



A review of comparison study between Corona Viruses (SARS-CoV, MERS-CoV) and Novel Corona Virus (Covid-19)

Una revisión del estudio comparativo entre los virus Corona (SARS-CoV, MERS-CoV) y el nuevo Corona virus (Covid-19)

W.S. Al-Qahtani¹, L.M. Alneghery², A.Q.S. Alqahtani³, M.D. ALKahtani⁴, S. Alkahtani^{5*},

¹*Department of Forensic Sciences, College of Criminal Justice, Naif Arab University of Security Sciences, Riyadh, Saudi Arabia.*

²*Department of Biology, College of Science, Al-Imam Mohammad Ibn Saud Islamic University, Riyadh, Saudi Arabia.*

³*Royal Commission Hospital, Pharmacy Department, Saudi Arabia.*

⁴*Department of Biology, College of Science, Princess Nourah Bint Abdulrahman University, Riyadh, Saudi Arabia*

⁵*Department of Zoology, College of Science, King Saud University, Riyadh, Saudi Arabia.*

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Abstract

Currently (March 2020) COVID-19 disease has recorded the most significant number of deaths and cases as compared to coronaviruses' types. Initially, the virus was referred to as 2019-nCoV. Subsequently, the International Committee on Taxonomy of Viruses (ICTV) named it the SARS-CoV-2 virus because it is significantly similar to the causative agent of (SARS-CoVs). All Nidovirales' viruses are positive-sense non-segmented and enveloped viruses. They have big genomes for the RNA viruses. Coronavirinae has the most significant documented RNA genomes, having around 30 kilobases (kb) of genomes. The critical differences in the families of Nidovirus are noted in the type, sizes, and the number of structural proteins. The variances cause substantial alterations in the morphology and structure of the viruses and nucleocapsids. Currently, the COVID-19 diseases have recorded the most significant number of deaths and cases as compared to other kinds of coronaviruses. In conclusion, since the outbreak of (COVID-19) disease in China, the illness is spreading very quickly across the globe. There was no evidence showing that the viruses were manufactured in laboratories or engineered till now. Extensive lab work on the mechanisms of infection and genetic factors such as polymorphism that may play an essential role in disease is needed urgently.

Keywords: SARS-CoV, SARS-CoV2 (COVID-19), Nidovirales, Pandemic.

Resumen

Actualmente (Marzo de 2020) la enfermedad COVID-19 ha registrado el mayor número de muertes y casos comparado a otros tipos de corona virus. Inicialmente al virus se le refería como 2019-nCoV. Luego, el Comité Internacional sobre Taxonomía de Virus (ICTV, por sus siglas en inglés) lo nombró el virus SARS-CoV-2 debido a su similitud significativa con el agente causante del (SARS-CoVs). Todos los virus Nidovirales son virus con polaridad positiva no-segmentados y con cubierta. Tienen genomas grandes para virus ARN. Coronaviridae tienen documentados los más significativos genomas ARN, teniendo alrededor de 30 kilobases(kb) de genomas. Las diferencias críticas en las familias de Nidovirus se notan en el tipo, tamaños, y número de proteínas estructurales. Las variaciones causan alteraciones substanciales en la morfología y estructura de los viriones y nucleocápsidos. En conclusión, desde el brote de la enfermedad en China, la enfermedad se ha esparcido muy rápidamente por el mundo. No hay evidencia hasta el momento de que los virus hayan sido fabricados o diseñados en el laboratorio. Intenso trabajo de laboratorio acerca de los mecanismos de acción y factores genéticos tales como el poliformismo que pueden jugar un rol esencial en la enfermedad son requeridos urgentemente.

Palabras clave: SARS-CoV, SARS-CoV2 (COVID-19), Nidovirales, Pandemia, Organización Mundial de la Salud (OMS).

* Corresponding author. E-mail: salkahtani@ksu.edu.sa

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1 Introduction

World Health Organization (WHO) indicated that viral diseases have continued to emerge, representing a serious public health issue. In the past twenty years, several viral endemics such as H1N1 influenza (2009) and the severe acute respiratory syndrome coronavirus (SARS-CoV) (2012-2013) have been documented. In most recent times, Saudi Arabia first recorded the Middle East respiratory syndrome coronavirus (MERS-CoV) in 2012 (Cascella *et al.*, 2020). Coronaviruses (CoVs) play a significant role in causing illness in animals and humans. Many human coronaviruses typically lead to relatively less severe respiratory illnesses. Nonetheless, two zoonosis coronaviruses, MERS-CoV and SARS-CoV, can lead to severe disease as well as death (Raj *et al.*, 2013; European Centre for Disease Prevention and Control, 2020).

