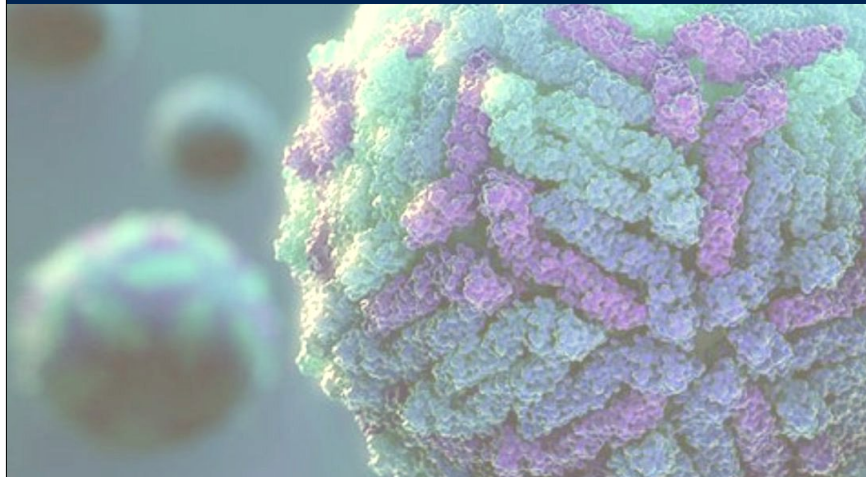




Genomic epidemiology and outbreak mapping of emerging virus infections

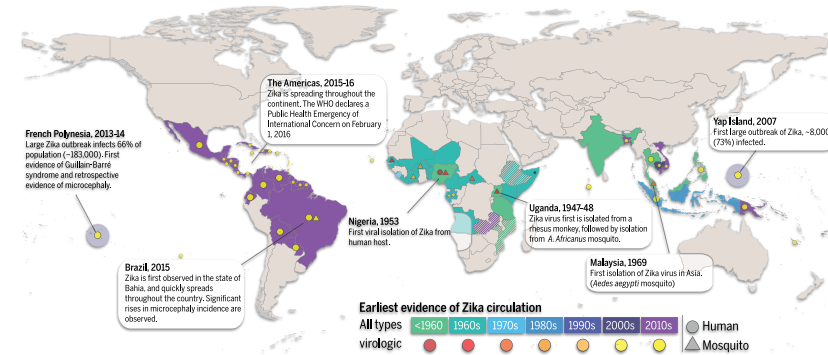


Nuno R. Faria, Ph.D. Sir Henry Dale Fellow nuno.faria@zoo.ox.ac.uk <http://evolve.zoo.ox.ac.uk>

Brief history of the Zika virus epidemic



Historical perspectives are typically obtained through serological studies that do not take into account evolutionary history of the pathogen



Lessler et al. *Science* Aug 2016

Zika virus surveillance

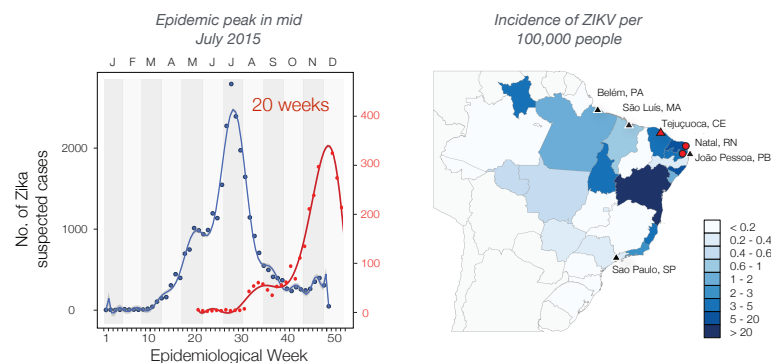
Temporal association between ZIKV notified cases and microcephaly



