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Original Scientific Paper

**EPIZOOTIOLOGICAL CHARACTERISTICS OF CORONAVIRUS INFECTIONS**

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**Summary**

Due to the modern way of life, the global exchange of goods, more frequent contacts, and the closer life with pets, domestic and exotic animal species, different species are also more often exposed to various coronaviruses (CoVs). Most CoVs are species-specific and are not transmitted between different species. Many CoVs have been found to spread very rapidly after introduction into the susceptible population and have remained endemic despite vaccination attempts and other measures to prevent their spread. The majority of animal CoV are present in susceptible population and can cause from mild to a severe clinical picture of the disease, including high mortality. Very rarely strains of animal CoVs are transmitted to humans and then spread rapidly among humans like severe acute respiratory syndrome CoV-2 (SARS CoV-2). The epizootiological characteristics of coronavirus infections are a consequence of their unique characteristics that can be classified into three basic epizootiological determinants. First of all, the virus itself has its own characteristics in terms of genetic characteristics and sustainability in the environment. In relation to the second epizootiological determinant, the macro-organism, it is necessary to emphasize that coronaviruses, more often than other families of viruses, adapt to primary species or even to a new species of animal in nature. This, so-called "jumping" the species barriers, is primarily conditioned by the biology of the virus, which often changes the antigenic composition and thus not only avoids the host's immune response but also finds new species in nature for its maintenance. For thousands of years, the environment greatly contributes to the fact that coronaviruses are a companion of populations of many animal species since there are certain characteristics of the environment (third epizootiological determinant) as sharing the same ecological niche by different species of animals (and humans).

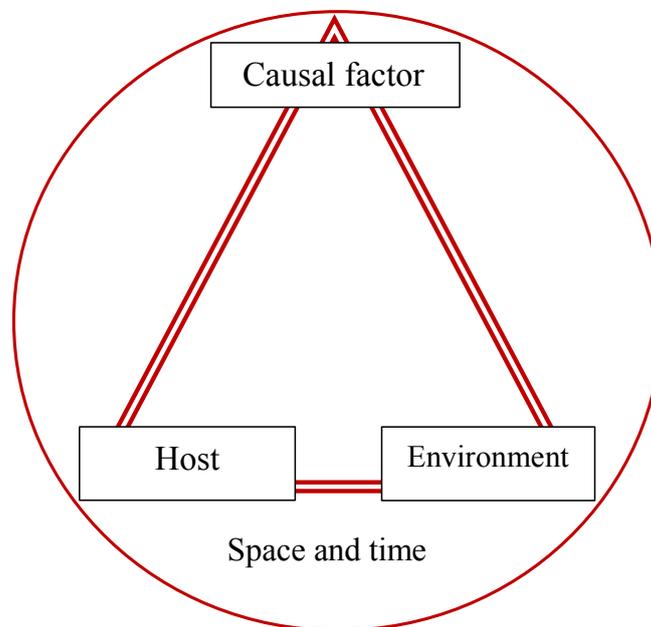
**Keywords:** epizootiological determinants, coronavirus, zoonoses

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## INTRODUCTION

The discovery of a new coronavirus (named SARS CoV-2) in Wuhan in 2019 in China and then its rapid spread across all continents has affected the lives of individuals to its foundations and placed a heavy burden on modern health systems of countries around the world. Despite rapid development and general prosperity, we are suddenly witnessing the fact that also modern human civilization is even more vulnerable and powerless in the face of a new virus. Daily reports of millions of cases and thousands of deaths due to disease (COVID-19) and the confrontation of the individual and society with each week new measures have become a constant that seems to have no end. Despite the measures in place and the mass vaccination in place, the control of this viral disease will also require finding the real causes that led to the SARS CoV-2 pandemic and re-examining the basic findings of potential of CoVs. The current pandemic is therefore also an opportunity and a challenge to look back as individuals and society and to become aware of the importance of coronavirus infections also in animals.

Epizootiological characteristics of all infectious diseases of animals (and humans), even those caused by coronaviruses, are observed through a three-pointed prism whose sides present the so-called epizootiological determinants: causal factor (microorganism), host and Environment (Fig. 1). An individual (new) disease occurs when the balance in the epidemiological triangle between the causative agent, the host and the environment is perfect.



**Figure 1** Epizootiological determinants

Taking this into account, it could be concluded that the development of infectious diseases caused by coronaviruses is a synergy of elements such as a) virulence,

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transmission, physiology, and virus resistance b) susceptibility and resistance of different species of animals and c) environmental conditions in which the first two epizootiological determinants are settled.

