

Maxwell Bohl

MS Microbiology

Sequencing and analysis of serially passaged influenza virus

Influenza viruses are human and animal pathogens. These airborne-spread viruses infect the respiratory tract of humans and can cause disease ranging from mild discomfort to death. In the United States roughly 30 million cases of seasonal influenza are reported yearly of which 500,000 require hospitalization. Previous students looked at how the imposition of genetic bottlenecks, like those experienced during transmission of the virus, resulted in viruses with reduced replication ability relative to the parental strain A/Victoria/361/2011 (H3N2). This project is a reconfirmation of those results and extend analysis to non-coding regions of the influenza virus strain. The replicative ability of these viruses was evaluated by comparing growth rates in cell culture over 48 hours relative to the parental virus. The genetic differences between the parental strain and the derived viruses were then analyzed by converting their genomes to DNA using reverse transcription polymerase chain reaction, and then sequenced using Illumina next generation sequencing. The changes in the derived virus lines were determined by comparing reference influenza genomes and the parental virus sequence. Further investigation into which of these changes affect viral protein function can then be done.