

# Molecular epidemiology of Chikungunya virus in its endemic regions

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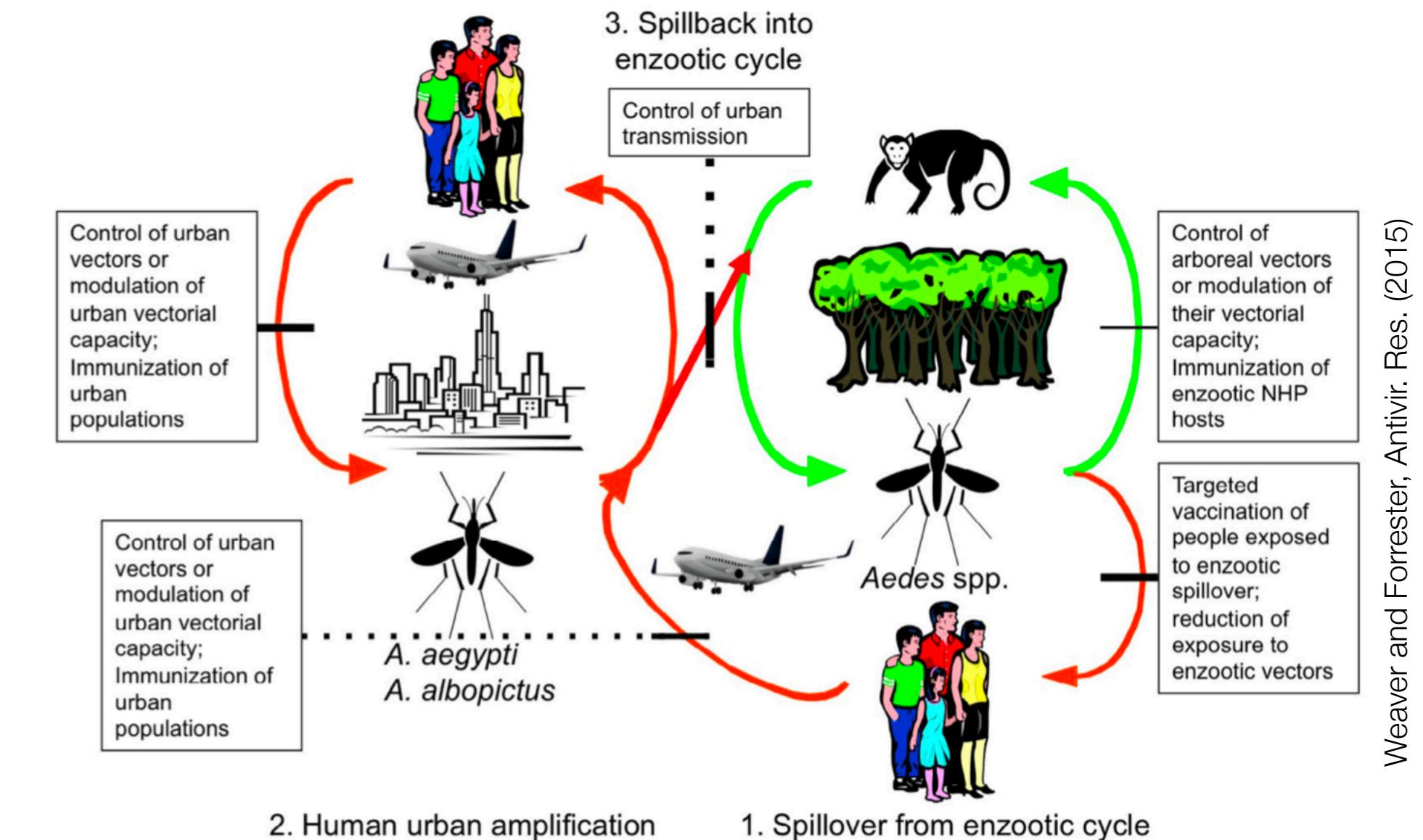
joint work with

Thomas Spicher, Markus Delitz and Andriano de Bernardi Schneider

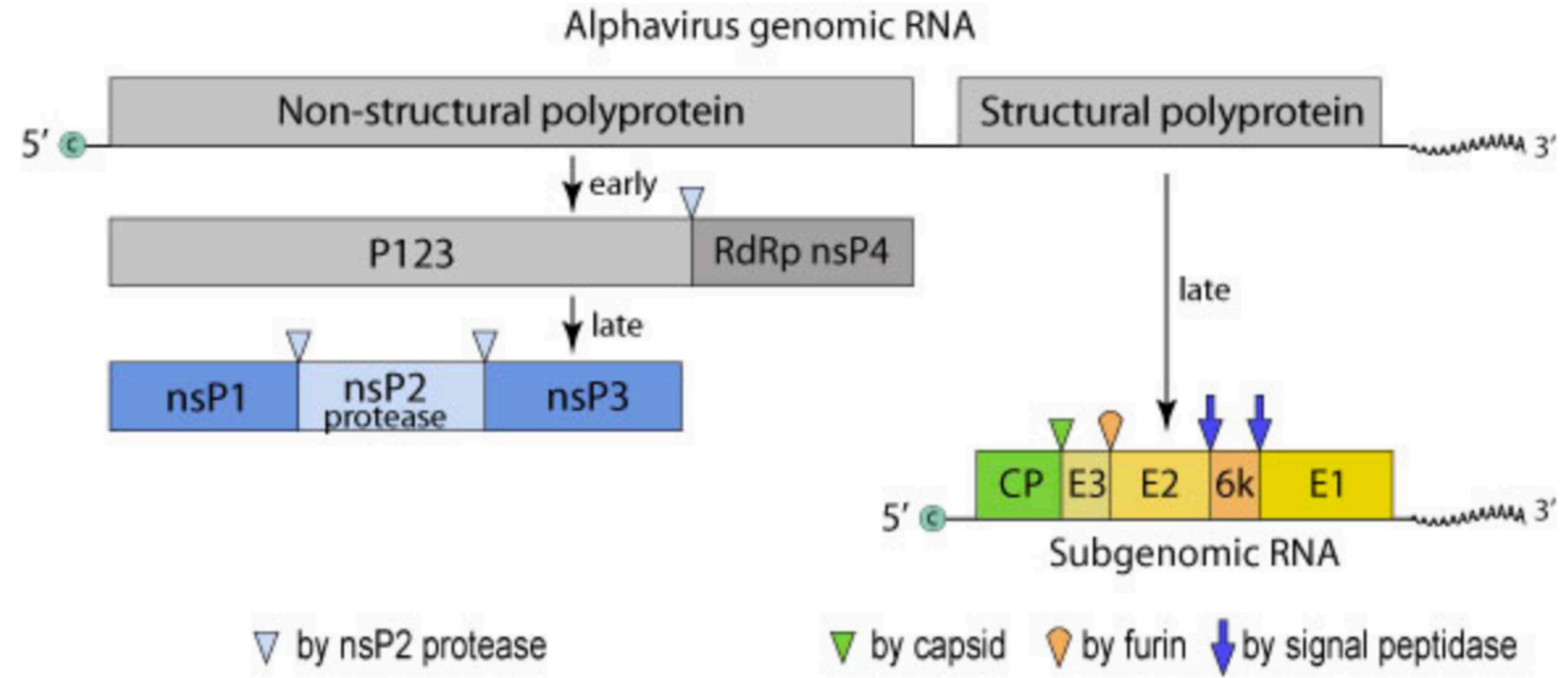
GCB 2020  
15 September 2020

# Chikungunya Virus (CHIKV)

- Family *Togaviridae* / genus *Alphavirus*; mosquito-borne (*Aedes* spp.)
- Single-stranded (+) sense RNA virus
- “Chikungunya” (Makonde language): “Disease that bend up the joints”
- Chikungunya fever: febrile illness, arthralgia, rash, rarely causes hemorrhagic complications
- Enzootic in tropical and subtropical regions of Africa
- First outbreak described 1952 in Tanzania
- No vaccine available

