Structure of the first isolated polinton-like virus and its host

Dr. Gabriela N. Condezo[1], Mr. Roberto Marabini[2], Mr. Javier Conesa[1], Mr. David Delgado[1], Mrs. Hilde K. Stabell[3], Mr. Gunnar Bratbak[3], Mrs. Carmen San Martín[1]
[1]Centro Nacional de Biotecnología (CNB-CSIC), Madrid, Spain, [2]Escuela Politécnica Superior. Universidad Autónoma de Madrid, Madrid, Spain, [3]Department of Biology. University of Bergen, Bergen, Norway

Viruses in the PRD1/Adenovirus (AdV) -like lineage infect bacteria, archaea and eukaryotic organisms and build their capsids with proteins with beta-jelly rolls orthogonal to the capsid surface (1). It has been suggested that Polintons (dsDNA transposons) are members of this lineage, because they encode genes very similar to viral proteins involved in replication, assembly, maturation, and possible structural proteins with jelly roll fold. These observations prompted the hypothesis that Polintons may have evolved from a PRD1-like ancestor (2). Subsequent evolution would have resulted in the "polintovirus" elements splitting into two different ways of life: the transposable, capsid-less integrating elements, and the bona fide viruses. Marine metagenome analyses have revealed a group of putative polinton-like viruses (PLVs) in eukaryotes. PLV genomes contain genes for single and double jelly roll proteins and a packaging ATPase, but lack the protease and integrase genes present in the polintons (3). Therefore, PLVs could represent a minimal version of the PRD1/AdV-like lineage in eukaryotic hosts. The study of this kind of virus could reveal the adaptations necessary for the jump from a bacterial to eukaryotic host. The first isolated PLV, TsV-N1, infects the unicellular eukaryotic algae Tetraselmis striata (4)

We have used cryo-electron microscopy to solve the structure of TsV-N1, and FIB-SEM volume electron microscopy on resin-embedded cells to analyse the structural changes induced by infection in the host. The high-resolution capsid structure (2.7 Å) corroborates the placement of TsV-N1 in the PRD1/AdV-like lineage and reveals similarities with those of bacteriophages in this lineage, although TsV-N1 infects a eukaryotic host. These similarities include: triangulation number T = 21d, size, genome arranged in concentric rings. However, the main differences with bacteriophages in this lineage are the absence of an inner membrane, the major capsid protein fold being more similar to other eukaryotic viruses, a complex cementing protein network and a high packing fraction, more similar to those of HK97-like viruses. TsV-N1 induces large changes in the host during the infection. Although this virus assembles in the nucleus, other cellular structures are modified too. Particularly striking is the disappearance of starch grains and the cell wall, suggesting that the virus hijacks energy sources for propagation. More studies must be carried out to understand how this virus reaches the nucleus. However, its similarities with AdV (no membrane, nuclear assembly) suggest that similar genome delivery mechanisms may be involved.

Keywords:

Polinton-like virus, cryo-EM, cellular-sections, volume-EM.

Reference:

[1] Krupovic et al., Nat Rev Microbiol 6, 941 (2008).
[2] Krupovic et al., Nat Rev Microbiol 13, 105 (2015).
[3] Yutin et al., BMC Biol 13, 95 (2015).
[4] Pagarete et al., Viruses 7, 3937 (2015).
[5]Supported by grants PID2019-104098GB-I00 and PID2022-136456NB-I00/AEI/10.13039/501100011033, CRIOMECORR (ESFRI-2019-01-CSIC-16), and BAG bi22006 at eBIC center.