THE NEW ARMENIAN MEDICAL JOURNAL
Vol.14 (2020), No 4, p. 37-42

GROWING TRENDS AND TRANSMISSION DYNAMICS OF NOVEL CORONAVIRUS – COVID 19

Woodman A.*[1], Al Jamea L.[2], Jebakumar A.Z.[3]

[1] Vice Deanship of Postgraduate Studies and Research, Prince Sultan Military College of Health Sciences, Dhahran, Saudi Arabia

[2] Department of Clinical Laboratory Sciences, Prince Sultan Military College of Health Sciences, Dhahran,Saudi Arabia

[3] Vice Deanship of Postgraduate Studies and Research, Prince Sultan Military College of Health Sciences, Dhahran, Saudi Arabia

Receive 22.02.2020; accepted for printing 14.07.2020

Abstract

Coronaviruses are a large family of viruses that cause disease ranging from the common cold to more severe cases such as Middle East Respiratory Syndrome and severe acute respiratory syndrome. Coronaviruses have been determined to be responsible for approximately 15% of upper respiratory tract infections in adults. Severe acute respiratory syndrome can cause severe pneumonia, with mortality approaching 10%. In 2019, novel coronavirus (COVID-19) has spread rapidly in Wuhan, Hubei Province, China. The first cases were strongly associated with the Huanan seafood market, where animals were sold for food. As of March 2020, the number of affected countries has tripled with 203,613 cases in over 114 countries and caused far higher morbidity and mortality than either Severe Acute Respiratory Syndrome or Middle East Respiratory Syndrome despite rapid identification and robust public health measures. However, genomic research has provided evidence that the virus was introduced to the market from a different, yet unknown location, although human-to-human transmission may have occurred earlier. COVID-19 caused far higher morbidity and mortality than either (severe acute respiratory syndrome) or (Middle East respiratory syndrome) despite rapid identification and robust public health measures disease severity independently predicted the composite endpoint. New therapies and clinical trials are needed for tracking the evolution of severe acute respiratory syndrome and limit the spread of the disease.

Keywords: *Coronaviruses, COVID-19, MERS-CoV, SARS-CoV, zoonotic disease*

Introduction

Diseases caused by animal coronaviruses have been discovered since the 1930's. The first human coronaviruses (HCVs) were reported in 1965, when respiratory specimens from patients with common colds that had been inoculated into organ cultures (OCs) of human fetal tracheal or nasal epithelium yielded cytopathic agents that were designed OC43 and OC38 [*Tyrrell D, Bynoe M, 1965; Bartlett J et al., 2003*]. The designation of these agents as coronaviruses was proposed in 1968 [*Almeida J et al., 1968; Bartlett J et al., 2003*].

Address for Correspondence:
Alexander Woodman, Ph.D., M.Sci., M.P.H.
Prince Sultan Military College of Health Sciences
Vice Deanship of Postgraduate Studies and Research cientific Research Unit, Al Amal Dhahran 34313, Saudi Arabia
Tel.: +1 310 498 4385
E-mail: alexwoodman.ucla@gmail.com

Coronaviruses (CoV) are a large family of viruses that cause disease ranging from the common cold to more severe cases such as Middle East Respiratory Syndrome (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS-CoV). Coronaviruses are zoonotic, meaning they are transmitted between animals and people [*Bartlett J et al., 2003; Trivedi S et al., 2019; Li G, De Clercq E, 2020*]. Detailed investigations found that SARS-CoV was transmitted from civet cats to humans and MERS-CoV from dromedary camels to humans (Fig. 1) [*Sheahan T, 2020*].

Coronavirus Family Classification

Coronaviruses are members of the subfamily *Coronavirinae* in the family *Coronaviridae*, which is divided into four genera based on their phyloge-