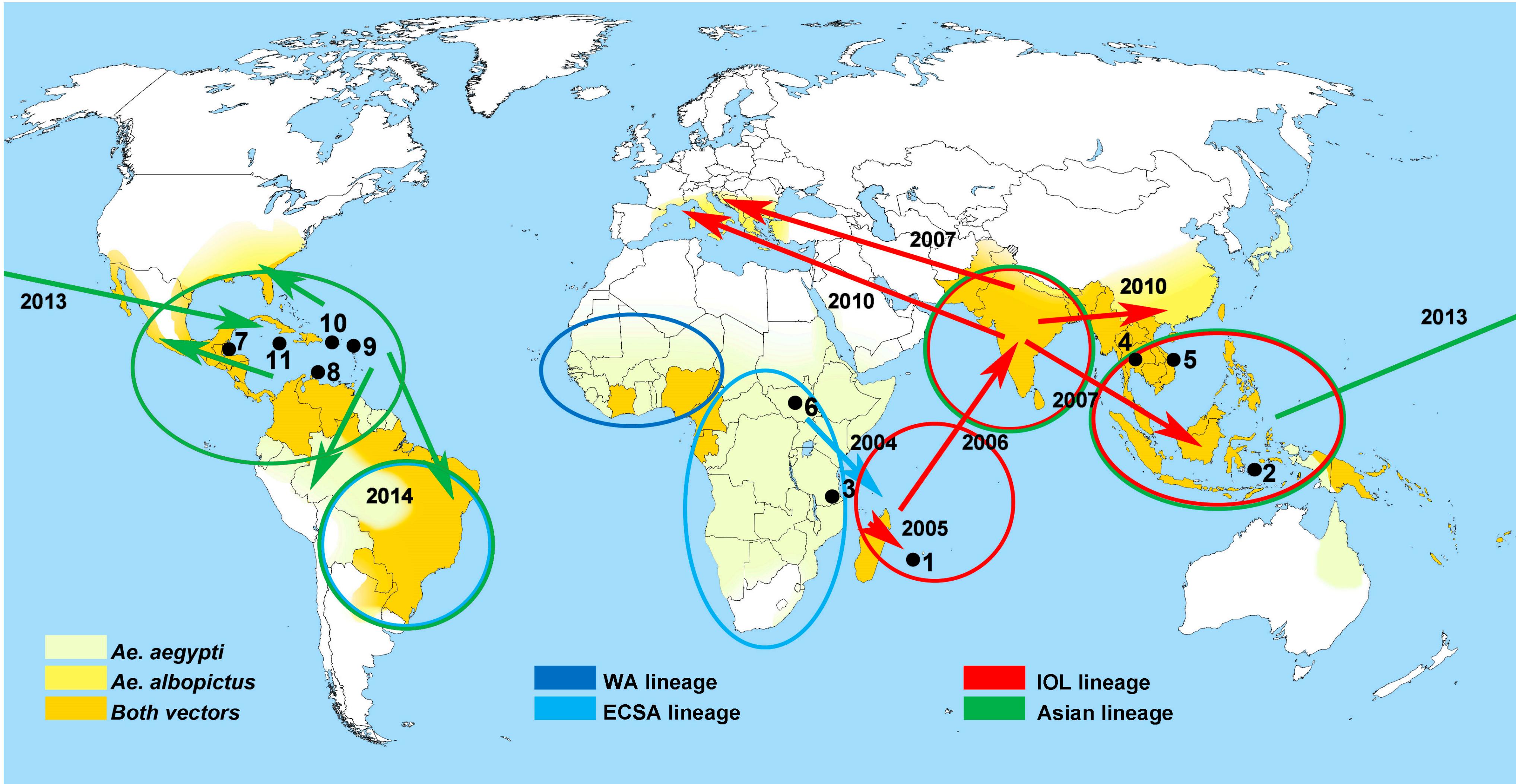


# Alphavirus Genome Organization

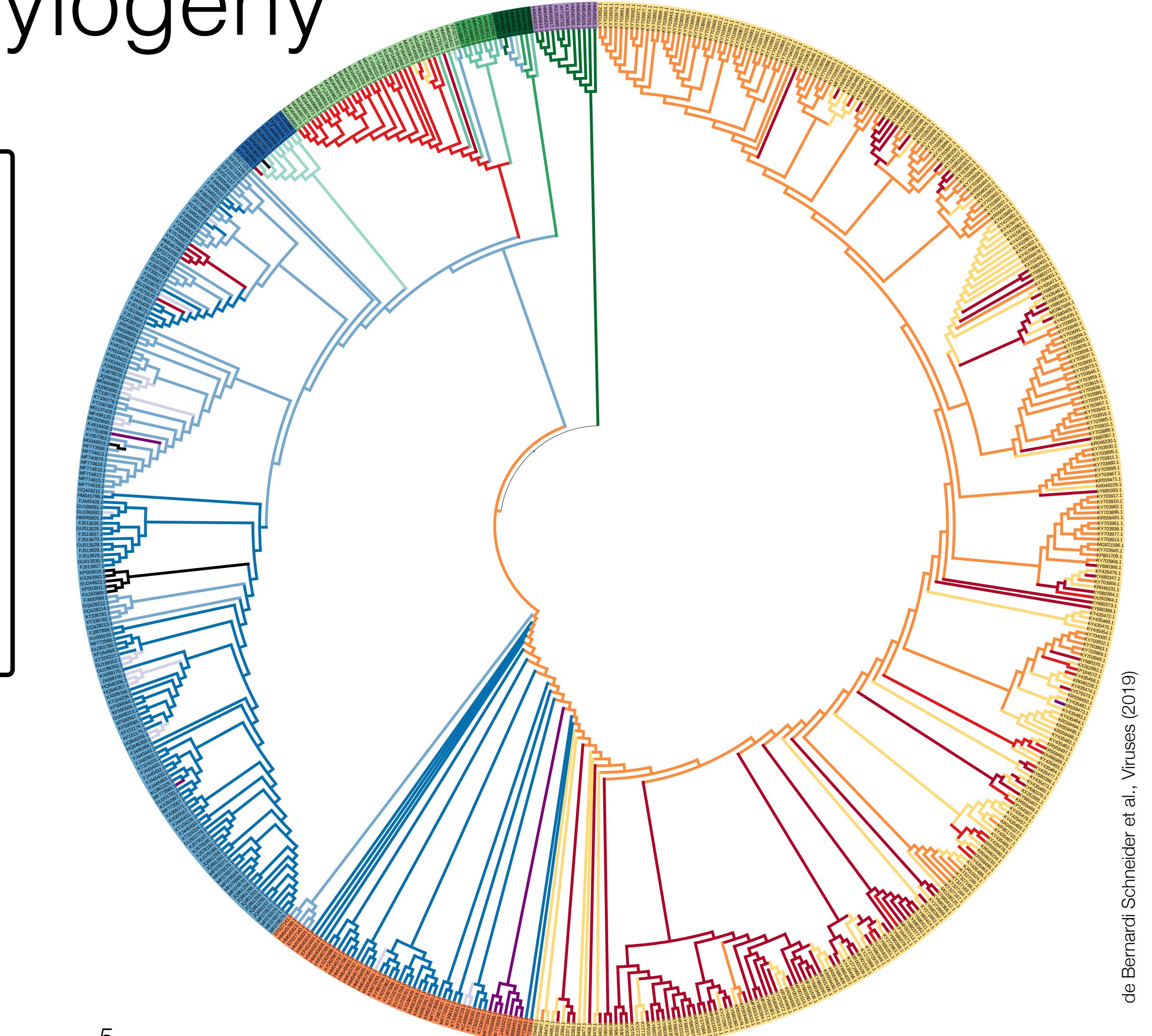
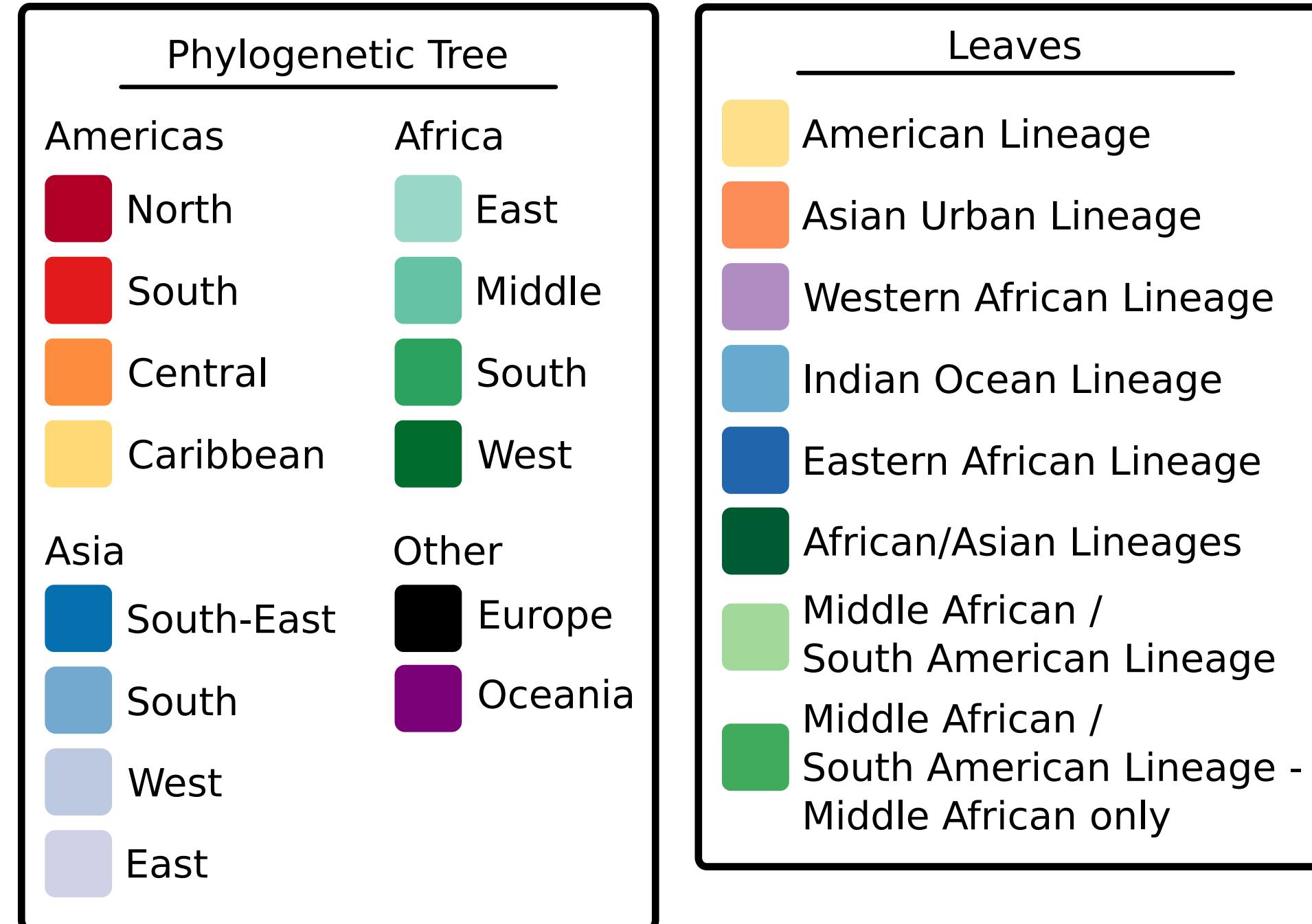


