

6TH CALL OF THE FAO-OIE ADVISORY GROUP ON SARS CoV-2 EVOLUTION IN ANIMALS

2nd December 2021

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Agenda

1. Animal reservoir and risk of emergence of variants
2. Monitoring for SARS-CoV-2 in animals
3. Collection and analysis of sequences from in animals
4. Research

Meeting notes

1. Animal reservoir and risk of emergence of variants

The meeting started with a discussion on the possible sources for emergence of the Omicron variant of concern (VOC). The Omicron VOC shares mutations with the other variants isolated from humans and animals. However, many of its numerous mutations are novel. The group agreed that, at this point, there is not enough evidence to pinpoint a single route of emergence. Different possibilities (not mutually exclusive) were discussed, such as mutation or recombination during persistent infection (e.g., in an immunocompromised human host), spill-back from an animal reservoir (following evolution or recombination), parallel evolution in an unsurveilled group of people. While current evidence precludes elimination of any of these scenarios, the most parsimonious hypothesis is the emergence of omicron from a chronically infected human host. At this stage, considering the lack of evidence, it would be useful to consider a range of hypotheses for further investigation.

It appears that there is currently no evidence from available sequence data that an animal reservoir is responsible for the emergence of Omicron. The group noted that the experience from the cases of infection in white-tailed deer (WTD) and mink populations have shown that even though SARS-CoV-2 can be maintained in animal species other than humans, uncontrolled circulation does not generate an accumulation of mutations as seen in the Omicron VOC. Nevertheless, while the few known cases of uncontrolled SARS-CoV-2 circulation in animal populations happened in short periods of time (few months), phylogenetic evidence suggests that Omicron VOC may have remained undetected for over a year.

The group noted the valuable work that had been done to determine the susceptibility of different animal species to SARS-CoV-2 and to identify potential animal reservoirs through field monitoring. However, it recognized that there were still significant gaps. For example, there were no data on susceptibility of several animal species which have a high level of direct or indirect contact with humans (e.g., rodents), monitoring or surveillance of animals had only been undertaken in a few species and in certain locations. There was a lack of animal surveillance data around clusters of new variants.

2. Monitoring for SARS-CoV-2 in animals

The group agreed on the importance of implementing targeted risk-based active surveillance in animal species. The design of animal surveillance studies could consider existing knowledge of species susceptibility; level of contact with humans or other animal species; co-circulation of other coronaviruses in animals; geographic location.

It was mentioned that the majority of animal susceptibility studies were performed using the Wuhan (original) strain and its early variants and not the most recent variants, and that it would be important to understand if animal susceptibility changes significantly in such cases.

3. Collection and analysis of sequences from in animals

The previous work done by IZSVe has set the basis for the future approach to the collection of animal sequence data. The group decided to work together on a table listing the frequency of relevant mutations in animal and human sequences using a whole genome sequence approach (opposed to focusing on the spike protein mutations only). Once this work is well underway, a mechanism for automatic update of the table with relevant information will be developed.

4. Research

It was noted that although rodents are susceptible to SARS-CoV-2 infection to various degrees, there has not been any large surveillance study done in a city which simultaneously has a high prevalence of COVID-19 cases in humans and a large rodent population (rats, mice, capybaras, etc.). This was flagged as a research gap, amongst others, by the group.

Studies had described the possibility for recombination events to occur between SARS-CoV-2 and other animal coronaviruses at the cellular level.

WHO will organise another COVID-19 R&D Blueprint meeting in mid-January. There will be the opportunity to submit relevant research proposals for funding at that time. Surveillance could be considered.

Immediate actions

- Analysis of available sequences to assess the presence/absence and frequency of different mutations in sequences from viruses isolated in animals and compare these to the mutations in Omicron and other human viruses – Richard Orton/Isabella Monne
- Establish a system for regular review and analyses of sequences from viruses isolated in animals
- Develop simple guidance for targeted active surveillance among spillover risk areas and for opportunistic surveillance – OIE (small expert group)
- Encourage countries to perform active surveillance using serological and molecular epidemiological approaches and to deposit whole genome sequences in publicly available databases -OIE
- Group to meet more often and support active review and analysis of sequences of viruses isolated from animals

The date of next meeting of the Advisory Group will be determined as needed.