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Focusing the AIDS response with phylogenetics: the Vancouver experience

Drs. Jeffrey B. Joy, P. Richard Harrigan, and Julio S.G. Montaner

BC Centre for Excellence in HIV/AIDS
Division of AIDS, Department of Medicine, University of British Columbia
Critical Questions for Deployment of Public Health Resources

• Public health officials are frequently faced with questions surrounding the efficient focus of limited resources.

• How to most efficiently choose places and populations to prioritize the deployment of interventions for maximum effect?

• How to find additional HIV positives?
HIV in British Columbia

• BC is the 3rd most populous province of Canada.
• Historically, highest rates of new HIV diagnoses.
• Marked decline attributed to large-scale rollout of fully subsidized TasP.
What is phylogenetics and how can a virus phylogeny help?

A virus phylogeny is a family tree of virus sequences
Phylogenetic Epidemiological Inferences

Temporal Distribution of Nodes (branching points)

Distribution of Branch Lengths
Phylogenetic Clustering

- HIV evolves very rapidly.
- Infections that retain significant genetic similarity are likely related by **recent transmissions**.
- Clusters of genetically similar infections can represent **localized outbreaks** of HIV transmission.
Caveats

• A “network” of genetic similarity is not a transmission network.
• We can’t exclude the possibility of intervening unidentified infections.
• Thus, branching events in a virus phylogeny do not represent transmission events.
• We consider only clusters of size 5+.
• Thus, we are considering things at the group level rather than at an individual level.
Phylogenetic Monitoring system

- Over 42,000 HIV genotypes from nearly 9,000 residents of BC living with HIV.
- Nearly 75% of estimated HIV prevalence in the province.
- All HIV genotypes automatically linked to clinical, demographic, and epidemiological variables.
- Including sub-populations (risk factors) and geography.
- De-identified prior to analysis.
- Phylogenetic trees and clusters regenerated daily.
- Currently tracking 170 clusters.
Monitoring system
Cluster 55

April 2014 to June 2014

new case

new cases

HIV drug resistance
no resistance
undetectable viral load
Cluster 55 Follow-up

- Enhanced public health follow-up for 9 individuals (8 with TDR*) to ensure linkage to care.
- Prior to follow-up, only 5 of 9 were on ART, only one with suppressed viral load.
- By end of follow-up, 8 had started ART, 6 suppressed viral loads.

* Transmitted drug resistance, K103N
Cluster 55 Conclusions

• Marked reduction of TDR in cluster 55.
• Large reduction in viral load of the cluster.
• Phylogenetics facilitated the prioritization and cost-effective delivery of:
  ▪ connection to care
  ▪ HIV testing
  ▪ enhanced partner care
  ▪ Treatment
  to populations with greatest risk.
Phylogenetically Targeted PrEP

- We have begun offering PrEP at no cost to partners of individuals in active HIV transmission clusters.
Next Steps

• In BC, phylogenetics has proven to be an efficient way to:
  o Identify populations at high risk of exposure to HIV transmission
  o Target public health interventions
    » HIV testing
    » PrEP
    » Enhanced partner care

• With the support of the Public Health Agency of Canada we are currently offering phylogenetic monitoring to other Provinces and Territories of Canada.
Phylogenetic Clustering of HIV in Canada

Canadian Province

- British Columbia
- Alberta
- Saskatchewan
- Ontario
- Quebec
Most Clusters Province Specific

- 156 provinces included in clusters
- 74 provinces included in clusters
- 44 provinces included in clusters
- 10 provinces included in clusters
- 1 province included in clusters

Number of Provinces Included in Cluster
Frequency
Conclusions

• Most clustering occurs within provinces through local transmission.

• Some interprovincial clustering.

• Provinces with lots of data display similar patterns:
  - Some large clusters - predominated by IDUs
  - Lots of smaller clusters

• Phylogenetic monitoring provides practical, actionable insights about HIV epidemics at multiple scales.
Conclusions

• As we reach 90-90-90 it will be increasingly difficult to find remaining pockets of HIV transmission.

• Phylogenetics provides rapid, real time, methods of:
  • Identifying additional HIV positive individuals and at risk subpopulations
  • Allows HIV testing, PrEP, partner care, and prevention efforts to be most efficiently deployed.

• Phylogenetic methods developed to combat the HIV epidemic will apply well to other emerging and established epidemics.