**Transmission dynamics and susceptibility patterns of SARS-CoV-2 in domestic, farmed and wild animals: Sustainable One health surveillance for conservation and public health to prevent future epidemics and pandemics**

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**Abstract:**

The exact origin of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and source of introduction into humans has not been established yet, though it might be originated from animals. Therefore, we conducted a literature review to understand the putative reservoirs, transmission dynamics, and susceptibility patterns of SARS-CoV-2 in animals. Rhinolophu*s* bats are presumed to be natural progenitors of SARS-CoV-2 related viruses. Initially pangolin was thought to be the source of spillover to human, but they might get infected from human or other animal species. So, the virus spillover pathways to humans remain unknown. Human-to-animal transmission has been testified in pet, farmed, zoo and free-ranging wild animals. Infected animals can transmit the virus to other animals in natural settings like, mink-to-mink, and mink-to-cat transmission. Animal-to-human transmission is not a persistent pathway, while mink-to-human transmission continues to be illuminated. Multiple companion and captive wild animals were infected by emerging alpha variant of concern (B.1.1.7 lineage) whereas Asiatic lions were infected by delta variant, (B.1.617.2). To date, multiple animal species- cat, ferrets, non-human primates, hamsters, and bats, showed high susceptibility to SARS-CoV-2 in experimental condition, while swine, poultry, cattle showed no susceptibility. The founding of SARS-CoV-2 in wild animal reservoirs can confronts the control of the virus in humans and might carry a risk to the welfare and conservation of wildlife as well. We suggest vaccinating pet, and captive animals to stop spillover and spillback events. We recommend sustainable one health surveillance at animal-human-environmental interface to detect and prevent future epidemics and pandemics by Disease X.

**Keywords:** Alpha variant,delta variant, COVID-19, horseshoe bat, mink, pangolin, Rhinolophu*s* bats.

1. **Introduction**

Several human cases of pneumonia were reported in Wuhan, China during December 2019. Later the causal agent was detected as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and the outbreak was linked to the seafood and live animal market in Wuhan (Zhu et al., 2020). The animal market is involved in trading poultry, snakes, hedgehogs, and other wildlife (Wu et al., 2020). Meat and carcasses were traded in that market at the time of the outbreak (Ashour, Elkhatib, Rahman, & Elshabrawy, 2020). SARS-CoV-2 enters host cells by its spike protein (S-protein). The receptor-binding domain (RBD) of S protein binds to angiotensin-converting enzyme 2 (ACE-2) for entering host cells. Then a cellular protease (TMPRSS2) acts on the S protein (Lam, Ratmann, & Boni, 2018; Wrapp et al., 2020) and divides it into 2 sub-units to merge the virus and the cell membrane (Hoffmann et al., 2020; Stopsack, Mucci, Antonarakis, Nelson, & Kantoff, 2020). ACE-2 receptors are very much preserved in different vertebrate species. So animals that have the receptor for this protein can be a vessel for entry (Lam, Ratmann, & Boni, 2018). SARS-CoV-2 can be harbored by any animal which possesses ACE-2 receptors (Damas et al., 2020; Lam et al., 2020; Lan et al., 2020).

Initially, bats are thought to be the reservoir of the virus (Mallapaty, 2020). Bats arereservoirs of several other emerging zoonotic pathogens like Nipah, Hendra, influenza, Ebola, rabies, and CoVs (Brook & Dobson, 2015). More than 200 novel CoVs have been detected in bats throughout the world (Chen, Liu, Yang, & Jin, 2014). It is believed that Middle East Respiratory Syndrome Coronavirus (MERS-CoV) and SARS-CoV may have originated in bats and transmitted through dromedary camels and civets, respectively (El-Sayed & Kamel, 2021). Not only SARS or MERS, other human CoVs like HCoV-NL63 and HCoV-229E have been also originated from bats (Lu, Wang, & Gao, 2015; Skirmuntt, Escalera-Zamudio, Teeling, Smith, & Katzourakis, 2020).

Furthermore, cats and dogs in contact with SARS-CoV-2 infected humans have been identified as SARS-CoV-2 positive. Therefore, there is occasional spillover evidence among human to animal species. Under experimental conditions, the virus can infect and replicate in the respiratory tracts of several animal species like ferrets, cats, hamsters, and rhesus macaques. Nevertheless, domestic cattle, sheep, and goats are not susceptible to SARS-CoV-2 in the experimental condition (OIE, 2021). Experimental studies showed that animals are not playing a crucial role in the transmission of SARS-CoV-2 (Parolin et al., 2021). Rather humans to human transmission help the persistence of the infection throughout the world.

The exact precursor for coronavirus is not established yet and has the possibility of wildlife origin. Phylogenetic analysis of SARS-CoV-2 sequences from different animals e.g; dog, cat, tiger, lion, mink, gorilla proved their relation to human sequences from the same region at the same time period (Barrs et al., 2020; Hamer et al., 2020; McAloose et al., 2020a; Pagani et al., 2021; Sailleau et al., 2020b; Segalés, Puig, & Rodon, 2020; Sit et al., 2020b). Animal strains showed various mutations in their nucleotide sequences, and some resultant mutates have given origin to new variants, harmful for the human population or other species of animals. Therefore, we thoroughly reviewed the available literature to understand the comprehensive transmission dynamics and susceptibility patterns of SARS-CoV-2 and its related viruses in domestic, farmed, and wild animal species, and to highlights the significance of sustainable One health surveillance at the animal-human-environment interface as an early warning tool to detect novel virus (disease X) to prevent future epidemics and pandemics globally.

1. **Material and method:**

We conducted a detailed literature search in the databases such as Scopus (<https://www.scopus.com/home.uri>), PubMed (<https://www.ncbi.nlm.nih.gov/pubmed/>), Web of Science (http://login.webofknowledge.com/), google scholar (<https://scholar.google.com/>), and preprint servers, using several keywords (Table 1). We also searched publicly available information from World Organization for Animal Health (OIE), the global initiative on sharing all influenza data (GISAID) (<https://www.gisaid.org/>; last access 10 July 2021), and the United States Department of Agriculture (USDA) (<https://www.aphis.usda.gov/aphis/ourfocus/animalhealth/sa_one_health/sars-cov-2-animals-us>). Then we selected the literatures based on the reporting of the natural and experimental infection in different animal species.

**Table 1: Keywords for searching published literature in different database**

|  |  |
| --- | --- |
| **Term** | **Keywords** |
| Descriptive term | Prevalence OR Incidence OR Frequency OR Occurrence OR Infection OR Detection OR Identification OR Isolation OR Characterization OR Investigation OR Survey OR Rate |
| Outcome term | “COVID-19” OR “SARS-CoV-2” |
| Population term | Bat OR Pangolin OR Dog OR Cat OR Domestic animals OR Pig OR Poultry OR Avian OR Turkey OR Chicken OR Goose OR Cattle OR Camel OR Bovine OR Equine OR Horse OR Wild animals OR Zoo animals OR Tiger OR Lion OR Canine OR Feline OR Mink OR Mammals OR Non-human primates OR Monkey OR Macaque OR Rodents OR Mice OR Rat OR Ferret OR Guinea pig OR Masked Civet |

1. **Results and discussions**

The origin of SARS-CoV-2 has not been confirmed yet, but it is clear that the virus was originated from animal species. Therefore, animal species, which can act as a reservoir, natural hosts, and intermediate hosts, should be well-known to health authorities. From this review, we assumed SARS-CoV-2 can affect several animal species globally (Kim et al., 2020a; Shafique, Ihsan, & Liu, 2020).

**3.1 Putative reservoirs of SARS-CoV-2 virus in animal hosts**

**3.1.1 SARS-CoV-2 related coronaviruses in bats**

(Rulli, D'Odorico, Galli, & Hayman, 2020) showed that land-use change, and livestock revolution enhance the zoonotic coronavirus transmission risk from Rhinolophid bats. Asian horseshoe bats usually harbor SARS-related coronaviruses. They stated that horseshoe bats habitat in china has more forest fragmentation and human-livestock density than any other country in the world. As a result, China becomes a hotspot for human-livestock-wildlife interactions with potential for SARS-related coronavirus spillover from animals to humans.

Soon after the emergence of SARS-CoV-2 in humans, researchers found that the viruses genome has similarities with coronaviruses from *Rhinolophus* bats (Fig-1) but the route of SARS-CoV-2 spread is still unknown (Wong et al., 2020). SARS-CoV-2 has a 96% genetic resemblance with the Horseshoe bat (*R. affinis*) CoV RaTG13, implying a probable bat origin of SARS-CoV-2 in humans (Lu et al., 2020a; Touati et al., 2020; Zhang & Holmes, 2020; Zhou et al., 2020b). Besides, the SARS-CoV-2 genome has an insertion site between the cleavage site of S1 and S2. This insertion has also been seen in *R. malaynus*. Two bat species namely *R. affinis* and *R. malaynus* can be the ancestral reservoir of SARS-CoV-2. Nevertheless, the direct transmission or spillover of SARS-CoV-2 from Horseshoe bats species to humans has not been established (Wong et al., 2020). Subsequently, additional SARS-CoV-2-related viral genome sequences from horseshoe bats have been detected in Eastern China (Zhou et al., 2020a), Japan (Murakami et al., 2020) and Cambodia (Hul et al., 2021) and Thailand (Wacharapluesadee et al., 2021).

In Cambodia, the SARS-CoV-2 like coronaviruses with 92.6% genome similarity with SARS-CoV-2 were detected in two Shamel’s horseshoe bats (*R. shameli*) archived swab samples captured back in 2010 (Hul et al., 2021). Moreover, *R. shameli* bats are not distributed in China (Lin et al., 2017) which implies that SARS-CoV-2 related viruses might have a much broader geographic spread than earlier thought, and proposes that Southeast Asia signifies a crucial zone to ponder in the continuing examine for the origins of SARS-CoV-2, and in monitoring the horseshoe bats for coronavirus diversity. Another virus called Rc-o319 was identified in Japanese horseshoe bat’s (*R. cornutus*) frozen droppings collected in 2013. This one has 81% genome similarity with SARS-CoV-2. The Japanese strain is too distant from SARS-CoV-2 and cannot bind to SARS-CoV-2’s receptor in human cells (Mallapaty, 2020). So, this strain will not infect humans easily. This discovery provides valuable information about the transmission of SARS-CoV-2 from bats to people.

Another species *R. acuminatus* harbor SARS-CoV-2 related coronavirus, RacCS203, in Thailand (Wacharapluesadee et al., 2021). Moreover, antibodies against SARS-CoV-2 were found in this same bat colony in Southern Thailand (Wacharapluesadee et al., 2021). But three distinct points indicate that bats are not responsible for transmitting the SARS-CoV-2 to humans (Jo et al., 2020; Li et al., 2020). Firstly, during the pandemic, local bat species were out and hibernated (Jo et al., 2020). Secondly, though other animal species were present in the market for sale, bats were not sold at that time. Finally, genomes of SARS-CoV-2 and other bat CoV sequences have 96% similarity (Jo et al., 2020).

Diagram

Description automatically generated

Fig.1: Transmission pathways and susceptibility of SARS-CoV-2 to domestic and wild animals

**3.1.2 SARS-CoV-2 related coronaviruses in pangolin**

Pangolins (Pholidota, Mammalia) are insects eating nocturnal animals, having eight species in Africa and Asia (Heighton & Gaubert, 2021). These critically endangered small animals are widely trafficked illegally for their meat and scales, which has high demand in China for traditional medicine purpose (Wong et al., 2020). The first SARS-CoV like CoV was named pangolin-CoV when it was identified in two Malayan pangolin’s (*Manis javanica*) carcasses that were trafficked for illegal wild animal market trade (Liu et al., 2020a). This was supported by the fact that pangolin CoV was closely related to SARS-CoV-2 (Fig-1) (Zhang, Xiao, Zhang, Roy, & Shen, 2020). The pangolin coronavirus genome shares 89% nucleotide and 98% amino acid resemblances with SARS-CoV-2 (Zhang, Xiao, Zhang, Roy, & Shen, 2020).

