

## POSTER 46

### PROBING THE HIV-1 GENOMIC RNA TRAFFICKING PATHWAY AND DIMERIZATION BY GENETIC RECOMBINATION AND SINGLE VIRION ANALYSES

Michael. D. Moore<sup>1</sup>, Olga A. Nikolaitchik<sup>1</sup>, Jianbo Chen<sup>1</sup>, Vinay K. Pathak<sup>1</sup>, Marie-Louise Hammarskjöld<sup>2</sup>, David Rekosh<sup>2</sup>, and Wei-Shau Hu<sup>1</sup>

<sup>1</sup>HIV Drug Resistance Program, National Cancer Institute, Frederick, MD 21702; <sup>2</sup>Myles H. Thaler Center for AIDS Research, University of Virginia, Charlottesville, VA 22908

HIV-1 virion packages two molecules of genomic RNA held together as a dimer. First, we sought to delineate the cellular location where HIV-1 RNA initiates dimerization. Using a cell-fusion-dependent recombination assay, we demonstrated that the two RNAs destined for copackaging into the same virion select each other mostly within the cytoplasm. Next, we analyzed how the RNA transport pathway used by the virus influences downstream events essential to viral replication. By replacing the HIV-1 Rev response element (RRE) with the constitutive transport element (CTE) from Mason-Pfizer monkey virus, we produced HIV-1 virus that exports its RNA from the nucleus using the Tap/Nxf1 pathway instead of the usual CRM-1 pathway. Analysis of RRE- and CTE-dependent HIV-1 viruses revealed that the export pathway taken is important for the ability of RNA molecules derived from two viruses to interact and be copackaged. These results further illustrate that at the point of dimerization the two main cellular export pathways are partially distinct. Lastly, by providing Gag *in trans* we have demonstrated that Gag is able to package RNA from either export pathway, irrespective of the transport pathway used by the *gag* mRNA. These findings provide unique insights into the process of RNA export in general, and more specifically, of HIV-1 genomic RNA trafficking.