Ongoing cross-species transmission of simian retroviruses and high HIV prevalence in Cameroon

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Background: Recent studies have shown ongoing exposure of humans to a wide variety of simian retroviruses, including SIV, HTLVs and SFVs. Moreover, the recent descriptions of HIV-1 group F in Cameroon and HIV-2 group D in Ivory Coast, confirm that our knowledge on HIV diversity is still incomplete. Here, we studied retroviral infections in humans living in rural forest areas in southern Cameroon, in order to explore other transmissions to humans as well as the extent of the HIV epidemic in these areas.

Methods: A total of 3288 blood samples were obtained from adults in 26 villages. All samples were tested for the presence of HIV antibodies by commercial Elisa. HIV, SIV, SFV and HTLV antibody positive samples were tested by PCR and sequence analysis to confirm and characterize retroviral infection. RT and protease (1800 bp) for HIV, integrase (2000 bp) for SIV, and PCR (410 bp) for HTLV. Results: In this rural forest areas, the overall HIV prevalence ranged between 6% and 9%, and was at least two times higher in women as compared to men, reaching 20% in women aged between 25 and 34 years. All HIV infections were HIV-1 group M. Genetic characterization of 158 HIV-1 strains showed predominance of CRF02_AG (80%), 12 other subtypes(CRF 02_AG, 01B) and 11% and has new possible CRFs. Importantly, 13 transmission clusters (20% of HIV-1 strains) including 21-30 strains were observed. Only 2 clusters comprised HIV-1 strains from west-Cameroon and only 1 strain was assigned to HIV-1 group O. Moreover, SFV and HTLV infections in the studied population were very high compared to the national estimate (4.3%).

Conclusions: Although HIV infections were observed in rural forest areas from Cameroon where humans are exposed to HIV, our study clearly shows contemporary transmission of simian retroviruses. The high HIV prevalence and high rates of transmission clusters in these rural areas indicate that, if a new HIV crosses the species barrier, conditions for rapid spread are present.

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Figure 1. HIV, SFV and HTLV Prevalence and genetic diversity

Figure 2. Ongoing cross-species transmission of simian retroviruses and high HIV prevalence in Cameroon

Figure 3. Phylogenetic analyses of newly identified HIV-1 strains

Figure 4. Phylogenetic analyses of newly identified HIV-1 strains

Figure 5. Phylogenetic analyses of newly identified HIV-1 strains