Along with the bat CoV, pangolin CoV was the second relative of SARS-CoV-2 (Zhang, Xiao, Zhang, Roy, & Shen, 2020). Besides, the spike protein of SARS-CoV is more like that of pangolin rather than that of bat (Goh, Dunker, Foster, & Uversky, 2020; Wang et al., 2020; Zhang, Xiao, Zhang, Roy, & Shen, 2020). The genetic analysis of the S glycoprotein of SARS-CoV-2 and related coronaviruses presumed that the RBD of SARS-CoV-2 S protein is a series of recombination events between the bat-CoV (RaTG13) and pangolin-CoV (MP789), might have ultimately directed to the advent of this novel coronavirus (Flores-Alanis, Sandner-Miranda, Delgado, Cravioto, & Morales-Espinosa, 2020).

But SARS-CoV-2 cannot be the descendant of pangolin CoV as the genetic variation is too high between them (Liu et al., 2020a). Besides, after screening 334 samples from Sunda pangolins from Peninsular Malaysia and Sabah between August 2009 to March 2019, no RNA of coronavirus could be detected (Lee et al., 2020). It was concluded that the earlier detection of SARS-CoV-2 related virus in pangolin reflects their exposure to infected humans, wildlife, or other animal species along the trading pathway (Lee et al., 2020). More interestingly, records from Wuhan’s market showed that 17 shops of the market sold 36,295 animals between May 2017 to November 2019, but no bat or pangolin was traded at that time period (Xiao, Newman, Buesching, Macdonald, & Zhou, 2021). So it is of utmost interest to the scientific community to know if pangolin is the natural host (Jaimes, André, Chappie, Millet, & Whittaker, 2020; Zhang, Wu, & Zhang, 2020) or the dead-end host (Frutos, Serra-Cobo, Chen, & Devaux, 2020) of SARS-CoV-2. Moreover, antibodies against SARS-CoV-2 were found in pangolin in Southern Thailand (Wacharapluesadee et al., 2021). Thus, future studies are required to prove the link between pangolin and SARS-CoV-2 (Cagliani, Forni, Clerici, & Sironi, 2020; Jaimes, André, Chappie, Millet, & Whittaker, 2020).

**3.2 Transmission dynamics of SARS-CoV-2 from humans to domestic and wild animals** After the emergence of SARS-CoV-2 in December 2019, several animal species are infected naturally from humans (Fig-1). Domestic animals like dogs, cats, and wild animals like tigers, lions, gorillas, leopards, puma, cougar, ferret, otter and mink have been infected by SARS-CoV-2 via reverse zoonoses (Table-2) (Enserink, 2020; Kiros et al., 2020; Oude Munnink et al., 2021). Animal species are primarily in contact with humans in settings like a household with pets, zoo, safari park, zoological centers, farms, etc. We compiled potential animal species which infected naturally and can act as a reservoir or intermediate or susceptible host.

**Table-2: Natural infection of SARS-CoV-2 in animal (do Vale et al., 2021; Hedman, Krawczyk, Helmy, Zhang, & Varga, 2021)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Animal species** | **Susceptibility** | **Infection level** | **Transmission** |
| **Companion animals** |  |  |  |
| Domestic Cat (*Felis catus*) | High | Sub-clinical | between cats |
| Dog (*Canis lupus familiaris*) | Less | Clinical and sub-clinical | not between dogs |
| **Zoo animals** |  |  |  |
| Tiger (*Panthera tigris*) | High | Clinical mostly | To another tiger |
| Lion (*Panthera leo*) | High | Clinical mostly | To another lion |
| Gorilla (*Gorilla gorilla*) | High | Clinical | - |
| Puma (*Puma concolor*) | - | Clinical | From human |
| Cougar (*Puma concolor*) | - | - | - |
| Snow leopard (*Prionailurus bengalensis euptilurus*) | Less | Mild clinical | From human |
| Asian small-clawed otter (*Aonyx cinereus*) | Unknown | Clinical | From human |
| **Farmed wild animals** |  |  |  |
| American Mink (*Neovison vison*) | High | Clinical | To and from human; to and from other mink; to feral cats |
| Ferret (*Mustela furo*) |  |  | From human |

**3.2.1 SARS-CoV-2 spillover events in companion animals**

**Domestic Cat:** SARS-CoV-2 can produce subclinical infection in cats. To date, 55 cats have been tested positive for SARS-CoV-2 by RT-PCR (Maurin et al., 2021). Natural infection in the cat has been reported in different countries including Spain, China, Hong Kong, Belgium, the USA, France, Germany, Russia, and the UK (Garigliany et al., 2020; Musso et al., 2020; Newman et al., 2020; Sailleau et al., 2020a; Segalés et al., 2020). At the beginning of the SARS-CoV-2 outbreak in China, antibodies against SARS-CoV-2 were detected in three different cats owned by three different patients, suggestive of human to cat transmission. Another study detected a considerable amount of antibodies against SARS-CoV-2 in serum samples from cats in Wuhan during and prior to the COVID-19 outbreak (Zhang et al., 2020c). Besides, serum samples collected from stray cats or hospital cats showed lower antibody titers. In contrast, SARS-CoV-2 was detected from symptomatic cat feces and vomitus in Belgium. Pet cats were also tested positive in New York, USA which suggests human-to-cat transmission (OIE, 2020). In Spain, eight cats were infected by humans (Ruiz-Arrondo et al., 2020). At least one infected human has one pet dog or cat in almost 25% of households in Texas, USA (Hamer et al., 2020). Cats from the abandoned household of SARS-CoV-2 patients and veterinary clinics showed seropositivity to SARS-CoV-2 in Wuhan, China (Zhang et al., 2020b). Furthermore, alpha (α) variant of concern (VOC) (lineage B.1.1.7) has been identified in a pet cat after contacted with infected COVID-19 owner in the USA (Hamer et al., 2021). The α VOC was also detected in cats from Thailand and Italy (Shu & McCauley, 2017). Interestingly, cats can be protected from SARS-CoV-2 if they become infected with other feline CoVs previously (Stout, André, Jaimes, Millet, & Whittaker, 2020). In conclusion, SARS-CoV-2 can affect cats more than dogs. To date, no spill-back event has been reported from cats to humans. But the shedding of the virus in cats increases the risk of cat-to-cat transmission. Besides, there is always the possibility of emerging new variants in animal species and subsequent infection to humans.

**Domestic Dog:** Natural infection of SARS-CoV-2 was found in domestic dogs in Hong Kong, USA, Germany, Japan, Canada, Brazil, Argentina, Mexico, Bosnia & Herzegovina (OIE).The first report of asymptomatic SARS-CoV-2 infectionwas found on 26 February 2020 in a Pomeranian dog in Hong Kong (Sit et al., 2020a). The owner of this dog was also tested positive for COVID-19 a few days ago (Sit et al., 2020a). After that, several dogs were found to be infected without showing any signs in Hong Kong. All of those dogs had a history of mutual living places with infected humans (Goumenou, Spandidos, & Tsatsakis, 2020; Patterson et al., 2020). Another dog was infected by its owner in the Netherlands (Delong, 2020). (Fritz et al., 2021) and (Patterson, 2020) detected high seroprevalence of SARS-CoV-2 in dogs from laboratory-confirmed COVID patients’ households in France and Italy, respectively. SARS-CoV-2 can reduce the smelling power of dogs (hyposmia, anosmia) (McNamara, Richt, & Glickman, 2020). Most recently a pet dog was found to be infected with α VOC, B.1.1.7 after being exposed to a COVID-19 patient (Hamer et al., 2021). Dogs from Thailand were also infected by the α VOC (Shu & McCauley, 2017).

Even scientists found limited productive replication of the virus in the canine nasal cavity with high ACE2 levels. The tropism and presence of the suitable receptor in dogs made are suitable for virus adaptation and reassortment (Bui et al., 2021). Due to the species’ suitability, continuous surveillance should be implemented in the dog population.

**3.2.2 SARS-CoV-2 spillover and spillback events in wild animals**

**3.2.2.1 SARS-CoV-2 spillover events from human to captive wild animals**

Several wild animal species naturally infected by SARS-CoV-2 from human which has been shown in Figure-1. To date, 15 tigers, 22 lions, and 3 gorillas have been infected by SARS-CoV-2 naturally (OIE, 2021). Two Malayan tigers (*Panthera tigris*), three Siberian tigers, and three African lions (*P. leo krugeri*) from Wildlife Conservation Society’s Bronx Zoo in New York acquired SARS-CoV-2 infection from the COVID-19 positive caretakers in the zoo (McAloose et al., 2020b) and all these animals developed mild respiratory signs and the infection might have occurred at asymptomatic or mild symptomatic animal caretakers in the zoo animals (WAHIS, 2020). Nine genomes were identified from these tigers, lions, and their keepers (McAloose et al., 2020b) of which, 2 distinct genotypes were detected (Lam, Ratmann, & Boni, 2018). It has been confirmed that transmission occurred from human to tiger but the exact route is still unclear (McAloose et al., 2020b). Two gorillas at the San Diego Zoo safari park in the USA, have been infected by COVID-19. Gorillas had mild symptoms like coughing and congestion. The zoo authority suspects that an asymptomatic worker who tested positive for SARS-CoV-2 might infect the gorillas. And most recently in a zoo in Hyderabad, India, 8 Asiatic lions are found to be infected by COVID-19 (Reuters, 2021). Natural infection was recorded in 1 cougar (*Puma concolor*) and 2 snow leopards (*Prionailurus bengalensis euptilurus*) from the USA, 1 leopard from the Czech Republic, 2 pumas (*P. concolor*) from Argentina and South Africa, 1 ferret (*Mustela furo*) from Slovenia (OIE, 2021). Moreover, the emerging α-variant (B.1.1.7) of SARS-CoV-2 was detected in dog and cat in the USA; gorilla, lions, leopard, and tiger in the Czech Republic; and lions from Sri Lanka (Shu & McCauley, 2017). Asiatic lions in India were infected with emerging delta variant (B.1.617.2) (Mishra et al., 2021) .

The serological evidence of SARS-CoV-2 was also reported in two household pet ferrets in Spain and antibodies endured at detectable levels in a seropositive SARS-CoV-2 status beyond 129 days of first detection (Giner et al., 2021). In this concern, serological assays may signify a viable opportunity to illuminate the host range of SARS-CoV-2 and in susceptible species including ferrets. Recently, SARS-CoV-2 has been detected in Asian small-clawed otters (*Aonyx cinereus*) at an aquarium in Georgia, USA (USDA, 2021). SARS-CoV-2 has infected several wild animal species and gradually increasing its host range. Though the wild animals were found to be infected by humans, the infection then can be transmitted among co-housed animals. Regular screening of staff and animals for SARS-CoV-2 should be done for early detection of the virus and any variants of concern in zoos and animal facilities.

**3.2.2.2 SARS-CoV-2 spillover and spillback events between farmed minks and humans**

Mink farming became popular due to the quality production of fur. Mink's fur is very valuable around the world. The global fur industry has grown recently and around 95 million mink and foxes were sacrificed for fur in 2014. The first farm was established in south Scotland in 1938 and industry expanded very rapidly and the number of farms rose to more than 100 in the late 140s and 1950s (Cuthbert, 1973). Fur production in Europe during 2018 was 34.7 million. Due to the concern about animal welfare, ethics, and inhuman killing, farming of mink for fur production was banned in the United Kingdom (2000), Austria (2005), Slovenia (2013), Republic of Macedonia (2014), Croatia (2018) and Serbia (2019). Outside Europe, mink farming is declared illegal in japan, New Zealand, and California, USA. Moreover, trading mink fur is banned in New Zealand, India, Brazil, and some states of the USA (California, Los Angeles, and San Francisco) (Bans, 2018).

The susceptibility of American mink (*Neovison vison*) to SARS-CoV-2 has already been established (Table-2). The virus causes respiratory disease with typical viral pneumonia in histopathology, which can be transmitted from each other. Till January 2021, 400 infected mink farms were identified in 8 countries in Europe- 290 farms in Denmark, 69 in the Netherlands, 21 in Greece, 13 in Sweden, 3 in Spain, 2 in Lithuania, 1 in France, and 1 in Italy (Authority et al., 2021). Minks from two different farms in the Netherlands showed respiratory and gastrointestinal disorders during April 2020. The mortality rate was estimated as 1.2-2.4% which was higher among pregnant animals. No variation in kid mortality was found. Interstitial pneumonia and other lung lesions were evident in necropsy findings. Viral RNA was detected from lung, throat, and rectal swabs, and also from the liver and intestines of the dead animals. The record of SARS-CoV-2 infected workers is evidence of possible human to animal transmission. However, sequencing of the initial data is suggestive in favor of mink to human transmission within mink farms (Munnink et al., 2021).

