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The origin and diversity of human retroviruses

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Abstract

Simian immunodeficiency viruses (SIV), T-cell lymphotrophic viruses (STLV), and foamy viruses (SFV) from non-human primates (NHP) have crossed the species barrier to humans at several occasions, leading to the HIV and HTLV epidemic and to sporadic cases of human infections with simian foamy viruses, respectively. Efficient infection and spread in humans differs between SFV, STLV and SIV, but seems also to differ among the different viruses from the same simian lineage, as illustrated by the different spread of HIV-1 M, N O, P or for the different HIV-2 groups. Among the four HIV-1 groups, only HIV-1 group M has spread worldwide and the actual diversity within HIV-1 M (subtypes, Circulating Recombinants) is the result of subsequent evolution and spread in the human population. HIV-2 did only spread to some extent in West Africa, and similarly as for HIV-1, the nine HIV-2 groups have also a different epidemic spread. Four types of HTLV, type 1 to 4, have been described in humans and for 3 of them simian counterparts (STLV-1, STLV-2, STLV-3) have been identified in multiple NHP species. The majority of human infections are with HTLV-1 which is present throughout the world as clusters of high endemicity. Humans are susceptible to a wide variety of SFVs and seem to acquire these viruses more readily than SIVs or STLVs but no signs of disease in humans nor human-to-human transmission of SFV has been documented yet. The current HIV-1 M epidemic illustrates the impact of a single cross-species transmission. The recent discovery of HIV-1 P, HIV-2 I, new HTLV-1 and HTLV-3 variants as well as SFV infections in humans in Central Africa, show that our knowledge of genetic diversity and cross-species transmissions of simian retroviruses are still incomplete.

Keywords

SIV; STLV; SFV; non-human primates; HIV; HTLV

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Introduction

The majority of emerging infectious diseases have a zoonotic origin and more than 70% originate from wildlife [1]. As such simian immunodeficiency viruses (SIV), T-cell lymphotrophic viruses (STLV), and foamy viruses (SFV) from non-human primates (NHP) have crossed the species barrier to humans at several occasions, leading to the HIV and HTLV epidemic and sporadic cases of human infections with simian foamy viruses respectively. Since the description of the first AIDS cases in the 1980's, the estimated cumulative number of HIV infections worldwide is around 60 million [2]. HTLV infections affect between 10 and 20 million people in the world [3] but in contrast to HIV, only 5% of infected individuals develop a disease associated with this virus [4]. The sporadic human SFV infections are apparently without any consequence for their health and human to human transmission has not been reported yet [5]. The most plausible routes for cross-species transmissions with simian retroviruses are exposure to infected blood or tissues, when NHPs are hunted or butchered for bushmeat, but injuries from pet NHPs can also play a role [6,7]. This review will present actual data on origin, genetic diversity and actual spread of these three retroviral infections in humans.

Origin and diversity of Human Immune Deficiency Viruses (HIV)

Simian Immune Deficiency Viruses (SIVs)

Shortly after the identification of HIV-1 as the cause of AIDS in 1983, the first simian lentivirus, SIVmac, was isolated in 1984 from captive rhesus macaques (*Macaca mulatta*) with clinical symptoms similar to AIDS at the New England Primate Research Center (NEPRC) [8,9]. Since SIVmac induced a disease in rhesus macaques with remarkable similarity to human AIDS, a simian origin of HIV was soon suspected. However, it became soon clear that macaques are not natural hosts of SIV infection but became infected with SIVsmm from captive sooty mangabeys that are naturally infected with this virus [10,11]. SIVs have since been isolated from many wild African NHP species, but not from wild Asian or new world NHPs [7,12]. Moreover, all these viruses seemed also non pathogenic for their host in contrast to what was observed in the captive Asian macaque species, suggesting that Asian NHP are not natural hosts for SIVs.

To date, SIVs have been identified in at least 45 different NHP species from Africa. SIVs are named according to the host species, and a three letter code refers to the common name of the corresponding NHP species; ex. SIVrcm for SIVs from red-capped mangabey, SIVgsn for greater spot nosed monkeys, etc (Table 1) [7]. The genetic diversity of NHP lentiviruses is complex and includes examples of co-evolution between the virus and the host, cross-species transmission, recombination between distant SIV lineages and certain species can even harbor different SIV lineages. Co-evolution over long time periods is the case for SIVs of the four different African green monkey species (*Chlorocebus* spec), the SIVs from the l'hoesti superspecies, (i.e. SIV lho from *C.lhoesti*, SIVsun from *C.solatus* and SIVpre from *C.preussi*) and SIVs form arboreal *Cercopithecus* species [13,14,15]. There are also numerous examples of cross-species transmissions of SIVs between NHP species with overlapping habitats or among species that live in polyspecific associations. For exemple, SIVs from African green monkeys have been transmitted to patas monkeys (*E.patas*) in

Senegal, West Africa and to yellow and chacma baboons in South Africa [16,17,18]. There are also more complex examples of cross-species transmissions of SIVs, followed by recombination between distant SIV lineages. This is the case for SIVcpz from chimpanzees, the 5' region of SIVcpz is most similar to SIVrcm from red-capped mangabeys, and the 3' region is closely related to the SIVgsn/mus/mon lineage infecting greater spot-nosed (*C. nictitans*), mustached (*C. cephus*), and mona (*C. mona*) monkeys [19]. Subsequently, chimpanzees have transmitted their virus to sympatric gorillas [20]. Finally, some NHPs are infected with more than one SIV lineage, often as a result of cross-species transmission and recombination, ex. SIVmnd-1 in mandrills from southern Gabon, and SIVmnd-2 in animals living in northern Gabon and Cameroon or SIVmus in mustached monkeys in which 3 different variants have been described [21, 22].

Despite the complex evolutionary history of SIVs, each NHP species is in general infected with a species-specific SIV which form monophyletic lineages in phylogenetic trees. The closest simian relatives of HIV-1 are SIVcpz from chimpanzees and SIVgor from gorillas. SIVs from sooty mangabeys are the closest relatives of HIV-2. These observations suggest that these NHP species are at the origin of HIV-1 and HIV-2, respectively. More in detailed studies showed that SIVs from chimpanzees and gorillas have crossed the species barrier on at least four occasions leading to HIV-1 group M, N, O and P in humans [6,23]. The different HIV-2 groups are the result from at least nine independant transmissions of SIVs from sooty mangabeys in west Africa [6,23,24].