- Non-segmented, single-stranded, (+)-sense RNA genomes of 11-12kB length
- Capped and polyadenylated
- Structured untranslated regions (UTRs)
- AV genomes appear to host cells as mRNA for immediate translation upon entry into the cytoplasm

# CHIKV Epidemic Spread

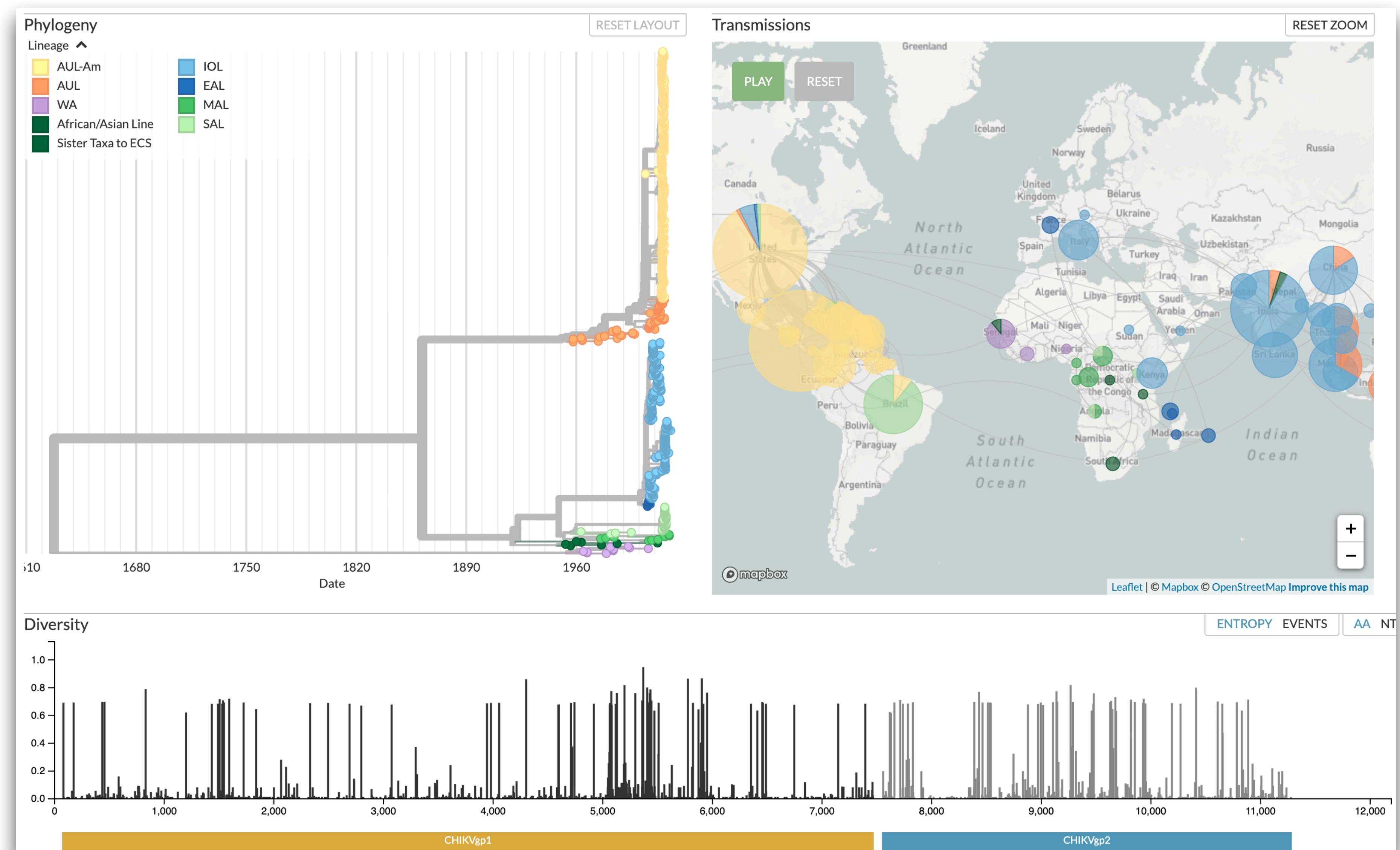


# Updated CHIKV Phylogeny



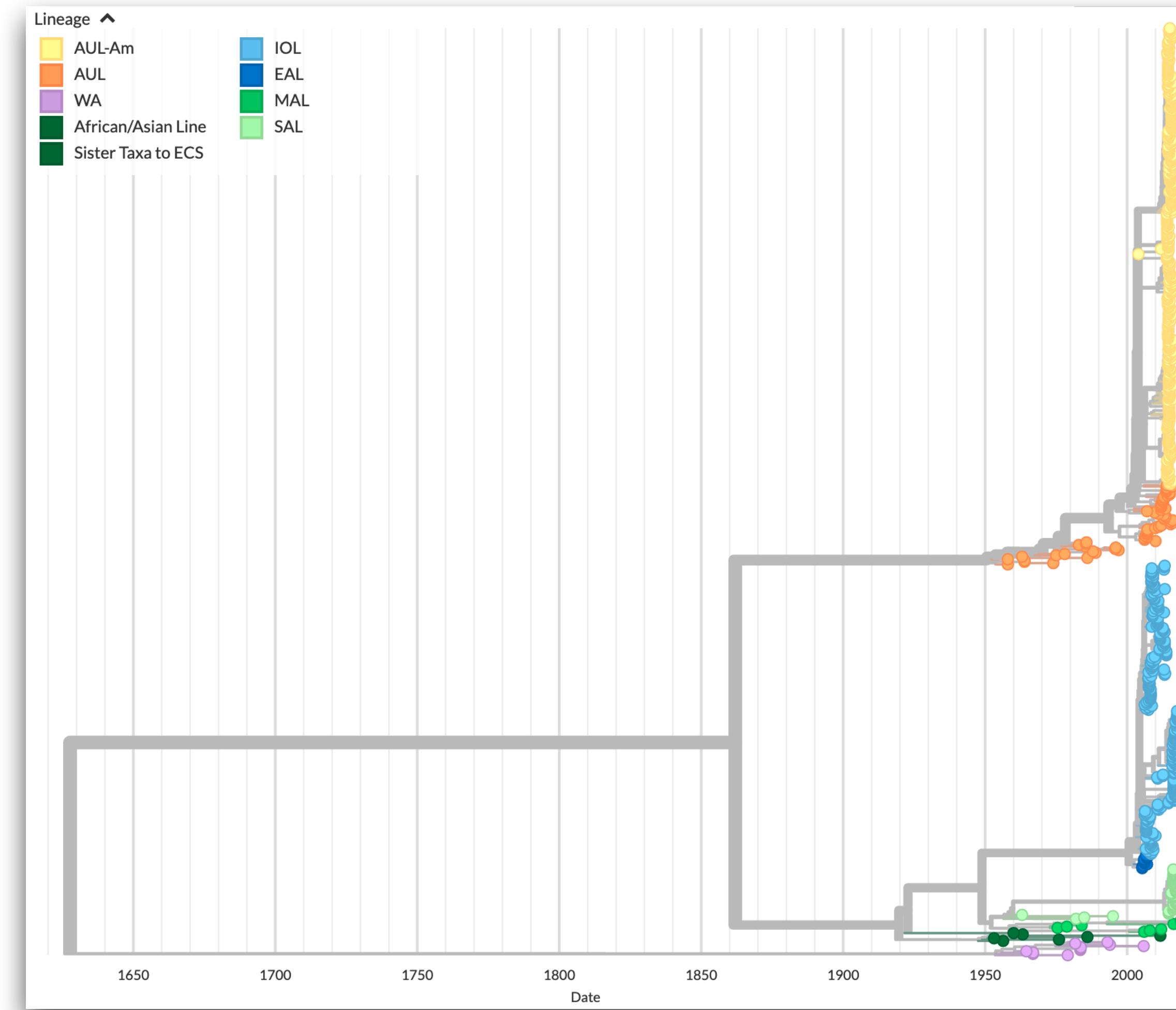
- 590 CHIKV genomes
- iq-tree / SH-aLRT

# CHIKV Molecular Epidemiology



# CHIKV Molecular Epidemiology

<https://nextstrain.org/community/ViennaRNA/CHIKV>