Local transmission in Brazil: 07 May 2015

WHO Public Health Emergency of International Concern: 01 Feb 2016

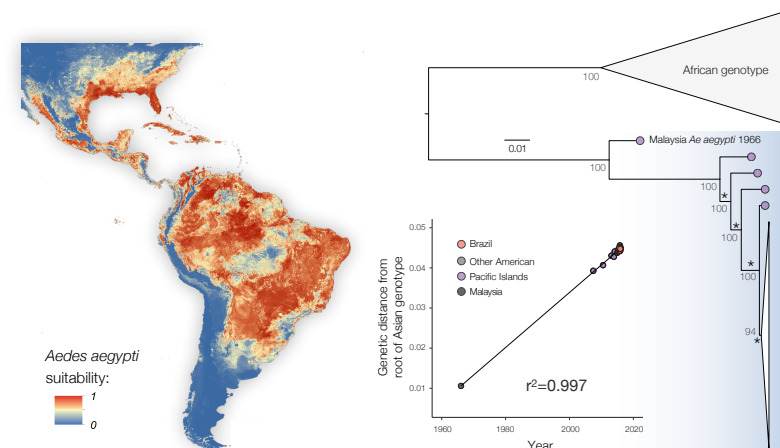
WHO/CDC confirm association between ZIKV infection and microcephaly: 13 Apr 2016



Faria et al. *Science* March 2016

Zika virus surveillance

Emergence of ZIKV as a function of local transmission regime, genotype



Kraemer et al. *eLife* 2014

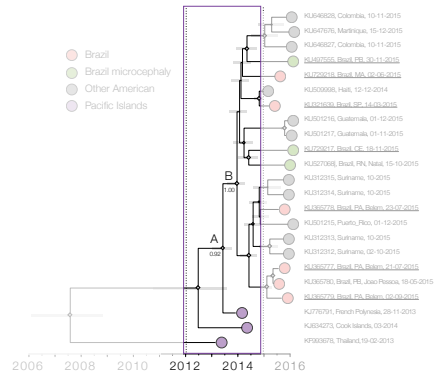
Faria et al. *Science* March 2016

Zika virus surveillance

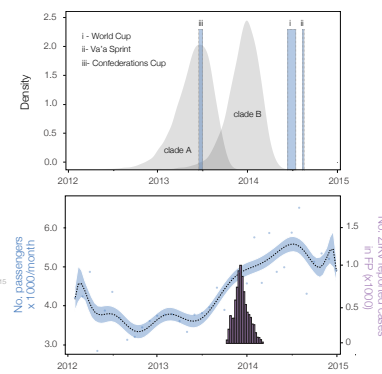
Emergence of ZIKV as a function of local transmission regime, genotype and global mobility



ZIKV Asian genotype molecular clock phylogeny



Combination of genetic and flight data



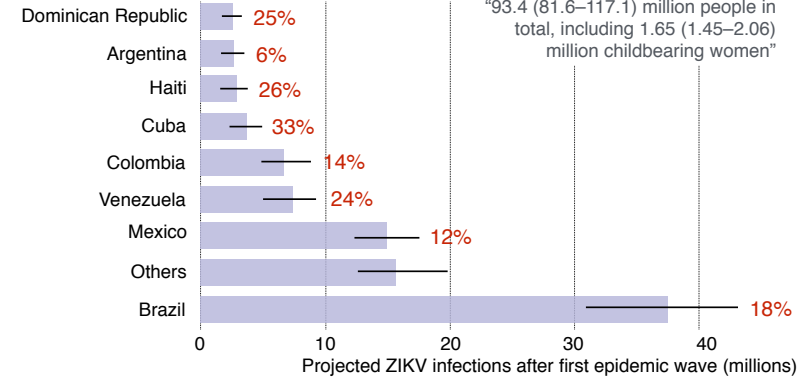
Faria et al. *Science* March 2016

Zika virus surveillance

37 million ZIKV infections in Brazil during the first epidemic wave



Estimated % population infected with ZIKV



Perkins et al. *Nature Microb* Jul 2016

Zika epidemiology and evolution

Real-time genomic surveillance during the Ebola and Zika epidemics



Ian Goodfellow in Sierra Leone 2015



Josh Quick in Guinea 2015

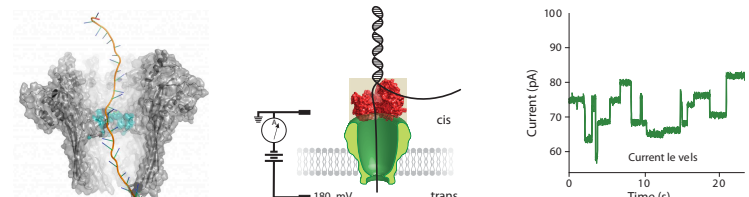


ZiBRA project in Brazil 2016



Zika virus surveillance

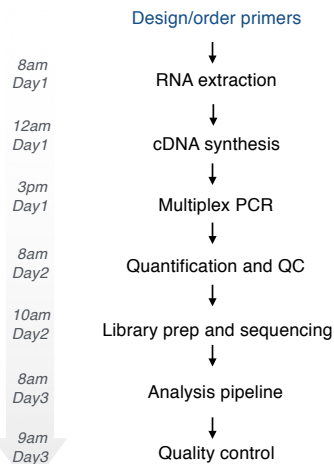
Previous MinION work on Ebola virus: Quick J, Loman N, et al. *Nature* 2016
Current MinION ZiBRA protocol: Quick J et al. *Nature Protocols* 2017



