

Genomic Surveillance

Intro

Roman Biek

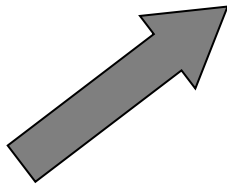
SPEEDIER kickoff meeting (Glasgow)

November 2018



University
of Glasgow

Genomic surveillance: closing the loop



Informing long-term
plans for control,
prevention and
elimination

Investigations and
diagnostics:
Katie Hampson

Effective tools for
visualization and
interpretation of
genomic data

Targeted strategy
for collecting
samples and high
quality metadata

GLUE platform
demo:
Rob Gifford
Josh Singer

Timely generation of
whole genome data in
country

Sequencing demo:
Kirstyn Brunner

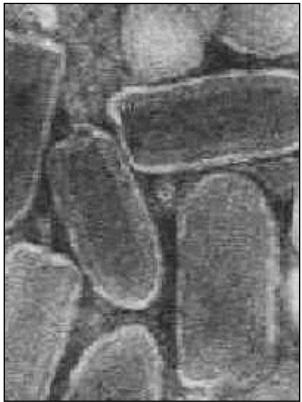
Outline

- Case study: using rabies virus genomics to understand cross-border incursions
- What do we expect a genomics surveillance platform to deliver?
- Opportunities and challenges
 - Sample collection and sequencing
 - Data processing, sharing and visualisation

Raccoon rabies in North America



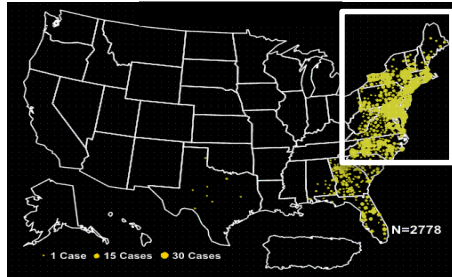
Raccoon (*Procyon lotor*)