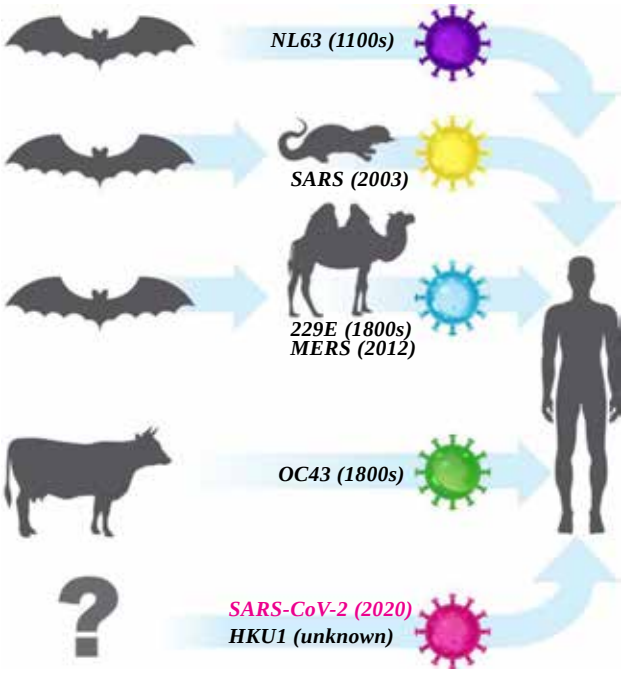

Figure 1. *Coronavirus is a zoonotic disease that can spread between animals and humans. The animal reservoir for COVID-19 is unknown*
Source: Timothy Sheahan, University of North Carolina, (Sheahan T, 2020)

netic relationships and genomic structures: *Alphacoronavirus*, *Betacoronavirus*, *Gammacoronavirus* and *Deltacoronavirus* [*Cui J et al., 2019*].

According to the literature, *Alphacoronavirus* and *Betacoronavirus* only infect mammals, while *Gammacoronavirus* and *Deltacoronavirus* infect birds, but some of them can also infect mammals [*Kirchdoerfer R et al., 2018; Cui J et al., 2019*]. Further the literature states that A*lphacoronaviruses* and *Betacoronaviruses* usually cause respiratory illness in humans and gastroenteritis in animals [*Cui J et al., 2019*]. The genus Coronavirus consists of enveloped, generally spherical virions with helical nucleocapsids, ranging from 100 to 120 *nm* in diameter. This new group of viruses was named coronavirus: corona due to its crown-like form of the surface projections [*Bartlett J et al., 2003*].

To overcome it is possible, due to the uniting the knowledge and will of all doctors in the world

However, these viruses mutate quickly and can jump from animals to humans, and from one human to another. In recent years, they have become a growing player in infectious-disease outbreaks worldwide [*Bartlett J et al., 2003; Kahn J, McIntosh K, 2005*].

Since 2003, at least five new HCVs have been identified, including SARS, which caused significant morbidity and mortality [*Kahn J, McIntosh K, 2005*]. Coronaviruses have been determined to be responsible for approximately 15% of upper respiratory tract infections in adults [*Bradburne A et al., 1967; Bartlett J et al., 2003*]. On the other hand, SARS-CoV can cause severe pneumonia, with morality approaching 10% (CDC, 2003). Coronavirus colds occur mainly in the winter and early spring. A longitudinal study in the United States indicated the large outbreaks of either 229E or OC43 infection tend to occur with a periodicity of 2-4 years [*Bartlett J et al., 2003; Kahn J, McIntosh K, 2005*].

Novel Coronavirus - SARS-CoV-2 or COVID-19

The pneumonia outbreak in Wuhan, Hubei Province, China has brought to the 2019 novel coronavirus (COVID-19). This new coronavirus, belonging to the Orthocoronavirinae subfamily is different from MERS-CoV and SARS-CoV (approximately 79% similarity) [*Dey S et al., 2020; Harapan H et al., 2020*]. Phylogenetic analysis of the SARS-CoV-2 genome shows that the virus is closely related (88%) to two SARS-like bat coronaviruses collected in 2018 in eastern China [*Dey S et al., 2020; Harapan H et al., 2020*].

Further research of genome sequences of SARS-CoV-2, RaTG13 and SARS-CoV, showed that the virus is more associated with BatCoV RaTG13. A bat coronavirus previously found in Rhinolophus affinis from Yunnan province, with 96.2% common genome sequence identity.

The study found that no evidence of recombination events from other bat-derived viruses such as BatCoV RaTG13, SARSCoV, and SARSr-CoVs was found in the SARS-CoV-2 genome. Taken together, these data suggest that bats may have been the original host of this virus. However, research is needed to find out if any intermediate hosts have contributed to the transmission of the virus to humans [*Dey S et al., 2020; Harapan H et al., 2020*].

