

# Novel Coronavirus disease (COVID-19)

## Fact sheet

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### Preamble

This document is published as a **working draft** and will be updated periodically as new information becomes available. Please check the **WHA website** [www.wildlifehealthaustralia.com.au](http://www.wildlifehealthaustralia.com.au) for the current version.

### Introductory statement

Coronaviruses are the cause of recently emerged diseases which cause significant respiratory symptoms in humans, including Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS). Evidence suggests bats are the maintenance hosts for both SARS and MERS viruses. Neither of these viruses are found in Australia (see WHA fact sheet "Coronaviruses in Australian Bats"). Coronaviruses have been shown to have the potential for cross-species transmission and an ability to evolve relatively rapidly, which makes them of interest as potential emerging infectious diseases.

In December 2019 a novel coronavirus disease (initially termed 2019-nCoV, then officially named COVID-19) emerged in humans in Wuhan, China, and spread progressively through the human population.

By 10 March 2020, there were over 110,000 human cases of disease confirmed globally (over 80,000 in China), with over 4000 fatalities recorded. There were cases in over 100 countries globally, as well as international cruise ships (WHO 2020b). WHO declared 2019-nCoV a "Public Health Emergency of International Concern" in late January 2020 (WHO 2020c).

### Aetiology and possible origin

Coronaviruses are single stranded, enveloped RNA viruses, 75-160 nm in diameter in the family *Coronaviridae*. The subfamily *Coronavirinae* 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).

Coronaviruses are considered to be zoonotic (passed from animals to humans) (WHO 2020a). 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). Previous emerging Betacoronaviruses causing respiratory disease in humans (SARS, MERS) have been shown to have recently moved from a bat host, via an intermediate animal host, to humans.

The virus responsible for COVID-19 (now termed SARS-CoV-2) is also a Betacoronavirus and is presumed to have transferred to humans from an (as yet) unidentified animal host, likely from the live animal market in Wuhan. It has been reported that the merchants at the market sold poultry, bats, marmots, snakes, birds, frogs, hedgehogs, rabbits and other farm animals (Ji et al. 2020) as well as tiger frogs, pheasants and other animals (Li et al. 2020; ProMed 2020).

SARS-CoV-2 is closely related to a known bat coronavirus (96% genome homology) and is less closely related to SARS virus (~80% homology) (Lu et al. 2020; Zhou et al. 2020). A possible snake origin based on viral genetics, was theorised (Ji et al. 2020), but this was quickly refuted by other virologists (Lu et al. 2020; Robertson 2020; Zhou et al. 2020). Pangolins were also proposed as a possible host or intermediate host for virus transmission from bats to humans (Cyranoski 2020). Many experts consider bats to be the most plausible and probable original host of SARS-CoV-2.

Routes of transmission between bats, and from bats to other hosts, including humans, are yet to be confirmed for coronaviruses (Smith et al. 2016).

## Epidemiology

Although coronaviruses appear to have a relatively narrow host range, 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).

There is no clear evidence of how SARS-CoV-2 moved from bats into humans and whether an intermediate host species was involved in transmission of the emergent disease in humans, as was shown to be the case for both SARS (civets) and MERS (camels).

## Public health concerns

COVID-19 disease is primarily a concern for humans, where infection can cause symptoms ranging from mild to severe. See the WHO website ([www.who.int/emergencies/diseases/novel-coronavirus-2019](http://www.who.int/emergencies/diseases/novel-coronavirus-2019)) for recommendations for the public to minimise risks of transmission between people. There is also a section devoted to dispelling false information ([www.who.int/emergencies/diseases/novel-coronavirus-2019/advice-for-public/myth-busters](http://www.who.int/emergencies/diseases/novel-coronavirus-2019/advice-for-public/myth-busters)).

Human-to-human spread of COVID-19 is of major concern and was confirmed early in the outbreak. Initially, most of the human cases occurring outside China were directly imported as a result of international travel of infected people (generally during the incubation stage).

Humans are thought to be most contagious during the symptomatic phase of the infection, although there is evidence that non-symptomatic patients may also be infectious. Greatest levels of viral shedding in humans is probably associated with patients with more severe symptoms.

## Potential involvement of Australian animals

There are published studies of coronaviruses in Australian animals, with a focus on bats (see WHA fact sheet “Coronaviruses in Australian Bats”). Although betacoronaviruses have been found in a variety of Australian bat species, there is NO evidence of SARS or SARS-like, MERS or MERS-like, SARS-CoV-2 or SARS-CoV-2-like viruses in Australian wildlife (including bats). SARS-CoV-2 is not closely related to any known Australian bat coronaviruses and there is no suggestion that SARS-CoV-2 is present in Australian wildlife, although further surveillance and studies are recommended.

There is very little evidence that livestock or pets such as dogs or cats can be infected with SARS-CoV-2. In March 2020, a dog in Hong Kong tested positive to SARS-CoV-2 following close exposure to its owners who were sick with COVID-19. The real-time PCR test showed the presence of genetic material from the virus but the dog was not showing any clinical signs of disease (OIE 2020). Further studies are needed to understand if and how different animals could be affected by SARS-CoV-2. It remains extremely unlikely that domestic animals play any role in transmission of this virus and there is no evidence to support restrictions to movement or trade of companion animals (OIE 2020).

There is no evidence to suggest that any animals (livestock, pets or wildlife) in Australia might be a source of infection of SARS-CoV-2. Regardless, appropriate personal hygiene (e.g. washing hands) is always recommended before and after contact with animals, including wildlife (see [National Wildlife Biosecurity Guidelines](#)). There is no justification in taking measures against companion animals which may compromise their welfare (OIE 2020).

The risk of transmission of SARS-CoV-2 from an infected human back to a wildlife host in the Australian situation is considered, empirically, to be very low.

## Conclusion

SARS-CoV-2 has most likely moved from a natural bat host into humans, possibly via an unidentified intermediate animal host. There is no evidence of SARS-CoV-2 or similar virus in Australian wildlife. This fact sheet will be updated as new information becomes available.

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## To provide feedback on this fact sheet

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