Coronaviruses in Australian bats

Fact sheet

Introductory statement

Coronaviruses appear to be widespread and endemic in global bat populations. Recent work suggests a similar situation exists in Australian bats. These viruses do not cause disease in their bat hosts but their potential for cross-species transmission and their ability to evolve relatively rapidly makes them of interest to those charged with the identification and management of emerging infectious diseases in Australia. Several recently emerging coronavirus diseases, which are not found in Australia, such as Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS), appear to have bats as their maintenance hosts.

Aetiology

Coronaviruses are single stranded, enveloped RNA viruses, 75-160 nm in diameter in the family Coronaviridae. All bat coronaviruses detected fall into the subfamily Coronavirinae, which is further divided into four genera Alpha-, Beta-, Gamma-, and Deltacoronavirus. SARS and MERS coronaviruses belong to the Betacoronavirus genus and all coronaviruses detected in bats are either alpha- or betacoronaviruses (Drexler et al. 2014).

Natural hosts

While coronaviruses infect a wide range of bird and mammal species, bats appear to be their natural hosts, with all coronaviruses recognised in other species having been derived from viruses residing in bats (Vijaykrishna et al. 2007). Coronaviruses have been isolated worldwide from a range of bat species. At least 109 bat species have been surveyed for coronaviruses. Viruses were found in 36 species with antibodies detected in a further seven species (Smith et al. 2011). Coronaviruses have been detected in 11 of the 18 families of bats, across Asia, Africa, Europe, North and South America and Australia (Drexler et al. 2014).
Occurrences in Australia

Two genotypes of alphacoronavirus and two genotypes of betacoronaviruses have been identified from seven species of Australian bats within five families, and in different regions of Australia. Anti-coronavirus antibodies have been identified from an additional 18 species (Table 1). Evidence of infection was widespread, from central Queensland (CQ), far-north Queensland (FNQ), south-east Queensland (SEQ), Northern Territory (NT) and Western Australia (WA), however many species and areas tested negative. No SARS-like betacoronaviruses were detected in Australia (Smith et al. 2016).

Prevalence was high (above 50%, and sometimes 100%) in insectivorous bat taxa (Miniopteridae and Vespertilionidae), including common species such as common bent-wing bats (Miniopterus schreibersii), little bent-wing bats (M. australis) and smaller horseshoe bats (Rhinolophus megaphyllus) (Smith et al. 2016).

There is further evidence of coronavirus exposure from bats in near northern neighbouring countries (e.g. Papua New Guinea, Malaysia, East Timor, Indonesia). See Smith et al. (2016) for more details. A survey undertaken on feral camels in Australia found no serological evidence of infection with MERS (Crameri et al. 2015).

Epidemiology

Coronaviruses appear to have a relatively narrow host range, but one bat species may be infected with multiple different coronaviruses. This potential mixing of viral species, along with their high mutation rate, permits significant genetic recombination allowing coronaviruses to change and evolve relatively rapidly (Smith et al. 2011). There is also evidence of mixing of viruses amongst bat hosts in Australia (Smith et al. 2016). Bat coronaviruses are usually detectable in faeces and oral swabs but not blood or serum, which indicates a tropism for the intestinal system of the host (Smith et al. 2016). Routes of transmission between bats, and from bats to other hosts, including humans, are yet to be confirmed, however both direct and environment contact have been proposed.

Clinical signs

Coronaviruses are generally endemic in bat populations and cause no clinical signs.

Pathology, laboratory diagnostic specimens and procedures

Coronaviruses elicit no discernible clinical pathology in bats. Samples of faeces, oral swabs or serum should be collected and submitted. PCR can be used to detect virus in faeces or oral swabs. Competition ELISA has been used to detect antibodies in serum. To date virus isolation has been unsuccessful (Smith et al. 2011).

Treatment, prevention and control

Treatment of infected bats is not required. Prevention of coronavirus infection is not possible as the virus is endemic in bat populations.
Table 1: PCR and antibody evidence of coronavirus infection in Australian bats, including geographic location of sampling [from Smith et al. (2016)]

