Should the susceptibility of cervid to coronaviruses be a matter of concern?

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Short Report

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Abstract

The susceptibility of the white-tailed deer (*Odocoileus virginianus*) to SARS-CoV-2 has highlighted cervids as a new coronavirus reservoir. Cervids are known hosts for other coronaviruses (such as bovine-like coronavirus) and can harbour several pathogens that cause serious diseases in humans. Moreover, herds of cervids are largely distributed among wildlife and are in close contact with humans, who often hunt or rear these animals. The increased incidence of severe acute coronavirus 2 (SARS-CoV-2) infections, especially in American countries, which serve as habitats for many cervids, including the white-tailed deer and other closely related species, can favour the transmission of coronaviruses from humans to wild animals. In this context, this letter briefly discusses some points that underscore the occurrence of SARS-CoV-2 infections in cervids as a matter of concern.

Full Text

Since the beginning of the coronavirus disease (COVID-19) pandemic, the origin of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been attributed to bats (Zhou et al., 2020). These animals have been implicated as the primary hosts for this virus due to their central role in the origins of severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS), the main coronavirus infections before COVID-19 (Zhou et al., 2020). Horseshoe bats and common pipistrelle bats are natural reservoirs for SARS-like-CoV and MERS-like-CoV, respectively (Lau et al., 2005; Woo et al., 2012). Moreover, bats harbour a series of zoonotic viruses, and several species of bats are widely distributed across the globe (Brook and Dobson, 2015; Wynne and Wang, 2013). Meanwhile, further studies have implicated other wild animals, such as civets, camels, and pangolins, as key members of the chains of transmission of coronaviruses to humans (Farag et al., 2015; Guan et al., 2003; Lopes et al., 2020). Currently, the detection of SARS-CoV-2 in companion animals, wild animals from zoos, and captive animals is alarming and raises concerns about other coronavirus-susceptible hosts (van Aart et al., 2021; Hamer et al., 2021; McAloose et al., 2020; do Vale et al., 2021).

In this context, recently, Palmer *et al.* (2021) reported that white-tailed deer (*Odocoileus virginianus*) are highly susceptible to SARS-CoV-2 infection, presenting efficient transmissibility (Palmer et al., 2021); these authors also showed that SARS-CoV-2-infected white-tailed deer presented subclinical infection with productive virus replication in the upper respiratory tract. Moreover, the infected animals shed infectious virus particles in their nasal secretions (Palmer et al., 2021). This means that the close contact between healthy white-tailed deer and infected animals may promote the transmission of SARS-CoV-2 through respiratory secretions.

Although the SARS-CoV-2 spillback from humans to wild cervids has not been reported previously, it is highly likely that cases of infection with this virus wildlife can emerge, leading to the establishment of cervids as potential reservoirs of coronavirus infection. Furthermore, previous studies had already reported that cervids can be infected with coronaviruses. Elk (Majhdi et al., 1997), sambar deer (Alekseev et al., 2008), sika deer (Yokoi et al., 2009), water deer (Kim et al., 2018), and white-tailed deer (Alekseev et

al., 2008) are susceptible hosts for bovine-like coronavirus. In cattle, bovine coronavirus (BCoV) can cause diarrhoea and respiratory illness and, have been reported to be transmitted via faecal-oral or respiratory routes (Zhang et al.). In 1994, a bovine-like coronavirus was isolated from a child (Zhang et al., 1994). According to molecular evolutionary approaches used in previous study, bovine-like coronaviruses were estimated to share a recent common ancestor with human CoV-OC43 (HCoV-OC43) (Hasoksuz et al., 2007), a coronavirus that causes common cold in humans (Birch et al., 2005). Additionally, cervids are also known to harbour pathogens that are transmitted to humans, such as rabies virus (Petersen et al., 2012), hepatitis E virus (Boadella et al., 2010; Medrano et al., 2012), Rift Valley fever virus (Wilson et al., 2018), Powassan virus (Nofchissey et al., 2013), West Nile virus (Miller et al., 2005), *Toxoplasma* sp. (Dubey et al., 2014), *Leptospira* spp. (Dubay et al., 2015), and *Mycobacterium bovis* (Lambert et al., 2016), which can cause serious diseases.

