

Understanding molecular mechanisms of non -enveloped virus entry and disassembly

Manidipa Banerjee¹, Kimi Azad¹, Saumya Bajaj¹, Mohit Kumar¹, Debajit Dey¹

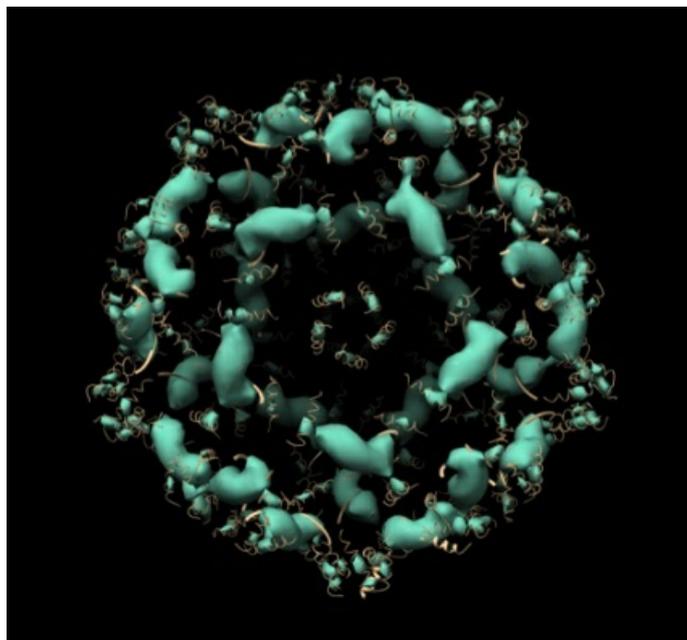
¹Kusuma School Of Biological Sciences, IIT-Delhi, New Delhi, India

E-mail: mbanerjee@bioschool.iitd.ac.in

Non-enveloped viruses employ small hydrophobic or amphipathic peptides to breach the host membrane barrier during cellular entry. The nature of capsid conformational changes required for the exposure of these peptides, and subsequent disassembly of the capsid and release of viral genome, remains unclear for most viruses. We are utilizing a non-enveloped insect RNA virus – Flock House Virus (FHV) - in order to understand capsid structural dynamics during cellular entry, membrane penetration and disassembly. FHV utilizes a small (44 amino acid) hydrophobic peptide called gamma for host membrane penetration. Using a combination of biophysical assays, cryoelectron microscopy and image reconstruction and molecular dynamics simulation studies, we have shown that the gamma peptide assumes an alpha helical hairpin structure, which is essential for its membrane disruptive function. We also established that effective disruption of membranes requires a pentameric version of full-length gamma. We have further carried out calorimetry-based analysis to identify conformationally altered states of the capsid during FHV disassembly – of which, a “puffed” capsid in the process of genome release and an empty, “eluted” capsid have been identified and characterized using biophysical techniques and electron microscopy. Detailed structural analysis of these intermediates is expected to provide a molecular roadmap of the viral disassembly pathway.

References:

- 1) Bajaj S et al. (2016) J Mol Bio 428(17):3540-56
- 2) Bajaj S, Banerjee M. (2016) Virology 496:106-15



Keywords: [nonenveloped virus](#), [disassembly](#), [membrane penetration](#)