The origin and simian reservoirs of HIV-1 in apes from West Central Africa

The first SIVcpz strains have been identified in two captive wild-born chimpanzees in Gabon [25]. Subsequent studies on captive chimpanzees from different geographic origin and subspecies showed a high degree of genetic diversity among SIVcpz strains that was associated with the chimpanzee subspecies [26]. These initial observations showed also that all HIV-1 strains were more closely related to SIVcpz*Ptt* from Central chimpanzees (*Pan troglodytes troglodytes*) in West Central Africa than to SIVcpz*Pts* from Eastern chimpanzees (*P. t. schweinfurtii*) in East Central Africa. However, data on SIVs from captive chimpanzees do not reflect the SIVcpz diversity and prevalence in the wild and studies on wild chimpanzees were needed to better document the origin and the reservoirs of the HIV-1 strains that circulate today in humans. Given the difficult access and the endangered status of chimpanzees, methods were first optimized for antibody and viral detection in faecal samples that can be collected non-invasively [27]. Subsequently, large scale studies have been conducted and today more than 6,000 fecal samples have been collected from the four different chimpanzee subspecies across Africa [27,28,29,30]. These studies showed that only the two subspecies from Central Africa are infected with SIVcpz and confirmed also that *P. t. troglodytes* and *P. t. schweinfurthii* are each infected with a subspecies-specific lineage. Within the SIVcpz*Ptt* and SIVcpz*Pts* lineages phylogeographic clusters are observed, which allowed to trace the reservoirs of the ancestors of the pandemic HIV-1 group M in south-east Cameroon [28,29,30]. Similarly, the ancestors of HIV-1 group N, have been identified in chimpanzee communities in south-central Cameroon [28,29,30]. In both chimpanzee subspecies, SIVcpz prevalences are heterogeneous with overall prevalence of 10% to 13%, that can reach even 30% or more in certain chimpanzee

communities [28,29,30]. Despite the fact that both chimpanzee subspecies represent significant reservoirs, only SIVcpz*Ptt* strains have been transmitted to humans.

In 2006, SIV infection was described for the first time in wild western lowland gorillas (*Gorilla gorilla gorilla*) in Cameroon [20]. SIVgor formed a monophyletic group within the HIV-1/SIVcpz radiation, and was more closely related to HIV-1 group O and P [20,31]. The close phylogenetic relationship of the recently discovered HIV-1 group P and SIVgor, suggested that group P is derived from SIVgor [31,32] and this was confirmed by a recent study that identified gorilla populations in south-west Cameroon that are infected with a strain that has equal or more homology to HIV-1 P than the SIVcpz ancestors to HIV-1 M and N [33]. However, no SIVgor strains sufficiently close to group O has been identified yet to be the direct ancestor of HIV-1 O. Today, more than 4,000 fecal samples from gorillas, mainly western lowland gorillas from Cameroon, have been tested. Compared to SIVcpz in chimpanzees, SIVgor is less widespread and prevalence is lower, although it can reach up to 20% in certain gorilla groups [20,31,33,34]. Despite the lower spread of SIVgor, gorillas have also transmitted their SIV to humans.

Different HIV-1 epidemics

The four HIV-1 groups have thus their origin in chimpanzees or gorillas from West Central Africa, and the initial genetic diversity of HIV-1 is associated with the different introductions of SIVs into humans. Among the four HIV-1 groups, only HIV-1 group M has spread worldwide. The other HIV-1 groups are less prevalent and remained mainly restricted to Cameroun. The geographic areas where HIV-1 O, N and P have been documented correspond to the areas where their ancestors or closely related SIVs have been identified [35]. The situation is different for the pandemic HIV-1 M lineage for which the epicenter is located in the western part of the Democratic Republic of Congo (DRC) at 1,000 km distance where the SIVcpz ancestors have been identified in Cameroon [28,36]. Although it cannot be excluded that SIVcpz*Ptt* strains closely related to HIV-1 M exist in chimpanzee populations living between southern Cameroon and Kinshasa, the virus most likely arrived in Kinshasa at the end of the 19th and beginning of 20th century due to commercial activities and exchanges with southern Cameroon [37]. As shown in a biopsy from 1960 and a serum from 1959, HIV-1 M strains circulated already among humans in Kinshasa 20 years before the first AIDS cases were observed in the United-States [38,39]. Molecular clock analyses showed that HIV-1 group M started to diverge in the human population at the beginning of the 20th century, around 1908 (confidence interval of 1884-1924) [39].

Genetic diversity and molecular epidemiology of the pandemic HIV-1 group M strain

Whereas the initial diversity of HIV-1, i.e. groups, is related to different cross-species transmission events, the actual diversity within HIV-1 M is the result of subsequent evolution and spread in the human population. Based on phylogenetic analysis, HIV-1 group M can be further subdivided into 9 subtypes (A-D, F-H, J, K), sub-subtypes (A1 to A4 and F1 and F2) and numerous circulating and unique recombinant strains, CRF and URFs respectively. Currently, more than 60 CRFs and numerous URFs have been reported [40]. Certain CRFs, like CRF01_AE and CRF02_AG, were already present early in the epidemic but many other CRFs emerged more recently. The genetic diversity within subtypes and

CRFs increases also over time. Subtype C predominates in the actual global epidemic representing almost half of HIV-1 infections, followed in decreasing order by subtype A (12%), subtype B (11%), CRF02_AG (8%), CRF01_AE (5%), subtype G (5%) and subtype D (2%) [55]. Other subtypes (F, H, J and K) and all other CRFs represented about 5% of infections in the world [41].

The classification of HIV strains has helped in tracking the course of the HIV pandemic. The highest genetic diversity, in terms of intra-subtype diversity and number of co-circulating subtypes and recombinants, is observed in the western part of the DRC [36]. This observation together with the fact that HIV-1 subtype A and D strains circulated already in Kinshasa, the capital city of DRC, around 1960, suggest that the epidemic is ancient in DRC [38,39]. Therefore, this part of Africa is considered as the epicenter where the initial diversification of the HIV-1 group M strains occurred and from where the different HIV-1 M variants started to spread across Africa and subsequently to other continents in the world. A high genetic diversity is also seen in the surrounding countries like Cameroon, Angola, Central African Republic, Gabon and Equatorial Guinea. In southern Africa, the epidemic is almost exclusively due to subtype C. In East Africa, subtype C predominates also in Burundi or Ethiopia, but subtypes A, C and D co-circulate in different proportions together with numerous unique recombinants involving subtypes A, C and D in other countries like Kenya, Tanzania, or Rwanda. In West Africa, 50% to 80 % of infections are caused by CRF02_AG. In the other continents, subtype/CRF distribution is also heterogeneous; subtype B predominates in North America and Western Europe, subtype A and CRF03_AB are widely present among IDUs in eastern Europe; subtypes B and F predominate in South America; CRF01_AE and subtype B co-circulate in south-east Asia; subtype C predominates in India [41,42]. However, as a result of the increasing human mobility and migration new HIV-1 variants are introduced and intermix with existing strains in different parts of the world. The geographic distributions of HIV-1 variants is thus a dynamic process. For example, only subtypes B and F were initially introduced in South America, but today a wide diversity of B/F recombinants circulate including at least 11 CRFs and numerous URFs [40]. A similar scenario has been observed in south-east Asia where subtype B predominated in the IDU population and CRF01_AE among heterosexually transmitted infections. Today, at least 10 CRFs and numerous URFs involving subtype B and CRF01_AE have been described [40]. Overall, with the intermixing of subtypes and CRFs, new recombinant viruses are generated and their numbers and complexity will increase since recombination involving viruses that are already recombinant will occur.

Genetic diversity and molecular epidemiology of non-pandemic HIV-1 group N, O and P

HIV-1 group O, described in 1990, remained restricted to West Central Africa, and especially in Cameroon where they represent today less than 1% of HIV-1 infections and the proportion of group O strains seems to decline overtime [43,44, Aghokeng et al. unpublished]. Sporadic cases of HIV-O infection have been described in east and west Africa, Europe and the United States but always in Cameroonians or in patients with a link to Cameroon [35]. The oldest case of HIV-1 group O infection is documented in a sailor from Norway who visited west central Africa during the 1960s [45]. A high genetic diversity

is seen among HIV-1 group O and the time of the HIV-1 group O radiation is estimated around 1920 (1890-1940) [46].