Cases of unexplained respiratory infections have been documented in Wuhan, China. Wuhan, the biggest metropolitan region in Hubei Province, reported the first case to China's WHO Office on December 31, 2019. The available literature links the first symptomatic people to early December 2019. The first cases were initially categorized as pneumonia with an unknown etiology as it was difficult to single out the causal agent. The local Center for Disease Control (CDC) and the Chinese Center for Disease Control and Prevention formed an intensive investigation program for the outbreak. The illness' causative agent is now linked to the novel virus that is associated with the family of coronavirus (CoV), COVID-19 (Cascella *et al.*, 2020). On February 11, 2020, Dr. Tedros Adhanom Ghebreyesus, the WHO's Director-General, reported that the new CoV caused COVID-19 disease, an acronym for "coronavirus disease - 2019". In the past twenty years, two coronavirus epidemics have recorded. The SARS-CoV first presented a great pandemic in China, leading to approximately 800 deaths and 8000 cases. Besides, the MERS-CoV started in Saudi Arabia leading to 800 deaths and 2,500 cases and still leads to sporadic cases (KHN Morning Briefing, 2020). The new virus has spread globally because of its aggressively contagious nature. On January 30, 2020, as per the 2005 International Health Regulations, the pandemic was declared as a Public Health Emergency of International Concern (PHEIC) by WHO as it was encountered in 18 states with four states recording

transmission among humans.

Additionally, on February 26, 2020, the first case of COVID-19 (not imported), was reported in America (The World Health Organization, 2020). At the initial stages, the virus was referred to as 2019-nCoV. Subsequently, the International Committee on Taxonomy of Viruses (ICTV) named it as the SARS-CoV-2 virus because it is substantially similar to the causative agent of (SARS-CoVs) (Cascella *et al.*, 2020). In the middle of this crisis, the researchers have used the "Statpearls" plan for the reason that it stands as a unique tool that can allow making real-time updates in the PubMed circles. The objective, thus, is to gather scientific evidence and information and to offer a picture of this area, which will be updated continuously (Cascella *et al.*, 2020).

2 Classification

Being the most prominent viruses' group and classified in Nidovirales order, coronaviruses (CoVs) include Roniviridae, Arteriviridae, and Coronaviridae families. Coronavirinae makes up one of the subfamilies classified in the family of Coronaviridae, the other one being Torovirinae. Coronavirinae is divided further into four classes; the alpha, beta, delta, and gamma coronaviruses. Initially, the viruses were classified into the categories based on serology although they are now classified according to phylogenetic clustering (David *et al.*, 1996). All Nidovirales' viruses are positive-sense non-segmented and enveloped viruses. They have big genomes for the RNA viruses. Corona viruses has the most significant documented RNA genomes, having around 30 kilobases (kb) of genomes. Other characteristics in the order of Nidovirales include i) highly conserved organization of genomes, with a big replicase gene leading to accessory and structural genes; ii) expression of most nonstructural genes through ribosomal frame shifting; iii) several unusual or unique enzymatic tasks encoded in the big replicase-transcriptase polyprotein, and iv) downstream genes expression by the manufacture of 3' encapsulated sub-genomes mRNAs. The name of Nidovirales' order is borrowed from these encapsulated 3' mRNAs because Nido is 'encapsulate' in Latin. The critical differences in the families of Nidovirus are noted in the type, sizes, and the number of structural proteins. The variances cause substantial alterations in the morphology and structure of the virions and nucleocapsids (Fehr and

Perlman, 2015).

