Unlocking the viral capsid: crown proteins and pore structural and functional analysis in dsRNA Virus

Clara Manesco*, Gabriela Garcia Hernández*, Han Wang*, Diogo de Matos Philip*, Keiichiro Koiwai**, Ikuo Hirono**and Kenta Okamoto*

*The Laboratory of Molecular Biophysics, Department of Cell and Molecular Biology, Uppsala University, Uppsala, Sweden, ** Laboratory of Genome Science, Tokyo University of Marine Science and Technology, Tokyo, Japan

Icosahedral, non-enveloped double-stranded RNA (dsRNA) viruses infect diverse hosts including crops, animals, and humans, causing significant societal impacts. Despite their diversity across taxons, these viruses share a conserved T=1 icosahedral capsid structure and a critical feature: a positively charged pore at each 5-fold vertex. In Artiviridae and Pistolviridae, that infect shrimp and salmon, these pores are obstructed by a surface crown protein (CrP).

Using Omono River virus (OmRV) as a model, we generated mutants disrupting these features[1]. CrP impairment does not affect infectivity or capsid structure, yet impacts cytopathic effect (CPE), vesicular virus factories, and propagation[2]. Pore impairments affect conserved positively charged residues in the 5-fold channels, hypothesized to facilitate NTP uptake for intraparticle genome synthesis—allowing packaged viral RNA-dependent RNA polymerases (RdRps) to synthesize genomes and evade host immune detection[3].

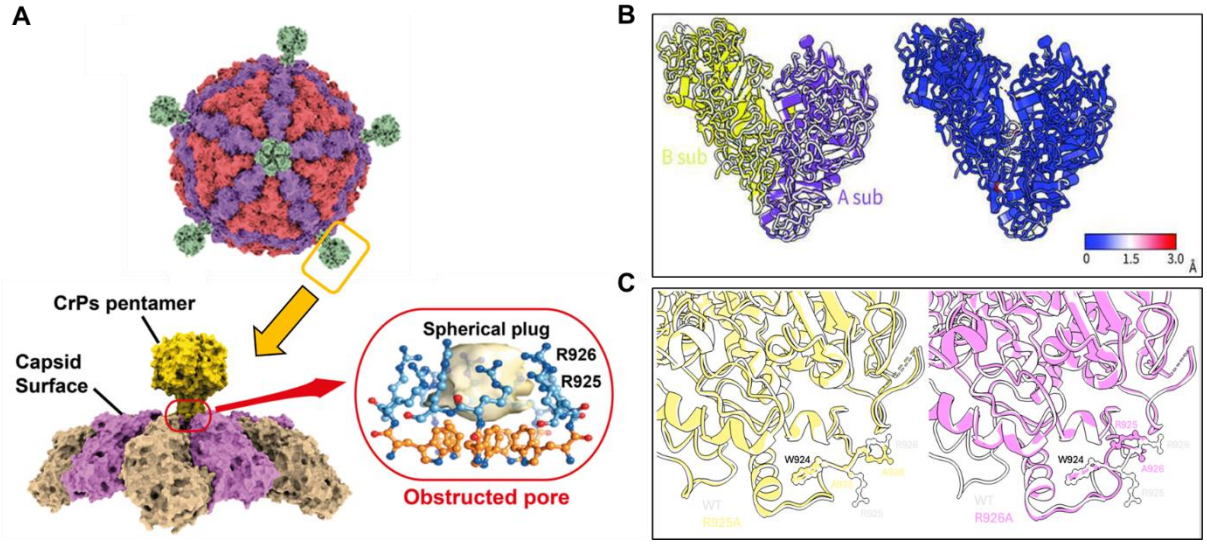

Figure 1: A) OmRV structure showing the CrPs and the obstructed pore consisting of an RR motif surrounding a spherical plug. B) Superimposition of the atomic models of the A and B subunits in OmRV-WT (white) and OmRV-CrP mutant (yellow and purple) with structural variations between OmRV-WT and OmRV-CrPdel highlighted by residual root mean square deviation (RMSD) values. C) Local structural variations on pore residues between OmRV-WT (white) and pore mutants: OmRV-R925A (yellow) , and OmRV-R926A (pink).

References: 1. Okamoto et al., **Structure** (2020); 2. Garcia Hernández et al., **Virology** (2026); 3. Manesco et al., **unpublished** (2026)