In December 2020, a free-ranging wild American mink was infected with SARS-CoV-2 in the USA. The animal was asymptomatic, and the infection was transmitted from a nearby affected commercial mink farm (Shriner et al., 2021). Besides, a mink farm in Denmark has reemergence of SARS-CoV-2 after 2 months of tested negative. The mutated virus is producing asymptomatic infection and the antibodies persist for a long period (OIE, 2021). Recently, the SARS-CoV-2 detected in two wild American mink in Spain highlights the potential significance of indirect transmission pathways of natural infection, seemingly wastewater, as a basis of infection (Aguiló-Gisbert et al., 2021) which suggest other aquatic roaming species of carnivores to investigate for their susceptibility to SARS-CoV-2 infection. Twelve feral cats and two dogs were infected by SARS-CoV-2 in the Netherland. The study concluded that the feral cats were infected from minks but whether the source of infection for the dogs were mink or humans was not clear (Enserink, 2020; van Aart et al., 2021).

A total of 644 human cases has been linked to mink farming in Denmark since June 2020. Moreover, more than half of these cases (N=338 cases) had a history of working with mink pelting, in six factories and two small facilities. It suggests that people who are involved in farming, culling, and pelting of mink have an increased risk of COVID-19 infection. Besides, till December 1, 2020, approximately 20% (289 farms) of all mink farms in Denmark have been infected with COVID-19 (WHO, 2020). The family dog of a mink farm owner has also been diagnosed with SARS-CoV-2. Immediately after identifying COVID-19 in mink farms, the authority took some steps to restrict the transmission. The control measures included entry and egress restriction, boosting of normal hygiene protocols for visitors to mink farms which include washing hands and changing clothes before and after animal handling (Hobbs & Reid, 2020b). The Danish government decided to 1). depopulate the infected mink farms till Mar 2021, 2). mandatory reporting of suspected or confirmed SARS-CoV-2 infections in Danish fur farms, 3). sampling and testing of fur animals (mink and ferrets), 4). safe handling of feed and manure, and 5). the quarantining, depopulation, and disinfection of the infected premises (Denis et al.; Hobbs & Reid, 2020b). Depopulation of mink farms is an inhumane act from an ethical point of view. Moreover, without characterizing the lethality or infectiousness of the isolated viruses from minks, farms were depopulated randomly. If we would know that the mink strain will not be lethal to humans, we could avoid the unnecessary killing of millions of minks. For this reason, we suggest banning mink farming for fur production as well as elaborate molecular characterization of mink variant viruses.

**3.3 Experimental infection of SARS-CoV-2 in domestic and wild animals**

The animal model for SARS-CoV-2 infection is important to understand the virus’s pathogenesis and to develop antivirals and vaccines. Non-human primates are best for this kind of experimental model, but they are expensive and difficult to restrain. Small animals like mice, ferrets, and hamsters have receptors for SARS-CoV and they were used for experimental studies (Glass, Subbarao, Murphy, & Murphy, 2004; Martina et al., 2003; Roberts et al., 2005). Domestic dogs and cats were also used for experimental purposes (Cleary et al., 2020; Sarkar & Guha, 2020). To check the antibody status, ELISA kits were also used (Deng et al., 2020). ACE-2 receptors are found only in few specific animal species (Damas et al., 2020). Animal species which are in contact with human cases of SARS-CoV-2 or in zoo or safari park, zoological centers, rehabilitation centers, or in farms are mainly used for experimental inoculation. We compiled the animal species which can act as reservoir, intermediate or susceptible host (Table-3).

**Table-3: Experimental infection of SARS-CoV-2 in different domestic and wild animal species (do Vale et al., 2021; Hedman, Krawczyk, Helmy, Zhang, & Varga, 2021)**

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Susceptibility to infection (none/extremely low/low/medium/high)** | **Symptoms** | **Transmission** |
| **Domestic animals** | | | |
| Dog (*Canis lupus familiaris*) | Less | No | No |
| Cat (*Felis catus*) | High | No | Yes |
| Pig (American Yorkshire crossbred pigs, *Sus scrofa*) | Not susceptible | No | No |
| Bird (Chicken, duck, turkey) | Not susceptible | No | No |
| Cattle (*Bos taurus*) | Very low | No | No |
| Camel (*Camelius dromedarius*) | Less | - | - |
| **Wild animals** | | | |
| Mice | Low | No | Yes |
| Golden Syrian Hamsters (*Mesocricetus auratus*) | High | Yes, but depends on the age | Yes |
| Mustelids (Ferrets) | High | Only in a small no of cases | Yes |
| Mink | High | In some cases | yes |
| Raccoon (*Nyctereutes procyonoides*) | High | No | Yes |
| Reptiles | None | - | - |
| Macaque (*Macaca fascicularis, M. mulatta*) | High | Yes | Yes |
| Egyptian fruit bat (*Rousettus aegyptiacus*) | High | No | Yes |
| Tree shrews (*Tupaia belangeri chinensis*) |  |  |  |
| Lagomorphs (*Oryctolagus cuniculus*) | High | No | No |
| White-tailed deer (*Odocoileus virginianus*) | High | No | Yes |
| Marmosets (*Callithrix jacchus*) | High | No | No |

**3.3.1. Susceptibility of SARS-CoV-2 in domestic animals**

**Domestic dogs-** Dogs were found to be less susceptible to SARS-CoV-2 during experimental inoculation (Hobbs & Reid, 2020a). The virus can accumulate in the kidney, the heart of dogs whereas in humans the predilection site is the lungs (Zhai et al., 2020). Simultaneous activities of ACE-2 and TMPRSS2 were not found in dogs’ lungs (Chen et al., 2020). Moreover, the required amino acids for the ACE-2 receptor cannot be found in canids (Mathavarajah & Dellaire, 2020). There is no evidence of SARS-CoV-2 detection from an oro-pharyngeal sample from the dog. But the rectal swabs tested positive for viral RNA in experimental infection (Hobbs & Reid, 2020a). However, two dogs were reported to be SARS-CoV-2 positive at a minute degree which can be described as low infection with a minimum likelihood of virus transmission (Leroy, Ar Gouilh, & Brugere-Picoux, 2020). After 4 days of intranasal inoculation of a Chinese strain of SARS-CoV-2 in a dog breed, beagle, the virus was found only in rectal swabs but not in other organs. The viable virus could not be found in inoculated dogs. Dogs shared housing with inoculated ones had no antibody or virus suggesting SARS-CoV-2’s lower affinity to dogs (Shi et al., 2020). Canids may play the role of the intermediate or dead-end host but not a reservoir of SARS-CoV-2 and they have very low ability for virus shedding and transmission.

**Domestic Cats-** Experimental infection in cats resulted in viral loads in the respiratory tract and small intestine. The airborne transmission was also documented in cats (Halfmann et al., 2020; Shi et al., 2020). Though the virus was isolated, and antibody was found in cats after experimental inoculation, but they did not show any signs. So, cats are more susceptible to SARS-CoV-2 than dogs. Interestingly, cats recovered from SARS-CoV-2 have protective immunity from being re-infected via experimental inoculation (Bosco-Lauth et al., 2020).

**Pigs-** Intra-nasal inoculation of SARS-CoV-2 in domestic pig (*Sus scrofa domesticus*) did not produce any antibody or revealed any virus (Schlottau et al., 2020; Shi et al., 2020). Even the in-house contact pigs had no virus or antibody (Shi et al., 2020). It suggested pigs are not susceptible to SARS-CoV-2. But pigs’ ACE-2 receptor may favor the binding of SARS-CoV-2 (Qiu et al., 2020).

**Birds-** Avian species are not susceptible to SARS-CoV-2. During the experiment, the Wuhan strain and German strain of SARS-CoV-2 showed neither RNA nor antibodies from the sample even they did not show any clinical signs as well (Schlottau et al., 2020; Wu, Wang, & Evans, 2019). Further studies showed neither RNA nor antibodies against the virus from the duck sample (Wu, Wang, & Evans, 2019). However, to date, chicken, duck, turkey, quail, and geese did not show any clinical signs or evidence of viral replication or antibodies during challenges with the SARS-CoV-2 viral strain (Suarez et al., 2020). But SARS-CoV-2 can use pigeon ACE-2 receptors (Qiu et al., 2020).

**Camel**- Camels are less susceptible to SARS-CoV-2 (Wong et al., 2020). Experimental studies are still very few regarding camels susceptibility to the virus. (Gai et al., 2020) immunized camel with SARS-CoV-2 spike protein RBD and collected the antibodies and used in humans to reduce the interaction with ACE-2 receptor.

**3.3.2 Susceptibility of SARS-CoV-2 in wild animals**

**Rodents**- Free-ranging rodents can catch the virus from humans and there is also the chance of reverse zoonosis of SARS-CoV-2 (Gryseels et al., 2020). It is also may be a concern that SARS-CoV-2 can adapt in wild rodents in natural environments and then again can transmit to humans (Konda, Dodda, Konala, Naramala, & Adapa, 2020).

**Mice**- Wild and transgenic mice were used for experimental purposes. Nevertheless, SARS-CoV-2 has a less binding capacity to murine ACE2 receptors (Lei et al., 2020; Letko, Marzi, & Munster, 2020; Wan, Shang, Graham, Baric, & Li, 2020). So, the researcher used transgenic mice with human ACE2 receptors rather than wild mice (Bao et al., 2020b). SARS-CoV-2 can exert a slight effect on hACE2 mice but not on WT-HB-01 mice. SARS-CoV-2 has a low affinity to mice without the hACE2 receptor. It was also observed that mice that were treated with human convalescent serum have fewer viral loads in their lungs (Boudewijns et al., 2020b). Deer mice are susceptible to SARS-CoV-2 after experimental inoculation but do not show any signs of illness. They can also transmit the virus to un-inoculated susceptible mice (Fagre et al., 2020). Sometimes, a serum sample from other rodent species gives negative ELISA test results for SARS-CoV-2 (Deng et al., 2020). Most recently two variants of concern (B.1.351 and P.1) of SARS-CoV-2 are able to infect laboratory mice with high titers in the lungs (Montagutelli et al., 2021). But there is also the possibility of wild rodents being the reservoirs of the virus (OIE, 2021). Future research should be directed to assess the spreading capability of SARS-CoV-2 to deer mice and deer mice to house mice and humans. Rodents are a model animal for SARS-CoV-2 vaccine development also (Dagotto, Yu, & Barouch, 2020; Dinnon et al., 2020; Jiang, Hillyer, & Du, 2020; Tian et al., 2020).

**Hamsters-** Golden Syrian hamsters (*Mesocricetus auratus*) were inoculated nasally with a strain from Hong Kong. Though they developed different signs, no animal died (Chan et al., 2020b). They transmitted the virus to naïve co-housed hamsters (Sia et al., 2020). Passive immunity increased the body’s defense and reduced the viral loads in hamsters (Chan et al., 2020a). STAT2 protein in hamsters impeded the viral spreading throughout the systems, though lung pathology increased (Boudewijns et al., 2020a). Chinese hamsters lose weight after experimental infection. The viral RNA and infectious virus were found in the nose, oropharynx, and trachea (Bertzbach et al., 2020).

**Mustelids-** Environmental samples from the Wuhan seafood market and samples from a COVID-19 patient were tested for virulence by (Shi et al., 2020). Intranasal inoculation of the virus in ferrets resulted in viral excretion in the upper respiratory tract but no virus was detected in the trachea, lungs, heart, liver, spleen, kidney, pancreas, small intestine, and brain. Rectal swabs had no detectable viral RNA. Fever and appetite loss were observed only in two ferrets on the 10th and 12th days of post-infection. Antibodies against SARS-CoV-2 were detected in ELISA and serum neutralization test (SNT). The same researcher detected viral RNA in the upper respiratory tract and trachea after 8 days of intra-nasal post-infection in ferrets (Shi et al., 2020). (Kim et al., 2020b) inoculated a Korean strain of SARS-CoV-2 intra-nasally in ferrets. Signs included high body temperature, decreased physical activity, sometimes coughing. Virus RNA was detected in serum, nostril washes, saliva, urine, feces, trachea, lungs, intestine, and kidneys. Other ferrets, housed together with these experimental animals, had antibodies that suggested transmission of the virus by direct contact and by indirect contacts via air (Kim et al., 2020b).