3 Genetic Materials (RNA Genome)

Coronaviruses have a positive-sense RNA genome of ~30 kb and non-segmented as shown in (Figure 1). These genomes contain a 5' cap structural make with a 3' poly tail that allows it to behave as an mRNA necessitating replicase polyproteins' translation. The encoding of nonstructural proteins (Nsps) by replicase gene takes two-thirds of the genome, approximately 20 kb, compared to the accessory and structural proteins that make up about 10 kb of the viral genome. Besides, the genome's 5' end has an untranslated region (UTR) containing multiple stem structures of loop needed for RNA transcription and replication as well as leader sequence (Scripps Research Institute, 2020). Besides, at the start of every accessory or structural gene are sequences of transcriptional regulatory (TRSs) that are needed for expressing every gene.

Furthermore, the 3'UTR has RNA structures needed for replication as well as the manufacture of the viral RNA. Classification of the coronaviruses genomes are 5'-leader-UTR- replicase-S, (Envelope)-M, (Spike)-E, (Membrane)-N, and (Nucleocapsid)-3'UTRpoly tail having accessory genes interspersing in the structure of genes at the 3' genome's end (Figure 1). Accessory proteins may be exclusively unimportant for replication within tissue culture. Nevertheless, some have shown to bear essential functions in viral pathogenesis (Scripps Research Institute, 2020). Analysis of data of public genomes' sequence from SARS-CoV-2 as well as related viruses concluded that there was no evidence showing that the viruses were manufactured in laboratories or engineered. "Through comparing available genomes' sequence information for known coronaviruses strains, it can be concluded that SARS-CoV-2 came as a result of natural processes," (Figure 1) (Scripps Research Institute, 2020). The scientists studied the genetic templates of spike proteins, outside virus armatures that it utilizes to penetrate and grab outer walls of animal and human cells. More particularly, they looked at two important spike protein's characteristics: receptor-binding domains (RBD), a type of a hook that holds host cells, the cleavage sites, and a molecular opener which allows the viruses to crack and enter the host cells (Table 1) (Schultze and Herrler, 1992;

Table 1. Receptors of Coronaviruses.

Virus	Receptor	References
Alpha coronaviruses		
HCoV-229E	APN	(Yeager \it et al., 1992)
HCoV-NL63	ACE2	(Hofmann it et al., 2005)
TGEV	APN	(Delmas it et al., 1992)
PEDV	APN	(Li it et al., 2007)
FIPV	APN	(Tresnan it et al., 1996)
CCoV	APN	(Benbacer it et al., 1997)
Beta coronaviruses		
MHV	mCEACAM	(Nedellec it et al., 1994)
BCoV	N-acetyl-9-O-acetylneuraminic acid	(Schultze it et al., 1992)
SARS-CoV	ACE2	(Li it et al., 2003)
MERS-CoV	DPP4	(Raj it et al., 2013)

Hofmann *et al.*, 2005; Li *et al.*, 2003; Li *et al.*, 2007; Fehr and Perlman, 2015).

4 Multiplication

The human Coronaviruses access cells, mostly, by particular receptors. Sialic acid-containing and Aminopeptidase-N receptors have been documented to act as OC43 and 229E, respectively (Benbacer *et al.*, 1997). After viruses enter the host cells and uncoated, the genomes are transcribed and translated. A distinctive characteristic of its replication is that the mRNAs createan "encapsulated set" having 3' ends (common); only the distinctive parts 5' ends becomes translated. Besides, 7 mRNAs are produced. The shortest codes of mRNA the nucleoproteins, and others direct the manufacture of more genome's segment. These proteins assemble at the cells' membrane, while genomes' RNA becomes incorporated as the mature particle is formed through

