Genomic epidemiology reveals multiple introductions and sustained transmission of Zika virus in Florida

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Outline

• Power of genomics for outbreak response
• Assembly of the team
• Genomic insights into FL outbreak
Genomic epidemiology

- Mutations provide markers of ancestry
- Viruses = high mutation and replication rates
- Genetic distance correlated with epi distance
- Rate of change provides molecular clock
Western African Ebola outbreak
Western African Ebola outbreak

Origin

• Single spillover from reservoir

• ~December 2013
Western African Ebola outbreak

Spread

Population centers were important hubs

Ladner et al. 2015
Western African Ebola outbreak

Transmission

Persistent Sources
(observed)

Asymptomatic

Re-introduction
(hypothetical)

Flare-up
2015
2014

GIN   LBR   SLE
Western African Ebola outbreak

Transmission

Flare-ups

Persistent Sources (observed)

Asymptomatic

Re-introduction (hypothetical)

Flare-up
2015
2014

Mate et al. 2015
Blackley et al. 2016
Global Zika virus spread

Weaver et al. 2016
Zika virus outbreak in Florida

Grubaugh et al., 2017. Nature
Timeline
July 29, 2016
1st confirmation of local transmission

To Your Health

U.S. confirms Florida Zika cases are first local transmission in any state

By Lena H. Sun and Brady Dennis

The Washington Post
Timeline

July 29, 2016
1st confirmation of local transmission

Aug 19
Contacted BPHL-Miami

To Your Health

Zika virus now actively spreading in Miami Beach, CDC expands travel advisory

The Washington Post

By Brady Dennis  August 19, 2016  Email the author
Timeline

- July 29, 2016
  1st confirmation of local transmission

- Aug 19
  Contacted BPHL-Miami

- Sept 15
  Received samples

- IRB approvals
- Time for sample ID/re-extraction
July 29, 2016
1st confirmation of local transmission

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Received samples

Sept 19
Sent initial report

USAMRIID technicians
Karla Prieto  Danny Reyes  Elyse Nagle
• Open lines of communication are critical for a timely and impactful response

Timeline

- July 29, 2016: 1st confirmation of local transmission
- Aug 19: Contacted BPHL-Miami
- Sept 15: Received samples
- Sept 19: Sent initial report
- Sept 22, 29: Calls with FLDOH

Open lines of communication are critical for a timely and impactful response.
In collaboration with the Florida Department of Health, we (Center for Genome Sciences, USAMRIID) have generated 11 Zika virus (ZIKV) genomes from urine samples collected from patients in Florida with locally acquired ZIKV infections. All genomes were sequenced using Illumina in combination with RNA Access targeted enrichment. Illumina reads were aligned to BelE19015 (KU365778.1 with missing terminal UTR regions filled with sequence from MRR786) and new consensus sequences were generated. A minimum of 3x read depth (in support of the consensus base) was required to make a consensus call. Across the different samples, genome coverage ranged from 57% to 99.6%. All samples were collected from patients in the Miami region during July 28 – August 31, 2016. All of these sequences form a phylogenetic clade together with the 4 Florida-derived genomes generated by
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Oct 2
Virological post

Oct 11
Joined forces
Zika virus transmission began multiple times

Likely ≥40 distinct intros
Sustained transmission of a couple lineages

Exchange between transmission zones

Lineage 1

Lineage 2

Exchange between transmission zones
Transmission 2-3 months before detection

Delayed detection of local transmission

Figure from Worobey, 2017. Nature
Conclusions

• Open science and individual initiative led to the self-assembly of a genomic epidemiology team

• Need to shift from reactive to proactive

• Genomic characterization should become standard part of response