

# GLOBAL HEALTH AND TROPICAL MEDICINE

## GHTM



### **Viral genomic surveillance: phylodynamic analysis of Zika virus and proposal of a nomenclature system**



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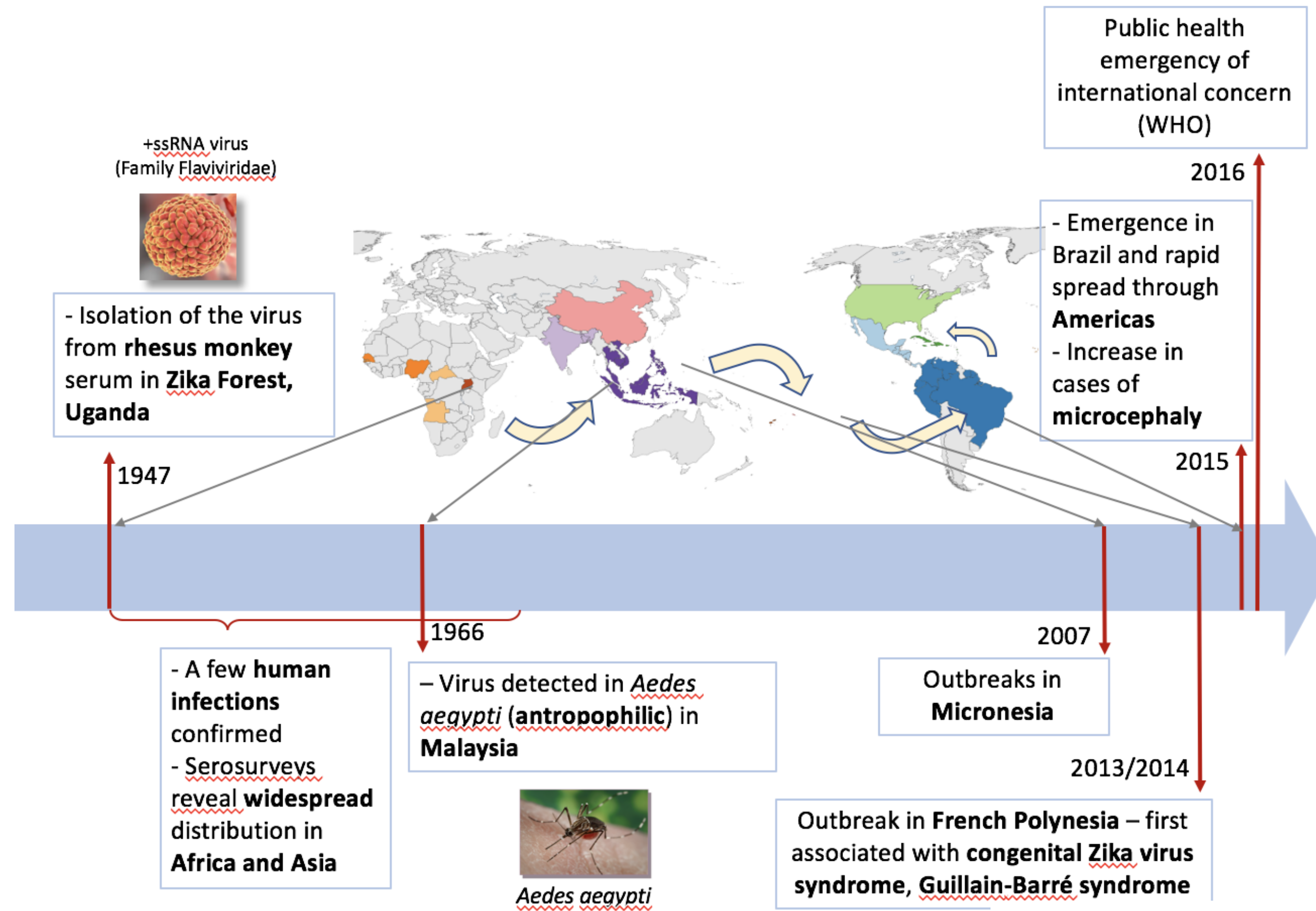