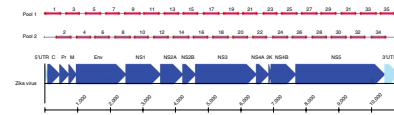
Portable sequencing

MinION portable genome sequencing in an outbreak context

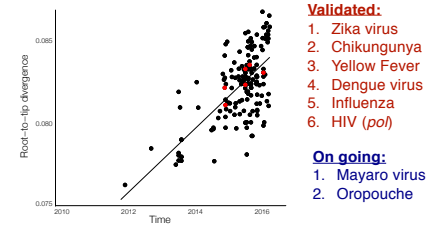
@ <http://zibraproject.github.io/>



Web-based primer design tool:



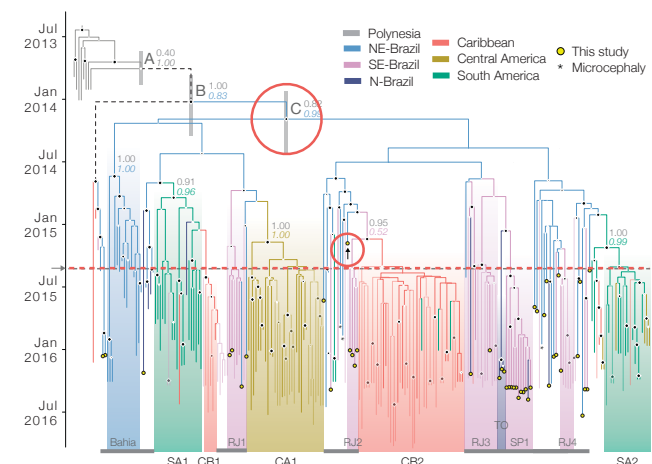
Consensus sequence quality control:



Quick et al. Nature Protocols, 2017

Portable sequencing

Origins of ZIKV-Am in NE Brazil, from where it spread to southeast Brazil and beyond



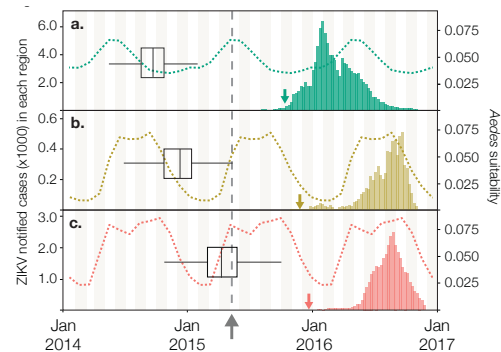
Faria et al, Nature, May 2017

ZIKV genome epidemiology

Cryptic circulation in several American regions for a near-complete season of transmission



Syndromic surveillance is often biased.
e.g. FSA (Bahia): 1 notified ZIKV case per 270 infections*



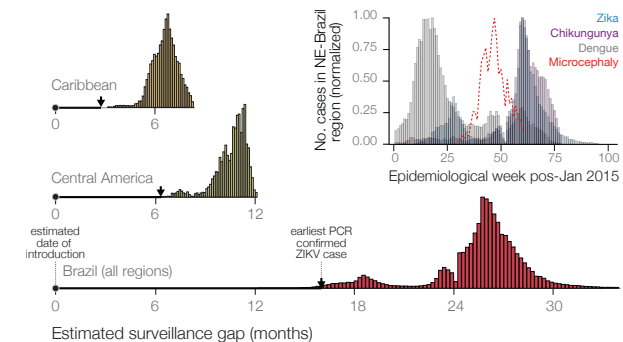
Faria et al, Nature, May 2017
*Lourenço et al, eLife, Sep 2017

ZIKV genome epidemiology

Genomic surveillance reveals vulnerability in current disease surveillance systems