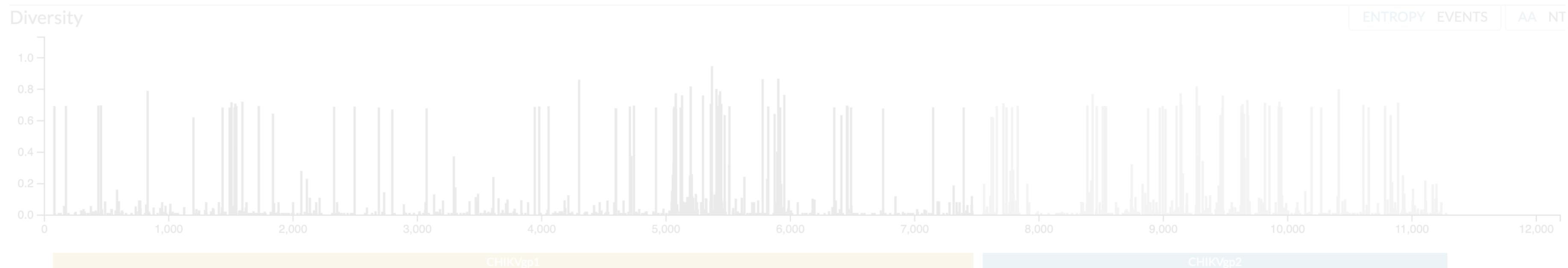


- 715 full CHIKV genomes
- nextstrain / time tree

# CHIKV Molecular Epidemiology



**Can we infer lineage-specific RNA structures?**

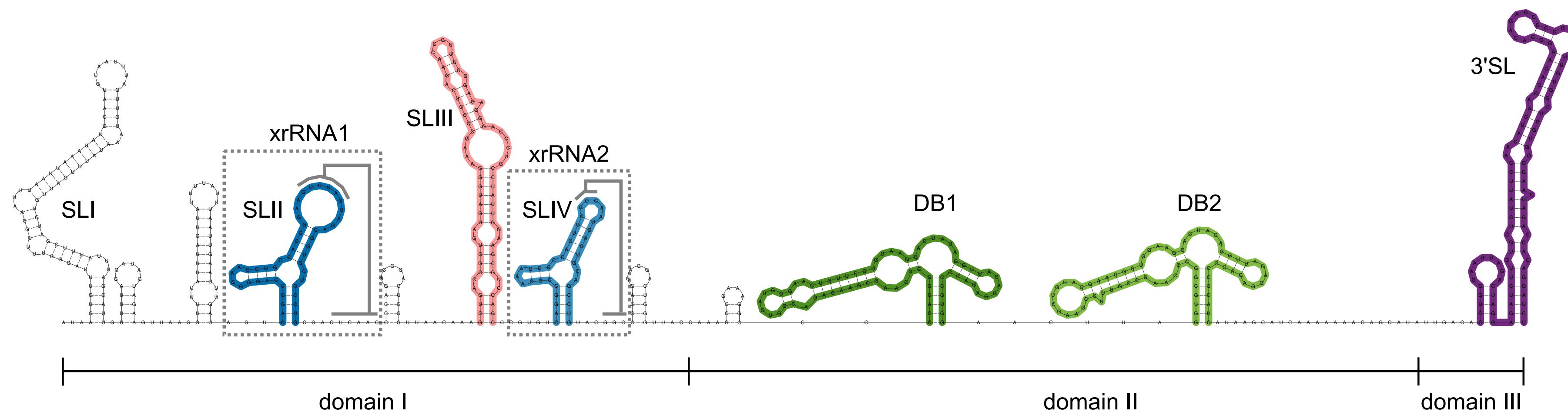


# Functional RNAs in Viruses

Functional RNAs are often evolutionarily conserved, typically at the secondary structure level

Examples:

- Exoribonuclease-resistant RNAs in Flaviviruses

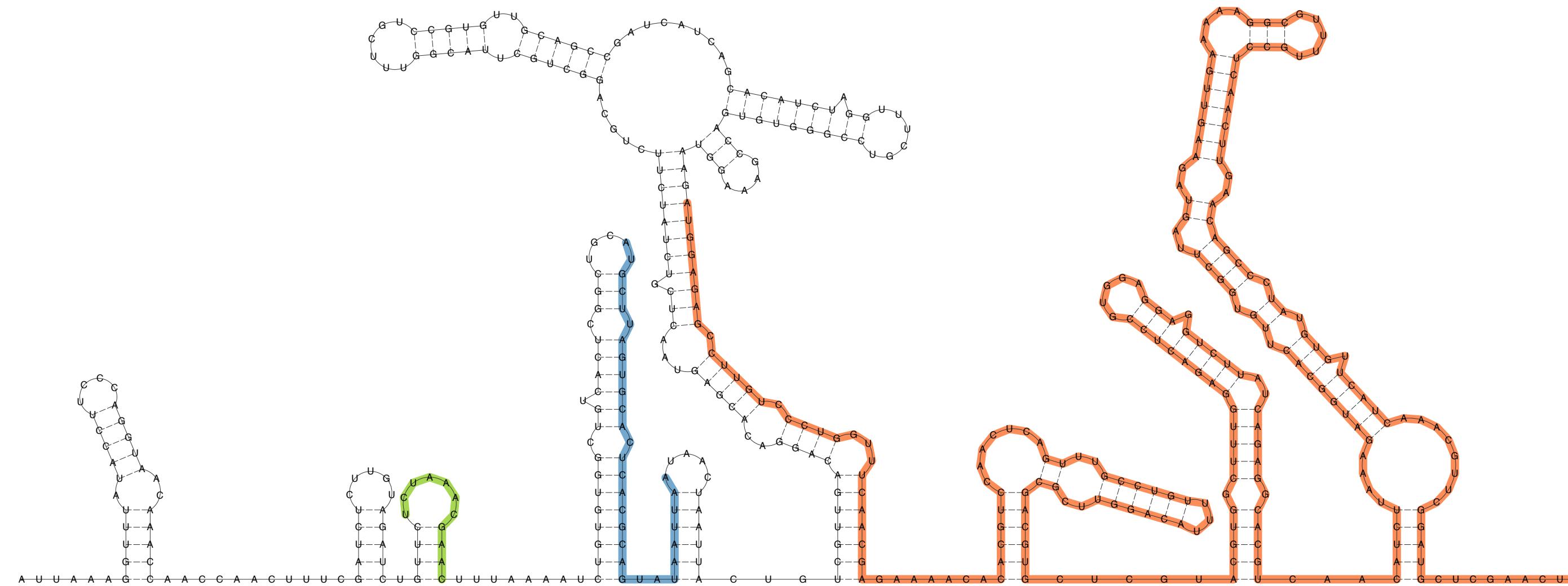


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## Examples:

- Exoribonuclease-resistant RNAs in flaviviruses
  - Cis-acting RNAs in SARS-CoV-2 (and other betacoronaviruses)

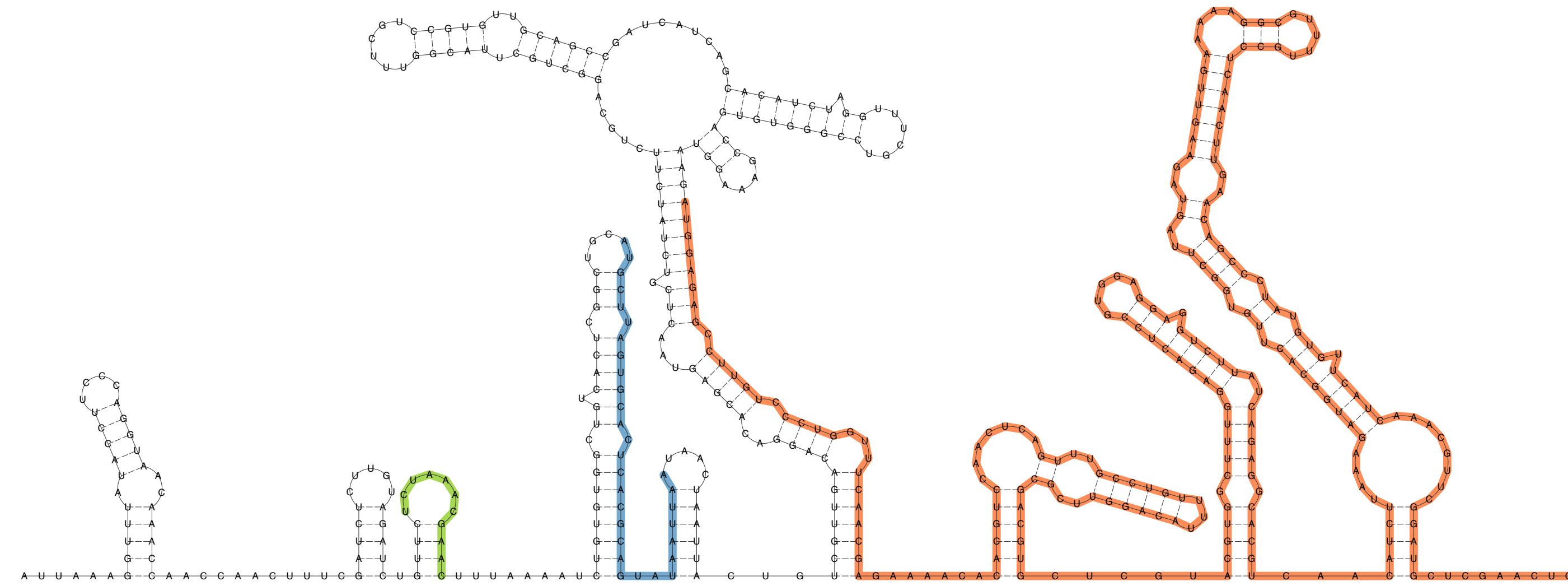


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We can find them by thermodynamic modelling and consensus structure prediction

# CHIKV 3'UTR

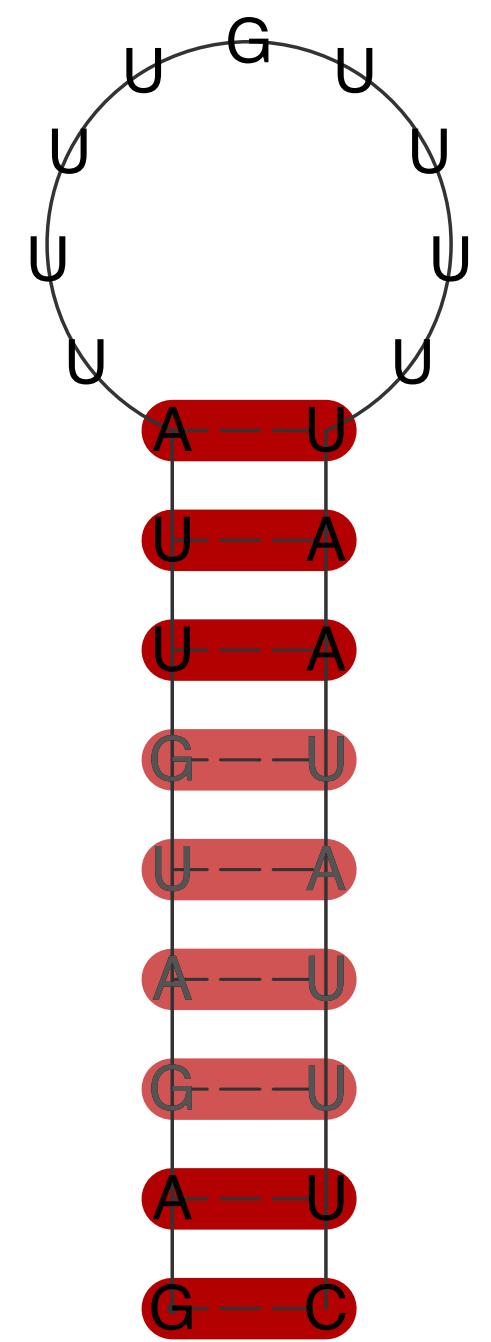


- 110 full length CHIKV 3'UTRs
- Variable length (510nt – 930nt)
- Structural RNA alignments + Covariance models
- Thermodynamic modelling based on ViennaRNA Package

