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.

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New tools to battle emerging viruses

Editorial overview

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Michael Buchmeier received his Ph.D. in virology and immunology from McMaster University in Hamilton, Ontario, Canada, and postdoctoral training at Scripps Clinic and Research Foundation. Until 2007 he was a Professor at The Scripps Research Institute. In 2008, Dr. Buchmeier joined the faculty of the University of California, Irvine, where he is associate director of the Pacific Southwest Center for Biodefense and Emerging Infectious Diseases, and a Professor in the Center for Virus Research and Center for Immunology.

Peter Kuhn

Peter Kuhn is an associate professor in the department of cell biology at the Scripps Research Institute in La Jolla, California. He also serves as life sciences director at the Scripps PARC Institute for Advanced Biomedical Sciences. Since joining Scripps Research in 2002, he has focused his research on developing novel approaches to therapeutic and diagnostic development in viral infectious diseases and cancer. His research has led to the structural elucidation and characterization of drug targets implicated in cancer and the structural description of the SARS Coronavirus proteome. Kuhn previously was an assistant professor at the Stanford Medical School and Stanford University's Synchrotron Radiation Laboratory, where he co-founded and co-lead the Joint Center for Structural Genomics within the Stanford Linear Accelerator Center at Stanford University in collaboration with Scripps Research. Kuhn holds a doctorate in physics from the Wadsworth Center at the New York State Department of Health and the State University of New York (SUNY). He also holds a master's degree in physics from SUNY and a bachelor's degree in physics from Julius Maximillians Universität in Würzburg, Germany.

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 the fatal infections of *Corvids* by West Nile to the inapparent or persistent 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.