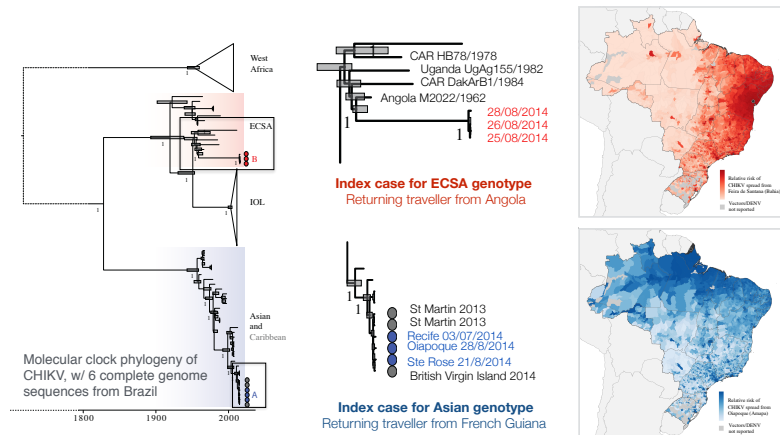
Co-circulation of arthropod-borne viruses makes epidemiological reconstructions from case reports alone challenging



Grubaugh, Faria et al, Cell, Mar 2018

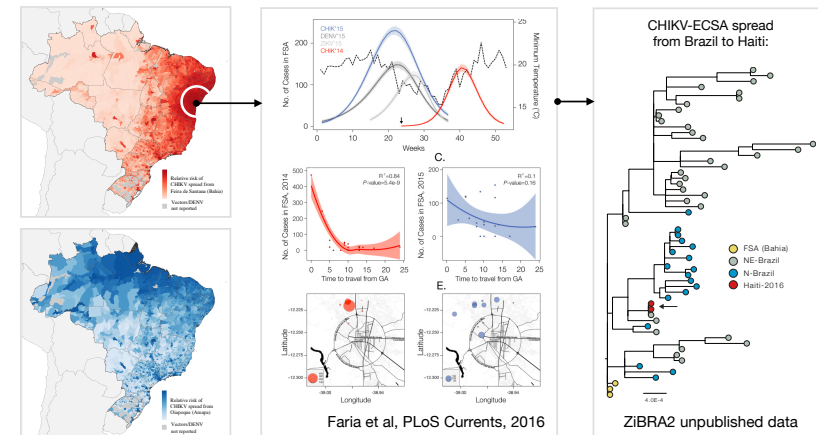
ZIKV genome epidemiology

Two chikungunya virus genotypes circulating in Brazil



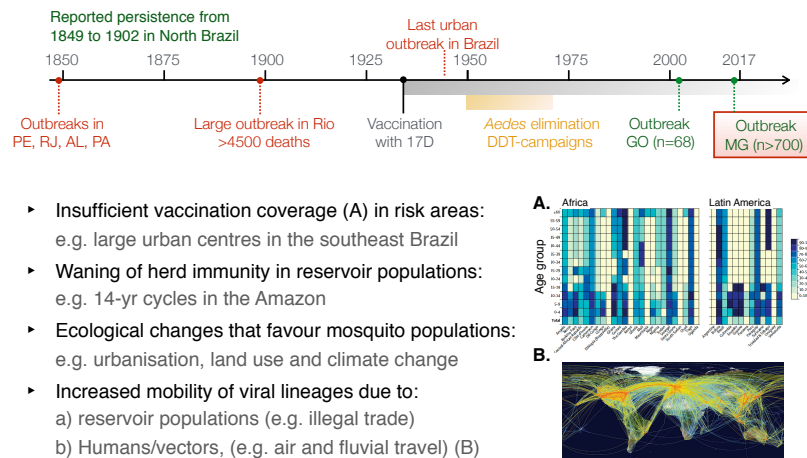
Spread of Chikungunya virus

Chikungunya ECSA virus genotype circulating in Brazil and Haiti



Spread of Chikungunya virus

Natural history and the (re)-emergence of yellow fever virus in Brazil

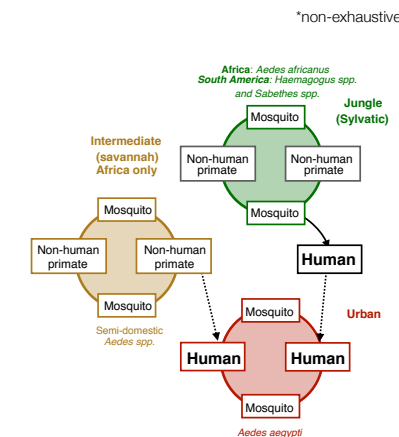


Real-time surveillance of YFV

Applied phylodynamic questions that can be addressed with genomic surveillance*



1. Are strains associated with particular transmission routes?
2. How fast is it transmitting and in what direction is it spreading?
3. When did an epidemic start and where did it come from?
4. Are hosts A, B and C epidemiologically linked?
5. Can we predict future virus transmission?



