Transmission analysis of multiple spillovers of SARS-CoV-2 from humans to white-tailed deer

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Introduction

- The emergence of a novel pathogen in a susceptible population can result in rapid spread of infection within the population.
- The high incidence SARS-CoV-2 in humans during the ongoing pandemic poses a risk of anthropogenic transmission to wildlife. Animal species infected with SARS-CoV-2 have the potential to then become reservoirs for infection and contribute to the emergence of new variants.
- Widespread SARS-CoV-2 infection and transmission was recently reported in wild white-tailed deer (*Odocoileus virginianus*), with 33% of sampled deer in Iowa, United States, testing positive for SARS-CoV-2 viral RNA (Kuchipudi *et al*., 2022).
- White-tailed deer are a free-living wild animal species present across the Americas and often live in close proximity to human populations, meaning people could be exposed to SARS-CoV-2 in deer through direct or indirect contact.
- Whole-genome sequencing combined with epidemiological parameters can provide insight into the transmission history of infectious diseases. Knowledge of the risk and direction of SARS-CoV-2 transmission between humans and potential reservoir hosts is essential for effective disease control and prioritisation of intervention measures.

Methods

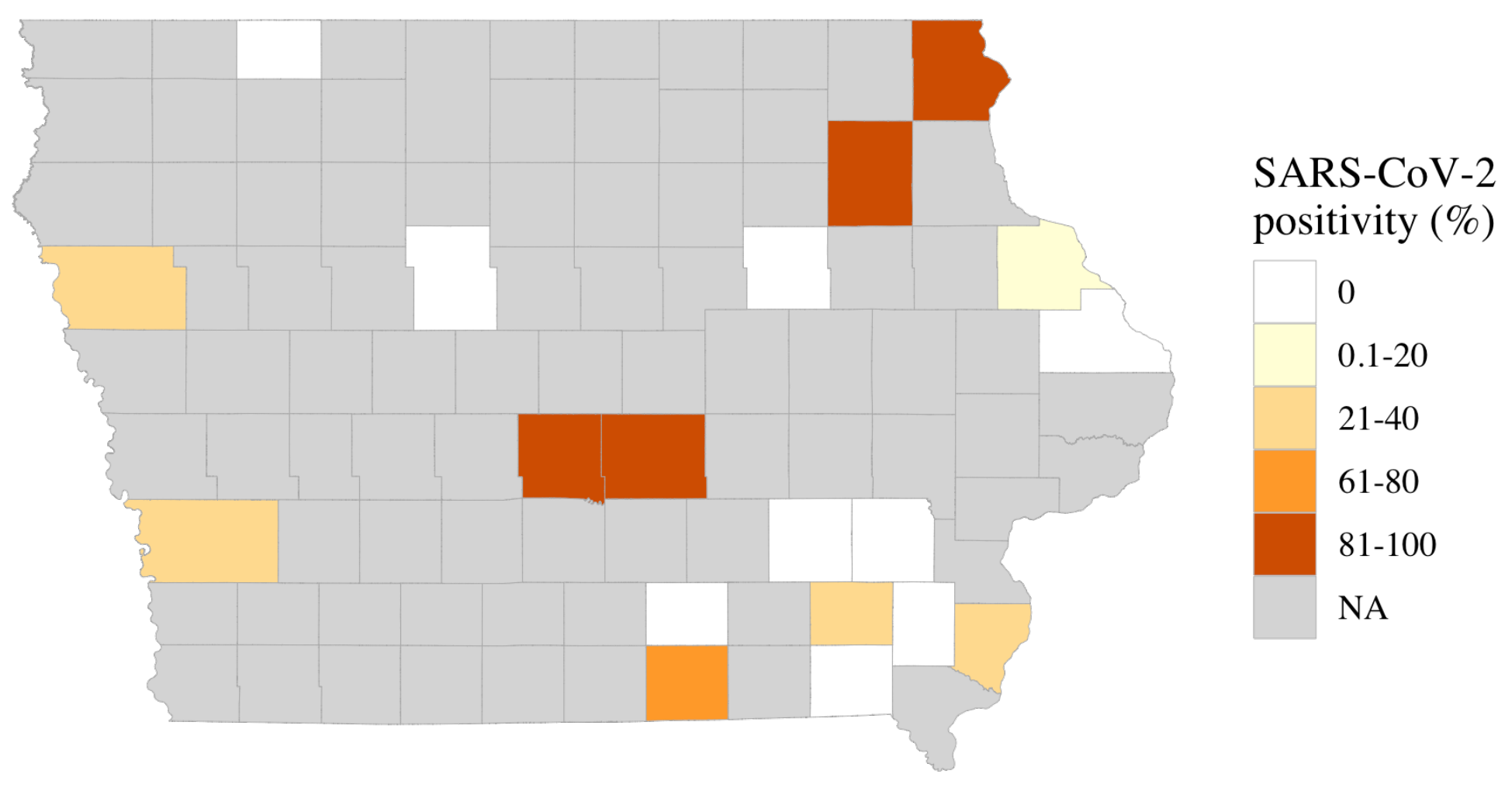
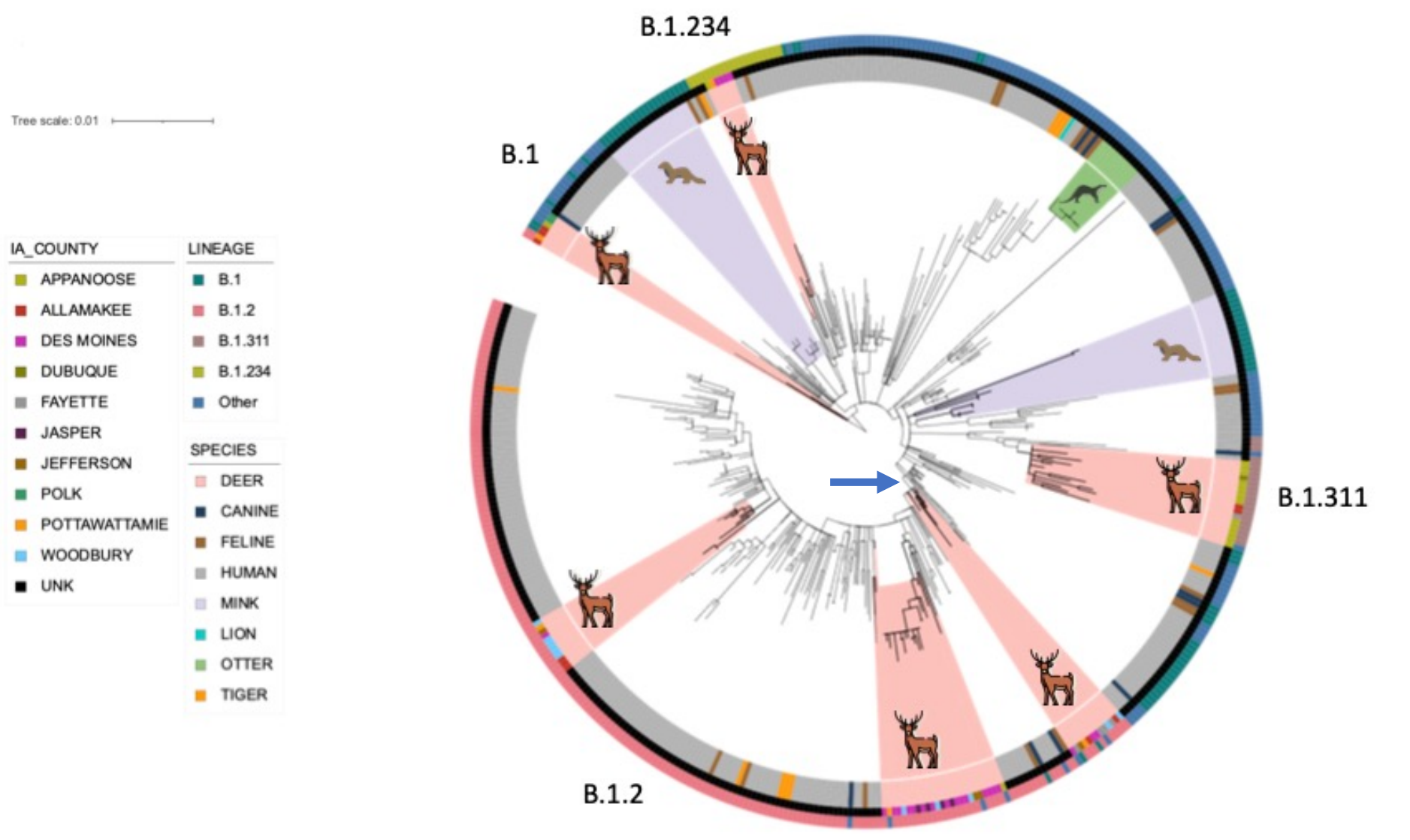


Figure 1. Counties in Iowa sampled for SARS-CoV-2 in deer between April 2020 and January 2021 with associated test positivity.

Retropharyngeal lymph node samples from white-tailed deer in Iowa, United States, were tested for presence of SARS-CoV-2 RNA (Kuchipudi *et al.*, 2022). Positive samples (figure 1) were sequenced and a phylogenetic tree was constructed from deer and publicly available SARS-CoV-2 sequences from Iowa (figure 2, Kuchipudi *et al*., 2022). The largest cluster with 52 deer and 141 human sequences was selected for further analysis (figure 2). We used a Bayesian framework (Didelot et al., 2017) to reconstruct the transmission history from a timed phylogenetic tree and infer who infected whom.



