Abstract

- Zika Virus (ZIKV) is a mosquito born virus
- ZIKV infection in pregnant women causes microcephaly in the developing fetus
- The genome of ZIKV is single stranded plus sense RNA
- ZIKV has untranslated regions (UTRs) that play important regulatory roles in productive infections
- The mechanisms by which these UTRs act in the cell are poorly understood
- In-vitro expression of UTRs can be used to "fish" for host proteins relevant in ZIKV infection and uncover potential druggable targets

Molecular Cloning

UTR Comparisons

ZIKV Genome

3' UTR Sequence Alignment

Cladogram based off 3' UTR sequence alignment between different pathogenic members of the Flavivirus family. Predictably, Brazilian and Uganadan ZIKV strains share the most similarities. The next most related virus is Dengue Fever virus.

Folded 3' UTRs

Brazillian ZIKV

Dengue Fever

JSV Virus

Uganda ZIKV

West Nile Virus

Yellow Fever Virus

The figure above illustrates the structural similarities between 3' UTRs of 5 different Flaviviridae species. The structure enclosed by the red circle is found in nearly every Flavivirus, suggesting evolutionary conservation and physiological relevance. Structures circled in orange are found in ZIKV, Dengue, and West Nile. Structures circled in yellow are found in ZIKV and Dengue, which is most similar to each other by both genome sequence and 3' UTR structure.

Pulling Down Host-Proteins

The 3' UTR is used as a "bait" to "fish" for relevant host proteins. Any protein that interacts with the 3' UTR will bind to it.

1. RNA is attached to a biotin molecule
2. Biotin-RNA complexes are attached to metal beads
3. RNA complexes bind host proteins in cell lysate
4. Proteins are eluted and characterized by mass spectrometry and/or Western blotting

References


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