



Donnelly Centre
for Cellular + Biomolecular Research
UNIVERSITY OF TORONTO



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Blencowe Lab Seminar

“Genome organization of dengue and Zika viruses”

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Abstract:

Dengue and Zika are closely related members of the Flaviviridae family of positive, single-stranded RNA viruses and are of global clinical importance. These viruses utilize an 11kb RNA genome for translation and replication, and much remains to be learnt about how the entire genome folds to enable virus function. Here, we performed high throughput RNA secondary structure and pair-wise interaction mapping on four dengue serotypes and four Zika strains within their virus particles. We identified structures that are associated with translation pausing, and are evolutionary conserved by integrating synonymous mutation rates into our analysis. Genome-wide interaction mapping revealed alternative structures, as well as extensive long-range RNA interactions – including the known circularization signals– within the virus particles. Many of these long-range interactions are conserved across the viruses and/or clustered into “hubs” that are shown to be functionally important. This comprehensive structural resource of dengue and Zika viruses reveals that viral genome organization is much more complex than previously appreciated and deepens our understanding of the molecular basis for viral pathogenesis.

Monday, March 19, 2018 | 11:00 am

Donnelly Centre James D. Friesen | Cecil C. Yip Red Seminar Room

Host: Benjamin (Ben) Blencowe, PhD