

Data Advisory Committee of the OHTN

Phylogenetics and public health surveillance

Art Poon

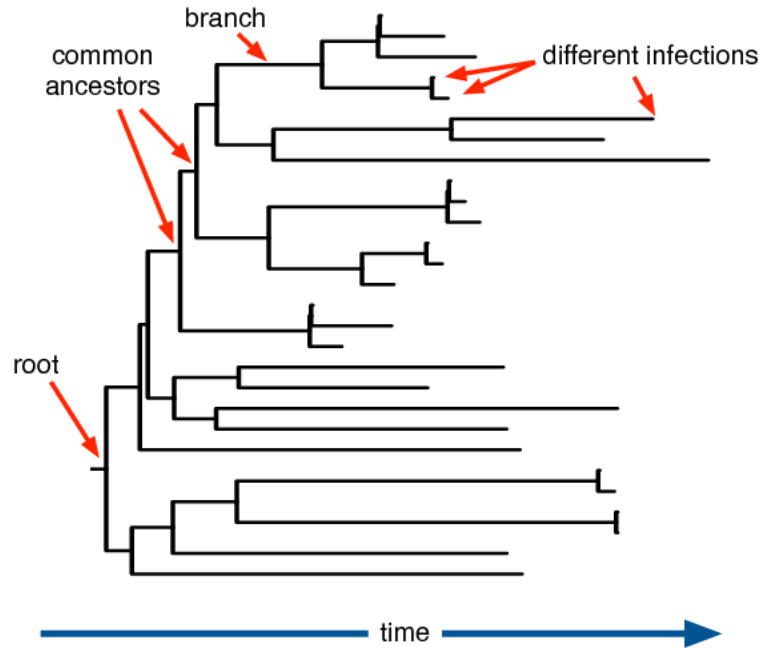
Department of Pathology & Laboratory Medicine;

Department of Microbiology & Immunology;

Department of Applied Mathematics, Western University



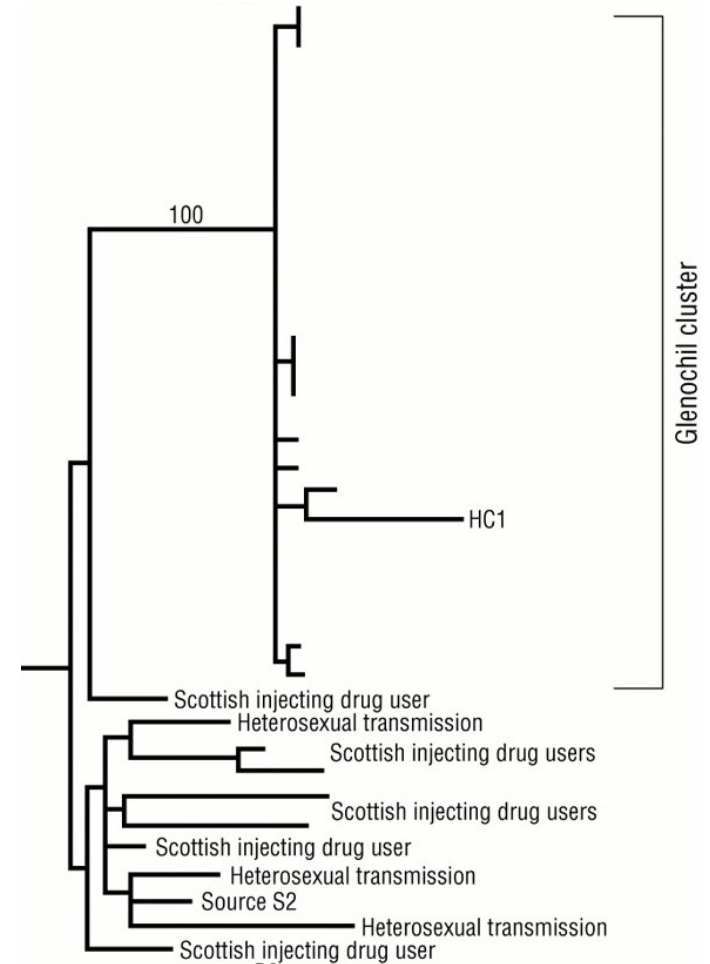
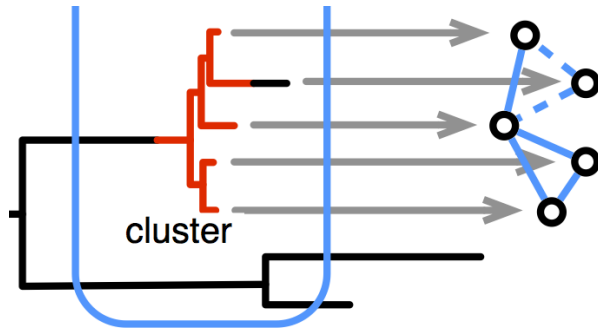
A molecular phylogeny is a hypothesis about how sequences are related by common ancestors



