

TICK-BORNE SEGMENTED RNA VIRUSES: MATHEMATICAL CHALLENGES AND OPPORTUNITIES

CARMEN MOLINA-PARIS

Vector-borne zoonotic diseases (VBZDs) are infectious diseases transmitted to animal hosts through the bite of infected blood-feeding arthropod vectors, (e.g., ticks or mosquitoes). VBZDs are often asymptomatic and non-lethal in animal hosts, but lead to severe and potentially lethal disease in humans or other spillover hosts, and have the potential to cause outbreaks or even pandemics (e.g., coronaviruses, avian or swine influenza, West Nile virus, Ebola virus, or Crimean-Congo hemorrhagic fever virus (CCHFV)). ZD transmission is a major risk to human health, and this risk, specifically for VBZDs, is increasing due to climate change and anthropomorphic factors (e.g., agricultural abandonment promoting large populations of vertebrate hosts for ticks).

We are interested in CCHFV, one of seven epidemic-prone diseases prioritised by the WHO and the most widespread tick-borne viral hemorrhagic fever in the world. CCHFV is a segmented RNA virus. This family of viruses possesses genomes with multiple discrete RNA strands, called segments, each a self-contained genetic element, complete with the required protein components for its expression and replication.

When such virus infects a cell, segments are independently transcribed and replicated, and subsequently assembled into new virus particles (or virions) to potentially infect new cells. Sometimes two genetically distinct RNA viruses can co-infect a host (vector) and enter the same cell. Consequently, during viral assembly, their segments can be exchanged, leading to the generation of virus particles that contain a new combination of segments, different from either of the progenitors. This process is known as reassortment, and results in the generation of viral progeny with new properties, e.g., accelerated replication kinetics or altered pathogenicity.

In this talk, I shall describe work-in-progress to study the CCHFV enzootic cycle and transmission. Bipartite graphs naturally describe contact rates between vectors and hosts, and will serve as the substrate on which infections occur along three distinct transmission routes: host to vector, vector to host, and vector to vector. The effects of small number of vectors associated to a particular host will be captured by allowing the bipartite graphs to be random and with block structure, to account for co-feeding vector clusters. I shall discuss mathematical challenges and opportunities when modelling tick-borne segmented RNA viruses.