Intranasal inoculation of a German strain of the virus was done in ferrets and then the ferrets were placed with naive ferrets in the same house. It was done to determine whether there is airborne transmission or not. After 19 days of inoculation, viral RNA was detected in challenged animals. Whereas naïve ferrets shed the virus after 17 days of exposure. The naïve ferrets then transmitted the virus to other ferrets via indirect contact. Viral RNA was found after 13-19 days of airborne transmission. Nasal swabs had more viral concentration than that of the throat and rectal swabs, but viable viruses were found from nasal and throat swabs but not from rectal swabs. Interestingly, whatever the route of transmission was (experimentally infected, direct, or indirect contact), all the ferrets had the same antibody level at days of post-infection (Richard et al., 2020). Moreover, another experiment showed that a German strain of SARS-CoV-2 can infect other ferrets housed together with experimental ferrets but showed no signs of disease (Beer, 2020; Schlottau et al., 2020).

**Raccoon-** Moderate susceptibility of raccoon (*Nyctereutes procyonoides*) was found in experimental infection by 105 median tissue culture infectiousdose (TCID50) intra-nasally. No clinical sign was observed but a viable virus was found in the raccoon. Antibody was detected also. The virus transmitted to contact animals had a high viral load in the nose and throat than the rectum (Freuling et al., 2020). The ACE-2 receptor of raccoon and domestic dogs are similar (Zhai et al., 2020).

**Reptiles-** Turtles’ andsnakes’ ACE-2 receptors interact with S protein RBD thus making them potential intermediate hosts of SARS-CoV-2 (Liu et al., 2020b). But later many researchers proved it wrong. Similarly, the many-branded krait (*Bungarus multicinctus*) and the Chinese cobra (*Naja atra*) use the same protein patterns as humans. That is why some hypothesized that these 2 snake species can act as wildlife reservoirs of SARS-CoV-2 (Ji, Wang, Zhao, Zai, & Li, 2020). But this study could not be replicated and proved to be not right due to the small number of protein sequences, vertebrate diversity, and outdated codon usage (Gong & Bao, 2018; Luan, Lu, Jin, & Zhang, 2020; Zhang et al., 2020a). Moreover, (Luan, Jin, Lu, & Zhang, 2020) snakes’ ACE2 cannot interact with the S protein of SARS-CoV-2 anymore. So, the snake cannot act as an intermediate host of SARS-CoV-2.

**Non-human primates-** Experimental studies have been done in rhesus macaques (*M. mulatta*) (Bao et al., 2020a; Hedman, Krawczyk, Helmy, Zhang, & Varga, 2021; Munster et al., 2020), cynomolgus macaques (*M. fascicularis*) (Hedman, Krawczyk, Helmy, Zhang, & Varga, 2021), New World monkey (*Callithrix jacchus*) (Maurin et al., 2021) and green monkeys (*Chlorocebus sabaeus*) (Woolsey et al., 2020). Rhesus macaques had a recurrent fever and there were no respiratory symptoms after inoculation of SARS-CoV-2 experimentally through oral, nasal, ocular, and tracheal route (Maurin et al., 2021; Munster et al., 2020). Some degrees of loss of weight was observed with the altered respiratory pattern, piloerection, anorexia, abdominal pain, dehydration, and paleness. Recovery after viral inoculation was observed between 9 to 17 days. The virus was identified from several organs of the respiratory and gastrointestinal tract. Viral antibodies persisted until the 10th day of inoculation (Munster et al., 2020). Shan et al. (2020) inoculated SARS-CoV-2 in the trachea of rhesus macaques. But only one macaque showed recurrent anorexia while others showed no signs. Moreover, the virus could not be detected in blood though a high level was found in oropharyngeal swabs. Another study also inoculated SARS-CoV-2 intratracheally in rhesus macaques. Subsequent signs included loss of body weight, transient anorexia, and hunched posture (Bao et al., 2020a). The virus was detected from several organs including the nose, lungs, GI tract, heart, bladder, etc. Antibodies against SARS-CoV-2 were identified in 14, 21, and 28 days of post-infection. When the macaques were re-infected by SARS-CoV-2 after 28 days of post-infection, no viral RNA or antibody was found in them. This indicated the macaques were protected against re-infection (Bao et al., 2020a). If macaques are vaccinated with adenovirus serotype 26 (Ad26) vector vaccine, they can be protected against SARS-CoV-2 (Mercado et al., 2020).

A comparative conducted by Lu et al. (2020b) found similar findings as others but there were higher viral titers in *Macaca* sp. compared with *C. jacchus.* Moreover, no virus was detected in the pulmonary tissues of *C. jacchus,* there were no macroscopic lesions observed in the lung tissues and finally animal did not develop a specific antibody response to SARS CoV-2. In summary, none of the non-human primates developed critical diseases but *Macaca* sp. was more susceptible to SARS CoV-2 infection than *C. jacchus.*

**Bats-** Experimental intra-nasal inoculation of a German strain in Rousettus fruit bats which are considered as a putative reservoir of this virus, resulted in oral viral shedding until 12 days of inoculation but there were no symptoms (Schlottau et al., 2020). The virus was detected in the respiratory, heart, skin, and intestinal tissue. Inoculated and contact bats had antibodies against SARS-CoV-2. Bat to bat transmission was observed between inoculated bats and contact bats (Schlottau et al., 2020). Experimental infection in Egyptian fruit bats (*R. aegyptiacus*) results in no clinical signs. But the viral RNA was detected in the oral cavity, trachea, lungs, lymph nodes, heart, skin, duodenum, and adrenal gland tissues whereas infectious viruses were found in the nose and trachea. The virus was transmitted to other contact animals (Schlottau et al., 2020).

**Tree shrews-** ChineseTree shrews (*Tupaia belangeri chinensis*) were experimentally infected via the intranasal route. Most females had elevated body temperature but no other signs. The virus was detected in younger animals especially, until 12 days of inoculation (Zhao et al., 2020). But tree shrews can act as intermediate hosts or asymptomatic carriers of SARS-CoV-2 (Zhao et al., 2020).

**Lagomorphs (Rabbit) -** (Damas et al., 2020; Gao, Luan, Cui, & Zhang, 2020; Kumar et al., 2020; Preziuso, 2020) reported binding of SARS-CoV-2 to lagomorphs’ ACE-2 receptor. New Zealand white rabbits (*Oryctolagus cuniculus*) shed the virus after experimental infection (Mykytyn et al., 2021). Rabbits are less infected by SARS-CoV-2 than hares and ferrets (Mykytyn et al., 2021). Farmed rabbits can infect with viruses, as like mink (Enserink, 2020), and can infect humans (Yekta, Vahid-Dastjerdi, Norouzbeigi, & Mortazavian, 2020). For this reason, advanced studies should be done to explore the adaptability of SARS-CoV-2 in the rabbit population and its infectiousness in humans.

**Cervids (Deer) -** White-Tailed Deer (WTD) (*Odocoileus virginianus*) has been identified as highly susceptible to infection with SARS-CoV-2 due to the high degree of resemblance of ACE2 receptors of white-tailed deer with human ACE2 (Palmer et al., 2021). Furthermore, infected animals were able to shed the SARS-CoV-2 virus through nasal secretions and feces. Notably, indirect contact WTD were infected and shed the virus, signifying effective SARS-CoV-2 transmission from experimental animals. As a result, the spillover of SARS-CoV-2 from humans to cervids might happen at captive deer farms and zoos. For example, farmed deer can mix with wild deer and other species where biosecurity measures are insufficient, this might stipulate possibilities to transmit the virus in feral wild animals.

**3.4 Sustainable one health surveillance for prevention and control of future epidemic and pandemic like Disease X**

The three organizations- Food and Agricultural Organization (FAO), OIE, and World Health Organization (WHO) are jointly working for a long time to reduce the impact of zoonotic and other important diseases. They emphasize preventing diseases directly or indirectly arise from animals at the human-animal interface. One ninety-three countries endorsed the 2015-30 Sustainable Development Goals which admitted the importance of a united approach to society and the environment. From a healthcare standpoint, they emphasized the importance of a One Health approach that embraces human, animal, and environmental health and realizes their serious interdependence. The contemporary pandemics (like SARS, MERS, 2009 H1N1 influenza, COVID-19) prominence the necessity for us all to make and respond more efficiently to infection spillover from animals to humans as well as the challenges posed by the degradation of the natural environment. The economic benefits of this approach sufficiently warrant the costs involved (Dobso et al., 2020).

The WHO Research and Development Blueprint publishes an annual list of priority diseases to guide governmental concentration to research and development on conditions that pose significant public health threats (Mehand, Al-Shorbaji, Millett, & Murgue, 2018). “Disease X,” a surrogate name serving as a reminder that the most critical disease risk is likely the one as yet unknown, capped the 2018 list (Mehand, Al-Shorbaji, Millett, & Murgue, 2018). The current Disease X is COVID-19, but there will certainly be more. The pandemic is not under full control yet, but we need to think about future mitigation strategies from now on.

The advent of the COVID-19 pandemic is a One Health challenge that pleads for collective attempts from various fields and experts. But a roadmap must be executed first, by placing a One Health approach in place. Though it is unknown when the next threat will arrive or what it will be, health systems and decision-makers can grab this COVID-19 pandemic as a chance to focus the multifaceted contacts among humans, animals, plants, and the environment and to reassembling our health systems to be better prepared for the next complex One Health confront that we will unavoidably tackle.

The transboundary disease risk of animal origin is increasing day by day due to several factors including changes in the landscape, ecology, and behavior of the human community which also increase the chance of generating more mutant viruses and adapt to a new host. SARS-CoV-2 is a hazard for free-ranging wild animals. So, a risk assessment should be conducted in a qualitative way (very low to high) to identify the risk of release, exposure, and infection by SARS-CoV-2. The risk will be determined by combining the “likelihood assessment scale” and “consequence assessment scale” (Logeot et al., 2021). Moreover, biosecurity measures should be taken to reduce the risk of human-animal contact and to prevent exposure of free-ranging wild animals to the virus. A guideline has been published in this regard (IUCN, 2020). The emergence of some deadly viruses including Ebola, Zika, Dengue, Nipah encephalitis, Bird flu, Swine flu, MERS-CoV, and current pandemic SARS-CoV-2 (Dhama et al., 2018; Dhama et al., 2012; Munjal et al., 2017; Singh et al., 2019) taught us the lesson for practicing strict biosecurity measures to prevent introduction or reemergence of the virus into the population which has already proved effective for preventing transboundary epizootics.

Functional wildlife health surveillance program is absent in most of the countries of the world. Wildlife and the environment are not getting priority in health security plans despite their importance for pandemic prevention. To reduce known and novel disease risk, wildlife health capacity, and operations should be strengthened in the One Health approach (Machalaba, Uhart, Ryser-Degiorgis, & Karesh, 2021). OIE expert groups have given a statement on wildlife trade and emerging zoonotic diseases also (OIE, 2020). The virus can transmit from humans to domestic animals and subsequently to wildlife. Some wild animal species like bats, primates, rodents live in groups. It facilitates the spreading of viruses from a single animal to a large group of animals. This spread increase risk of the establishment of the virus in wildlife and the emergence of viral strains capable of transmitting back to humans or domestic animals through reverse zoonoses. Though several species of animals have been infected to date, we still do not know exactly which animal species will be adapted to the virus. Knowledge of animal reservoirs and the transmission cycle will mitigate the gaps between animal to human spread in the future.

Moreover, veterinary laboratories all over the world were well equipped which helped to support the public health response for COVID-19 during the pandemic (OIE, 2021). This resource should be used in the future also for surveillance of both humans and animals worldwide. We should also eliminate the possibility of SARS-CoV-2 establishment in novel animal hosts to reduce the animal to human transmission (Olival et al., 2020; Sun et al., 2020). Continuous sero- and genomic surveillance will guarantee effective vaccine production. We need to think about vaccines also for pet animals as they can be an asymptomatic carrier of the virus. A company named Applied DNA Sciences and EvviVax is producing a vaccine candidate name LinearDNATM COVID-19 for use in cats against COVID-19. The vaccine is under trial in domestic felines after receiving approval from the United States Department of Agriculture (Brook, 2020; Sharun et al., 2021). The renowned company Zoetis has produced a vaccine for dogs and cats and found it effective in a preliminary trial. They are experimentally using the vaccine in captive bonobos and orangutans at the San Diego zoo in the USA (Daly, 2021). But vaccination of pet and farmed animals is complex. Vaccination in companion animals will be feasible only when they are in contact with the immunocompromised human. But it is very difficult for farmed animals. We saw that minks were infected by humans and it can be prevented by strict biosecurity and immunization of workers in those farms. Vaccination of mink can only be then complementing the biosecurity measures. We will get over the COVID-19 pandemic eventually. Nevertheless, we should not wait until the next pandemic before applying the One Health approach to secure a healthier future for our nation and the world.