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# History of Zika virus

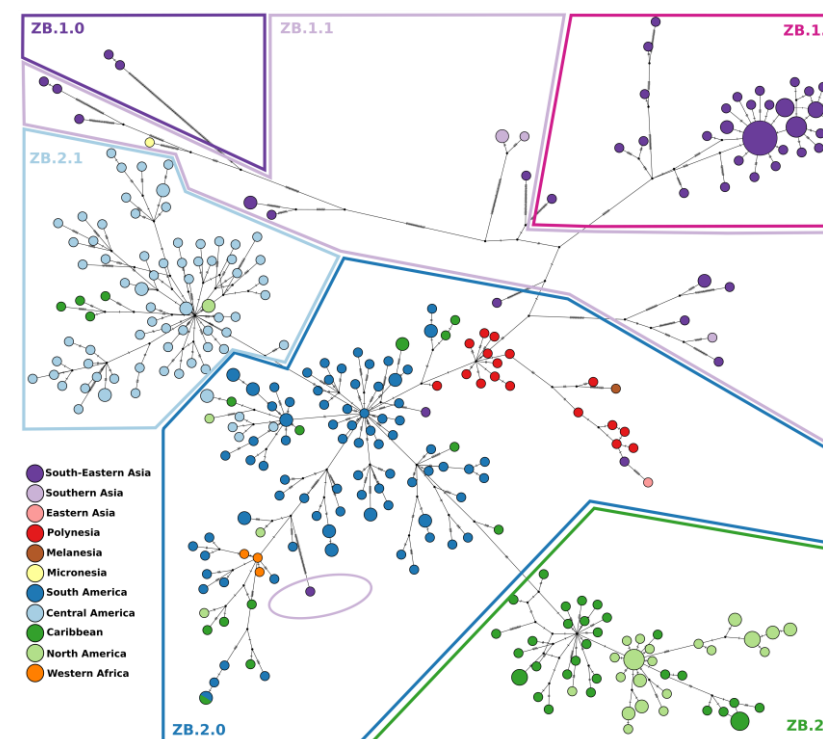




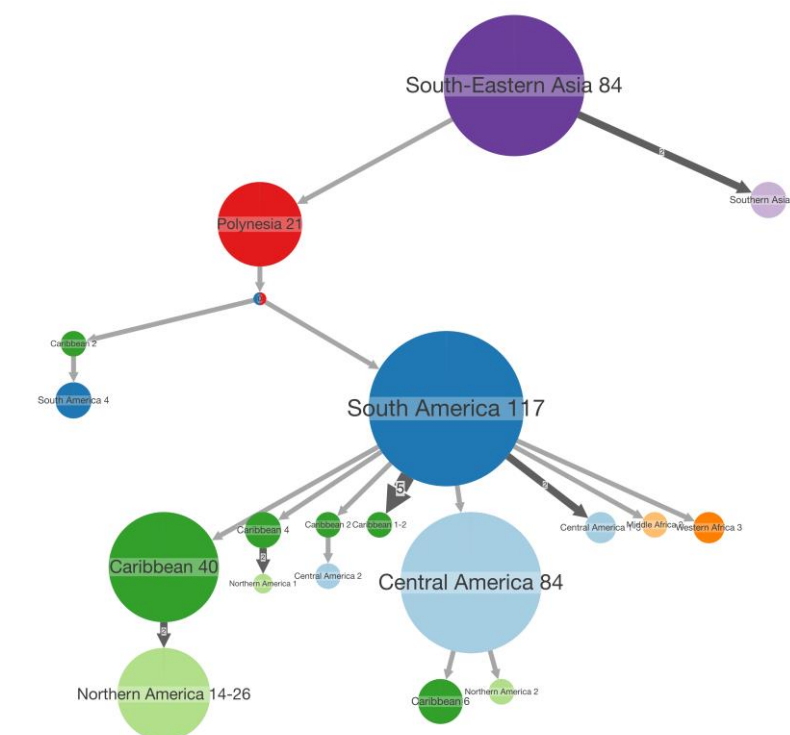
# Evolution and spread of Zika virus

## Steps for definition of genetic subgroups:

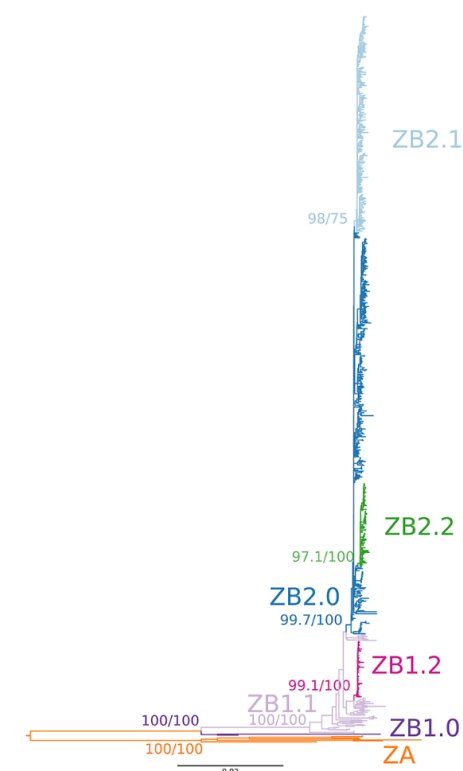
### 1. Identification of genetic clusters



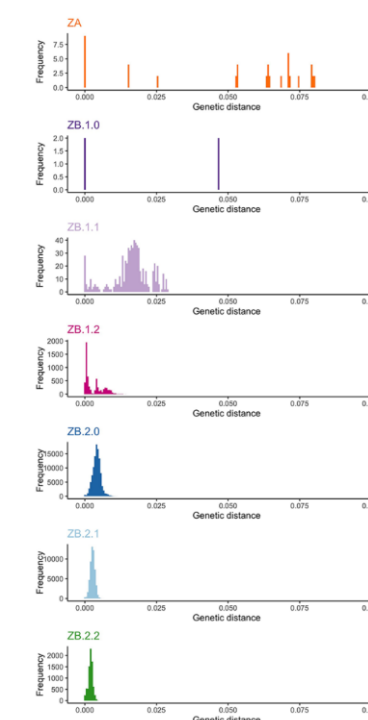
