Coronavirus Infections in Animals: Risks of Direct and Reverse Zoonoses

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Abstract—The publications on animal coronavirus infections that have the greatest emerging potential, as well as official data from the World Organization for Animal Health (OIE) on cases of animal infection with COVID-19, are analyzed. Like most infectious diseases common to humans, coronavirus infections were first discovered in animals. Due to the increased rate of replication and recombination activity compared to other viruses, mutations occur more often in the genome of coronaviruses, which contribute to the acquisition of new qualities in order to consolidate in the host organism. Examples of cross-species transmission are not only SARS-CoV, MERS-CoV, and SARS-CoV-2, which are dangerous to humans, but also coronaviruses of agricultural and domestic animals, between which there is a genetic relationship. There are several known cases of zoo, wild, domestic, and farm animals displaying symptoms characteristic of COVID-19 and identification of the genome of the SARS-CoV-2 virus in them. The issue of cross-species transmission of coronavirus infections, in particular the reverse zoonosis of SARS-CoV-2 from animals to humans, is widely discussed. According to the conclusions of many researchers, including OIE experts, there is no direct evidence base for infection of humans with COVID-19 from animals. However, people with suspected COVID-19 and with a confirmed diagnosis are still advised to isolate not only from people but also from animals. A number of methods for specific prevention, diagnosis, and immunization against a wide range of coronavirus infections are being developed at the All-Russia Research Institute for Animal Protection.

Keywords: coronaviruses, animals, virus carrier, SARS-CoV, spread of COVID-19, animal coronavirus infections, emergent viruses, cross-species transmission, coronavirus vaccine, immunoprophylaxis

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tional Committee on Taxonomy of Viruses (ICTV) and four out of nine betacoronavirus species were identified only in bats. Thus, bats are probably their main natural reservoirs. Periodically, the taxonomy of coronavirus infections is supplemented, as, for example, in the case of SARS-CoV-2.

Alpha- and beta-coronaviruses can cause severe and acute illness in pets. Animal alphacoronaviruses include porcine transmissible gastroenteritis (TGEV), porcine epidemic diarrhea (PEDV), porcine respiratory coronavirus (PRCV), feline enteric coronavirus (FECV), and the recently emerged swine acute diarrhea coronavirus syndrome (SADS-CoV). Betacoronaviruses include pathogens of buffalo (BuCoV), horses (ECoV), rabbits (RbCoV), cattle (BCoV), canine respiratory coronavirus (CRCoV), etc. Gamma-coronaviruses (chicken infectious bronchitis virus (IBV), dolphin and whale (BDcCoV and BWC0V), and turkey (TCoV)) and delta-coronaviruses (porcine coronavirus—PDCoV) infect birds and mammals. Due to the unique mechanism of CoV replication, a high frequency of occurrence of genetic mutations is observed, which together ensure the ability of CoV to adapt rapidly to new hosts and ecological niches [1, 2]. Carrier animals are involved in the global ecosystem also as the fundamental links of zoonotic viral infections—primary and secondary reservoirs [3, 4]. SARS-CoV, MERS-CoV, and SARS-CoV-2 betacoronaviruses have the highest emergent zoonotic potential. Both domestic and wild animals, in particular bats, are involved in their occurrence and spread [5]. The peculiarities of the antiviral immune reactions of these animals created a convenient foundation for the intensive development of the progenitors of the three viruses listed above [6].

At the moment, the scientific community is faced with the task of developing a strategy to prevent a potential fourth outbreak of a new coronavirus infection, which is very likely given the lack of study of the ecology of both coronaviruses and potential carriers of the infection in the wild. Representatives of the order Chiroptera (wing-handed) are involved in the emergence of many epidemiological outbreaks of zoonotic viral infections, as well as those common to other animals and humans. Among the human viruses whose precursors have been observed in these animals, filoviruses (Ebola and Marburg) [7, 8], paramyxoviruses (Nipah, Hendra) [9], and, of course, CoV [10] are distinguished. More than 30 CoV species have already been identified, for which bats are a natural reservoir [11]. These animals are the only mammals capable of long flights, which increases the number of contacts with other animals [12].