However, phylogenetic tree analysis of numerous HIV-1 O strains did not allow to identify subtypes like in HIV-1 M and a consensus classification for HIV-1 group O is still pending [35]. As a consequence of the cocirculation of HIV-1 M and O, cases of dual M and O infections, and several HIV1 M/O recombinant viruses have been observed in Cameroun but also in France [47,48,49,50].

HIV-1 N has been documented in less than 20 patients since his first description in 1998. With the exception of 1 case, all are documented in Cameroon [35,51]. The low numbers of HIV-1 N infections and the lower intragroup genetic diversity suggest a more recent introduction of the HIV-1 N lineage into the human population around 1963 (1948-1977) [46]. Finally, HIV-1 group P has been described in 2009 and despite extensive screening, only two patients have been identified today and estimates on dates are uncertain, but probably between 1845 and 1989 [32,52,53].

Origin and spread of HIV-2 in the human population

HIV-2 is most closely related to SIVsmm infecting sooty mangabeys (*Cercocebus atys*) in West Africa [54,55] and at least 9 cross-species transmissions have been observed, leading to nine HIV-2 groups [6,23,24]. HIV-2 did only spread to some extent in West Africa, and similarly as for HIV-1, the different HIV-2 groups have also a different epidemic spread. Only groups A and B were able to spread to some extent in the human population in West Africa. Overall, HIV-2 group A predominates. HIV-2 group B is less prevalent and co-circulates with HIV-2 A mainly in Ivory Coast and Ghana [56]. Recombinants between HIV-2 groups A and B have also been reported, and the first circulating recombinant form of HIV-2 (CRF01_AB) has been identified recently in three patients living in Japan [57,58]. Detailed analysis showed that this CRF most likely originated in West Africa, because a similar strain was isolated in 1990 from a patient living in Ivory Coast [58]. The other HIV-2 groups have been documented in one or two individuals (group F only) and represent most likely dead end infections or infections associated with very low spread. Except for groups G and H, groups C, D, E, F and I were isolated in rural areas where people are frequently in contact with SIV infected mangabeys (pets or bushmeat) [23,24]. The ancestors of the epidemic HIV-2 group A and B viruses, as well as for group C, G, H and I were identified in wild sooty mangabey populations from the Taï forest in Ivory Coast, in the eastern part of the sooty mangabey range [24,59]. HIV-2 D, E and F strains have been isolated in Sierra Leone or Liberia and are most closely related to SIVsmm strains from that area [23].

Today HIV-2 prevalences are decreasing and HIV-1 becomes predominant in West Africa most likely because HIV-2 is less pathogenic and less transmissible [60]. Dual infections with HIV-1 and HIV-2 have been frequently observed in areas where both viruses co-circulate, but today no recombinant virus between HIV-1 and 2 has been documented yet.

Origin and diversity of Human T-Lymphotropic Viruses (HTLV-1 to 4)

Simian T-Lymphotropic Viruses (STLV)

Four types of HTLV, type 1 to 4, have been described in humans and for 3 of them simian counterparts (STLV-1, STLV-2, STLV-3) have been identified. The first STLV was isolated in 1982 in Japan [61] and subsequent studies on NHP showed that STLV is endemic in many NHP species from Africa and Asia but absent in NHP from the new world [3,62]. Table 1 summarizes STLV infections in african NHPs. STLV-1 has been characterized in at least 30 different in African and Asian NHP species [4,7]. Today, the STLV-2 lineage is composed of only two strains isolated from two captive bonobos (*Pan paniscus*) but from different captive groups [63,64]. Despite extensive surveys on STLV infection in wild NHP, there is no evidence today for STLV-2 infection in other NHP species. STLV-3 has a wide geographic distribution among NHPs in Africa [65].

A high genetic diversity is seen among the different STLV-1 and 3 strains, with presence of numerous subtypes. Phylogenetic analyses show that STLV-1 and 3 strains from different NHP species cluster by geography and not according to species origin as is seen for SIVs. This means that different NHP species living in the same area can be infected with identical STLVs and suggests that these viruses are easily transmitted among different NHP species. For example, in Gabon greater spot-nosed monkeys, red capped mangabeys and mustached monkeys are all infected with subtype D [22]; in the Tai National Park in Côte d'Ivoire western red colobus and chimpanzees are infected with the same STLV-1 [66]; in Asia different macaque species are infected by STLV-1's of the Asian/Austronesian PTLV-1 clade [67]. On the other hand, different subtypes co-circulate also within the same NHP species and co-circulation of STLV-1 and 3 within the same species has also been documented [68,69],

Origin of HTLV

PTLV-1 viruses, including HTLV-1 and STLV-1, are the most widely spread variants and at least ten subtypes (A to J) of closely related HTLV-1 and/or STLV-1 have been described. In certain subtypes, human and simian viruses are interspersed, others are mainly comprised of simian strains, including or not sporadic human counterparts. For the cosmopolitan subtype A, which has spread globally, no simian counterpart is observed yet [3]. For example in Central Africa, STLV-1 strains from chimpanzees or mandrills cannot be distinguished from HTLV-1 strains of subtype B or D, respectively [70] and human and simian subtype F strains from Gabon and Cameroon are also very closely related [22,71]. Like STLV-1, STLV-3 is also widespread among African NHPs. Four separate subtypes are reported for STLV-3, and human HTLV-3 strains are interspersed with STLV-3 strains from subtype B and D [65]. This intermixing and the close relatedness between certain simian and human strains in the PTLV-1 and 3 lineages suggest that many independent cross-species transmission events are at the origin of the genetic diversity of HTLV-1 and 3 in humans and suggest also past and probably ongoing cross-species transmissions of STLVs from numerous NHP species to humans [72]. On the other hand HTLV-2 and STLV-2 form distinct monophyletic clades, without evidence for recent interspecies transmissions. Also, for the recently described HTLV-4, no simian counterpart has been identified yet.

Genetic diversity and molecular epidemiology of HTLV

Since the first descriptions of STLV-1 and HTLV-1 around 1980, the virus has infected between 10 to 20 million people worldwide [3]. HTLV-1 is present throughout the world, but in contrast to HIV, the HTLV epidemic is characterized by clusters of high endemicity [3]. The majority of HTLV-1 strains belong to the cosmopolitan subtype A which has spread globally. Subtype A can be further subdivided in a transcontinental, west African, north African and Japanese subgroup. Subtype B and D are present in Central Africa, and the Melanesian subtype C counts for almost all HTLV infections in the different islands of the Pacific area [3,73]. The other HTLV subtypes are documented in few individuals mainly in Central Africa.

HTLV-2 is less widespread and 4 subtypes are observed. The major subtypes, A and B, are both documented in Amerindians and intravenous drug–using populations in the US and Europe and subtype C is nearly exclusive in Brazilian populations [74,75]. These observations led initially to the hypothesis that HTLV-2 was restricted to the new world. However, sporadic cases of HTLV-2 infection have been described in different areas from Central Africa. More precisely, a unique divergent subtype D strain was identified in a Pygmy living in the Democratic Republic of Congo (DRC) [76] and HTLV-2 subtype B strains were isolated from Pygmies living in Cameroon and Gabon [77,78].

