Structural biology of viruses and capsid assembly

Chun-Jung Chen[1]

[1]*Life Science Group, Scientific Research Division, National Synchrotron Radiation Research Center, Hsinchu 300092, Taiwan*

[*]*E-mail: cjchen@nsrrc.org.tw*

Abstract

Viral capsid proteins (CPs) are important in the viral life cycle. CP forms the capsid shell that protects genomes and is responsible for both host specificity and receptor binding to transport the viral genome into infected host cells, or for intracellular trafficking. Recombinant CPs could assemble into virus-like particles (VLPs) that preserve the structural properties and antigenicity of mature infectious virions. Our previous studies of the VLP architectures of grouper nervous necrosis virus [1] and shrimp nodavirus [2] provided new insights to develop an appropriate treatment, such as epitope mapping for vaccine developments, to prevent viral infection in fish and shrimp aquaculture industry. We recently characterized structures of honeybee-infecting Lake Sinai virus (LSV), belonging to tetraviruses, in various states [3].

Understanding honeybee-infecting viruses' structural insight and diversity is critical to maintaining pollinator health and managing the spread of diseases in ecology and agriculture. The LSV2 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. Delta-N48 LSV1 CP interacts with ssRNA via particular positively charged domain regions. Cryo-EM reconstructions, combined with synchrotron 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 exist in LSV VLPs across varied pH conditions, indicating that autoproteolysis for γ peptide release, which was generally observed in other known viruses, is not required for LSV maturation. An introduction of a double mutation of M83E/D461F on the LSV2 CP potentially triggers a self-cleavage process on the specific scissile bond of LSV2 CP. 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 [4].

References

1. N.-C. Chen, M. Yoshimura, H.-H. Guan, T.-Y. Wang, Y. Misumi, C.-C. Lin, P. Chuankhayan, A. Nakagawa, S. I. Chan, T. Tsukihara, T.-Y. Chen and C.-J. Chen, *PLoS Path*., 2015, **11**(10): e1005203.

2. N.-C. Chen, M., Yoshimura, N. Miyazaki, H.-H. Guan, P. Chuankhayan, C.-C. Lin, S.-K. Chen, P.-J. Lin, Y.-C. Huang, K. Iwasaki, A. Nakagawa, S. I. Chan and C.-J. Chen, *Commun. Biol.,* 2019*,* **2**:72.

3. N.-C. Chen, C.-H. Wang, M. Yoshimura, Y.-Q. Yeh, H.-H. Guan, P. Chuankhayan, C.-C. Lin, P.-J. Lin, Y.-C. Huang, S. Wakatsuki, M.-C. Ho and C.-J. Chen, *Nat. Commun*., 2023, **14**, 545.

4. D. Cox-Foster, *et al*., *Science*, 2007, **318**, 283–287.