The susceptibility of cervids to SARS-CoV-2 has become a matter of concern due to the existence of a large number of cervid species and their wide distribution, which could enable the dissemination of a serious pathogen among wild animals. The circulation of SARS-CoV-2 in wildlife population may enable viral strains to evolve and adapt to new hosts, leading to transmission of a new pathogen to human populations (Banerjee et al., 2021). Although the transmission of viruses from humans to free-living wildlife requires a series of opportunities, the plausible transmission of SARS-CoV-2 to wildlife may occur indirectly via human faeces, considering that viral shedding of SARS-CoV-2 in stool samples occurs in a notable number of patients (Doorn et al., 2020). Furthermore, there are several opportunities for farmed and captive animals to be infected by SARS-CoV-2 (Fagre et al., 2020; Freuling et al., 2020; Kim et al., 2020). The large herding of some cervids, such as reindeer (*Rangifer tarandus*), white-tailed deer, roe deer (*Capreolus* sp.), and others, represents a favourable chance for these cervids to be involved in pathogen transmission to humans.

Cervids are distributed across Europe, Asia, and the Americas. They compose the family Cervidae (detailed in Table 1), which represents a diverse group into the order Artiodactyla, showing diversity in size, habitat, and behaviour (Klein, 1992). In addition to their high population densities, the larger body size of these animals can trigger a series of problems involving humans and cervids, such as injuries due to vehicle collisions and cervid-associated crop loss (McShea, 2012). Hunting and habitat destruction represent major threats for cervids (González and Duarte, 2020; McShea, 2012). They are hunted for their meat in most regions they inhabit. Although there are appropriate cervid-hunting regimens, some species of cervids are overhunted (Duarte et al., 2012a; McShea, 2012).

While some species of cervids such as red deer (*Cervus elaphus*), are more sensitive to the presence of humans, other species such as roe deer, can cope with human disturbance near settlements (Jiang et al., 2008). In this context, white-tailed deer appear to be adapted to human presence and activities. This species thrives and is found in a diverse range of habitats (Branan et al., 1985; Lagory, 1986; Laurent et al., 2021). However, although the population density of white-tailed deer remains stable in Canada and the USA, Latin American populations of this deer are declining due to overhunting and progressive habitat losses (Gallina, 2015).

The habitat of white-tailed deer overlap with those of members from the genus *Mazama*. This genus includes cervids inhabit tropical forests. In Central America and Mexico, both the white-tailed deer and the Central American red brocket deer (*Mazama temama*) are found (Bello, 2015; Duarte et al., 2012b). In South America, white-tailed deer are restricted to the northern region and can be found in some countries together with the red brocket deer (*Mazama americana*) (Duarte et al., 2012b, 2012c). For instance, in Suriname, white-tailed deer inhabit coastal marshes, while red brocket deer inhabit the rainforest; the habitat ranges of these two species overlap slightly at the margins (Branan et al., 1985).

Although the preference of cervids for different habitats may impact their physiology and morphology, the close evolutionary relationship they share among themselves may reflect the genetic similarity between them. In this context, white-tailed deer share a close evolutionary relationship with red brocket deer (Figure 1). The Bayesian phylogenetic tree presented herein was constructed based on the mitochondrial cytochrome b nucleotide sequences of 49 cervid species, and camels which served as the outgroup, using the Mr.Bayes v.3.2 software (Ronquist et al., 2012) and applying the general time-reversible model (GTR) (Rodríguez et al., 1990), selected using using MEGA X software (DNA model selection) (Kumar et al., 2018). Phylogenetic analysis showed that the genus *Mazama* is not a monophyletic group. For instance, *M. guazoupira*, *M. chunyi* and *M. nemorivaga* are not nested in the same clade with red brocket deer. Moreover, the Central American red brocket deer (*M. temama*), red brocket deer (*M. americana*), Brazilian dwarf brocket (*M. nana*), and small red brocket (*M. bororo*) are close to the genus *Odocoileus* (Figure 1). Thus, considering that these cervids are closely related species, their potential susceptibility to SARS-CoV-2 must be taken into account.

All cervids from the gender *Mazama*, except the Central American red brocket deer, are closely related to white-tailed deer and are widely distributed in South America. The red brocket deer is one of the most abundant and widely distributed cervids in Neotropical forests (Varela et al., 2010). They inhabit almost all South American countries, except for Uruguay and Chile. Red brocket deer populations have been frequently threatened by commercial and subsistence hunting (Duarte et al., 2012c). Their meat is an important food source for people living close to Neotropical forests and is sold in urban and rural markets close to the Amazon (Varela et al., 2010). The red brocket deer is sympatric with two Brazilian endemic cervids: the Brazilian dwarf brocket and the small red brocket, which are threatened by hunters and predation by feral dogs (Duarte et al., 2012d, 2012e). These endemic species are found close to regions with a high density of human population.