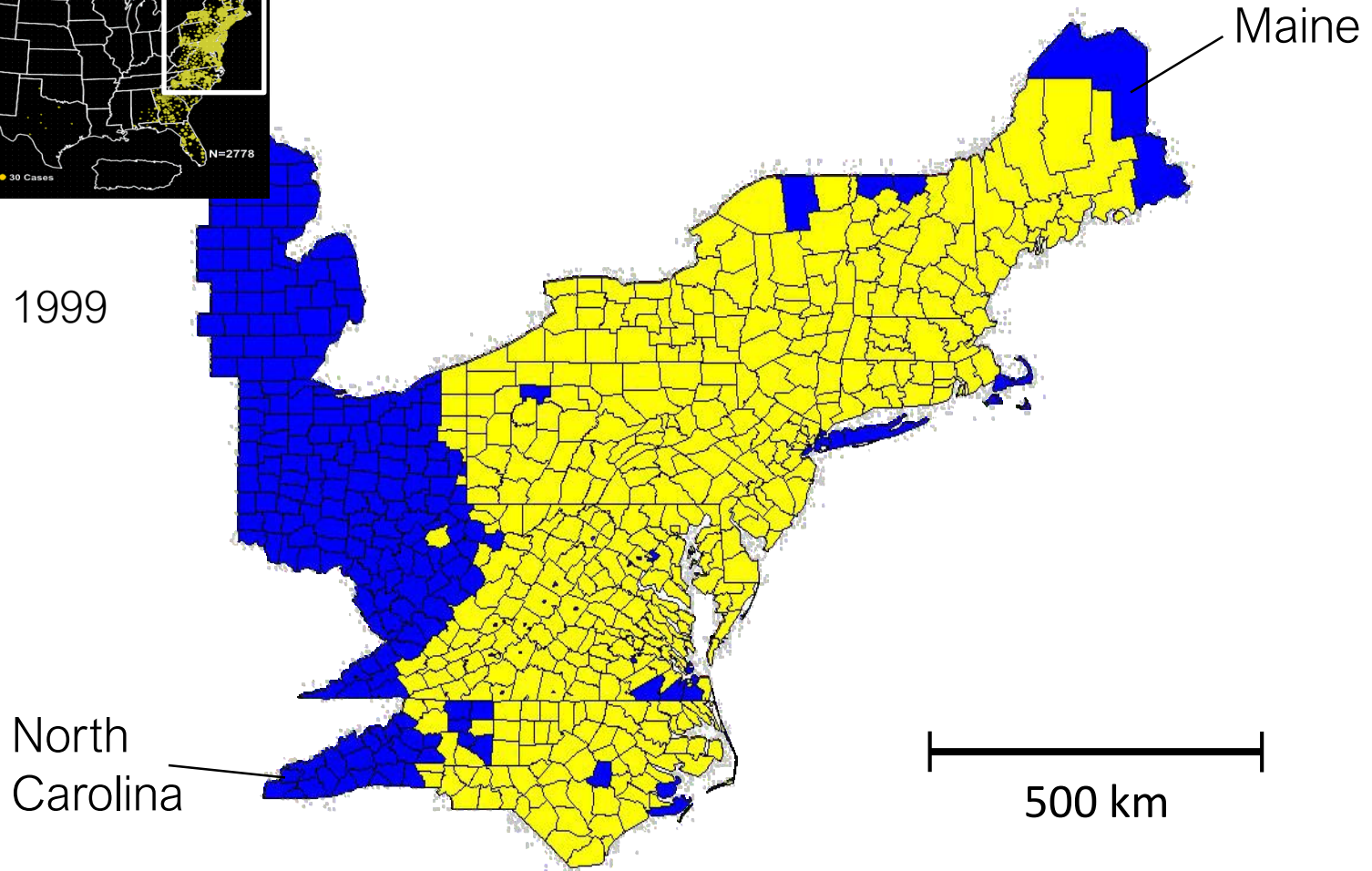
Rabies virus



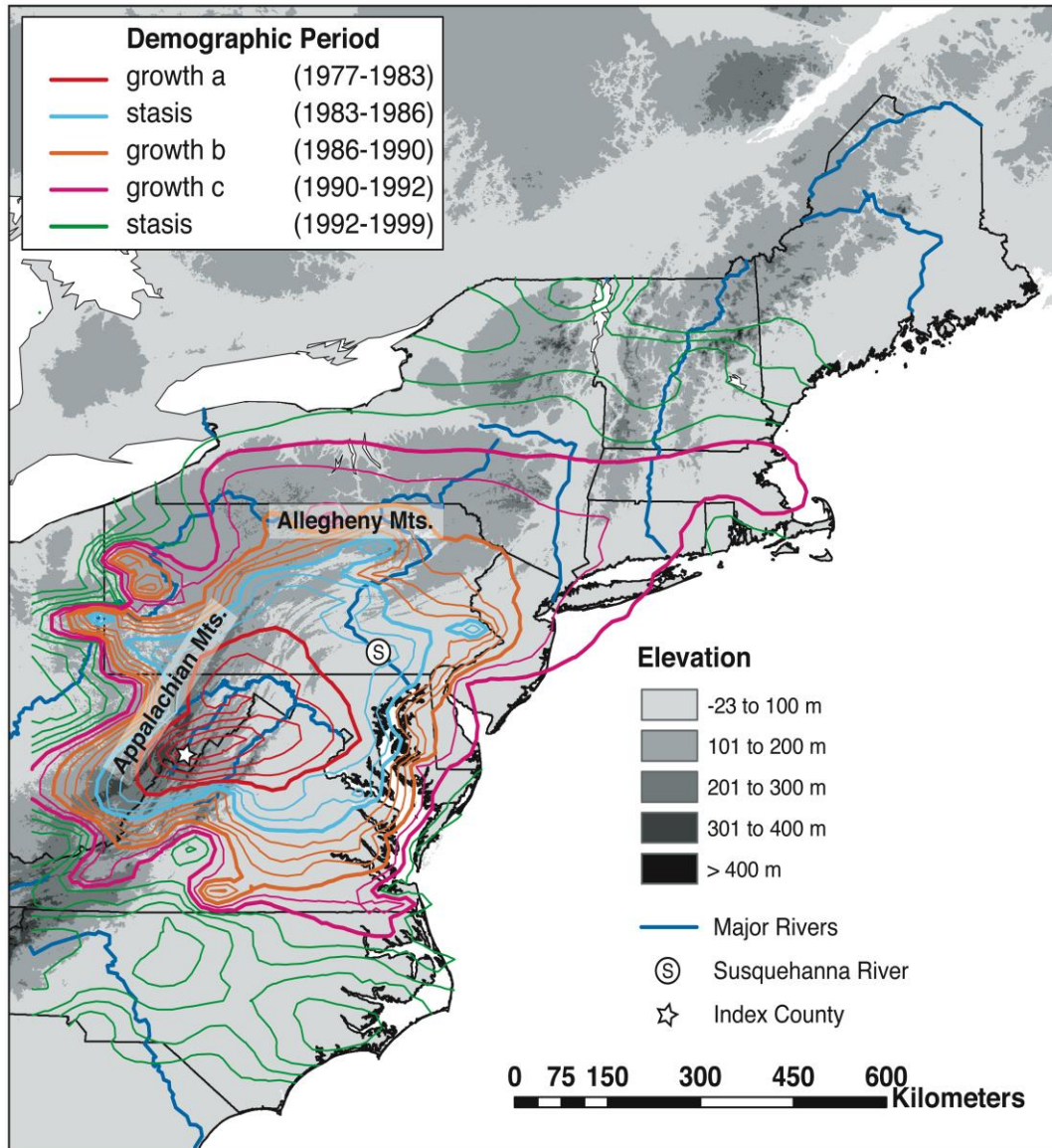
Raccoon rabies – spatial invasion



1977 - 1999



