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LARGE CATTLE CORONAVIRUS: EPIZOOTIC STATUS, GENOME STRUCTURE, CLINICAL SYMPTOMS AND PREVENTION-MINI REVIEW

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Received: 18.05.2023
Accepted: 02.09.2023

Bovine diarrhea is of multifactorial origin, causing heavy mortality risk and having a negative impact on animal welfare along with high economic loss in animal husbandry. Coronoviruses are one of the main enteropathogenic viruses of humans and newborn calves. A review of the available data indicates that further research is needed to understand the underlying pathogenesis mechanisms of BCoV respiratory and intestinal diseases, as well as the variables and interactions between the virus, host, and environmental factors that can exacerbate the disease or lead to increased spread and transmission. Further extensive research is needed to determine the correlates and attributes of immune defense needed to develop effective vaccines/regimens that can prevent severe disease and limit the spread of the virus.
Keywords: *coronavirus, RNA (ribonucleic acid), epidemiology, genome*
DOI: https://doi.org/10.59849/2409-4838.2023.3.77

INTRODUCTION

Viral diseases occur as a result of the pathogen entering the body of an animal. The interaction of a virus with an animal organism is a biological process. The genus Coronovirus belongs to little-studied viruses and was separated into an independent group in 1968 [1-4]. The modern classification of coronaviruses is presented in the following form:

Coronaviruses (CoV) belong to the Coronavirinae subfamily of the Coronaviridae family, phylum Nidovirales. CoVs are currently classified into four genera: alphacoronaviruses, betacoronaviruses, gammacoronaviruses, and deltacoronaviruses, while alphacoronaviruses and betacoronaviruses are mammalian CoVs and members of the other two genera cause disease in all birds [14, 16].

Despite differences in natural hosts, coronovirus virions share many common biological features in their morphological structure. Five main features determine the belonging of the virus to the genus of coronoviruses. The average size of the virion is 80-160 nm, the presence of RNA, membranes with lipids, the peculiar morphology of virions and the reproduction of viruses in the cytoplasmic vesicles of the cell.

MAIN PART

The genomic RNA of coronoviruses is a single-stranded linear "plus" RNA molecule with a molecular weight of 5.5-8.1 mD and a sedimentation coefficient of 48-70 S. Of great epidemiological importance are the infectious bronchitis virus of birds, infectious gastroenteritis of pigs, hemagglutinating encephalomyelitis of pigs and coronovirus of large horned animals. Mouse hepatitis viruses are known to be coronoviruses. The main way for the introduction of coronoviruses from an infected cell is its lysis. There is an antigenic relationship between human coronoviruses and murine hepatitis virus [9, 10, 19].

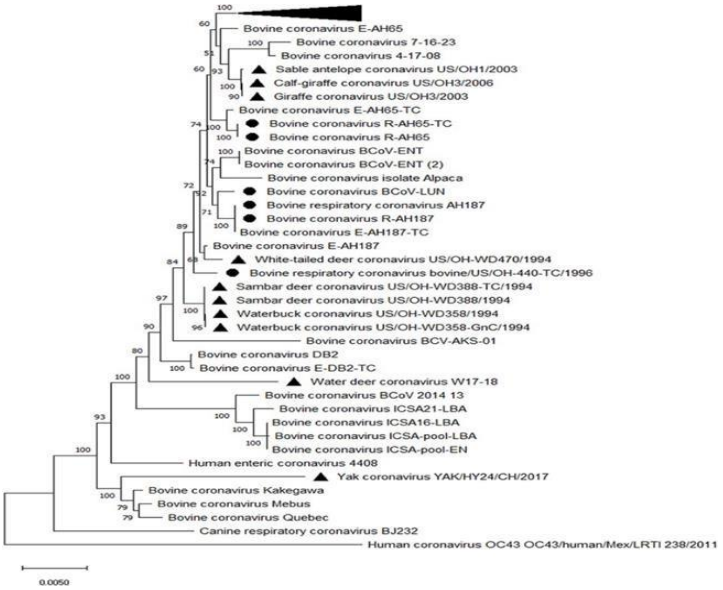

Fig. 1. Phylogenetic analysis of the complete genomes of enteric and respiratory BCoVs from wild ruminants and bovine CoVs (source: https://doi.org/10.3390/v12020183)

The phylogenetic tree of the hemagglutinin esterase protein (HE), glycoprotein (S), nucleocapsid protein (N), and ORF1 genes in Figure 1 revealed similar clusters throughout the genome.

Determining how target genes can influence the disease process is important because coronaviruses are increasingly spreading in livestock around the world, and can be helpful if the disease process of other coronaviruses is not understood. A possible common mechanism of spread between species may provide more data on the etiology of the disease and potential treatment options in the future [24].

Table 1.

The gastric BCoV degree of positiveness in Different countries

Spread area by years	Countries	Spreading speed (%)
2010-2019	Korea	5.6-58.2
	Turkey	1
	Australia	14
	New Zealand	21.6
	Algeria	20.73
	Iran	7.2.
	China	12.20-69
	India	8.88-16
	Thailand	12
2009	Canada	57-66
2000-2009	Ireland	22.9-60.7
	Italy	9.6-65
	Brazil	22-67

Table 1 shows the gastric BCoV degree of positiveness in different countries [24].

It shows that, in 2000-2009, the gastric BCoV degree of positiveness in Italy and Ireland was 9.60-65.85% and 22.9-60.7%, respectively. From 2010 to 2019, a positive BCoV was detected for the first time in Australia. In China, a positive BCoV rate has been detected for the first time since 2020. Other countries respectively as mentioned in table 1.