HTLV-3 infections have only been recently identified in a handful of individuals, all living in rural areas in southern Cameroon [65]. HTLV-4 consists so far of a unique human strain obtained from a hunter living in Cameroon [79]. The recent discovery of HTLV-3 and HTLV-4 and novel STLV-1-like viruses among people who hunt and butcher NHPs suggests that cross-species transmissions are still ongoing [66, 72, 79].

Foamy Viruses

Simian Foamy Viruses [SFV]

SFVs have been identified in almost all African and Asian NHP, but also in several NHP species in South America [65,80]. SFVs are ancient and have co-evolved with their NHP primate hosts 30-40 millions years ago [81]. Although, SFVs are species-specific occasional cases of cross-species transmissions among NHP have been documented. The transmission of SFVwrc from western red colobus to chimpanzees in a predator/prey system has been documented in the Tai forest in Ivory Coast, and SFV form a *Cercopithecus* species has been detected in a wild chimpanzee in Cameroon [82,83].

SFV infections in humans

Importantly, humans are not naturally infected with a foamy virus but several cases of zoonotic transmissions have been reported around the world among individuals who are exposed to NHPs, like zoo workers, animal handlers or hunters [5,84,85,86]. In Cameroon, about 1% of villagers, exposed to NHP through hunting, butchering or keeping of pet monkeys were found to be SFV antibody positive, and genetic analysis showed infection with SFV strains from DeBrazza's monkeys, mandrills and gorillas [87]. Persons living in rural villages in the Democratic Republic of Congo [DRC] were infected at a 0.5% SFV

prevalence rate and molecular characterization of the SFV strains confirmed infection with SFVs from local NHP species, i.e. Angolan colobus and red tailed monkeys [88]. Between 18% to 36% of individuals who were severely bitten and injured while hunting wild chimpanzees and gorillas in Cameroon and Gabon had detectable SFVcpz or SFVgor sequences in their blood [84, 89]. An SFV prevalence of 16% was observed in zookeepers in China, and studies from Thaïland, Nepal, Bangladesh and Indonesia reported that 8% of persons in various contexts (including zookeepers, hunters, Temples and urban) were SFV infected [85,90]. Finally, up to 5.3% SFV infection is seen in persons with occupational NHP exposure in research institutions or zoos in the USA [86].

Humans are thus susceptible to a wide variety of SFVs and seem to acquire these viruses more readily than SIVs or STLVs but no signs of disease in humans nor human-to-human transmission of SFV has, however, been documented. Therefore, the lack of human-to-human SFV transmission represents an informative marker of contact between human and NHPs.

Conclusion

As shown above a wide diversity of simian retroviruses have been transmitted to humans most probably through exposure to blood or other secretions of infected animals, during hunting and butchering of bushmeat, or by injuries likes bites or scratches during hunting of from pet NHPs. The chance for cross-species transmissions certainly increases when frequency of exposure and retrovirus prevalence is high, which could partially explain the higher rate of cross-species transmissions observed for SFV. In addition to the type and intensity of contacts between NHP and humans, host and viral characteristics play a role in subsequent efficient infection in the new host. SIVwrc infecting western red colobus illustrate the role of viral adaptation and host factors. Overall, 50% to 80% of them are infected with SIVs and together with mangabeys they are heavily hunted for bushmeat [91,92]. However, in contrast to SIVsmm which has been transmitted at least 9 times to humans, no SIVwrc cross-species transmission to humans has been documented yet. Efficient infection and spread in humans differs between SFV, STLV and SIV, but seems also to differ among the different viruses from the same simian lineage, as illustrated by the different spread of HIV-1 M, N O, P or for the different HIV-2 groups.

Efficient virus spread of the virus in the human population depends on the capacity of the virus to adapt to the new host, and then on transmission modes together with social and environmental factors. The current HIV-1 M pandemic illustrates the impact of a single cross-species transmission and its transmission among different human populations where conditions for efficient epidemic spread were present. Already 13 transmissions involving 3 different NHP species to humans have been documented, 4 for HIV-1 and 9 for HIV-2. Most likely other cross-species occurred in the past but remained undetected, because the virus could not adapt to his new host or was not introduced into an environment where conditions for efficient and rapid spread were present. Today humans are still exposed to a wide diversity of SIVs through hunting and butchering NHPs for bushmeat [22,68,69,95,96,97,98,99]. The recent discovery of HIV-1 P in 2009 in two Cameroonian patients, a new HIV-2 in 2013 in Ivory Coast, new HTLV-1 and HTLV-3 variants as well as

SFV infections in humans in Central Africa, clearly illustrate that our knowledge of genetic diversity and cross-species transmissions of simian retroviruses are still incomplete [24,32,65,66,72,84,87,89]. Cross-species transmission of other SIVs from mangabeys, chimpanzees, gorillas or other NHP species has to be considered given the high prevalence of SIVs in some primate populations and species [>50%]. The increasing presence of humans in tropical forest areas (logging and mining industries) and subsequent increasing contact and exposure to SIV infected primates through hunting and bushmeat preparation together with the socio-economic and demographic factors today are in favor of global expansion with new viral infections.

REFERENCES

1. Jones KE, Patel NG, Levy MA, et al. Global trends in emerging infectious diseases. Nature. 2008; 451:990–993. [PubMed: 18288193]
2. The Joint United Nations Programme on HIV/AIDS (UNAIDS). (www.unaids.org); accessed in January 2014
3. Gessain A, Cassar O. Epidemiological Aspects and World Distribution of HTLV-1 Infection. Front Microbiol. 2012; 3:388. eCollection 2012. [PubMed: 23162541]
4. Gessain A. Human retrovirus HTLV-1: descriptive and molecular epidemiology, origin, evolution, diagnosis and associated diseases. Bull Soc Pathol Exot. 2011; 104:167–180. [PubMed: 21796326]
5. Switzer, WM.; Heneine, W. Foamy Virus Infection of Humans. In: Liv, D., editor. Molecular Detection of Human Viral Pathogens. CRC Press; 2011.
6. Hahn BH, Shaw GM, De Cock KM, Sharp PM. AIDS as a zoonosis: scientific and public health implications. Science. 2000; 287:607–614. [PubMed: 10649986]
7. Locatelli S, Peeters M. Cross-species transmission of simian retroviruses: how and why they could lead to the emergence of new diseases in the human population. AIDS. 2012; 26:659–73. Review. [PubMed: 22441170]
8. Daniel MD, Letvin NL, King NW, et al. Isolation of T-cell tropic HTLV-III-like retrovirus from macaques. Science. 1985; 228:1201–1204. [PubMed: 3159089]
9. Kanki PJ, McLane MF, King NW, et al. Serologic identification and characterization of a macaque T-lymphotropic retrovirus closely related to HTLV-III. Science. 1985; 228:1199–1201. [PubMed: 3873705]
10. Fultz PN, McClure HM, Anderson DC, Swenson RB, Anand R, Srinivasan A. Isolation of a T-lymphotropic retrovirus from naturally infected sooty mangabey monkeys (*Cercocebus atys*). Proc Natl Acad Sci U S A. 1986; 83:5286–5290. [PubMed: 3014542]
11. Apetrei C, Kaur A, Lerche NW, et al. Molecular epidemiology of simian immunodeficiency virus SIVsm in U.S. primate centers unravels the origin of SIVmac and SIVstm. J Virol. 2005; 79:8991–9005. [PubMed: 15994793]
12. Ayouba A, Duval L, Liégeois F, et al. Nonhuman primate retroviruses from Cambodia: high simian foamy virus prevalence, identification of divergent STLV-1 strains and no evidence of SIV infection. Infect Genet Evol. 2013; 18:325–334. [PubMed: 23612320]
13. Wertheim JO, Worobey M. A challenge to the ancient origin of SIVagm based on African green monkey mitochondrial genomes. PLoS Pathog. 2007; 3:e95. [PubMed: 17616975]
14. Beer BE, Bailes E, Goeken R, et al. Simian immunodeficiency virus (SIV) from sun-tailed monkeys (*Cercopithecus solatus*): evidence for host-dependent evolution of SIV within the C. lhoesti superspecies. J Virol. 1999; 73:7734–7744. [PubMed: 10438863]
15. Bibollet-Ruche F, Bailes E, Gao F, et al. New simian immunodeficiency virus infecting De Brazza's monkeys (*Cercopithecus neglectus*): evidence for a *Cercopithecus* monkey virus clade. J Virol. 2004; 78:7748–7762. [PubMed: 15220449]
16. Bibollet-Ruche F, Galat-Luong A, Cuny G, et al. Simian immunodeficiency virus infection in a patas monkey (*Erythrocebus patas*): evidence for cross-species transmission from African green