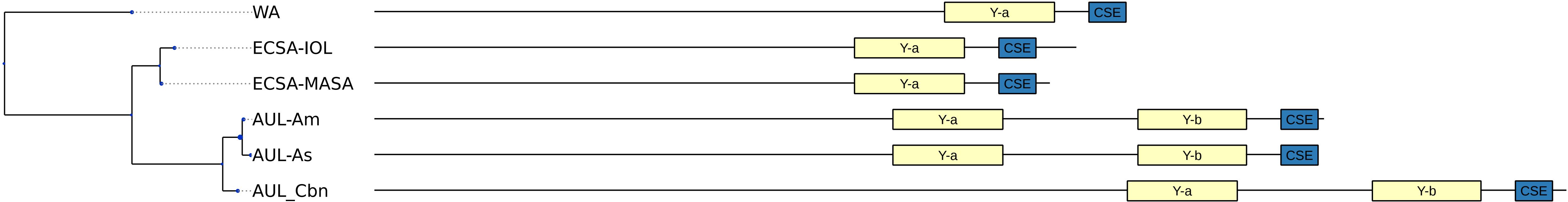
# CHIKV 3'UTR: Conserved RNA Structures



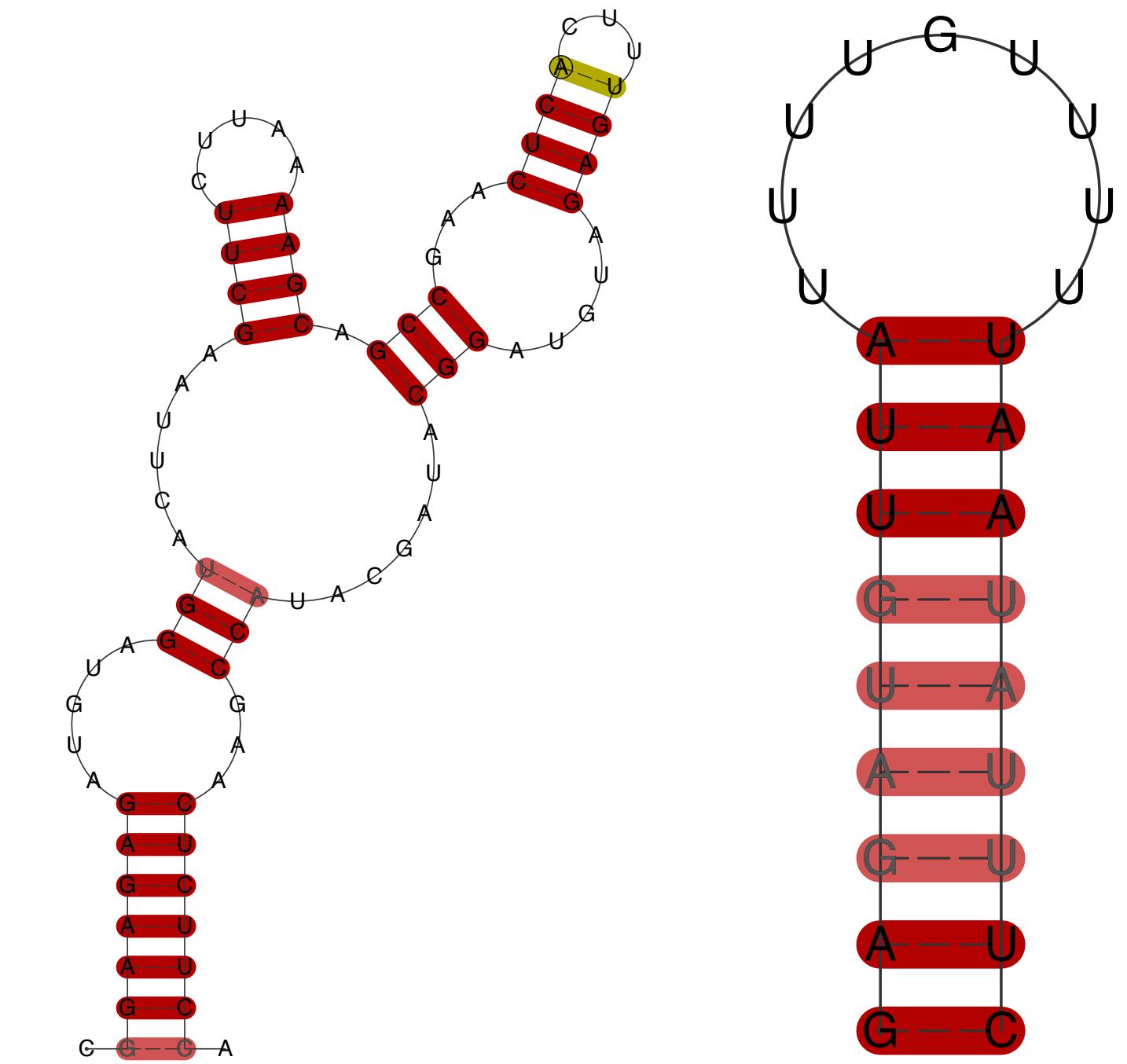
Conserved Sequence Element (CSE)



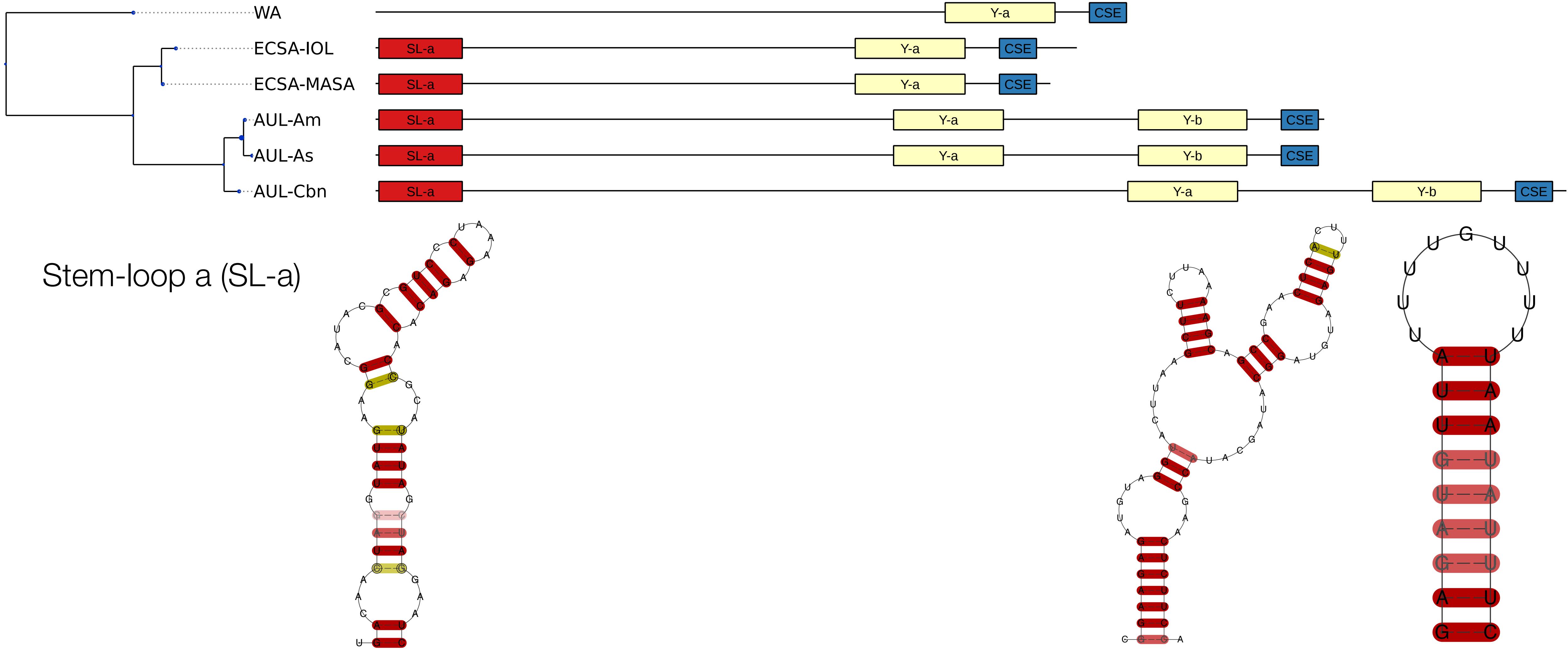
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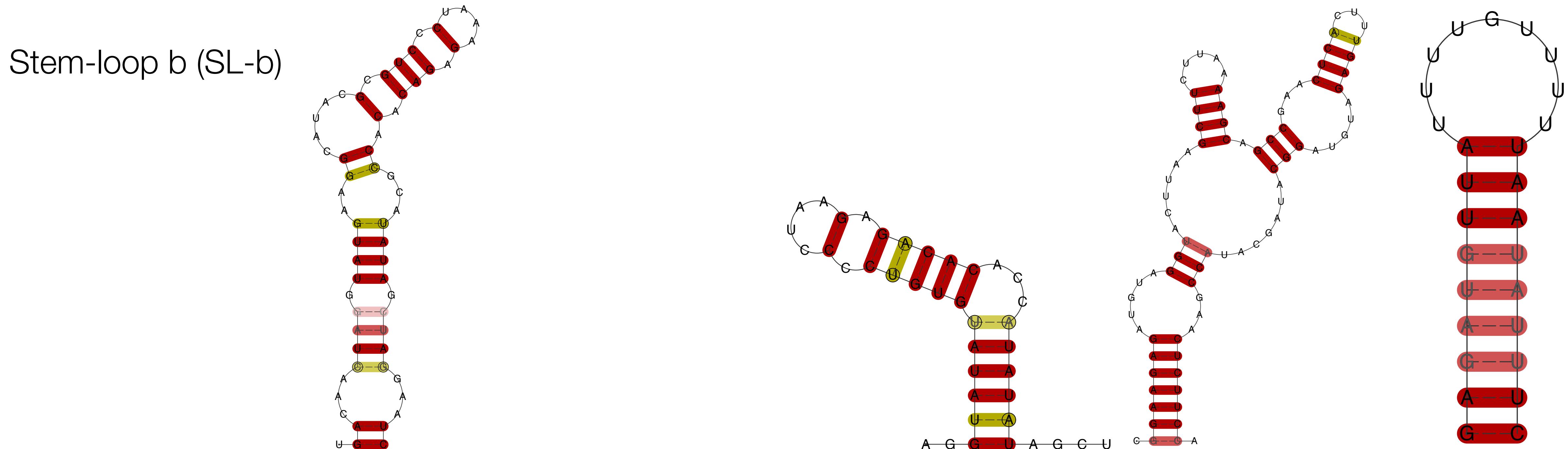
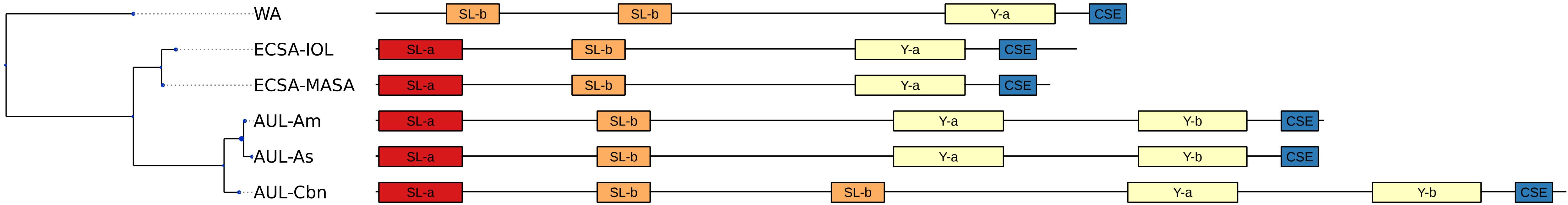
Y-shaped Element (SL-Y)