The coronavirus family consists of several hundred (over 300) known and isolated viruses (Fauquet et al., 2005). It is considered to be the phylogenetically oldest virus, considering that in most cases, in the species in which they usually cause infections, the disease usually proceeds asymptotically. Namely, in the case of viruses (microorganisms) that are present in the population of a susceptible species for a long period of time, a balance is achieved, which implies adaptation of the animal species to the virus, on the one hand, and weakening of virus virulence, on the other. The reason for that is purely biological: on the one side it is not beneficial for the virus to kill its host, and on the part of the animal species, those individuals (that continue the species) that are genetically more resistant to given virus infection survive.

Most CoVs are species-specific and are not transmitted between different species of animals and to humans (Decaro et al., 2020). Many CoV species have been found to spread very rapidly after introduction into the susceptible population and have remained endemic despite vaccination attempts and other measures to prevent their spread. Strains of animal CoV are rare and can cause a severe clinical picture of the disease in humans after infection and then spread rapidly among humans. Since 2002, three cases of new CoV infections have been identified in humans, causing great alarm and relatively high mortality in infected people. In 2002, viral diseases were first detected in people with clinical signs of severe acute respiratory syndrome virus (SARS), in 2012 Middle East Respiratory Syndrome (MERS) and in 2019 a new SARS CoV-2 causing coronavirus disease (COVID-19). During the COVID-19 pandemic, natural transmissions of SARS CoV-2 from infected people to dogs, cats, mink, ferrets, raccoons, tigers, lions, and gorillas were recorded, and experimental experiments demonstrated susceptibility to SARS CoV-2 in many species. animals and there is a risk that some species of animal could become a reservoir of SARS CoV-2 virus, which could further complicate the control of the spread of the disease. Due to the emergence of SARS CoV-2 infections and many new variants of the SARS CoV-2 virus already detected in humans and minks in 2020, emergency measures have been taken in several countries to prevent transmission to humans and banned mink farming in many countries (OIE, 2020).

Prior to 2002, when the first outbreak of SARS CoV occurred, the study of human CoV was not very common, as in humans these CoVs did not cause major complications with infection. The human alphacoronavirus HCoV-229E is known to originate from bats and was detected in alpacas prior to human transmission. HCoV-OC43 spread from rodents to cattle and was transmitted to humans around 1890, and has been circulating within the human population ever since (Vijgen et al., 2005; Jevšnik Virant et al., 2021). Following the first SARS CoV epidemic, a new human alphacoronavirus, HCoV-NL63, was detected in humans and transmitted to humans from bats. The beta-coronavirus HCoV-HKU1 has also been spread from humans to rodents. All four of these human CoVs occur seasonally, especially in winter, and most often cause mild signs of respiratory infections in humans (Corman et al., 2018). The identification of different CoVs and SARS like

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coronaviruses in bats and other wild animals suggest that some CoVs detected as human pathogen emerged because of interspecies transmission (Guan et al., 2003). These findings highlight the potential human health risk posed by coronaviruses in wild animals. To predict risk for coronavirus host transition, adaptation and disease outbreaks, we need to have deeper understanding of coronavirus reservoirs, such as bats (Rihtarič et al., 2010; Muth et al., 2018).

In veterinary medicine, coronaviruses that cause diseases in cats (and related species, such as civets), dogs (and related species, such as raccoons), pigs, cattle, horses, monkeys (Rhesus macaques) as well as small mammals (weasels, ferrets), rodents (rats, mice, bat guinea pigs and rabbits) and birds are important (Siddell et al., 1983).

### **The first epizootiological determinant – corona virus**

In the order *Nidovirales*, there is, among others, the family *Coronaviridae*, which includes the genera *Coronavirus* and *Torovirus*. CoVs are a genetically diverse group of viruses that occur in different species of animals and humans. All CoVs belong to the family *Coronaviridae*, which consists of four genera named *Alphacoronavirus*, *Betacoronavirus*, *Gammacoronavirus* and *Deltacoronavirus* (Figure 6), and within each genus CoVs are further classified into subgenera.