<https://www.cdc.gov/yellowfever/transmission>

Real-time surveillance of YFV

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Medawar
pathogenesis research

- A. Idealised YF sylvatic phylogenetic tree**
-
- Genome from human
● Genome from monkey
- B. Idealised YF urban phylogenetic tree**
-
- Genome from human
● Genome from monkey
- Africa:** *Aedes africanus*
South America: *Haemagogus* spp. and *Sabethes* spp.
- Jungle (Sylvatic)**
- Mosquito
- Non-human primate
- Non-human primate
- Mosquito
- Human
- Urban
- Human
- Mosquito
- Mosquito
- Aedes aegypti*

Real-time surveillance of YFV

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publichealthresearch

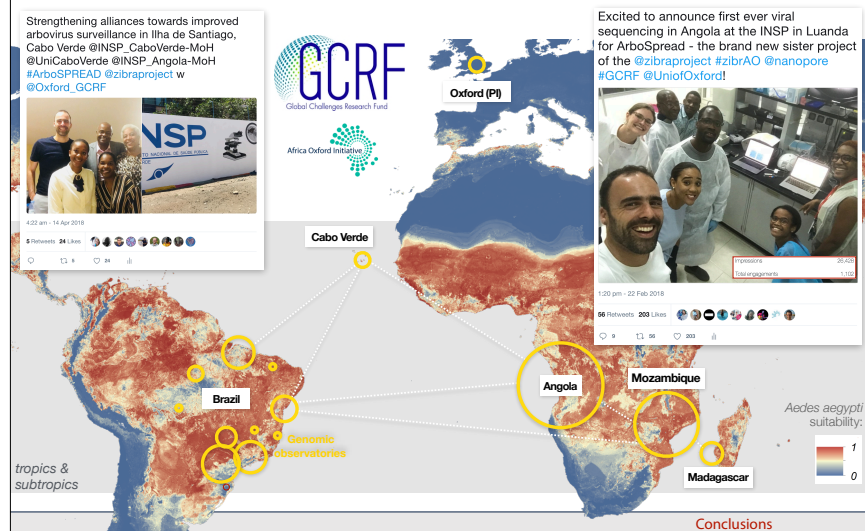


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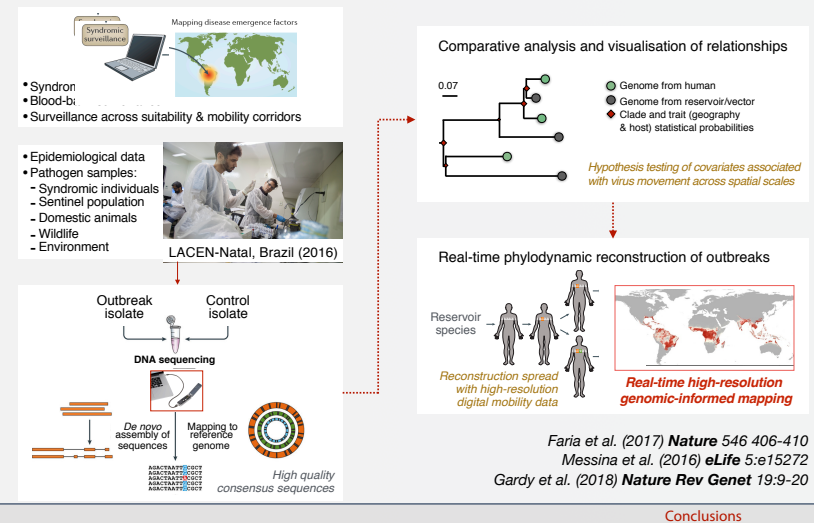
Medawar
Institute for Health Research



ArboSPREAD, a network for real-time genomic surveillance of arboviruses



Towards a real-time genomic-informed surveillance of arthropod-borne viruses across suitable corridors



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Thank you!