Starting from December 2019, COVID-19 has spread rapidly in Wuhan, Hubei Province, China. As of February 7, 2020, 31,000 human infections with COVID-19 have been confirmed in China

with at least 630 reported deaths. Additional cases have been confirmed in several countries including the United States [*Carlos W et al., 2020*]. As of March 2020, the number of affected countries has tripled with more than 118,000 cases in 114 countries, and over 4,291 people have lost their lives (Fig. 2, 3) [*ECDC, 2020; Roser M et al., 2020; WHO, 2020*]. As a result of the rapid spread of the virus around the world, the World Health Organization (WHO) has described the coronavirus pandemic as the "defining global health crisis of our time" [*Roser M et al., 2020; WHO, 2020*].

As of September 7th 2020, 27.2 million COVID-19 cases have been confirmed globally, of which 18.2 million deaths, and 891,000 recovered cases. As of January 2021, 87.2 million cases have been confirmed globally, of which 48.8 million were recovered, and 1.88 million died (Fig. 4, 5) [Roser M et al., 2020; WHO, 2020].

Transmission and Clinical Findings

The incidence of COVID-19 is most commonly seen in adult male patients, with an average age of 34 to 59 years. COVID-19 is also more likely to infect people with chronic comorbidities such as cardiovascular, cerebrovascular disease, and diabetes. The largest proportion of severe cases occurs in adults over 60 years of age. Severe cases

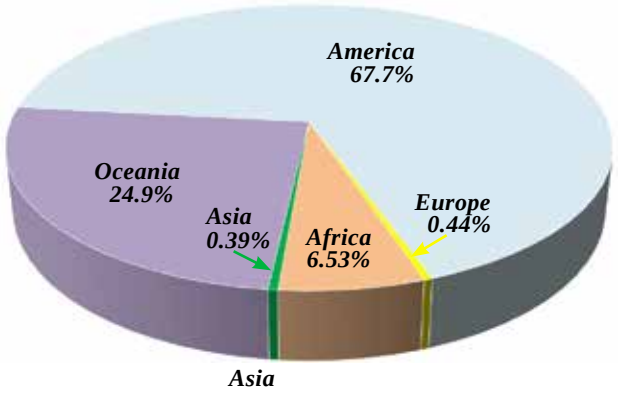

Figure 3. *Overall percentage of regionally confirmed cases as of 17 March 2020 [ECDC, 2020; Roser M et al., 2020; WHO, 2020]*

can also be associated with coinfections of bacteria and fungi [*Dey S et al., 2020; Guan W, 2020; Harapan H et al., 2020*].

Although, the pathogenesis of COVID-19 is still not widely known, in humans, COVID-19 mainly affects the cells in the airways lining the alveoli, binding to receptors and enters the cell [*Bastola A et al., 2020; Li Q et al., 2020*]. According to case studies, the virus infects the lower respiratory tract. Patients initially develop a fever, cough and aches, and can progress to shortness of breath and complications from pneumonia [*Huang C et al., 2020*].

