

# 2<sup>ND</sup> CALL OF THE FAO-OIE ADVISORY GROUP ON SARS CoV-2 EVOLUTION IN ANIMALS

20<sup>th</sup> January 2021

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## Agenda

1. Latest findings, knowledge gaps, and priorities in relation to SARS-CoV-2 viral evolution in animals
2. Options to collate and synthesize a list of mutations observed in SARS-CoV-2 in animals

## Meeting notes

### 1. Latest findings in relation to SARS-CoV-2 viral evolution in animals

The Group started the meeting by discussing the findings of a recent study done by one of the Group members which indicated that viral neutralizing antibodies to SARS-CoV-2 had been detected in bats and pangolins in Thailand. 4 out of 100 bats were PCR positive to SARS-CoV-2, while 1 out of the 10 confiscated pangolins had SARS-CoV-2 neutralizing antibodies. Whole genome sequencing indicated that the virus found was 92% identical to SARS-CoV-2 genome, with some differences at the level of the spike protein. These findings indicate that pangolins are susceptible to SARS-CoV-2 infection, in addition to SARS-CoV-1 infection that had been previously demonstrated, although not yet published.

A discussion followed concerning an article published [in Nature in November 2020](#). The article in question describes the finding of viruses closely related to SARS-CoV-2 in archived horseshoe bat sera and droppings from Japan and Cambodia. Although the viruses had not been fully sequenced at the time of the writing, the finding confirms that viruses closely related to SARS-CoV-2 are relatively common in *Rhinolophus* bats, and in bats found outside China. **The Group reaffirmed the importance of testing archived sera of species known or suspected to be susceptible to SARS-CoV-2 infection, especially in Southeast Asia, as well as sampling wild animals confiscated from illegal trade operations.**

While on the human health side numerous SARS-CoV-2 variants of concern have been identified, no animal variant with changing antigenicity, or increasing transmissibility and pathogenicity has been identified since the “mink variants”. At the moment, it appears that Cluster 5 viruses have died out and that mink isolates do not grow in human cells. However, it is not yet clear what would be the result of animal infection with either of the human variants of concern. **Up to now, any virus detected in companion animals (except for mink) has been virtually identical to those found in humans.** The Group affirmed that it should be studied how many species of mink there are, how many production types, and how do those factors affect susceptibility. There is active and/or passive surveillance data from mink farms in North America, Europe and Russia but a dearth of information from other areas with significant fur farming industries.

It was noted that there may be forthcoming sequences from [gorillas](#).

The Group briefly mentioned an article published [in December in Emerging Infectious Diseases](#) related to the susceptibility of pigs to infection with SARS-CoV-2, to say that the low level of viral replication shown by some individuals when infected under experimental conditions does not translate into species susceptibility on the field. Readers should be careful in extrapolating findings of experimental susceptibility to field susceptibility when experiments are not done in an ecologically relevant way.

The group noted that one more susceptible species had been found through experimental infection – [White-tailed deer](#) (*Odocoileus virginianus*), " a species in which ACE2 is similar to that of humans. This is the first ruminant found to be susceptible to infection with SARS-CoV-2 (cattle and small ruminants are not susceptible), and these experimentally infected deer transmitted the virus to indirect -contact non-infected fawn. The group remarked that SARS-CoV-2 may jump the species barrier into domesticated animals, but the significance of such an event depends on the pathogenicity in that species and/or transmissibility to humans.

The Group observed that it would be interesting to know whether there is information on the underlying viral populations at the sub-consensus level in minks, and then on the intra-host and intra-farm diversity and the size of transmission bottlenecks. Based on the variants emerging in minks, it could be suggested that the transmission bottleneck is narrow, as only specific virus populations seem to disseminate between individuals and farms.

Finally, the Group raised two questions related to animal surveillance. **While passive surveillance of animal populations would be enough for now to detect eventual onwards transmission and establishment of host pools, with the exception of mink, racoon dogs and other fur producing species, the case of wildlife is different. The Group defended that it was crucial that a strategy was implemented to sample wild animals held in confiscation centres. The latter would clarify questions related to SARS-CoV-2 persistence in wildlife and viral evolution.**

## **2. Options to collate and synthesize a list of mutations observed in SARS-CoV-2 in animals**

The OIE will question its network of Laboratory Focal Points about which laboratories are doing genetic sequencing and antigenic characterization of SARS-CoV-2 animal isolates in order to promote better resource sharing and lessen duplication of work.

One of the members of the Group will start a registry of the SARS-CoV-2 mutations found in animals. This table will be regularly updated by the Group.

The next call of the Advisory Group shall take place on the 12<sup>th</sup> March.