- 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 Yirell *et al*
BMJ 314 (1997): 1446.

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

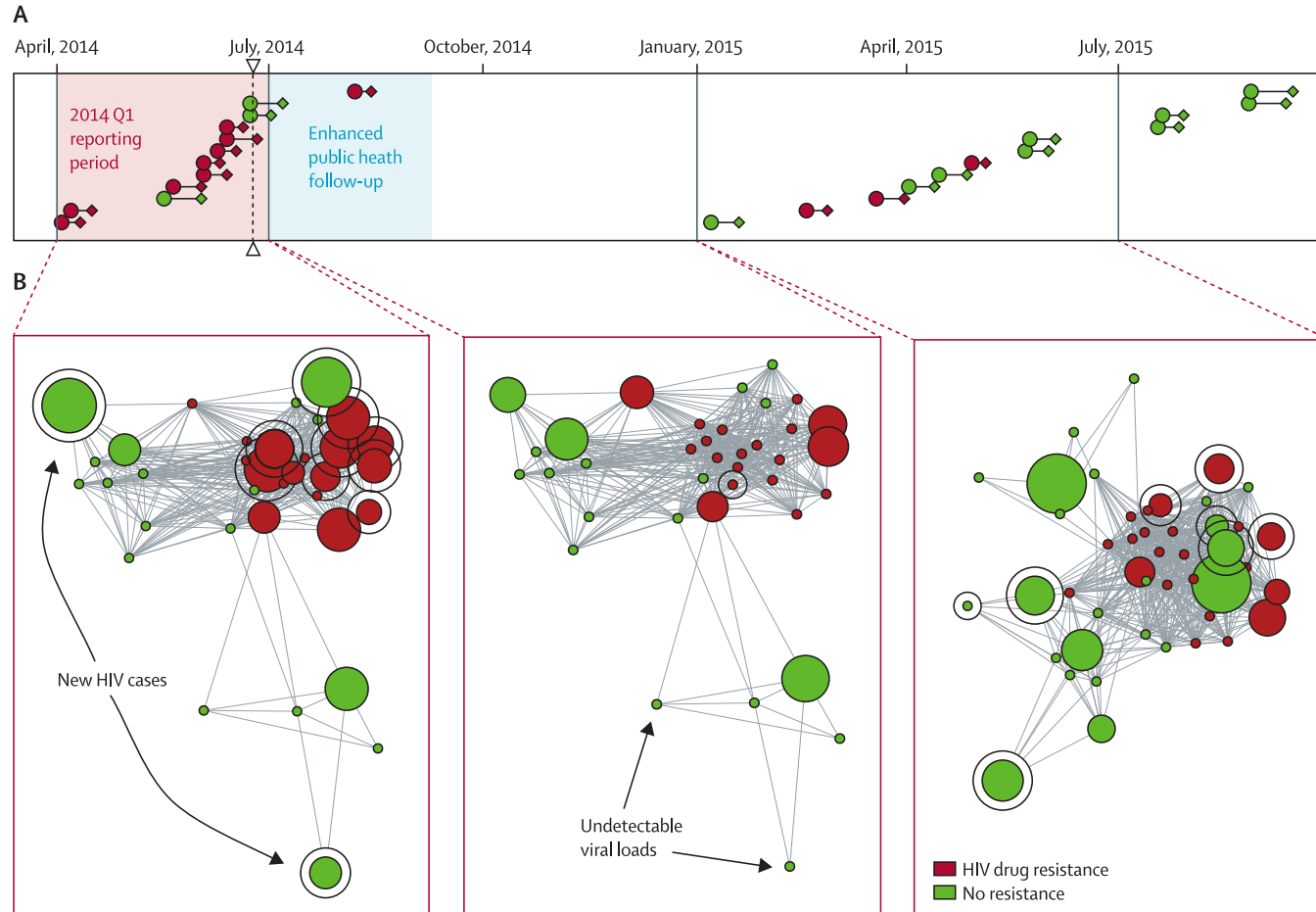


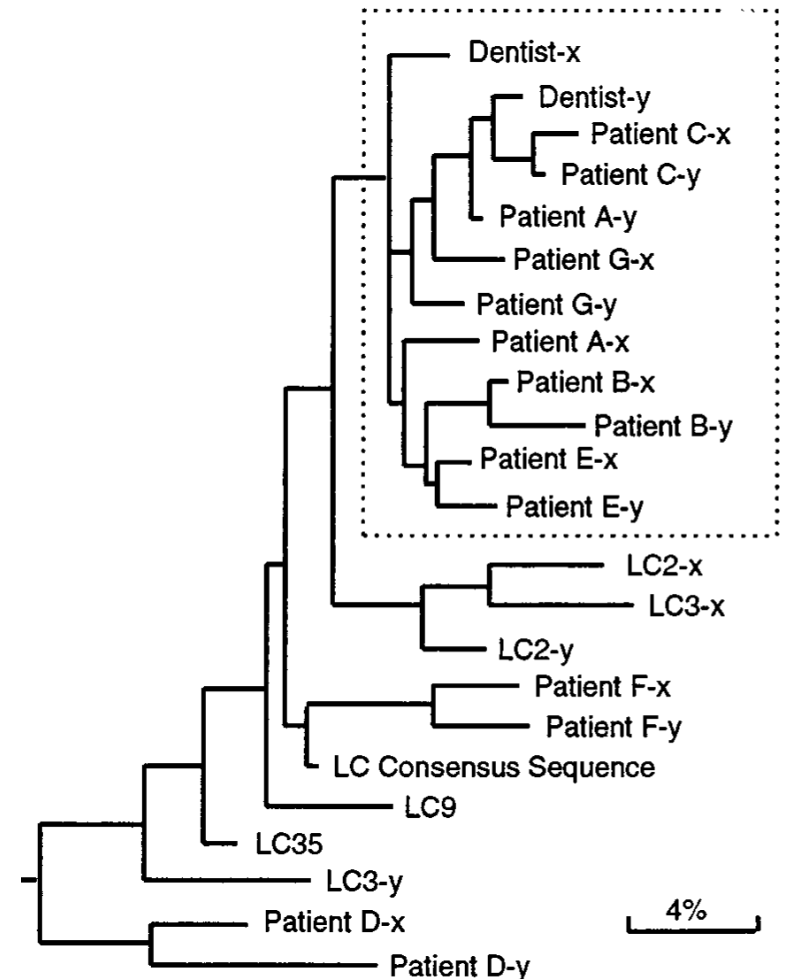
Figure from Poon *et al.* Lancet HIV 3.5 (2016): e231.

How does cluster-based public health work in BC?

- System analyzes the anonymized clinical database every hour.
- Reports are reviewed by joint committee of public health and lab staff.
- If the appearance of new cases in a cluster is deemed of significant health concern, the medical health officer uses the *pre-existing protocol* to request the secure transfer of identifying information for no fewer than 5 individuals. **The "networks" are never de-identified.**
- Public health contacts those 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).

