INFEKTOL GLASN 2022;42(1):9-15
https://doi.org/10.37797/ig.42.1.2

Pregledni rad | Review paper

Human coronaviruses in the 'One Health' context

Humani koronavirusi u kontekstu 'Jednog zdravlja'

Tatjana Vilibić-Čavlek[1,2], Thomas Ferenc[3], Vladimir Stevanović[4], Mateja Vujica[5], Maja Bogdanić[1], Safdar Ali[6], Irena Tabain[1], Ljubo Barbić[4]

[1] Department of Virology, Croatian Institute of Public Health, Zagreb, Croatia
[2] School of Medicine University of Zagreb, Zagreb, Croatia
[3] Department of Radiology, Merkur University Hospital, Zagreb, Croatia
[4] Faculty of Veterinary Medicine University of Zagreb, Zagreb, Croatia
[5] Institute of Emergency Medicine of Krapina-Zagorje County, Krapina, Croatia
[6] Faculty of Public Health, University of Debrecen, Hungary

Keywords:
seasonal coronaviruses
SARS-CoV
MERS-CoV
SARS-CoV-2
One Health

Ključne riječi:
sezonski koronavirusi
SARS-CoV
MERS-CoV
SARS-CoV-2
Jedno zdravlje

Summary

Seven human coronaviruses have been identified so far: four seasonal coronaviruses (HCoV-229E, HCoV-OC43, HCoV-NL63, HCoV-HKU1) and three novel coronaviruses (SARS-CoV, MERS-CoV, SARS-CoV-2). While seasonal coronaviruses cause only mild symptoms, novel coronaviruses cause severe and potentially fatal infections. All known coronaviruses originated in animals. Bats are considered as an origin for the majority of coronaviruses capable of infecting humans; however, rodents are proposed as natural hosts for HCoV-OC43 and HCoV-HKU1. Different animal species could serve as intermediate hosts including alpacas (HCoV-229E), livestock (HCoV-OC43), civet cats (SARS-CoV), camels (MERS-CoV), and pangolins (SARS-CoV-2). In Croatia, SARS-CoV-2 was detected in humans, pet animals, wildlife, and the environment. The COVID-19 pandemic has highlighted the role of the 'One Health' approach in the surveillance of zoonotic diseases.

Primljeno: 07-09-2021
Received: 07-09-2021

Prihvaćeno: 09-10-2021
Accepted: 09-10-2021

✉ **Corresponding author:**
Assoc. Prof. Tatjana Vilibić-Čavlek, PhD, MD,
specialist in clinical microbiology
Department of Virology, Croatian Institute of Public Health,
Zagreb, Croatia
E-mail: tatjana.vilibic-cavlek@hzjz.hr

Sažetak

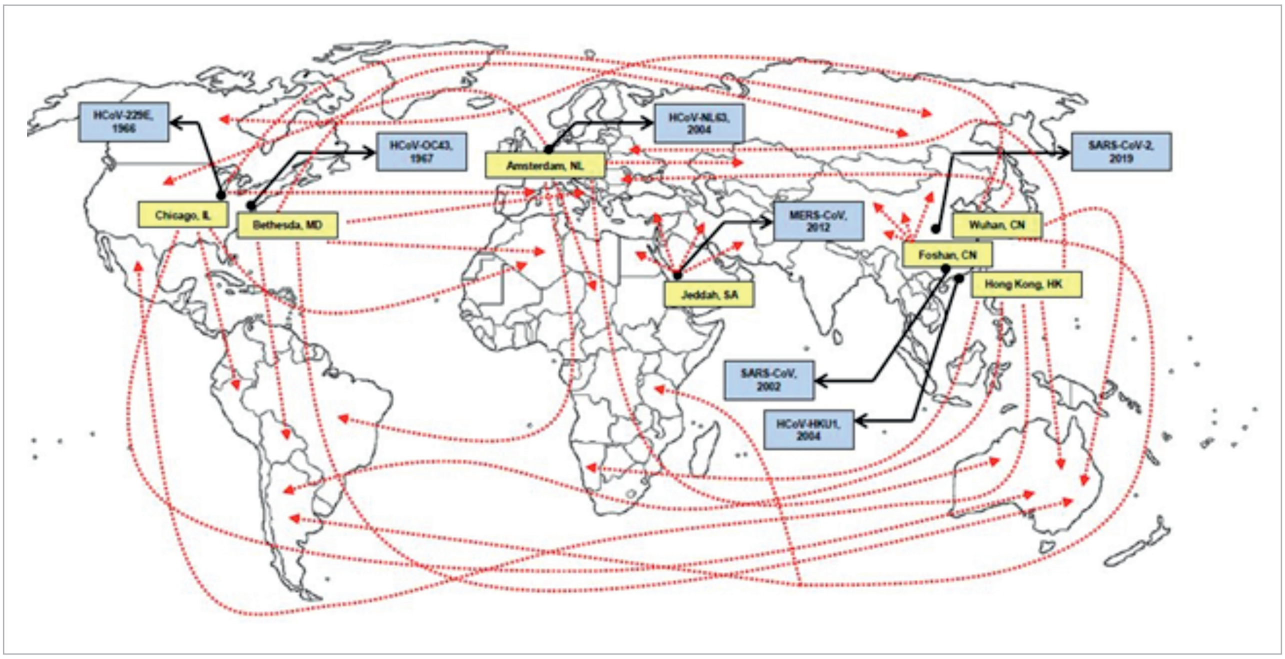
Do sada je otkriveno sedam humanih koronavirusa: četiri sezonska koronavirusa (HCoV-229E, HCoV-OC43, HCoV-NL63, HCoV-HKU1) i tri nova koronavirusa (SARS-CoV, MERS-CoV, SARS-CoV-2). Dok sezonski koronavirusi uzrokuju tek blage infekcije, novi koronavirusi su uzročnici teških i potencijalno smrtonosnih infekcija. Svi poznati koronavirusi su podrijetlom od životinja. Šišmiši se smatraju izvorom većine koronavirusa koji uzrokuju infekcije u ljudi, međutim prirodnim rezervoarima HCoV-OC43 i HCoV-HKU1 se smatraju glodavci. Različite životinjske vrste predstavljaju prijelazne domaćine uključujući alpake (HCoV-229E), stoku (HCoV-OC43), cibetke (SARS-CoV), deve (MERS-CoV) te ljuskaše (SARS-CoV-2). Na području Hrvatske SARS-CoV-2 je dokazan u ljudi, kućnih ljubimaca, divljih životinja te okolišu. Pandemija COVID-19 naglašava ulogu pristupa 'Jedno zdravlje' u nadzoru zoonoza.