Until the early 2000s, coronavirus infections were considered relevant to veterinary medicine but not to public health. The identification in 2002 of the severe acute respiratory syndrome-related coronavirus (SARS-CoV) and the epidemic spread of the infection in China changed the opinion of virologists. Himalayan civets became the source of infection for humans (a SARS-like CoV, homologous to SARS-CoV by 99.8%, was isolated from a civet and a raccoon dog) [13]. Successful experimental infection of civets has made it possible to consider them as a SARS-CoV reservoir. A precursor to SARS-CoV has previously been identified in a population of Chinese red horseshoe bats, which should be considered a natural reservoir of the disease. Bats are considered ideal incubators for new pathogenic viruses, including CoV, as they have asymptomatic virus carriers due to limited immune-inflammatory responses. When viruses enter the body, pro-inflammatory cytokines are activated in most mammals, which leads to inflammatory diseases and death [14, 15].

A second animal outbreak of the previously unknown Middle East respiratory syndrome coronavirus (MERS-CoV, Betacoronavirus) was reported in 2012 in Saudi Arabia. The natural reservoir is the one-humped camel (MERS-CoV isolated, 100% homologous to what was in humans). In 2014–2015 based on 1309 rectal and nasal swabs from camels, two members of the Betacoronavirus genus (MERS-CoV and HKU23-CoV) and one member of the Alphacoronavirus genus were found to be genetically homologous to a CoV previously identified in the *Vicugna pacos* alpaca in the United States in 2007 and HCoV-229E in humans [16]. Camelids are an ideal intermediate host for zoonotic infections due to close, repeated contact with humans. One-humped camels are a reservoir of 37 zoonotic infections, 13 of a viral nature.

In December 2019, in the city of Wuhan, in the Chinese province of Hubei, work began on identification of the viral agent SARS-CoV-2, which has a number of genetic and phenotypic similarities to SARS-CoV [17, 18]. A group of researchers conducted an extensive pilot study. It included many different species of small domestic and farm animals, which were intranasally vaccinated with 105 plaque-forming units of the SARS-CoV-2 virus. The results raised many questions about the possibility of small domestic animals, in particular cats, being involved in the SARS-CoV-2 transmission pathways [18]. It was found that 15% of cat plasma samples taken during the COVID-19 outbreak were seropositive for the SARS-CoV-2 receptor binding domain, indicating their possible infection. The highest neutralization titer was also observed in three cats whose owners had COVID-19. However, 39 plasma samples studied in March–May 2019 were negative [19]. This experimental route of infection is unnatural, since the probability of occurrence of real conditions under which an extremely large dose of a viral pathogen will be directly administered intranasally to animals is extremely low. Data have been obtained only on the possibility of using cats and ferrets as model animals but nothing more [20].
Currently, one of the most discussed topics is the involvement of companion animals in the transmission chain of emerging coronavirus infections, since these animals are in close contact with humans. There is not yet sufficient evidence that small domestic animals are involved in the emergence and spread of emerging CoVs. They may play an important role as intermediate hosts that enable transmission of the virus from natural hosts to humans. In addition, pets themselves can become ill when infected with bat-borne pathogens or closely related coronaviruses: genomic sequences very similar to pig epidemic diarrhea virus (PEDV) have been found in bats, and swine acute diarrhea coronavirus syndrome (SADS-CoV) probably appeared as a result of the transmission of coronavirus from bats to pigs (the first case occurred in 2016 in China).

Throughout the COVID-19 pandemic, which is caused by human-to-human transmission, cases of SARS-CoV-2 infection in animals have been quite rare, but their number and the range of animals infected continue to grow. There are 625 animal cases worldwide, affecting 17 species in 32 countries. The first case of infection was identified in Hong Kong in February 2020, when the SARS-CoV-2 virus was detected in a dog living with an infected owner; the infection was asymptomatic. The second case was recorded in March 2020 in Belgium in a cat with signs of damage to the respiratory and gastrointestinal tracts. The animal belonged to a patient infected with COVID-19.

The next event that confirmed the possibility of infection of different species of animals was the detection of COVID-19 infection in 5 tigers and 3 lions in 2 zoo enclosures in the United States. If on March 27, 2020, one of the tigers was ill, then by April 3, 2020, the rest of the tigers and lions had fallen ill. The symptoms noted were a dry cough, wheezing, and loss of appetite (one animal). The tigers and lions were isolated; no disease of other animals was detected. Within a few days their condition was stable with improvement. Presumably, the infection came from one of the zoo workers—an asymptomatic carrier of the virus. In April 2020, the competent authority of the Netherlands reported the infection of mink in fur farms and the suspicion of human infection from them. In the following months, a number of countries announced the detection of the SARS-CoV-2 virus in fur animals on fur farms (Denmark, Spain, Greece, Poland, etc.).

