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Sequence Note

Genetic Analysis of HIV Type 2 from Ghana and Guinea-Bissau, West Africa

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ABSTRACT

The phylogenetic variability of part of the long terminal repeat (LTR) region of HIV-2 strains isolated in 1995 from five individuals residing in Bissau, the capital city of Guinea-Bissau, and collected from seven persons from Kumasi, Ghana in 1996–1997, was analyzed. All Guinean samples and all but one Ghanaian sample clustered with HIV-2 subtype A. One Ghanaian sample (14%) was classified as HIV-2 subtype B. This study adds to previous reports on HIV-2 subtype distribution in West Africa indicating local prevalence of HIV-2 subtype B in Ivory Coast and neighboring Ghana.

HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (HIV-2) is common in West Africa (Ivory Coast, Ghana, Guinea-Bissau, Senegal, The Gambia, Cape Verde Islands, Mali)[1,2] and in India.[3] In addition, HIV-2 infection has been documented mainly in African immigrants.[4] In geographic regions where both HIV-1 and HIV-2 are prevalent, their spread has been unequal. Studies have shown that HIV-2 is perinatally and sexually less transmissible than HIV-1.[5,6] Although HIV-2 AIDS appears to be similar to HIV-1-induced AIDS, the rate of disease progression in HIV-2-infected individuals is much slower than in those with HIV-1.[6,7] The ratio of HIV-1 versus HIV-2 infections is rapidly increasing over time. In Ghana, Hishida *et al*. reported that HIV seroprevalence of HIV/AIDS patient or suspected cases in 1990–1992 for HIV-1, HIV-2, and dual infection were 65, 21, and 14%, respectively.[8] According to the data of 1999 HIV sentinel surveillance in Ghana, HIV-1, HIV-2, and dual infection rates were 92.8, 2.8, and 4.4%, respectively.[9] Seven HIV-2 genetic subtypes, A to G, have been reported to date.[10–12] HIV-2 subtype A viruses have been documented in diverse locations across western Africa[1,2] as well as in Europe,[4] India,[3] and South Korea.[13] Subtype B exhibits a more restricted geographical distribution and has been reported mainly in Ivory Coast[14] and Ghana,[15] with a few cases documented in Europe[16] and the Middle East.[17] Subtypes C, D, E, F, and G are each represented by single sequences that were obtained from HIV-2-seropositive individuals living in rural areas of Liberia (subtypes C and D), Sierra Leone (subtypes E and F), or Ivory Coast (subtype G).[10–12]

The present study focuses on HIV-2 subtype distribution among HIV-2-seropositive individuals in Guinea-Bissau (n = 5) and Ghana (n = 7). Ninety-four Guinean individuals attending an outpatient clinic at the Tropical Medicine Center of Bissau, the capital city of Guinea-Bissau, in 1995 were screened for HIV-1 and HIV-2 antibodies by enzyme-linked immunosorbent assay (ELISA) (Innotest HIV-1/HIV-2 Ab sp; Innogenetics, Zwijnaarde, Belgium). Reactive specimens were subsequently confirmed by Western blot analysis (New Lav Blot 1–2; Sanofi Diagnostics Pasteur, Marnes-la-Coquette,

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France). Twenty-one of 94 (22.3%) Guinean individuals tested positive for HIV-2. Eighteen of 21 Guinean samples were confirmed HIV-2 positive by nested polymerase chain reaction (PCR) using long terminal repeat (LTR) and/or *env* primers (primers L100/L200 and L101/L201 for LTR, and primers SE24/SE25bis and SE28/SE27bis for *env*) as described previously.[18]

Five Guinean HIV-2-positive samples and seven samples isolated from HIV-2-positive individuals from Ghana (Kumasi) in 1996–1997 were used for subtyping purposes. Genomic DNA was extracted from primary peripheral blood mononuclear cells (PBMCs) of HIV-2-seropositive individuals. A 324-base pair fragment encoding part of the LTR region (nucleotides 60 to 383 according to HIV-2 ROD; accession number X05291) was PCR amplified as described previously.[18] PCR products were purified with a QIAquick gel extraction kit (Qiagen, Valencia, CA). The recovered PCR products were subjected to direct sequencing in both directions, using an ABI PRISM dye terminator cycle sequencing Ready Reaction kit (Applied Biosystems, Foster City, CA) and an automatic sequencer (ABI model 373A: Applied Biosystems). The newly determined HIV-2 LTR sequences were aligned with 15 previously documented sequences of HIV-2 isolates representing HIV-2 subtypes A, B, and G, for which LTR sequence information is currently available. Distance calculation, tree construction, and bootstrap analysis were realized with the software package TREECON, as previously described.[19]

