A018-04-290823

Viruses

Structures of honeybee-infecting Lake Sinai virus reveal domain functions and capsid assembly with dynamic motions

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Keywords: Lake Sinai virus, cryo-EM structures, Colony Collapse Disorder

Understanding the structural insight and diversity of honeybee-infecting viruses is critical to maintain pollinator health and manage the spread of diseases in ecology and agriculture. We determine cryo-EM structures of *T*=4 and *T*=3 capsids of virus-like particles (VLPs) of Lake Sinai virus (LSV) 2 and delta-N48 LSV1, belonging to tetraviruses, at resolutions of 2.3–2.6 Å in various pH environments [1]. Structural analysis shows that the LSV2 capsid protein (CP) structural features, particularly the protruding domain and C-arm, differ from those of other tetraviruses. The anchor loop on the central β-barrel domain interacts with the neighboring subunit to stabilize homo-trimeric capsomeres during assembly. For a comparison, we also determine the cryo-EM structure of the *T*=3 delta-N48 LSV1 VLP at 2.6 Å. Delta-N48 LSV1 CP interacts with ssRNA via the positively charged domains of the rigid helix α1', α1' –α1 loop, β-barrel domain, and C-arm. Cryo-EM reconstructions, combined with X-ray crystallographic and small-angle X-ray scattering analyses, indicate that pH affects capsid conformations by regulating reversible dynamic particle motions and sizes of LSV2 VLPs. C-arms with continuous densities exist in all LSV2 and delta-N48 LSV1 VLPs across varied pH conditions, indicating that autoproteolysis cleavage for g peptide release, which was generally observed in other known *T*=4 and *T*=3 viruses, is not required for LSV maturation. Interestingly, an introduction of a double mutation of M83E/D461F on the LSV2 CP, mimicking the key residues at the autoproteolysis sites from other tetraviruses Providence virus (PrV) and *Nudaurelia* capensis ω virus (NωV), potentially triggers a self-cleavage process on the specific scissile bond of LSV2 CP. Moreover, the observed linear domino-scaffold structures of various lengths, made up of trapezoid-shape capsomeres, provide a basis for icosahedral *T*=4 and *T*=3 architecture assemblies. These findings advance understanding of honeybee-infecting viruses that can cause Colony Collapse Disorder [2, 3, 4].

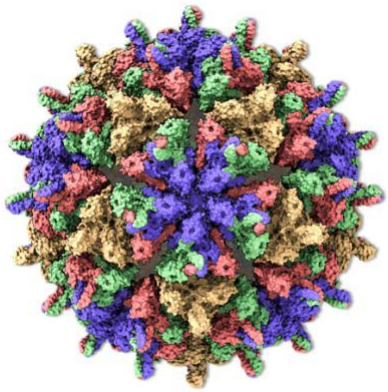

Figure 1. The structure of *T*=4 LSV2 VLP.

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