Despite the relatively small number of cases detected in 2020–2021, as surveillance activities and laboratory tests were carried out, the number of outbreaks steadily increased. Thus, in December 2021 alone, the World Organization for Animal Health (OIE) received urgent messages about the detection of the SARS-CoV-2 virus (https://www.oie.int/app/uploads/2022/01/sars-cov-2-situation-report-8.pdf): 1 from Canada (white-tailed deer), 1 from Colombia (lion), 1 from Croatia (lynx, lion), 2 from Denmark (lions), 1 from Finland (cat), 2 from Poland (American minks), 1 from Singapore (lion), 3 from Switzerland (cats and dogs), 1 from Thailand (cats and dogs), 2 from Great Britain (dog and tigers), and 1 from the Unites States (lynx and tigers). Of particular concern to virologists are cases of detecting infection in wild animals (mink, deer), in the population of which it is extremely difficult to carry out anti-epizootic measures. The formation of natural foci and, possibly, the endemity of COVID-19 disease in limited areas among wild animals will become a constant threat to farm animals and humans.

Two CoVs have been identified in dogs Canis lupus familiaris: Alphacoronavirus, which causes inflammatory intestinal diseases, and Betacoronavirus, which affects the respiratory organs [21, 22]. Both viruses exhibit high replication activity and regular rapid evolutionary development. Canine intestinal CoV was discovered in 1971 in Germany in service dogs with acute viral enteritis [23]. Canine respiratory CoV was identified in 2003 in the United Kingdom. The close affinity of canine respiratory CoV with bovine CoV and HCoV-OC43 has been established [24]. It was possible to reproduce experimentally the infection in puppies using bovine CoV [25]. Based on the homology between CoVs of different species, it can be assumed that dogs, like cats, are involved in the cross-species transmission of these viruses. However, a number of researchers found that, in Wuhan, dogs were immune to SARS-CoV-2 after intranasal inoculation of an extremely high number of plaque-forming units of the virus [18]. Over several months of the pandemic, no SARS-like CoVs were identified in Hubei Province dogs and no antibodies to these viruses were found; that is, dogs are not involved in the transmission of SARS-CoV-2, and even the possibility of their carriage as a biological dead end is extremely unlikely.

Some authors are convinced that if SARS-CoV-2 infection in cats is confirmed, then these animals will become a biological dead end for the virus. For a critical discussion of the fact of carriage of SARS-CoV-2 and its transmission by cats, it is necessary to conduct a full-scale cohort clinical study, moreover, blinded and randomized, which will exclude the influence of the human factor on the results, since an incorrect interpretation can lead to irreversible consequences. In addition, it is necessary to apply methods for detecting subgenomic RNA of the virus, which most likely indicates the fact of SARS-CoV-2 replication in animal cells.

It is assumed that the development of SARS-CoV compared to MERS-CoV occurred much more rapidly due to human intervention in the wild [26–28]. It is impossible to predict the vector of genetic development of CoV, which poses a danger of the emergence of a virus with unknown properties. In addition, as a result of uncontrolled transmission, CoV does not
have time to adapt to any one animal, which does not reduce its ability to overcome the interspecies barrier and does not stabilize the replication activity acquired due to bats [29]. Two scenarios for emerging CoVs have been proposed differing in the degree of human intervention in wildlife.

The first scenario does not imply a pronounced human influence on the CoV transmission chain, namely, a deliberate invasion of the life activity of wild animals, leading to a meeting of species the natural ranges of which do not intersect. It is reliably known that MERS-CoV has been circulating in the camel population for decades, as evidenced by the lower genetic affinity for potential CoV precursors in bats (75–87%) compared to SARS-CoV (95%) [26–28]. The MERS-CoV virus has recently entered the human body, which explains its low adaptation to the new host, which is expressed in the relatively low ability to transmit between people [30]. Animal coronaviruses pose an epidemiological hazard due to their increased ability for cross-species transmission, replication, and recombination activity. Homologous coronaviruses with common characteristics are found in many species, indicating their continuous evolutionary development.

The second scenario assumes that humans make the greatest contribution to creating conditions for new emerging coronaviruses by invading nature, removing wild animals from their range, providing contacts between species that never occur in natural conditions, and naturally creating new transmission routes of coronaviruses between wild animals and humans. The OIE expert panels have stated that there is no evidence of transmission of the virus that causes COVID-19 from animals to humans. However, infected people need to limit contact with animals. In case of infection of the owner, it is advisable to transfer pets to relatives or isolate them in a separate room, while strictly observing the rules of personal hygiene. Pets living with people infected with SARS-CoV-2 should be kept indoors, and contact with other animals should be excluded.