Seasonal changes are one of the most important and predictable systems affecting humans and ecosystems. The spread of many pathogenic infections is seasonal, for example, respiratory diseases in humans and rotaviruses in children are more common in winter [20, 21, 23]. In addition, nodular dermatitis of large ruminants' spreads depending on seasonal changes also [22]. Annual seasonal fluctuations can cause changes in the susceptible organism and infection biology and lead to epidemics, but other factors leading to seasonal epidemics should be considered [5, 6, 8]. The coronavirus pandemic, which is a viral disease that the planet is facing in the modern period, has shown that in order to prevent such diseases and stay prepared for the possible occurrence of such risks in the futures. Thus, just 5 months after the global pandemic caused by the SARS-CoV-2 virus in China at the end of 2019, millions of people were symptomatically or asymptomatically infected with the virus, and 360,000 of them died [18]. There for, it is very important to study viral diseases in depth and reduce biological threats.

Pathogenic viruses, spreading in the environment with different serotypes, change their own serotypes, mutating and causing epizootics, epidemics and even pandemics. Along with humans, coronaviruses are observed in diarrhea in animals, including calves. In the US, BCoV-WD is more common in northern states [11, 13, 17].

According to statistics, 75-95% of infectious diarrhea in calves in Azerbaijan is caused by Escherichia coli, Rotavirus, Coronavirus and Cryptosporidium, including rotovirus 27-36%, coronavirus 20-26%.

Clinical signs

Coronoviruses that cause respiratory and intestinal diseases in farm animals and other ruminants can be found in the respiratory tract and intestines of healthy farm animals [7]. BCoV is excreted in faeces and nasal secretions and is associated with 3 different clinical syndromes in farm animals [15]: calf (neonatal) diarrhea [12], winter dysentery characterized by hemorrhagic diarrhea in adult animals [22, 23].

Preventive care

After an illness, calves develop immunity against coronavirus for up to a year. Colostral immunity in newborn calves provides them with resistance to disease or prevents the disease from becoming severe. For specific prophylaxis, live and inactivated vaccines are used. Calves are vaccinated orally after birth, and cows are vaccinated parenterally to induce colostral immunity. In addition, for oral-nasal administration, the coronavirus vaccine uses a multivalent that combines type I, II, and III viruses. Currently, an associated inactivated vaccine with aluminum hydroxide against rotavirus, coronavirus and intestinal diarrhea of newborn calves has been developed. Timely epizootological control and prevention of infection in healthy farms are the basis of preventive measures. To do this, all new animals entering the farm are kept in quarantine, the calves are looked after separately and they are not allowed to be kept together with older animals. In the maternity ward, veterinary and sanitary rules are observed and regular disinfection is carried out. Other preventive measures include epidemiological monitoring and biosecurity rules [1].

CONCLUSION

A review of the available data indicates that further research is needed to understand the underlying pathogenesis mechanisms of BCoV respiratory and intestinal diseases, as well as the variables and interactions between the virus, host, and environmental factors that can exacerbate the disease or lead to increased spread and transmission. Further extensive research is needed to determine the correlates and attributes of immune defense needed to develop effective vaccines/regimens that can prevent severe disease and limit the spread of the virus. The lack of awareness of the mechanisms that

regulate interspecies transmission of BCoV and identify a wide range of its hosts predetermines the importance of studying this area. Finally, detailed studies are needed in wildlife waters (including wild ruminants or other susceptible species) to better understand the similar bovine CoV ecology or the threats such ecology poses to human or animal health.

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İRİ MALLARIN KORONAVİRUSU: EPİZOOTİK VƏZİYYƏT, GENOMLARIN STRUKTURU, KLİNİKİ ƏLAMƏTLƏRİ VƏ PROFİLAKSİYA-İCMAL

V.C. Abbasov

İri Buynuzluların dihareasi multifaktorial mənşəli olmaraq ağır ölüm riski yaradır və heyvandarlıqda yüksək ekonomik zərərlə bərabər heyvan rifahına mənfi təsir edir. Koronoviruslar da bu qəbildən olmaqla insanların və yeni doğulmuş buzovların əsas enteropatogen viruslarındandır. Məlumatların icmalı onu göstərir ki, BCoV-nun tənəffüs və bağırsaq xəstəliklərinin patogenezinin əsas mexanizmlərini və xəstəliyi şiddətləndirən və ya yayılmasının artmasına və ötürülməsinə səbəb ola bilən viral, ev sahibi və ətraf mühit amilləri arasında dəyişənləri və qarşılıqlı əlaqəni anlamaq üçün əlavə tədqiqatlara ehtiyac var.

Açar sözlər: *koronavirus, RNT (ribonuklein turşusu), epidemiologiya, genom*

КОРОНАВИРУС КРУПНОГО СКОТА: ЭПИЗООТИЧЕСКИЙ СТАТУС, СТРУКТУРА ГЕНОМА, КЛИНИЧЕСКИЕ СИМПТОМЫ И ПРОФИЛАКТИКА-ОБЗОР

В.Ч. Аббасов

Диарея крупного рогатого скота имеет многофакторное происхождение, вызывая высокий риск смертности и оказывая негативное влияние на благополучие животных, а также высокие экономические потери в животноводстве. Короновирусы относятся к основным энтеропатогенным вирусам человека и новорожденных телят. Анализ данных показывает, что необходимы дальнейшие исследования для понимания основных механизмов патогенеза BCoV респираторных и кишечных заболеваний, а также переменных и взаимодействий между вирусом, хозяином и факторами окружающей среды, которые могут усугубить заболевание или привести к увеличению распространения и передачи.

Ключевые слова: *коронавирус, РНК (рибонуклеиновая кислота), эпидемиология, геном.*