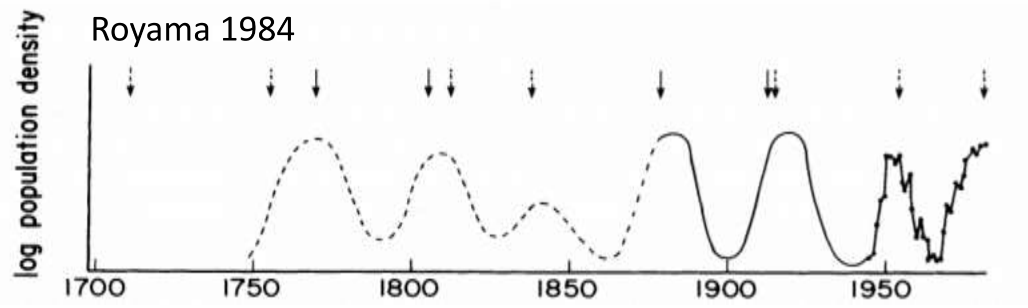


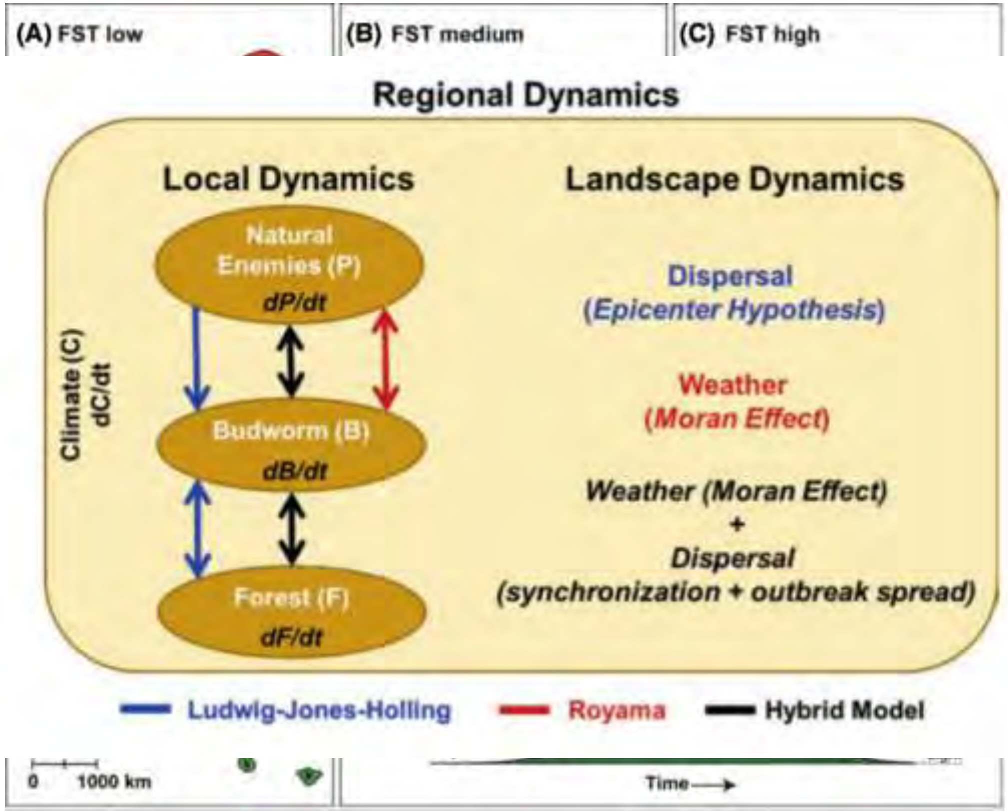
Adj. R2 : -0.045
P-value: 0.611

Apanteles expanding its range?

Apanteles fumiferanae




Royama 1984



- Demographic complexity makes it difficult to quantify genetic structure and movement.
- Signals the reflect the mechanisms driving spatio-temporal outbreak dynamics can be obfuscated as the outbreak progresses.
- Timing matters …

Other ongoing work

- Mapping inter- and intra-taxa spatial variation in potentially adaptive loci (SBW and MPB).
- Simulation modelling to examine the consequences of cyclic population dynamics on spatial genetic structure.
- Simulation modelling to examine the consequences of rapid range expansion on identifying signatures of selection in “real” landscapes.

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