

**Data Advisory Committee of the OHTN**

# Phylogenetics and public health surveillance

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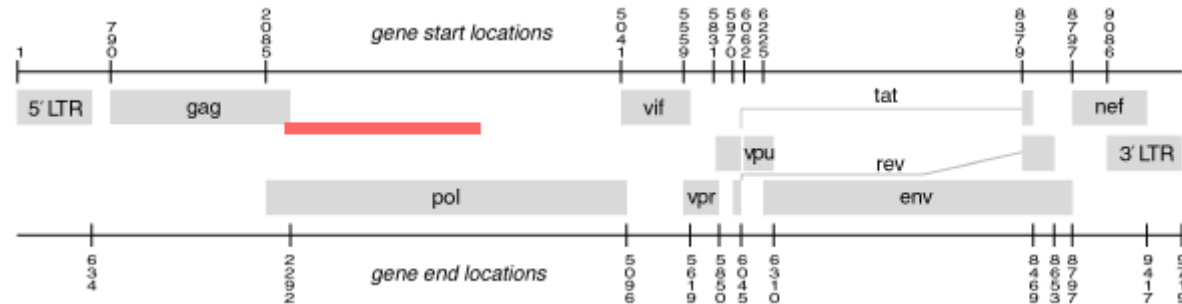
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# The HIV genome evolves very quickly

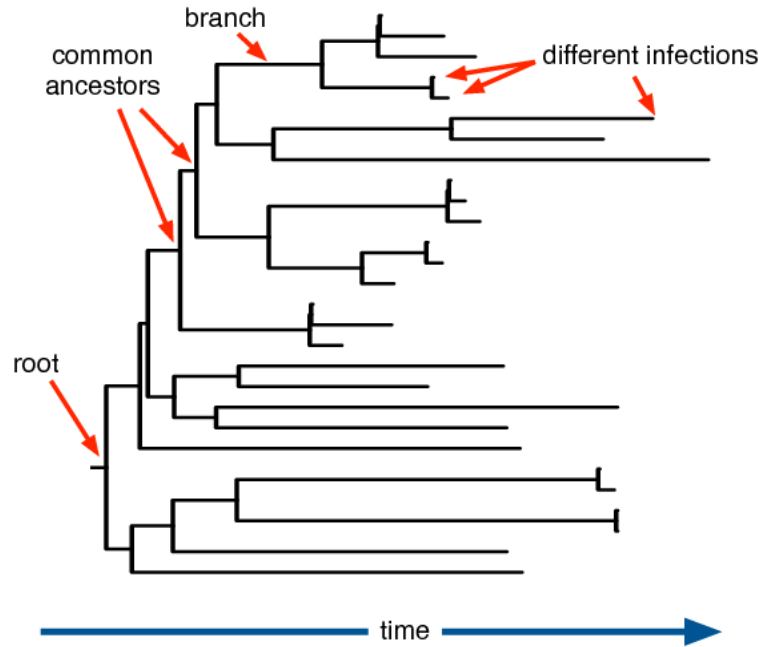
- A mutation occurs when the enzyme that converts the HIV genome into DNA adds the wrong nucleotide.
- Our cells also make enzymes that force the HIV genome to mutate — most mutations break something.



- Sequencing the region encoding the main targets of drug treatment is used to predict if an infection is becoming resistant.

Image generated by Los Alamos National Laboratory HIV Sequence Locator tool.

