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The origin of HIV revisited: Are we closer to the answer or not?

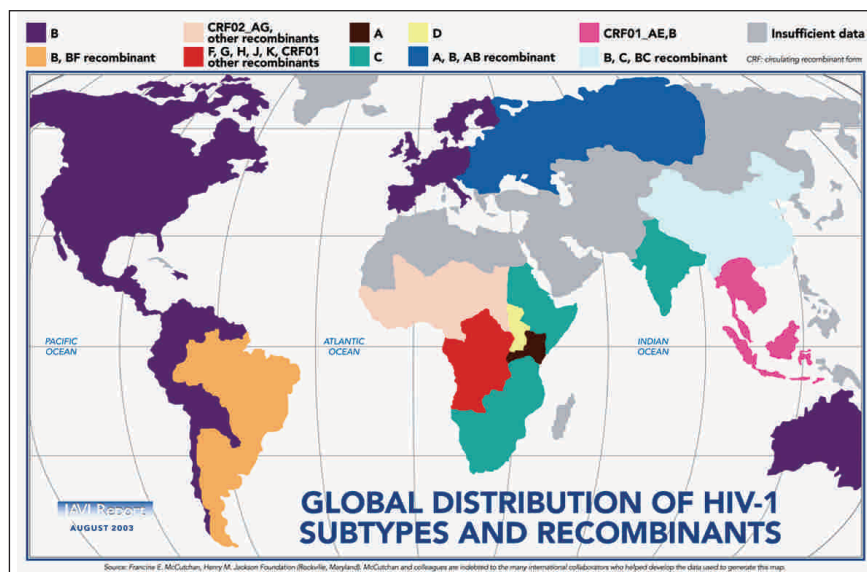
To the editor: There is general consensus among scientists that the Human Immunodeficiency Virus (HIV) crossed from non-human primates to man as a result of consumption of, or contact with blood from bush meat by local inhabitants of sub-Saharan Africa. In particular, *Pan troglodytes troglodytes*, which carries the SIVcpz form of Simian Immunodeficiency Virus (SIV) has been postulated as the progenitor of HIV-1. In addition, HIV-2 is closely related to SIVmac based on the extremely close sequence homology between the human forms and their simian counterparts.¹

There are two types of HIV namely HIV-1 and HIV-2 (less cytopathic than HIV-1). HIV-1 is divided into three groups (types) namely **M** (Major), **N** (New) and **O** (Outlier). Group **M** has nine clades (subtypes) - designated A through K, with

no E or I based on the short sequences, mostly within the HIV envelope.² In the 2003 International AIDS Vaccine Initiative (IAVI) report, the various clades and recombinant forms of HIV-1 are shown in their global geographical distribution (figure 1).² Western Europe, Australia and the USA essentially harbour the clade B form of HIV-1; Southern Africa, East Africa, the horn of Africa and India harbour clade C, while clades B, C and BC recombinant are found in the Far East. Eastern Europe harbours clades A, B, and AB recombinant. Central Africa harbours F, G, H, J, K, CRF01, other recombinants, with A and D in adjacent areas of east Africa – none of which harbour clade B. In West Africa and some of the adjacent North African countries where HIV-2 is predominant, the HIV-1 clades are CRF02_AG and other recombinants, but not clade B, while in South America the clades are B and BF recombinant. There are geographical areas of the world where there is insufficient data to classify their predominant HIV-1 clades namely North Africa, Middle East, central Asia, parts of the former Russian Federation, some Pacific Islands and Madagascar (Africa). It is important to note that the prevalence of HIV in some of these regional blocks is on the increase.

Apart from the remarkable compartmentalization of various clades and recombinants in specific global areas, clade B, in essence, is absent from Africa, the presumed origin of the progenitor of HIV-1 i.e. SIVcpz. In addition, it is significant that in the short period since the first evidence of HIV-1 was documented in human sera (circa 1959); various clades have essentially become restricted to specific geographical areas of the world despite global migration. The question is: why is clade B absent in Africa? Central Africa, where the first polio vaccine using monkey kidney cultures were implicated, shows various clades with no evidence of clade B, which is found in Australia, Western Europe and the USA. The IAVI global map of clade distribution suggests the inescapable notion of the independent origin of each clade rather than a common origin of all clades from the African continent. It is difficult to explain the strict demarcation of each clade to specific geographical areas strictly using genetic mutation as a possible reason. Considering these observations and available scientific evidence, it is suggested that the origin of HIV-1 is still unknown and this necessitates objective re-evaluation. We hypothesize that HIV originated from various parts of the world with different clades at about the same or closely-related time. What triggered its emergence is a more productive process to follow than its origin. The jury is still out on this one!

Figure 1: Global distribution of HIV-1 subtypes and Recombinants



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