HIV-1 Transmission Networks Among Men Who Have Sex With Men in Asia

To the Editor—We read with great interest the recent article by Yang et al [1], which reports the high incidence of human immunodeficiency virus type 1 (HIV-1) infection and syphilis among men who have sex with men (MSM) in Jiangsu and Changzhou cities in China. The potential role of transmission networks in fueling the AIDS epidemic among MSM in Asia was also highlighted in the editorial section of the same issue [2]. Because regional data on transmission networks remain largely inadequate, we examined the population history of HIV-1 transmission networks by estimating the temporal origin of genetically similar virus variants circulating at a population level across Asia. Using phylodynamic information, we also attempted to explain the continued expansion of HIV-1 among MSM as seen today in the region.

We studied 192 HIV-1 positive treatment-naive MSM recruited in Singapore and Malaysia between 2006 and 2012. The protease sequence data generated from an antiretroviral resistance surveillance program were analyzed using neighbor-joining and maximum likelihood phylogenetic reconstructions to identify transmission networks, following guidelines described elsewhere [3, 4]. Bayesian coalescent analysis was carried out to delineate the divergence time of each networks. A total of 12 transmission networks of different sizes (involving 3–23 MSM subjects) were identified in Singapore and Malaysia, most of which emerged after the mid-1990s (Figure 1). New networks continued to emerge thereafter, despite increased access to combination antiretroviral therapy in both of these countries. Branch length analysis of the time-stamped phylogenetic trees also showed a relatively short transmission interval (time between transmission events), ranged from 0.1 to 6.5 years, suggesting that HIV-1 was transmitted at great speed within these networks. Similar phylodynamic studies conducted recently in China and Hong Kong also uncovered the presence of multiple transmission networks among MSM [6, 7] (Figure 1). Population history estimation for HIV-1 showed a trend of continuous emergence of new networks and coexistence of multiple MSM subepidemics from various common ancestors in these Asian countries. This is in alignment with the high HIV-1 incidence among MSM reported across Asia [8], establishing the role of transmission networks in contributing to the rise in new HIV-1 infections. These networks, if left uninterrupted by means of effective intervention strategies, such as early initiation of combination antiretroviral therapy or preexposure prophylaxis, will most likely continue to grow, resulting in sustained transmission among MSM.
Figure 1. Divergence times of human immunodeficiency virus type 1 (HIV-1) transmission networks among men who have sex with men in Asia. The divergence time (in calendar years) of the most recent common ancestor for the transmission networks observed in Malaysia and Singapore were estimated based on the HIV-1 protease gene using Bayesian coalescent relaxed clock-based analysis in BEAST software (version 1.7.4) [5] and a general time-reversible nucleotide substitution model with a gamma distribution and a proportion of invariant sites. Under similar conditions, the origin of the transmission networks found in Hong Kong and mainland China (northern China) were estimated based on the HIV-1 pol and gag gene sequences, respectively, also using BEAST software. The mean divergence times (circles) for each transmission network and the 95% highest posterior distribution are indicated.

Note

Potential conflicts of interest. All authors: No reported conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

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