Size Matters: Impact of Serial Bottleneck Events on Influenza A Evolution

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Influenza A virus (IVA) mutates rapidly and generates genetic variation in the viral population. As influenza viruses are transmitted host-to-host, there is a substantial reduction in the viral population size as only a portion of the viral population in the infected host is transmitted to the new host, herein called a bottleneck event. To determine the impact of serial bottleneck events A/Victoria/361/2011 (H3N2) influenza virus was serially passaged under narrow bottleneck conditions resulting in a virus with dilapidated viral fitness, referred to as the "dilapidated virus" (DV). The DV was passed through a series of larger bottlenecks which produced a "recovered virus" (RV). To characterize the RV, next-generation sequencing (NGS) is used. Sequences from the RV, DV, and parental virus are compared to understand mutational patterns associated with fitness recovery. A long-range reverse-transcription quantitative polymerase chain reaction (LR-RT-qPCR) to quantitate virus loads in biological samples will be developed to replace plaque assay-based quantitative methods. A qPCR-based method of viral quantification will be faster and less expensive than plaque assays, streamlining workflow in the laboratory.