monkeys (*Cercopithecus aethiops sabaeus*) in the wild. J Gen Virol. 1996; 77:773–781. [PubMed: 8627266]

17. Jin MJ, Rogers J, Phillips-Conroy JE, et al. Infection of a yellow baboon with simian immunodeficiency virus from African green monkeys: evidence for cross-species transmission in the wild. J Virol. 1994; 68:8454–8460. [PubMed: 7966642]
18. Van Rensburg EJ, Engelbrecht S, Mwenda J, et al. Simian Immunodeficiency Viruses (SIVs) from eastern and southern Africa: detection of a SIVagm variant from a chacma baboon. J Gen Virol. 1998; 79:1809–1814. [PubMed: 9680146]
19. Bailes E, Gao F, Bibollet-Ruche F, et al. Hybrid origin of SIV in chimpanzees. Science. 2003; 300:1713. [PubMed: 12805540]
20. Van Heuverswyn F, Li Y, Neel C, et al. Human immunodeficiency viruses: SIV infection in wild gorillas. Nature. 2006; 444:164. [PubMed: 17093443]
21. Souquiere S, Bibollet-Ruche F, Robertson DL, et al. Wild Mandrillus sphinx are carriers of two types of lentivirus. J Virol. 2001; 75:7086–7096. [PubMed: 11435589]
22. Liégeois F, Boué V, Mouacha F, et al. New STLV-3 strains and a divergent SIVmus strain identified in non-human primate bushmeat in Gabon. Retrovirology. 2012; 9:28. [PubMed: 22462797]
23. Sharp PM, Hahn BH. Origins of HIV and the AIDS pandemic. Cold Spring Harb Perspect Med. 2011; 1:a006841. Review. [PubMed: 22229120]
24. Ayouba A, Akoua-Koffi C, Calvignac-Spencer S, et al. Evidence for continuing cross-species transmission of SIVsmm to humans: characterization of a new HIV-2 lineage in rural Côte d'Ivoire. AIDS. 2013; 27:2488–2491. [PubMed: 23939239]
25. Peeters M, Honore C, Huet T, et al. Isolation and partial characterization of an HIV-related virus occurring naturally in chimpanzees in Gabon. AIDS. 1989; 3:625–630. [PubMed: 2512955]
26. Gao F, Bailes E, Robertson DL, et al. Origin of HIV-1 in the chimpanzee *Pan troglodytes troglodytes*. Nature. 1999; 397:436–441. [PubMed: 9989410]
27. Santiago ML, Lukasik M, Kamenya S, et al. Foci of endemic simian immunodeficiency virus infection in wild-living eastern chimpanzees (*Pan troglodytes schweinfurthii*). J Virol. 2003; 77:7545–7562. [PubMed: 12805455]
28. Keele BF, Van Heuverswyn F, Li Y, et al. Chimpanzee reservoirs of pandemic and nonpandemic HIV-1. Science. 2006; 313:523–526. [PubMed: 16728595]
29. Van Heuverswyn F, Li Y, Bailes E, et al. Genetic diversity and phylogeographic clustering of SIVcpz*Ptt* in wild chimpanzees in Cameroon. Virology. 2007; 368:155–171. [PubMed: 17651775]
30. Li Y, Ndjango JB, Learn GH, et al. Eastern chimpanzees, but not bonobos, represent a simian immunodeficiency virus reservoir. J Virol. 2012; 86:10776–10791. [PubMed: 22837215]
31. Neel C, Etienne L, Li Y, et al. Molecular epidemiology of simian immunodeficiency virus infection in wild-living gorillas. J Virol. 2010; 84:1464–1476. [PubMed: 19906908]
32. Plantier JC, Leoz M, Dickerson JE, et al. A new human immunodeficiency virus derived from gorillas. Nat Med. 2009; 15:871–872. [PubMed: 19648927]
33. D'arc, M.; Ayouba, A.; Esteban, A., et al. Gorillas in south-west Cameroon are the reservoir of HIV-1 group P ancestors; Conference on Retroviruses And Opportunistic Infections; Atlanta, GA. 2013. Abstract 484
34. Etienne L, Locatelli S, Ayouba A, et al. Noninvasive follow-up of simian immunodeficiency virus infection in wild-living nonhabituated western lowland gorillas in Cameroon. J Virol. 2012; 86:9760–9772. [PubMed: 22740419]
35. Mourez T, Simon F, Plantier JC. Non-M variants of human immunodeficiency virus type 1. Clin Microbiol Rev. 2013; 26:448–461. [PubMed: 23824367]
36. Vidal N, Peeters M, Mulanga-Kabeya C, et al. Unprecedented degree of human immunodeficiency virus type 1 [HIV-1] group M genetic diversity in the Democratic Republic of Congo suggests that the HIV-1 pandemic originated in Central Africa. J Virol. 2000; 74:10498–10507. [PubMed: 11044094]
37. Pepin, J. The origins of AIDS. Cambridge University Press; Cambridge: 2011.

