

# 15<sup>TH</sup> CALL OIE AD HOC GROUP ON COVID-19 AT THE ANIMAL-HUMAN INTERFACE

22<sup>nd</sup> November 2021

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## Agenda

1. Summary of recent work
  - a. Experimental infection of white-tailed deer – Juergen Richt (K State)
  - b. US studies on WTD - Thomas DeLiberto (USDA APHIS)
  - c. RNA detection studies – Vivek Kapur (Penn State)
2. Implications
  - a. Discussion
  - b. Recommendations

## Meeting notes

### 1. Summary of recent work

The research published by [Damas et al. in August 2020](#) concerning the prediction of host susceptibility to SARS-CoV-2 infection by comparative and structural analysis of ACE2 in vertebrates has prompted numerous follow-up studies focused on different species. White-tailed deer (WTD), which were flagged as susceptible in the study, are the most widely distributed wild ungulate in the Americas.

Experimental infection of white-tailed deer: the rationale, methods, and conclusions of a research paper by [Cool et al. \(August 2021, pre-print\)](#) titled *Infection and transmission of ancestral SARS-CoV-2 and its alpha variant in pregnant white-tailed deer* were presented to the group. In this work, the researchers showed that adult white-tailed deer were highly susceptible to SARS-CoV-2 infection and could transmit the virus through direct contact as well as vertically from doe to fetus. Additionally, it was determined that the alpha VOC B.1.1.7 isolate of SARS-CoV-2 outcompeted the ancestral lineage A isolate in white-tailed deer. These findings were demonstrated by the genome of the virus shed from nasal and oral cavities from principal infected and contact animals, and from virus present in tissues of principal infected deer, fetuses and contact animals. Sequencing findings revealed that there was minimal viral adaptation to WTD, to the contrary of what is verified in the case of other susceptible hosts, such as cats and mink. CEEZAD, [Meekins](#)

[et al. \(October 2021\)](#), has published a review titled *Natural and Experimental SARS-CoV-2 Infection in Domestic and Wild Animals* and plans to produce a regular update.

US studies on WTD: building on the findings of the aforementioned studies, in addition to the research published by [Palmer et al. \(March 2021\)](#), who showed that WTD became subclinically infected upon intranasal inoculation and that indirect contact animals became infected, [Chandler et al. \(November 2021\)](#) did a serosurveillance study to assess the prevalence of SARS CoV-2 infection in WTD in four USA states. The sampling was opportunistic, utilizing archived sera collected for chronic wasting disease and Tuberculosis surveillance. 624 pre-pandemic (2011-2019) and post-pandemic (2020-2021) serum samples from wild deer were assessed for SARS-CoV-2 exposure using a surrogate virus neutralization test. Antibodies were detected in 152 samples (40%) from 2021 and were not detected in samples prior to 2020, suggesting that WTD in the populations assessed had been exposed to SARS-CoV-2 in 2020 and 2021. In addition to Chandler *et al.*'s research, [Hale et al. \(November 2021, pre-print\)](#) detected SARS-CoV-2 using rRT-PCR in 129 out of 360 (35.8%) free-ranging WTD from northeast Ohio, USA, sampled between January and March 2021. The findings were reported to the OIE as an emerging disease in animals. Considering the high prevalence of SARS-CoV-2 infection in the tested USA WTD populations, a large-scale surveillance operation is underway, aiming to test up to 40,000 samples over 4 months. This study will inform further actions and assist in viral characterization, identification of routes of transmission, and characterization of deer-human interactions that increase transmission risks. Surveillance efforts have engaged multiple stakeholders and communities including USA States, tribes, federal agencies.

Further viral nucleic acid detection studies: [Kuchipudi et al. \(November 2021, pre-print\)](#) used samples collected in Iowa from April 2020 through January of 2021 to test the hypothesis that SARS-CoV-2 was circulating in deer. SARS-CoV-2 was detected in one-third of WTD sampled, likely resulting from multiple human-to-deer spillover events alongside with deer-to-deer transmission. During the presentation, it was affirmed that WTD may have silently become a reservoir for SARS CoV-2. The spillover from humans to deer coincided with increase in cases in humans including the November 2020 peak in Iowa, as well as with the onset of winter and the peak deer hunting season. Possible sources of WTD infection could be contaminated food and feed, the environment or an intermediary host. The route(s) of spillover, the potential for WTD to remain a reservoir of SARS-CoV-2, or opportunities for spillback from WTD to humans needs further investigation.

## 2. Implications

Discussion: The group discussed the population dynamics of WTD, whose females and young form families which live within a limited radius. WTD, being social with a high level of interaction, create the opportunity for SARS-CoV-2 infections to spread rapidly within epidemiological groups. This is further catalyzed by males, who can travel long distances (60+ km) between family units, creating opportunities for viral spread. It was noted that the infection pattern seemed to be the same between free ranging/wild deer and farmed deer. The current state of knowledge does not allow to say if there has been reinfection of WTD with different viral strains. However, it seems that there is variability in SARS-CoV-2 strains while circulating in WTD populations. Interestingly, although the infection of WTD is asymptomatic, their level of neutralizing antibodies is higher than other species with symptomatic infections, such as humans.

It was suggested that, in the future, researchers should investigate the possibility of recombination between different coronaviruses in deer populations and assess the susceptibility of different cervid species to infection with SARS-CoV-2. Limiting these studies to serosurveillance, on a first stage, would mitigate the cost that is associated with molecular studies involving sequencing. Opportunistic sampling can be done to speed up operations while limiting costs. However, serosurveillance would not provide the important information that molecular techniques do, such as the identification of recombination and proof of onward transmission.

It is likely that similar spillover events from humans to deer will have occurred in other countries. However, little is known about surveillance efforts in wildlife around the world. The group highlighted the value of gathering such information. The abovementioned studies also suggest that passive surveillance alone lacks power, and that thoughtful, targeted surveillance studies are needed to detect and describe spillover events.

Recommendations:

- Further discuss implications with the Chair and with public health partners and report back to the group with proposed actions e.g., update or development of guidance
- Review existing OIE guidance on monitoring of animal populations
- Consider guidance on biosecurity
- Gather information on surveillance in wildlife (including deer) from OIE Members
- The group will support OIE and its partners in developing criteria and recommendations for surveillance in wildlife populations. OIE will update its guidance according to the latest findings.

The next call of this *ad hoc* Group shall be scheduled on a need-basis.