

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

10<sup>th</sup> December 2020

**Participants:** Ann Cullinane (Chair, IEC, Ireland), Bart Haagmans (Erasmus MC, Netherlands), Daniel Haydon (Glasgow University, UK), Frank Konings (WHO), Isabella Monne and Francesco Bonfante (IZSVE, Italy), Linfa Wang (Duke-NUS, Singapore), Leo Poon (HKU, Hong Kong), Nicola Lewis (RVC, UK), Cristian de Battisti and Sophie VonDobschuetz (FAO), OIE Preparedness & Resilience Department.

## Agenda

1. Opening and short introductions
2. Advisory Group's take on the Terms of Reference and direction of the group
3. Latest findings in relation to SARS-CoV-2 viral evolution in animals
4. Discussion on knowledge gaps and priority research areas in relation to SARS-CoV-2 viral evolution

## Meeting notes

### 1. Opening and short introductions

The meeting was opened by Keith Hamilton, Head of the OIE Preparedness and Resilience Department. Keith noted the joint condition of this group, that shall operate as a joint Advisory Group to FAO and OIE, and highlighted the recent events related to SARS-CoV-2 mutations found in mink populations which recently raised public health concerns. Keith noted that this group will not duplicate the work of WHO's viral evolution group but rather work in synergy with it. Sophie VonDobschuetz and Cristian de Battisti from FAO also welcomed the participants and emphasized the importance of having a joint mechanism that can be activated when the need arises, and which can advise WHO on matters of viral evolution in animals. Ann Cullinane led the group through a round-the-screen introduction.

### 2. Advisory Group's take on the Terms of Reference and direction of the group

The group revised the TOR and adapted them as it seemed fit. The revised TOR are as follows:

- 1- Advise FAO and OIE on risks related to the evolution of SARS-CoV-2 (through mutation or recombination) in animal populations, specifically:
  - a. List knowledge gaps and priority research areas in relation to SARS-CoV-2 viral evolution, thereby contributing to the R&D Blueprint
  - b. Monitor, review, assess the latest information in relation to SARS-CoV-2 viral evolution in all animals, focusing on animal infection resulting from human-to-animal transmission and considering both spillover events and long term transmission and establishment of viral circulation.
  - c. Collate and synthesize a list of mutations observed in SARS-CoV-2 in animals.
- 2- Liaise with the WHO viral evolution group

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

- Work on a review of fresh and archived sera samples is being done by a member of the group to have a better picture of the range of susceptible species and their level of susceptibility. A surrogate virus neutralization assay that is not species-specific is being used for this purpose. This is a long-term work that will take some time to come to fruition.

- Another member of the group is doing numerous plaque reduction neutralization tests (PRNT) for cat and dog samples, finding very good seroconversion for both species.
- Studies are ongoing in the Netherlands focusing on SARS-CoV-2 mutations in mink populations have not yet arrived at any conclusions on correlation between specific sets of mutations and a consistent change to the behaviour of the virus.
- Results from Danish studies that reported increased antigenicity of SARS-CoV-2 as a result of the “Cluster 5” mutation are being replicated for confirmation by laboratories in a number of countries.
- At this point there is no evidence that the reported mutations could affect human vaccine efficacy.
- Studies that have looked at viruses from cats infected with SARS-CoV-2 have not found cat-associated mutations to the SARS-CoV-2 genome.

#### **4. Discussion on knowledge gaps and priority research areas in relation to SARS-CoV-2 viral evolution**

- The members of the Advisory Group agree that future work focusing on the implication of SARS-CoV-2 mutations should assess their capacity to increase the antigenicity, transmissibility, and pathogenicity of the virus.
- While performing molecular surveillance studies looking for recombination, it is recommended to do whole genome sequencing rather than focusing only on the spike protein of the virus. On a similar note, it is recommended that researchers do not solely consider the ACE2 receptor when evaluating susceptibility.
- While hamsters and mink are good animal models for laboratory studies, the species targeted for active surveillance should be those that are known to be susceptible and have regular or close contact with humans.
- When discussing the mapping of mink populations that is being done by FAO and OIE, experts asked why racoon dogs are the second in the priority line and suggested that pangolins and civets, which are susceptible, are mapped too.
- The members of the Advisory Group recommend that adequate expertise is used in structuring national/regional active surveillance in animal populations to avoid waste of resources and time. The concern at this point is that the virus is transmitted to an animal host that does not present clinical signs, but which allows for onwards transmission and viral evolution within its population. This scenario could bring us yet another new zoonotic coronavirus a few years from now.
- In general, there are many knowledge gaps about the risk of viral evolution of SARS-CoV-2 in different animals and about the implications of different mutations for viral characteristics.

The next call of the Advisory Group shall take place on a date to be determined in January.