Spread is not homogeneous in space and time



Mountains

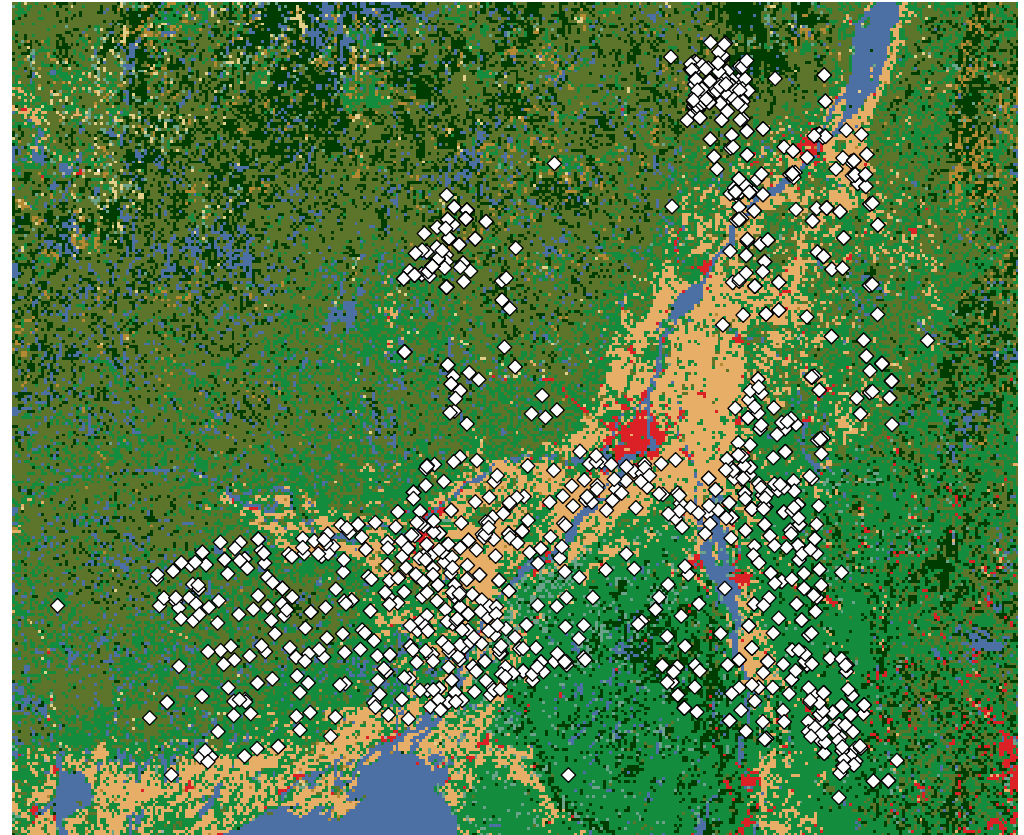
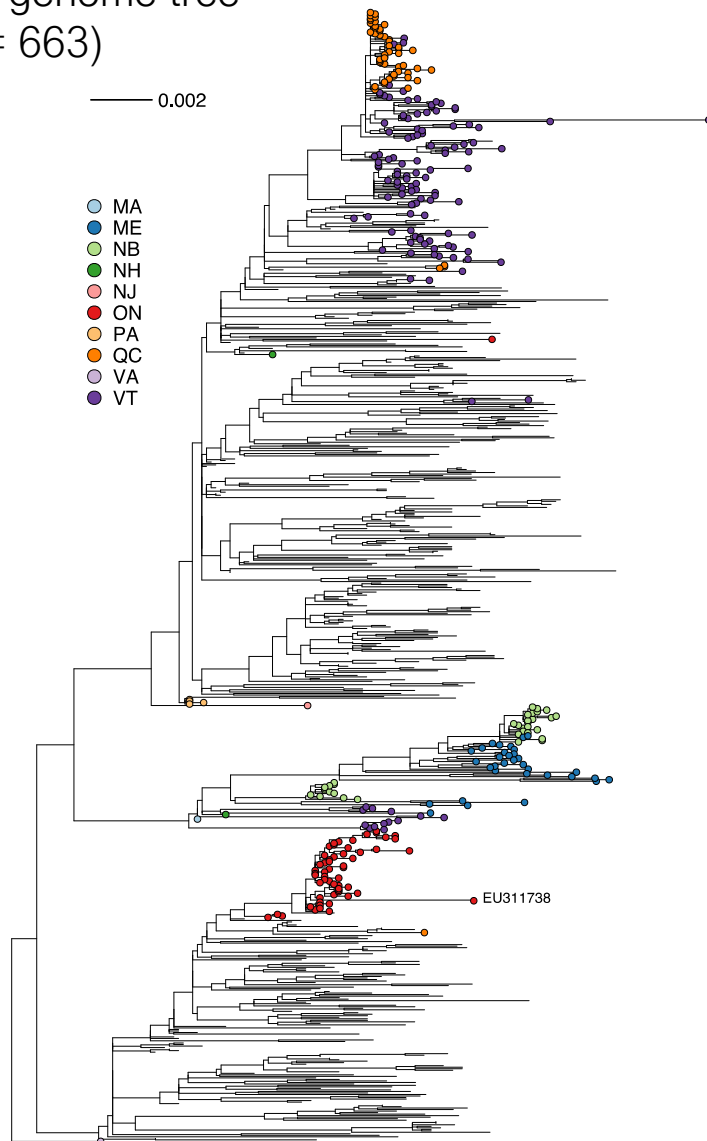


