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

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Julius Chia[1,2], Avelin F. Aghokeng[2,1], Emilande Guichet[2], Ahidjo Ayouba[2], Steve Ahuka-Mundeke[2], Nicole Vidal[2], William Switzer[3], Eric Delaporte[2], Eitel Mpoudi Ngole[1], Martine Peeters[2]

1. Projet PRESICA and IMPM/CREMER, Yaoundé, CAMEROON; 2. IRD-UMI233, Université Montpellier 1, Montpellier, France; 3. Centers for Disease Control and Prevention, Atlanta, GA.

Contact: martine.peeters@ird.fr

ABSTRACT

Background: Recent studies have shown ongoing exposure of humans to a wide variety of simian retroviruses, including SIVs, HTLVs and SFVs. Moreover, the recent descriptions of HIV-1 group P in Cameroon, and HIV-2 group I 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, to further explore other transmissions to humans as well as the extent of the HIV epidemic in these areas.

Methodology: A total of 3288 blood samples were obtained from adults in 26 villages. All samples were tested for the presence of HIV antibodies using commercial assays, and a subset of individuals with highest probability of exposure to non-human primates were tested for the presence of SIV and SFV antibodies by an in-house xMAP assay. HTLV antibodies were detected 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 for SIV (300 bp) and SFV (425 bp), tax (200 bp) and/or LTR (450-900bp) 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 188 HIV-1 strains showed predominance of CRF02-AG (58%), 12 other subtypes/CRFs, URFs (10%) and two new possible CRFs. Importantly, 13 transmission clusters (20% of HIV-1 strains) including 2 to 10 strains were observed. Only 3 clusters comprised HIV-1 strains from 1 women and 1 man. In the other clusters, strains derived from women predominated, with one cluster of 10 strains exclusively from women, residing in 4 different villages on a major road for logging transport. HTLV infection was confirmed by PCR in 30/2501(1.2%) individuals in Cameroon, prevalences were similar among women and men but increased with age from 0.7% (18-24y) to 1.8% (>45y). HTLV-1 subtype B predominated, but a new HTLV-1 subtype F and HTLV-3 B variant related to STLVs from local NHPs were observed. Although, 23 on a subset of 813 samples reacted weakly with SIV antigens, no virus was amplified by PCR. Among 69 SFV antibody reactive samples, only one SFV infection with a chimpanzee virus, was confirmed by PCR in a 65 years old male reporting hunting.

Conclusions: Although no SIV infections were observed in rural forest areas from Cameroon where humans are exposed to NHPs, 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 SIV crosses the species barrier, conditions for rapid spread are present.

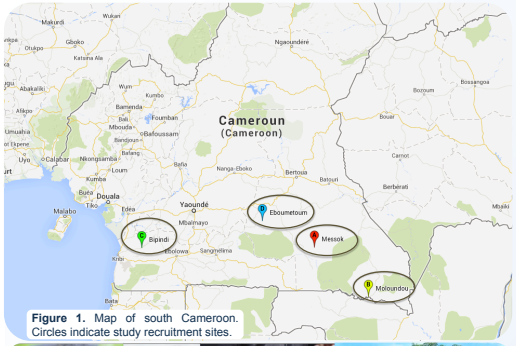


Figure 1. Map of south Cameroon. Circles indicate study recruitment sites.



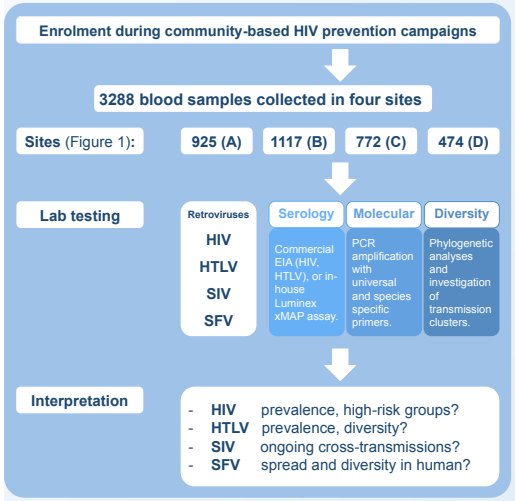
Background and Justification

The human immunodeficiency virus (HIV) epidemic illustrates the risk that cross-species transmissions of retroviruses from non-human species may represent for humans. Indeed, the virus which is currently carried by about 35 million people worldwide, with up to 70% of infected peoples living in developing countries, is responsible of about 1.5 million deaths every year. While efforts are being mobilized to reduce the burden of HIV/AIDS infection by improving the prevention and access to antiretroviral treatment, prevention of other cross-species transmissions of retroviruses that may lead to similar picture is essential.

