

EVENT DESCRIPTIONS

From October 2016 to May 2017, an outbreak of swine acute diarrhea syndrome coronavirus (SADS-CoV) affected four pig farms in Guangdong province, China. Since that time, no cases of the disease were reported in Guangdong until it re-emerged in February 2019 (Zhou et al 2019) . Retrospective investigations suggest the disease has been present in swine herds in southern China since August of 2016 (Zhou 2018a).

Similar to other swine enteric coronaviruses, clinical signs include acute diarrhea and vomiting, and rapid mortality (within 2-6 days) in piglets less than 5 days of age. Infected sows suffer only mild diarrhea. The mortality rate can be very high, up to 90% in young piglets. Disease control measures include separation of sick sows and piglets from the rest of the herd (Zhou et al., 2018b) and vaccination with an inactivated SADS-CoV vaccine (Zhou et al. 2019).

After the outbreaks of SADS-CoV on pig farms, researchers conducted a retrospective investigation and found SADS-related CoVs (HKU2 strains) with 96–98% sequence identity in 9.8% (58 out of 591) of anal swabs collected from bats (predominantly horseshoe bats: *Rhinolophus* spp.) in the same vicinity (Zhou et al., 2018b).



Figure 1 : Map showing location of Guangdong province

TRIAGE

This event was considered in scope for the Community for Emerging and Zoonotic Diseases (CEZD), and was primarily rated relevant or highly relevant by the community after its initial public report in 2018. Upon publication of research studies that demonstrated the capability of SADS-CoV to replicate in human cells, a community discussion was held to discuss the zoonotic potential of this pathogen. This is a novel virus that has so far only been reported in China. Very little is currently known about the virus. Extrapolation can be made from the behaviour of related viruses, but this should be interpreted with caution. An update of the risk profile is provided to include new outbreak information from 2019, review the zoonotic implications of new research in 2020 and identify potential concerns, data gaps, and pathways/scenarios that may warrant further consideration.

ETIOLOGY

SADS-CoV (a.k.a. swine enteric alpha coronavirus (SeACoV) and porcine enteric alphacoronavirus (PEAV)) is a novel alphacoronavirus (enveloped, RNA) that is very closely related to HKU2 strains found in bats. Based on phylogenetic analysis (Gong et al., 2017) (Zhou et al., 2019), other closely related alphacoronaviruses include various bat strains, human coronavirus 229E (a cause of the common cold), and porcine epidemic diarrhea virus (PEDV). Other, slightly more distant, alphacoronaviruses include porcine respiratory coronavirus and transmissible gastroenteritis virus. More distantly related betacoronaviruses include SARS-CoV, SARS-CoV-2 and MERS-CoV (see Figure 2). The re-emerged SADS-CoV showed high sequence homology and phylogeny with all existing SADS-CoV isolates to date (Zhou, et al. 2019).