Oral vaccination



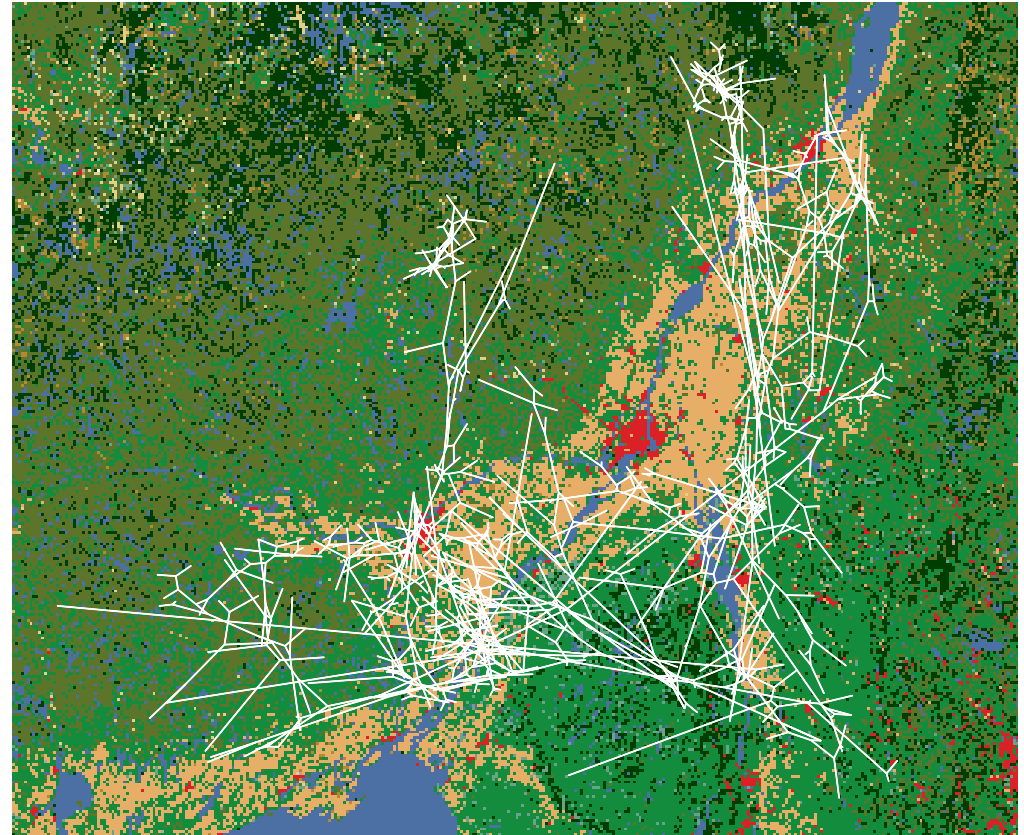
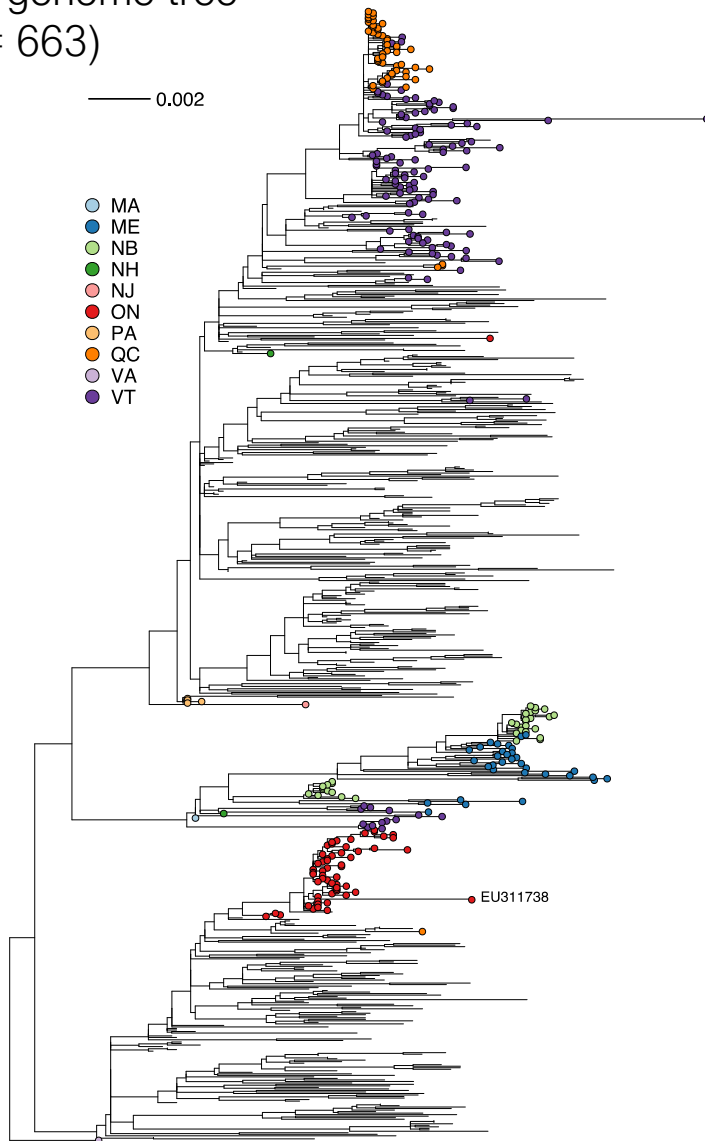
Genomic epidemiology at US/Canada border

Full genome tree
(n = 663)