HIV-1 resulted from at least four cross-species transmissions of simian immunodeficiency viruses (SIVs) from chimpanzees and gorillas in West Central Africa, while HIV-2 viruses resulted from at least nine independent transmissions of SIVs infecting sooty mangabeys in West Africa only. Current data indicate that humans are still exposed to a wide variety of simian retrovirus, including SIVs, Human T-lymphotropic virus (HTLVs), simian foamy virus (SFVs), and contemporary cross-species transmissions with STLVs and SFVs have been reported. Moreover, the recent descriptions of HIV-1 group P in Cameroon and HIV-2 group I in Ivory Coast, confirm these ongoing exposures, and indicate that our knowledge on HIV diversity is still incomplete.

In this study, we investigated in southern Cameroon, where populations are exposed to non-human primates through hunting and butchering, retroviral infections in humans and we further explored other transmissions to humans as well as the extent of the HIV epidemic in these areas.

Methods



Results

HIV Prevalence, Distribution and Diversity

HIV	MESSOK (%)	MOLOUNDOU (%)	BIPINDI (%)	EBOUMETOUM (%)
Male	14/408 **(3.4)**	24/465 **(5.2)**	10/341 **(2.9)**	7/222 **(3.1)**
Female	51/517 **(9.9)**	77/652 **(11.8)**	32/431 **(7.4)**	28/250 **(11.2)**
Total	65/925 **(7.0)**	101/1117 **(9.0)**	42/772 **(5.4)**	35/474 **(7.3)**

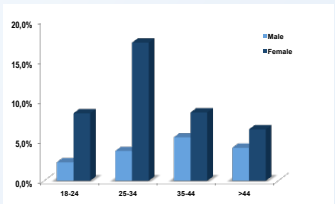


Figure 2. Overall HIV prevalence per age groups

Observed HIV prevalence varied from 5.4% to 9.0%. High prevalence were found in women, reaching almost 20% in women aged 25-34 years. A broad HIV-1 genetic diversity was observed, with the CRF02_AG strain predominating.

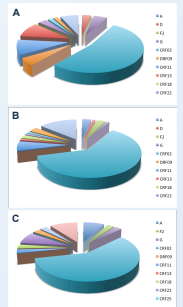


Figure 3. HIV-1 Subtypes and CRFs distribution in Messok (A), Moloundou (B) and Bipindi (C).

HTLV and SFV Prevalence and genetic diversity

SITES	HTLV		SFV	
	Serology pos.	PCR confirmed	Serology pos.	PCR confirmed
Messok	30/955 **(3.1%)**	13/30	13/255 **(5.1%)**	0/13
Moloundou	19/1110 **(1.7%)**	14/19	6/180 **(3.3%)**	0/6
Eboumetoum	9/431 **(2.1%)**	3/9	50/471 **(10.6%)**	1/50
Total	58/2496 **(2.3%)**	**30/58**	69/906 **(7.6%)**	1/69

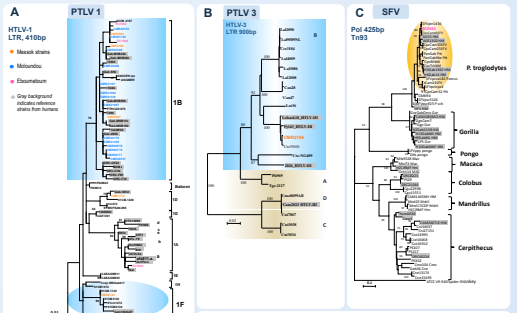


Figure 5. Phylogenetic trees of newly identified HTLV-1 strains (A), HTLV-3 strains (B), and SFV strains (C).

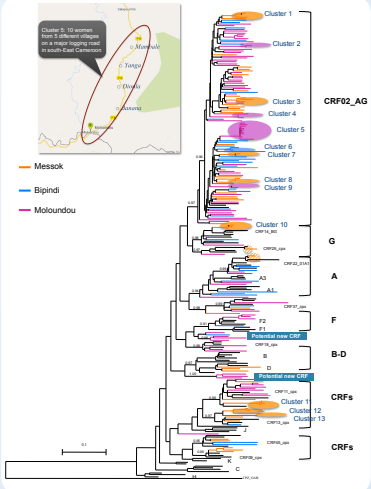


Figure 4. Phylogenetic analyses of newly identified HIV-1 strains.13 Transmission clusters were identified and 10/13 involved only women. Potential new recombinants forms were also identified.

Conclusion

This study showed that prevention of HIV infection is still a major challenge in Cameroon rural areas where observed HIV prevalence are very high compared to the national estimate (4.3%).

In young women, the prevalence was two to five times higher than the national prevalence. In addition, the figure of transmission clusters that involve several women indicates that specific information and prevention strategies should be implemented and must involve the community.

We observed no SIV infection in these rural forest regions where humans are exposed to NHP, but the identification of several other NHP retroviruses as HTLV and SFV highlights the risks of possible new cross-transmission of SIVs other than SIVcpz, SIVgor or SIVsmm and supports the necessity of regular surveillances.

ACKNOWLEDGEMENTS

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