### 2 – Identification of transmission routes



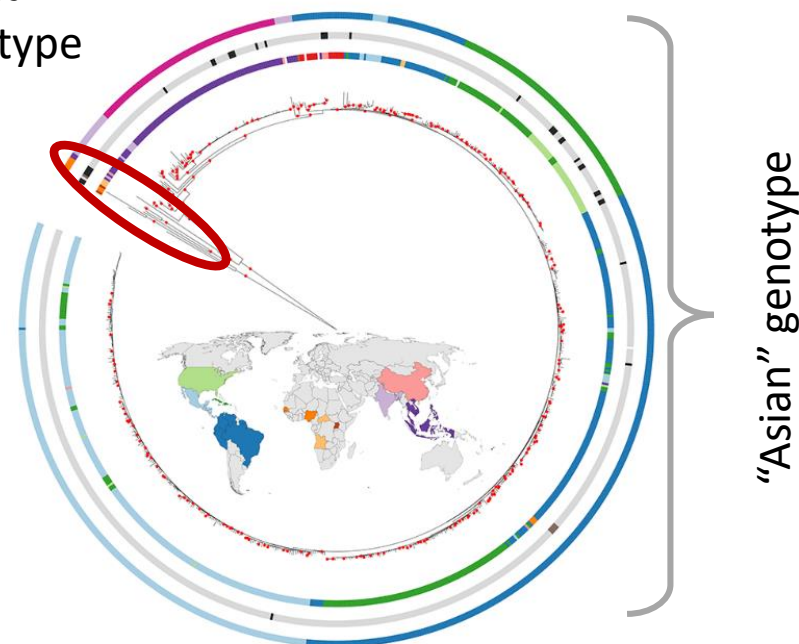
### 3 - Phylogenetic support



### 4 - Between and within-group genetic distances



“African”  
genotype



759 publicly available sequences  
(full-length coding region of 10,269  
nucleotides)