Further symptoms are fatigue, sore throat, head-

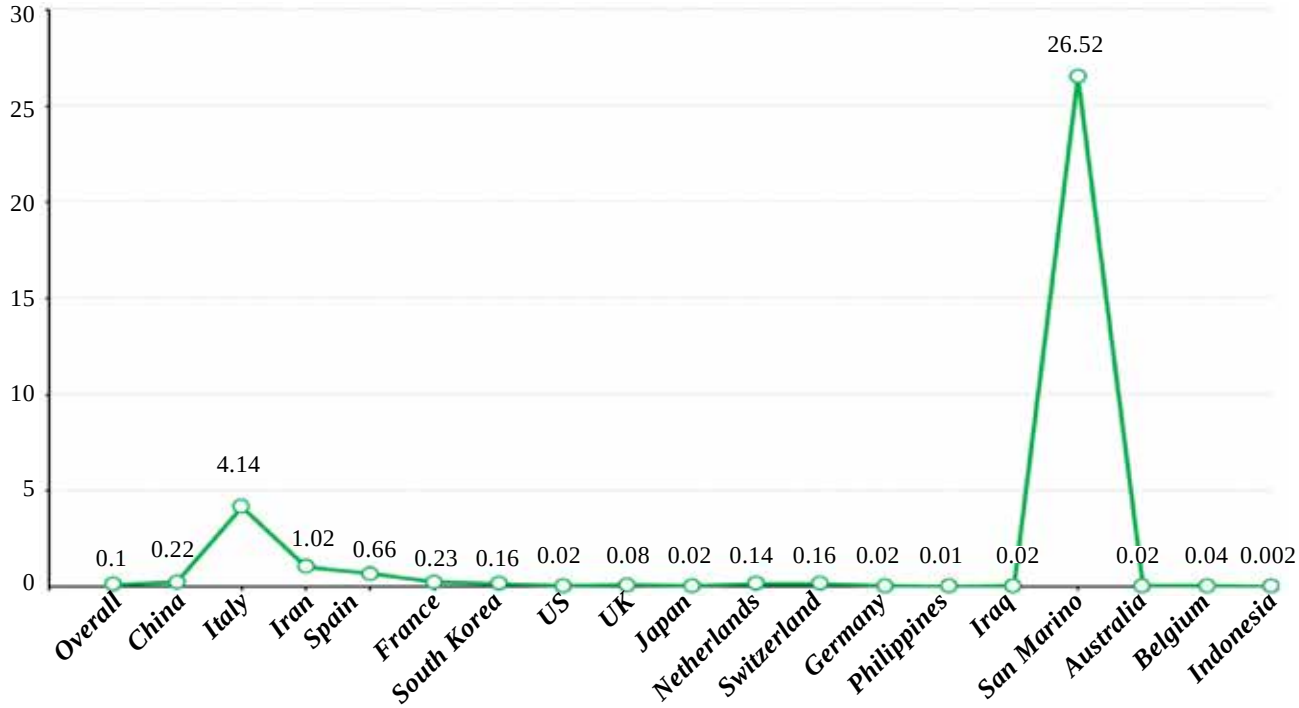

Figure 2. *COVID-19 Death rate per 100,000, March 2020 [Roser M et al., 2020; WHO, 2020]*

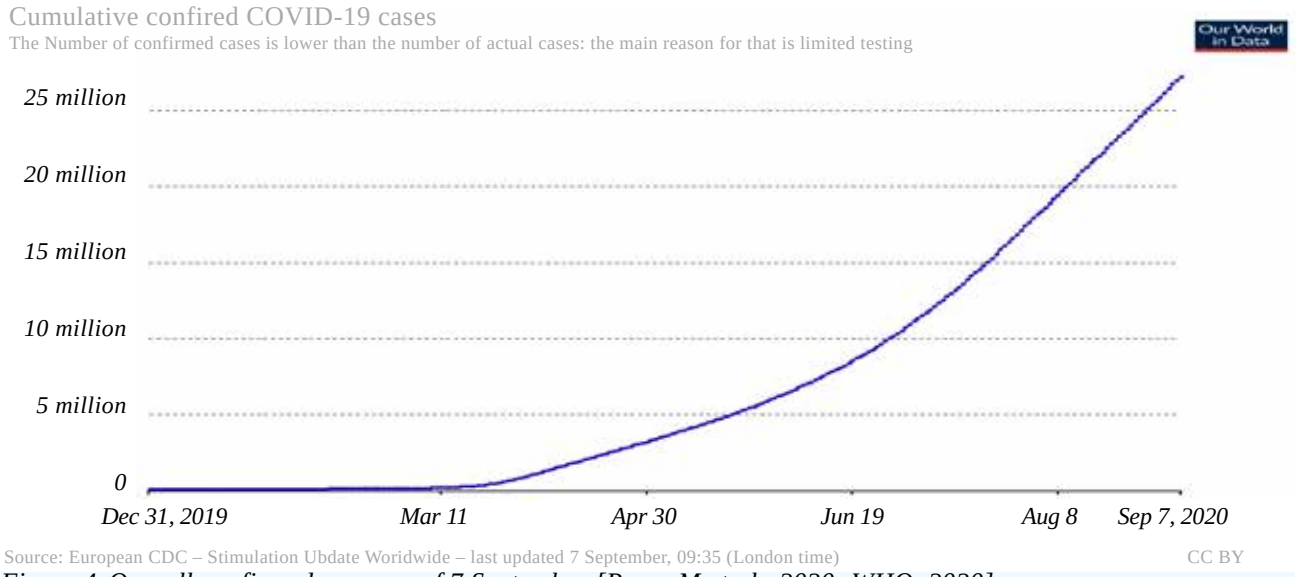

Figure 4. Overall confirmed cases as of 7 September [Roser M et al., 2020; WHO, 2020]

