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Claudia Filippone, Edouard Betsem, Sylviane Bassot, Patricia Tortevoeye, Alain Froment, et al.. High frequency of HTLV-1 infection in Bantus and Pygmies from rural Cameroon bitten by non-human primates during hunting: High frequency of HTLV-1 infection in Bantus and Pygmies from rural Cameroon bitten by non-human primates during hunting. 16th International Conference on Human Retroviruses: HTLV and Related Viruses, Jun 2013, Montreal, Canada. 11 (Suppl 1), pp.P57, 2014, 10.1186/1742-4690-11-S1-P57 . pasteur-00924958

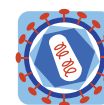
HAL Id: pasteur-00924958

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Submitted on 7 Jan 2014

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POSTER PRESENTATION

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High frequency of HTLV-1 infection in Bantus and Pygmies from rural Cameroon bitten by non-human primates during hunting

Claudia Filippone^{1,2*}, Edouard Betsem^{1,2,3}, Sylviane Bassot^{1,2}, Patricia Tortevoe^{1,2}, Alain Froment⁴, Arnaud M Fontanet⁵, Antoine Gessain^{1,2}

From 16th International Conference on Human Retroviruses: HTLV and Related Viruses
Montreal, Canada. 26-30 June 2013

HTLV-1 infection is endemic in Central Africa, as well as the closely related STLV-1 found in several non-human primates (NHPs). Like other retroviruses, acquisition through interspecies transmission is strongly suggested but needs to be investigated. We analyzed 269 selected individuals (254 men, 15 women, average age 43.5 years) for whom a direct contact (mainly a severe bite) with a NHP occurred. This happened mostly during hunting activities and involved bleeding and body fluids exchange with at least saliva/blood contact. The same number of persons who live in the same villages/settlements but did not report any bite by NHPs was matched according to sex, age and ethnicity. Both groups include either Pygmies or Bantus living in the rain forest of South Cameroon. Plasma were tested for HTLV serology by WB, and proviral DNA was searched in buffy-coat DNA by 3 HTLV generic and one HTLV-1 specific PCR. HTLV-1 prevalence was of 8.5% (23/269) among bitten individuals *versus* 1.5% (4/269) observed in the controls ($p < 0.001$). The 23 HTLV-1+ bitten individuals reported a gorilla (17), chimpanzee (3) or monkey (3) bite. Interestingly, 13/23 were coinfecting by a simian foamyvirus, for which cross-species transmission from NHP to humans through bites is demonstrated. Moreover, familial studies excluded the other established routes of virus acquisition among some positive bitten individuals. Lastly, a phylogenetic analysis showed a HTLV-1 subtype F in a bitten subject closely related to the STLV-1 strain from a *Cercocebus agilis* with whom he was in contact, thus strengthening these new findings.

Authors' details

¹Institut Pasteur, Unité d'Epidémiologie et Physiopathologie des Virus Oncogènes, Département de Virologie, Paris, France. ²CNRS, UMR3569, Paris, France. ³Faculté de Médecine et des Sciences Biomédicales, Université de Yaoundé I, Yaoundé, Cameroun. ⁴Institut de Recherche pour le Développement, Musée de l'Homme, Paris, France. ⁵Institut Pasteur, Unité de Recherche et d'Expertise Epidémiologie des Maladies Emergentes, Département d'Infection et Epidémiologie, Paris, France.

Published: 7 January 2014

doi:10.1186/1742-4690-11-S1-P57

Cite this article as: Filippone et al.: High frequency of HTLV-1 infection in Bantus and Pygmies from rural Cameroon bitten by non-human primates during hunting. *Retrovirology* 2014 **11**(Suppl 1):P57.

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* Correspondence: claudia.filippone@pasteur.fr

¹Institut Pasteur, Unité d'Epidémiologie et Physiopathologie des Virus Oncogènes, Département de Virologie, Paris, France

Full list of author information is available at the end of the article