In addition, rapid diagnosis, observance, isolation, and quarantine measures are needed to formulate for the future prevention and control of pandemic potential disease spread. Moreover, intensive medical care facilities, public health awareness buildup program, networking, rapid communication, and international collaboration are needed to develop against any pandemic potential emerging virus to prevent haunting the lives of billions of human populations (Bonilla-Aldana, Dhama, & Rodriguez-Morales, 2020; Dhama et al., 2020; Malik et al., 2020; Rodriguez-Morales et al., 2020).

1. **Conclusion:**

SARS-CoV-2 is assumed to emerge from an animal source and later spillover to humans. Even though SARS-CoV-2 related viruses have been detected in Rhinolophus bats and pangolin but the exact source and route of introduction into the human population has not been established yet. Multiple domestic and wild animal species have been infected naturally from humans and some species demonstrated susceptibility in experimental settings. Moreover, alpha variant, B.1.1.7 has been detected in pet dog and cat after contacting with COVID-19 positive owner whereas beta variant, B.1.351 has been detected in rodents in experimental condition. Humans are at risk of contracting mutated strains from animals as they can be an asymptomatic carrier of the virus. The continuing spillover and spillback of SARS-CoV-2 in a wide range of animals in farming, captive and free ranging interfaces make inferences for human and animal health, welfare and conservation. Besides, authorities should take steps to make traditional animal markets safer to reduce public health risks. But capturing wild mammals for food or breeding should be banned also. Moreover, we recommend a combined one health surveillance in both human and animals to prevent future epidemics and pandemics. Vaccination of pet, farmed and captive wild animals in accordance with vaccination in humans should be done.

**Acknowledgment**

We gratefully acknowledge all researchers for submitting SARS-CoV-2 related articles in animals into databases that was used for writing this manuscript. The authors are thankful to the Institute of Epidemiology Disease Control and Research (IEDCR), EcoHealth Alliance, NY, USA, and Chattogram Veterinary and Animal Sciences University (CVASU) for their continued support to our research team. The authors did not receive any external funds to conduct this research. However, the research team was partially supported by NIH U01AI153420-01 (PI Epstein) through EcoHealth Alliance.

**Ethical approval:** No ethical approval was needed.

**Conflict of interest**: The authors declare that they have no conflict of interest.

**References:**

Aguiló-Gisbert, J., Padilla-Blanco, M., Lizana, V., Maiques, E., Muñoz-Baquero, M., Chillida-Martínez, E., . . . Rubio-Guerri, C. (2021). First Description of SARS-CoV-2 Infection in Two Feral American Mink (Neovison vison) Caught in the Wild. *Animals, 11*(5), 1422.

Ashour, H. M., Elkhatib, W. F., Rahman, M., & Elshabrawy, H. A. (2020). Insights into the recent 2019 novel coronavirus (SARS-CoV-2) in light of past human coronavirus outbreaks. *Pathogens, 9*(3), 186.

Authority, E. F. S., Prevention, E. C. f. D., Control, Boklund, A., Gortázar, C., Pasquali, P., . . . Broglia, A. (2021). Monitoring of SARS‐CoV‐2 infection in mustelids. *EFSA Journal, 19*(3), e06459.

Bans, F. F. (2018). https://[www.furfreealliance.com/fur-bans/](http://www.furfreealliance.com/fur-bans/) (accessed on 3 July, 2021).

Bao, L., Deng, W., Gao, H., Xiao, C., Liu, J., Xue, J., . . . Xu, Y. (2020a). Reinfection could not occur in SARS-CoV-2 infected rhesus macaques. *bioRxiv*.

Bao, L., Deng, W., Huang, B., Gao, H., Liu, J., Ren, L., . . . Qin, C. (2020b). The pathogenicity of SARS-CoV-2 in hACE2 transgenic mice. *Nature, 583*(7818), 830-833. doi: 10.1038/s41586-020-2312-y

Barrs, V. R., Peiris, M., Tam, K. W., Law, P. Y., Brackman, C. J., To, E. M., . . . Sit, T. H. (2020). SARS-CoV-2 in Quarantined domestic cats from COVID-19 households or close contacts, Hong Kong, China. *Emerging infectious diseases, 26*(12), 3071-3074.

Beer, M. (2020). COVID‐19: Experimental infection of fruit bats, ferrets, pigs and chicken with SARS‐CoV‐2 at Friedrich‐Loeffler‐Institut. *ProMed‐mail. Archive*(20200407.7196506).

Bertzbach, L. D., Vladimirova, D., Dietert, K., Abdelgawad, A., Gruber, A. D., Osterrieder, N., & Trimpert, J. (2020). SARS‐CoV‐2 infection of Chinese hamsters (Cricetulus griseus) reproduces COVID‐19 pneumonia in a well‐established small animal model. *Transbound Emerg Dis*.

Bonilla-Aldana, D. K., Dhama, K., & Rodriguez-Morales, A. J. J. A. A. V. S. (2020). Revisiting the one health approach in the context of COVID-19: a look into the ecology of this emerging disease. *8*(3), 234-237.

Bosco-Lauth, A. M., Hartwig, A. E., Porter, S. M., Gordy, P. W., Nehring, M., Byas, A. D., . . . Bowen, R. A. (2020). Experimental infection of domestic dogs and cats with SARS-CoV-2: Pathogenesis, transmission, and response to reexposure in cats. *Proceedings of the National Academy of Sciences, 117*(42), 26382-26388.

Boudewijns, R., Thibaut, H. J., Kaptein, S. J., Li, R., Vergote, V., Seldeslachts, L., . . . Van Weyenbergh, J. (2020a). STAT2 signaling as double-edged sword restricting viral dissemination but driving severe pneumonia in SARS-CoV-2 infected hamsters. *bioRxiv*.

Boudewijns, R., Thibaut, H. J., Kaptein, S. J. F., Li, R., Vergote, V., Seldeslachts, L., . . . Dallmeier, K. (2020b). STAT2 signaling as double-edged sword restricting viral dissemination but driving severe pneumonia in SARS-CoV-2 infected hamsters. *bioRxiv*, 2020.2004.2023.056838. doi: 10.1101/2020.04.23.056838

Brook. (2020). Applied DNA, EvviVax, and GVS Receive Regulatory Approval to Conduct Veterinary Clinical Trial for Linear COVID-19 Vaccine Candidate. Available at: https://[www.businesswire.com/news/home/20201130005340/en/Applied-DNA-EvviVax-andGVS-Receive-Regulatory-Approval-to-Conduct-Veterinary-Clinical-Trial-for-Linear-COVID-19-Vaccine-Candidate](http://www.businesswire.com/news/home/20201130005340/en/Applied-DNA-EvviVax-andGVS-Receive-Regulatory-Approval-to-Conduct-Veterinary-Clinical-Trial-for-Linear-COVID-19-Vaccine-Candidate) (Accessed on: March 28, 2021).

Brook, C. E., & Dobson, A. P. (2015). Bats as 'special' reservoirs for emerging zoonotic pathogens. *Trends Microbiol, 23*(3), 172-180. doi: 10.1016/j.tim.2014.12.004

Bui, C. H. T., Yeung, H. W., Ho, J. C. W., Leung, C. Y. H., Hui, K. P. Y., Perera, R., . . . Chan, M. C. W. (2021). Tropism of SARS-CoV-2, SARS-CoV and influenza virus in canine tissue explants. *J Infect Dis*. doi: 10.1093/infdis/jiab002

Cagliani, R., Forni, D., Clerici, M., & Sironi, M. (2020). Computational inference of selection underlying the evolution of the novel coronavirus, severe acute respiratory syndrome coronavirus 2. *Journal of virology, 94*(12).

Chan, J. F.-W., Zhang, A. J., Yuan, S., Poon, V. K.-M., Chan, C. C.-S., Lee, A. C.-Y., . . . Wen, L. (2020a). Simulation of the clinical and pathological manifestations of Coronavirus Disease 2019 (COVID-19) in a golden Syrian hamster model: implications for disease pathogenesis and transmissibility. *Clinical Infectious Diseases, 71*(9), 2428-2446.

Chan, J. F.-W., Zhang, A. J., Yuan, S., Poon, V. K.-M., Chan, C. C.-S., Lee, A. C.-Y., . . . Yuen, K.-Y. (2020b). Simulation of the Clinical and Pathological Manifestations of Coronavirus Disease 2019 (COVID-19) in a Golden Syrian Hamster Model: Implications for Disease Pathogenesis and Transmissibility. *Clinical Infectious Diseases, 71*(9), 2428-2446. doi: 10.1093/cid/ciaa325

Chen, D., Sun, J., Zhu, J., Ding, X., Lan, T., Zhu, L., . . . Wang, X. (2020). Single-cell screening of SARS-CoV-2 target cells in pets, livestock, poultry and wildlife. *bioRxiv*.

Chen, L., Liu, B., Yang, J., & Jin, Q. (2014). DBatVir: the database of bat-associated viruses. *Database, 2014*.

Cleary, S. J., Pitchford, S. C., Amison, R. T., Carrington, R., Robaina Cabrera, C. L., Magnen, M., . . . Page, C. P. (2020). Animal models of mechanisms of SARS‐CoV‐2 infection and COVID‐19 pathology. *British journal of pharmacology, 177*(21), 4851-4865.

Cuthbert, J. (1973). The origin and distribution of feral mink in Scotland. *Mammal Review, 3*(3), 97-103.

Dagotto, G., Yu, J., & Barouch, D. H. (2020). Approaches and challenges in SARS-CoV-2 vaccine development. *Cell host & microbe*.

Daly, N. (2021). First great apes at U.S. zoo receive COVID-19 vaccine made for animals. Available at: https://[www.nationalgeographic.com/animals/article/first-great-apes-at-uszoo-receive-coronavirus-vaccine-made-for-animals](http://www.nationalgeographic.com/animals/article/first-great-apes-at-uszoo-receive-coronavirus-vaccine-made-for-animals) (Accessed on: March 27, 2021).

Damas, J., Hughes, G. M., Keough, K. C., Painter, C. A., Persky, N. S., Corbo, M., . . . Zhao, H. (2020). Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. *Proceedings of the National Academy of Sciences, 117*(36), 22311-22322.

Delong, J. (2020). Dutch Minister confirms dog, three cats have caught novel coronavirus. *American Reporter*.

Deng, J., Jin, Y., Liu, Y., Sun, J., Hao, L., Bai, J., . . . Tian, K. (2020). Serological survey of SARS‐CoV‐2 for experimental, domestic, companion and wild animals excludes intermediate hosts of 35 different species of animals. *Transboundary and emerging diseases, 67*(4), 1745-1749.

Denis, M., Vandeweerd, V., VERBEEKE, R., Laudisoit, A., REID, T., HOBBS, E., & WYNANTS, L. Information available to support the development of medical countermeasures and interventions against COVID-19.

Dhama, K., Karthik, K., Khandia, R., Chakraborty, S., Munjal, A., Latheef, S. K., . . . Singh, R. J. F. i. i. (2018). Advances in designing and developing vaccines, drugs, and therapies to counter Ebola virus. *9*, 1803.

Dhama, K., Sharun, K., Tiwari, R., Dadar, M., Malik, Y. S., Singh, K. P., . . . immunotherapeutics. (2020). COVID-19, an emerging coronavirus infection: advances and prospects in designing and developing vaccines, immunotherapeutics, and therapeutics. *16*(6), 1232-1238.

Dhama, K., Verma, A. K., Rajagunalan, S., Deb, R., Karthik, K., Kapoor, S., . . . Chakraborty, S. J. P. j. o. b. s. P. (2012). Swine flu is back again: a review. *15*(21), 1001-1009.