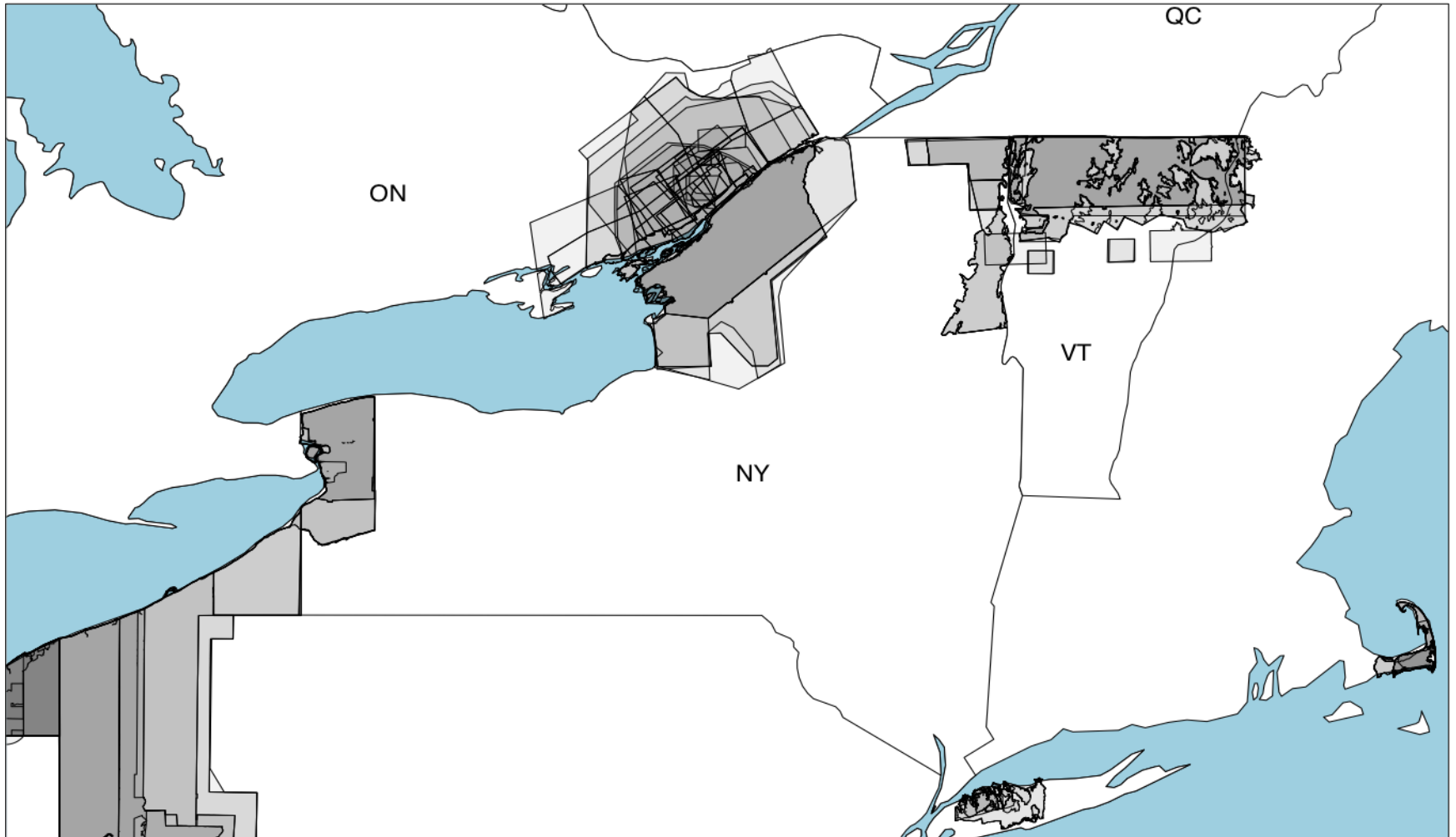


Genomic epidemiology at US/Canada border

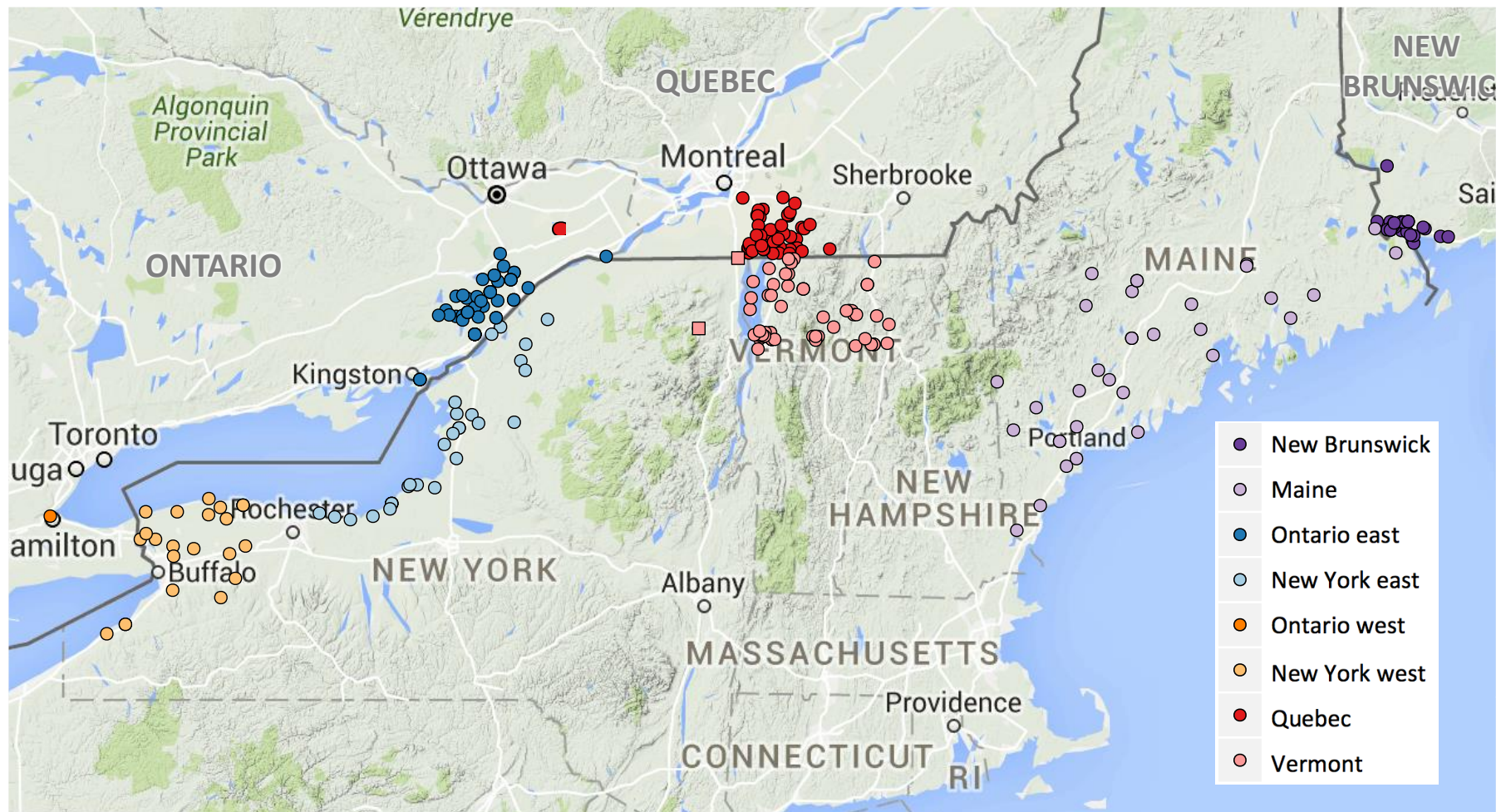