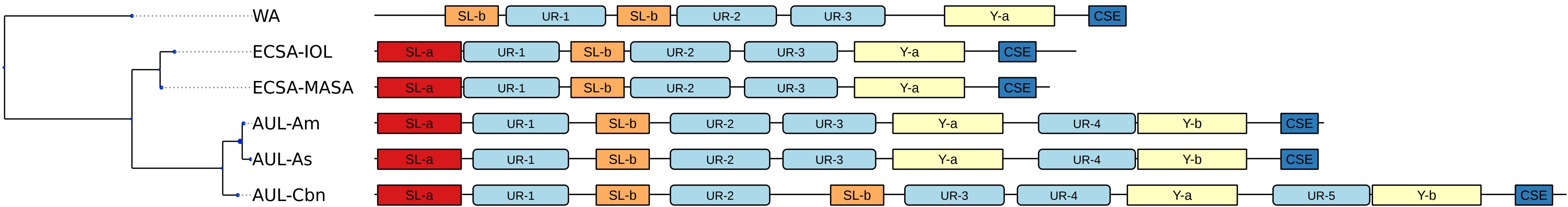
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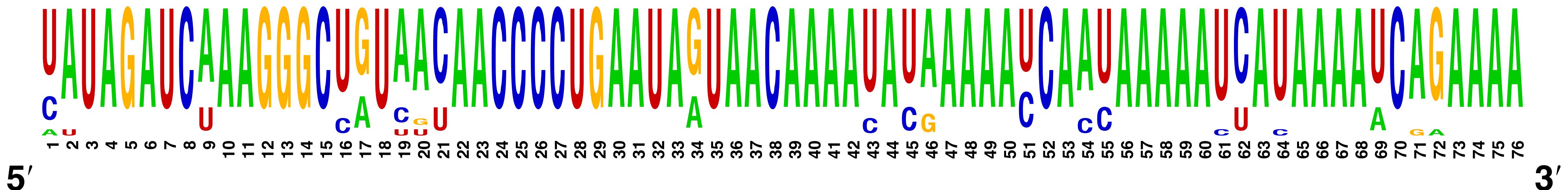
# CHIKV 3'UTR: Conserved RNA Structures



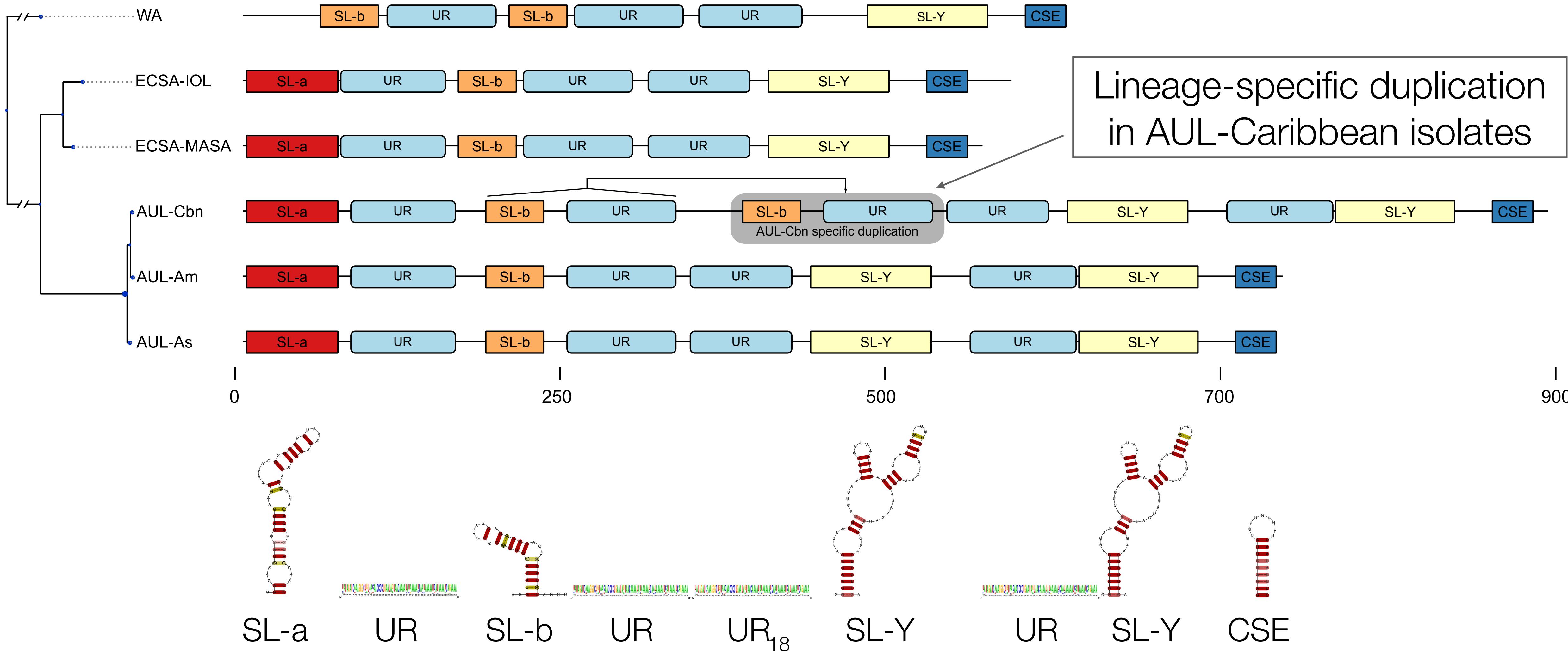
# CHIKV 3'UTR: Conserved RNA Elements



Unstructured repeat (UR)

