

**Ph.D Scholar:** Uma Sharma

**Department:** Department of Biotechnology, Jamia Millia Islamia, New Delhi-110025

**Faculty:** Faculty of Natural Sciences, Jamia Millia Islamia, New Delhi-110025

**Ph.D. Thesis Title:** “Molecular characterization of HIV-1 in infants born to HIV-1 positive mothers”

**Supervisor:** Prof. Mohammad Husain, Dept. of Biotechnology, Jamia Millia Islamia, New Delhi- 110025

**Co-Supervisors:** Dr Sunil Gupta, Additional Director, National Centre for Disease Control, 22-Sham Nath Marg, Delhi-110054, Dr. S. Venkatesh, Director, National Centre for Disease Control, 22-Sham Nath Marg, Delhi-110054

## **Abstract**

**Key words:** HIV-1, DBS, DNA PCR, Heterogeneity, *nef*, *vpu*, *p24*

HIV-1 infection transmitted from an infected mother to her child is the most important mode of transmission in children. Diagnosis of HIV-1 in children is very important at very young age so that they can live a disease free life. In this study a total of 1646 Dry Blood Spot of infants aged 6 weeks to 18 months were tested by DNA PCR. Out of these, 269 (16.34%) were HIV-1 positive. Positivity was slightly higher in males (17.4%) than females (14.8%). It was observed that the infants on mixed feed (breast feed + formula feed) showed a much higher transmission rate in comparison to the exclusive breast or replacement feed suggesting that the mixed feeding practice aggravates the situation.

Identifying the genetic variability in vertically transmitted viruses in early infancy is important to understand the virus characteristics and disease progression. Molecular characterization of *nef*, *vpu* and *p24* gene was also carried out in 85 infant's samples. To investigate and compare the genotypic characteristics of transmitted viruses in early infancy, these infants were categorized in two age groups; acute ( $\leq 6$  months) and early ( $> 6$ -18 months).

Most of the sequences belonged to subtype C followed by A1. Phylogenetic analysis revealed that both the age groups were genetically related to each other. Synonymous substitutions were frequent. The study showed appreciable differences in virus population due to difference in age group of infants. *Nef* was the most variable; *vpu*

was moderately variable while *p24* was the least variable gene. Amino acid variability was decreasing with the increasing age of the infants indicating that the infants were gradually evolving towards positive selection for robust virus population. The study revealed that the epitopes LTFGWCFKL, TPQDLNTML and RMYSPVSIL may be the good candidates for vaccine construct.