

Cryo-electron microscopy structure of archaeal virus APBV1

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Archaeal viruses have evolved to infect hosts often thriving in extreme conditions. For example, viruses infecting hyperthermophilic archeons can resist extreme temperatures. Rod-shaped virus APBV1 (*Aeroperum pernix* bacilliform virus 1) infects a hyperthermophile *Aeroperum pernix*, which grows optimally at 100°C [1]. Due to shortage of information on archaeal virion structures, key determinants behind temperature resistance have remained elusive. Our cryo-electron microscopy analysis provided details of unique structural organisation of APBV1 which allowed better understanding of viral adaptation to hostile environment.

As major virion protein virus is a very small protein (10kDa) the APBV1 particles appeared as smooth rods on microphotographs recorded initially on CCD camera. Determination of helical parameters became possible only after the data was collected with direct electron detector (Strubi, Oxford). Helical parameters established from the Fourier-Bessel analysis of 2D class averages and corresponding power spectra allowed to obtain experimental cryo-EM map at 3.7Å resolution and to build a model of the major virion protein (VP1) *de novo* [2]. The curvature of the alpha helices of VP1 is critical for incorporation of subunits in the helical lattice without gaps. The extreme thermostability of APBV1 is based on cooperative assembly of multiple VP1 subunits arranged in a helical array. Tight packing of the subunits held together by extended hydrophobic contacts makes the virion very rigid and remarkably stable.

APBV1 is one of the smallest known viruses and high degree of compaction of its genome is an important feature. The double stranded circular DNA genome adopts an unusual form of a left-handed superhelix. The folding of the DNA inside the virion is guided by its interactions with the positively charged residues of VP1 exposed on the inner surface of the protein capsid. The whole assembly is closed by specific capping structures at either end, which we propose to play a role in DNA packing and delivery.

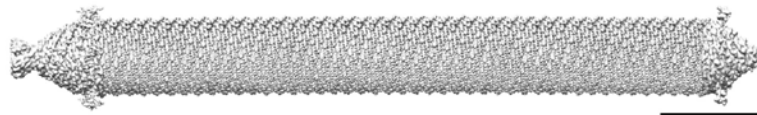


Figure 1: Cryo-electron microscopy map of APBV1 virion (bar: 20nm)

References

- [1] - T. Mochizuki, T. Yoshida, R. Tanaka, P. Forterre, Y. Sako and D. Prangishvili, *Virology* **402**, 347 (2010). J.D. Watson and F.H.C. Crick, *Nature* **171**, 737 (1953).
- [2] - A. Desfosses, R. Ciuffa, I. Gutsche and C. Sachse, *J Struct Biol* **185**, 15 (2014).