Self-assembly of viral capsids and packing of genome

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1. Abstract

Assembly of viral capsids containing genetic material, is a key process in viral reproduction cycle. The capsid assembly differs qualitatively among viruses: bacteriophages and double stranded DNA viruses initially assemble empty capsids, into which DNA is driven by an ATP packaging motor; the single stranded RNA / DNA viruses package their genomes concurrently with the capsid assembly, resulting in a co-assembly of the virus genome and capsid proteins. We have explored a simplified model of an elastic filament confined to a sphere with replica-exchange MD simulations combined with energy minimization approaches. In contrast to a general assumption that viral DNA is packed in an inverse spool configuration, we show that compartmentalization into multiple domains (either multiple spools or intertwined rings resembling twisted topological links) is a preferred ground state at high densities. We further explored the role of the kinetics of packing via nonequilibrium simulations of DNA pushed into a capsid by a molecular motor. We observe structures with spool-like symmetry in the outer shells and melted or twisted-nematic core regions, which are in agreements with recent experimental observations. Finally, we studied the co-assembly process with ssRNA and capsid proteins with icosahedral symmetry. We explored the stability of assembled virions and found that it depends in a complex fashion on both genome topology (branchidness) and degree of confinement. Our model predicts that MS2 bacteriophage should prefer a linear genome topology, which is compatible with the Hamiltonian path hypothesis of RNA conformation in the virions.

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