38. Zhu T, Korber BT, Nahmias AJ, Hooper E, Sharp PM, Ho DD. An African HIV-1 sequence from 1959 and implications for the origin of the epidemic. Nature. 1998; 391:594–597. [PubMed: 9468138]
39. Worobey M, Gemmel M, Teuwen DE, et al. Direct evidence of extensive diversity of HIV-1 in Kinshasa by 1960. Nature. 2008; 455:661–664. [PubMed: 18833279]
40. Los Alamos HIV database. (http://www.hiv.lanl.gov/) ; accessed in January 2014
41. Hemelaar J, Gouws E, Ghys PD, Osmanov S, WHO-UNAIDS Network for HIV Isolation and Characterisation. Global trends in molecular epidemiology of HIV-1 during 2000-2007. AIDS. 2011; 25:679–689. [PubMed: 21297424]
42. Aldrich C, Hemelaar J. Global HIV-1 diversity surveillance. Trends Mol Med. 2012; 18:691–694. [PubMed: 22796205]
43. De Leys R, Vanderborght B, Vanden Haesevelde M, et al. Isolation and partial characterization of an unusual human immunodeficiency retrovirus from two persons of west-central African origin. J Virol. 1990; 64:1207–1216. [PubMed: 2304140]
44. Ayouba A, Mauclère P, Martin PM, et al. HIV-1 group O infection in Cameroon, 1986 to 1998. Emerg Infect Dis. 2001; 7:466–467. [PubMed: 11384531]
45. Jonassen TO, Stene-Johansen K, Berg ES, et al. Sequence analysis of HIV-1 group O from Norwegian patients infected in the 1960s. Virology. 1997; 231:43–47. [PubMed: 9143301]
46. Wertheim JO, Worobey M. Dating the age of the SIV lineages that gave rise to HIV-1 and HIV-2. PLoS Comput Biol. 2009; 5:e1000377. [PubMed: 19412344]
47. Vergne L, Bourgeois A, Mpoudi-Ngole E, et al. Biological and genetic characteristics of HIV infections in Cameroon reveals dual group M and O infections and a correlation between SI-inducing phenotype of the predominant CRF02_AG variant and disease stage. Virology. 2003; 310:254–266. [PubMed: 12781713]
48. Peeters M, Liegeois F, Torimiro N, et al. Characterization of a highly replicative intergroup M/O human immunodeficiency virus type 1 recombinant isolated from a Cameroonian patient. J Virol. 1999; 73:7368–7375. [PubMed: 10438826]
49. Takehisa J, Zekeng L, Ido E, et al. Human immunodeficiency virus type 1 intergroup [M/O] recombination in Cameroon. J Virol. 1999; 73:6810–6820. [PubMed: 10400779]
50. Vessière A, Leoz M, Brodard V, et al. First evidence of a HIV-1 M/O recombinant form circulating outside Cameroon. AIDS. 2010; 24:1079–1082. [PubMed: 20386379]
51. Simon F, Mauclere P, Roques P, et al. Identification of a new human immunodeficiency virus type 1 distinct from group M and group O. Nat Med. 1998; 4:1032–1037. [PubMed: 9734396]
52. Vallari A, Holzmayer V, Harris B, et al. Confirmation of putative HIV-1 group P in Cameroon. J Virol. 2011; 85:1403–1407. [PubMed: 21084486]
53. Sauter D, Hue S, Petit SJ, et al. HIV-1 Group P is unable to antagonize human tetherin by Vpu, Env or Nef. Retrovirology. 2011; 8:103. [PubMed: 22171785]
54. Hirsch VM, Olmsted RA, Murphey-Corb M, Purcell RH, Johnson PR. An African primate lentivirus (SIVsm) closely related to HIV-2. Nature. 1989; 339:389–392. [PubMed: 2786147]
55. Gao F, Yue L, White AT, et al. Human infection by genetically diverse SIVSM-related HIV-2 in west Africa. Nature. 1992; 358:495–499. [PubMed: 1641038]
56. Faria NR, Hodges-Mameletzis I, Silva JC, et al. Phylogeographical footprint of colonial history in the global dispersal of human immunodeficiency virus type 2 group A. J Gen Virol. 2012; 93:889–899. [PubMed: 22190015]
57. Yamaguchi J, Vallari A, Ndembi N, et al. HIV type 2 intergroup recombinant identified in Cameroon. AIDS Res Hum Retroviruses. 2008; 24:86–91. [PubMed: 18275352]
58. Ibe S, Yokomaku Y, Shiino T, et al. HIV-2 CRF01_AB: first circulating recombinant form of HIV-2. J Acquir Immune Defic Syndr. 2010; 54:241–247. [PubMed: 20502347]
59. Santiago ML, Range F, Keele BF, et al. Simian immunodeficiency virus infection in free-ranging sooty mangabeys (*Cercocebus atys atys*) from the Tai Forest, Cote d'Ivoire: implications for the origin of epidemic human immunodeficiency virus type 2. J Virol. 2005; 79:12515–12527. [PubMed: 16160179]

60. Van Tienen C, van der Loeff MS, Zaman SM, et al. Two distinct epidemics: the rise of HIV-1 and decline of HIV-2 infection between 1990 and 2007 in rural Guinea-Bissau. J Acquir Immune Defic Syndr. 2010; 53:640–647. [PubMed: 19841588]

61. Hayami M, Komuro A, Nozawa K, et al. Prevalence of antibody to adult T-cell leukemia virus-associated antigens (ATLA) in Japanese monkeys and other non-human primates. International journal of cancer. 1984; 33:179–183.

62. Mahieux R, Gessain A. HTLV-3/STLV-3 and HTLV-4 viruses: discovery, epidemiology, serology and molecular aspects. Viruses. Jul; 2011 3(7):1074–90. doi: 10.3390/v3071074. Epub 2011 Jul 8. Review. [PubMed: 21994771]

63. Digilio L, Giri A, Cho N, Slattery J, Markham P, Franchini G. The simian T-lymphotropic/leukemia virus from *Pan paniscus* belongs to the type 2 family and infects Asian macaques. J Virol. 1997; 71:3684–3692. [PubMed: 9094642]

64. Van Brussel M, Salemi M, Liu HF, et al. The simian T-lymphotropic virus STLV-PP1664 from Pan paniscus is distinctly related to HTLV-2 but differs in genomic organization. Virology. 1998; 243:366–379. [PubMed: 9568035]

65. Gessain A, Rua R, Betsem E, Turpin J, Mahieux R. HTLV-3/4 and simian foamy retroviruses in humans: discovery, epidemiology, cross-species transmission and molecular virology. Virology. 2013; 435:187–199. Review. [PubMed: 23217627]

66. Calvignac-Spencer S, Adjogoua EV, Akoua-Koffi C, et al. Origin of human T-lymphotropic virus type 1 in rural Cote d'Ivoire. Emerging infectious diseases. 2012; 18:830–833. [PubMed: 22516514]

67. Van Dooren S, Verschoor EJ, Fagrouch Z, Vandamme AM. Phylogeny of primate T lymphotropic virus type 1 (PTLV-1) including various new Asian and African non-human primate strains. Infection Genetics and Evolution. 2007; 7:374–381.

