

SIVcpz in Wild Chimpanzees

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West-central African chimpanzees (*Pan troglodytes troglodytes*) harbor strains of simian immunodeficiency virus (SIVcpz) that are closely related to all three groups of human immunodeficiency virus 1 (HIV-1) (M, N, and O) and have thus been implicated as a reservoir for human infection (1). Yet, because all SIVcpz strains identified to date have been derived from captive chimpanzees, little is known about the prevalence, geographic distribution, and genetic diversity of SIVcpz in the wild. Here, we describe a prevalence study and detection of SIVcpz in wild-living apes.

Sampling blood from endangered primates is generally neither feasible nor ethical. We therefore developed noninvasive methods to detect and characterize SIVcpz in wild chimpanzees by analyzing fecal and urine samples for SIVcpz antibodies and virion RNA (2). The sensitivity of antibody detection by enhanced chemiluminescent immunoblot was tested in captive chimpanzees of known HIV-1/SIVcpz infection status and found to be 100% for urine and 65% for feces (specificity in each instance was 100%). The sensitivity of polymerase chain reaction amplification of virion RNA from feces of SIVcpz-infected chimpanzees was 66%. Using these techniques, we studied 28 *P. t. verus* from the Tai Forest, Cote d'Ivoire, 24 *P. t. schweinfurthii* from Kibale National Park, Uganda, and 6 *P. t. schweinfurthii* from Gombe National Park, Tanzania (Fig. 1A). Of the 58 wild-living chimpanzees tested, only one healthy 23-year-old sexually active male (Ch-06) from Gombe was positive for SIVcpz infection. Two different urine samples from Ch-06 contained SIVcpz antibodies (Fig. 1B), and three fecal samples were positive for SIVcpz virion RNA. Sequence analysis of a 2195-base pair *pol/vif* fragment amplified from fecal samples revealed a highly divergent SIVcpz strain (TAN1) that differed from west-central African SIVcpz and HIV-1 groups M, N, and O by 28 to 30% of amino acid sequences. The most similar sequence was SIVcpzANT from a captive *P. t. schweinfurthii* (3), which differed by 23%. In a phylogenetic tree, SIVcpzTAN1 and SIVcpzANT clustered together in a statistically highly significant manner (Fig. 1C).

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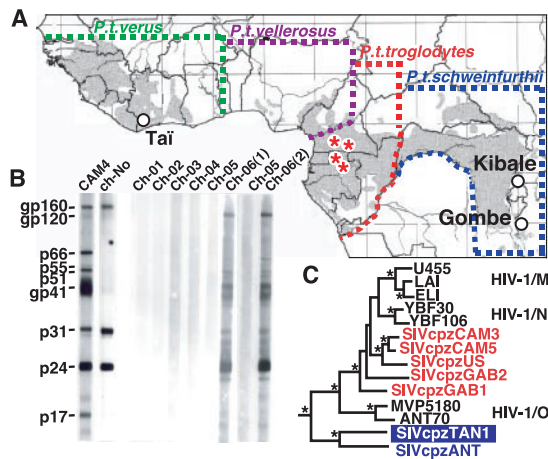


Fig. 1. (A) Locations of Tai, Kibale, and Gombe chimpanzees and the four recognized chimpanzee subspecies (5). Red asterisks indicate the origins of four captive SIVcpz-infected *P. t. troglodytes* apes (6, 7). (B) Urine immunoblots of Ch-06, two infected captive chimpanzees CAM4 (6) and ch-No (3), and negative samples. (C) Maximum likelihood tree of TAN1 Pol/Vif sequences (GenBank accession number AF382822) and other SIVcpz (*P. t. troglodytes*, red; *P. t. schweinfurthii*, blue) and HIV-1 strains (asterisks denote >95% bootstrap values).

The discovery of SIVcpzTAN1 in a single wild-living Gombe chimpanzee provides insight into the origins and evolutionary history of HIV-1 and SIVcpz. First, the geographic boundaries for SIVcpz must now be extended from Gabon and Cameroon in west-central Africa to the easternmost limit of the chimpanzee range in Tanzania. Second, both *P. t. schweinfurthii* and *P. t. troglodytes* are now shown to be naturally infected by SIVcpz. Third, the considerable divergence of both SIVcpzTAN1 and SIVcpzANT from HIV-1 groups M, N, and O indicates that *P. t. schweinfurthii* did not serve as the zoonotic source for epidemic HIV-1. Fourth, the prevalence of natural SIVcpz infection is surprisingly low. To infer whether true SIVcpz infections went undetected because of falsely negative test results, we used conserva-

tive estimates of assay sensitivities and specificities to calculate the likelihood of a 10% (or greater) SIVcpz prevalence in the Tai and Kibale apes. These probabilities were extremely low: 0.0072 and 0.000025, respectively (2). Thus, the prevalence of SIV in these chimpanzees is far lower than in other primates such as African green monkeys, where it can reach 90% in adults (1).

This report leaves open two important questions: Where are the endemic foci of SIVcpz infection in wild chimpanzees today and what is the natural history of such infection? We can explain the absence of SIVcpz infection in chimpanzees from the Tai Forest [and from over 2000 captive chimpanzees exported from west Africa (4)] by assuming that the geographic isolation of *P. t. verus* predated infection by the SIVcpz progenitor. However, the lack of SIVcpz in the *P. t. schweinfurthii* apes from Kibale is an enigma. It is possible that low SIVcpz transmission efficiency, declining chimpanzee population size, and habitat fragmentation have all led to low prevalence rates—or even virus extinction—in certain communities. It is also possible that the prevalence of SIVcpz in *P. t. schweinfurthii* is generally lower than in *P. t. troglodytes* and that this explains why representatives of the SIVcpzTAN1/ANT lineage have not been found in humans. Additional field studies are needed to understand fully the epidemiology and natural history of this medically important family of viruses. The present report demonstrates the feasibility of noninvasive approaches that make such work possible in a scientifically rigorous yet ecologically sensitive manner.

References and Notes

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