Table 1. Comparison of quantitative RNA levels detected in plasma and ultracentrifuged saliva pellets.

		Plasma (copies/ml)			
		Negative	10^3	10^4	10^5
Saliva (copies/ml)	Negative	3	5	6	0
	10^3	1	2	7	1
	10^4	0	0	1	1
Positive saliva (n)		1/4	2/7	8/14	2/2

The general correlation between level of plasma HIV-1 RNA and positivity of corresponding saliva may indicate a direct relationship between blood and saliva viral load. However, a given amount of HIV-1 RNA found in blood plasma sometimes corresponded to levels of saliva RNA that differed by as much as 100-fold (Table 1). Therefore, it is difficult to determine whether the HIV-1 RNA found in saliva comes mostly from blood plasma or whether it is produced locally by epithelial and T cells present in the oral mucosa. Since different pools of virus may be produced by different body compartments, information obtained on viral load, phenotype, and genotype in peripheral blood may not be pertinent to other body compartments.

Our study has demonstrated that cell-free HIV-1 RNA was present in a significant portion of saliva samples from infected individuals. Low levels of virus, defective particles, and the presence of inhibitory substances may all contribute to the low infectivity of saliva.

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Further evidence of the presence of genetically aberrant HIV-1 strains in Cameroon and Gabon

To date, the most genetically divergent HIV-1 variants have been isolated from a Cameroonian couple (HIV_{ANT70}) [1] and a Cameroonian patient ($HIV_{MVP5180}$) [2] and their complete nucleic acid sequences have been determined [2,3]. These variants have been classified as O group viruses, where O stands for 'outliers' [4]. The GPMAWY (HIV_{ANT70}) and GPMRWRS ($HIV_{MVP5180}$) amino-acid sequences at the tip of the V3 loop are very different from all the other V3 loops reported so far. In a previous study, we reported on the antigenic evidence of the presence of HIV_{ANT70} like viruses in Cameroon and Gabon [5]. Nine sera (4.8%) from HIV-positive individuals from Cameroon and five (2.5%) from Gabon were reactive in a HIV_{ANT70} V3-loop peptide solid-phase enzyme-linked immunosorbent assay (ELISA). For two of these sera, HIV_{CA9} (Cameroon) and HIV_{VI686} (Gabon), the corresponding peripheral blood mononuclear cells (PBMC) were available. In order to confirm a genetic relationship with the HIV-1_{ANT70} virus, we undertook sequencing and phylogenetic analysis. A 280 base-pair fragment of the *pol* gene was amplified by the polymerase chain reaction (PCR) on DNA extracted from cultured PBMC. PCR fragments were subsequently cloned and sequenced. The newly obtained sequences were aligned with the corresponding *pol* gene fragments of strains belonging to different subtypes documented by Myers *et al.* [4] and a phylogenetic tree was generated (Fig. 1). The classification of the reference strains in genetic subtypes, based on the 280 base-pair fragment of the *pol* gene, was identical to their position in the phylogenetic tree based on sequences of the total *pol* gene [4]. The new samples, HIV_{CA9} and HIV_{VI686}, cluster with HIV_{ANT70} and $HIV_{MVP5180}$. Within this cluster, HIV_{CA9} and HIV_{VI686} are more closely related to HIV_{ANT70} than to the $HIV_{MVP5180}$ isolate. The genetic distance between HIV_{ANT70} and $HIV_{MVP5180}$ was 7.5%. Genetic distances to HIV_{ANT70} are 4.4%

(HIV_{CA9}) and 2.6% (HIV_{VI686}), whereas distances to $HIV_{MVP5180}$ are 9.5% (HIV_{CA9}) and 7.9% (HIV_{VI686}). These values are high compared with the other HIV-1 strains included in this study, where intra-subtype distances were up to 3.6% and inter-subtype distances were 4.8–8.3%.

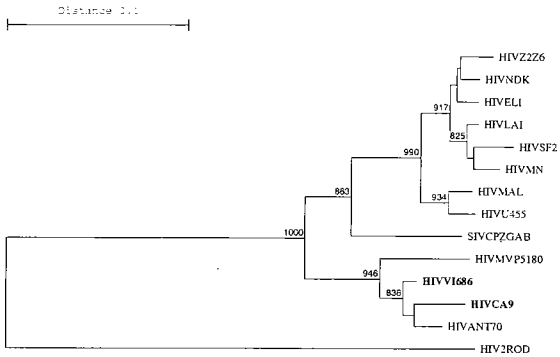

Fig. 1. Phylogenetic tree based on 280 unambiguously aligned positions of 10 HIV-1, one simian immunodeficiency virus $(SIV)_{CPZ}$ and one HIV-2 sequence. The sequences determined in this study are indicated in bold type. Tree topologies were inferred by neighbour-joining as described previously [6]. The root of the tree is placed so as to equalize its distance to the outgroup sequence $HIV2_{ROD}$ and its average to the HIV-1 and SIV_{CPZ} sequences. The distance between two sequences is obtained by summing the lengths of the connecting horizontal branches, using the scale on top. The number of bootstrap trees out of 1000 replications supporting a particular phylogenetic group in more than 70% is placed alongside the node considered. Branches supported by less than 70% of the bootstrap trees are not reliable. The nucleotide sequence data of HIV_{CA9} and HIV_{VI686} were deposited in the EMBL, GenBank and DDBJ Nucleotide Sequence Databases under the following accession numbers: X78476, X78477.

In conclusion, seroreactivity in the HIV_{ANT70} V3-loop peptide ELISA leads to the identification of viruses genetically related to HIV_{ANT70}. Further efforts to assess the true prevalence of these divergent isolates in Cameroon and neighbouring countries are necessary, in order to select vaccine prototype strains representative of particular geographical areas in Africa.

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Transmission of zidovudine-resistant HIV-1 through heterosexual contacts

In general, variants of HIV-1 bearing a point mutation at codon 215 as well as at residues 41, 67, 70 and 219 in the reverse transcriptase (RT) gene, develop in patients receiving long-term zidovudine therapy and are associated with phenotypical resistance to the drug [1]. The occurrence of primary HIV-1 infections caused by resistant variants of HIV have important implications for clinicians in terms of prognosis and approach to antiretroviral treatment. However, few observations in subjects with mutant HIV-1 primary infection have been made to date [2]; although the case of a child infected with HIV-1 from another child through unrecognized exposure [3] caused general alarm. In fact, the child was infected by a mutant virus and transmission occurred in the home, in the absence of sexual or percutaneous exposure. Fortunately, similar modes of HIV-1 transmission without an obvious exposure are rare. Conversely, the risk of acquiring resistant viruses is increasing because of the earlier and greater use of antiretrovirals and the transmission of HIV-1 through heterosexual contacts.

We used two methods to study the transmission of viruses with zidovudine-related mutations. In the first, viral isolates were obtained from heterosexual couples shortly after the primary infection of one partner (the recipient). Nucleotide-sequence analysis showed that the mutant viruses were transmitted between only one of the four couples studied [4]. In the second study (unpublished), we evaluated eight heterosexual couples who were having regular unprotected sexual intercourse, during which the male HIV-1-infected carrier (the donor) transmitted