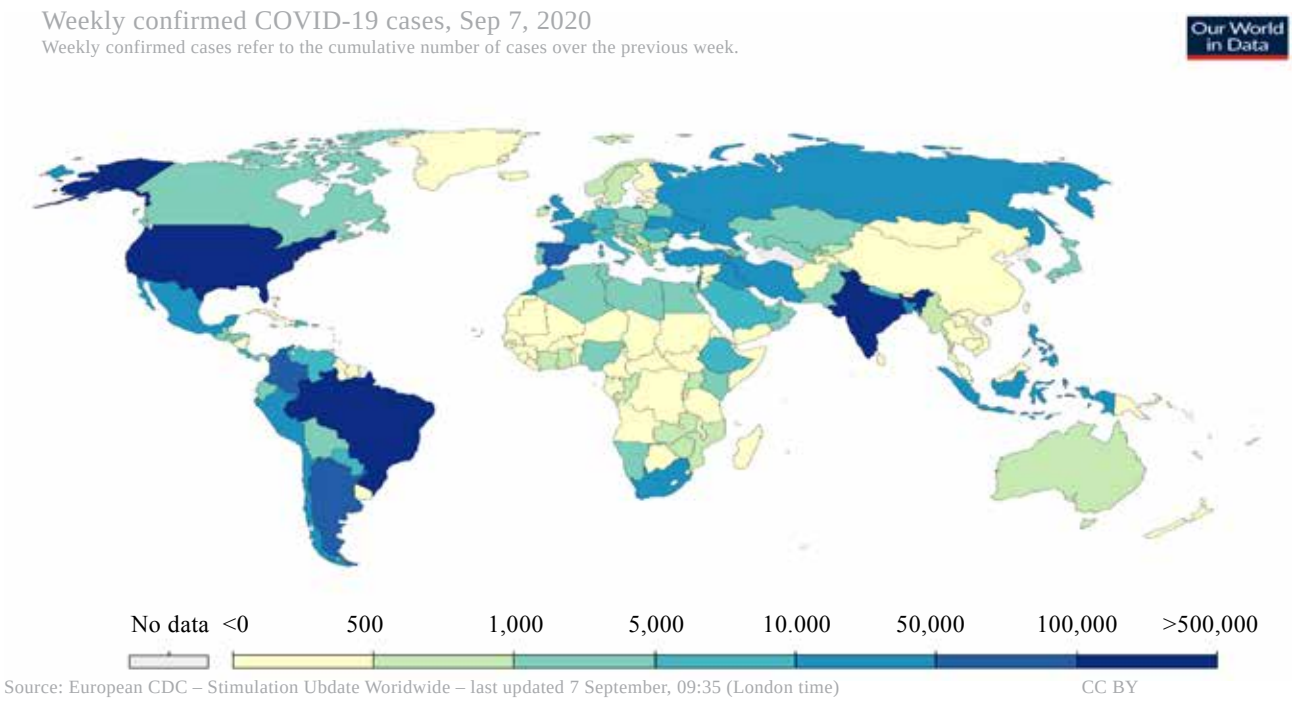

Figure 5. Weekly confirmed cases as of 7 September [Roser M et al., 2020; WHO, 2020]

ache, and nausea, with vomiting and diarrhea. Huang et al. (2020) found that 98% of the patients in their study had fevers, of which 78% had a temperature higher than 38°C. They reported that 76% of the patients had coughs, 44% of patients experienced fatigue and muscle pain, and 55% of patients had dyspnea [*Huang C et al., 2020*].

Studies have shown that fever occurred in only 43.8% of patients with COVID-19, during initial stage but developed in 87.9% following hospitalization [*Guan W, 2020*]. Severe pneumonia occurred in 15.7% of cases. No radiologic abnormality was noted on initial stage in 23.9% and 5.2% of severe and non-severe cases respectively, while diarrhea was uncommon [*Guan W, 2020*]. Around only 1% of patients had a direct contact with wildlife, while more than three quarters were local residents of Wuhan, or had contacted with people from Wuhan. These findings echoed the latest reports, including the outbreak of a family cluster, transmission from an asymptomatic individual, and the three-phase outbreak patterns [*Bastola A et al., 2020; Guan W, 2020*].

At the same time, a study of nine pregnant women

who developed COVID-19 in late pregnancy found that COVID-19 does not cause significantly worse symptoms than non-pregnant women, and there is no evidence of intrauterine infection caused by vertical transmission [*Chen H et al., 2020*].