68. Liegeois F, Lafay B, Switzer WM, et al. Identification and molecular characterization of new STLV-1 and STLV-3 strains in wild-caught nonhuman primates in Cameroon. Virology. 2008; 371:405–417. [PubMed: 17976676]

69. Ahuka-Mundeke S, Mbala-Kingebeni P, Liegeois F, et al. Identification and molecular characterization of new simian T cell lymphotropic viruses in nonhuman primates bushmeat from the Democratic Republic of Congo. AIDS research and human retroviruses. 2012; 28:628–635. [PubMed: 21827287]

70. Mahieux R, Chappey C, Georges-Courbot MC, et al. Simian T-cell lymphotropic virus type 1 from Mandrillus sphinx as a simian counterpart of human T-cell lymphotropic virus type 1 subtype D. J Virol. 1998; 72:10316–10322. [PubMed: 9811783]

71. Nerrienet E, Meertens L, Kfutwah A, Foupouapouognigni Y, Gessain A. Molecular epidemiology of simian T-lymphotropic virus (STLV) in wild-caught monkeys and apes from Cameroon: a new STLV-1, related to human T-lymphotropic virus subtype F, in a *Cercocebus agilis*. Journal of General Virology. 2001; 82:2973–2977. [PubMed: 11714973]

72. Zheng H, Wolfe ND, Sintasath DM, et al. Emergence of a novel and highly divergent HTLV-3 in a primate hunter in Cameroon. Virology. 2010; 401:137–145. [PubMed: 20353873]

73. Verdonck K, Gonzalez E, Van Dooren S, Vandamme AM, Vanham G, Gotuzzo E. Human T-lymphotropic virus 1: recent knowledge about an ancient infection. Lancet Infect Dis. 2007; 7:266–281. [PubMed: 17376384]

74. Alcantara LC, Shindo N, Van Dooren S, et al. Brazilian HTLV type 2a strains from intravenous drug users (IDUs) appear to have originated from two sources: Brazilian Amerindians and European/North American IDUs. AIDS research and human retroviruses. 2003; 19:519–523. [PubMed: 12892061]

75. Salemi M, Vandamme AM, Desmyter J, Casoli C, Bertazzoni U. The origin and evolution of human T-cell lymphotropic virus type II (HTLV-II) and the relationship with its replication strategy. Gene. 1999; 234:11–21. [PubMed: 10393234]

76. Vandamme AM, Salemi M, Van Brussel M, et al. African origin of human T-lymphotropic virus type 2 (HTLV-2) supported by a potential new HTLV-2d subtype in Congolese Bambuti Efe Pygmies. J Virol. 1998; 72:4327–4340. [PubMed: 9557723]

77. Letourneur F, d'Auriol L, Dazza MC, et al. Complete nucleotide sequence of an African human T-lymphotropic virus type II subtype b isolate (HTLV-II-Gab): molecular and phylogenetic analysis. The Journal of general virology. 1998; 79:269–277. [PubMed: 9472611]

78. Mauclere P, Afonso PV, Meertens L, et al. HTLV-2B strains, similar to those found in several Amerindian tribes, are endemic in central African Bakola Pygmies. The Journal of infectious diseases. 2011; 203:1316–1323. [PubMed: 21459818]

79. Switzer WM, Salemi M, Qari SH, et al. Ancient, independent evolution and distinct molecular features of the novel human T-lymphotropic virus type 4. Retrovirology. 2009; 6:9. [PubMed: 19187529]

80. Muniz CP, Troncoso LL, Moreira MA, et al. Identification and characterization of highly divergent simian foamy viruses in a wide range of new world primates from Brazil. PLoS One. 2013; 8:e67568. [PubMed: 23844033]

81. Switzer WM, Salemi M, Shanmugam V, et al. Ancient co-speciation of simian foamy viruses and primates. Nature. 2005; 434:376–380. [PubMed: 15772660]

82. Leendertz FH, Zirkel F, Couacy-Hymann E, et al. Interspecies transmission of simian foamy virus in a natural predator-prey system. J Virol. 2008; 82:7741–7744. [PubMed: 18508895]

83. Liu W, Worobey M, Li Y, et al. Molecular ecology and natural history of simian foamy virus infection in wild-living chimpanzees. PLoS Pathog. 2008; 4:e1000097. [PubMed: 18604273]

84. Betsem E, Rua R, Tortevoye P, Froment A, Gessain A. Frequent and recent human acquisition of simian foamy viruses through apes' bites in central Africa. PLoS Pathog. 2011; 7:e1002306. [PubMed: 22046126]

85. Jones-Engel L, May CC, Engel GA, et al. Diverse contexts of zoonotic transmission of simian foamy viruses in Asia. Emerging infectious diseases. 2008; 14:1200–1208. [PubMed: 18680642]

86. Switzer WM, Bhullar V, Shanmugam V, et al. Frequent simian foamy virus infection in persons occupationally exposed to nonhuman primates. Journal of Virology. 2004; 78:2780–2789. [PubMed: 14990698]

87. Wolfe ND, Switzer WM, Carr JK, et al. Naturally acquired simian retrovirus infections in central African hunters. Lancet. 2004; 363:932–937. [PubMed: 15043960]

88. Switzer W, Tang S, Ahuka-Mundeke S, et al. Novel simian foamy virus infections from multiple monkey species in women from the Democratic Republic of Congo. Retrovirology. 2012; 9:100. [PubMed: 23217108]

89. Mouinga-Ondeme A, Caron M, Nkoghe D, et al. Cross-Species Transmission of Simian Foamy Virus to Humans in Rural Gabon, Central Africa. Journal of Virology. 2012; 86:1255–1260. [PubMed: 22072747]

90. Huang F, Wang H, Jing S, Zeng W. Simian Foamy Virus Prevalence in Macaca mulatta and Zookeepers. AIDS research and human retroviruses. 2012; 28:591–593. [PubMed: 22236106]

91. Leendertz S, Junglen S, Hedemann C, et al. High Prevalence, Coinfection Rate, and Genetic Diversity of Retroviruses in Wild Red Colobus Monkeys (*Piliocolobus badius badius*) in Tai National Park, Cote d'Ivoire. Journal of Virology. 2012; 84:7427–7436. [PubMed: 20484508]

92. Refisch J, Koné I. Impact of commercial hunting on monkey populations in the Taï region, Côte d'Ivoire. Biotropica. 2005; 37:136–144.

93. Peeters M, Courgnaud V, Abela B, et al. Risk to human health from a plethora of simian immunodeficiency viruses in primate bushmeat. Emerg Infect Dis. 2002; 8:451–457. [PubMed: 11996677]

94. Aghokeng AF, Ayouba A, Mpoudi-Ngole E, et al. Extensive survey on the prevalence and genetic diversity of SIVs in primate bushmeat provides insights into risks for potential new cross-species transmissions. Infect Genet Evol. 2010; 10:386–396. [PubMed: 19393772]

95. Ahuka-Mundeke S, Ayouba A, Mbala-Kingebeni P, et al. A novel multiplexed HIV/SIV antibody detection assay identified new simian immunodeficiency viruses in primate bushmeat in the Democraphic Republic of Congo. Emerg Infect Dis. 201; 17:2277–2286. [PubMed: 22172157]

96. Worobey M, Telfer P, Souquiere S, et al. Island biogeography reveals the deep history of SIV. Science. 2010; 329:1487. [PubMed: 20847261]

97. Apetrei C, Metzger MJ, Richardson D, et al. Detection and partial characterization of simian immunodeficiency virus SIVsm strains from bush meat samples from rural Sierra Leone. J Virol. 2005; 79:2631–2636. [PubMed: 15681464]

Table 1

African non-human primates infected with SIV and STLV.

