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.
The isolation of Hendra and Nipah viruses from bats in the vicinity of the outbreaks, and the subsequent detection of coronaviruses similar to the severe acute respiratory syndrome coronavirus from various bat species, led to speculation that bats may be reservoirs for potentially zoonotic viruses. These events stimulated a global search for bat viruses that resulted in the detection and sometimes isolation of over 200 viruses from almost all viral families. These observations suggested that bats may harbour a substantial diversity of viruses rivalling or surpassing that in rodents. The book Bats and Viruses, Current Research and Future Trends, edited by Eugenia Corrales-Aguilar and Martin Schwemmle, aims to compile current (as of 2018 and some cases, late 2019) information on bat viruses, bat immunological responses to viral infection, the search for new bat viruses by metagenomics technologies and isolation techniques, and the establishment bat colonies to explore bat-virus interactions. Despite providing a vast compilation of useful information about this important topic, the book suffers from attempting to assemble “current” information in print form on a very rapidly evolving area of investigation. A search (bat virus) of PubMed revealed almost 300 articles published in the first 6 months of 2020, mostly focusing on severe acute respiratory syndrome coronavirus 2 and COVID-19.

Bats and Viruses begins with an introduction on the diversity of Chiroptera, the mammalian order to which bats belong, the array of viruses known to parasitise bats, and factors that are thought to contribute to the spillover of bat viruses to other animals, very occasionally leading to pandemics. The next 6 chapters catalogue bats belonging to specific viral families: Flaviviruses, Alphaviruses, influenza A-like viruses, Coronaviruses, Hantaviruses, and Polyomaviruses. In some cases, such as the insect-transmitted Flaviviruses and Alphaviruses, and the Hantaviruses, it is difficult to discern whether association of the viruses with bats is incidental or whether the bat hosts are reservoirs for the viruses and play a significant role in their transmission to other animals. The chapter on bat influenza A-like viruses provides an excellent overview about the recently discovered H17N10 and H18N11 viruses. It illustrates how bat viruses can differ significantly from their much better studied cousins hosted by birds, which have spilled into domestic animals and humans with often devastating consequences. The chapter on coronaviruses summarises information available until 2018. Although the authors could not have anticipated COVID-19, the field of pandemic coronaviruses has exploded this year and a reader wanting information about these viruses may be better served by the consulting the literature published in the past few months. The chapter on Polyomaviruses summarises the discovery of these viruses in bat species from several continents. Then, using this trove of genetic information, the authors provide evidence, albeit circumstantial, on the possibility of recombination within intermediate hosts and host switching. They speculate on the possibility of coinfection of Rhinolophus species with coronavirus and polyomaviruses promoting cross-species transmission and spillover of the coronaviruses.

The isolation of new bat viruses has proven difficult and the “hunting” for new bat viruses has depended to a large extent on the detection and sequencing of viral genomes. The authors provide valuable information on virus isolation techniques and susceptible cell lines as well as the challenges (and mitigating strategies) of using metagenomics for detecting bat viruses.

Field studies, especially on Hendra and Nipah viruses in their natural reservoir pteropid hosts, have provided information on virus-host interactions. However, the chapter on in vivo modes of infection points to the value of controlled experiments involving the infection of carefully maintained and standardised bat colonies. The author discusses the challenges for laboratories considering setting up bat colonies. In-vivo studies can provide valuable insights. However, in the opinion of this reader, studies on interactions of medically relevant viruses in bats that are not their natural hosts must be viewed with some caution. Bat-virus relationships are governed by millennia of co-evolution and are very likely specific to the bat species. Infection by a virus in a conveniently available species that is not its natural host may not tell the whole story. Some have addressed this problem by studying viruses in their captured autochthonous or closely related bat species.

Bats and Viruses also reviews the rapidly growing field of bat-virus interactions as they relate to host innate and adaptive responses. These responses likely underpin the unique evolutionary journey of bats as flying mammals that has led to unique adaptations and more balanced and benign bat-virus relationships than observed in other non-volant mammals. In the book’s final chapter the authors address the question “Are bats special?” and speculate how the need to detoxify by-products of heightened activity required for flight may have led to the evolution of increased threshold for detection of pathogen and damage-associate molecular patterns and a decrease in the threshold for protective responses once triggered. They conclude “Although all mammalian groups are special in their own way, in the context of virus host, bats are indeed special in different ways”.

Vikram Misra