Dinnon, K. H., Leist, S. R., Schäfer, A., Edwards, C. E., Martinez, D. R., Montgomery, S. A., . . . Adams, L. E. (2020). A mouse-adapted model of SARS-CoV-2 to test COVID-19 countermeasures. *Nature, 586*(7830), 560-566.

do Vale, B., Lopes, A. P., da Conceição Fontes, M., Silvestre, M., Cardoso, L., & Coelho, A. C. (2021). Bats, pangolins, minks and other animals-villains or victims of SARS-CoV-2? *Veterinary research communications*, 1-19.

Dobso, A. P., Pim, S. L., Hannah, L., Kaufman, L., Ahumad, J. A., Bernstein, A., . . . Kinnair, M. F. (2020). Ecology and economics for pandemic prevention: Investments to prevent tropical deforestation and to limit wildlife trade will protect against future zoonosis outbreaks. *Science, 369*(6502).

El-Sayed, A., & Kamel, M. (2021). Coronaviruses in humans and animals: the role of bats in viral evolution. *Environmental Science and Pollution Research*, 1-12.

Enserink, M. (2020). Coronavirus rips through Dutch mink farms, triggering culls: American Association for the Advancement of Science.

Fagre, A., Lewis, J., Eckley, M., Zhan, S., Rocha, S. M., Sexton, N. R., . . . Kading, R. (2020). SARS-CoV-2 infection, neuropathogenesis and transmission among deer mice: Implications for reverse zoonosis to New World rodents. *bioRxiv*.

Flores-Alanis, A., Sandner-Miranda, L., Delgado, G., Cravioto, A., & Morales-Espinosa, R. (2020). The receptor binding domain of SARS-CoV-2 spike protein is the result of an ancestral recombination between the bat-CoV RaTG13 and the pangolin-CoV MP789. *BMC research notes, 13*(1), 1-6.

Freuling, C. M., Breithaupt, A., Müller, T., Sehl, J., Balkema-Buschmann, A., Rissmann, M., . . . Wernike, K. (2020). Susceptibility of raccoon dogs for experimental SARS-CoV-2 infection. *bioRxiv*.

Fritz, M., Rosolen, B., Krafft, E., Becquart, P., Elguero, E., Vratskikh, O., . . . Leroy, E. M. (2021). High prevalence of SARS-CoV-2 antibodies in pets from COVID-19+ households. *One Health, 11*, 100192. doi: 10.1016/j.onehlt.2020.100192

Frutos, R., Serra-Cobo, J., Chen, T., & Devaux, C. A. (2020). COVID-19: Time to exonerate the pangolin from the transmission of SARS-CoV-2 to humans. *Infection, Genetics and Evolution, 84*, 104493.

Gai, J., Ma, L., Li, G., Zhu, M., Qiao, P., Li, X., . . . Gong, R. (2020). A potent neutralizing nanobody against SARS-CoV-2 with inhaled delivery potential. *bioRxiv*.

Gao, S., Luan, J., Cui, H., & Zhang, L. (2020). ACE2 isoform diversity predicts the host susceptibility of SARS‐CoV‐2. *Transboundary and Emerging Diseases*.

Garigliany, M., Van Laere, A.-S., Clercx, C., Giet, D., Escriou, N., Huon, C., . . . Desmecht, D. (2020). SARS-CoV-2 natural transmission from human to cat, Belgium, March 2020. *Emerging infectious diseases, 26*(12), 3069.

Giner, J., Villanueva-Saz, S., Tobajas, A. P., Pérez, M. D., González, A., Verde, M., . . . Lira-Navarrete, E. (2021). SARS-CoV-2 seroprevalence in household domestic ferrets (Mustela putorius furo). *Animals, 11*(3), 667.

Glass, W. G., Subbarao, K., Murphy, B., & Murphy, P. M. (2004). Mechanisms of host defense following severe acute respiratory syndrome-coronavirus (SARS-CoV) pulmonary infection of mice. *The Journal of Immunology, 173*(6), 4030-4039.

Goh, G. K.-M., Dunker, A. K., Foster, J. A., & Uversky, V. N. (2020). Shell disorder analysis suggests that pangolins offered a window for a silent spread of an attenuated SARS-CoV-2 precursor among humans. *Journal of Proteome Research, 19*(11), 4543-4552.

Gong, S. r., & Bao, L. l. (2018). The battle against SARS and MERS coronaviruses: reservoirs and animal models. *Animal models and experimental medicine, 1*(2), 125-133.

Goumenou, M., Spandidos, D. A., & Tsatsakis, A. (2020). Possibility of transmission through dogs being a contributing factor to the extreme Covid‑19 outbreak in North Italy. *Molecular medicine reports, 21*(6), 2293-2295.

Gryseels, S., De Bruyn, L., Gyselings, R., Calvignac‐Spencer, S., Leendertz, F. H., & Leirs, H. (2020). Risk of human‐to‐wildlife transmission of SARS‐CoV‐2. *Mammal Review*.

Halfmann, P. J., Hatta, M., Chiba, S., Maemura, T., Fan, S., Takeda, M., . . . Iwatsuki-Horimoto, K. (2020). Transmission of SARS-CoV-2 in domestic cats. *New England Journal of Medicine, 383*(6), 592-594.

Hamer, S. A., Ghai, R. R., Zecca, I. B., Auckland, L. D., Roundy, C. M., Davila, E., . . . Hamer, G. L. (2021). SARS-CoV-2 B.1.1.7 variant of concern detected in a pet dog and cat after exposure to a person with COVID-19, USA. *Transbound Emerg Dis*. doi: 10.1111/tbed.14122

Hamer, S. A., Pauvolid-Corrêa, A., Zecca, I. B., Davila, E., Auckland, L. D., Roundy, C. M., . . . Jenkins-Moore, M. (2020). Natural SARS-CoV-2 infections, including virus isolation, among serially tested cats and dogs in households with confirmed human COVID-19 cases in Texas, USA. *bioRxiv*.

Hedman, H. D., Krawczyk, E., Helmy, Y. A., Zhang, L., & Varga, C. (2021). Host Diversity and Potential Transmission Pathways of SARS-CoV-2 at the Human-Animal Interface. *Pathogens, 10*(2), 180.

Heighton, S. P., & Gaubert, P. (2021). A timely systematic review on pangolin research, commercialization, and popularization to identify knowledge gaps and produce conservation guidelines. *Biological Conservation, 256*, 109042.

Hobbs, E. C., & Reid, T. J. (2020a). Animals and SARS-CoV-2: Species susceptibility and viral transmission in experimental and natural conditions, and the potential implications for community transmission. *Transbound Emerg Dis*. doi: 10.1111/tbed.13885

Hobbs, E. C., & Reid, T. J. (2020b). Animals and SARS‐CoV‐2: Species susceptibility and viral transmission in experimental and natural conditions, and the potential implications for community transmission. *Transbound Emerg Dis*.

Hoffmann, M., Kleine-Weber, H., Schroeder, S., Krüger, N., Herrler, T., Erichsen, S., . . . Nitsche, A. (2020). SARS-CoV-2 cell entry depends on ACE2 and TMPRSS2 and is blocked by a clinically proven protease inhibitor. *cell, 181*(2), 271-280. e278.

Hul, V., Delaune, D., Karlsson, E. A., Hassanin, A., Tey, P. O., Baidaliuk, A., . . . Mazet, J. (2021). A novel SARS-CoV-2 related coronavirus in bats from Cambodia. *bioRxiv*.

IUCN, S., WHSG & OIE. (2020). Guideline for working with free-ranging wild mammals in the era of the COVID-19 pandemic.

Jaimes, J. A., André, N. M., Chappie, J. S., Millet, J. K., & Whittaker, G. R. (2020). Phylogenetic analysis and structural modeling of SARS-CoV-2 spike protein reveals an evolutionary distinct and proteolytically sensitive activation loop. *Journal of molecular biology, 432*(10), 3309-3325.

Ji, W., Wang, W., Zhao, X., Zai, J., & Li, X. (2020). Cross‐species transmission of the newly identified coronavirus 2019‐nCoV. *Journal of medical virology, 92*(4), 433-440.

Jiang, S., Hillyer, C., & Du, L. (2020). Neutralizing antibodies against SARS-CoV-2 and other human coronaviruses. *Trends in immunology, 41*(5), 355-359.

Jo, W. K., de Oliveira‐Filho, E. F., Rasche, A., Greenwood, A. D., Osterrieder, K., & Drexler, J. F. (2020). Potential zoonotic sources of SARS‐CoV‐2 infections. *Transbound Emerg Dis*.

Kim, D., Lee, J.-Y., Yang, J.-S., Kim, J. W., Kim, V. N., & Chang, H. (2020a). The architecture of SARS-CoV-2 transcriptome. *cell, 181*(4), 914-921. e910.

Kim, Y.-I., Kim, S.-G., Kim, S.-M., Kim, E.-H., Park, S.-J., Yu, K.-M., . . . Casel, M. A. B. (2020b). Infection and rapid transmission of SARS-CoV-2 in ferrets. *Cell host & microbe, 27*(5), 704-709. e702.

Kiros, M., Andualem, H., Kiros, T., Hailemichael, W., Getu, S., Geteneh, A., . . . Abegaz, W. E. (2020). COVID-19 pandemic: current knowledge about the role of pets and other animals in disease transmission. *Virol J, 17*(1), 1-8.

Konda, M., Dodda, B., Konala, V. M., Naramala, S., & Adapa, S. (2020). Potential Zoonotic Origins of SARS-CoV-2 and Insights for Preventing Future Pandemics Through One Health Approach. *Cureus, 12*(6).

Kumar, A., Pandey, S. N., Pareek, V., Narayan, R. K., Faiq, M. A., & Kumari, C. (2020). Predicting susceptibility for SARS‐CoV‐2 infection in domestic and wildlife animals using ACE2 protein sequence homology. *Zoo biology*.

Lam, H. M., Ratmann, O., & Boni, M. F. (2018). Improved algorithmic complexity for the 3SEQ recombination detection algorithm. *Molecular biology and evolution, 35*(1), 247-251.

Lam, T. T.-Y., Jia, N., Zhang, Y.-W., Shum, M. H.-H., Jiang, J.-F., Zhu, H.-C., . . . Liao, Y.-S. (2020). Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. *Nature, 583*(7815), 282-285.

Lan, J., Ge, J., Yu, J., Shan, S., Zhou, H., Fan, S., . . . Zhang, L. (2020). Structure of the SARS-CoV-2 spike receptor-binding domain bound to the ACE2 receptor. *Nature, 581*(7807), 215-220.

Lee, J., Hughes, T., Lee, M.-H., Field, H., Rovie-Ryan, J. J., Sitam, F. T., . . . Daszak, P. (2020). No Evidence of Coronaviruses or Other Potentially Zoonotic Viruses in Sunda pangolins (Manis javanica) Entering the Wildlife Trade via Malaysia. *Ecohealth, 17*(3), 406-418. doi: 10.1007/s10393-020-01503-x

Lei, C., Qian, K., Li, T., Zhang, S., Fu, W., Ding, M., & Hu, S. (2020). Neutralization of SARS-CoV-2 spike pseudotyped virus by recombinant ACE2-Ig. *Nature communications, 11*(1), 1-5.

Leroy, E. M., Ar Gouilh, M., & Brugere-Picoux, J. (2020). The risk of SARS-CoV-2 transmission to pets and other wild and domestic animals strongly mandates a one-health strategy to control the COVID-19 pandemic. *One Health, 10*, 100133. doi: 10.1016/j.onehlt.2020.100133

Letko, M., Marzi, A., & Munster, V. (2020). Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses. *Nature microbiology, 5*(4), 562-569.

Li, X., Zai, J., Zhao, Q., Nie, Q., Li, Y., Foley, B. T., & Chaillon, A. (2020). Evolutionary history, potential intermediate animal host, and cross‐species analyses of SARS‐CoV‐2. *Journal of medical virology, 92*(6), 602-611.

Lin, X.-D., Wang, W., Hao, Z.-Y., Wang, Z.-X., Guo, W.-P., Guan, X.-Q., . . . Li, M.-H. (2017). Extensive diversity of coronaviruses in bats from China. *Virology, 507*, 1-10.