Introduction

The recent emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) highlights the continuous threat to human health posed by coronaviruses. Seven coronaviruses that infect humans have been identified to date: seasonal human coronaviruses (HCoV-229E, HCoV-OC43, HCoV-NL63, HCoV-HKU1), severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS-CoV) and SARS-CoV-2. While seasonal coronaviruses cause only mild symptoms (common cold), novel coronaviruses (SARS-CoV, MERS-CoV, and SARS-CoV-2) cause severe and potentially fatal infections[1]. The emergence and spreading of human coronaviruses are presented in Figure 1.

Figure 1. Emergence and spreading of human coronaviruses

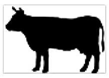
Slika 1. Pojava i širenje humanih koronavirusa



All known coronaviruses originated in animals (Table 1). This review focuses on human coronavirus infections in the 'One Health' context.

Table 1. Zoonotic origin of human coronaviruses

Tablica 1. Zoonotsko podrijetlo humanih koronavirusa

Virus	Year of isolation/ Godina izolacije	Natural host/ Prirodni domaćin	Intermediate host/ Prijelazni domaćin	Geographic distribution/ Geografska rasprostranjenost
HCoV-229E	1966		 ?	Worldwide/ Diljem svijeta
HCoV-OC43	1967			Worldwide/ Diljem svijeta
SARS-CoV	2002			China/ Kina
HCoV-NL63	2004		?	Worldwide/ Diljem svijeta
HCoV-HKU1	2004		?	Worldwide/ Diljem svijeta
MERS-CoV	2012			Middle East/ Srednji Istok
SARS-CoV-2	2019		 ?	Worldwide/ Diljem svijeta

Seasonal human coronaviruses (HCoV-229E, HCoV-NL63, HCoV-OC43 and HCoV-HKU1)