The white-tailed deer and brocket deer are widely distributed across various countries in the American subcontinent; these represent some of the most prominent COVID-19-affected regions in the world. At the time of writing this article, the COVID-19 cases in the Americas accounted for 39% of all COVID-19 cases worldwide. Moreover, although the American population represents only 13% of the global population, 48% of all COVID-19-associated deaths occurred in America. Thus, the close coexistence between SARS-CoV-2-infected populations and cervids places these animals within the transmission chain of coronaviruses.

In addition, during the pandemic, South American countries have relaxed their regulations and environmental policies, which has exacerbated deforestation (López-Feldman et al., 2020). Consequently, as human habitation ventures deeper into once-inaccessible tropical biomes, the potential contact with coronavirus-susceptible hosts can contribute to the transmission of these viruses to wildlife (Harvey, 2021). In this context, the progressive and continued environmental destruction and the conflicting coexistence between humans and wild animals may favour the exchange of pathogens. Thus, cervids may be involved in a pathogen-transmission chain because they are globally widespread, inhabit regions close to areas inhabited by humans, and can harbour a series of human pathogens, including coronaviruses. Therefore, molecular epidemiological surveillance must target cervids due to their potential to harbour SARS-CoV-2 or related coronaviruses, in order to take effective measures to control future outbreaks of coronavirus infections.

Declarations

Funding

Not applicable

Availability of data and material

All the data obtained from the NCBI GenBank databases included in this research study were associated with accession codes/numbers for research or reanalysis.

Code availability

Not applicable

Ethics approval

This research included secondary biological data with no possibility of individual identification. The Unifesp Research Ethics Committee was consulted and it was determined that this study did not require ethical approval.

Conflict of interest statement

The author state that there are no conflicts of interest to declare.

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Tables

General cervid informations

Subfamily	Species	Popular name	Red list	Population trend	Geographic distribution
Cervinae	<i>Axis axis</i>	Chital	LC	Unknown	Asia
	<i>Axis porcinus</i>	Hog deer	EN	Decreasing	Asia
	<i>Axis kuhlii</i>	Bawean Deer	CR	Decreasing	Asia (Indonesia)
	<i>Cervus canadensis</i>	Wapiti	LC	Increasing	Asia and North America
	<i>Cervus elaphus</i>	Red deer	LC	Increasing	Europe, Asia (Russia) and Middle East
	<i>Cervus nippon</i>	Sika deer	LC	Increasing	Asia
	<i>Dama dama</i>	Dama deer	LC	Unknown	Europe
	<i>Dama mesopotamica</i>	Persian Fallow Deer	EN	Increasing	Asia (Iran)
	<i>Elaphurus davidianus</i>	Père David's Deer	EW	Unspecified	
	<i>Przewalskium albirostris</i>	White-lipped Deer	VU	Unknown	Asia (China)
	<i>Rucervus duvaucelii</i>	Barasingha	VU	Decreasing	Asia (India and Nepal)
	<i>Rucervus eldii</i>	Eld's Deer	EN	Decreasing	Asia
	<i>Rusa alfredi</i>	Philippine Spotted Deer	EN	Decreasing	Asia (Philippines)
	<i>Rusa marianna</i>	Philippine Deer	VU	Decreasing	Asia (Philippines)
	<i>Rusa timorensis</i>	Javan Deer	VU	Decreasing	Asia (Indonesia)
	<i>Rusa unicolor</i>	Sambar	VU	Decreasing	Asia
Hydropotinae	<i>Hydropotes inermis</i>	Water Deer	VU	Decreasing	Asia (China and Korea)
Muntiacinae	<i>Elaphodus cephalophus</i>	Tufted Deer	NT	Decreasing	Asia (China)
	<i>Muntiacus atherodes</i>	Bornean Yellow Muntjac	NT	Decreasing	Asia (Malasya)
	<i>Muntiacus feae</i>	Fea's Muntjac	DD	Unknown	Asia (Myamar and Thailand)
	<i>Muntiacus</i>	Gongshan	DD	Decreasing	Asia (China and