(Kuchipudi *et al*., 2022)

Figure 2. Phylogenetic tree of SARS-CoV-2 deer isolates and publicly available sequences from Iowa. Blue arrow indicates cluster selected for transmission analysis.

Results

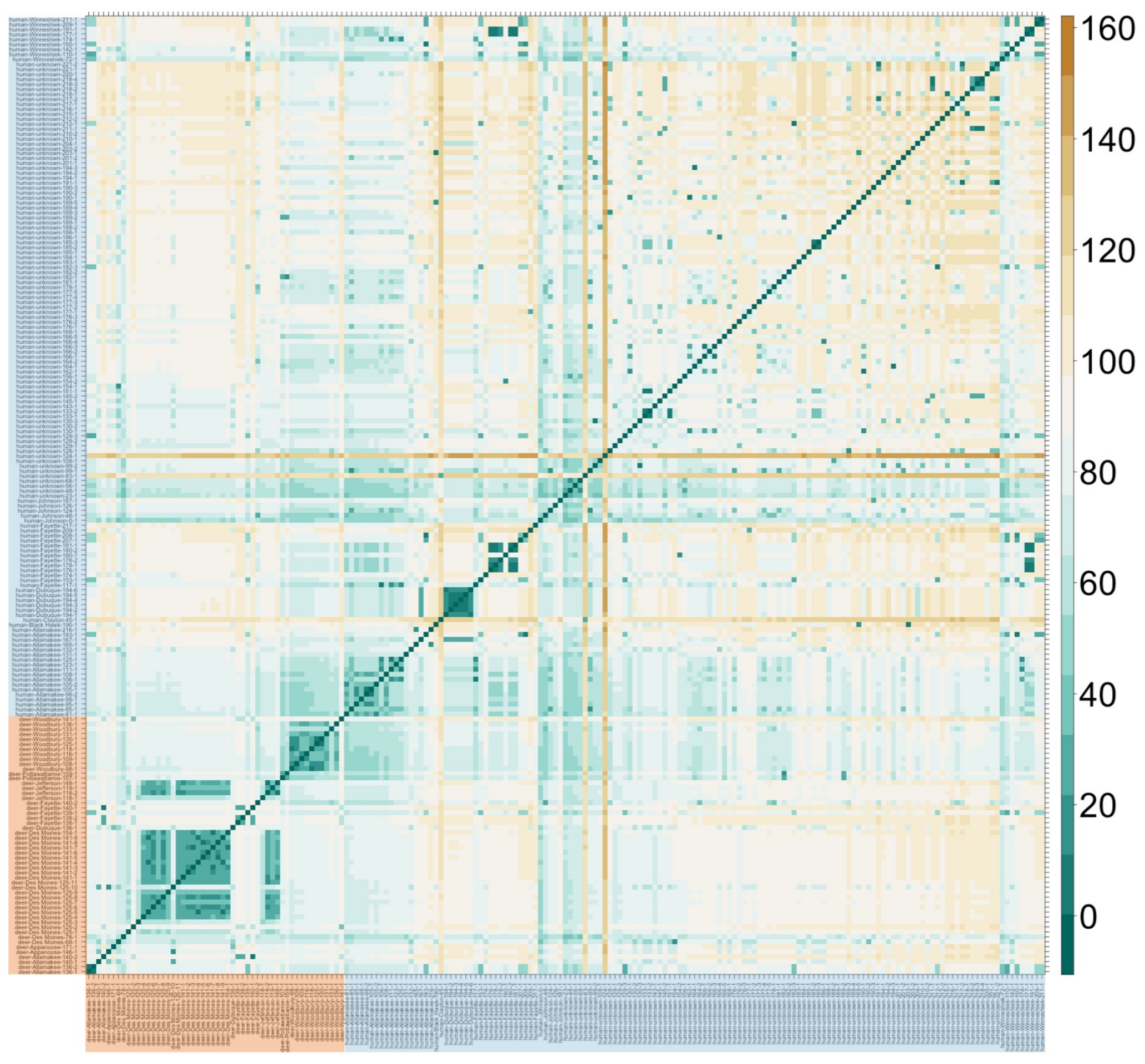


Figure 3. Estimated number of intermediate cases in the transmission chain between each pair of sampled individuals. Deer cases are highlighted in orange and human cases in blue.

- Analysis of the 193 SARS-CoV-2 sequences estimated the time of the most recent common ancestor to 26 December 2019 for human sequences and 31 March 2020 for deer.
- The inferred number of unsampled cases was high in both deer and human populations (figure 3), with a case finding rate of <5.5%.
- Clusters of deer SARS-CoV-2 sequences were interspersed among human isolates, consistent with multiple spillover events from humans to deer and onwards transmission within deer populations (figure 4).
- We found no evidence of direct transmission from deer to human.

