



Commentary

HIV Phylogeographic Analyses and Their Application in Prevention and Early Detection Programmes: The Case of the Tijuana–San Diego Border Region



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As the deadline for the UNAIDS 90–90–90 target approaches, huge challenges in HIV diagnosis, access to treatment and follow up have become evident. This initiative aims to have 90% of people living with HIV diagnosed, 90% of diagnosed people receiving antiretroviral therapy (ART) and 90% of people receiving ART under viral suppression by 2020 (http://www.unaids.org/sites/default/files/media_asset/90-90-90_en_0.pdf, n.d.). In this regard, huge improvements have been made on ART programmes around the world, especially in resource-limited settings. Nevertheless, identifying new and undiagnosed HIV infections is an important issue in large areas of the world where stigmatization and ignorance towards HIV infection and its transmission routes still prevail. This is the case of most Latin American countries, which generally present concentrated epidemics with a wide variety of epidemiological scenarios, most of which are characterized by late presentation of individuals living with HIV to clinical care (Crabtree-Ramirez et al., 2011). In Mexico, a middle-income country with a strong ART programme, it is estimated that more than half of HIV-infected individuals are unaware of their serologic status (<http://www.censida.salud.gob.mx/descargas/2009/VIHSIDAenMexico2009.pdf>, n.d.). Cases like this render ART programmes alone unable to control the epidemics and constitute a major challenge for the ambitious 90–90–90 target to become a reality. Knowledge on HIV transmission dynamics is needed in order to focus and strengthen prevention and early detection programmes, urgently needed in Latin America. In recent years, HIV phylogenetic and phylogeographic analyses have been ever more recognized as a fundamental tool for studying HIV transmission dynamics, which can result in the generation of public health policies improving HIV prevention programmes (Grabowski & Redd, Mar 2014). Phylogenetic and clustering analyses can provide useful information on clinical and demographic

factors shaping HIV transmission in specific geographic areas, and when geographic data is available, can identify the specific location and spread of HIV transmission hotspots. Large multinational efforts such as PANGEA-HIV (Pillay et al., Mar 2015) have been created to use viral sequence data to assess transmission of HIV in the context of generalized epidemics. Moreover, recent studies have demonstrated the possibility of identifying HIV transmission hotspots in near real time by the secondary phylogenetic analysis of HIV sequences obtained for routine drug resistance testing in concentrated epidemics with a high sampling density (Poon et al., 2015).

In this issue of E-Biomedicine, Mehta et al. (Mehta et al., 2015) present a phylogeographic study to assess the characteristics of HIV transmission in the Tijuana–San Diego crossing of the Mexico–U.S. border region. This work is a good example of how phylogenetic and phylogeographic analyses on already existing HIV sequence data can provide useful information on HIV transmission dynamics in an especially complex HIV transmission hotspot. The Tijuana–San Diego border is probably the busiest land border crossing in the world, characterized by a large transnational commercial sex network, a large population of people who inject drugs (PWID), and a large population of men who have sex with men (MSM) (Strathdee et al., 2012). The prostitution district in Tijuana is frequented by thousands of U.S. and foreign tourists each year and this region geographically overlaps with a neighbourhood known for its high density of PWID. Risk behaviour for HIV acquisition is high in the border region and is strongly associated with economic disparities, with a high frequency of male clients negotiating condom-less sex with female sex workers (FSW), who accept higher rates for unprotected sex out of economic necessity and are also often PWID (Strathdee et al., 2012; Martinez-Donate et al., 2015; Robertson et al., 2014). In their study, Mehta et al. describe the epidemics in Tijuana and San Diego as highly separated, the last one dominated by MSM clusters. Nevertheless, the authors identified bi-directional mixed international clusters including FSW, PWID and MSM, describing this border region as a “melting pot” of risk groups. International clusters had higher proportion of females, heterosexuals and PWID, highlighting the importance of commercial sex in HIV transmission across the border and pointing areas of opportunity for prevention interventions. Moreover, albeit with considerable overlap in both directions, a shift in viral migration from Tijuana to San Diego was observed comparing 2014 to the 1990s, when the

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opposite was true. It is important to mention that even with a relatively low sampling density, clusters providing useful epidemiological information were found yielding useful conclusions to inform public health policies. Also, the lack of male individuals in clusters including FSW is also informative as it underscores the need to focus detection efforts in their customers and partners.

Following WHO recommendations to implement HIV drug resistance (DR) surveillance in the region, many Latin American countries are making efforts to implement HIVDR surveys nationally, with the support of WHO-accredited national and regional laboratories. Thus, even with an important limitation in sequencing capacity, generation of HIV sequence data linked to basic socio-demo-geographic data is expected to grow significantly in the next few years. These data could also be used in phylogenetic and transmission network analysis to inform HIV transmission dynamics in the region, always with a cautious interpretation due to sampling limitations. Eventually, these data could improve targeting of prevention and early detection efforts to place this region of the world closer to the 90–90–90 target in 2020.

Disclosure

The authors declare no conflicts of interest.

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