

## Characterising Active HIV-1 Transmission Clusters in Queensland Using Molecular Phylogenetic Analysis

Davis CA<sup>1</sup>, Reid S<sup>1</sup>, [Gilks C](#)<sup>1</sup>

<sup>1</sup> School of Public Health, University of Queensland, Brisbane, Queensland, Australia

**Background:** There has been a resurgence of HIV-1 infections in Australia over the previous two decades. Molecular phylogenetic analysis (Mphy) has improved understanding of how HIV-1 spreads in populations, including identifying active (recent and increasing in size) transmission clusters for public health action. This study aimed to characterise putative transmission clusters through secondary use of linked, de-identified epidemiological and HIV-1 molecular sequences using Mphy.

**Methods:** All data was secondary and linked data, including 1,766 unique baseline HIV-1 genotypic resistance (partial pol) sequences tested between 2008-2013 of which 1,563 sequences were linked to notification case reports. Mphy included testing for subtype (jpHMM), high-level drug resistance (H-LDR) to at least one drug (Stanford HIVDB), and active (1+ recent diagnoses) clusters (HyPhy). Cluster size (small 2-4, moderate 5-19, and large 20+) and membership was examined using descriptive and multivariate statistics.

**Results:** One-third (32.0% or 565) of all sequences comprised 43 moderate and 7 large (B62, B52, C32, B28, B25, B24, and B20) clusters, 29.4% (519) sequences comprised small clusters (298 in pairs), and 38.6% (682) were singletons. Most sequences (78.8%) were subtyped as HIV-1B including 78.6% of clusters. H-LDR was identified in 10.9% of sequences and 33% of clusters. All large clusters were active (mean=3.3 sequences/yr); most (6) were HIV-1B and 3 included an active H-LDR sequence. Twenty-one (48.8% of) moderate-sized clusters were active (mean 1.1 sequences/yr); most (19) were HIV-1B and 5 included an active H-LDR sequence. Thirty-eight (17.4% of) small clusters were active; most (29) were HIV-1B and 7 included an active H-LDR sequence. Multivariate results of membership in large clusters will be discussed in more detail.

**Conclusion:** Mphy of linked sequences is useful in identifying numerous large and moderate-sized active transmission clusters, including H-LDR sequences. Implications for enhanced surveillance and public health action will be discussed.

Craig was in part funded by a Australian Postgraduate Award APA.