

Impact of the Bottleneck Effect on Influenza A
Julia Gall
Microbiology

Influenza virus mutates rapidly and the genetic diversity in a population is affected by bottleneck events, which are when population sizes is suddenly reduced, demonstrated when the virus jumps to a new species. This study may increase understanding of how Influenza virus can jump from animals to human. To determine the impact of these events, an influenza virus, A/Victoria/361/2011 (H3N2), was repeatedly exposed to bottleneck events and a virus population with poor viral fitness, “dilapidated virus” (DV) was discovered. The DV was then repeatedly passed through bottlenecks and a “recovered virus” (RV) population with improved fitness was identified. To assess the viral fitness, we will evaluate a real-time quantitative polymerase chain reaction (qPCR) protocol for monitoring virus replication, replacing labor-intensive plaque assays and establishing a new standard protocol in the lab. Ideally, qPCR data will not have any significant differences compared to plaque assays, although qPCR may give higher virus counts because it will detect non-viable and viable viruses. To characterize the RV, next-generation sequencing (NGS) will be used. NGS has the unique ability to report nearly all sequences from individual genomes in mixed populations, thereby yielding the proportion of mutations in the RV compared to the DV and parental virus.