

LOCAL GEOGRAPHIC DIFFERENCES IN LONG-LASTING HIV-1 CLUSTERS IN NEW SOUTH WALES

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Background:

Sequence cluster analysis is a powerful tool to identify potential transmission cluster in phylogenetic trees, which represent potential active transmission, or long-lasting that are linked by epidemiological features.

Methods:

Phylogenetic trees for the *pol* region of subtype B were estimated using 2,927 virus sequences sampled in NSW from 1992 to 2016. A cluster analysis using ClusterPicker v1.2.5 implementing a node support of 0.99 was performed to identify long-lasting clusters. Epidemiological characteristics and geographic location (SLA and LHD) were mapped onto these clusters to allow the identification of major drivers of transmission dynamics.

Results:

The phylogenetic tree showed a star-like topology well-known for the exponential expansion typical in HIV-1. Up to 100-fold more sequences were sampled in the inner city of Sydney compared to the rest of the state, which is in concordance with incidence rates. Of all sequences, 385 were within 39 long-lasting clusters of at least 5 sequences with a node support of 0.99. A marked increase in overall number of clusters from 2009 onwards was observed. The largest cluster contained 26 sequences and covered at time span of almost nine years. Strikingly, ten of the 39 subtype B clusters identified have been circulating for over ten years and seven of these contained sequences sampled in 2016, hence these include ongoing transmission clusters. The longest lasting cluster has been ongoing for over 22 years and includes 18 sequences. Interestingly, 38% of the sequences within the long-lasting clusters were from the south-eastern suburbs but only 10% and 9% from Sydney's west and north, respectively.

Conclusion:

There is a geographic difference in long-lasting subtype B virus clusters and the inner city of Sydney is a major hub for the HIV epidemic in NSW. This data supports the current HIV prevention strategies which are currently focused in this region.

Disclosure of Interest Statement:

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