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Perspective

The Structure and Expression of Viruses

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PERSPECTIVE

By their very nature, humans are inquisitive. Starting with the invention of the wheel, discoveries are achieved via observation and effort. In the seventeenth century, Edward Jenner employed 'attenuated' cow smallpox to immunise the French people, and observation was crucial in his creation of vaccines. With the independent and revolutionary work of Iwanonski and Beijerick, the name 'virus' would be established almost a century later. They demonstrated that a filtrate of infected material can cause disease in tobacco leaves that were previously healthy. Structural virology took a leap forward with the invention of numerous essential methods like as mass spectrometry, electron, and cryo-electron microscopy, all guided by the scientific method of observation, hypothesis, and experiment. We wanted to show substantial improvements in defining the three-dimensional structures of viruses, including their assembly processes, in this issue of Current Opinion in Virology.

Viruses are most frequently associated with disease-causing agents that constitute a substantial threat to humanity. HIV and arthropod-borne diseases including dengue, yellow fever, and zika are examples of extreme epidemics. To cause their recipients to produce infectious progeny, all viruses must go through a series of processes. In humans, virus interaction almost always triggers an immunological response that results in viral clearance. On the other hand, removing a pathogen from an organism might have serious negative implications, as seen with Flavivirus infections. Dengue viruses 1, 2, 3 and 4 have highly similar capsid architectures, which cause the formation of non-interchangeable neutralising antibodies that can cross-react with other Flaviviruses, resulting in potentially dangerous hemorrhagic episodes through a mechanism known as antibody-dependent enhancement (ADE). Because of a combination of cellular and structural biology, our understanding of the molecular processes controlling this occurrence is improving. According to Morrone and Lok, the orientation of antibody binding to viral proteins and the Dengue virion's maturation state are both influenced by ADE. Understanding the structural dynamics of antibody binding can also help in the development of effective immunisations against diseases that could affect 390 million people globally.

Scientists have been studying the amazing uniformity of such capsids for decades. Cryo-electron microscopy advances are demonstrating that perfect symmetry adherence is not required for virus assembly. For the longest time, determining the high-resolution structures of virus capsids required icosahedral symmetry to boost the resolution. Details on capsid assembly were lost as a result. Local asymmetry is an essential component of capsids. These structural properties may be necessary essential critical biological functions such as genome packing and protein-protein interactions, such as capsid maturation rearrangements. The reader will get a comprehensive review of the structural elements of HIV development in this issue. The complicated change in capsid protein required for HIV infectivity gives light on capsid protein biology as well as components of the viral life cycle such as viral enzyme activities, viral budding, and RNA recognition.

Caspar and Klug postulated in 1962 (and many others validated over the next half-century) that viral capsids tend to be exceedingly regular when assembled. The overall conservation of capsid protein folds, even though amino acid conservation is not a requirement, is a striking feature that may be partly responsible for such periodicity: even though amino acid conservation is not a requirement, viral proteins assume common topologies, such as the HK97 fold, which Duda and Teschke explore in this issue. In recent years, researchers have taken an unusual turn, viewing viruses as "bad news wrapped in proteins" rather than "bad news wrapped in proteins" (Peter Medawar). Viruses most commonly target receptive cells and distribute their DNA via specialised viral:host protein:protein interactions. As a result, once the assembly qualities and circumstances of a particular virus are established, it may theoretically be employed as a nano compartment for targeted chemical delivery, as their genomes demonstrate. We can now regard these pathogenic entities as molecular nano machines, rather than pathogenic entities.

The genome is packaged in bacteriophages and some animal viruses, for example, by a molecular motor

known as the portal protein complex. The power density generated by these complexes is twice that of man-made automotive engines. That force is required to bundle DNA into capsids to a near-crystalline density, which must satisfy various physical restrictions, as outlined in Jardine's review, which are only observed in portals carrying viral capsids. These findings have provided new perspectives on such systems as well as new insights into the biophysical properties of macromolecules. The use of viruses as nanotechnology tools is another relatively young field of research. They comply with the minimum of prerequisites for building nanomaterials successfully. They self-assemble into biodegradable containers quickly and consistently, permitting for interior and/or exterior adjustments.

We compiled the reviews in this issue as a result of our quest and interest to learn information regarding nature's nano machines that have been developed by evolution. We learned of Michael Rossmann's death as we were putting together this Overview. Professor Rossman is well-known regarding his contributions to structural biology and structural virology. He solved major virus structures using X-ray crystallography and, more recently, cryo-electron microscopy, spanning from the tiniest picorna viruses to the largest viruses. His zeal for structural virology was inexhaustible, and his contributions to structural methodologies, virus structure, and biological insights were invaluable.