HIV transmission links between past and newly diagnosed infections: a molecular epidemiology study

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Abstract

Background **Understanding the driving forces of HIV infection is crucial for developing intervention strategies. We aimed to infer these forces from genetic linkages between past and newly diagnosed cases by a molecular approach.**

Methods **We recruited newly diagnosed HIV patients from all three HIV specialist clinics in Hong Kong, China, between 2016 and 2018 to collect their HIV sequences with corresponding behavioural and clinical data. We retrieved archived HIV sequences from 1994 to 2012 separately. We pooled and analysed sequences by constructing a network with 1·5% TN93 distance threshold and measured node degree centrality. We did univariate analyses to identify factors associated with genetic links with archived sequences among newly diagnosed patients, and used a generalised linear model to differentiate archived sequences having links with new cases adjusting for diagnosis year.**

Findings **2778 partial *pol* sequences were amalgamated for network construction, of which 426 were newly diagnosed. The network contained 1908 (69%) nodes and 23 305 edges. Some 703 (3%) edges linked 192 archived samples with 135 new cases. Of 239 newly diagnosed patients with genetic connections, those linked with past infections were more likely to be subtype B (odds ratio 3·31; p<0·0001) and be 30 years or younger (2·26; p=0·0065). Men who have sex with men (MSM) linked with past infections were less likely to be engaged in chemsex (0·52; p=0·039) or users of a mainland Chinese gay dating mobile application (0·39; p=0·035). Generalised linear model showed that people with past infections linked to new cases were younger (p=0·0002), had a higher degree centrality (p<0·0001), were less likely to be subtype CRF01_AE (p=0·0019), and infected through heterosexual contact (p<0·0001) or injection drug use (p=0·0002) compared with MSM contact.**

Interpretation **HIV transmission chains linking new with past infections in Hong Kong were driven by younger MSM. Chemsex, emergence in recent years, only clustered in and contributed to some new infections. Formation of transmission linkages over time signified the importance of targeting new and established infections in developing prevention strategies.**

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Contributors
THK contributed to data analysis and interpretation, and drafting of the Abstract. NSW and DPCC contributed to data analysis. GCYL, KCWC, OTYT, WSL, KMH, MPL, WL, SNC, SWCT, and WCY contributed to the acquisition of data. SSL conceptualised the study, contributed to the study design and data interpretation, and critically amended the Abstract. All authors have seen and approved the final version of the Abstract for publication.

Declaration of interests
We declare no competing interests.

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