<table>
<thead>
<tr>
<th>Suborder</th>
<th>Family</th>
<th>Genus</th>
<th>Species</th>
<th>Location¹</th>
<th>PCR positive²</th>
<th>Antibody positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pteropodiformes</td>
<td>Hipposideridae</td>
<td>Hipposideros</td>
<td>H. ater</td>
<td>FNQ, NT, WA</td>
<td>+</td>
<td>+</td>
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<td></td>
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<td></td>
<td></td>
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<td>+</td>
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<tr>
<td>Rhinoloceris</td>
<td></td>
<td>R. aurantia</td>
<td></td>
<td>NT</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Megadermatidae</td>
<td>Macroderma</td>
<td>M. gigas</td>
<td></td>
<td>NT, WA</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Pteropodidae</td>
<td>Pteropus</td>
<td>P. alecto</td>
<td></td>
<td>SEQ</td>
<td>+</td>
<td>+</td>
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<tr>
<td></td>
<td></td>
<td>P. conspicullatus</td>
<td></td>
<td>FNQ, N/T</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td></td>
<td>P. poliocephalus</td>
<td></td>
<td>SEQ</td>
<td>-</td>
<td>+</td>
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<td>R. megaphyllus</td>
<td></td>
<td>FNQ</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Vespertilioniformes</td>
<td>Emballonuridae</td>
<td>Taphozous</td>
<td>Taphozous spp.</td>
<td>WA</td>
<td>N/T</td>
<td>+</td>
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<tr>
<td>Miniopteridae</td>
<td>Miniopterus</td>
<td>M. australis</td>
<td></td>
<td>CQ, FNQ, SEQ, WA</td>
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<td>+</td>
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<tr>
<td></td>
<td></td>
<td>M. schreibersii</td>
<td></td>
<td>NT, SEQ</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Molossidae</td>
<td>Chaerophon</td>
<td>C. jobensis</td>
<td></td>
<td>WA</td>
<td>N/T</td>
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<tr>
<td>Mormopterus</td>
<td>M. beccarii</td>
<td></td>
<td></td>
<td>SEQ</td>
<td>-</td>
<td>+</td>
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<td>Vespertilionidae</td>
<td>Chalinolobus</td>
<td>Chalinolobus spp.</td>
<td></td>
<td>WA</td>
<td>N/T</td>
<td>+</td>
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<tr>
<td>Myotis</td>
<td>M. macropus</td>
<td></td>
<td></td>
<td>FNQ, SEQ</td>
<td>-</td>
<td>+</td>
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<td></td>
<td></td>
<td>+</td>
<td>N/T</td>
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<tr>
<td>Scotorepens</td>
<td>Scotorepens</td>
<td></td>
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<td>SEQ</td>
<td>N/T</td>
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<tr>
<td>Vespadelus</td>
<td>V. pumilus</td>
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<td>N/T</td>
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<td>V. troughtoni</td>
<td></td>
<td>FNQ</td>
<td>-</td>
<td>+</td>
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</tbody>
</table>

¹ Central Queensland (CQ), far-north Queensland (FNQ), south-east Queensland (SEQ), Northern Territory (NT) and Western Australia (WA)
² Positive (+), negative (-), not tested (N/T)

Surveillance and management

Wildlife disease surveillance in Australia is coordinated by the Wildlife Health Australia. The National Wildlife Health Information System (eWHIS) captures information from a variety of sources including Australian government agencies, zoo and wildlife parks, wildlife carers, universities and members of the public. Coordinators in each of Australia’s States and Territories report monthly on significant wildlife cases identified in their jurisdictions. There is no targeted surveillance program for bat coronaviruses and no records of bat coronavirus in eWHIS.

NOTE: access to information contained within the National Wildlife Health Information System dataset is by application. Please contact admin@wildlifehealthaustralia.com.au.
We encourage those with laboratory confirmed cases of this condition in native Australian or feral animals to submit this information to the national system for consideration for inclusion in the national database. Please contact us at admin@wildlifehealthaustralia.com.au.

Statistics

A survey of 2,195 Australasian bats, sampled between 1997 and 2009 from Queensland, the Northern Territory and Western Australia, as well as neighbouring countries, identified coronaviruses in seven species and detected anti-coronavirus antibodies from an additional 18 species (Table 1). The authors also identified a population of Australian bats that were infected with a coronavirus prevalence of at least 17% (Smith et al. 2016).

Research

Key questions include:

- What are the human health risks associated with Australian bat coronaviruses?
- Are these viruses endemic to Australian bats or is there potential for new viruses to be introduced via bats residing outside Australia?
- What is the potential for cross species infection with Australian bat coronaviruses?

To assist in answering these questions and gain a more complete epidemiological picture of coronavirus infections, where resources allow, Australian bats should continue to be tested with results entered into the national Wildlife Health Information System. Knowledge of the prevalence of infection and the range of bat species involved will also assist.

Human health implications

In other parts of the world, coronaviruses can cause a range of disease syndromes including respiratory and gastrointestinal disease in humans and gastrointestinal, neurological and hepatic disease in animals.

While SARS and MERS have caused serious disease in humans the coronaviruses isolated from Australian bats are not closely related to the causative agents of these diseases. No human health implications have been identified to date.

Conclusions

Coronaviruses appear to be widespread and endemic in the world’s bat populations. While relatively little work has been carried out on Australian bats, preliminary data indicates that a similar situation exists here. As humans continue to move into new areas it is likely that contact with novel coronaviruses will increase. The risk remains unknown.

Acknowledgements

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References and other information


To provide feedback on this fact sheet

Wildlife Health Australia would be very grateful for any feedback on this fact sheet. Please provide detailed comments or suggestions to admin@wildlifehealthaustralia.com.au. We would also like to hear from you if you have a particular area of expertise and would like to produce a fact sheet (or sheets) for the network (or update current sheets). A small amount of funding is available to facilitate this.

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