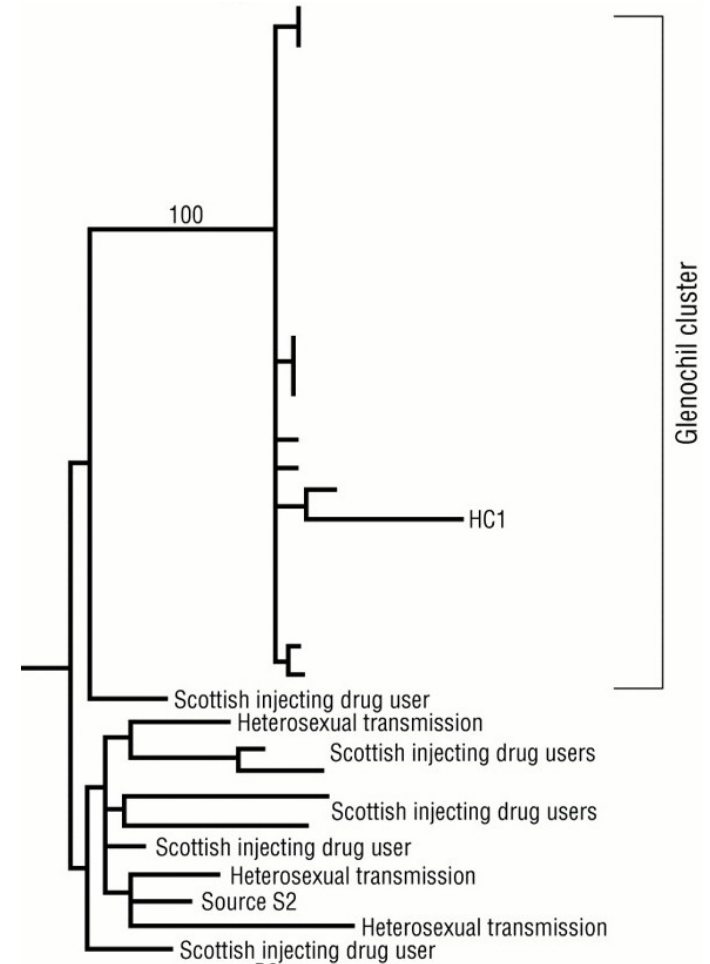
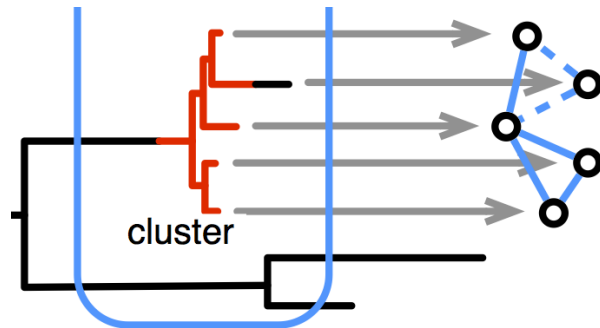
# A molecular phylogeny is a hypothesis about how sequences are related by common ancestors



- We infer that two sequences share a common ancestor from their genetic similarity.

## Clusters of genetically similar infections may represent transmission outbreaks

- HIV evolves rapidly - a new infection becomes unique within weeks.
- If two infections are still similar when diagnosed, they are probably related through an unknown number of recent transmission events.



HIV-1 *gag* phylogeny from Yirrell *et al* BMJ 314 (1997): 1446.