	<i>gongshanensis</i>	Muntjac			Myanmar)
	<i>Muntiacus muntjak</i>	Southern Red Muntjac	LC	Decreasing	Asia
	<i>Muntiacus putaoensis</i>	Leaf Muntjac	DD	Decreasing	Asia (India and Myanmar)
	<i>Muntiacus reevesi</i>	Reeves' Muntjac	LC	Decreasing	Asia (China)
	<i>Muntiacus rooseveltorum</i>	Roosevelts' Muntjac	DD	Decreasing	Asia (Laos)
	<i>Muntiacus vaginalis</i>	Northern Red Muntjac	LC	Decreasing	Asia
	<i>Muntiacus vuquangensis</i>	Large-antlered Muntjac	CR	Decreasing	Asia
Odocoileinae	<i>Alces alces</i>	Moose	LC	Increasing	Asia, Europe and North America
	<i>Blastocerus dichotomus</i>	Marsh Deer	VU	Decreasing	South America
	<i>Capreolus capreolus</i>	European Roe Deer	LC	Increasing	Europe and Middle East
	<i>Capreolus pygargus</i>	Siberian Roe Deer	LC	Decreasing	Asia
	<i>Hippocamelus antisensis</i>	Taruca	VU	Decreasing	South America
	<i>Hippocamelus bisulcus</i>	Patagonian Huemul	EN	Decreasing	South America
	<i>Mazama americana</i>	Red brocket	DD	Unknown	South America
	<i>Mazama bororo</i>	Small Red Brocket	VU	Decreasing	South America (Brazil)
	<i>Mazama chunyi</i>	Peruvian Dwarf Brocket	VU	Decreasing	South America (Bolivia and Peru)
	<i>Mazama gouazoubira</i>	Gray brocket	LC	Decreasing	South America
	<i>Mazama nana</i>	Brazilian Dwarf Brocket	VU	Unknown	South America
	<i>Mazama nemorivaga</i>	Amazonian Brown Brocket	LC	Decreasing	South America
	<i>Mazama pandora</i>	Yucatan Brown Brocket	VU	Decreasing	Central America and North America (Mexico)

<i>Mazama rufina</i>	Dwarf Red Brocket	VU	Decreasing	South America
<i>Mazama temama</i>	Central American Red Brocket	DD	Decreasing	Central America and North America (Mexico)
<i>Odocoileus hemionus</i>	Mule deer	LC	Stable	North America
<i>Odocoileus virginianus</i>	White tailed deer	LC	Stable	America
<i>Ozotoceros bezoarticus</i>	Pampas Deer	NT	Decreasing	South America
<i>Pudu mephistophiles</i>	Northern Pudu	DD	Decreasing	South America
<i>Pudu puda</i>	Southern Pudu	NT	Decreasing	South America (Argentina and Chile)
<i>Rangifer tarandus</i>	Reindeer	VU	Decreasing	Europe, Asia (Russia) and North America (Canada)

Table 1 – Classification of cervids was based on NCBI Taxonomy Database (<https://www.ncbi.nlm.nih.gov/taxonomy/>). Geographic, populational and extinction risk data were extracted from the International Union for Conservation of Nature's (IUCN) Red List of Threatened Species. The IUCN Red List includes categories ordered in decreasing risk of collapse: extinct in the wild (EW), critically endangered (CR), endangered (EN), vulnerable (VU), near threatened (NT), least concern (LC). The category data deficient (DD) does not indicate a level of risk.

Figures

Figure 1

Bayesian phylogenetic inference based on (n = 49) mitochondrial cytochrome b (cyt b) nucleotide sequences of cervids. Camel was included as outgroup. White-tailed deer (*Odocoileus virginianus*), susceptible host to SARS-CoV-2, are highlighted in the tree, nested with gender *Odocoileus* and gender *Mazama*. All sequences were obtained from NCBI Genbank database (<http://ncbi.nlm.nih.gov/Genbank>). To infer phylogenetic Bayesian tree, substitution models selection was based on the Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC), using MEGA X software (DNA model selection). General time-reversible (GTR) model with gamma distribution and proportion of invariant sites (GTR+G+I) was selected according to the best perform. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Phylogenetic analyses were conducted in MrBayes and the trees were formatted with the FigTree v1.3.1 software (<http://tree.bio.ed.ac.uk/software/figtree/>).