### Poster presentation

## **Open Access**

# **Identification and Biological Characterization of Unique B/C Recombinant Strains of HIV-1 In Southern States of India** Siddappa N Byrareddy\*<sup>‡1,2</sup>, PK Dash<sup>1</sup>, A Mahadevan<sup>3</sup>, Anita Desai<sup>2</sup>, N Jayasuryan<sup>4</sup>, P Satishchandra<sup>5</sup>, V Ravi<sup>2</sup>, SK Shankar<sup>3</sup> and U Ranga<sup>1</sup>

Address: <sup>1</sup>Molecular Virology Laboratory, Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore, India, <sup>2</sup>Department of Neurovirology, Bangalore, India, <sup>3</sup>Department of Neuropathology, Bangalore, India, <sup>4</sup>Department of Neurology, National Institute of Mental Health and Neurosciences, Bangalore, India and <sup>5</sup>Microtest Innovations Pvt. Ltd, Bangalore, India

Email: Siddappa N Byrareddy\* - sidhu@jncasr.ac.in

\* Corresponding author \$Presenting author

from 2005 International Meeting of The Institute of Human Virology Baltimore, USA, 29 August – 2 September 2005

Published: 8 December 2005

Retrovirology 2005, 2(Suppl 1):P126 doi:10.1186/1742-4690-2-S1-P126

#### Background

HIV-1 subtype-C strains are associated with more than half the infections globally. The molecular nature of the viral subtypes circulating in India is not adequately characterized. In the largest study ever to appear from India, we recently reported a predominance of subtype-C infections in the southern states of the country (Siddappa N.B et al AIDS in press). Unexpectedly, we identified 3 unique B/C recombinant viruses in our cohort that contained envelope of subtype-B origin.

#### **Methods**

608 seropositive volunteers were enrolled during 2000–2004 for this study. Genomic DNA from the blood samples was characterized using a novel PCR that differentially identified subtype-C viruses in the viral LTR. A subset of 115 samples was also analyzed in the env, using DNA sequencing and / or HMA.

#### Results

Out of a total of 608 samples, 602 (99%) were identified to be subtype-C in LTR. Additionally, two subtype-A one subtype-B and 3 B/C recombinants were also identified. Interestingly, env sequences of two of three B/C recombinant viruses phylogenetically clustered with subtype-B strains of the USA and the third one with Thai-B. Subtype-C viruses are hypothesized to have evolved to greater levels of attenuation, hence are less pathogenic to the host. This hypothesis was further supported by the observation that the prominent recombinants of subtype-C (B/C and C/D) invariably retain env sequences derived from subtype-C. In this backdrop, the B/C recombinant viruses we identified in southern India attain importance as these recombinants contain naturally evolved B-env. We are presently isolating molecular clones of these unique B/C recombinants for further characterization of subtype-C viruses.

#### Conclusion

Globally, the number of circulating recombinant forms of HIV-1 is rapidly increasing. Importantly, the overall incidence of the recombinants is also on the rise. Our identification of two different types of unique B/C recombinants in southern India, at a significant frequency, warrants an extensive nationwide investigation to determine if a new epidemic is emerging in India.