Liu, P., Jiang, J.-Z., Wan, X.-F., Hua, Y., Li, L., Zhou, J., . . . Zou, J. (2020a). Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)? *PLoS Pathogens, 16*(5), e1008421.

Liu, Z., Xiao, X., Wei, X., Li, J., Yang, J., Tan, H., . . . Liu, L. (2020b). Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS‐CoV‐2. *Journal of medical virology, 92*(6), 595-601.

Logeot, M., Mauroy, A., Thiry, E., De Regge, N., Vervaeke, M., Beck, O., . . . Van den Berg, T. (2021). Risk assessment of SARS‐CoV‐2 infection in free‐ranging wild animals in Belgium. *Transbound Emerg Dis*.

Lu, G., Wang, Q., & Gao, G. F. (2015). Bat-to-human: spike features determining ‘host jump’of coronaviruses SARS-CoV, MERS-CoV, and beyond. *Trends Microbiol, 23*(8), 468-478.

Lu, R., Zhao, X., Li, J., Niu, P., Yang, B., Wu, H., . . . Zhu, N. (2020a). Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet, 395*(10224), 565-574.

Lu, S., Zhao, Y., Yu, W., Yang, Y., Gao, J., Wang, J., . . . Ma, C. (2020b). Comparison of nonhuman primates identified the suitable model for COVID-19. *Signal transduction and targeted therapy, 5*(1), 1-9.

Luan, J., Jin, X., Lu, Y., & Zhang, L. (2020). SARS‐CoV‐2 spike protein favors ACE2 from Bovidae and Cricetidae. *Journal of medical virology, 92*(9), 1649-1656.

Luan, J., Lu, Y., Jin, X., & Zhang, L. (2020). Spike protein recognition of mammalian ACE2 predicts the host range and an optimized ACE2 for SARS-CoV-2 infection. *Biochemical and biophysical research communications, 526*(1), 165-169.

Machalaba, C., Uhart, M., Ryser-Degiorgis, M.-P., & Karesh, W. B. (2021). Gaps in health security related to wildlife and environment affecting pandemic prevention and preparedness, 2007–2020. *Bulletin of the World Health Organization, 99*(5), 342.

Malik, Y. S., Sircar, S., Bhat, S., Sharun, K., Dhama, K., Dadar, M., . . . Chaicumpa, W. J. V. q. (2020). Emerging novel coronavirus (2019-nCoV)—current scenario, evolutionary perspective based on genome analysis and recent developments. *40*(1), 68-76.

Mallapaty, S. (2020). Coronaviruses closely related to the pandemic virus discovered in Japan and Cambodia. *Nature, 588*(7836), 15-16.

Martina, B. E., Haagmans, B. L., Kuiken, T., Fouchier, R. A., Rimmelzwaan, G. F., Van Amerongen, G., . . . Osterhaus, A. D. (2003). SARS virus infection of cats and ferrets. *Nature, 425*(6961), 915-915.

Mathavarajah, S., & Dellaire, G. (2020). Lions, Tigers and Kittens too: ACE2 and susceptibility to CoVID-19. *Evolution, medicine, and public health, 2020*(1), 109-113.

Maurin, M., Fenollar, F., Mediannikov, O., Davoust, B., Devaux, C., & Raoult, D. (2021). Current Status of Putative Animal Sources of SARS-CoV-2 Infection in Humans: Wildlife, Domestic Animals and Pets. *Microorganisms, 9*(4), 868.

McAloose, D., Laverack, M., Wang, L., Killian, M. L., Caserta, L. C., Yuan, F., . . . Mauldin, M. R. (2020a). From People to Panthera: Natural SARS-CoV-2 Infection in Tigers and Lions at the Bronx Zoo. *11*(5). doi: 10.1128/mBio.02220-20

McAloose, D., Laverack, M., Wang, L., Killian, M. L., Caserta, L. C., Yuan, F., . . . Cronk, B. D. (2020b). From people to Panthera: Natural SARS-CoV-2 infection in tigers and lions at the Bronx Zoo. *MBio, 11*(5).

McNamara, T., Richt, J. A., & Glickman, L. (2020). A critical needs assessment for research in companion animals and livestock following the pandemic of COVID-19 in humans. *Vector-Borne and Zoonotic Diseases, 20*(6), 393-405.

Mehand, M. S., Al-Shorbaji, F., Millett, P., & Murgue, B. (2018). The WHO R&D Blueprint: 2018 review of emerging infectious diseases requiring urgent research and development efforts. *Antiviral Research, 159*, 63-67.

Mercado, N. B., Zahn, R., Wegmann, F., Loos, C., Chandrashekar, A., Yu, J., . . . Barouch, D. H. (2020). Single-shot Ad26 vaccine protects against SARS-CoV-2 in rhesus macaques. *Nature, 586*(7830), 583-588. doi: 10.1038/s41586-020-2607-z

Mishra, A., Kumar, N., Bhatia, S., Aasdev, A., Kanniappan, S., Thayasekhar, A., . . . Dubey, C. K. (2021). Natural infection of SARS-CoV-2 delta variant in Asiatic lions (Panthera leo persica) in India. *bioRxiv*.

Montagutelli, X., Prot, M., Levillayer, L., Salazar, E. B., Jouvion, G., Conquet, L., . . . Behillil, S. (2021). The B1. 351 and P. 1 variants extend SARS-CoV-2 host range to mice. *bioRxiv*.

Munjal, A., Khandia, R., Dhama, K., Sachan, S., Karthik, K., Tiwari, R., . . . Iqbal, H. J. F. i. m. (2017). Advances in developing therapies to combat Zika virus: current knowledge and future perspectives. *8*, 1469.

Munnink, B. B. O., Sikkema, R. S., Nieuwenhuijse, D. F., Molenaar, R. J., Munger, E., Molenkamp, R., . . . Brouwer, M. (2021). Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. *Science, 371*(6525), 172-177.

Munster, V. J., Feldmann, F., Williamson, B. N., Van Doremalen, N., Pérez-Pérez, L., Schulz, J., . . . Brumbaugh, B. (2020). Respiratory disease in rhesus macaques inoculated with SARS-CoV-2. *Nature, 585*(7824), 268-272.

Murakami, S., Kitamura, T., Suzuki, J., Sato, R., Aoi, T., Fujii, M., . . . Horimoto, T. (2020). Detection and Characterization of Bat Sarbecovirus Phylogenetically Related to SARS-CoV-2, Japan. *Emerg Infect Dis, 26*(12), 3025-3029. doi: 10.3201/eid2612.203386

Musso, N., Costantino, A., La Spina, S., Finocchiaro, A., Andronico, F., Stracquadanio, S., . . . Emmanuele, G. (2020). New SARS-CoV-2 Infection Detected in an Italian Pet Cat by RT-qPCR from Deep Pharyngeal Swab. *Pathogens, 9*(9), 746.

Mykytyn, A. Z., Lamers, M. M., Okba, N. M., Breugem, T. I., Schipper, D., van den Doel, P. B., . . . Koopmans, M. P. (2021). Susceptibility of rabbits to SARS-CoV-2. *Emerging Microbes & Infections, 10*(1), 1-7.

Newman, A., Smith, D., Ghai, R. R., Wallace, R. M., Torchetti, M. K., Loiacono, C., . . . Rooney, J. A. (2020). First reported cases of SARS-CoV-2 infection in companion animals—New York, March–April 2020. *Morbidity and Mortality Weekly Report, 69*(23), 710.

OIE. (2020). COVID-19 (SARS-COV-2), Hong Kong (SAR - PRC). Available online: https://[www.oie.int/wahis\_2/public/wahid.php/Reviewreport/Review?page\_refer=MapFullEventReport&reportid=33832](http://www.oie.int/wahis_2/public/wahid.php/Reviewreport/Review?page_refer=MapFullEventReport&reportid=33832) (accessed on 9 November 2020).

OIE. (2021). World organization for animal health.

Olival, K. J., Cryan, P. M., Amman, B. R., Baric, R. S., Blehert, D. S., Brook, C. E., . . . Daszak, P. (2020). Possibility for reverse zoonotic transmission of SARS-CoV-2 to free-ranging wildlife: A case study of bats. *PLoS Pathogens, 16*(9), e1008758.

Oude Munnink, B. B., Sikkema, R. S., Nieuwenhuijse, D. F., Molenaar, R. J., Munger, E., Molenkamp, R., . . . Koopmans, M. P. G. (2021). Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. *Science, 371*(6525), 172-177. doi: 10.1126/science.abe5901

Pagani, G., Lai, A., Bergna, A., Rizzo, A., Stranieri, A., Giordano, A., . . . Zehender, G. (2021). Human-to-Cat SARS-CoV-2 Transmission: Case Report and Full-Genome Sequencing from an Infected Pet and Its Owner in Northern Italy. *Pathogens, 10*(2), 252.

Palmer, M. V., Martins, M., Falkenberg, S., Buckley, A., Caserta, L. C., Mitchell, P. K., . . . Diel, D. G. (2021). Susceptibility of white-tailed deer (Odocoileus virginianus) to SARS-CoV-2. *J Virol*. doi: 10.1128/jvi.00083-21

Parolin, C., Virtuoso, S., Giovanetti, M., Angeletti, S., Ciccozzi, M., & Borsetti, A. (2021). Animal Hosts and Experimental Models of SARS-CoV-2 Infection. *Chemotherapy*. doi: 10.1159/000515341

Patterson, E. I. (2020). Evidence of exposure to SARS-CoV-2 in cats and dogs from households in Italy. doi: 10.1101/2020.07.21.214346

Patterson, E. I., Elia, G., Grassi, A., Giordano, A., Desario, C., Medardo, M., . . . Patterson, G. T. (2020). Evidence of exposure to SARS-CoV-2 in cats and dogs from households in Italy. *Nature communications, 11*(1), 1-5.

Preziuso, S. (2020). Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Exhibits High Predicted Binding Affinity to ACE2 from Lagomorphs (Rabbits and Pikas). *Animals, 10*(9), 1460.

Qiu, Y., Zhao, Y.-B., Wang, Q., Li, J.-Y., Zhou, Z.-J., Liao, C.-H., & Ge, X.-Y. (2020). Predicting the angiotensin converting enzyme 2 (ACE2) utilizing capability as the receptor of SARS-CoV-2. *Microbes and infection, 22*(4-5), 221-225.

Reuters. (2021). Gorillas at San Diego Zoo Safari Park diagnosed with COVID-19. https://[www.reuters.com/article/us-health-coronavirus-usa-gorillas-idUSKBN29G2L9](http://www.reuters.com/article/us-health-coronavirus-usa-gorillas-idUSKBN29G2L9) (accessed on 7 July, 2021)

Eight lions in indian zoo test positive for COVID-19. https://[www.reuters.com/world/india/eight-lions-indian-zoo-test-positive-covid-19-2021-05-04/](http://www.reuters.com/world/india/eight-lions-indian-zoo-test-positive-covid-19-2021-05-04/) (accessed on 3 July, 2021).

Richard, M., Kok, A., de Meulder, D., Bestebroer, T. M., Lamers, M. M., Okba, N. M., . . . Koopmans, M. P. (2020). SARS-CoV-2 is transmitted via contact and via the air between ferrets. *Nature communications, 11*(1), 1-6.

Roberts, A., Vogel, L., Guarner, J., Hayes, N., Murphy, B., Zaki, S., & Subbarao, K. (2005). Severe acute respiratory syndrome coronavirus infection of golden Syrian hamsters. *Journal of virology, 79*(1), 503-511.

Rodriguez-Morales, A. J., Bonilla-Aldana, D. K., Tiwari, R., Sah, R., Rabaan, A. A., & Dhama, K. J. J. P. A. M. (2020). COVID-19, an emerging coronavirus infection: current scenario and recent developments-an overview. *14*(1), 5-12.

Ruiz-Arrondo, I., Portillo, A., Palomar, A. M., Santibanez, S., Santibanez, P., Cervera, C., & Oteo, J. A. (2020). Detection of SARS-CoV-2 in pets living with COVID-19 owners diagnosed during the COVID-19 lockdown in Spain: A case of an asymptomatic cat with SARS-CoV-2 in Europe. *medRxiv*.

Rulli, M. C., D'Odorico, P., Galli, N., & Hayman, D. (2020). Land use change and livestock revolution as contributors to Coronavirus emergence risk.