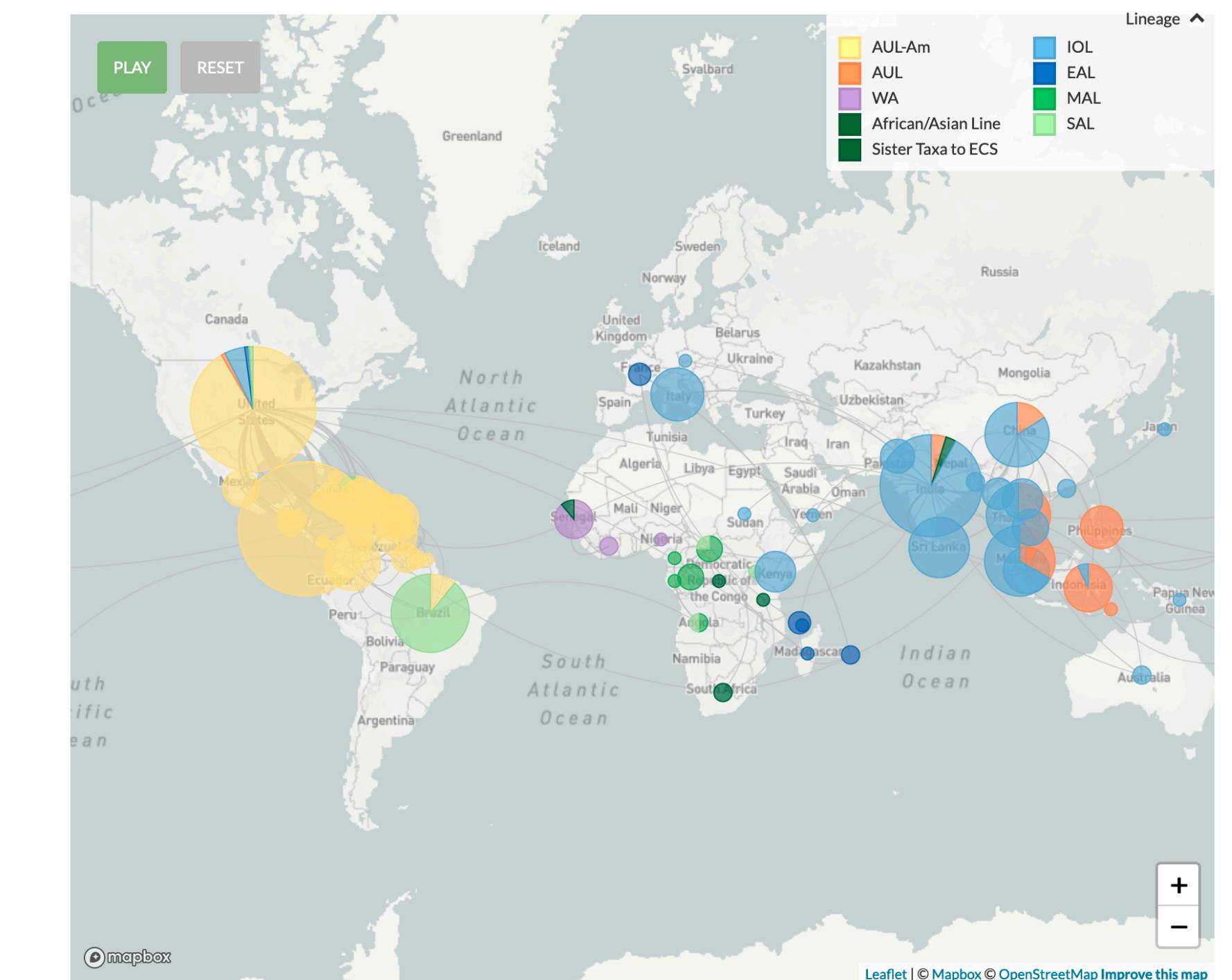
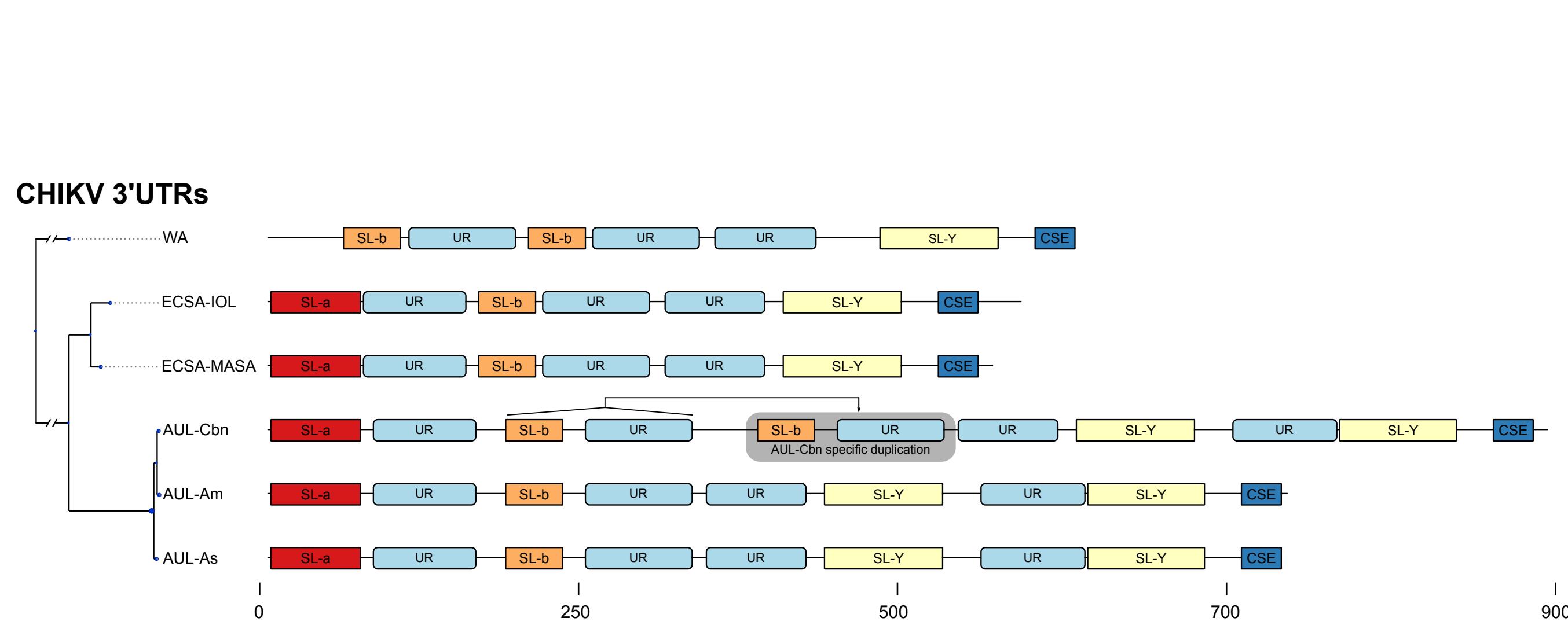


# CHIKV 3'UTR Overview



# Summary

- Conclusive mapping of sequence repeats to structured and unstructured 3'UTR regions
- Individual lineages show varied replication potential in mosquito / vertebrate cells
- CHIKV nextstrain build can help identifying lineage-specific RNA structures in coding regions



# Acknowledgements

## University of Vienna

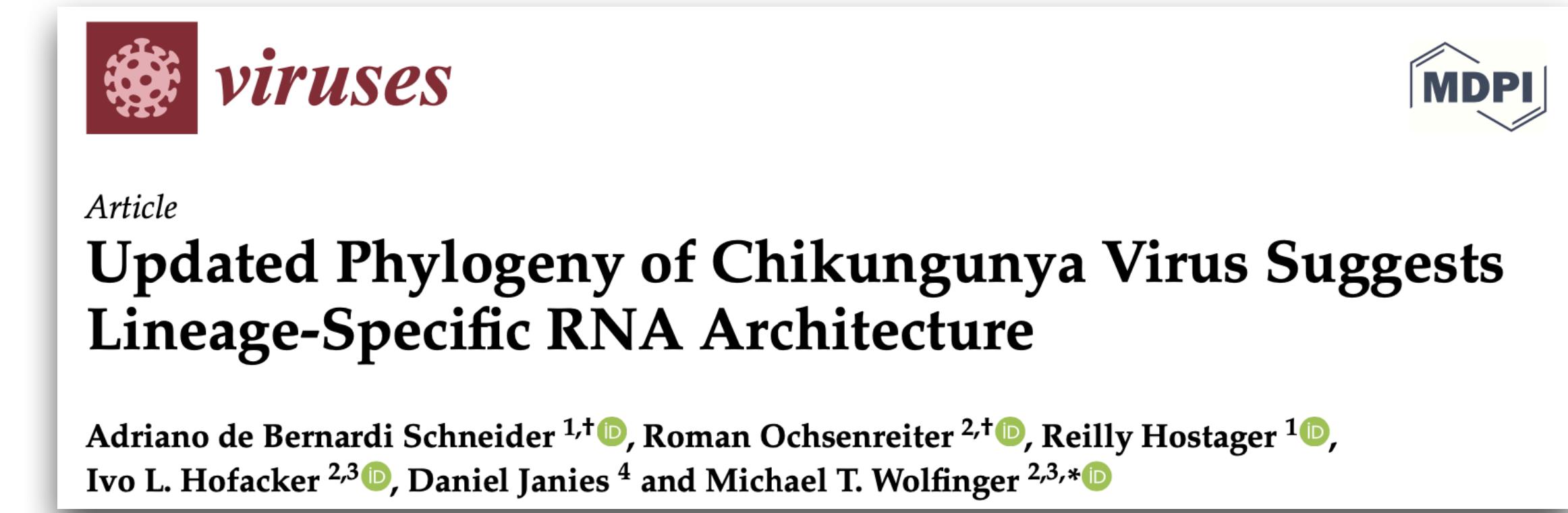
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