

CHARACTERISTICS ASSOCIATED WITH HIV-1 TRANSMISSION CLUSTERS IN NEW SOUTH WALES'

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Background:

Despite treatment as prevention rollout, the number of newly diagnosed HIV-1 infections in NSW was stable between 2004 and 2015. To gain a deeper understanding into transmission dynamics, a molecular epidemiological approach was taken to determine characteristics of transmission clusters.

Methods:

The statewide HIV sequence database was linked with the HIV notifications. Phylogenetic tree construction was performed for three periods (2004 to 2007, 2008 to 2011, and 2012 to 2015). Clusters were identified using genetic distance threshold of 0.015 and support > 0.7. Univariate and multivariate analysis was undertaken to determine factors associated with cluster membership.

Results:

There were 2552 linked sequences, 1904 subtype B. The proportion of sequences in a cluster increased from 16% (2004-2007) to 30% (2008 to 2011) to 38% (2012 to 2015), with increases in cluster size. For subtype B sequences 2012 to 2015 (n=760), 94% male, 60% < 40 years, 86% MSM, 29% seroconversion symptoms. The two largest clusters (n=10 & 13) were predominantly metropolitan MSM. For non-B sequences 2004 to 2015 (n=580): 68% male, 65% <40 years, 43% MSM, 20% seroconversion symptoms. These were predominantly transmission pairs, with largest cluster size of 5. On multivariate analysis, factors independently associated with subtype B and non-B cluster membership were acquisition in Australia, early infection stage and diagnosis post- 2012. Age <30 years was associated with B subtype clusters.

Conclusion:

Transmission clusters in NSW are predominantly comprised of early stage of infection acquired in Australia in the previous five years. Campaigns focused on increased HIV testing among MSM may have led to the identification of new cases in these clusters in recent years. Factors associated with cluster membership are the same in B and non-B subtypes, although cluster size is larger in B subtypes. Ongoing analysis of transmission dynamics can help inform future public health strategies.

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