Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
New tools to battle emerging viruses

Editorial overview

Michael J Buchmeier and Peter Kuhn

In the wake of world changing episodes like the invasion of and spread across North America by West Nile Virus in 1999, the 2003 SARS pandemic, and the current and continuing spread of Chickungunia virus into Southern Europe, it has become evident that to all but the most shortsighted of observers that the study of Viral zoonoses is critical to any effort to understand and counteract emerging viral infections. Animals have proven to be important reservoirs of nearly all-recent emerging viruses, including SARS, avian flu, arenaviruses, hantaviruses, and West Nile. The mechanisms of spread and persistence of viruses in the animal hosts is diverse, ranging from lifelong infections of their natural hosts by arena and hantaviruses. What has been particularly troubling about these outbreaks is the rapidity with which they are able to move across countries, continents and oceans with ease. Also of concern is the ability these agents have shown to be able to jump host species and quickly generate new cross-over viruses. The highly pathogenic nature of such cross-over viruses, ill adapted to their human hosts, has lead to rapid, severe disease with high fatality rates. Such characteristics, unfortunately, also make these agents potentially good bioweapons. Key information about the extent of distribution of heretofore unknown agents in Nature is not readily available, and the clear message is that zoonotic outbreaks are not going to disappear at anytime soon. Recent history bears this out. For example when SARS shocked the World in 2003 the question of the origin of the virus was paramount, yet it was not until well after the epidemic that we learned that SARS like viruses are enzootic in bat populations throughout Asia. Although it has been shown that relatively few mutations in the SARS glycoprotein can generate the human tropism seen in the virulent SARS viruses, how those mutations occur, and what environmental or ecological conditions led to their appearance, are still unresolved. Indeed one current theory of the origin of SARS coronavirus is that it arose suddenly in or around the Summer of 2002 by a recombinational event between two as yet unknown progenitors. Clearly the scale and cost of surveillance efforts to track these emerging pathogens is beyond the scope of existing programs, however progress toward understanding their pathogenic mechanisms and designing effective countermeasures is not, and as a result novel new approaches and capabilities have been developed in response to the threat. The articles in this section focus on three of these issues.

Remy Charrel has shown, through his work in phylogenetics, the diversity of the arenaviridae, an important group of rodent-borne agents represented on many continents, and important etiologic agents for humans in both the Old and New Worlds. Clearly the extent and diversity of these viruses exceeds the previous estimates, ad such work will help us to assess the true magnitude of the problems of human exposure.
Richard Kuhn has been at the forefront of viral structural biology for many years, and his recent work on the structure of the Dengue virus serves as a signal contribution in the area of new and emerging viruses. The structural data has provided novel new insights into the design of antiviral drugs and antibodies against Dengue.

The past decade has revealed a significant role for the innate immune response in viral infections, and thus it should come as no surprise that viruses like Vaccinia have evolved the means to modulate these responses. The work of Grant McFadden has yielded important insights into the molecules involved and their mechanisms of action.

Thus together these three articles highlight three important aspects of the field of emerging viral disease, these are by no means exclusive, but will serve to provide the reader with important examples to expand upon.