A multidisciplinary team of pulmonologists and radiologists from 10 countries has developed guidelines for the use of chest X-ray (CXR) and computed tomography (CT) in patients with COVID-19. The team recommended that chest imaging be indicated in patients with poor or impaired respiratory function, or if identified as risk groups for disease progression [*Gallo Marine M et al., 2020*].

Thus, the most common CT findings are ground glass opacities or bilateral compaction in the lower peripheral lung fields. However, in the early stages of the disease or with mild symptoms, chest imaging may be normal. Specific CT findings such as traction bronchiectasis (a subtype of bronchiectasis with bronchial dilatation in abnormal lung parenchyma), extensive distribution of abnormalities, and lymph node involvement have also been reported in critically ill patients. In addition, an architectural distortion has been described, which refers to a violation of normal architecture as defined by the American College of Radiology [*American College of Radiology, 2003*; *Gallo Marine M et al., 2020*].

X-ray studies in children were described in a retrospective study of 20 hospitalized children with coronavirus in China, where CT often showed consolidation with the surrounding halo mark, as well as opacities of ground glass. Although these signs are not pathognomonic for COVID-19, they can confirm this diagnosis [*Gallo Marine M et al., 2020*].

The incubation period of HCV infection ranges from 2 to 7 days, and the usual illness lasts from 3 to 18 days (means 7 days) [*Bartlett J et al., 2003; Rota P et al., 2003; Trivedi S et al., 2019*; *Li G, De Clercq E, 2020*]. The median incubation period of COVID-19 is 6 days, with a range of up to 14 days [*Bartlett J et al., 2003; Trivedi S et al., 2019; Li G, De Clercq E, 2020*].

COVID-19 caused far higher morbidity and mortality than either (SARS-CoV) or (MERS-CoV) despite rapid identification and robust public health measures disease severity independently predicted the composite endpoint. Many factors can contribute to the severity of lower respiratory tract infections. The sequence of the viral genome and the degree of viral replication (viral load) can influence severity and initiate an inflammatory response that can cause immunopathology. The airway microbiome and bacterial co-infections can similarly increase severity. Some hosts are more susceptible to severe disease based on genetic and environmental factors [*Shang W et al., 2020; Cheng A, Williamson D, 2020*]. Unfortunately, no drug or vaccine has yet been approved to treat HCVs. Several vaccine options have been developed, approved by national regulatory authorities, and disseminated among general public. However, the effects of the proposed vaccines are still being [*CDC, 2020; WHO, 2020*]. New interventions are likely to require months to years to develop and implement the vaccine [*CDC, 2020; WHO, 2020*].

Conclusion

The current COVID-19 pandemic is an international health crisis causing millions of deaths and increasing the economic burden worldwide. As such, identifying and testing the factors predicting COVID-19 disease progression is vital to improving health outcomes. Factors including age, comorbidities, immune response, chest radiographs, laboratory markers, and organ dysfunction indicators may individually or collectively predict worse outcomes. Nevertheless, new therapies and clinical trials are needed for tracking the evolution of SARS-CoV-2 and limit the spread of the disease.

Limitations

The data consolidated in this literature review must be considered along with some limitations. The data comes primarily from studies and reports published during the pandemic. Thus, these data cannot be considered definitive and is recommended to be revised and reviewed by other researchers. It is vital to continue research in this new area and identify factors that can potentially predict complications of COVID-19.

