

Genetic Variability of Hiv Type 1 In Kenya

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Abstract

PIP: The AIDS epidemic is a rapidly growing problem in Nairobi, where the seroprevalence in pregnant women increased from 4% in 1988 to over 10% in 1991. 22 HIV-1-seropositive pregnant women and 1 HIV-1-infected baby (K88) attending the Pumwani Maternity Hospital of Nairobi between 1990 and 1992 were studied as part of a cohort study of maternal risk factors in mother-to-child transmission. A 250-base pair (bp) fragment of the env gene encoding C2V3 was amplified mostly from DNA isolated from primary peripheral blood mononuclear cells and subsequently sequenced. The 23 newly determined HIV env sequences were aligned with 23 previously known sequences of HIV-1 isolates of diverse geographical origin and the sequence of the HIV-1-related chimpanzee isolate SIVcpz-gab, on the basis of primary structure. Distance calculation, tree construction, and bootstrap analysis were realized with the software package TREECON. In the tree, 8 major branches could be observed containing sequences representative of 8 different subtypes A, B, C, D, E, F, G, and H, besides the outlier group O. 19 of 23 Kenyan isolates clustered with D687, Z321, U455, and SF170, which were members of genetic subtype A. Phylogenetic analyses favored positioning of K976 as a divergent A subtype strain. For 4 strains (K29, K88, K98, and K112) the subtype A classification based on the gag gene was also observed on the basis of phylogenetic analysis of the C2V3 coding part of the env gene. The predicted amino acid sequence of the V3 region for these strains was also presented. The finding that among 23 HIV-1 isolates collected in Nairobi, 19 were classified in subtype A versus 3 in subtype D, together with a much larger variation between subtype A strains as compared to subtype D strains, suggests an earlier introduction of a subtype A strain, multiple introductions of subtype A strains, and/or faster diversification of subtype A strains as compared to subtype D strains.