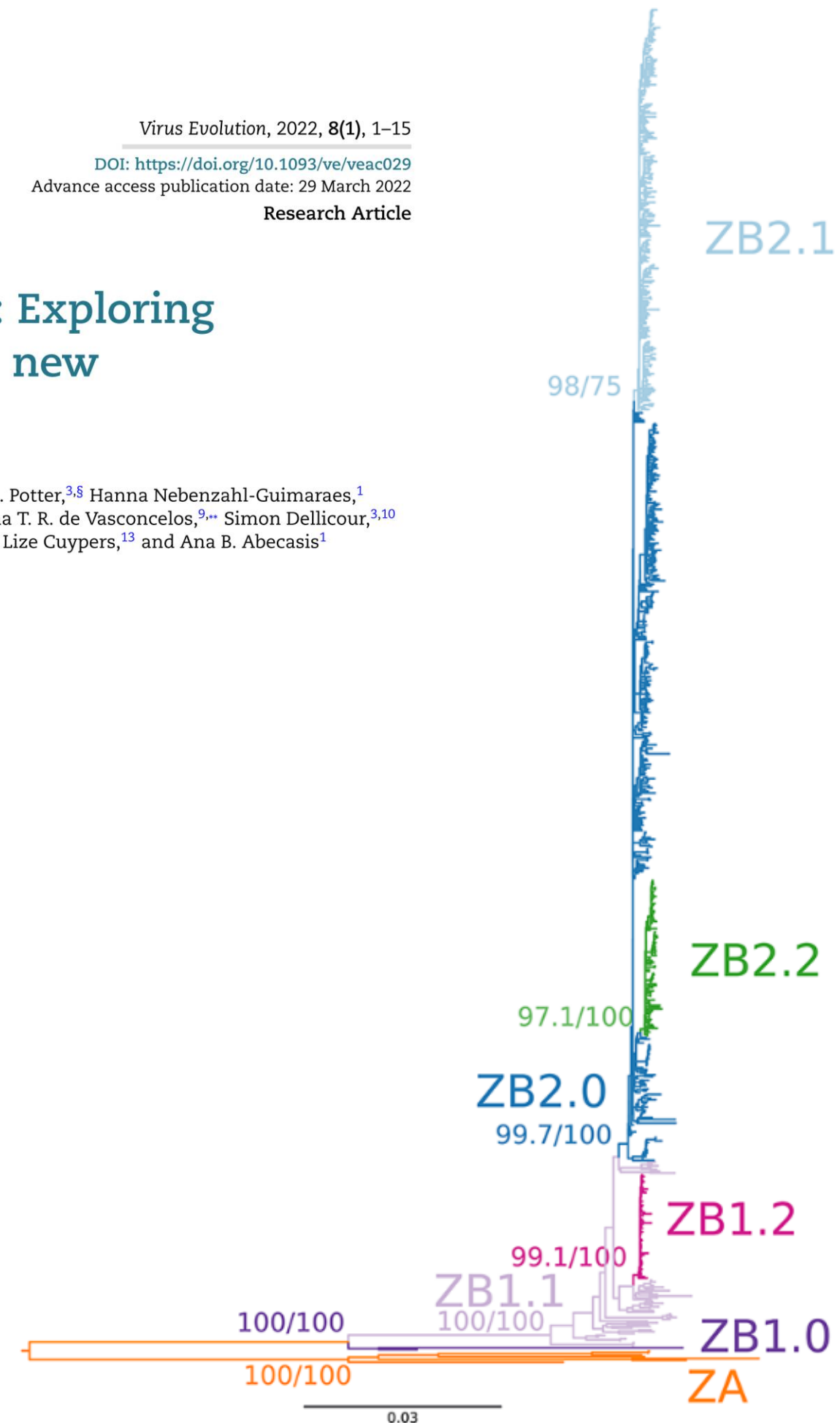
# Zika virus nomenclature proposal



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Research Article

## Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal

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- Reflects divergence levels
- Avoids geographical references
- Flexible to be updated with future lineages



