

Human-animal spillover of SARS-CoV-2: Implications for public health

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ABSTRACT

Summary: COVID-19 pandemic caused by the recently emerged severe acute respiratory syndrome coronavirus (SARS-CoV-2) is a significant public health catastrophe in a century. While the precise origin of SARS-CoV-2, and its mode of introduction into the human population, is not yet fully resolved, there is evidence that SARS-CoV-2 originated from bats. As zoonotic viruses infecting humans can spill back into susceptible animal hosts, SARS-CoV-2 has demonstrated the ability to infect many non-human animal host species. The list of animal species susceptible to SARS-CoV-2 infection continues to grow and includes domestic animals, primates, pet animals, and zoo animals. In addition, based on the ability of the spike protein to bind to the ACE-2 receptor, computational predictions have identified dozens of additional possible animal hosts for SARS-CoV-2. In addition, there are multiple reports of human infections from SARS-CoV-2 infected animals. We discovered widespread natural infection of wild white-tailed deer with SARS-CoV-2 in the USA, suggesting their role as a potential SARS-CoV-2 reservoir. Establishing an animal reservoir could facilitate the continued circulation of SARS-CoV-2 independent of circulation in humans. In addition, deer could pass on the infection to other susceptible wild animals such as rodents, foxes, and raccoons resulting in the establishment of SARS-CoV-2 enzootic transmission cycles. Such a scenario could result in virus adaptation and the emergence of novel variants that could escape the protection of current human SARS-CoV-2 vaccines. This presentation will discuss our recent findings on natural SARS-CoV-2 infection of deer and the long-term implications of human-animal-human spillover of SARS-CoV-2.