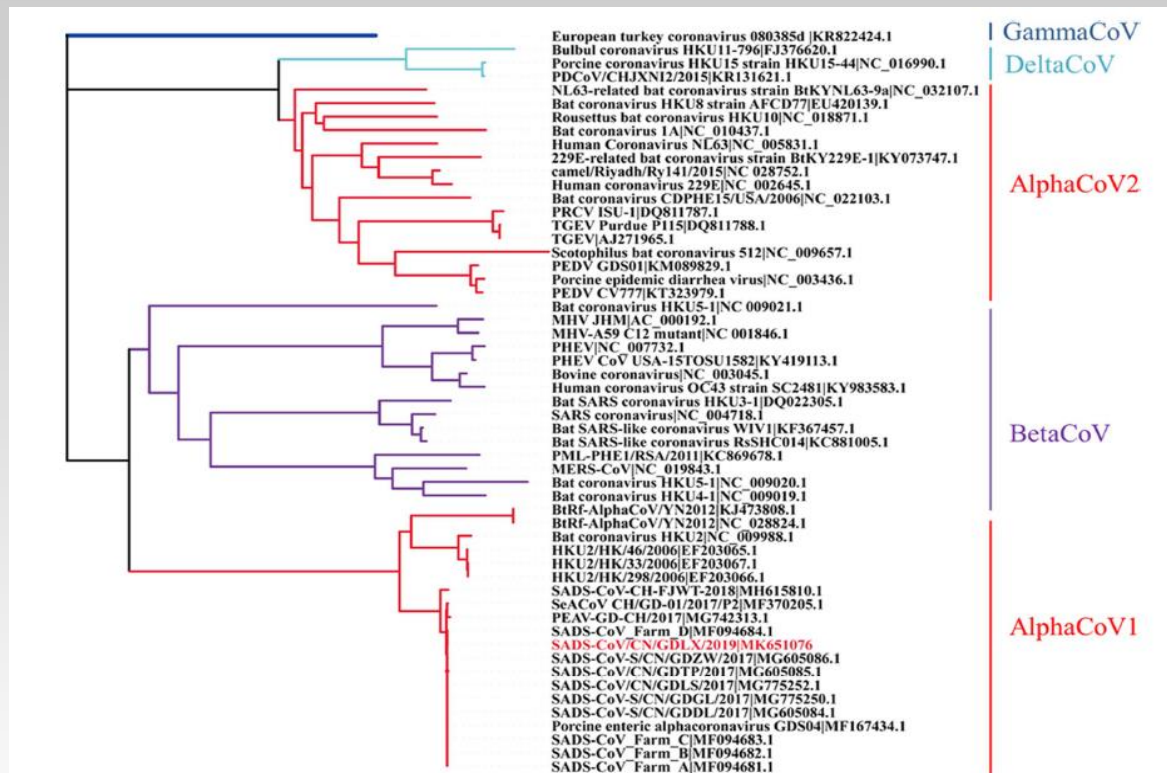


Figure 2 : Phylogenetic analysis of the S gene of SADS-CoV and reference coronavirus species (Zhou et al, 2019)

TRANSMISSION

Based on their research and phylogenetic analysis, Zhou et al. (2018b) could not say conclusively whether the virus was introduced into pigs from bats just once or multiple times. Either way, the mortality rate indicates that once on a farm, it is capable of spreading between pigs for at least a short period of time.

The related virus, PEDV, is highly transmissible with a very low infectious dose. It can remain stable in the environment for several weeks, especially at low environmental temperatures (Scott et al., 2016).

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Emerging Disease Risk Profile

Swine Acute Diarrhea Syndrome Coronavirus (SADS-CoV) in China

PATHWAYS OF INTRODUCTION TO CANADA

This novel virus has not yet been reported in other regions of the world, though now that it has been identified, further surveillance is warranted. Potential pathways of spread between countries therefore remain unknown; however, they may resemble those associated with similar viruses, such as PEDV.

A root cause investigation concluded that the most likely pathway for introduction of PEDV to the USA was the flexible containers used to transport bulk feed (Scott et al., 2016). These containers could become contaminated in the source country due to exposure to contaminated contents, wild birds, flood water, or other sources (Scott et al., 2016).

The *Feeds Regulations* in Canada do not specifically restrict the use/reuse of the packaging material used for feed (Justice Department of Canada, 1983). There is a restriction found in the *Health of Animals Regulations* requiring procedures to prevent cross-contamination, but this is related to ruminant feeds and prohibited material (i.e., generally protein that originated from a mammal other than a porcine or equine) (Justice Department of Canada, 2018).

Canada does not recognize China as officially free of any swine diseases, so the importation of live swine, germplasm, or raw or inedible porcine-origin commodities is not permitted. In addition, China's swine slaughter system has not been approved, so neither raw nor processed pork is eligible for import. These commodities would also not be accepted in-transit through the USA.

Processed (heat treated) pet chews containing porcine ingredients are currently allowed to be imported from CFIA-approved manufacturing facilities in China. However, the practice of repurposing pet food or treats into swine rations is prohibited in Canada (Canadian Food Inspection Agency, 2012).