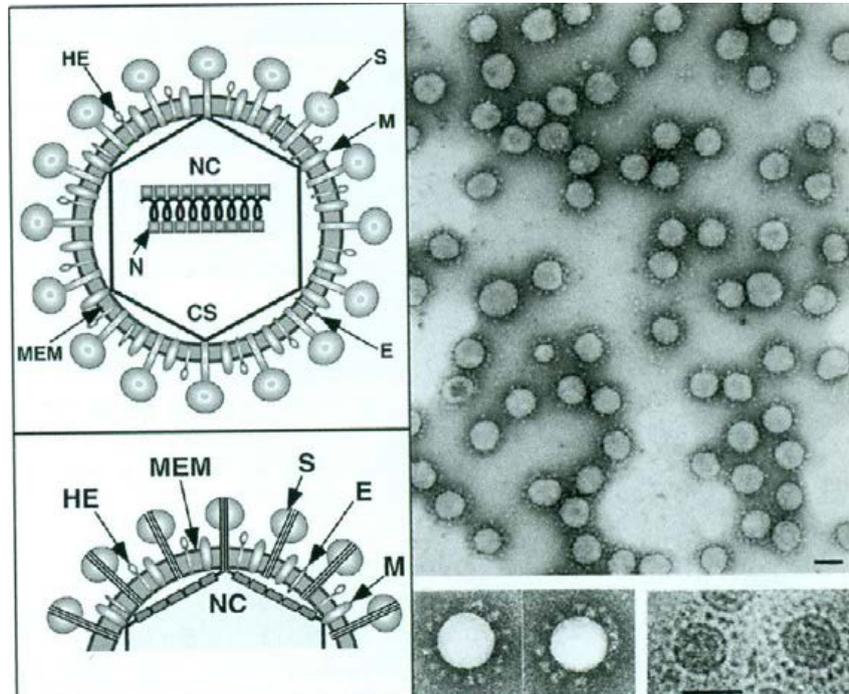
*Coronaviridae* is a family with a large number of viruses, that cause infectious diseases of mammals and birds with pronounced variations in clinical symptoms of the respiratory, reproductive, intestinal, urinary tract as well as nervous system disorders, liver damage, changes in joints and other systems, organs and tissues. These are RNA viruses, which have a sheath from which spikes protrude into the space, the so-called peplomere. Coronaviruses are relatively adapted to the species in which they cause primarily asymptomatic infections.

In the environment, coronaviruses can be easily inactivated with fat solvents, formalin, hypochlorite,  $\beta$ -propiolactone. The temperature of 56 °C inactivates them in one hour. They are relatively stable in an acidic environment (pH 3.0, 20 to 22 °C, for days). At a temperature of -70 or -80 °C or lyophilized at +4 °C they retain infectivity for years. In a humid atmosphere, they retain infectivity for up to two days, and when dried, they are inactivated in less than 24 hours. At low temperatures (-10 °C), they retain infectivity for several months. It is important that some coronaviruses (enteral) can remain infectious even after passing through the acidic environment of the stomach. This is especially true for coronaviruses that cause enteritis in young suckling animals and in which the buffering properties of milk significantly increase the pH value in the stomach. In dead animals, they lose their infectivity very quickly.

The epizootiological significance of individual coronavirus structures (Figure 2) is reflected in the fact that the spectrum of susceptible animal species is largely conditioned by the peplomer protein ("S" protein of the spike) (Figure 3) (Sanchez et al., 1999). The segments of this protein cause the binding to cells receptors and the conjugation of the virus to the cell, which in the initial phase of infection takes place on the plasma membrane but also within the endosomes of the receptive cell (Hajjerma et al., 2003). The cells contain, as receptors, aminopeptidase-N molecules (enteral viruses of cats,

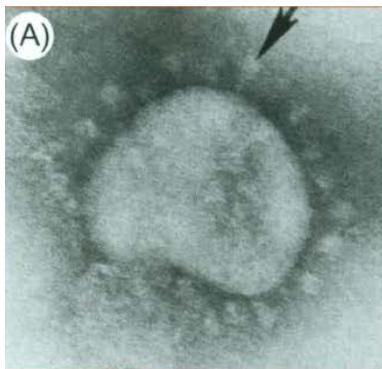
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dogs and pigs), ACE (angiotensin-converting enzyme 2), cell adhesion molecules, sialic acid molecules and heparin sulfate (Tresnan et al., 1996).