# Clustering has become a popular method for real-time molecular epidemiology

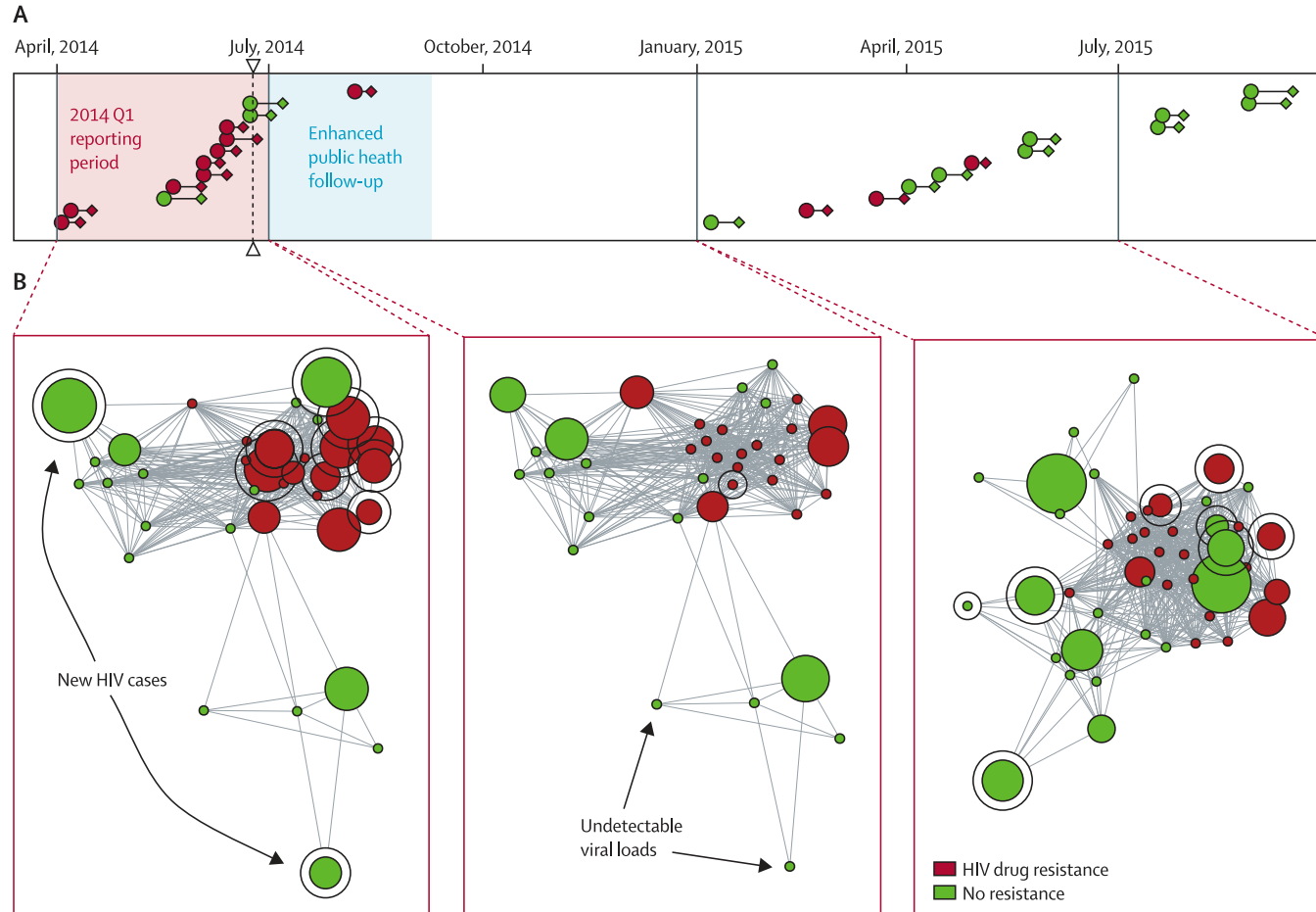


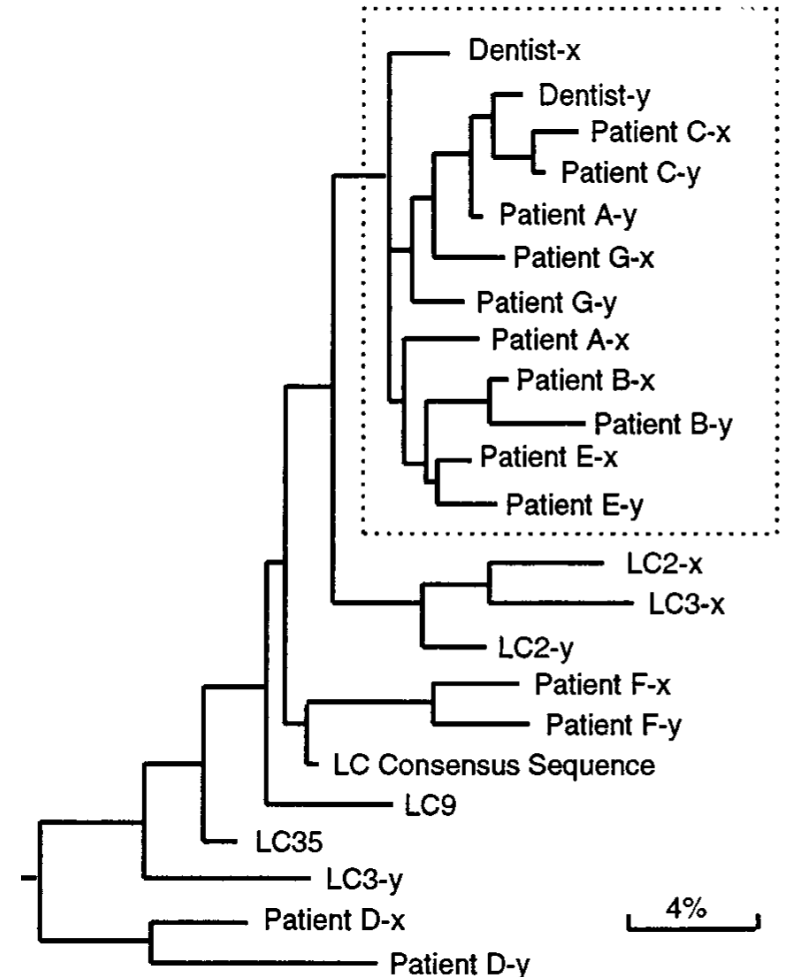
Figure from Poon *et al.* Lancet HIV 3.5 (2016): e231.

