

Acquisition of HIV by African-born residents of Victoria, Australia : insights from molecular epidemiology

ABSTRACT

African-born Australians are a recognised "priority population" in Australia's Sixth National HIV/AIDS Strategy. We compared exposure location and route for African-born people living with HIV (PLHIV) in Victoria, Australia, with HIV-1 pol subtype from drug resistance assays and geographical origin suggested by phylogenetic analysis of env gene. Twenty adult HIV positive African-born Victorian residents were recruited via treating doctors. HIV exposure details were obtained from interviews and case notes. Viral RNA was extracted from participant stored plasma or whole blood. The env V3 region was sequenced and compared to globally representative reference HIV-1 sequences in the Los Alamos National Library HIV Database. Twelve participants reported exposure via heterosexual sex and two via iatrogenic blood exposures; four were men having sex with men (MSM); two were exposed via unknown routes. Eight participants reported exposure in their countries of birth, seven in Australia, three in other countries and two in unknown locations. Genotype results (pol) were available for ten participants. HIV env amplification was successful in eighteen cases. HIV-1 subtype was identified in all participants: eight both pol and env; ten env alone and two pol alone. Twelve were subtype C, four subtype B, three subtype A and one subtype CRF02-AG. Reported exposure location was consistent with the phylogenetic clustering of env sequences. African Australians are members of multiple transnational social and sexual networks influencing their exposure to HIV. Phylogenetic analysis may complement traditional surveillance to discern patterns of HIV exposure, providing focus for HIV prevention programs in mobile populations.

Keyword: HIV; Pediatric; African-born residents; Molecular epidemiology; Australia