HCoV-229E, HCoV-NL63, HCoV-OC43, and HCoV-HKU1 are globally distributed pathogens associated with the common cold in humans. These viruses have been in perpetual circulation since their discovery and annually cause a variety of respiratory symptoms that more frequently involve children than adults [2,3]. In temperate climates, the highest infection rates are observed in winter and early spring months whereas tropical regions demonstrate year-round circulation with increased infection rates during certain months [2-6]. HCoV-229E, HCoV-NL63, HCoV-OC43 and HCoV-HKU1 account for 1.1-15%[6,7], 1-9.3%[2,6,8,9], 1.3-5%[6,10] and 1-6%[2,6], respectively of all reported acute respiratory infections. Furthermore, over 90% of adults show seropositivity for at least one seasonal human coronavirus while neutralizing (NT) antibodies to HCoV-NL63 have been found in the absolute majority of the adult population[4,11]. Coinfections with other viruses are relatively common, mainly HCoV-NL63 and HCoV-HKU1 with respiratory syncytial virus and influenza viruses[2,4,12]. Bats are considered an origin for the majority of coronaviruses capable of infecting humans[4,7]. However, some authors also propose an association with rodents as natural hosts[7,13]. A study from Corman *et al.*[14] (2015) has found that viruses discovered in fecal specimens of hipposiderid bats from Ghana are genetically related to HCoV-229E. In addition, the phylogenetic analysis identified a close relationship between HCoV-229E and Alpaca-CoV. These findings suggest that alpacas (camelids) may be an intermediate host in the bat-human cycle, however that has yet to be determined because these species do not share habitats[7,15]. HCoV-NL63 is also closely related to bat coronaviruses[7-9,12,15]. A study from Huynh *et al.*[8] reported that HCoV-NL63 could replicate in the lung cells of tricolored bats as well as in primate or human cells. These observations indicate that bats may also be the origin of this coronavirus. The potential intermediate host of HCoV-NL63 is still unknown[16]. A study from Ghana evaluated the possible role of domestic livestock species in the transmission of this virus to humans, however, none of the animal samples (pigs, sheep, donkeys, goats, cattle) tested positive[16]. HCoV-OC43 is considered to have originated from rodents whereas cattle are widely accepted as an intermediate host in the human transmission cycle[7,13]. Furthermore, there is also an association between rodents and HCoV-HKU1, however with no known intermediate host[7,16]. The general clinical spectrum of infections related to HCoVs varies from asymptomatic to common cold-like symptoms (rhinorrhea, nasal congestion, sore throat, cough, and fever)[4,6,17]. However, some strains are presumably associated with sporadic but more severe manifestations like febrile seizures (HCoV-229E, HCoV-OC43, HCoV-NL63, HCoV-HKU1), meningitis (HCoV-OC43, HCoV-HKU1), encephalitis (HCoV-OC43), flaccid paralysis (HCoV-229E, HCoV-OC43) and multiple sclerosis (HCoV-OC43, HCoV-229E)[4,7,11,12,17,18]. Although all four viruses have been detected in human fecal specimens, their significance as enteric pathogens appears to be minor as fecal-oral transmission has not yet been reported[4,7,14,17].

SARS-CoV

The first known case of SARS-CoV was reported in November 2002 in the Guangdong Province, China; however, the detection of the virus occurred in April 2003[19]. More than one-third of early cases were in food handlers[20]. By July 2003, SARS-CoV had spread to over 30 countries, resulting in more than 8098 confirmed cases, including 774 deaths[21]. After that, no cases were detected, and the SARS-CoV pandemic was declared over on 5th July 2003. Reported cases in all other countries have acquired the infection through travel to endemic areas, and only limited local transmission through close contact was reported[22]. The virus was first isolated from Himalayan palm civets[1]. A number of pet animals (cats, dogs) whose owners were diagnosed with SARS-CoV tested reverse-transcription polymerase chain reaction (RT-PCR) positive. Rats, mice, poultry, pigs, and rabbits seem resistant to infection[23]. In addition to palm civets, six wildlife species were found to be positive by either RT-PCR and/or serology–the raccoon dog, the Chinese ferret badger, cynomolgus macaques, fruit bats, snakes, and wild pigs[21,24]. SARS-CoV is thought to be transmitted most readily by respiratory droplets in close person-to-person contact, but also through contaminated surfaces or objects[21]. Clinical symptoms of SARS-CoV infection are rather non-specific and may mimic influenza or atypical pneumonia[25]. In 10%-20% of patients, respiratory illness is severe and requires mechanical ventilation[22]. The case fatality for SARS is 3%-15%[23]; however, it may be as high as 45% in patients older than 60 years, particularly those with pre-existing comorbidity[26].

MERS-CoV

MERS-CoV was first reported in a patient who died from severe acute respiratory syndrome in a hospital in Jeddah, Saudi Arabia in 2012[27]. Since then, many outbreaks have been reported on the

Arabian Peninsula[28]. In total, 27 countries have reported MERS-CoV cases since 2012, leading to more than 2580 cases and 858 known deaths due to the infection and related complications[29]. The origin of MERS-CoV has been widely discussed. Initially, it was believed that MERS-CoV, like many other coronaviruses, originated in bats based on the phylogenetic similarity of certain bat coronaviruses with MERS-CoV[30]. Dromedary camels were lately introduced as possible virus reservoirs. The first evidence to link the virus to dromedary camels came from a serological study on multiple animal species including dromedary camels, cattle, sheep, goats, water buffalo, and various other camelid species. MERS-CoV NT antibodies were only found in dromedary camels[31]. Equids (horses, donkeys, mules) were also screened for MERS-CoV antibodies, but evidence for equid infections has not been confirmed[32]. The virus is endemic in camel populations of East Africa and the Middle East and camels seem to be the only animal host responsible for the spillover of human infections[33]. Humans become infected from direct or indirect contact with dromedary camels; however, human-to-human transmission is also possible among household contacts and in healthcare settings. MERS-CoV can cause severe disease and has been fatal in approximately 35% of patients[29].