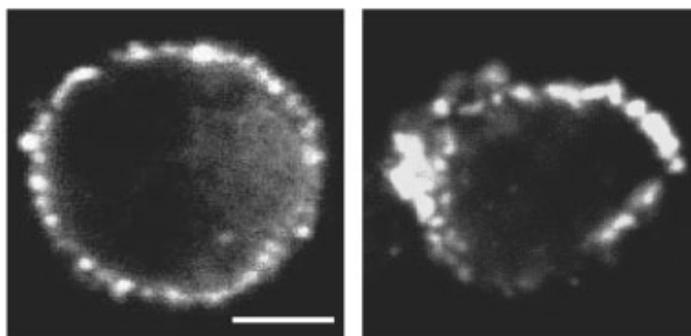
**Figure 2** Coronavirus structure. Top left: Schematic diagram of viral structure. Bottom left: section of the virus surface. Top right: electronic scan of viral particles (transmissible porcine gastroenteritis virus-TGE) Staining: uranyl acetate or sodium phosphotungstat (bottom left from right). At the very bottom right is the visualization using cryo-electron microscopy, a non-stained TGE virus. The particles contain the internal structures of the virus in the envelope as well as the pronounced peplomers. MEM: lipid membrane, S: spike protein (peplomere, "Spike"), M: large virus membrane protein, E: small virus membrane protein, HE: hemagglutinin esterase, N: nucleocapsid protein, CS: virus core envelope, NC: nucleocapsid.

Coronavirus replication is complex. Viral RNA serves as information for the synthesis of RNA polymerase used to transcribe complementary RNA molecules (negative polarity). The next phase is the transcription of this molecule into RNA of positive polarity, but also a larger number of small information RNA molecules that cause the translation and synthesis of a larger number of viral proteins.



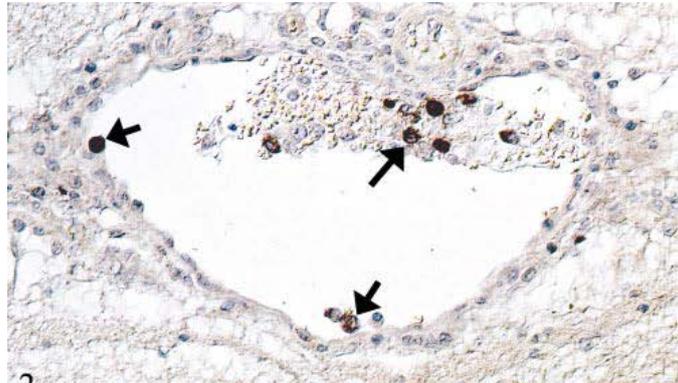
**Figure 3** The arrow shows a spike (peplomer) that contains the "S" protein.

Synthesis, processing, maturation, as well as transport of several viral envelope glycoproteins, show unusual properties. For example, the M envelope protein is directed exclusively to the cisterns of the endoplasmic reticulum located prior to the Golgi membrane. As a result, the virus only buds at that location of the cell, and not from the plasma membrane. This is followed by the transport of viral particles into the vesicles of the plasma membrane, after which the virus leaves the cell, by the mechanism of exocytosis. It should be noted that at this stage, in addition to the large number of virus particles leaving the cell membrane, a significant percentage of mature viruses remain bound to the cell from which they originated (Figures 4 and 5). This is of great importance in relation to the ratio of immune pathogenetic mechanisms in tissue and organ damage (Dewerchin et al., 2006).



**Figure 4** Localization of viruses and viral proteins on the cell surface (monocytes).

During the replication of the coronavirus, polymerase errors occur during transcription and accumulation of point mutations in the genetic material of the virus occurs (genetic "drift"). Likewise, frequent recombination occur between genetic materials of different as well as similar coronaviruses (Haijema et al., 2003). These mechanisms can be of great importance for understanding the existence and creation of new generations of genetically different coronaviruses that occurs in nature. Certainly, this enables a constant potential source of new viruses with new phenotypic characteristics, including the possibility of infecting new species of animals and changing the tropism and virulence of coronaviruses (Dong et al., 2007).



**Figure 5** Veins (leptomeninks). Coronaviruses antigen in monocytes, in the vascular lumen as well as bound to endothelial cells (arrows).

### **Second epizootiological determinant - host**

A large number of animal species can be infected with a coronavirus that is specific for that species of coronavirus, but infections with coronaviruses that are specific, ie. adapted to another species are also possible. Figure 6 (Fehr and Perlman, 2015) lists the genera of coronaviruses in humans and animals. Selected and chosen elements related to the first two epizootiological determinants of coronavirus infections of different animal species are listed.