Genus	Species/subspecies	Common name	SIV lineage	SIV prevalence[a]	STLV type	STLV prevalence[a]	Human counterparts of SIV and STLV[b]
Pan	*troglodytes troglodytes*	Central African chimpanzee	SIVcpz*Ptt*	0-30%	1	na	**HIV-1 group M and N**, HTLV-1 subtype B
	troglodytes schweinfurthii	Eastern chimpanzee	SIVcpz*Pts*	0-30%	na	na	
	troglodytes verus	West African chimpanzee	neg	0%	1	70%	HTLV-1 subtype J?
	troglodytes ellioti	Gulf of Guinea chimpanzee	neg	0%	1	na	
	paniscus	Bonobo	neg	na	2	na	STLV-2 from bonobos are closest simian strains to HTLV-2
Gorilla	*gorilla gorilla*	Western lowland gorilla	SIVgor	0-5%	1	na	**HIV-1 group P and O?**, HTLV-1 subtype B
Colobus	*guereza*	Mantled guereza	SIVcol-1,col-2	18%	?	*na*	
	angolensis	Angolan colobus	?	na	3	8%	
	satanus	Black colobus	SIVblc*	30%	na	na	
Piliocolobus	*badius badius*	Western red colobus	SIVwrc*Pbb*	50-80%	1	50%	HTLV-1 subtype J?
	badius temminckii	Temminck's red colobus	SIVwrc*Pbt*	10%	na	na	
	tholloni	Tshuapa red colobus	SIVtrc*	24%	1, 3	na	
	rufomitratus tephrosceles	Ugandan red colobus	SIVkrc*	23%	1	6%	
Procolobus	*verus*	Olive colobus	SIVolc	na	na	na	
Lophocebus	*albigena*	Gray-cheeked mangabey	?	na	1, 3	20%	HTLV-1 subtype F?
	aterrimus	Black crested mangabey	SIVbkm*	na	3	12%	
Papio	*anubis*	Olive baboon	?	na	1	9%	
	cynocephalus	Yellow baboon	[SIVagm-ver]*	na	3	na	
	ursinus	Chacma baboon	[SIVagm-ver]*	na	1	na	
	hamadryas	Sacred baboon	na	na	3	50%	
Theropithecus	*gelada*	Gelada baboons	na	na	3	na	
Cercocebus	*atys*	Sooty mangabey	SIVsmm	50%	1	23%	**HIV-2 group A to I**, HTLV-1 sm subtype
	torquatus	Red-capped mangabey	SIVrcm	50%	1, 3	na	HTLV-3 subtype B
	agilis	Agile mangabey	SIVagi	na	1, 3	80%	HTLV-1 subtype F?
Mandrillus	*sphinx*	Mandrill	SIVmnd-1, mnd-2	33%	1	20%	HTLV-1 subtype D and F
	leucophaeus	Drill	SIVdrl	22%	na	na	
Allenopithecus	*nigroviridis*	Allen's swamp monkey	SIVasm*	na	1	na	
Miopithecus	*talapoin*	Angolan talapoin	SIVtal*	na	na	na	
	ogouensis	Gabon talapoin	SIVtal	17%	1	na	
Erythrocebus	*patas*	Patas monkey	[SIVagm-sab]*	7%	1	na	

Genus	Species/subspecies	Common name	SIV lineage	SIV prevalence[a]	STLV type	STLV prevalence[a]	Human counterparts of SIV and STLV[b]
Chlorocebus	*sabaeus*	Green monkey	SIVagm-sab	47%	1	na	
	aethiops	Grivet	SIVagm-gri	na	1	na	
	tantalus	Tantalus monkey	SIVagm-tan	50%	1	na	
	pygerythrus	Vervet monkey	SIVagm-ver	na	1	na	
Cercopithecus	*diana*	Diana monkey	?	na	na	na	
	nictitans	Greater spot-nosed monkey	SIVgsn	1%	1, 3	2%	HTLV-3 subtype D?, HTLV-1 subtype F?
	mitis	Blue monkey	SIVblu*	na	na	na	
	albogularis	Sykes's monkey	SIVsyk	46%	1	na	
	mona	Mona monkey	SIVmon	na	1, 3	na	HTLV-3 subtype D?
	lowei	Lowe's mona monkey	?	na	na	na	
	campbelli	Campbell's monkey	?	na	na	na	
	pogonias	Crowned guenon	?	na	1	7%	HTLV-1 subtype D?
	denti	Dent's mona monkey	SIVden	na	na	na	
	cephus	Mustached guenon	SIVmus-1,mus-2,mus-3	1%	1	3-30%	
	erythrotis	Red-eared monkey	SIVery*	33%	na	na	
	ascanius	Red-tailed monkey	SIVasc*	25%	1	1.5%	
	lhoesti	l'Hoest's monkey	SIVlho	na	na	na	
	solatus	Sun-tailed monkey	SIVsun	na	na	na	
	preussi	Preuss's monkey	SIVpre*	22%	na	na	
	hamlyni	Owl-faced monkey	?	na	na	na	
	neglectus	De Brazza's monkey	SIVdeb	20-40%	1	20%	
	wolfi	Wolf's monkey	SIVwol	12%	1	12%	

? only serological evidence for SIV infection

[ ]: SIV infections resulting from cross-species transmissions of local African green monkey species. na: not available

* only partial sequences are available

[a] prevalence observed in wild NHP primate populations are shown,

[b] HIV strains are indicated in bold, ? means that the precise NHP species at the origin of the human HTLV cannot be identified because multiple NHP species are infected with same STLV subtype

Table 2

Comparison of SIV, SFV and STLV infections in their natural hosts and humans

	SIV	STLV	SFV
Spread in NHP	Africa	Africa and Asia	Africa, Asia, South-America
Evolution in natural NHP host	Species-specific lineages : result of virus-host co-evolution, cross-species transmissions, recombination	No species-specific lineages but geographic clustering : frequent cross-species transmissions, co-circulation of several STLV types and subtypes in same NHP species	Virus-host co-evolution ; some exemples of cross-species transmissions
Cross-species transmissions to humans	chimpanzee, gorilla, sooty mangabeys	Chimpanzee, gorilla, bonobo, mandrill, sooty mangabeys, red-capped mangabeys, western red colobus, several Cercopithecus species	Chimpanzee, gorilla, mandrill, angolan colobus, thsuapa red colobus, several cercopithecus species, macaca species in asia
Human infections	60 million HIV infections since discovery early 1980s	10-12 million HTLV infections	No spread in humans
Human epidemics	HIV-1 M global HIV-1 O 1% of HIV in Cameroon HIV-1 N <20 cases in Cameroon HIV-1 P, 2 patients from Cameroon HIV-2 A West Africa HIV-2 B, eastern part of West Africa HIV-2 C-I sporadic cases in West Africa	HTLV-1 A global HTLV-1 B and D, West and Central Africa HTLV-1 C Melanesia HTLV-1 E, F, G, H, J, sporadic cases in West and Central Africa HTLV-2 A US and Europe HTLV-2 B, Europe, US and Central Africa HTLV-2 C Brazil HTLV-2 D sporadic case in Central Africa HTLV-3 sporadic cases in central Africa HTLV-4 single case in Central Africa	Sporadic human infections : Hunters in Central Africa, rural populations in central Africa, Asia, primate keepers US
Human disease	AIDS	Adult T-cell leukemia/lymphoma, Tropical spastic paraparesis and HTLV-1 associated myelopathy	No disease