SARS-CoV-2

SARS-CoV-2 is a novel coronavirus that emerged in Wuhan, China in December 2019. In January 2020, the World Health Organization (WHO) declared it a public health emergency of international concern and on March 11th, a global pandemic was declared[34]. The discovery of diverse bat coronaviruses closely related to SARS-CoV-2 indicates that bats are possible reservoirs of SARS-CoV-2. Pangolins are another wildlife host probably linked with SARS-CoV-2[35]. However, unlike bats, the infected pangolins showed clinical signs and histopathological changes, including interstitial pneumonia and inflammatory cell infiltration in diverse organs suggesting pangolins are unlikely to be the reservoir of SARS-CoV-2 but more likely acquired the virus after spillover from the natural hosts[36]. Several animal species in zoological facilities have tested positive for SARS-CoV-2 including large cats (lions, tigers, snow leopards, cougars) and gorillas. At this time, there is no evidence that animals play a significant role in spreading of the SARS-CoV-2. However, reports from infected mink farms suggest that in these environments there is the possibility for the spread of SARS-CoV-2 from mink to humans. Recent experimental studies have shown that cats, dogs, ferrets, hamsters, and tree shrews can become infected and spread the virus to other animals of the same species in laboratory settings[37]. In addition, SARS-CoV-2 has been detected in naturally infected cats and dogs, most of whom were living in close contact with infected humans[38]. Human-to-human SARS-CoV-2 transmission can occur through direct, indirect, or close contact with infected persons through infected secretions such as saliva and respiratory secretions or respiratory droplets. Asymptomatic persons can also transmit the virus[39]. The clinical spectrum of symptomatic SARS-CoV infection ranges from mild to critical. In addition, asymptomatic infections have been well documented. The overall case fatality rate was reported to be 2.3%[40].

SARS-CoV-2 in Croatia in the 'One Health' context

The COVID-19 pandemic in Croatia is part of the worldwide pandemic. Four epidemic waves have been recorded with a total of 1,073,386 cases and 15,336 deaths due to COVID-19 reported up to 14th March 2022[41]. Several seroprevalence studies were conducted after the first and second waves in different population groups showing significant differences in the seropositivity rates (Table 2). The seropositivity rates detected by enzyme-linked immunosorbent assay varied from 2% to 11.1% and 8.8% to 25.1% after the first and second waves, respectively. The prevalence of NT antibodies was 2.2-5.5% after the first wave and 2.6-18.2% after the second pandemic wave[42-49]. In a meta-analysis by Rostami *et al.*[50] (2020) on SARS-CoV-2 seroprevalence worldwide, almost 400,000 people from 23 countries were included with seroprevalence rates in the general population ranging from 0.37% to 22.1% (pooled estimate of 3.38%). On a more regional level, the estimated overall seroprevalence in Western Europe was 3.17% (95%CI 1.96-4.38%), in Southern Europe, including Croatia, was 4.41% (95%CI 2.20-6.61%), in Eastern Europe was 0.66% (95%CI 0.51-0.83%), and in Northern Europe was 5.27% (3.97-6.57%). In their recent meta-analysis (2022), the Iranian group of authors[51] reported the estimated overall SARS-CoV-2 seroprevalence in Europe of 5% (95%CI 4-6%). The highest seroprevalence rates were in England (20%), Switzerland (8%), Germany (7%), and Spain (6%), while the lowest seroprevalence rates were detected in Lithuania (1%), Greece (1%), Hungary (1%), and Croatia (1%). One systematic review reported seroprevalence rates among selected population subgroups[52]. In healthcare workers, the lowest seroprevalence was detected in Italy (0.7%) and the highest (45.3%) in England. The blood donors possessed the lowest seroprevalence in Germany (0.91%), and the highest

Table 2. Seroprevalence of SARS-CoV-2 in Croatia (April 2020 - December 2021)

Tablica 2. Seroprevalencija SARS-CoV-2 na području Hrvatske (travanj 2020.- prosinac 2021.)

