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Taiwan scientists discover vaccinia protein structure

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Singapore: Scientists at Academia Sinica have solved the crystal structure of a vaccinia envelope A27 protein and showed that the protein trimer is the structural unit critical for vaccinia virus egress and also helps in controlling viral fusion suppressor complex formation. The research titled, 'Crystal structure of vaccinia viral A27 protein reveals a novel structure critical for its function and complex formation with A26 protein', was published in PLoS Pathogens on August 23, 2013.

The study sheds light on the viral fusion regulation mechanism of the vaccinia virus. Revelation of viral membrane protein structure will aid in design of improved vaccine in the future. The two teams of scientists were led by Dr Andrew H J Wang at the Institute of Biological Chemistry and Dr Wen Chang at the Institute of Molecular Biology.

The first authors in the study include Tao-Hsin Chang, a current Oxford University PhD student who solved the crystal structure while working at Dr Wang's lab and Shu-Jung Chang, a PhD student in National Yang-Ming University. The research is funded by Academia Sinica and National Science Council of Taiwan.

Vaccinia mature virus has more than 20 envelope proteins, including the A27 protein, which is conserved in pathogenic poxviruses such as variola and monkey poxivuses. Dr Wang's lab used X-ray crystallography to determine the structure of the A27 protein, which forms a novel hexamer consisting of four parallel strands and two anti-parallel strands. Based on the crystal structure, Dr Chang's lab generated a series of mutant vaccinia viruses that interrupt A27 protein-protein contact interface resulting in attenuation of virus egress and virus spreading in cells.

Furthermore, Dr Chang's lab also demonstrated that A27 protein complex formation through the coiled-coiled domain is crucial to its biological activity in vivo, and revealed how A27 regulates virus-induced membrane fusion through its ability to form complexes with A26 protein.