“NEAR REAL-TIME” GENOMIC SEQUENCING OF ZIKA VIRUS POSITIVE MOSQUITOES AND CLINICAL CASES

Gustavo Palacios[1]
[1]Center for Genome Sciences, USAMRIID, Frederick, USA

ZIKV was first discovered in 1947 and was not initially considered a major threat to human health. However, over the last year, ZIKV has spread worldwide and has been shown to be associated with a range of often severe birth defects now known collectively as congenital ZIKV syndrome. The important health implications were compounded by the fast rate at which ZIKV has been able to spread throughout the Americas.

Whole genome sequencing has been extensively used in the past to characterize disease outbreaks. However, these activities have been typically performed after the threat has subsided, mainly due to the difficulties of first-responders to engage in “research” activities not considered crucial to the public health response. Next-generation sequencing (NGS) has revolutionized the field allowing the generation of whole viral genome sequences in “near real-time” and providing information relevant for the reconstruction of transmission chains, for understanding the spatial movement of the virus, and for dating introduction events. In this work, we used ZIKV-tailored NGS tools for the characterization of complete genomes from clinical specimens to study the origin of both travel-related and locally-acquired ZIKV cases in the US.

In collaboration with the Florida Department of Health, we have generated 20 ZIKV genomes from urine samples collected from patients in Florida with locally acquired ZIKV infections. All genomes were sequenced with the RNA Access targeted enrichment system on an Illumina MiSeq. All samples were collected from patients in the Miami region during July 28 – October 31 2016. All of these sequences, in conjunction with other ZIKV complete genomes obtained worldwide were utilized to characterize the introduction of the virus in the continental US.

The distribution of these viral genomes and their relation with the recovered from mosquitoes and from other caribbean countries allowed us to infer the more likely scenario of introduction to the US. The genomes generated from the locally acquired cases in Florida form two distinct subclades within this group, which are separated from each other by 18 substitutions. Based on epidemiological data combined with tMRCA estimates, we believe that these results are most consistent with at least two introductions resulting in local transmission in Florida. Under this hypothesis, we estimate that both introductions likely occurred during the first half of 2016 (median estimates during April 2016). The data collected demonstrate the power of "Near Real-Time" genomic sequencing and the potential of these technologies to transform outbreak management.