Tested group/ Testirana skupina	Testing period/ Razdoblje testiranja	Tested/ Testirani	SARS CoV-2 IgG ELISA		SARS-CoV-2 VNT		References/ Literatura
			Positive/ Pozitivni	95%CI	Positive/ Pozitivni	95%CI	
Healthcare workers/ Zdravstveni radnici	April-May/Travanj-svibanj 2020	592	16 (2.7%)	1.5-4.3	9 (1.5%)	0.7-2.9	[43]
Children and adolescents/ Djeca i adolescenti	May/Svibanj 2020	240	9 (3.9%)	1.7-7.0	7 (2.9%)	1.2-5.9	[44]
	October-November/ Listopad-studeni 2020	308	27 (8.8)	5.0-12.5	26 (8.4%)	5.6-12.1	
Hemodialysis patients/ Bolesnici na hemodijalizi	May/Svibanj 2020	136	9 (6.6%)	3.1-12.1	0 (0%)	0-2.7*	[46, 48]
Veterinary personnel/ Veterinari	May/Svibanj 2020	122	6 (4.9%)	1.8-10.4	0 (0%)	0-2.9*	[46]
	Mar/Ožujak 2021	121	22 (18.2%)	11.8-26.2	11 (9.1%)	4.6-15.7	
Professional football players/ Profesionalni nogometaši	May-July/ Svibanj-srpanj 2020	305	6 (2%)	0.9-4.2	NT	NA	[49]
General population/ Opća populacija	May-Jul/ Svibanj-srpanj 2020	1088	24 (2.2%)	1.4-3.2	2 (0.2%)	0-0.6	[45]
	Dec/Prosinac 2020-Feb/Veljača 2021	1436	360 (25.1%)	22.8-27.4	268 (18.7%)	16.7-20.8	
	Jun-July/	354	170 (48.0%)	42.7-53.4	NT	NA	
	Lipanj-srpanj 2021**						CIPH; unpublished data
	Dec/Prosinac 2021**	406	196 (48.3%)	43.3-53.3	NT	NA	
Professional athletes/ Profesionalni sportaši	Jun/Lipanj 2020	90	10 (11.1%)	5.5-19.5	5 (5.5%)	1.8-12.5	[48]
Solid organ transplant recipients/ Primatelji solidnih organa	Sep-Nov/Rujan-studeni 2020	512	103 (20.1%)	16.7-23.8	16 (3.1%)	1.8-5.0	[47]

*One-sided 97.5%CI; **Adult general population; CIPH=Croatian Institute of Public Health; NT=Not tested; NA=Not applicable

in Italy (23.3%), whereas students and teachers in Germany, had the lowest (0.6%) and in England the highest seroprevalence rates (11.7%). Galanis *et al.*[53] (2021) conducted a meta-analysis on the seroprevalence of SARS-CoV-2 antibodies among healthcare workers. The authors demonstrated the estimated overall seroprevalence of 8.7% (95%CI 6.7-10.9%), whereas the seroprevalence was higher in reports from North America (12.7%), compared to those from Europe (8.5%), Africa (8.2%), and Asia (4%).

Higher seropositivity rates were detected after the third and fourth pandemic waves (48.0 and 48.3%, respectively using ELISA). It is important to note that COVID-19 vaccination started at the end of December 2020 which may at least partly influence the obtained seroprevalence results in 2021 and 2022. A very recently published study (systematic review and meta-analysis of standardized population-based studies) observed that global SARS-CoV-2 seroprevalence has risen considerably over time. Similar to the Croatian results, the seroprevalence in Europe high-income countries has increased to 50% in 2021 (Q2, April-July) with a further steady increase to 95.9% in 2022 (Q1, January-March)[54].

In addition to human cases, SARS-CoV-2 was detected in pet animals. The first large-scale serosurvey of SARS-CoV-2 in dogs and cats from Zagreb and the Split region was conducted from February to June 2020. A small number of seropositive animals (dogs 0.31%, cats 0.76%) with a low neutralizing antibody titer after the first wave suggest infections are rare and are following human infections[55]. The second study (July-December 2020) included two dog populations from Zagreb: dogs from households with confirmed human COVID-19 cases and dogs admitted to the Veterinary Teaching Hospital (Faculty of Veterinary Medicine, University of Zagreb) for any given reason (general population). In COVID-19-infected households, 25.64% of dogs had detectable NT antibodies compared to 2.20% in the general population[56]. In addition, SARS-CoV-2 IgG antibodies were detected in 13.8% of cat serum samples collected in the Veterinary Teaching Hospital in December 2020[48].

The presence of SARS-CoV-2 was also analyzed in the wildlife (June 2020-February 2021). Blood, muscle extract, and fecal samples of free-living wild boars (*Sus scrofa*), red foxes (*Vulpes vulpes*) and jackals (*Canis aureus*), and blood and cloacal swabs of yellow-legged gulls (*Larus michahellis*) were tested. Using ELISA, SARS-CoV-2 antibodies were detected in 2.9% of red foxes, 3.9% of wild boars, and 4.6% of jackals; however, surrogate NT antibodies as well as SARS-CoV-2 RNA were not detected[57].

Conclusions

The COVID-19 pandemic has highlighted the role of the 'One Health' approach in the surveillance of zoonoses[58]. In addition to human cases, SARS-CoV-2 infections were confirmed in pet animals and wildlife. The detection of SARS-CoV-2 in humans, animals, and the environment implies that the 'One Health' approach is crucial to controlling COVID-19 and future pandemics[48].

