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[KL1] Where did it all begin?

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Purpose of the Study HIV-1 and HIV-2, the causative agents of AIDS, were acquired by humans in the 20th century. Their origins lie among the simian immunodeficiency viruses (SIVs). Host-specific SIVs have been found in more than 30 species of primates in sub-Saharan Africa. To understand the evolutionary origins of the human viruses we have performed extensive phylogenetic analyses of the SIVs, and sampled wild primate populations to find the closest relatives of HIV-1 and HIV-2.

Disentangling the evolution of the SIVs has been difficult because of numerous events of recombination between divergent lineages, implying transmissions between different host species. After removing the mosaic viruses, it becomes apparent that the primary split among SIVs is into two groups, one found in terrestrial monkeys, the other in arboreal species. Among the terrestrial viruses, one that evolved in sooty mangabeys (SIV_{smm}) in West Africa has subsequently been transmitted numerous times to humans to form HIV-2. Chimpanzees acquired two viruses from different species of monkeys (one terrestrial, one arboreal), which recombined to form a new virus with a unique genome structure. This virus, SIV_{cpz}, was subsequently transmitted to humans on three occasions giving rise to HIV-1.

The numbers of examples of SIV_{cpz} and SIV_{smm} characterized have been extremely limited. To learn more about these viruses, and the origins of HIV-1 and HIV-2, non-invasive techniques have been developed and used to greatly increase the number of strains sampled from wild populations of sooty mangabeys and chimpanzees. We have found the closest SIV_{smm} relatives of the two epidemic forms of HIV-2 in Cote d'Ivoire. The closest SIV_{cpz} relatives of HIV-1 infect one particular subspecies of chimpanzees, *Pan troglodytes troglodytes*, in West Central Africa. We have now found widespread endemic infection in these apes, with SIV_{cpz} prevalence rates over 20% in some communities. SIV_{cpz} strains exhibit a local phylogeographic clustering, allowing us to trace the origins of pandemic (group M) and non-pandemic (group N) HIV-1 to distinct, geographically isolated chimpanzee communities in

southern Cameroon. Thus, 25 years into the AIDS epidemic, the origins of this newly emerged disease have been elucidated.

Plenary Session: Keynote Lectures (Past, Present and Future)

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