In Russia, the main scientific institution dealing with infections in animals is the Federal Center for Animal Health, the All-Russia Research Institute for Animal Protection (ARRIAH) of the Rosselkhoznadzor. In 1995, the institution was awarded the status of coordinator of the CIS countries for rabies, the OIE reference laboratory for avian influenza, and the OIE reference laboratory for Newcastle disease. In 2019, the institute was given the status of coordinator of the CIS countries for avian influenza and Newcastle disease. Application for the FAO Reference Center for Zoonotic Coronaviruses was filed in 2021.

The main achievements of the last two years have been the development of a set of tools and methods for diagnosing and preventing COVID-19 in animals:

- guidelines for the detection of SARS-CoV-2 virus RNA by RT-PCR (March 21, 2020);
- regulatory and technical documentation for the “Test System for the Detection of SARS-CoV-2 Virus RNA in Biomaterial from Animals, Food Products, and Environmental Objects by RT-PCR” (April 4, 2020);
- guidelines for the selection, storage, and transportation of animal biomaterial samples for laboratory studies to identify the pathogen COVID-19 (based on FAO and OIE data, May 27, 2021);
- guidelines for the detection of antibodies to the SARS-CoV-2 virus in the blood sera of susceptible animals by enzyme immunoassay (January 22, 2021);
- regulatory and technical documentation for the “Diagnostic Kit for the Detection of Antibodies to the SARS-CoV-2 Virus in the Blood Sera of Susceptible Animals in ELISA” (December 28, 2021).

The results of testing diagnostic preparations proved their high efficiency. Thus, the specificity and sensitivity of the developed enzyme immunoassay method with respect to the neutralization reaction for postvaccination sera amounted to 100 and 92.6%, respectively [31]. With the assistance of the Rosselkhoznadzor, monitoring programs were implemented in the populations of fur animals (mink, sable, polecat) at 34 fur farms, 36 livestock farms (cattle and small cattle, pigs, poultry), 274 private households, and petting zoos. A total of 1773 animal biomaterial samples were studied. The genome of the SARS-CoV-2 virus was identified in a cat in Tyumen’ oblast.

Due to the worsening of the epidemic situation, the identification of infected animals, including multiple outbreaks of the disease in the mink population in fur farms in a number of countries around the world, the task of developing a vaccine against animal COVID-19 has become urgent. When creating a vaccine, veterinary experience gained in relation to other coronavirus infections of animals was applied. One of the requirements for the vaccine was its universality, that is, the possibility of application for different types of animals. At the initial stage, ARIAH produced eight experimental samples, but the best performance was observed in the whole-virion inactivated preparation, where aluminum hydroxide was used as an adjuvant. Double immunization with an interval of 21 days made it possible to induce the production of intense immunity lasting at least six months. The registration certificate for the vaccine against coronavirus infection (COVID-19) of carnivorous animals sorbed inactivated Karnivak-Kov was issued on March 26, 2021. The features of the drug include the following:
The vaccine is a whole-virion inactivated preparation that provides a full spectrum of immunological protection against the pathogen SARS-CoV-2.

The adjuvant used contributes to the development of an active immune response while having a low reactogenicity.

The target animals are cats, dogs, and all types of fur-bearing animals (potentially, other types of warm-blooded animals).

The vaccination dose is 1 mL.

Revaccination is after 21 days.

The duration of immunity is at least 6 months.

The use of the vaccine does not require special conditions and precautions.

Taking into account the forecasting of the situation with COVID-19 in animals, the ARRIAH work plans include the following: conducting monitoring studies among groups of animals at high risk of infection; study of the properties of viruses when they are detected (antigenicity, immunogenicity, virulence, tropism for various cultures, etc.); improvement of methods of laboratory diagnostics and means of specific prevention; educational activities and publication of methodological materials; and participation in international projects for the study of coronaviruses, including the IAEA/FAO.

Thus, coronavirus infections pose the greatest emergent danger due to unpredictable mutations and cross-species transmissions. At the moment, according to the OIE, there is no evidence base for human infection with COVID-19 from animals; however, a person with a coronavirus infection is advised to limit contact not only with other people but also with pets to eliminate all possible risks of cross-species transmission. One of the leading roles in the control of future emerging infections, including coronaviruses, should be played by veterinary control and immunization of animals using vaccine preparations.

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**CONFLICT OF INTEREST**

The authors declare that they have no conflicts of interest.

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