# How does cluster-based public health work in BC?

- Cluster reports are reviewed by joint committee of public health and lab staff.
- If a cluster is deemed of significant concern, the medical health officer uses the *pre-existing protocol* to request the secure transfer of identifying information for no fewer than 5 individuals. (Public health already has personal IDs.)
- **Cluster "networks" are never de-identified.**
- Public health contacts individuals to confirm access to treatment and re-offer the same prevention services that are offered for every new diagnosis (e.g., anonymous partner referral).

## What are the risks?

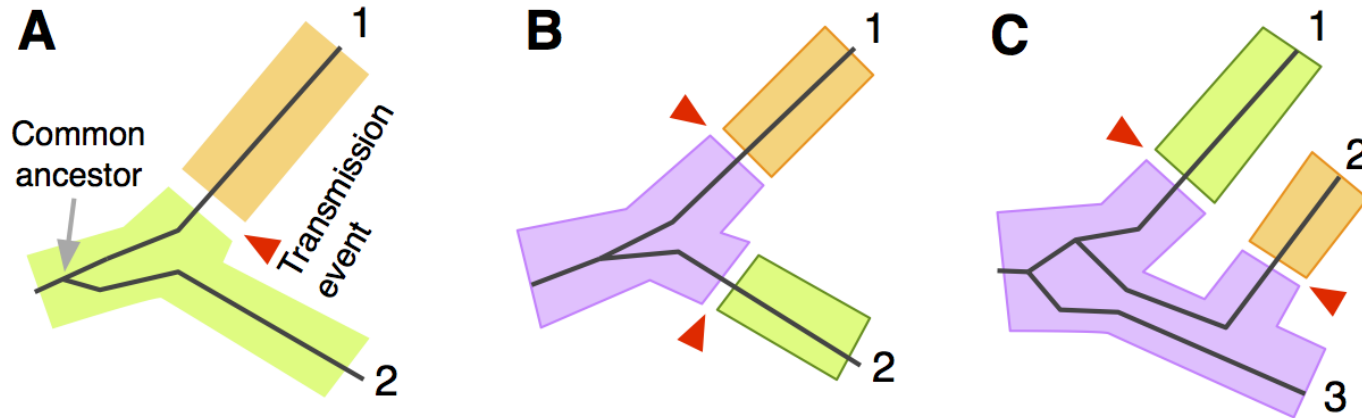
- Phylogenetic and cluster analyses have been used in the prosecution of people in HIV transmission cases.
- Police subpoena clinical and research labs to access data for such cases (these have *always* been refused in BC).
- "Criminalization of HIV non-disclosure [...] is doing more harm than good in terms of its impact on public health and human rights." ([Oslo declaration](#)).



Phylogeny from Ou *et al.* Science 256 (1992): 1165.

# Source attribution

- Generally speaking, the kinds of sequences used for resistance genotyping and public health monitoring *cannot* be used to infer "who infected whom".



- Overcoming this limitation is (unfortunately) active area of research.
- e.g., "next-generation sequencing", Bayesian inference.

