

# 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 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 <sup>1</sup>	PCR positive <sup>2</sup>	Antibody positive <sup>2</sup>
<i>Pteropodiformes</i>	<i>Hipposideridae</i>	<i>Hipposideros</i>	<i>H. ater</i>	FNQ	-	-
				NT	-	+
				WA	N/T	-
		<i>Rhinonictis</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>	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	-	+

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

<sup>2</sup> 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.

## 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. See the WHA website for more information:

[www.wildlifehealthaustralia.com.au/ProgramsProjects/eWHISWildlifeHealthInformationSystem.aspx#requests](http://www.wildlifehealthaustralia.com.au/ProgramsProjects/eWHISWildlifeHealthInformationSystem.aspx#requests).

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](mailto: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).

## 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.

## 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.

## Acknowledgements

We are extremely grateful to the many people who had input into this fact sheet and would specifically like to thank Drs Peter Holz, Craig Smith, Hume Field. Alison Peel and the agencies and organisations that provided expert knowledge, comment and external review. Without their ongoing support production of these fact sheets would not be possible.

Updated: 23 November 2020

## References and other information

Boardman WSJ, Baker ML, Boyd V, Crameri G, Peck GR, Reardon T, Smith IG, Carague CGB, Prowse TAA (2020) Serological evidence of exposure to a coronavirus antigenically related to Severe Acute Respiratory Syndrome virus (SARS-CoV-1) in the Grey-headed flying fox (*Pteropus poliocephalus*). *Transboundary and Emerging Diseases*

Crameri G, Durr PA, Barr J, Yu M, Graham K, Williams OJ, Kayali G, Smith D, Peiris M, Mackenzie JS (2015) Absence of MERS-CoV antibodies in feral camels in Australia: Implications for the pathogen's origin and spread. *One Health* **1**, 76-82.

Drexler JF, Corman VM, Drosten C (2014) Ecology, evolution and classification of bat coronaviruses in the aftermath of SARS. *Antiviral Research* **101**, 45-56.

Holz PH, Lumsden LF, Druce J, Legione AR, Vaz P, Devlin JM, Hufschmid J (2018) Virus survey in populations of two subspecies of bent-winged bats (*Miniopterus orianae bassanii* and *oceanensis*) in south-eastern Australia reveals a high prevalence of diverse herpesviruses. *PLoS ONE* **13**, e0197625.

Jeong J, Smith C, Peel A, Plowright R, Kerlin D, McBroom J, McCallum H (2017) Persistent infections support maintenance of a coronavirus in a population of Australian bats (*Myotis macropus*). *Epidemiology & Infection* **1-9**.

Prada D, Boyd V, Baker ML, O'Dea M, Jackson B (2019) Viral Diversity of Microbats within the South West Botanical Province of Western Australia. *Viruses* **11**, 1157.

Smith C (2017) Persistent or long-term coronavirus infection in Australian bats. *Microbiology Australia* **38**, 8-11.

Smith C, de Jong C, Meers J, Henning J, Wang L-F, Field H (2016) Coronavirus infection and diversity in bats in the Australasian region. *EcoHealth* **13**, 72-82.

Smith C, Field H, Wang L-F (2011) Bat coronaviruses. In 'Investigating the role of bats in emerging zoonoses: balancing ecology, conservation and public health interest.' (Eds SH Newman, H Field, J Epstein, C de Jong.) pp. 102-122. (Food and Agriculture Organization of the United Nations Rome, Italy).

Vijaykrishna D, Smith G, Zhang J, Peiris J, Chen H, Guan Y (2007) Evolutionary insights into the ecology of coronaviruses. *Journal of Virology* **81**, 4012-4020.

Wong AC, Li X, Lau SK, Woo PC (2019) Global epidemiology of bat coronaviruses. *Viruses* **11**, 174.

Woo PC, Wang M, Lau SK, Xu H, Poon RW, Guo R, Wong BH, Gao K, Tsoi H-w, Huang Y (2007) Comparative analysis of twelve genomes of three novel group 2c and group 2d coronaviruses reveals unique group and subgroup features. *Journal of Virology* **81**, 1574-1585.

## 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](mailto: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.

## Disclaimer

This fact sheet is managed by Wildlife Health Australia for information purposes only. Information contained in it is drawn from a variety of sources external to Wildlife Health Australia. Although reasonable care was taken in its preparation, Wildlife Health Australia does not guarantee or warrant the accuracy, reliability, completeness or currency of the information or its usefulness in achieving any purpose. It should not be relied on in place of professional veterinary or medical consultation. To the fullest extent permitted by law, Wildlife Health Australia will not be liable for any loss, damage, cost or expense incurred in or arising by reason of any person relying on information in this fact sheet. Persons should accordingly make and rely on their own assessments and enquiries to verify the accuracy of the information provided.



Find out more at [www.wildlifehealthaustralia.com.au](http://www.wildlifehealthaustralia.com.au)  
email [admin@wildlifehealthaustralia.com.au](mailto:admin@wildlifehealthaustralia.com.au)  
or call +61 2 9960 6333