

8TH CALL OF THE FAO-OIE ADVISORY GROUP ON SARS CoV-2 EVOLUTION IN ANIMALS

2nd March 2022

Participants: Ann Cullinane (Chair, IEC, Ireland), Bart Haagmans (Erasmus MC, The Netherlands), Evelyne Picard-Meyer (ANSES), John Dennehy (Queens College), John Korslund (USDA APHIS), Leo Poon and Malik Peiris (HKU), Linfa Wang (Duke-NUS, Singapore), Marc Johnson (University of Missouri), Marine Wasniewski (ANSES), Nicola Lewis (RVC, UK), Richard Orton (Glasgow University, UK), Virginie Lattard (VetAgroSup), Vivek Kapur (Penn State University, USA), Stephane de la Rocque (WHO), OIE Preparedness & Resilience and Science Departments

Agenda

1. Findings in white-tailed deer (Vivek Kapur, Penn State University)
2. Update on hamsters (Malik Peiris or Leo Poon, HKU, and Richard Orton, Glasgow University)
3. SARS-CoV-2 sequences in wastewater (Marc Johnson, University of Missouri, and John Dennehy, Queens College and The Graduate Center of CUNY)
4. Surveillance in urban rodents and wastewater (Marine Wasniewski (ANSES), Evelyne Picard-Meyer (ANSES), Virginie Lattard (VetAgroSup))
5. Early observations in mink post-vaccination monitoring (John Korslund, USDA APHIS)

Meeting notes

1. Findings in white-tailed deer

The meeting started with a follow-up on the discussion from the previous call regarding findings in white-tailed deer. There seem to be a few possibilities for the source of the infection in white-tailed deer populations: fomites (masks, food, tissues, etc.) left by humans; contaminated environment, including wastewater; intermediary host; or direct transmission from humans. These hypotheses are in decreasing order of probability. Since the previous meeting, two important studies have been made available through pre-prints: a serological screen in wild ruminants, including fallow deer, red deer, roe deer, mouflon and wisent in Germany which did not find any evidence of SARS-CoV-2 infection in 2021/22 ([Wernike et al, 2022](#)), and a study from Canada ([Pickering et al, 2022](#)) which found some evidence supporting long-term adaptation of SARS-CoV-2 in deer populations in Ontario and a potential case of deer-to-human transmission. The group reiterated that deer and other susceptible animals should continue to be monitored, including through active surveillance, in order to anticipate any negative consequences of viral evolution in susceptible animal populations.

2. Update on hamsters

The possibility to do further work on the case of infected hamsters in Hong Kong is somewhat limited since all involved hamsters have been culled and the relevant areas have been sanitized. Enquiries into the origin of the hamster batches for upstream epidemiological investigation have proven unfruitful.

With the information currently available it was possible to determine that 3 or 4 independent events of hamster-to-human transmission of the Delta variant with onwards human-to-human transmission have occurred. After sequence analysis, it appears that the introduction of SARS-CoV-2 into the hamster population occurred around September 2022. Interestingly, all the isolated sequences (human and hamster) had the D427G mutation in the spike protein, which is rare otherwise. Given the current Omicron

outbreak in Honk Kong, it has not been possible to determine if the pet shop/hamster outbreak was an isolated event. In any case, more than 100 human infections have resulted from this event

3. SARS-CoV-2 sequences in wastewater

The researchers responsible for a recent Nature article called *Tracking cryptic SARS-CoV-2 lineages detected in NYC wastewater* ([Smyth et al, 2022](#)) joined the call to discuss their findings with the Advisory Group. The research group collected wastewater from 14 New York City wastewater treatment plants (covering 8.5 million people) between January and June 2021 and proceeded to sequencing all SARS-CoV-2 found in the water and focusing their analysis on N terminal domain and receptor binding domain of the spike protein of the virus. Surprisingly, 2% of all sequences in some sewersheds belonged to rats (Mammalian 12S rRNA sequence). It was found that the frequency of particular sequences that had not been detected elsewhere fluctuated with time in different locations that were sampled. Some mutations that are rare in humans are frequently seen in wastewater samples, including Q493K and Q498H/Y which, based on previous research, has been associated with adaptation to mice. It was also suggested that the unusual mutations could be derived from Alpha or pre-Alpha lineages. Although the researchers are open to considering an animal origin for the cryptic sequences, more specifically a rodent origin, they do not discard the hypothesis of evolution of these sequences in an immunocompromised population. Incidentally, the rats living in the sampling locations did not present antibodies against SARS-CoV-2, although SARS-CoV-2 was present in their feces – possibly from wastewater consumption. More studies/more samples from various locations around the globe are needed to understand if this phenomenon relates to extreme convergent evolution or is it relates to viral adaptation to a rodent host.

4. Surveillance in urban rodents and wastewater

A team of French researchers joined the call to present an ongoing project for monitoring infection with SARS-CoV-2 and its variants in urban rodent populations. The project is still underway and includes field and laboratory work. The laboratory work covers *in vivo* infection of different rodent species with SARS-CoV-2 and its variants – it was shown that mice infected with the Beta variant could infect naïve contact mice and that the contact mice that were infected could transmit the virus to a second pool of naïve mice. On the field, researchers are assessing rodent contamination close to wastewater and the presence of SARS-CoV-2 in wastewater. Rodents will be trapped in four/five sewers of French cities with high population density. Thus far, only the first location (Besançon) has been covered – although SARS-CoV-2 could be detected in all samples of wastewater, viral RNA could not be found in nasal swabs and lung samples. The research team will share further results once they become available.

5. Early observations in mink post-vaccination monitoring

The group was briefed on the use of a SARS-CoV-2 vaccine in farmed mink in the USA using anecdotal information. The Zoetis vaccine has been given emergency permission for use in mink based on safety data. It is a two-dose vaccine, the first inoculation done after weaning and the second one 3 weeks after. It is estimated that 90% of the US mink herds have been given the vaccine. However, since there is no mandate for post-vaccination monitoring at national level, the data is scattered and state-based. Some states require mandatory vaccination and others do not. Overall, no clinical illness has been reported to state veterinarians after vaccination. Still, subclinical or asymptomatic infections cannot be ruled out. There is not yet data on vaccine efficacy against Delta and Omicron variants. Once the Zoetis vaccine obtains full licensure, efficacy data will have to be provided.

Immediate actions

- Assist wastewater group in finding collaborators to provide samples from different countries.
- Group to meet often and support active review and analysis of sequences of viruses isolated from animals.

The next meeting of the Advisory Group will take place on a date to be determined in April.