### **Porcine coronavirus infections**

Transmissible porcine gastroenteritis (TGE) is a highly contagious disease, and both dogs and cats are susceptible. Due to the low population density, wild boars are not a significant reservoir of the virus in nature. The virus, the causative agent of TGE, has a very similar antigen as the coronaviruses of dogs, cats and humans, so there is a potential for cross-immunity. The virus was isolated from mice on the farm during the epizootic as well as from birds (starlings). In piglets, the intake of 10-100 virus particles is sufficient to cause clinically manifest disease. This amount is 10,000 times higher in adult pigs.

The virus enters the farm through carriers or mechanical vectors (contaminated equipment, dirt). In an uninfected farm, the epizootic occurs suddenly, all categories of pigs become ill, with a high mortality rate. Within a few weeks, the epizootic affects all animals that become immune. However, in such groups, some pigs remain carriers.

There is another epizootiological scenario that is characteristic of large farms where, in accordance with the breeding technology, there is always a certain population of susceptible piglets. In that case, there is a low degree of mortality, milder symptoms that are most often observed in piglets immediately after weaning as a consequence of the weakening of the protective effect of maternal immunity (especially the effect of IgA from milk).

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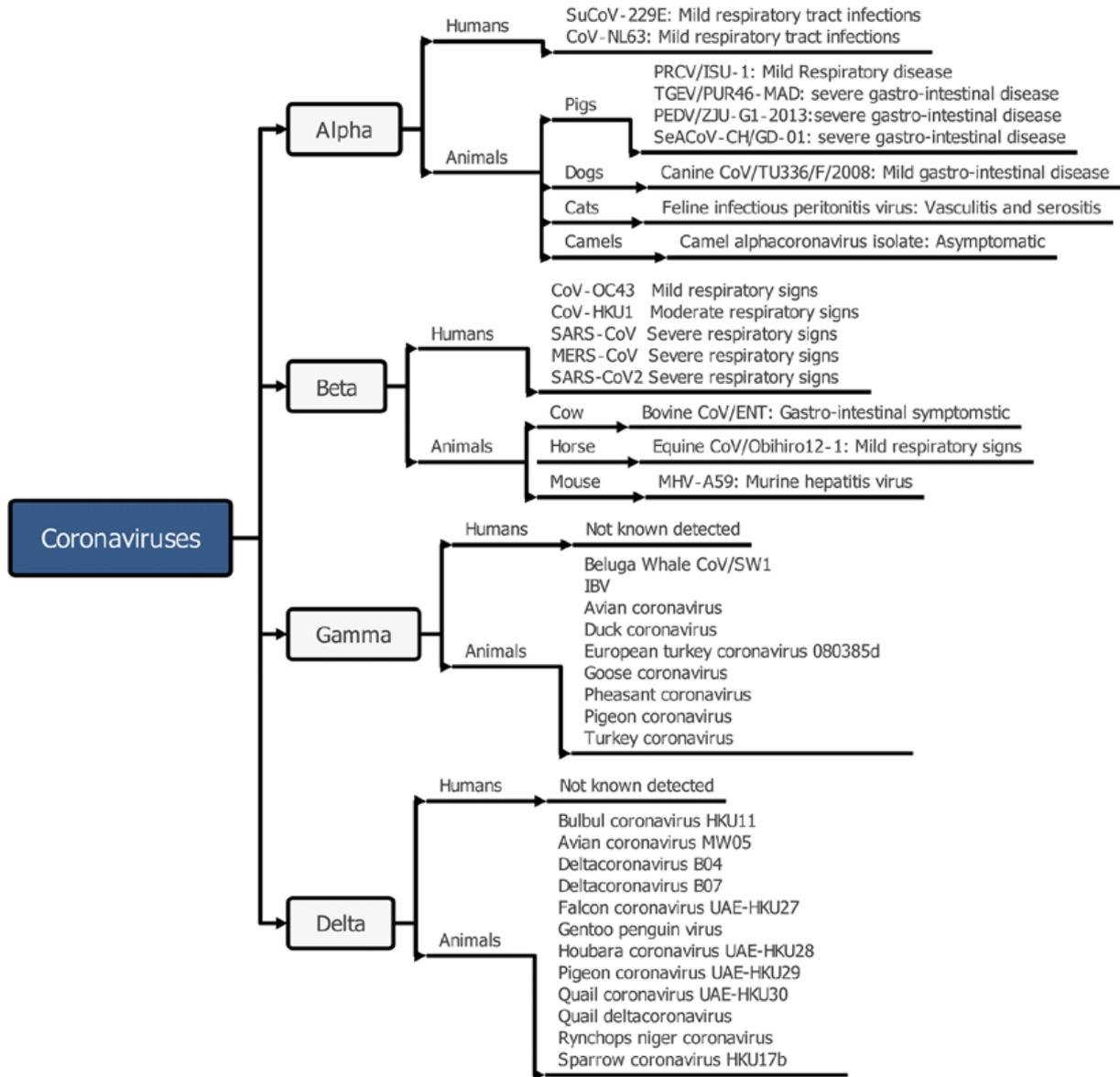


Figure 6 Coronaviruses in humans and animals.