Sailleau, C., Dumarest, M., Vanhomwegen, J., Delaplace, M., Caro, V., Kwasiborski, A., . . . Comtet, L. (2020a). First detection and genome sequencing of SARS‐CoV‐2 in an infected cat in France. *Transbound Emerg Dis*.

Sailleau, C., Dumarest, M., Vanhomwegen, J., Delaplace, M., Caro, V., Kwasiborski, A., . . . Le Poder, S. (2020b). First detection and genome sequencing of SARS-CoV-2 in an infected cat in France. *Transbound Emerg Dis, 67*(6), 2324-2328. doi: 10.1111/tbed.13659

Sarkar, J., & Guha, R. (2020). Infectivity, virulence, pathogenicity, host-pathogen interactions of SARS and SARS-CoV-2 in experimental animals: a systematic review. *Veterinary research communications*, 1-10.

Schlottau, K., Rissmann, M., Graaf, A., Schön, J., Sehl, J., Wylezich, C., . . . Harder, T. (2020). Experimental transmission studies of SARS-CoV-2 in fruit bats, ferrets, pigs and chickens.

Segalés, J., Puig, M., & Rodon, J. (2020). Detection of SARS-CoV-2 in a cat owned by a COVID-19-affected patient in Spain. *117*(40), 24790-24793. doi: 10.1073/pnas.2010817117

Segalés, J., Puig, M., Rodon, J., Avila-Nieto, C., Carrillo, J., Cantero, G., . . . Noguera-Julián, M. (2020). Detection of SARS-CoV-2 in a cat owned by a COVID-19− affected patient in Spain. *Proceedings of the National Academy of Sciences, 117*(40), 24790-24793.

Shafique, L., Ihsan, A., & Liu, Q. (2020). Evolutionary trajectory for the emergence of novel coronavirus SARS-CoV-2. *Pathogens, 9*(3), 240.

Shan, C., Yao, Y.-F., Yang, X.-L., Zhou, Y.-W., Gao, G., Peng, Y., . . . Jiang, R.-D. (2020). Infection with novel coronavirus (SARS-CoV-2) causes pneumonia in Rhesus macaques. *Cell research, 30*(8), 670-677.

Sharun, K., Dhama, K., Pawde, A. M., Gortázar, C., Tiwari, R., Bonilla-Aldana, D. K., . . . Attia, Y. A. (2021). SARS-CoV-2 in animals: potential for unknown reservoir hosts and public health implications. *Veterinary Quarterly*(just-accepted), 1-31.

Shi, J., Wen, Z., Zhong, G., Yang, H., Wang, C., Huang, B., . . . Sun, Z. (2020). Susceptibility of ferrets, cats, dogs, and other domesticated animals to SARS–coronavirus 2. *Science, 368*(6494), 1016-1020.

Shriner, S. A., Ellis, J. W., Root, J. J., Roug, A., Stopak, S. R., Wiscomb, G. W., . . . DeLiberto, T. J. (2021). SARS-CoV-2 exposure in escaped mink, Utah, USA. *Emerging infectious diseases, 27*(3), 988.

Shu, Y., & McCauley, J. (2017). GISAID: Global initiative on sharing all influenza data - from vision to reality. *Euro Surveill, 22*(13). doi: 10.2807/1560-7917.es.2017.22.13.30494

Sia, S. F., Yan, L.-M., Chin, A. W., Fung, K., Choy, K.-T., Wong, A. Y., . . . Nicholls, J. M. (2020). Pathogenesis and transmission of SARS-CoV-2 in golden hamsters. *Nature, 583*(7818), 834-838.

Singh, R. K., Dhama, K., Chakraborty, S., Tiwari, R., Natesan, S., Khandia, R., . . . Karthik, K. J. V. Q. (2019). Nipah virus: epidemiology, pathology, immunobiology and advances in diagnosis, vaccine designing and control strategies–a comprehensive review. *39*(1), 26-55.

Sit, T. H., Brackman, C. J., Ip, S. M., Tam, K. W., Law, P. Y., To, E. M., . . . Chu, D. K. (2020a). Infection of dogs with SARS-CoV-2. *Nature, 586*(7831), 776-778.

Sit, T. H. C., Brackman, C. J., Ip, S. M., Tam, K. W. S., Law, P. Y. T., & To, E. M. W. (2020b). Infection of dogs with SARS-CoV-2. *586*(7831), 776-778. doi: 10.1038/s41586-020-2334-5

Skirmuntt, E. C., Escalera-Zamudio, M., Teeling, E. C., Smith, A., & Katzourakis, A. (2020). The potential role of endogenous viral elements in the evolution of bats as reservoirs for zoonotic viruses. *Annual Review of Virology, 7*, 103-119.

Stopsack, K. H., Mucci, L. A., Antonarakis, E. S., Nelson, P. S., & Kantoff, P. W. (2020). TMPRSS2 and COVID-19: Serendipity or Opportunity for Intervention? *Cancer discovery, 10*(6), 779-782.

Stout, A. E., André, N. M., Jaimes, J. A., Millet, J. K., & Whittaker, G. R. (2020). Coronaviruses in cats and other companion animals: Where does SARS-CoV-2/COVID-19 fit? *Veterinary Microbiology*.

Suarez, D. L., Pantin-Jackwood, M. J., Swayne, D. E., Lee, S. A., Deblois, S. M., & Spackman, E. (2020). Lack of susceptibility of poultry to SARS-CoV-2 and MERS-CoV. *bioRxiv*.

Sun, J., He, W.-T., Wang, L., Lai, A., Ji, X., Zhai, X., . . . Zhou, J. (2020). COVID-19: epidemiology, evolution, and cross-disciplinary perspectives. *Trends in molecular medicine, 26*(5), 483-495.

Tian, J.-H., Patel, N., Haupt, R., Zhou, H., Weston, S., Hammond, H., . . . Guebre-Xabier, M. (2020). SARS-CoV-2 spike glycoprotein vaccine candidate NVX-CoV2373 elicits immunogenicity in baboons and protection in mice. *bioRxiv*.

Touati, R., Haddad-Boubaker, S., Ferchichi, I., Messaoudi, I., Ouesleti, A. E., Triki, H., . . . Kharrat, M. (2020). Comparative genomic signature representations of the emerging COVID-19 coronavirus and other coronaviruses: High identity and possible recombination between Bat and Pangolin coronaviruses. *Genomics, 112*(6), 4189-4202.

USDA. (2021). United States Department of Agriculture (USDA). Confirmation of COVID-19 in otters at an aquarium in Georgia. https://[www.aphis.usda.gov/aphis/newsroom/stakeholder-info/sa\_by\_date/sa-2021/sa-04/covid-georgia-otters](http://www.aphis.usda.gov/aphis/newsroom/stakeholder-info/sa_by_date/sa-2021/sa-04/covid-georgia-otters) (accessed on 3 June, 2021).

van Aart, A., Velkers, F., Fischer, E., Broens, E., Egberink, H., Zhao, S., . . . de Rooij, M. (2021). SARS-CoV-2 infection in cats and dogs in infected mink farms. *Authorea Preprints*.

Wacharapluesadee, S., Tan, C. W., Maneeorn, P., Duengkae, P., Zhu, F., Joyjinda, Y., . . . Lim, B. L. (2021). Evidence for SARS-CoV-2 related coronaviruses circulating in bats and pangolins in Southeast Asia. *Nature communications, 12*(1), 1-9.

Wan, Y., Shang, J., Graham, R., Baric, R. S., & Li, F. (2020). Receptor recognition by the novel coronavirus from Wuhan: an analysis based on decade-long structural studies of SARS coronavirus. *Journal of virology, 94*(7).

Wang, J., Xu, X., Zhou, X., Chen, P., Liang, H., Li, X., . . . Hao, P. (2020). Molecular simulation of SARS-CoV-2 spike protein binding to pangolin ACE2 or human ACE2 natural variants reveals altered susceptibility to infection. *The Journal of general virology, 101*(9), 921.

Wong, G., Bi, Y.-H., Wang, Q.-H., Chen, X.-W., Zhang, Z.-G., & Yao, Y.-G. (2020). Zoonotic origins of human coronavirus 2019 (HCoV-19/SARS-CoV-2): why is this work important? *Zoological research, 41*(3), 213.

Woolsey, C., Borisevich, V., Prasad, A. N., Agans, K. N., Deer, D. J., Dobias, N. S., . . . Medina, L. (2020). Establishment of an African green monkey model for COVID-19. *bioRxiv*.

Wrapp, D., Wang, N., Corbett, K. S., Goldsmith, J. A., Hsieh, C.-L., Abiona, O., . . . McLellan, J. S. (2020). Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. *Science, 367*(6483), 1260-1263.

Wu, L., Wang, D., & Evans, J. A. (2019). Large teams develop and small teams disrupt science and technology. *Nature, 566*(7744), 378-382.

Wu, Y., Guo, C., Tang, L., Hong, Z., Zhou, J., Dong, X., . . . Qu, X. (2020). Prolonged presence of SARS-CoV-2 viral RNA in faecal samples. *The lancet Gastroenterology & hepatology, 5*(5), 434-435.

Xiao, X., Newman, C., Buesching, C. D., Macdonald, D. W., & Zhou, Z.-M. (2021). Animal sales from Wuhan wet markets immediately prior to the COVID-19 pandemic. *Sci Rep, 11*(1), 11898. doi: 10.1038/s41598-021-91470-2

Yekta, R., Vahid-Dastjerdi, L., Norouzbeigi, S., & Mortazavian, A. M. (2020). Food Products as Potential Carriers of SARS-CoV-2. *Food control*, 107754.

Zhai, X., Sun, J., Yan, Z., Zhang, J., Zhao, J., Zhao, Z., . . . Su, S. (2020). Comparison of severe acute respiratory syndrome coronavirus 2 spike protein binding to ACE2 receptors from human, pets, farm animals, and putative intermediate hosts. *Journal of virology, 94*(15).

Zhang, C., Zheng, W., Huang, X., Bell, E. W., Zhou, X., & Zhang, Y. (2020a). Protein structure and sequence reanalysis of 2019-nCoV genome refutes snakes as its intermediate host and the unique similarity between its spike protein insertions and HIV-1. *Journal of Proteome Research, 19*(4), 1351-1360.

Zhang, Q., Zhang, H., Gao, J., Huang, K., Yang, Y., Hui, X., . . . Zhang, Y. (2020b). A serological survey of SARS-CoV-2 in cat in Wuhan. *Emerging Microbes & Infections, 9*(1), 2013-2019.

Zhang, Q., Zhang, H., Gao, J., Huang, K., Yang, Y., Hui, X., . . . Shi, Z. L. (2020c). A serological survey of SARS-CoV-2 in cat in Wuhan. *9*(1), 2013-2019. doi: 10.1080/22221751.2020.1817796

Zhang, T., Wu, Q., & Zhang, Z. (2020). Probable pangolin origin of SARS-CoV-2 associated with the COVID-19 outbreak. *Current biology, 30*(7), 1346-1351. e1342.

Zhang, Y. Z., & Holmes, E. C. (2020). A Genomic Perspective on the Origin and Emergence of SARS-CoV-2. *cell, 181*(2), 223-227. doi: 10.1016/j.cell.2020.03.035

Zhang, Z., Xiao, K., Zhang, X., Roy, A., & Shen, Y. (2020). Emergence of SARS-like coronavirus in China: an update. *Journal of Infection, 80*(5), e28-e29.

Zhao, Y., Wang, J., Kuang, D., Xu, J., Yang, M., Ma, C., . . . Ding, K. (2020). Susceptibility of tree shrew to SARS-CoV-2 infection. *Sci Rep, 10*(1), 1-9.

Zhou, H., Chen, X., Hu, T., Li, J., Song, H., Liu, Y., . . . Shi, W. (2020a). A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein. *Current biology : CB, 30*(11), 2196-2203.e2193. doi: 10.1016/j.cub.2020.05.023

Zhou, P., Yang, X. L., Wang, X. G., Hu, B., Zhang, L., Zhang, W., . . . Shi, Z. L. (2020b). A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature, 579*(7798), 270-273. doi: 10.1038/s41586-020-2012-7

Zhu, N., Zhang, D., Wang, W., Li, X., Yang, B., Song, J., . . . Tan, W. (2020). A Novel Coronavirus from Patients with Pneumonia in China, 2019. *N Engl J Med, 382*(8), 727-733. doi: 10.1056/NEJMoa2001017