

# **Epidemiological Correlates of HIV Phylogenetic Diversification Rate in British Columbia**

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## **Background**

Identifying HIV transmission risk factors can inform the prioritization of health care services. Although phylogenetic clustering of HIV sequences is routinely performed to evaluate characteristics associated with transmission, clusters membership over-simplifies the range of transmission activity across a population. We introduce an alternative method to investigate HIV transmission risk factors in British Columbia (BC), Canada, based on patients' viral diversification rates.

## **Methods**

For 8,103 people living with HIV (PLHIV) in BC in March 2018, we recovered the oldest available HIV protease and RT sequences from the BC Drug Treatment Program database. We inferred 100 bootstrap approximate maximum likelihood phylogenetic trees and for each tip, we calculated its diversification rate as an estimate of its transmission rate. Patient attributes significantly associated with high viral transmission were evaluated using a gamma generalized linear model.

## **Results**

Having a high HIV diversification rate was positively associated with being younger, using injection drugs, having hepatitis C virus, having a high recent viral load, and residing within the Northern BC Health authority (Table 1). In contrast, having ever had AIDS and identifying as black were both significantly associated with lower diversification rates (Table 1).

## **Conclusions**

By identifying risk factors associated with HIV transmission using the viral diversification rate among PLHIV, we can confidently recommend prioritized provision of treatment and prevention services for key groups. Additionally, these analyses highlight that HIV diversification rates can illuminate differences in individuals' transmission activity, regardless of phylogenetic cluster membership.