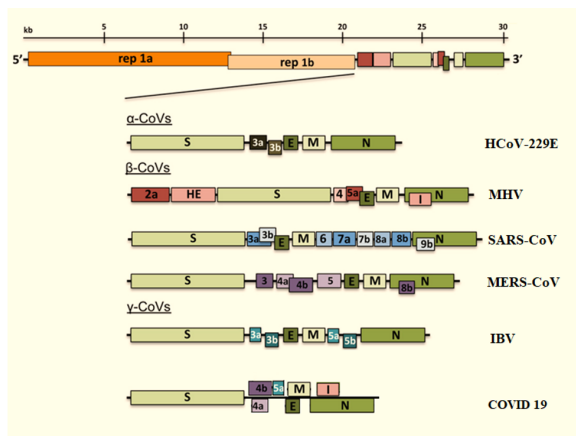


Figure 1: Genomic Representative' Orientation α , β , COVID 19, and γ CoVs. A representation with depiction of MHV genome on the top with expanded areas below showing the accessory and structural proteins in the MHV, MERS-CoV, and SARS-CoV 3' regions. Genome's size and separate genes are conducted through approximating by use of the legend appearing at the diagram's top although not represented to scale. human coronavirus 229E, HCoV-229E, MHV, SARS-CoV, mouse hepatitis virus, severe acute respiratory syndrome coronavirus, Middle East respiratory syndrome coronavirus, MERS-CoV, IBV, COVID 19, infectious bronchitis virus, and SARS-CoV2 virus.

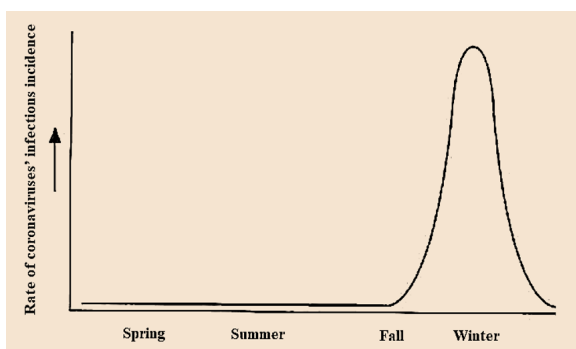


Figure 2. Coronaviruses' infections seasonal incidence.

budding from the layers of internal cells (Yeager *et al.*, 1992; Delmas *et al.*, 1992; Tyrrell and Myint, 1996;).

5 Pathogenesis

Researches in human volunteers and organ cultures indicate that coronaviruses are highly fastidious and

develop in differentiated epithelial cells (respiratory) only. Infected cells turn vacuolated, indicate damaged cilia as well as form syncytia. Cells' damage triggers the creation of inflammatory mediators that maximize nasal secretions and lead to swelling and local inflammation. The responses consequently stimulate sneezing, cause airways' obstruction, and raise mucosa's temperature (Miura and Holmes, 2009; Dominguez *et al.*, 2013).

6 Etiology

CoVs can be termed as RNA viruses (positive-stranded) that are crown-like in appearance when viewed on an electrons' microscope (corona is Latin for crown) because of the presence of glycoproteins (spike-like) in the envelope. Orthocoronavirinae subfamily of the (order Nidovirales) Coronaviridae family groups into 4 CoVs genera: Alphacoronavirus (alphaCoV), Deltacoronavirus (deltaCoV), Gammacoronavirus (gammaCoV), and Betacoronavirus (betaCoV). In addition, the genus of betaCoV divides into 5 lineages or sub-genera (Ashour, 2020). The genomic grouping has indicated that possibly rodents and bats are the gene's sources for betaCoVs and alphaCoVs. On the other hand, avian species represent the gamma CoVs and deltaCoVs gene sources (Ashour, 2020). Infections' waves pass through populations in the winter period and lead typically too small outbreaks for schools, families etc (Figure 2). Immunity never persists, and the subjects can be re-infected, at times in a year. This pattern, therefore, varies with that of the rhinovirus infections that are high during the spring and fall and usually elicits lasting immunity. About 20% of colds are as a result of coronaviruses (Hossam *et al.*, 2020; European Centre for Disease Prevention and Control, 2020). The coronavirus transmission rate has not been examined in detail. Coronavirus is typically transmitted through inhaling contaminated droplets, although it can also be spread through hands to the eyes or nasal mucosa. Members of the big viruses' family can lead to respiratory, enteric, neurological, and hepatic diseases in various animal species that include camels, cattle, bats, and cats. To the present day, seven human CoVs (HCoVs) - able to infect human beings - have been documented. Some HCoVs were recorded in the mid-1960s, whereas others were detected during the new millennium (Giuseppina *et al.*, 2013; Peng, *et al.*, 2020; Singhal,

2020).

