

The Architecture of African Swine Fever Virus

By YAN Fusheng (Staff Reporter)

frican swine fever virus (ASFV) is a giant and complex DNA virus that causes domestic pigs and wild boars to suffer from acute, febrile and highly contagious and lethal diseases. The last year has witnessed numerous outbreaks worldwide, causing a huge economic loss. Nearly all infected animals ended up dead and culling pigs has been so far the most effective way to contain ASFV outbreaks, because no vaccine or treatment is currently available. To fight against the virus, there is an urgent demand to get to known it above all.

A timely process has been made by Chinese scientists on revealing the fine structure of the virus, which will provide clues to explore fundamental mechanisms for how the virus makes its moves to get to its victims and infect their cells. These further understandings would then serve as useful guidelines for

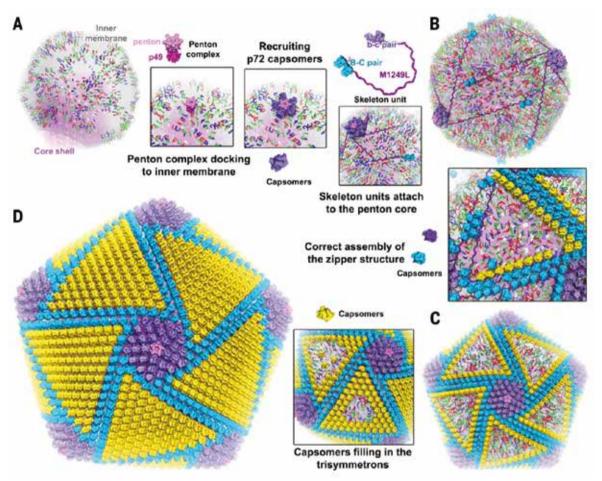
designing anti-virus drugs and vaccines. The research was conducted by a joint team led by RAO Zihe and WANG Xiangxi at the CAS Institute of Biophysics (IBP) and BU Zhigao at the Harbin Veterinary Research Institute of the Chinese Academy of Agricultural Sciences (CAAS), which was reported in *Science* in October 2019.

The scientists isolated the epidemic strain of the spreading virus in China and continuously collected high-quality data from cryo-electron microscopy (EM). Using an optimized image reconstruction strategy, they successfully solved the three-dimensional structure of the ASFV capsid, a protein shell surrounding the virus, with a resolution of 4.1 Å. They also revealed the ASFV's five-layer unique structural feature – from surface to core bearing the outer membrane, capsid, double inner membrane, core shell and the virus genome.

They found that the ASFV capsid contains more



The five-layer structure of the African swine fever virus (ASFV) and how it looks at the capsid layer, a layer of protein shell. (Credit: CAS)



A proposed assembly line for the ASFV capsid, a protein shell surrounding the virus. (Credit: Science)

than 30,000 protein subunits and is assembled into a spherical particle with a diameter of about 260 nanometers. The assembly pathway of the virus, as proposed in the research, is even superior to an industrial assembly line, because the virus may not assemble layer by layer, the parts may coordinate and interactively build into the final architecture as a whole.

In short, these structural details not only unveil the basis of capsid stability and assembly, but also provide important clues for revealing the mechanism of how the African swine fever virus invades the host cells and evades and combats host anti-virus immunity.

Reference

Nan Wang, Dongming Zhao, Jialing Wang, Yangling Zhang, Ming Wang, Yan Gao, Fang Li, Jingfei Wang, **Zhigao Bu*, Zihe Rao*, Xiangxi Wang***, (2019) Architecture of African swine fever virus and implications for viral assembly. Science 366, 640. doi: 10.1126/science.aaz1439.