The greatest danger of virus transmission is the movement of pigs within the farm. Protracted transmission of the virus on the farm, exogenous re-infections as well as the constant secretion of the virus by carriers indicate that any seropositive animal must be considered a potential source of infection.

The course of the epizootic, the territorial distribution as well as the clinical signs in pigs, depending on the characteristics of the virus. Initially, high levels of virulence and contagiousness lead to the rapid spread of the infection. Later, after a few months, there is a weakening of the epizootic (and virulence of the virus) and over a period of several years, there is no disease, even when large populations of pigs are susceptible. The change in virulence is thought to be due to the presence of "herd" immunity. It is unusual that the change in virulence (weakening) is maintained for a longer period of time, ie. for

years. However, as a consequence of a sudden change in virulence, new TGE epizootics occur (Yanga et al., 1995).

Transmission of the virus is fecal-oral, and the virus enters the susceptible animal by ingestion of contaminated material (Herrewegh et al., 1995). Infection can spread aerogenously. The virus is in the feces 24 hours after infection, and the highest concentrations are in the period from the 2nd to the 5th day, when there are  $10^7$  infectious virus particles in one gram of feces. In adult pigs, secretion is intermittent during episodes of diarrhea. However, even when there are no symptoms in pigs on the farm, there is enough virus in the feces of adult pigs to spread the infection quickly on the farm.

There are several reasons for the greater susceptibility of very young piglets: 1. lower gastric acidity at that age as a consequence of the buffering action of milk, 2. slower renewal of enterocytes from the base of intestinal villi, 3. neonatal immune system is not fully developed and 4. neonatal piglets are particularly susceptible to dehydration and electrolyte loss.

The most severe symptoms are found in very young animals (vomiting, profuse watery diarrhea of yellow color, rapid weight loss and dehydration). Most pigs on the farm are usually infected and die within a few days. Animals older than 2-3 weeks rarely die. Slightly older pigs in fattening show signs of transient watery diarrhea; vomiting is rare. In adult pigs, the disease is asymptomatic, but epizootics with high mortality have been reported, with clinical symptoms such as anorexia, pyrexia, vomiting, diarrhea and agalactia predominating.

In some regions of the world (Europe), virulent strains of TGE-causing swine coronavirus are replaced by epizootic swine respiratory coronavirus. This respiratory virus is a genetic variant of the TGE virus with a greater or lesser deletion in the peplomer protein (S protein). This virus also elicits a strong immune response against the TGE virus.

Infection with porcine haemagglutinating encephalomyelitis coronavirus in adult animals is inapparent. The virus spreads by aerosols, and the respiratory tract is the site of primary virus replication. In piglets younger than 3 weeks, there is weakening and vomiting. There are also neurological disorders (opisthotonus, sitting posture, paralysis, convulsions).

The porcine epizootic diarrhea virus causes similar symptoms as TGE, but in most cases this causative agent is less contagious.

The TGE virus in pigs is thought to be derived from genetically related canine coronavirus (CCoV) and from a less virulent version of porcine respiratory coronavirus (PRCV), which is widespread in pig farms where it causes only mild respiratory infections (Saif et al., 2019). The porcine epidemic diarrhea virus (PED) causes mainly high mortality among suckling piglets and originates from bat CoV. The first cases of deaths and diarrhea in piglets caused by the PED virus were detected in Europe and also in Slovenia between 2014 and 2015 (Toplak et al., 2015). In the next two years, real-time RT-PCR and sequencing confirmed the same strain of the virus in many pig farms throughout Slovenia. Determination and phylogenetic comparison of the entire genome of the Slovenian strain of PED virus (SLO / JH-11/2015, KU297956) with strains in the gene bank showed very similarity with PED strains from France, Germany and Belgium

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and with OH851 strain, which was first identified in 2013 in the US (Toplak et al., 2016) and later in other parts of the world (Wang et al., 2019). In 2012, a new delta porcine CoV (PDCV) was identified, which causes severe diarrhea in pigs in pigs and is derived from avian deltacoronavirus (Wille et al., 2020).

