

7TH CALL OF THE FAO-OIE ADVISORY GROUP ON SARS CoV-2 EVOLUTION IN ANIMALS

2nd February 2021

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Agenda

1. Update from Hong Kong
2. SARS-CoV-2 sequences in hamsters and other rodents
3. Animal vaccines (Zoetis)
4. Update on SARS-CoV-2 infection in white-tailed deer

Meeting notes

1. Update from Hong Kong

The meeting started with an update on the epidemiology and genetic sequencing findings of the recent outbreak of COVID-19 in Hong Kong which involved imported hamsters and humans. The current findings ([Yen et al, 2022](#)) indicate that there were at least 3 separate introductions of SARS-CoV-2 Delta strain into the human population at a time when COVID-19 cases caused by this strain had not been detected in Hong Kong for at least 2 months. Genetic sequences retrieved from the human cases and the infected hamsters shared 4 new mutations in the spike protein. Considering the genetic sequencing information in addition to the epidemiological observations, the experts agreed that there was enough evidence to support the hypothesis of hamster to human transmission of SARS-CoV-2 and subsequent onwards transmission between humans.

2. SARS-CoV-2 sequences in hamsters and other rodents

The group received an overview of the information available on GISAID and other platforms relative to SARS-CoV-2 sequences in hamsters, which is limited to the outbreak in Hong Kong and to a couple of experimental studies. The 4 non-silent mutations found in the AY.127 sequence (which infected hamsters and humans) were discussed. These are mutations which have been seen before only in rare occasions, but it is not clear whether they relate to adaptation of the virus to hamsters and/or which implications they have.

An analysis of the mutations in the Omicron variant against the mutations seen in known animal sequences was also shared with the group. There was not a significant overlap of mutations, therefore no significant connections were found. Members of the group suggested that a similar exercise was conducted with coronaviruses known to infect animals, such as Murine coronavirus.

Since the majority of mutations in the omicron variant are associated with expression of the SARS-CoV-2 spike protein and have led to escape from virus neutralization, this may indicate that mutations were a result of selection pressure in a population with a significant level of immunity to earlier strains rather than in a wild or immuno-naive rodent population. This might support the hypothesis that omicron emerged in humans rather than mice.

3. Infections in animals and animal vaccines

A representative of Zoetis joined the meeting to discuss the experience of vaccinating animals in the USA. It was pointed out that it is likely that there is a significant underreporting of SARS-CoV-2 cases in animals, which gives a biased picture of the actual epidemiological situation in non-human hosts. It was also mentioned that most of the current findings regarding experimental infection of animals were achieved with the earlier strains (closer to Wuhan-1 strain) and describe the infection/disease in juvenile animals. The clinical picture is likely different in older animals. Field data also indicated that other sporadic animal to human transmission events may have occurred, highlighting the importance of One Health approaches to investigating animal and human cases.

Zoetis has developed a vaccine using a recombinant spike protein which has been used in mink farms, zoos, and other settings with high concentration of animals. Vaccinated zoo animals seem to have less severe clinical signs and make full recoveries. However, they may still transmit the virus to humans. More than 3 million vaccine doses have been used in mink in the USA with zero adverse events and/or safety observations reported regarding the mink use. More recently, the vaccine has been used in more than 10,000 animals in zoos, aquariums and similar settings also with positive results. Zoetis has received requests from entities in other countries and is preparing broader deployment of the vaccine. Its technology allows for the quick adaptation of the vaccine to existing and future variants.

4. Update on SARS-CoV-2 infection in white-tailed deer

The samples of retropharyngeal lymph nodes of white-tailed deer collected in Iowa from April 2020 through January of 2021 that are mentioned in the publication of [Kuchipudi et al. \(2022\)](#) are being further analysed with molecular techniques. So far, about 4/5 of the samples have been sequenced and SARS-CoV-2 has been found in 51,7% of the samples. There is a strong spatiotemporal correlation between the animal infections and the peak of human infection/hunting season. It was noted that multiple human to deer spillovers have occurred in Iowa and that there is no evidence yet of deer to human transmission.

The group was also informed of a recent study done in white-tailed deer in Staten Island, NY, USA, where a significant percentage of the sampled deer, especially yearlings, showed evidence of infection with the Omicron variant. It was pointed out that white-tailed deer are looking more and more like a probable silent reservoir, but longitudinal studies are still needed before that can be said with certitude.

Immediate actions

- Analysis of available sequences to assess the presence/absence and frequency of different mutations in sequences from animal coronaviruses and compare these to the mutations in Omicron – Richard Orton
- Establish a system for regular review and analyses of sequences from viruses isolated in animals
- Continue to share findings about infection in hamsters
- Group to meet more 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 the 2nd of March.