

Poster presentation

Open Access

P20-05. Emergence of HIV-1 circulatory recombinant forms (CRFs) and unique recombinant forms (URFs) in North India: functional and pathogenic implications

U Neogi^{*1}, V Sood¹, AS Bano¹, A Wanchu² and AC Banerjea¹

Address: ¹Department of Virology, National Institute of Immunology, New Delhi, India and ²PGIMER, Chandigarh, India

* Corresponding author

from AIDS Vaccine 2009
Paris, France. 19–22 October 2009

Published: 22 October 2009

Retrovirology 2009, **6**(Suppl 3):P375 doi:10.1186/1742-4690-6-S3-P375

This abstract is available from: <http://www.retrovirology.com/content/6/S3/P375>

© 2009 Neogi et al; licensee BioMed Central Ltd.

Background

After documentation of first case of HIV/AIDS in commercial sex worker in 1986 in India, it has now spread to all the states over a period of 22 years and become a major public health problem in India. Sex trafficking and injecting drug users are the main source for driving HIV-1 epidemic here. HIV-1 is also spreading due to the mother-to-child transmission and by other unspecified route. The detail genetic analysis of HIV-1 genotypes in India would help us define the biological significance of the global diversity of HIV-1 strains and improve our understanding of the disease progression.

Methods

LTR, *Nef*, *Vpr* and *Env* genes were amplified and sequenced from genomic DNA of HIV-1 infected individuals from Punjab/Haryana and Delhi. Various genotyping and bioinformatics tools were used to analyze the sequences.

Results

We have found novel mosaic URFs B/C LTR, B/C and B/C/D recombinant *Nef*, B/C/D recombinant *Vpr* and CRF02_AG envelope along with dominant subtype C after analyzing near about 100 HIV-1 infected patients from different risk groups (heterosexual and vertical transmission).

Conclusion

Extensive recombinations involving multiple HIV-1 subtypes were observed by us in northern India. The co-existence of several subtypes and social networks of HIV-1 transmission could quickly lead to the generation of highly diverse forms of unique intersubtype recombinants. Mixing of different lineages and clades of HIV-1 strains could rapidly lead to the evolution of new recombinant strains. Recombinant viruses have already contributed substantially to the global pandemic, and the likelihood of generating recombinant viruses will continue to increase as the different HIV-1 subtypes are spreading worldwide. This provides insights into the understanding the genesis and functional implications of HIV-1 epidemic in India. Such temporal studies are very important to monitor the spatio-dynamics of the emerging strains. They will obviously have enormous implications in designing region specific T-cell based vaccines.