### **Cats coronavirus infections**

Coronavirus in cats can cause relatively mild enteritis but also a very severe infection in the form of peritonitis, often fatal (Pedersen, 1983). Peritonitis is thought to occur as a result of mutations in the enteral coronavirus, during natural infection, with the virus altering tropism toward macrophages (Pedersen et al., 1984). Serotype 2 feline coronavirus possesses segments of the canine coronavirus genome. Any strain of the virus can cause any form of the disease. There are a large number of coronavirus strains in nature that cause enteral form or peritonitis. However, it is difficult to publish accurate epidemiological studies on the distribution of coronavirus infections in cats, due to their high antigen (and genetic) similarity (Haijema et al., 2003).

The disease usually occurs in young or very old cats. Very young animals are protected by maternal immunity, but after weaning, they become susceptible to enteral coronavirus that is secreted by the mother cat. Having created their own immune response, such kittens remain carriers. In such animals, a balance between viruses and immune mechanisms is maintained for a long period of time. However, in the case of stress or weakened immunity, the virus mutates to form variants that have tropism for macrophages and that lead to the development of peritonitis (Poland et al., 1996).

### **Dogs coronavirus infections**

It is usually a mild gastrointestinal infection. However, in the recent period, there are strains of canine coronavirus that have increased virulence and cause multisystem diseases such as disorders of the respiratory tract and other organ systems (pyrexia, anorexia, depression, diarrhea, leukopenia and nervous disorders). Wild canids (coyotes), cats, and raccoons are also susceptible (Helfer-Baker et al., 1980). Coronaviruses, which are genetically similar to bovine coronaviruses, have been isolated from dogs in Europe and North America. Dogs can be infected with the virus that causes TGE.

Transmission of the virus is fecal-oral. The virus passes through the stomach due to its resistance to acidic environments.

Affected dogs secrete the virus between 6 and 9 days. However, this period may be longer in some dogs. Transmission largely depends on the density of the dog population. It has been observed that in the population of dogs kept individually (domestic dogs), 20% of them are seropositive. This percentage is 80% in dogs kept in kennels (Herrewegh et al., 1995).

### **Mice coronavirus infections**

Mouse hepatitis is caused by a coronavirus that has tropism for a large number of tissues. The range of tropism begins at the intestinal tract and ends at the respiratory tract. Between these two extremes, the virus can have tropism for the vascular endothelium,

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lymphatic tissues, hematopoietic system, liver and central nervous system. However, all of these viruses multiply in the liver tissue.

Mouse coronavirus is highly contagious, and young animals are particularly susceptible. In adults, the disease is asymptomatic. When the epizootic passes, as a result of maternal immunity, the disease does not exist in its clinical form. Polytropic strains of the virus are less contagious.

In mouse coronaviruses, persistent infections are observed in the population as a consequence of the constant evolution of the virus (mutation), which constantly infects already infected mice. Thus, the virus is constantly maintained in the population.

Coronavirus can also cause sialodacryoadenitis in mice. There are a number of strains of the rat virus. In the rat population, this virus is highly contagious and possesses tropism for the nasal respiratory epithelium. From there, it spreads to the salivary glands and lungs. The most pronounced symptoms are found in young animals.

### **Cattle coronavirus infections**

Bovine coronavirus (BCoV) cause diarrhea in calves, winter dysentery (bloody diarrhea) of adult animals and respiratory disorders, in which case they contribute to the multifactorial etiology of "transport fever". The BCoV is genetically and antigenically closely related to the human coronavirus (HCoV-OC43) and can infect a large number of wild animals (dogs and turkeys). It is also isolated from a large number of wild animals (camels, giraffes, etc.).

Most often, calves younger than 3 weeks, after a decrease in the concentration of maternal antibodies, are affected. Animals up to 3 months of age can also become ill. Mixed infections (rotavirus, torovirus, cryptosporidium, *E. coli*) are common, and are usually seasonal. Namely, during the winter, the concentration of the virus is higher in the environment (longer survival). As for winter dysentery, the name indicates when it occurs, and the virus can circulate in nature in a large number of ruminant species (deer, caribou, etc.). Respiratory disease in cattle is observed at the age of 2 to 6 months. After the enteral form of the disease, the virus remains in the upper segments of the respiratory tract for a long period of time, being secreted into the environment. In this way the infection is maintained on farms. Also, new variants of the virus can be introduced through the carrier, from another source.