Phylogenetically, all Guinean samples and six (86%) Ghanaian samples are classified as HIV-2 subtype A; one Ghanaian sample (14%; NJ205) belongs to HIV-2 subtype B. Within subtype A, four Ghanaian samples (NJ42, NJ79, NJ206, and NJ207) strongly clustered with HIV-2 ROD, previously isolated from a person of the Cape Verde Islands (Fig. 1). Our results indicate that at least two different subtypes of HIV-2, subtype A and subtype B, cocirculated in Kumasi, Ghana between 1990 and 1997. So far only HIV-2 subtype A has been found in Guinea-Bissau.[20] In Ghana, cocirculation of HIV-2 subtypes A and B has already given rise to HIV-2 A/B recombinants.[15]

This study adds to the previous reports on HIV-2 subtype distribution in Guinea-Bissau and Ghana. Regarding HIV-2 subtype distribution, so far subtype B has mainly been identified in Ivory Coast, where the majority of HIV-2 infections are due to subtype B (71%, 20 of 28),[14] and to less extent in Ghana. The reason for this local prevalence of HIV-2 subtype B is unclear. There are currently no studies indicating differences in pathogenesis and transmissibility for HIV-2 subtypes. However, data on molecular epidemiology of HIV-2 subtypes remain scarce, and on the basis of our current knowledge it is

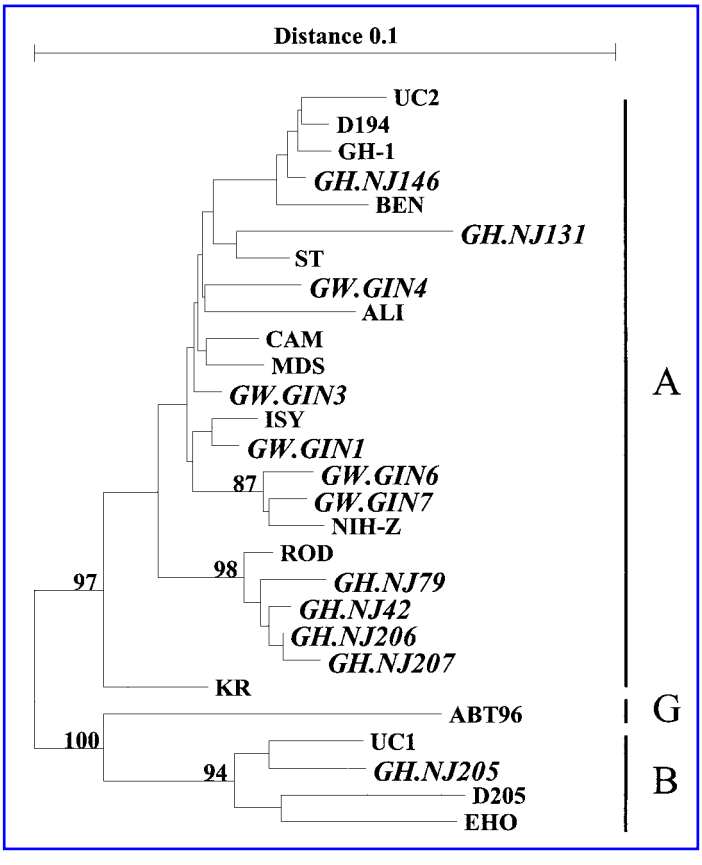

FIG. 1. Phylogenetic tree based on 346 unambiguously aligned positions of 28 HIV-2 sequences encoding part of the LTR. Sequences determined in this study are represented in italic. A total of 1000 bootstrap samples were analyzed. Bootstrap values are given in percentages at the internodes if they exceed the 70% level. The distance between two sequences is obtained by summing the lengths of the connecting branches by using the scale at the top. The tree is rooted arbitrarily. Strain names of samples from Guinea-Bissau and Ghana identified in this study are preceded by country codes GW and GH, respectively.

speculative to address evolutionary advantage to either subtype. As the earliest samples documented for HIV-2 subtype distribution in Ivory Coast were of both subtype A and B, sharing a similar range of diversity, it seems plausible to believe that the relative success of subtype A in most West African countries is due to a founder effect. Further studies of HIV-2 isolates may reveal the differences in biological properties between HIV-2 subtypes A and B.

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SEQUENCE DATA

The HIV-2 LTR nucleotide sequence data were deposited in the EMBL, GenBank, and DDBJ nucleotide sequence databases under the following accession numbers: AY039114–AY039125.

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