REFERENCES

[1] Chen B, Tian E-K, He B, Tian L, Han R, Wang S, et al. Overview of lethal human coronaviruses. Sig Transduct Target Ther. 2020; 10;5(1):89.

[2] Principi N, Bosis S, Esposito S. Effects of Coronavirus Infections in Children. Emerg Infect Dis. 2010; 16(2):183–88.

[3] Park S, Lee Y, Michelow IC, Choe YJ. Global Seasonality of Human Coronaviruses: A Systematic Review. Open Forum Infect Dis. 2020; 7(11):ofaa443.

[4] Ogimi C, Kim YJ, Martin ET, Huh HJ, Chiu C-H, Englund JA. What's New With the Old Coronaviruses? J Pediatric Infect Dis Soc. 2020; 9(2):210–17.

[5] Audi A, AlIbrahim M, Kaddoura M, Hijazi G, Yassine HM, Zaraket H. Seasonality of Respiratory Viral Infections: Will COVID-19 Follow Suit? Front Public Health. 2020; 8:567184.

[6] Al-Khannaq MN, Ng KT, Oong XY, Pang YK, Takebe Y, Chook JB, et al. Diversity and Evolutionary Histories of Human Coronaviruses NL63 and 229E Associated with Acute Upper Respiratory Tract Symptoms in Kuala Lumpur, Malaysia. Am J Trop Med Hyg. 2016; 94(5):1058–64.

[7] Corman VM, Muth D, Niemeyer D, Drosten C. Hosts and Sources of Endemic Human Coronaviruses. Adv Virus Res. 2018; 100:163–88.

[8] Huynh J, Li S, Yount B, Smith A, Sturges L, Olsen JC, et al. Evidence supporting a zoonotic origin of human coronavirus strain NL63. J Virol. 2012; 86(23):12816–25.

[9] Hu B, Ge X, Wang L-F, Shi Z. Bat origin of human coronaviruses. Virol J. 2015; 12:221.

[10] Abidha CA, Nyiro J, Kamau E, Abdullahi O, Nokes DJ, Agoti CN. Transmission and evolutionary dynamics of human coronavirus OC43 strains in coastal Kenya investigated by partial spike sequence analysis, 2015-16. Virus Evol. 2020; 6(1):veaa031.

[11] Morgello S. Coronaviruses and the central nervous system. J Neurovirol. 2020; 26(4):459–73.

[12] To KKW, Hung IFN, Chan JFW, Yuen K-Y. From SARS coronavirus to novel animal and human coronaviruses. J Thorac Dis. 2013; 5(Suppl 2):S103–8.

[13] Cui J, Li F, Shi Z-L. Origin and evolution of pathogenic coronaviruses. Nat Rev Microbiol. 2019; 17(3):181–92.

[14] Corman VM, Baldwin HJ, Tateno AF, Zerbinati RM, Annan A, Owusu M, et al. Evidence for an Ancestral Association of Human Coronavirus 229E with Bats. J Virol. 2015; 89(23):11858–70.

[15] Tao Y, Shi M, Chommanard C, Queen K, Zhang J, Markotter W, et al. Surveillance of Bat Coronaviruses in Kenya Identifies Relatives of Human Coronaviruses NL63 and 229E and Their Recombination History. J Virol. 2017; 91(5):e01953-16.

[16] El-Duah P, Meyer B, Sylverken A, Owusu M, Gottula LT, Yeboah R, et al. Development of a Whole-Virus ELISA for Serological Evaluation of Domestic Livestock as Possible Hosts of Human Coronavirus NL63. Viruses. 2019; 11(1):43.

[17] Rajapakse N, Dixit D. Human and novel coronavirus infections in children: a review. Pediatr Int Child Health. 2021; 41(1):36–55.

[18] Talbot PJ, Ekandé S, Cashman NR, Mounir S, Stewart JN. Neurotropism of human coronavirus 229E. Adv Exp Med Biol. 1993; 342:339–46.

[19] Ksiazek TG, Erdman D, Goldsmith CS, Zaki SR, Peret T, Emery S, et al. A novel coronavirus associated with severe acute respiratory syndrome. N Engl J Med. 2003; 348:1953–66.

[20] Breiman RF, Evans MR, Preiser W, Maguire J, Schnur A, Li A, et al. Role of China in the quest to define and control severe acute respiratory syndrome. Emerg Infect Dis. 2003; 9:1037–41.

[21] Centers for Disease Control and Prevention. Severe acute respiratory syndrome (SARS) [Internet]. Available at: https://www.cdc.gov/sars/about/fs-sars.html. Accessed 10 April 2022.

[22] Sampathkumar P, Temesgen Z, Smith TF, Thompson RL. SARS: epidemiology, clinical presentation, management, and infection control measures. Mayo Clin Proc. 2003; 78(7):882–90.

