

Poster presentation

Open Access

## Development of a Quantum Dot-based Assay System for Detection of Specific HIV-1 LTR Sequence Variants

Asiedua Asante\*<sup>‡1</sup>, Michael Nonnemacher<sup>1</sup>, Aikaterini Alexaki<sup>1</sup>, Elisabeth Papazoglou<sup>2</sup>, Peter Lelkes<sup>2</sup> and Brian Wigdahl<sup>1</sup>

Address: <sup>1</sup>Department of Microbiology and Immunology and Institute for Molecular Medicine and Infectious Disease, Philadelphia, PA, USA and <sup>2</sup>School of Biomedical Engineering, Science, and Health Systems, Drexel University College of Medicine, Philadelphia, PA, USA

\* 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):P9    doi:10.1186/1742-4690-2-S1-P9

Analysis of human immunodeficiency virus type 1 (HIV-1) long terminal repeat (LTR) sequence variation within the CCAAT/enhancer binding protein (C/EBP) and stimulating protein (Sp) transcription factor binding sites has identified variants that correlate with HIV-associated dementia (HIVD). CdSe/ZnS nanocrystals have facilitated the investigation of nano- and pecto-scale biological components. Quantum dot-conjugated oligonucleotides homologous to specific variants of Sp site III and C/EBP site I, were utilized to quantitate the relative abundance of specific LTR variants. Quantum dot-conjugated oligonucleotides containing the Sp site III 5T binding site variant (C-to-T change at position 5) or the C/EBP site I 3T site variant, were reacted with plasmid DNA containing increasing concentrations of plasmid with the homologous LTR sequence variant. The results suggest that quantum dot-conjugated oligonucleotides specific for sequence variants within the LTR can be used as reporter molecules for identification and quantitation of HIV-1 genetic variation.