

Coronaviruses in Australian bats

Fact Sheet

November 2020

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 emerged human diseases, such as Severe Acute Respiratory Syndrome (SARS-CoV-1), Middle East Respiratory Syndrome (MERS-CoV) and COVID-19 (SARS-CoV-2), are caused by coronaviruses that appear to have bats as their original or natural 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. All coronaviruses detected in bats are either alpha- or betacoronaviruses (Drexler et al. 2014). SARS-CoV-1, MERS-CoV and SARS-CoV-2 belong to the betacoronavirus genus and this genus is of greatest interest for those assessing the zoonotic potential of coronaviruses.

Natural hosts

While coronaviruses infect a wide range of bird and mammal species, bats appear to be the natural hosts of many coronaviruses. There is evidence to suggest that all coronaviruses recognised in other species originally derived from bats (Vijaykrishna et al. 2007), although others suggest that alpha- and betacoronaviruses originated in bats and gamma- and deltacoronaviruses originate in birds (Wong et al. 2019).

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 globally with antibodies detected in a further seven species (Smith et al. 2011). Coronaviruses have been detected in at least 11 of the 18 families of bats, across Asia, Africa, Europe, North and South America and Australia (Drexler et al. 2014).

Occurrences in Australia

There have been no detections to date of SARS-CoV-1, MERS-CoV, SARS-CoV-2 or closely related viruses in Australian bats or other wildlife. Serological evidence of exposure to a coronavirus antigenically related to SARS-CoV-1 (“SARS-CoV-1-like”) has been found in various bat species (Smith et al 2016, Prada et al 2019, Boardman et al 2020).

A widespread study found two genotypes of alphacoronavirus and two genotypes of betacoronaviruses in seven species of Australian bats within five families, and in different regions of Australia. Anti-coronavirus antibodies were 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) (Smith et al. 2016).

Alphacoronaviruses were more widespread (by host species and by geographic spread) than betacoronaviruses in this study. No SARS-like betacoronaviruses were detected in Australia in this study. Viral genome and/or antibody 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*). No betacoronavirus genomes were detected in Australian *Rhinolophus* bats (a taxon of interest as SARS-CoV-1 is believed to have originated from this genus) but the presence of antibodies in this genus indicated previous exposure to, or infection with, alpha- or betacoronaviruses (Smith et al. 2016).

A study in SW Western Australia found a low level of antibodies to coronaviruses in a range of Australian microbats from family Vespertilionidae and Molossidae. Faecal PCR revealed a number of (mostly novel) alphacoronaviruses. No betacoronaviruses were detected by PCR (Prada et al. 2019).

Boardman et al. (2020) found serological evidence of exposure to a “SARS-CoV-1-like” coronavirus in grey-headed flying-foxes (*Pteropus poliocephalus*) in South Australia .

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-CoV (Cramer et al. 2015).

Table 1: PCR and antibody evidence of coronavirus infection in Australian bats, including geographic location of sampling [from Smith et al. (2016), Prada et al (2019) and Boardman et al. (2020)]. Only species with at least one positive result are shown. For full results refer to original sources.