[23] WHO. Consensus document on the epidemiology of severe acute respiratory syndrome (SARS). 2003.

[24] Cyranoski D, Abbott A. Virus detectives seek source of SARS in China's wild animals. Nature. 2003; 423:467.25.

[25] Hui DS, Wong KT, Antonio GE, Lee N, Wu A, Wong V, et al. Severe acute respiratory syndrome: correlation between clinical outcome and radiologic features. Radiology. 2004; 233(2):579–85.

[26] Peiris JS, Chu CM, Cheng VC, Chan KS, Hung IF, Poon LL, et al.; HKU/UCH SARS Study Group. Clinical progression and viral load in a community outbreak of coronavirus-associated SARS pneumonia: a prospective study. Lancet [serial online]. 2003.

[27] Chen X, Chughtai AA, Dyda A, MacIntyre CR. Comparative epidemiology of Middle East respiratory syndrome coronavirus (MERS-CoV) in Saudi Arabia and South Korea. Emerg Microbes Infect. 2017; 6(6):e51.

[28] Ebrahim SH, Maher AD, Kanagasabai U, Alfaraj SH, Alzahrani NA, Alqahtani SA, Assiri AM, Memish ZA. MERS-CoV Confirmation among 6,873 suspected persons and relevant Epidemiologic and Clinical Features, Saudi Arabia - 2014 to 2019. EClinicalMedicine. 2021; 41:101191.

[29] World Health Organization. Middle East respiratory syndrome coronavirus (MERS-CoV) [Internet]. Available at: https://www.who.int/health-topics/middle-east-respiratory-syndrome-coronavirus-mers#tab=tab_1. Accessed 2 April 2022.

[30] Mobaraki K, Ahmadzadeh J. Current epidemiological status of Middle East respiratory syndrome coronavirus in the world from 1.1.2017 to 17.1.2018: a cross-sectional study. BMC Infect Dis. 2019; 19(1):351.

[31] Reusken CBEM, Haagmans BL, Müller MA, Gutierrez C, Godeke G-J, Meyer B, et al. Middle East respiratory syndrome coronavirus neutralising serum antibodies in dromedary camels: a comparative serological study. Lancet Infect Dis. 2013; 13(10):859–66.

[32] Meyer B, García-Bocanegra I, Wernery U, Wernery R, Sieberg A, Müller MA, et al. Serologic assessment of possibility for MERS-CoV infection in equids. Emerg Infect Dis. 2015; 21(1):181–82.

[33] Mohd HA, Al-Tawfiq JA, Memish ZA. Middle East Respiratory Syndrome Coronavirus (MERS-CoV) origin and animal reservoir. Virol J. 2016; 13:87.

[34] Guo G, Ye L, Pan K, Chen Y, Xing D, Yan K, et al. New Insights of Emerging SARS-CoV-2: Epidemiology, Etiology, Clinical Features, Clinical Treatment, and Prevention. Front Cell Dev Biol. 2020; 8:410.

[35] Hu B, Guo H, Zhou P, Shi Z-L. Characteristics of SARS-CoV-2 and COVID-19. Nat Rev Microbiol. 2021; 19(3):141–54.

[36] Xiao K, Zhai J, Feng Y, Zhou N, Zhang X, Zou J-J, et al. Isolation of SARS-CoV-2-related coronavirus from Malayan pangolins. Nature. 2020; 583(7815):286–89.

[37] Centers for Disease Control and Prevention. COVID-19 and Animals [Internet]. Available at: https://www.cdc.gov/coronavirus/2019-ncov/daily-life-coping/animals.html. Accessed 5 April 2022.

[38] Patterson EI, Elia G, Grassi A, Giordano A, Desario C, Medardo M, et al. Evidence of exposure to SARS-CoV-2 in cats and dogs from households in Italy. Nat Commun. 2020; 11(1):6231.

[39] WHO. Transmission of SARS-CoV-2: implications for infection prevention precautions, Available at: https://www.who.int/news-room/commentaries/detail/transmission-of-sars-cov-2-implications-for-infection-prevention-precautions. Accessed 30 March 2022.

[40] Hasan MN, Haider N, Stigler FL, Khan RA, McCoy D, Zumla A, et al. The Global Case-Fatality Rate of COVID-19 Has Been Declining Since May 2020. Am J Trop Med Hyg. 2021; 104(6): 2176–84.

[41] Coronavirus – Statistical data for Croatia and EU [Koronavirus-statistički podaci za Hrvatsku i EU]. Available at: https://www.koronavirus.hr/. Accessed 6 April 2022.

[42] Jerković I, Ljubić T, Bašić Ž, Kružić I, Kunac N, Bezić J, et al. SARS-CoV-2 Antibody Seroprevalence in Industry Workers in Split-Dalmatia and Šibenik-Knin County, Croatia. J Occup Environ Med. 2021; 63(1):32–7.