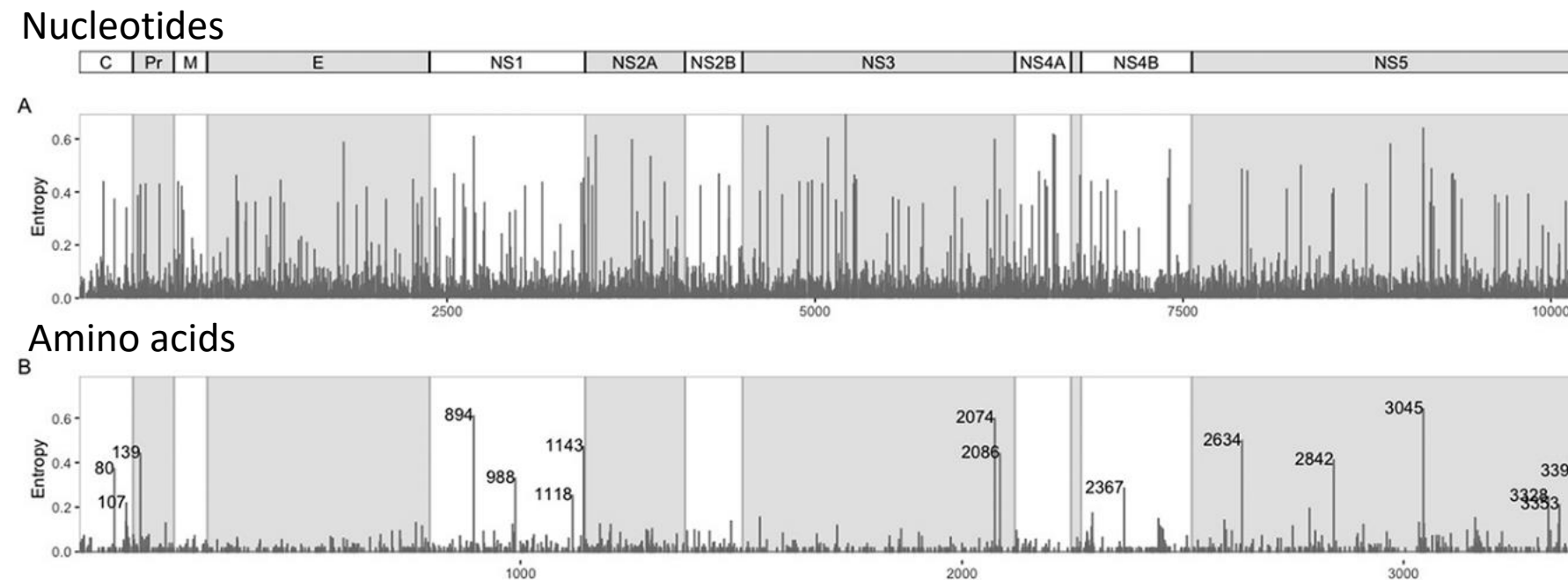
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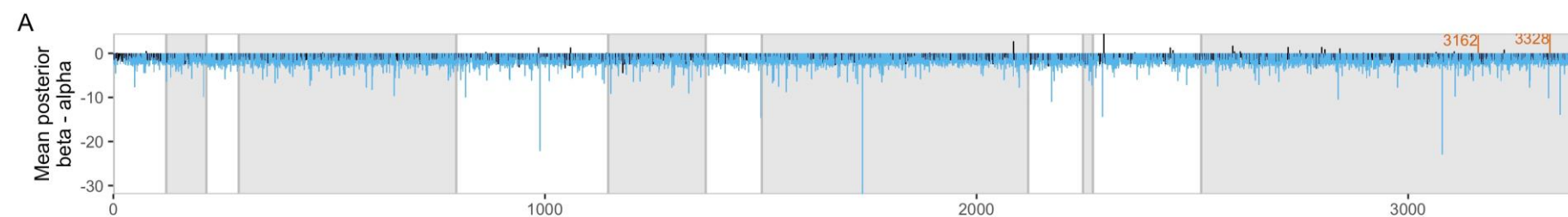
# Mutations of interest

