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Diversity in virus assembly: biology makes things complicated

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Icosahedral viruses have an elegance of geometry that implies a general path of assembly. However, structure alone provides insufficient information. Cowpea Chlorotic Mottle Virus (CCMV), an important system for studying virus assembly, consists of 90 coat protein (CP) homodimers condensed around an RNA genome. The crystal structure (Speir et al, 1995) reveals that assembly causes burial of hydrophobic surface and formation of β hexamers, the intertwining of N-termini of the CPs surrounding a quasi-sixfold. This structural view leads to reasonable and erroneous predictions: (i) CCMV capsids are extremely stable, and (ii) β hexamer formation is critical to assembly. Experimentally, we have found that capsids are based on a network of extremely weak (4-5 kT) pairwise interactions and that pentamer formation is the critical step in assembly kinetics. Because of the fragility of CP-Cp interaction, we can redirect assembly to generate and dissociate tubular nanostructures. The dynamic behavior of CCMV reflects the requirements and peculiarities of an evolved biological system; it does not necessarily reflect the behavior predicted from a more static picture of the virus.