

**POSTER 65****NEW BIOINFORMATIC ALGORITHM TO DETECT RECENT HIV-1 INFECTION**

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**Background:** Characterizing the prevalence and incidence of HIV-1 infection in populations is a public health imperative. Although HIV-1 prevalence rates are readily derived from routine HIV-1 testing modalities, measurements of HIV-1 incidence are determined using sensitive serologic assays that require laboratory procedures in addition to standard clinical testing. New inexpensive methods to efficiently measure HIV-1 incidence would provide an important advance in epidemiologic surveillance. Recently we used sensitive single genome sequencing techniques to detect increases in HIV-1 diversity with time after infection (Kearney et al., 2009). We developed new bioinformatics approach to analyze commercial genotypes to investigate whether indirect measures of genetic diversity obtained from population based genotypes are useful in distinguishing recent (<1 y) from chronic ( $\geq$  1y) HIV-1 infection.

**Methods:** Patients with recent (N=15) or chronic (N=13) HIV-1 infection with no prior exposure to antiretroviral therapy were identified; all patients provided written informed consent and standard genotyping (TRUGENE) was performed. Using TRUGENE base-calling algorithm, we determined the number of ambiguous bases, and calculated the frequency of all sequenced bases that were ambiguous. Differences in numbers of ambiguous bases were compared using standard t testing, and sensitivity and specificity determined.

**Results:** All patients with recent HIV infection had documented HIV-1 seroconversion event within the year prior to genotyping. Individuals with chronic HIV-1 infection had documented positive western blot  $\geq$  1 year prior to genotyping. Analysis of Median ambiguity in patients with acute infection (0.11 ambiguous bases/ bases sequenced, range 0 -0.76) was c. 9 fold lower than that measured in chronically infected individuals (0.98 ambiguous bases/bases sequenced, range 0.22 – 2.2 ambiguous bases/sequenced bases.  $p < 0.0003$ ). Assay sensitivity was 0.8 and specificity was 0.77.

**Conclusions:** Bioinformatic analyses of commercially available, population based genotypes distinguished recent from chronic HIV-1 infection. As current DHHS guidelines recommend standard genotyping for all individuals with newly identified HIV-1 infection, analysis of these standard genotypes can lead to new inexpensive determination of incidence rates.