Disassembly pathway of an empty icosahedral viral capsid

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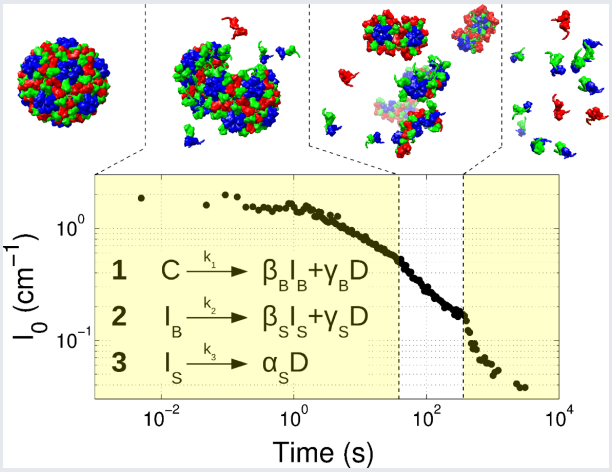
RNA viruses are ubiquitous pathogens causing serious health issues and economic concerns worldwide. Their survival depends upon their ability to efficiently self-assemble and disassemble in host cells. A common architecture for RNA viruses consists of an icosahedral capsid made of 90 copies of a dimeric polypeptide subunit arrayed in quasi-equivalent environments. Despite a huge body of work dedicated to the atomic structure of viral protein complexes, the disassembly pathways of icosahedral viruses are still ill known and the nature of the intermediate species is much debated.



Empty viral capsids derived from an icosahedral plant virus widely used in physical and nanotechnological investigations were fully dissociated into subunits by a rapid change of pH. The process was probed *in vitro* at high spatiotemporal resolution by time-resolved small-angle X-ray scattering (TR-SAXS) using a high brilliance synchrotron source. A powerful custom-made global fitting algorithm allowed us to reconstruct the most likely pathway parametrized by a set of stoichiometric coefficients. We determined the shape of two successive intermediate species made of 35 and 16 subunits on average, by *ab initio* calculations. Interestingly, none of these two unexpected species was previously identified in self-assembly experiments, which suggests that the disassembly pathway is not a mirror image of the assembly pathway.

These findings shed new light on the mechanisms and the reversibility of the assembly/disassembly of natural and synthetic virus-based systems. They also demonstrate that both the structure and dynamics of an increasing number of intermediate species become accessible to experiments.

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