Scott et al. (2016) considered the introduction of PEDV to the USA via human travel, but it was considered unlikely due to the existence of travel biosecurity measures and biosecurity practices on commercial swine premises. Introduction via carriage in the human nasal passage was considered a plausible scenario. Mechanical transmission via migratory birds was also considered, but was determined to be unlikely due to the long travel routes taken by birds from Asia (United States Department of Agriculture, 2015).

Bioterrorism and illegal importation practices are also potential pathways.

SPECIES SUSCEPTIBILITY

It is unknown if species other than swine are susceptible to SADS-CoV. There is currently no evidence of infection in humans. Farm workers who had close contact with sick pigs were tested for antibodies to the virus, but no positives were found out of 35 workers tested (Zhou et al., 2018b). However, this is very preliminary information on a novel virus. In addition, coronaviruses have long genomes that display high plasticity, resulting in a propensity for host jumps (Forni et al., 2017).

Recent laboratory studies indicate that SADS-CoV can replicate effectively in monkey, pig, cat and primate (including human) cell lines, however, the virus does not use the human coronavirus receptors for docking and entry (Edwards et al, 2020). Porcine Epidemic Diarrhea Virus, which has been circulating in pig populations for many years, also demonstrates the ability to replicate in human cells in-vitro, with no evidence of transmission of this virus into human populations. (Liu et al, 2015)



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DETECTION AND SPREAD

The ability of SADS-CoV to rapidly spread between farms is unknown; however, when PEDV entered the USA, it spread to more than 200 herds in thirteen states in less than 2 months. Once in North America, there are several potential mechanisms of spread for PEDV that may also be relevant for SADS-CoV, such as: trucks, feed, animals, manure, and other fomites (Scott et al., 2016). Nine months after it was discovered in the USA, PEDV was detected in Canada. The weight of evidence gathered during the outbreak investigation suggested that the outbreak was associated with swine feed containing a contaminated lot of spray-dried porcine plasma (Aubry et al., 2017).

Molecular assays for detection of SADS-CoV genomic material and serological assays for detection of antibodies to SADS-CoV have been developed (Zhou et al., 2018b; Zhou et al., 2018c). In Canada, the National Centres for Animal Disease is developing tools for molecular detection (RT-PCR) of SADS-CoV, including the development of a synthetic positive control to evaluate the PCR. SADS-CoV is not a listed disease for the OIE, CFIA or provinces. However, PEDV is notifiable or reportable in several provinces.

KNOWLEDGE GAPS AND PRIMARY CONCERNS

This is a novel virus associated with a high level of uncertainty. Relevant knowledge gaps include:

- Coronavirus diversity and distribution in bats, and in particular, the susceptibility of bat species in North America to SADS-CoV
- SADS-CoV prevalence in pigs in China and globally
- Infectivity between pigs, and ability of the virus to maintain transmission in the pig population in the absence of bats
- Survival in the environment of SADS-CoV
- Susceptibility of humans or other species to SADS-CoV
- Excretion of SADS-CoV from infected pig feces, droplets from the respiratory system and materials from the reproductive system.
- Persistence of SADS-CoV in pig material: blood, offal, pork etc.

Primary concerns associated with this event include:

- That this area of China appears to be a hotspot for emerging diseases, such as SARS
- The potential for SADS-CoV to enter the Canadian swine population via a pathway similar to PEDV, and result in economic impacts to the swine industry
- The potential for as yet undiscovered human health impacts, or mutation of the virus to develop pathogenicity in humans



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Zhou L, Sun Y, Wu J-l, Mai K-j, Chen G-h, Wu Z-x,[...] Ma J-y, 2018c. Development of a TaqMan-based real-time RT-PCR assay for the detection of SADS-CoV associated with severe diarrhea disease in pigs. *Journal of Virological Methods* 255: 66-70.

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