

# **5<sup>th</sup> Annual Joint Bioinformatics Workshop**

**July 19, 2005**  
2229 Seamans Center  
University of Iowa

by

**Christopher J. Moressi**  
University of Iowa

## ***In Vitro Analysis of Feline Immunodeficiency Virus Vector Integration***

### ***ABSTRACT***

Currently, nothing is known regarding the integration preferences of non-primate lentiviral vectors derived from feline immunodeficiency virus (FIV) in human or murine cells. It was discovered in our study that FIV closely corresponded with the integration preferences of HIV. A total of 132 integration sites into the human genome were mapped in our study and analyzed according to gene locality, go terms, and physics properties of flanking sequence. Approximately 68% of the FIV integrations events occurred within a RefSeq transcript and introns regions were preferred of exon regions. Of the 90 RefSeq genes targeted, 50 were represented on a publicly available HepG2 microarray data set. The median expression level for these 50 genes was 6.3-fold higher than that of all the genes on the array, demonstrating that FIV integration favors actively transcribed genes. Furthermore FIV integrations occurred throughout the whole RefSeq transcript which is similar to the integration preference of HIV. These data suggest that while FIV integration preferences are more similar to HIV than to MLV, significant differences exist between FIV and HIV vectors.