

# The 29th Annual Canadian Conference on HIV/AIDS Research Le 29e Congrès annuel canadien de recherche sur le VIH/sida

Session: **EPH3**: Saturday May 2 – 15:00:17:00 – HIV in Priority Populations and Global Health Issues: Epidemiology and Prevention

Track: Epidemiology and Public Health  
Subject: HIV in Priority Populations and Global Health Issues: Epidemiology and Public Health Aspects

Presentation Type: Oral

Title of Abstract: **Sporadic Clustered Outbreaks of HIV among MSM Persist in Treatment-as-Prevention Era**

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## Abstract

**Background:** Phylogenetic analyses of the interrelationships of viral sequences, using novel statistical tools, provide molecular epidemiological frameworks to reconstruct HIV transmission networks. We applied these methods to gain novel insights on HIV transmission patterns across Quebec, uncover cryptic at-risk populations, and elucidate epidemic drivers that cannot be identified by traditional epidemiological approaches.

**Methods:** Genetic analyses were performed on subtype B *pol* sequences derived from newly-infected Men having Sex (MSM, n=4800) and Heterosexuals subgroups, including People who Inject Drugs (PWID) and Migrants from Haiti and the Americas (n=1836). Phylogenetic analyses were also conducted on non-B viral subtypes originating from Migrants from Africa, Asia and Europe (n=1578). Growth trajectories of transmission networks (6+ members/cluster) from 2004 to 2017 were analyzed using Maximum-Likelihood MEGA10 and/or HIV-TRACE (Transmission Cluster Engine) platforms.

**Results:** Among MSM, half of the subtype B epidemic is attributable to viral strains (n=1839) leading to “dead-end” transmissions (n= 1478) or short-lived clusters (2-5 members) (n=850). The remaining half of viral infections (n=2371) could be ascribed to sporadic large outbreaks, averaging 42 members/cluster. There has been a 48% decline in new singleton/small cluster transmissions over the 2011-2017 (n=673) vs. 2004-2010 (n=1271) periods, concomitant to advances in Treatment-as-Prevention paradigms. In contrast, ongoing genesis and/or expansion of clustered outbreaks persist over the 2011-2017 (n=1056) and 2004-2010 periods (n=1110). Heat maps of individual clusters can distinguish “actively-growing” clusters and “newly emerging” clusters from older low-risk clusters. HIV-TRACE maps showed differential features of forty large cluster sub-epidemics (e.g. subjects’ ages, recency of infection, geographic locations). Phylogenetics uncovered the cryptic introduction and spread of subtype B and non-B subtype sub-epidemics among migrants to the province.

**Discussion:** The ability to predict, identify and respond to emerging “active” HIV transmission clusters may tailor public health interventions to avert transmission cascades and control the HIV epidemic.