

3RD CALL OF THE FAO-OIE ADVISORY GROUP ON SARS CoV-2 EVOLUTION IN ANIMALS

12th March 2021

Participants: Ann Cullinane (Chair, IEC, Ireland), Bart Haagmans (Erasmus MC, Netherlands), Isabella Monne, Luca Tassoni and Francesco Bonfante (IZSVe, Italy), Linfa Wang (Duke-NUS, Singapore), Leo Poon (HKU), Nicola Lewis (RVC, UK), Cristian de Battisti, Junxia Song and Ihab El Masry (FAO), OIE Preparedness & Resilience Department.

Agenda

1. Latest findings in relation to SARS-CoV-2 viral evolution in animals
2. Progress in collating a list of SARS-CoV-2 animal variants

Meeting notes

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

The meeting started with a discussion on mink farming and the associated risk pathways for introduction of SARS-CoV-2 to farmed mink populations. It was noted that, at this point, it is not possible to distinguish seropositivity due to a past infection and presence of immunity from seropositivity from a current infection, which complicates surveillance at farm-level. It was also noted that it is not clear yet how the virus was transmitted between farms in the Netherlands, despite several hypothesis having been investigated. The Group observed that there has not been much discussion around mink feeding and that there are places where mink are fed leftover raw meat from nearby slaughterhouses, which could pose a risk of SARS-CoV-2 transmission due to surface contamination of the meat by infected operators. A parallel was made with past influenza outbreaks detected in mink farms that were caused by feeding raw pork to mink that was contaminated with influenza viruses (<https://orbit.dtu.dk/en/publications/consequences-of-outbreaks-of-influenza-a-virus-in-farmed-mink-neo>). **The Group will issue a statement regarding the risk of using raw meat to feed farmed animal populations.**

2. Progress in collating a list of SARS-CoV-2 animal variants

Luca Tassoni and Isabella Monne presented the Group the first effort in the collation of a list of variants of interest. There are over 900 sequences from animals, of which the overwhelming majority are from infected mink. So far, the work has been focused on mink and cat sequences due to their availability and to the higher susceptibility of these species. Mutations of interest were identified according to criteria such as frequency of the mutation, geographical spread of the mutation, persistence of the mutation and its potential to be transmitted from animals to humans.