Abstract

It has been 40 years since smallpox was declared eradicated, a feat that was only made possible by the discovery of vaccines. The discovery of vaccinations started through a process known as variolation. The process of variolation was eventually optimized and the concept of vaccination was applied to various diseases reducing the global burden of these diseases on the healthcare system. Most vaccines in the past were geared towards the modulation of the B cells as they are directly related to the production of antibodies. However, more recent studies are focusing their attention towards T cells. This study aims to understand what is happening in T cells during the peak of the adaptive immune response to the most successful vaccine in the world. The Activated CD8, Activated CD4, Naive CD4 and Resting CD4 subsets were put through a differential gene expression analysis conducted through Rstudio and GenePattern. Gene ontology was also performed through Database for Annotation, Visualization, and Integrated Discovery (DAVID). As expected, resting T cells showed an upregulation of genes related to homing, Naive CD4 T cells showed a more random expression of genes and the two activated subsets expressed similar genes. Interestingly, cytotoxic genes were found in CD4 subsets which is a potential future area of study. Data for this study was obtained from a HG-U133 plus 2.0 microarray. While this method was cutting edge at the time of this study, there are several downfalls to this method. Other limitations came in the form of the age of the samples, the limited participant size, and the lack of access to the lab due to the on-going pandemic. Future studies should be geared towards performing the same analysis with newer technologies and a larger sample size.

Keywords: *Vaccinia, CD4 T cells, CD8 T cells, GenePattern, Gene Ontology*