

Immunological characterization of HIV-1 Recent and

Long-term Infections in Cameroon

Service Site: FDA, White Oak

Sai Keerthana Cherukuri saikc@umd.terpmail.edu Science and Global Chnage Neurobiology and Physiology



College_Park

scholars

Research Objective

The objective of this study is to measure whether the infection is recent or long term for a cohort of clinical samples from

Cameroon.

Experience

Working the the FDA was very rewarding. All the concepts that I was learning in my classes such as Genetics and the skills that I acquired in Organic Chemistry Lab, I was able to apply them in my work at the FDA. While I was working there, I had the opportunity to be exposed to other disciplines such as bioinformatics. This sort of exposure helped me broaden my interests towards statistics and helped me appreciate them more. I am now able to understand in specifics the interdisciplinary relationships between the various subjects.

We analyzed (n=136) HIV-positive individuals plasma samples from Cameroon. Plasma viral load was determined using the Abbott Real-Time HIV-1 Assay Kit (0.6 ml HIV-1 RNA US). The HIV RNA isolation was done using the m2000sp system and amplified by the m2000rt (Abbott Molecular, Inc., Des Plains, IL). All samples were tested using the LAg-Avidity assay (Sedia Biosciences Corporation, Portland, OR) per manufacturer's recommendations. Briefly, using Sedia HIV-1 Lag-Avidity EIA kit, we measured the HIV-1 antibody avidity which classifies the samples as being recent or long-term infection by comparing the EIA result with an established calibrator. The calibrators and controls are set with specific numerical values which help classify the timing of infection. The normalized OD values less than 1.5 are labeled as recent infection and the samples with greater than 1.5 are labeled as a chronic or long-term infection. The proportion of individuals

this prompted me to take classes such a

who were misclassified as recent were determined using a predetermined algorithm of a LAg Avidity score of <1.5 normalized optical density units (ODn) and presence of an HIV viral load >1000 copies/ml.

For ongoing genomic characterization HIV-1 env coding regions, including V1-C5 of gp120 and the gp41 ectodomain of HIV-1 consisting of ~1.4kb, were successfully amplified and sequenced by next generation sequencing (NGS) using the Illumina MiSeq platform.