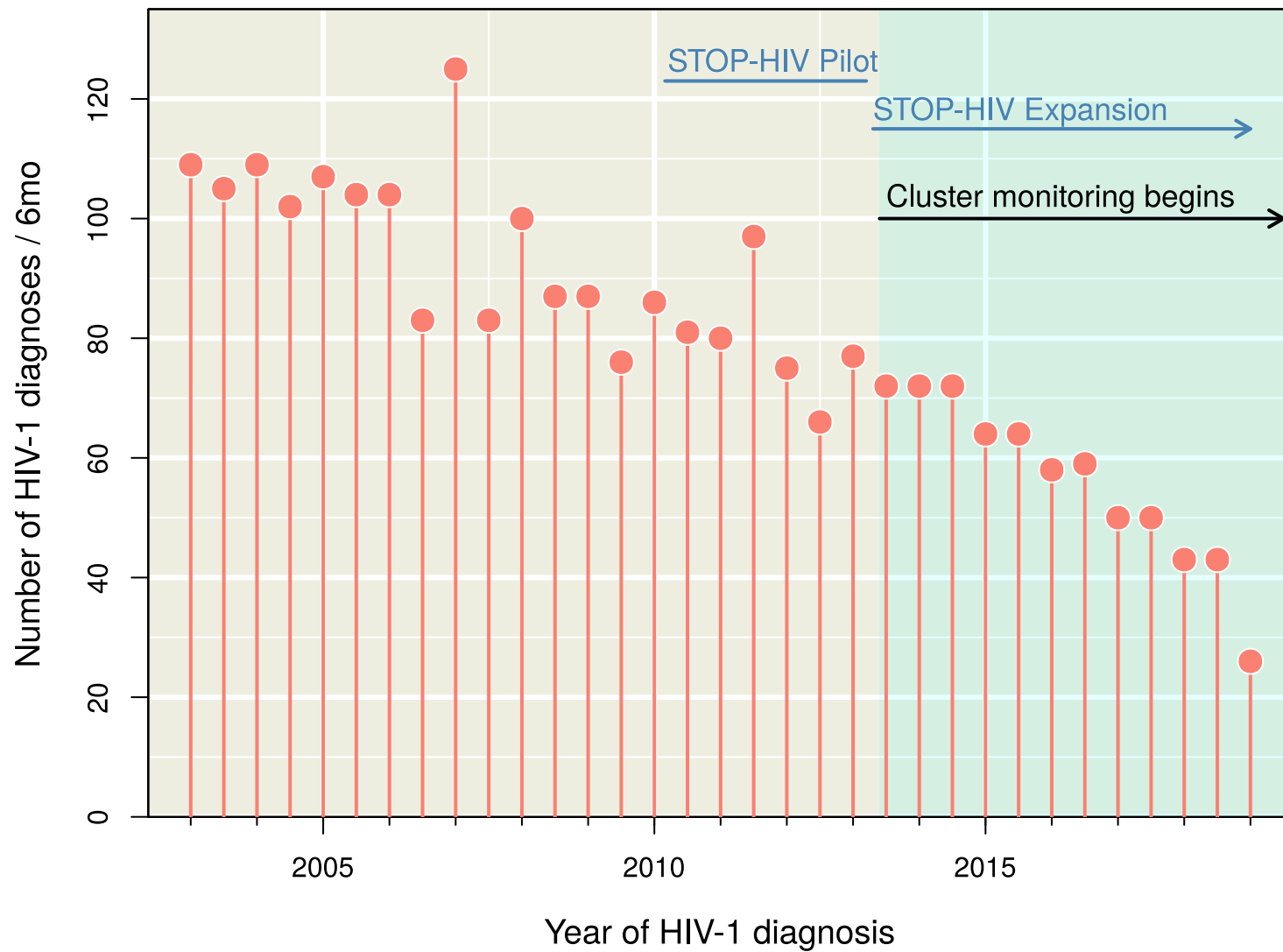


## How do we minimize risk?

- These risks already exist in the absence of cluster analysis for public health (*i.e.*, routine clinical genotyping).

*Confer benefits to public health without elevating risks to individuals.*

- All phylogenetic outputs are immediately destroyed.
- No information from this system has ever been used in the prosecution of a person living with HIV.



Data from Vancouver Coastal Health STOP HIV/AIDS monitoring reports.