Genome Selection by RNA Viruses

Robijn Bruinsma

1. Abstract

Small, single-stranded (ss) RNA viruses self-assemble spontaneously in solutions that contain the viral RNA (vRNA) genome molecules and viral capsid proteins. The self-assembly of empty capsids is generally understood on the basis of free energy minimization. During the self-assembly of complete viral particles in the cytoplasm of an infected cell, the viral genome molecules must be selected from a large pool of very similar host messenger RNA molecules. The talk proposes that vRNA selection should not be understood on the basis of global free energy minimization. Instead, vRNA selection takes places early in the assembly process with vRNA molecules minimizing the activation energy of a critical nucleus in which RNA packaging signals interact with a limited number of capsid proteins. The physics of this ""selective nucleation"" process will be illustrated via a simple, numerically soluble model.

and it is not known whether this also can be understood by free energy minimization. We address this question using a simple mathematical model, the Spanning Tree Model, that was recently proposed for the assembly of small ssRNA viruses a. We present a statistical physics analysis of the properties of this model. RNA selection takes place via a kinetic mechanism that operates during the formation of the nucleation complex and that is related to Hopfield kinetic proofreading.