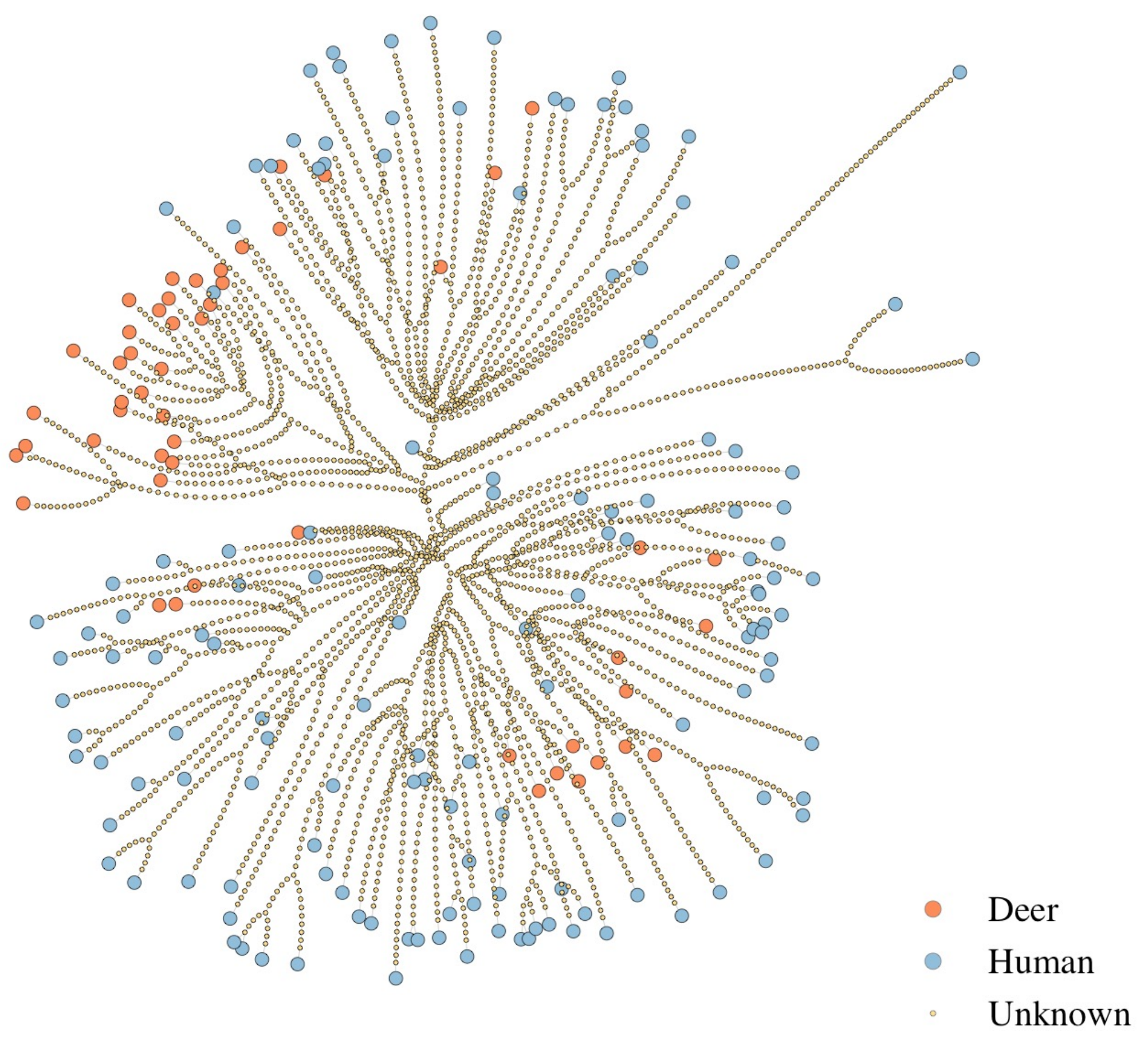


Figure 4. Inferred transmission network. The size of nodes (cases) and length of edges (transmission events) are weighted based on if the case was sampled. Unsampled cases are shown as smaller nodes.

Conclusion

- Based on analysed SARS-CoV-2 sequences, deer-to-human transmission does not appear to have occurred. However, due to the high number of unsampled cases in both deer and human populations, spillback to humans cannot be ruled out.
- The extensive transmission of SARS-CoV-2 in wild deer populations and the low case finding highlights the need for surveillance at the human-animal interface. Without active surveillance in susceptible animal populations, the virus could circulate and evolve undetected for extended periods of time.
- Already existing disease surveillance programmes in deer could be extended to monitor SARS-CoV-2 occurrence and mutations with potential to affect transmissibility, virulence or other adverse phenotypic changes.

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References:

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