Genetic diversity



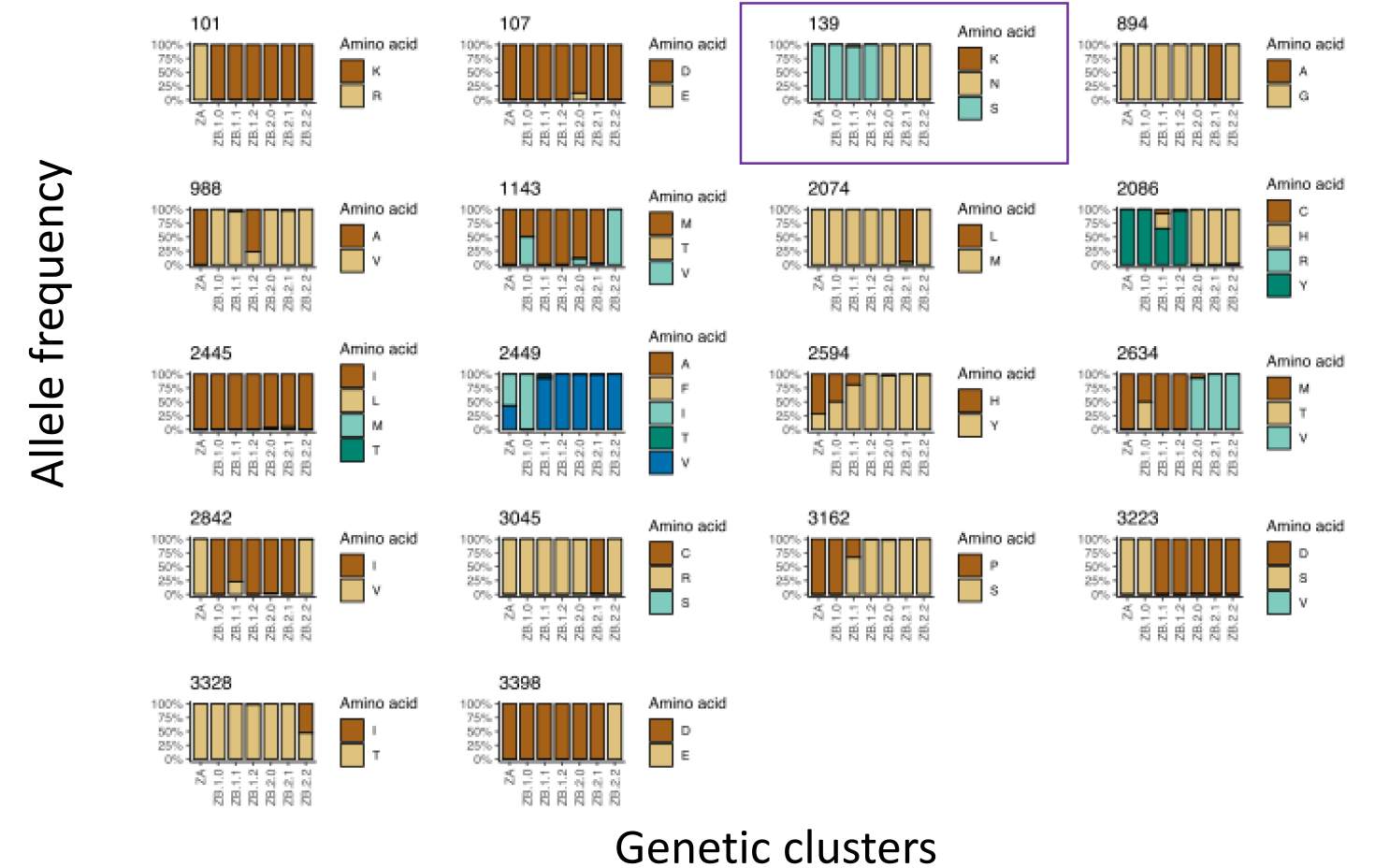
Protein **E** and **prM** - targets of vaccine development (Heinz and Stiasny 2017; Nambala and Su 2018)

## Detection of selective pressure



Mutation **S139N** - increases neurovirulence in neonatal mouse models (Yuan et al., 2017)

## Amino acid frequency in each genetic cluster





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