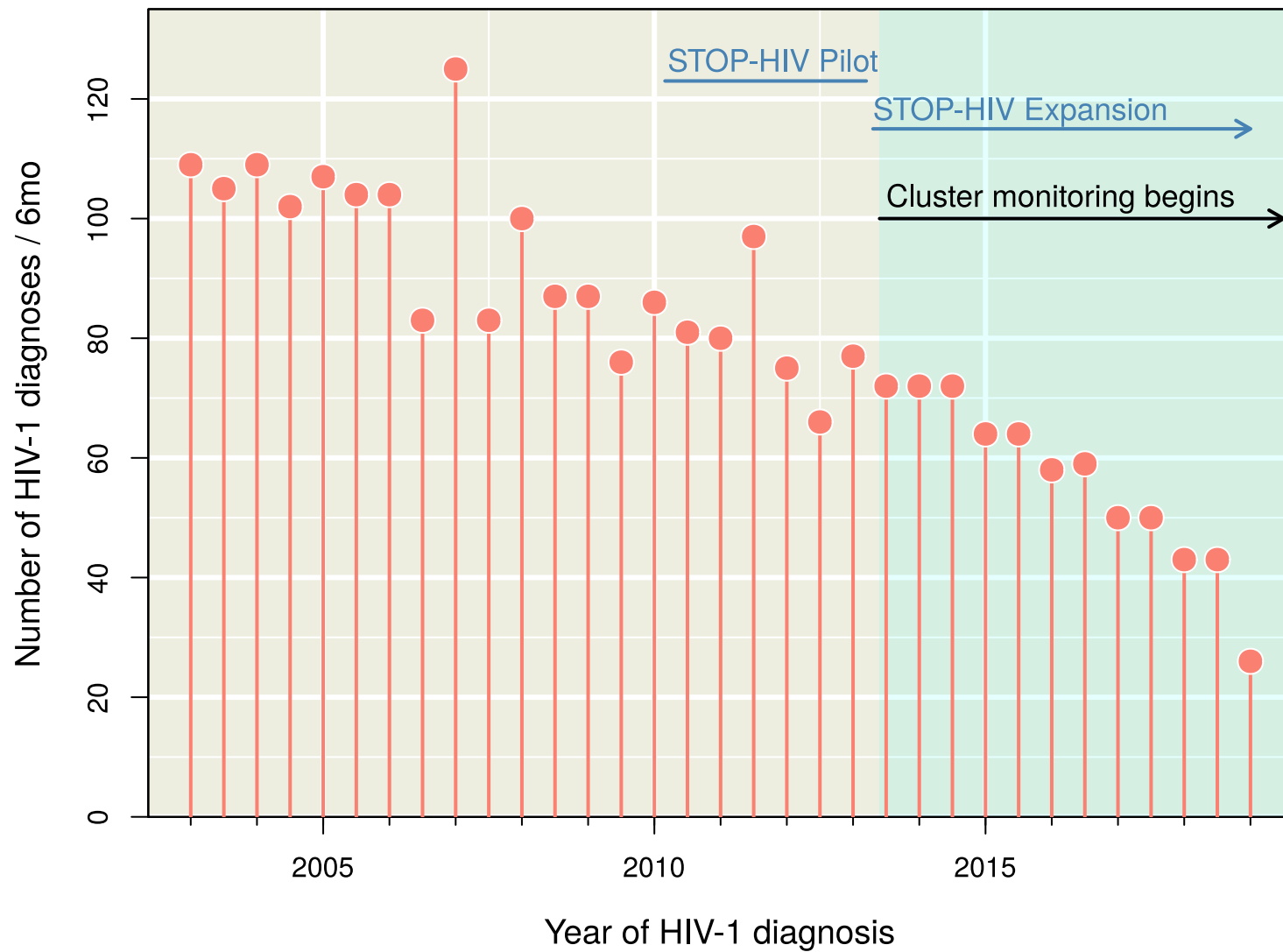
What are the risks?

- 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).
- The development of *source attribution* methods to reconstruct "who infected whom" is an active area of research in phylogenetics.



How do we minimize risk?

- Most of these risks already exist in the absence of cluster analysis (clinical genotyping).
- Guiding principle: **Confer benefits to public health without increasing personal risk.**
- System is physically and network secured.
- All phylogenetic data 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.