It is important that calves or heifers that arrive at the cattle fattening farm with higher concentrations of specific anti-coronavirus antibodies, have less pronounced symptoms, and the carrier period is also shorter.

Within the *Betacoronavirus* genus BCoVs share a global nucleotide identity of 96% with human coronavirus HCoV-OC43 (Jevšnik Virant et al., 2021). Vijgen and co-workers demonstrated, using molecular clock analysis, that HCoV-OC43 has zoonotic origin and transmitted from bovine to human around 1890 (Vijgen et al., 2005). CoVs are unique among RNA viruses, because of their replication and transcription mechanism and therefore CoVs are characterized by a high potential of evolution, adaptation, and interspecies jumping (Woo et al., 2009).

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### **Birds coronavirus infections**

Avian coronaviruses are one of the first viruses isolated from this family. Infectious bronchitis is one of the most important diseases in poultry, and so far a large number of serotypes (over 10) have been isolated. The only reservoirs in nature are chickens. The clinical signs depend on a number of factors: bird age, flock genetics and immune status, mode of infection and nutritional factors (especially the presence of calcium in food), virulence of virus strains as well as the presence of stress (cold) and other microorganisms (Poland et al., 1996). The disease can appear explosive on the farm, when all the birds get sick in a few days. Mortality can be up to 75 % (usually 25-30 %). Higher mortality is found in broilers, as a result of secondary bacterial infections. In laying hens, there are symptoms of damage of the reproductive tract, but also systemic health disorders.

After getting sick, the birds are carriers for more than 100 days. The virus can be isolated from the caecum even when it is not present in the respiratory tract.

The infection is spread by droplets, with the the respiratory tract being the route of viral entry, as well as the ingestion of contaminated material (feces). The virus can also be introduced to the farm through secondary sources of infection (people, equipment, food). There are three forms of the disease: respiratory, reproductive and nephritis. In the environment, the virus that causes infectious bronchitis in poultry can survive for several days, and in cold periods of the year, for several weeks. It is interesting to note that epizootics can also occur in vaccinated flocks in the cases when immunity is weakened or when a new serovariety of the virus appears.

Turkeys can be infected with the turkey coronavirus, in which case the symptoms most often appear as a consequence of enteritis. There is only one serotype of this virus in which the peplomer protein ("C"), despite the great similarity in the genetic material (90 %), differs significantly from that of the causative agent of infectious chicken bronchitis. It has been established that bovine coronavirus can infect young turkeys.

Birds of all ages can get sick, but the symptoms are most pronounced in the young categories (the first few weeks of life). Symptoms may be more severe in the case of mixed infections.

### **SARS CoV-2 pandemic and difficulties in control of infection**

The SARS CoV-2 virus is transmitted faster and more efficiently through the air than is known for influenza viruses and most other respiratory pathogens and can also persist for several days on contaminated surfaces. But all the ways in which the virus spreads and the reasons why there are differences in the immune response in those infected are not yet fully understood. It should be borne in mind that the current pandemic has emerged in modern times, when it has become self-evident that there is a free exchange of various goods between countries and continents, and we are directly or indirectly connected daily with people and goods from different parts of the world. Not only clinically infected people are important in the spread and control of SARS CoV-2 virus infections, but undetected infections play a key role, in which the virus can only be detected by mass testing. In the vast majority of these, the immune system successfully fights with the

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SARS CoV-2 virus and infected persons show no clinical signs of the disease and gain at least a few months of natural protection against re-infection. Clinically undetectable carriers of SARS CoV-2 virus will therefore continue to be an important source of infection in the future, which will be very difficult to control. Similar problem was observed as main obstacle for controlling the outbreaks in all CoVs infections detected also in animals.

### CONCLUSION

Phylogenetically, coronaviruses are considered to be the oldest. This means that during the development of animal species there was enough time for viruses from this family not only to adapt to certain species, without causing significant clinical symptoms with long-term virus carriers, but also to "skip" from one species animals to another (and human), due to the characteristics of their genetic material. In order to understand all aspects of the SARS-CoV-2 pandemic, it is necessary to know the epizootiological characteristics of corona viral infections in the animal kingdom. This is the only way to correctly interpret the different panzootic/pandemic scenarios caused by coronaviruses. At the same time, only by knowing the epizootiological determinants, effective measures for the control and suppression of coronavirus viral infections can be determined not only in animals but also in humans.

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