[43] Vilibic-Cavlek T, Stevanovic V, Tabain I, Betica-Radic L, Sabadi D, Peric L, et al. Severe acute respiratory syndrome coronavirus 2 seroprevalence among personnel in the healthcare facilities of Croatia, 2020. Rev Soc Bras Med Trop. 2020; 53:e20200458.

[44] Lenicek Krleza J, Zrinski Topic R, Stevanovic V, Lukic-Grlic A, Tabain I, Misak Z, et al. Seroprevalence of SARS-CoV-2 infection among children in Children's Hospital Zagreb during the initial and second wave of COVID-19 pandemic in Croatia. Biochem Med (Zagreb). 2021; 1(2):020706.

[45] Vilibic-Cavlek T, Stevanovic V, Ilic M, Barbic L, Capak K, Tabain I, et al. SARS-CoV-2 Seroprevalence and Neutralizing Antibody Response after the First and Second COVID-19 Pandemic Wave in Croatia. Pathogens. 2021; 10(6):774.

[46] Vilibić-Čavlek T, Stevanović V, Barbić Lj, Milašinčić Lj, Antolašić Lj, Hruškar Ž, et al. Temporal trends of SARS-CoV-2 seroprevalence in Croatia. In Proceedings of the Symposium with International Participation-Veterinary Days, Vodice, Croatia, 26–29 October 2021; pp. 9–16. (In Croatian)

[47] Mrzljak A, Jureković Ž, Pavičić-Šarić J, Stevanović V, Tabain I, Hruškar Ž, et al. Seroprevalence of SARS-CoV-2 in Croatian solid-organ transplant recipients. Biochem Med (Zagreb). 2021; 31(3):030901.

[48] Vilibic-Cavlek T, Stevanovic V, Brlek-Gorski D, Ferencak I, Ferenc T, Ujevic-Bosnjak M, et al. Emerging Trends in the Epidemiology of COVID-19: the Croatian 'One Health' Perspective. Viruses. 2021; 13(12):2354.

[49] Vince A, Zadro R, Sostar Z, Ljubin Sternak S, Vranes J, Skaro V, et al. SARS-CoV-2 Seroprevalence in a Cohort of Asymptomatic, RTPCR Negative Croatian First League Football Players. J Pharm Pharmacol Res. 2021; 5(4): 218-35.

[50] Rostami A, Sepidarkish M, Leeflang MMG, Riahi SM, Nourollahpour Shiadeh M, Esfandyari S, et al. SARS-CoV-2 seroprevalence worldwide: a systematic review and meta-analysis. Clin Microbiol Infect. 2021;27(3):331-40.

[51] Azami M, Moradi Y, Moradkhani A, Aghaei A. SARS-CoV-2 seroprevalence around the world: an updated systematic review and meta-analysis. Eur J Med Res. 2022;27(1):81.

[52] Vaselli NM, Hungerford D, Shenton B, Khashkhusha A, Cunliffe NA, French N. The seroprevalence of SARS-CoV-2 during the first wave in Europe 2020: A systematic review. PLoS One. 2021;16(11):e0250541.

[53] Galanis P, Vraka I, Fragkou D, Bilali A, Kaitelidou D. Seroprevalence of SARS-CoV-2 antibodies and associated factors in healthcare workers: a systematic review and meta-analysis. J Hosp Infect. 2021; 108:120-34.

[54] Bergeri I, Whelan MG, Ware H, Subissi L, Nardone A, Lewis HC, et al; Unity Studies Collaborator Group. Global SARS-CoV-2 seroprevalence from January 2020 to April 2022: A systematic review and meta-analysis of standardized population-based studies. PLoS Med. 2022; 19(11):e1004107.

[55] Stevanovic V, Vilibic-Cavlek T, Tabain I, Benvin I, Kovac S, Hruskar Z, et al. Seroprevalence of SARS-CoV-2 infection among pet animals in Croatia and potential public health impact. Transbound Emerg Dis. 2021; 68(4):1767–73.

[56] Stevanovic V, Tabain I, Vilibic-Cavlek T, Mauric Maljkovic M, Benvin I, Hruskar Z, et al. The Emergence of SARS-CoV-2 within the Dog Population in Croatia: Host Factors and Clinical Outcome. Viruses. 2021;13(8): 1430.

[57] Jemeršić L, Lojkić I, Krešić N, Keros T, Zelenika TA, Jurinović L, et al. Investigating the Presence of SARS CoV-2 in Free-Living and Captive Animals. Pathogens. 2021; 10(6):635.

[58] Ruckert A, Zinszer K, Zarowsky C, Labonté R, Carabin H. What Role for One Health in the COVID-19 Pandemic? Can J Public Health. 2020; 111:641–4.