Physical Ingredients Controlling Stability and Structural Selection of Empty Viral Capsids

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Viruses are fascinating biological entities, in the fuzzy frontier between life and inert matter, and stand out in the biological context by their efficiency and relative simplicity. Contrary to most biological organisms, viral particles are made of a minimal number of components that in the simplest cases are just a one-protein-thick shell protecting a single chain of RNA or DNA inside. Despite the lack of sophisticated biological machinery, viruses have found the way to efficiently infect the host, assemble, and egress the cell following, in many cases, a coordinated sequence of passive and spontaneous processes. This strongly suggests that, during their life cycle, viruses must rely on general physical mechanisms to succeed in their different tasks and to achieve the required resistance against possible extreme environmental conditions [1]. Moreover, their outstanding properties have stirred the interest in the study of viruses to develop novel strategies aimed at stopping viral infections, or at using their remarkable abilities for bio and nanotechnological applications.

One of the most amazing characteristics of viruses is their ability to self-assemble forming infective particles well-defined in size, in the range of 10 to 500 nm, and structure[2]. The most prevalent architecture found in viruses is the spherical capsid with icosahedral symmetry adopted by about half of all known viral species, and classified in terms of a discrete sequence of triangulation numbers[3], T, i.e. T=1,3,4,7,9...

Typically, each native virus adopts a unique architecture, but the coat proteins of many viruses have the capability to self-assemble *in vitro* into different structures by changing the assembly conditions. However, the mechanisms determining which of the possible capsid shapes and structures is selected by a virus are still not well known.
We present a coarse-grained model to analyze and understand the physical mechanisms controlling the size and structure selection in the assembly of empty viral capsids[4]. Using this model and Monte Carlo simulations, we have characterized the phase diagram and stability of T=1,3,4,7 and snub cube shells (see Fig. 1). In addition, we have studied the tolerance of different shells to changes in physical parameters related to ambient conditions, identifying possible strategies to induce misassembly or failure. Finally, we discuss the factors that select the shape of a capsid as spherical, faceted, elongated or decapsidated.

Our model sheds important light on the ingredients that control the assembly and stability of viral shells. This knowledge is essential to get capsids with well-defined size and structure that could be used for promising applications in medicine or bionanotechnology.

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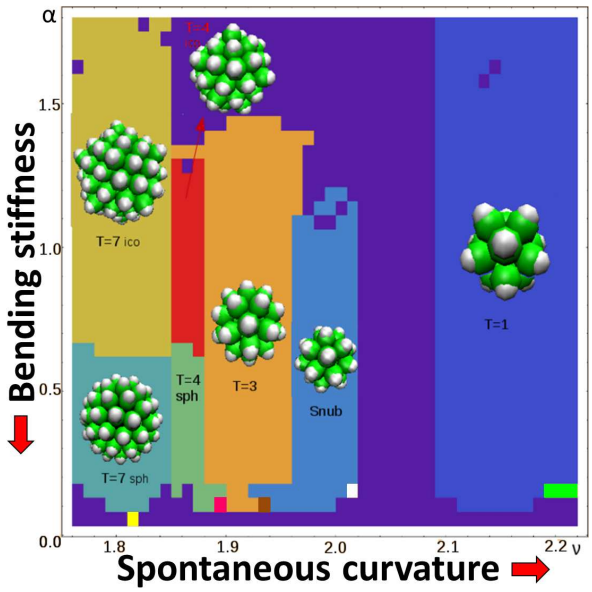

Figure 1: Stability phase diagram of the different viral structures with one type of capsomers obtained as a function of the parameters that control the bending stiffness and the spontaneous curvature in the model: T=7 elongated (yellow), spherical (cyan) and icosahedral (dark yellow); T=4 elongated (magenta), spherical (light green), and icosahedral (red); T=3, elongated (maroon), and spherical (orange); snub cube, elongated (white) and spherical (blue) and T=1, elongated (green) and spherical (dark blue).

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