REFERENCES

1. *Almeida JD, Berry DM, Cunningham CH, Hamre D, Hofstad MS., et al.* Coronaviruses. Nature, 1968; 220(650): 2
2. *American College of Radiology*. Illustrated breast imaging reporting and data system (BI-RADS). American College of Radiology. 2003. Retrieved from: https://ci.nii.ac.jp/naid/10014560841/
3. *Bartlett JG, Blacklow NR, Gorbach SL.* Textbook of nfectious diseases. 2003; 2115
4. *Bastola A, Sah R, Rodriguez-Morales AJ, Lal BK, Jha R., et al.* The first 2019 novel coronavirus case in Nepal. The Lancet Infectious Diseases. 2020; 20(3): 279-280
5. *Bradburne AF, Bynoe ML, Tyrrell DA.* Effects of a "new" human respiratory virus in volunteers. British Medical Journal. 1967; 3(5568): 767
6. *Carlos WG, Dela Cruz CS, Cao B, Pasnick S, Jamil S.* Novel Wuhan (2019-nCoV) coronavirus. American journal of respiratory and critical care medicine. 2020; 201(4): P7-P8
7. *Centers for Disease Control and Prevention (CDC).* Coronavirus Disease 2019 (COVID-19). 2020. Retrieved from: https://www.cdc.gov/coronavirus/2019-ncov/index.html
8. *Chen H, Guo J, Wang C, Luo F, Yu X., et al.* Clinical characteristics and intrauterine vertical transmission potential of COVID-19 infection in nine pregnant women: a retrospective review of medical records. Lancet. 2020; 395(10226): 809-815
9. *Cheng AC, Williamson DA.* An outbreak of COVID-19 caused by a new coronavirus: what we know so far. Medical Journal of Australia. 2020; 212(9): 393-394
10. *Cui J, Li F, Shi Z.* Origin and evolution of pathogenic coronaviruses. Nat Rev Microbiol. 2019; 17: 181-192
11. *Dey SK, Rahman MM, Siddiqi UR, Howlader A.* Analyzing the epidemiological outbreak of COVID-19: A visual exploratory data analysis approach. Journal of Medical Virology. 2020; 92(6): 632-638
12. *European Centre for Disease Prevention and Control (ECDC).* COVID-19 situation update worldwide, as of 17 March 2020. Retrieved from: https://www.ecdc.europa.eu
13. *Gallo Marine B, Aghagoli G, Lavine K, Yang L, Siff EJ., et al.* Predictors of COVID□19 severity: A literature review. Reviews in medical virology. 2020; e2146
14. *Guan WJ, Ni ZY, Hu Y, Liang WH, Ou CQ., et al.* Clinical characteristics of 2019 novel coronavirus infection in China. N Engl J Med 2020; 382:1708-1720
15. *Harapan H, Itoh N, Yufika A, Winardi W, Keam S., et al.* Coronavirus disease 2019 (COVID-19): A literature review. J Infect Public Health. 2020; 13(5): 667-673
16. *Huang C, Wang Y, Li X, Ren L, Zhao J., et al.* Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. The Lancet. 2020; 395(10223): 497-506
17. *Kahn JS, McIntosh K.* History and recent advances in coronavirus discovery. The Pediatric infectious disease journal. 2005; 24(11): S223-S227
18. *Kirchdoerfer RN, Wang N, Pallesen J, Wrapp D, Turner HL., et al.* Stabilized coronavirus spikes are resistant to conformational changes induced by receptor recognition or proteolysis. Scientific reports. 2018; 8(1): 1-11
19. *Li G, De Clercq E.* Therapeutic options for the 2019 novel coronavirus (2019-nCoV). Nature Reviews Drug Discovery. 2020; 19: 149-150
20. *Li Q, Guan X, Wu P., et al.* Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia. N Engl J Med. 2020; 382:1199-1207
21. *Roser M, Ritchie H, Ortiz-Ospina E.* Coronavirus Disease (COVID-19) – Statistics and Research. Our World in Data. 2020
22. *Rota PA, Oberste MS, Monroe SS, Nix WA, Campagnoli R., et al.* Characterization of a novel coronavirus associated with severe acute respiratory syndrome. Science. 2003; 300(5624): 1394-1399
23. *Shang W, Yang Y, Rao Y, Rao, X.* The outbreak of SARS-CoV-2 pneumonia calls for viral vaccines. NPJ Vaccines. 2020; 5(1): 1-3
24. *Sheahan T.* COVID-19, University of North Carolina. 2020. Retrieved from: https://www.wsj.com/articles/what-we-know-about-the-coronavirus-11579716128?tesla=y
25. *Trivedi SU, Miao C, Sanchez JE, Caidi H, Tamin A., et al.* Development and evaluation of a Multiplexed Immunoassay for simultaneous Detection of serum IgG Antibodies to six Human Coronaviruses. Scientific reports. 2019; 9(1): 1-8
26. *Tyrrell DAJ, Bynoe ML.* Cultivation of a novel type of common-cold virus in organ cultures. British Medical Journal. 1965; 1(5448): 1467
27. *World Health Organization.* Coronavirus disease (COVID-19) outbreak. 2020. Retrieved from: https://www.who.int/emergencies/diseases/novel-coronavirus-2019