ABSTRACT

Background: Global vaccine concepts either include the subtypes A, B, C, and CRF01_AE for insert design or mosaic inserts derived from published databases with low West African subtype representation. The conventional view that West African HIV variants are largely CRF02_AG would justify the inclusion of subtype A sequences in a global design. We challenge this justification by presenting the significant contribution of subtype G in the HIV-1 epidemic in four Nigerian cities using a multiregion hybridization assay (MHA) that can identify and differentiate between subtype G and CRF02_AG.

Methods: Viral RNA was extracted from plasma of 71 volunteers for a cohort for prevalence, risk factor, and subtype study conducted in Nigeria. Twelve were from Kaduna, 18 from Abuja, 30 from Makurdi, and 11 from Enugu and all were subjected to the G/CRF02_AG MHA, a high throughput assay. This MHA was designed to contain 7 regions: 3 (pol [RT], pol [INT], tat) through the inclusion of subtype A sequences in a global design. We challenge this justification by presenting the significant contribution of subtype G in the HIV-1 epidemic in four Nigerian cities using a multiregion hybridization assay (MHA) that can identify and differentiate between subtype G and CRF02_AG.

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Results: Overall, subtype G represents 25% while CRF02_AG contributes 44% and their recombinants represent 21%. 10% of the samples are neither subtype G nor CRF02_AG. Notably, 13 out of 15 recombinants contain subtype G gp120 sequences. Our data agree with previous reports showing a higher percentage of subtype G in southern Nigeria (Enugu) as compared to the north (Kaduna).

Conclusions: Subtype G and subtype G-positive gp120 recombinants represent a significant portion of HIV-1 infections in Nigeria, suggesting that the total number of subtype G infections in Western Africa may be more of a burden than previously thought and should inform global vaccine designs.

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CONCLUSIONS

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