POSTER PRESENTATION



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Genetic variability and high proportion of HIV-1 BF1 recombinant strains among vertically infected children in São Paulo, Brazil

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Introduction

The enormous genetic variability of human immunodeficiency virus type 1 (HIV-1) continues to present a major challenge for vaccine design and frustrate efforts to halt the epidemic. A proper understanding of this phenomenon is a prerequisite for proper epidemiology, genetic diagnosis, and successful drugs and vaccines. In this study, we undertook a detailed molecular epidemiological investigation on HIV-1 vertically-infected children born from 1993 to 2008 in the state of São Paulo, Brazil.

Material and methods

HIV-1 proviral DNA was extracted from the peripheral blood mononuclear cells of 48 participants. The near fulllength genomic (NFLG) and partial fragments were determined by overlapping nested PCR and direct sequencing. The data were phylogenetically analyzed.

Results

Of the 48 samples (median age 11.8 years, range 4-20.6 years) studied, 3 (6.2%) NFLGs and 39 (81.2%) partial fragments were successfully subtyped. Of the successfully subtyped sequences, 20 (47.6%) were subtype B sequences, 17 (40.4%) BF1 recombinants, and 5 (11.9%) subclade F1. Two of the partial BF1 chimeric isolates shared an identical recombination structure. Predictions of viral tropism using the computer program geno2pheno [co receptor] for phenotype prediction were determined for 15 subjects. X4 or X4 dual or mixed-tropic viruses were seen in 3 (20%) of participants and the V3 sequences of 12 patient virus strains (80%) were predicted to be R5-tropic virus.

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Conclusions

Our data provided evidence of unexpectedly high proportion of BF1 recombinants viruses transmitted from the first mother-to-child since the earliest days of the epidemic to the present time in Brazil. These findings offers additional insights to understanding the diversity of HIV-1 strains currently circulating in Brazil, with future implications for diagnosis, therapy, and efficient vaccine development.

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