Reconstruction of newly found viruses
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Viruses are very small entities that only propagate through means of parasitism. In the past decade, sequencing technology has improved the way scientists can discover viruses from the environment and has led to a massive amount of newly found viruses infecting a wide variety of hosts. These new viruses have been connected to their relatives based on their genetic similarities which has led to new insights on how many, if not all viruses are related. These new relationships can also be used to investigate how some medically relevant viruses have evolved. It is important to know how viruses evolve to create a predictive framework to combat the advent of new dangerous human viruses.

In this study, two newly discovered viruses were characterized based on specific aspects of their relationship to medically significant viruses. The flaviviruses are the most common human infecting viruses, and cause millions of infections globally worldwide. The first virus, the Southern Pygmy Flavilike virus was found in a study to infect a marine invertebrate, the Southern pygmy squid, reflecting its split from common flaviviruses ~500 million years ago. By reconstructing a structural element, the “E-protein” of the SpSFV and comparing it with for instance the dengue virus, elements that are important for infecting mammals, and by extension humans would stand out and can be easily identified. Because the mammal infecting flaviviruses have adapted and are specific to their hosts, the differences between the invertebrate flaviviruses and the vertebrate flaviviruses can highlight structural features that are necessary for the virus to infect mammals, and by extension humans. The reconstruction of this “ancient” flavivirus “E-protein” was successful in insect cells (Sf-9) cells. By modifications to its native gene sequence, the protein could be released into the culture fluid and analysed by several different assays. To accurately reconstruct a protein structure, a highly concentrated and purified protein is required. The release of this protein into the culture fluid in this study is an important step in the large-scale expression and consequent structure determination of this protein.

The second virus of this study, the Hubei partitilike virus 11 is an insect infecting partitivirus. Since partitiviruses normally don’t infect insects, reconstructing this virus and comparing it to fungi infecting partitiviruses could lead to discovering which structural virus features are necessary to infect insects. This virus was successfully expressed in insect Sf-9 cells and assembly into the characteristic virus icosahedral geometry was confirmed using microscopy. However, the number of particles were too few to be used for the highest resolution type work. Therefore, additional upscaling of insect culture which produce these virus-like particles is required. Once the insect culture volume has been increased substantially, solving the structure of the Hubei.PLV 11 may become possible.