Tanya Kostova Vassilevska
National Science Foundation
e-mail: tvassile@nsf.gov

A model of intracellular virus replication with implications for virus evolution

Viruses are the simplest living organisms. In order to survive, a virus has to successfully invade a host cell, overcome cellular degradation mechanisms, produce progeny and export it to infect other cells; eventually evade immune response and jump to a new host to start the cycle again. The first challenge to virus survival is successful reproduction in the host cell. For RNA viruses, such reproduction includes a balance between several competing processes: production of RNA-derived RNA polymerase (RdRp), production of viral protein, RNA replication by the RdRp, formation of virions by combination of genomic RNA and structural viral protein and degradation of these products. Here we design a model representing these processes for positive-sense single stranded viruses (such as the family of Picorna or Flavi viruses) as a system of ODEs derived from stoichiometric enzyme-substrate reactions and explore the asymptotic dynamics of the model. The possible regimes are (1) virus extinction, (2) stable steady state and (3) a regime where RNA and RdRp are produced in excess (tend to infinity in the model) while the structural protein is fully utilized (converges to 0). If the net production of virions is a measure of virus fitness (such a claim is supported by the view that larger virus populations can maintain higher diversity and therefore be more adaptable), then we show that viruses that have evolved to utilize scenario (3) have higher fitness than viruses that establish equilibrium progeny production within the cell.