

Beans, viruses... and synchrotron radiation. Probing the self-assembly dynamics of icosahedral virus by time-resolved small-angle X-ray scattering

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Viruses are entities that fascinate physicists and biologists. They oppose a relative simplicity in their structure to a surprising sophistication in their function. Although inert, their hundreds or even thousands of molecular components spontaneously assemble and disassemble in a heterogeneous and crowded cellular medium, with near-atomic precision and low error rate. Some single-stranded RNA viruses can even be self-assembled into infectious particles in test tubes from their purified components. This ability to self-assemble always defies theoretical understanding and the kinetic pathways remain largely unknown.

We work on viruses whose spherical capsids adopt icosahedral symmetry with quasi-equivalence and are able to self-assemble around their RNA genome. We focus here on the cowpea chlorotic mottle virus (CCMV), which infects a variety of beans. Its capsid, which displays an icosahedral symmetry $T = 3$, is made of 180 chemically identical and structurally quasi-equivalent copies of a single protein. The assembly implies that 90 dimers of this protein (subunits) find the viral RNA (genome) and fit perfectly around it. We show how our time-resolved X-ray scattering (TR-SAXS) experiments carried out on the ID02 and SWING beamlines at ESRF and SOLEIL synchrotron sources respectively, complemented by *ad hoc* numerical algorithms, have led to significant advances in the understanding of the self-assembly of icosahedral viruses.

In the technically simpler case of empty capsids, we reconstruct the form of metastable intermediate species during assembly (~half a capsid [1]) and disassembly (~half a capsid then two pentameric units [2]). Then, we reveal the very rich dynamic phenomena that occur during the packaging of the genome and of a synthetic polyelectrolyte [3]. These latest data have allowed us to revisit the assembly model of icosahedral viruses, which seemed firmly established on the basis of indirect data.

References

[1] - D. Law-Hine, M. Zeghal, S. Bressanelli, D. Constantin, G. Tresset, *Soft Matter* **12**, 6728–6736 (2016).

[2] - D. Law-Hine, A.K. Sahoo, V. Bailleux, M. Zeghal, S. Prevost, P.K. Maiti, S. Bressanelli, D. Constantin, G. Tresset, *J. Phys. Chem. Lett.* **6**, 3471–3476 (2015).

[3] - M. Chevreuil, D. Law-Hine, J. Chen, S. Bressanelli, S. Combet, D. Constantin, J. Degrouard, J. Möller, M. Zeghal, G. Tresset, *Nat. Commun.* **9**, 3071 (2018).