Full genome tree
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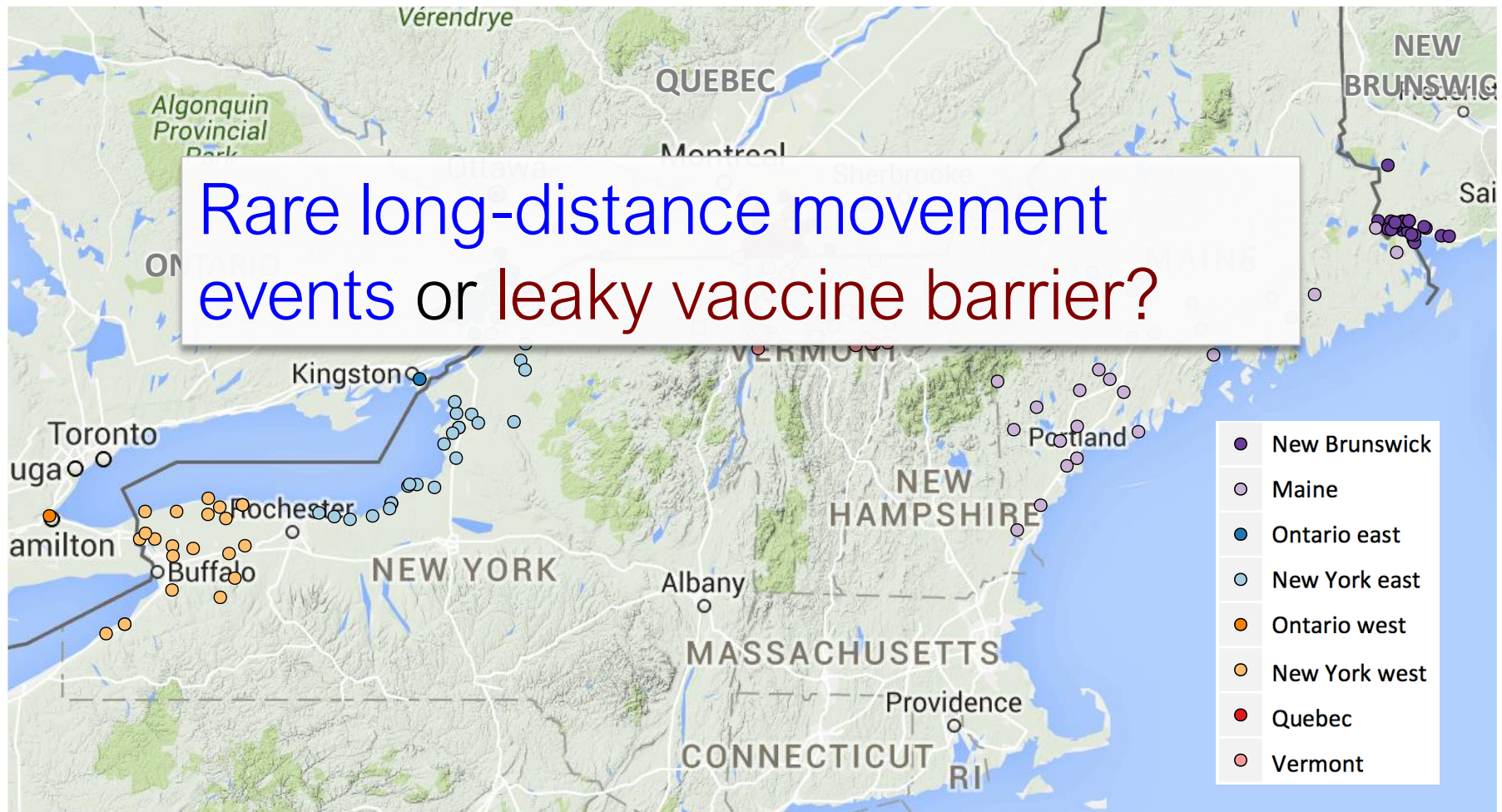
Oral vaccination zones



