

Bat-associated diseases



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Emerging infectious diseases pose a significant threat to human and animal health. Increasingly, emerging and re-emerging infectious diseases are of zoonotic origin and are derived from wildlife. Bats have been identified as an important reservoir of zoonotic viruses belonging to a range of different virus families including SARS-Coronavirus, Rabies virus, Hendra virus, Nipah virus, Marburg virus and Ebola virus.

Bats have been reported to harbour more zoonotic viruses per species than rodents and are now recognised as a significant source of zoonotic agents. The spill-over of virus from bats to humans, often through an intermediate, results in rare infections however, the consequences of infection are often fatal disease.

Bats are mammals belonging to the order *Chiroptera*, and are the only mammal that has true flight capabilities. Over 1200 species of bats exist worldwide, being found in all continents except for Antarctica. This species diversity is second only to rodents. Bats have unique and specialised capabilities including echolocation, hibernation/flight.

For many reasons bats are the perfect reservoir species for infectious diseases. They often live in large colonies or roosts, are able to travel considerable distances and they enjoy remarkable longevity for their body size. Human activities, such as deforestation, are increasing interactions between bats, humans, and livestock, thereby increasing the opportunities for zoonotic spill-over. For these reasons, bats present a significant potential source of emerging infectious diseases.

The discovery of Hendra virus in fruit bats in Australia and spill-overs resulting in deaths of both horses and humans began a global renaissance in virus discovery from bats. Research over the past

decade has resulted in the detection and isolation of many new viruses from bats, some of which have been associated with diseases of humans and animals. In Australia, apart from Hendra virus, Australian Bat Lyssavirus and Menangle virus are two examples of bat-borne viruses that have resulted in disease. In addition to these two viruses, many other viruses, particularly those of the *Paramyxoviridae* family have been isolated from Australian fruit bats, including Cedar virus, a seemingly non-pathogenic member of the *Henipavirus* genus.

Other virus families that have been found in bats include *Rhabdoviridae*, *Coronaviridae*, *Filoviridae*, *Paramyxoviridae*, *Togaviridae*, *Flaviviridae*, *Bunyaviridae*, *Reoviridae*, *Herpesviridae*, *Adenoviridae*, *Poxviridae*, *Retroviridae* and *Orthomyxoviridae*.

The articles in this issue highlight some of more serious of these viruses that have spilled over into humans. The recent outbreak of Ebola virus in west Africa demonstrates the potential of these bat viruses to result in significant human disease. One hypothesis of the origin of this outbreak was that a two-year-old boy who died in December 2013 in the village of Meliandou, Guéckédou Prefecture, Guinea, was the index case. It has been suggested that the boy became infected whilst playing around a tree that was the home of a large colony of Angolan free-tailed bats. The presence of virus in this bat colony was not able to be confirmed as the tree had been burnt and the bats moved on prior to any investigation. The single introduction of virus into humans resulted in an outbreak that lasted over two years and resulted in over 28 000 cases and 11 000 deaths.

A greater understanding the infectious diseases present in bats and the potential of these to cause disease in humans and animals is important to mitigate the risks. Additional work globally is needed to understand how to identify and characterise these novel infectious agents and potentially proactively develop vaccines and therapeutics that could be deployed if human disease was to eventuate.

Biography

Glenn Marsh is a Senior Research Scientist and Team Leader for Dangerous Pathogens in CSIRO. His research interests include development of animal models for high consequence viruses and using molecular tools to identify virulence determinants.