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The Refined Crystal Structures of Flock House Virus and Virus-like-particles Reveal Structural Features Important to the Virus Maturation and Assembly. Zhongguo Chen, Vijay Reddy, John E. Johnson, Dept. of Molecular Biology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA.

Flock house virus (FHV) is a member of Nodaviridae, a group of icosahedral insect viruses with a bipartite, single stranded RNA genome. Each virus particle is assembled from 180 copies of capsid protein containing 407 amino acid residues in a $T=3$ quasi symmetry and encapsidates the bipartite genome. During maturation, the capsid protein is auto-cleaved into two polypeptides with the cleavage of the scissile bond between Asn363-Ala364.

We refined 4 crystal structures of FHV, one authentic virus and 3 virus-like particles (VLP), to near atomic resolution. All 4 structures share similar features, except that a Ca ion and a sulfate ion can be found in the VLP structures at the quasi three-fold axes, but not in the authentic FHV. The fold of the capsid protein is a canonical virus β sandwich with residues 92-320 forming the core of the β domain. An internal helical domain is formed by three α helices from the N and C-termini in the interior of capsid. A portion of the duplex RNA genome can be imaged in the crystal structure, however, the B factors are high, indicating disorder or non-strict conformation to the icosahedral symmetry. Segment 72-82 is flexible with higher B factors. We postulate that the flexibility of this segment helps in catalyzing the cleavage of the scissile bond, and plays an essential role in the capsid maturation, as well as the formation of subunit contacts during the assembly.