Transboundary incursions into Canada



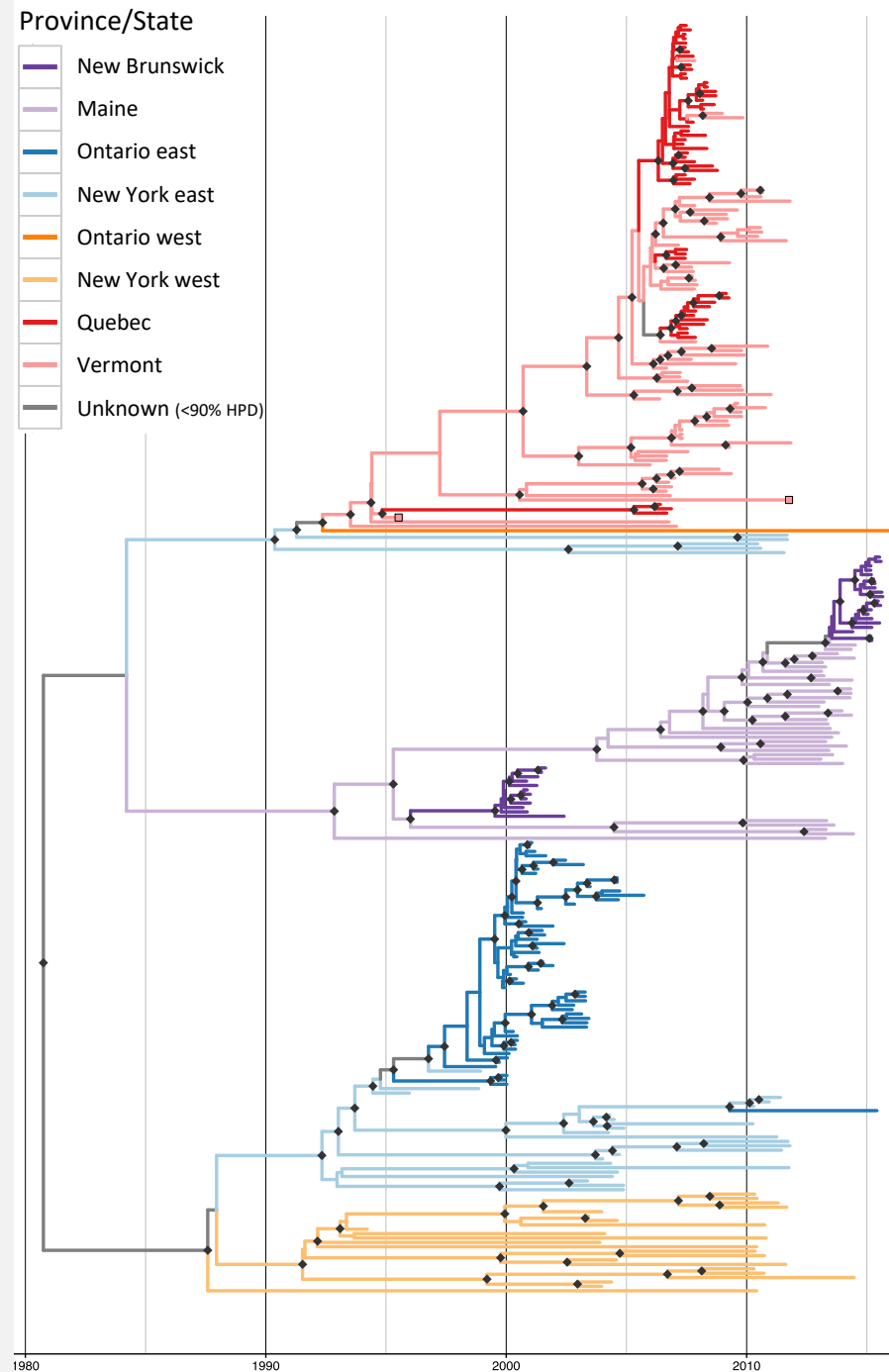
Transboundary incursions into Canada



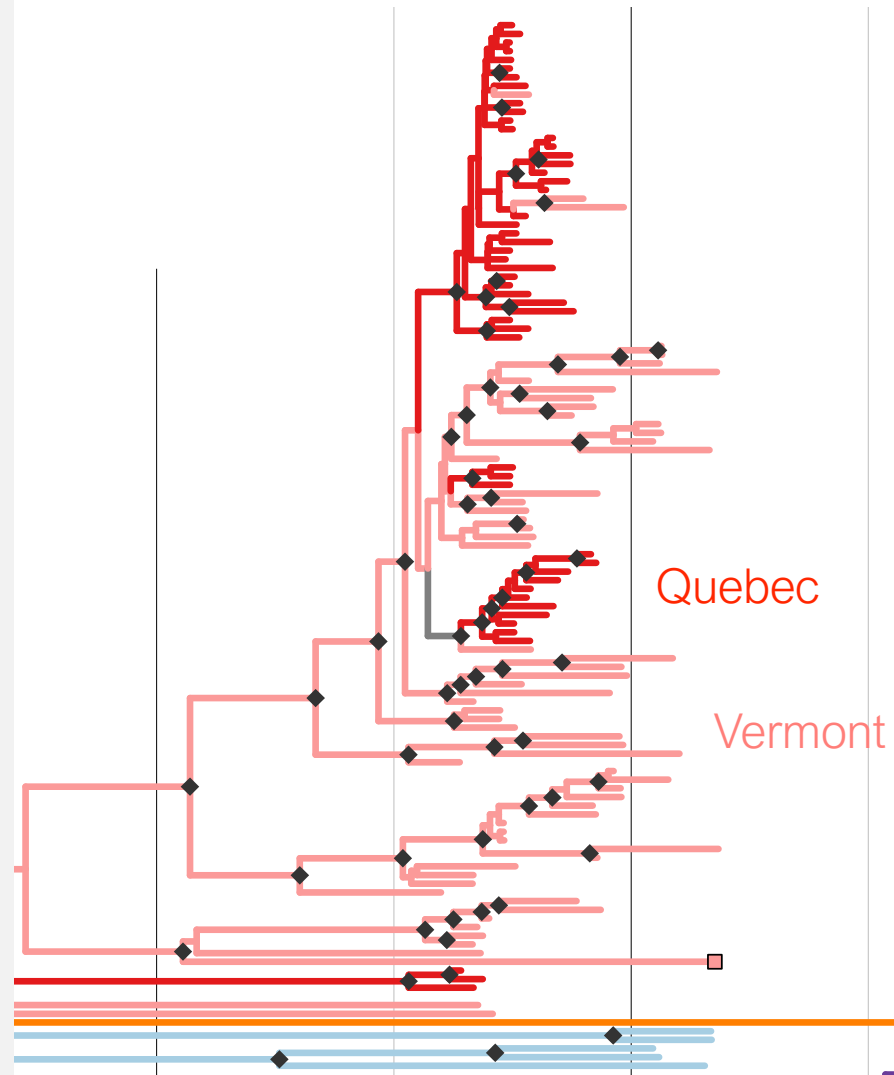
Phylogeny based on >200
virus genomes

Ten independent incursion
events over two decades

Trewby et al., EID 2017



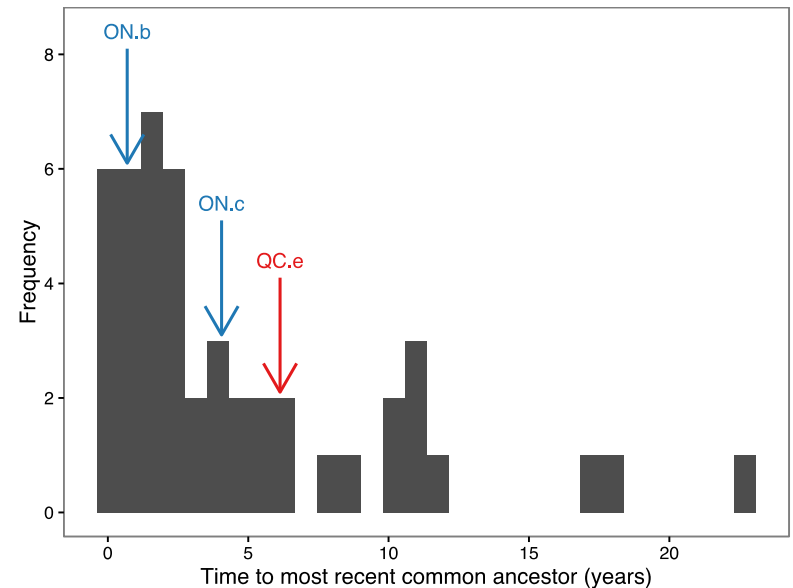
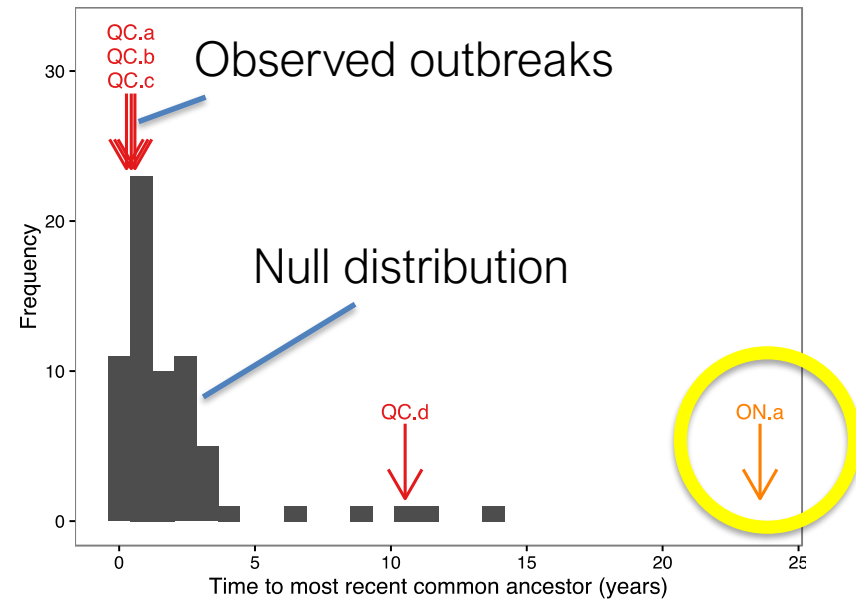
Example Vermont/Quebec:
Repeated, bi-directional
movement of virus across
vaccine corridor



Are outbreak caused by local US strains circulating near the border?

Out of 8 outbreaks

- 7 caused by local strains
- 1 caused by long distance movement



General lessons

- Fine scale viral movement (e.g. multiple border crossings) only detectable from genomic data
- Identifying sources of incursions requires extensive sequence data with good spatial coverage for comparison

What do we expect a genomics surveillance platform to deliver?

- Rapid identification of viral lineages: incursion or continuous transmission of resident strains?
- Geographic source attribution
- Apparent extinction of lineages: measure of elimination success

=> Statistical frameworks required (integration with epidemiological data)

Opportunities and challenges

1. Sample collection and sequencing

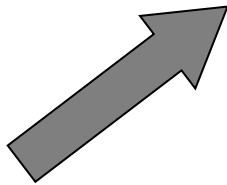
- Building on existing surveillance platform
- Access to archived samples – what to sequence?
- RNA extraction of positive samples
- Training in use of portable sequencers
- Data storage and transfer

Opportunities and challenges

2. Data processing, sharing and visualisation

- Rapid and accurate tree building
- Integration of genomic and sub-genomic sequence data
- Effective visualisation
- Automated interpretation?

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