

5TH CALL OF THE FAO-OIE ADVISORY GROUP ON SARS CoV-2 EVOLUTION IN ANIMALS

1st September 2021

Participants: Ann Cullinane (Chair, IEC, Ireland), Isabella Monne, Francesco Bonafante and Luca Tassoni (IZSve, Italy), Malik Peiris (HKU), Nicola Lewis (RVC, UK), OIE Preparedness & Resilience Department.

Agenda

1. Latest findings in relation to SARS-CoV-2 viral evolution in animals
2. Advances in the inventory of priority mutations to be tracked in SARS-CoV2 infections in animals

Meeting notes

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

The meeting started with a discussion on the [detection](#) of natural infection with SARS-CoV-2 in white-tailed deer. A recent [pre-print](#) describing vertical transmission of infection with SARS-CoV-2 in pregnant white-tailed deer was also discussed. The Advisory Group was concerned by the fact that white-tailed deer populations do not show clinical signs of infection and seem able to spread the virus to other animals in natural settings. Considering the frequent proximity of humans to deer populations through hunting, visits to parks and zoos, etc., it was deemed a priority to look for more evidence of SARS-CoV-2 infection in deer populations globally (agent detection in addition to serological surveillance), as well as to investigate SARS-CoV-2 evolution in deer hosts and its potential spill-back into human populations. The Advisory Group will issue a statement recommending surveillance of deer populations using existing mechanisms and established wildlife conservation groups.

The discussion advanced to the topic of vaccination of animal populations against SARS-CoV-2. The Advisory Group showed interest in seeking data from countries that are vaccinating farmed mink populations and wild/kept endangered species to learn more about post-vaccination surveillance.

Finally, a new [pre-print](#) covering surveillance of wastewater in New York was discussed. This paper sparked the group's interest since new lineages never described before and which contain mutations rarely observed in clinical samples were found in the wastewater. This type of surveillance is relevant not only for inference of disease prevalence in a region, but also to track viral evolution.

2. Advances in the inventory of priority mutations to be tracked in SARS-CoV2 infections in animals

IZSve informed the group that the systematic review mentioned during the previous call had been completed. IZSve will need assistance from the rest of the group to screen all the papers that were selected in the systematic review.

The inventory was updated since the last discussion. All new sequences were downloaded, including the entire genome and not just the spike protein. Almost 1000 mutations against the original Wuhan sequence were identified and characterized. Finding differences in animal sequences is tricky in terms of interpretations since these are mostly spillover except for minks. A discussion is ongoing with colleagues from the University of Glasgow Centre for Virus Research about how to evaluate evolutionary convergence and to identify mutations that are meaningful for animals.

The date of next meeting of the Advisory Group is yet to be determined.