Suborder	Family	Genus	Species	Location ¹	PCR positive ²	Antibody positive ²			
<i>Pteropodiformes</i>	<i>Hipposideridae</i>	<i>Hipposideros</i>	<i>H. ater</i>	FNQ	-	-			
				NT	-	+			
				WA	N/T	-			
			<i>Rhinonicteris</i>	<i>R. aurantia</i>	NT	+	-		
		<i>Megadermatidae</i>	<i>Macroderma</i>	<i>M. gigas</i>	NT	-	+		
	WA				N/T	+			
		<i>Pteropodidae</i>	<i>Pteropus</i>	<i>P. alecto</i>	SEQ	+	+		
					<i>P. conspicillatus</i>	FNQ	N/T	+	
						<i>P. poliocephalus</i>	SEQ	-	+
					SA		-	+	
			<i>P. scapulatus</i>	NT	N/T	+			
	<i>Rhinolophidae</i>	<i>Rhinolophus</i>	<i>R. megaphyllus</i>	FNQ	+	+			
				SEQ	-	+			
<i>Vespertilioniformes</i>	<i>Emballonuridae</i>	<i>Taphozous</i>	<i>Taphozous</i> spp.	WA	N/T	+			
	<i>Miniopteridae</i>	<i>Miniopterus</i>	<i>M. australis</i>	CQ	+	+			
				FNQ	+	+			
				SEQ	+	+			
				WA	N/T	+			
					<i>M. schreibersii</i>	NT	+	+	
			SEQ	+	+				
	<i>Molossidae</i>	<i>Chaerephon</i>	<i>C. jobensis</i>	WA	N/T	+			
				<i>Mormopterus</i>	<i>M. beccarii</i>	SEQ	-	+	
			<i>A. australis</i>	WA	+	+			
			<i>O. sp</i>	WA	+	-			
	<i>Vespertilionidae</i>	<i>Chalinolobus</i>	<i>Chalinolobus</i> spp.	WA	N/T	+			
				<i>C. gouldii</i>	WA	+	+		
				<i>C. morio</i>	WA	+	+		
				<i>Falsisterellus</i>	<i>F. mackensiei</i>	WA	+	-	
				<i>Myotis</i>	<i>M. macropus</i>	FNQ	-	+	
						SEQ	+	N/T	
				<i>Nyctophilus</i>	<i>N. geoffroyi</i>	<i>N. geoffroyi</i>	WA	+	-
							<i>N. gouldi</i>	WA	+
	<i>N. major</i>	WA	/T				+		
		<i>Scotorepens</i>	<i>Scotorepens</i> spp.	SEQ	N/T	+			
	<i>Vespadelus</i>		<i>V. baverstocki</i>	WA	+	-			
				<i>V. pumilus</i>	SEQ	+	N/T		
				<i>V. regulus</i>	WA	+	+		
				<i>V. troughtoni</i>	FNQ	-	+		

¹ Central Queensland (CQ), far-north Queensland (FNQ), Northern Territory (NT), south-east Queensland (SEQ), South Australia (SA) and Western Australia (WA)

² Positive (+), negative (-), not tested (N/T)

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 (Woo et al. 2007). 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. There is evidence for persistent infections of coronavirus in at least one Australian bat, *Myotis macropus* (Jeong et al. 2017; Smith 2017).

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 but it does not differentiate between host response to alpha- or betacoronaviruses.

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.

Research

Key questions include:

- Are there any human health risks associated with Australian bat coronaviruses?
- Are these viruses endemic to Australian bats and is there potential for new viruses to be introduced via bats residing outside Australia?
- Can coronaviruses that have spilled over and established in humans (e.g. SARS-CoV-2) be transmitted from humans to bats?
- What is the potential for cross-species infection with Australian bat coronaviruses?
- Do the known zoonotic coronaviruses (SARS-CoV-1, SARS-CoV-2 or MERS-CoV) occur in Australian bats?

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.

Surveillance and management

Wildlife Health Australia administers Australia's general wildlife health surveillance system, in partnership with government and non-government agencies. Wildlife health data is collected into a national database, the electronic Wildlife Health Information System (eWHIS). Information is reported by a variety of sources including government agencies, zoo based wildlife hospitals, sentinel veterinary clinics, universities, wildlife rehabilitators, and a range of other organisations and individuals. Targeted surveillance data is also collected by WHA. See the WHA website for more information <https://wildlifehealthaustralia.com.au/Our-Work/Surveillance> and <https://wildlifehealthaustralia.com.au/Our-Work/Surveillance/eWHIS-Wildlife-Health-Information-System>.

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).

A survey of 11 species of insectivorous bats in SW WA undertaken 2016-2018 examined 571 faecal samples and over 640 serum samples and found both molecular and serological evidence of coronaviruses (Prada et al. 2019).

A survey of 213 bent-winged bats (*Miniopterus orianae*) from different locations in SE Australia during 2015-2017 did not find evidence of coronavirus on molecular testing of oral swabs (Holz et al. 2018).

A survey of 301 grey-headed flying-foxes from SA found 31.6% had antibodies reactive to SARS-CoV-1 antigen (Boardman et al. 2020).

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-CoV-1, MERS-CoV and SARS-CoV-2 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, existing data indicates that a similar situation exists here. As humans continue to move into new geographic areas it is likely that contact with novel coronaviruses will increase. The risk remains unknown.

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Wildlife Health Australia recognises the Traditional Custodians of Country throughout Australia. We respectfully acknowledge Aboriginal and Torres Strait Islander peoples' continuing connection to land, sea, wildlife and community. We pay our respects to them and their cultures, and to their Elders past and present.

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