7 Epidemiology (Pandemic) mortality and morbidity

On December 31, 2019, the Chinese government notified the World Health Organization (WHO) of an outbreak of the novel strains of coronavirus leading to severe illness that was later named SARS-CoV-2. By February 20, 2020, approximately 167,500 cases of COVID-19 have been recorded; but most mild cases have probably gone undiagnosed. Deaths from the virus have totaled to over 6,600 individuals (Wu X *et al.*, 2020). After the endemic started, scientists from China sequenced the genomes of SARS-CoV-2, making the information available to investigators globally. The resulting genomes' sequence information has indicated that the Chinese government quickly detected the endemic and that COVID-19 cases have increased due to human-human transmission after the single introduction inhuman beings (Dongchi *et al.*, 2020). Andersen and colleagues at other institutions of research utilized this sequencing information to examine the evolution and origins of SARS-CoV-2 through assessing the several tell-tale characteristics of this virus. In this part, we performed statistical comparisons for HCoV-229E, SARS-CoV, COVID 19, MERS-CoV, MHV, and morbidity and mortality based on deaths and cases recorded by the World Health Organization (WHO). Currently (March 2020) COVID-19 disease has registered the most significant number of deaths and cases as compared to other coronaviruses' types (Table 2) (Tesini, 2020).

Table 2. The degree of corona viruses' deaths and cases (statistics).

Virus	Global Cases	Global Deaths
SARS-CoV2	271364	11252
MERS-CoV	2500	850
SARS-CoV	> 8000	774

8 Possible origins of the virus

Based on genomes sequence analysis, Anderson together with his collaborators found out that the highly likely origins of SARS-CoV-2 follow one of two probable scenarios. In one of the situations, the virus developed to its pathogenic state by natural selection in non-human hosts and jumped to human beings. In the same way, previous coronavirus epidemics have emerged, where human beings have contracted the viruses after exposure to camels (MERS) and civets (SARS). The researchers indicated bats as highly likely reservoirs for SARS-CoV-2 because they are similar to bats' coronavirus. There have been no identified cases of bats-humans transmission (Yan *et al.*, 2019).

Nonetheless, research suggests that the intermediate host likely involved humans and bats. In this case, both of the unique characteristics of SARS-CoV-2's spike proteins - the RBD portion which binds on cells as well as the cleavage site which opens the viruses up - could have developed to their state before entering human beings. In this scenario, the existing epidemic could have emerged quickly as soon as human beings were infected because the virus could have already developed the characteristics that make it pathogenic and capable of spreading between individuals. In the other scenario, non-pathogenic versions of the viruses jumped from animal hosts into human beings and then developed to their pathogenic state in humans. For example, some coronaviruses from pangolins, armadillo-like mammals located in Africa and Asia, have RBD structures similar to those of SARS-CoV-2. Coronaviruses from pangolins could probably have been passed to humans, directly or through intermediary hosts such as ferrets or civets. The other distinctive spike protein SARS-CoV-2 characteristics, the cleavage sites, could have developed in human hosts, possibly through limited unidentified circulation in humans before the start of the endemic. The researchers concluded that SARS-CoV-2 cleavage sites appear similar to cleavage sites with strains of bird's flu which have been indicated to transmit with ease between individuals. SARS-CoV-2 would have developed like virulent cleavage sites in the human cells and quickly started the endemic, as coronaviruses could probably have become more capable of spreading among people (Fang *et al.*, 2020).

9 The potential factors are helping to spread the COVID-19 virus quickly

The COVID-19 is related to other coronaviruses but is highly transmittable and causing severe disease. It is capable of indirect transmission to humans because it can remain on environmental surfaces and instruments that can become a new infection source when coming into contact with the human (Al-Qahtani, 2020; Cai *et al.*, 2020; Peng *et al.*, 2020).

Human coronaviruses cause neck, throat, and lung infections. They are most commonly spread through an infected person by:

- Respiratory droplets produced while cough or sneeze closely
- Sustained direct interaction, like touching or shaking hands
- Handling anything with the virus on it, then exposing to the mouth, nose or eyes before washing hands
- Existing evidence indicates that person-to-person transmission is effective when there is direct contact.

10 Possible risk factors

On the basis of published data from the World Health Organization (WHO) as well as a recent study (Wu C *et al.*, 2019; The World Health Organization, 2020), new Coronaviruses can cause death easily, and some of the risk factors include smoking, being elderly, age of patients (it is also probably being a male could increase risk) as well as having other diseases, for example, greatly increases the risk of death from COVID-19 disease. Researchers concluded that 399 patients having at least one more disease (including diabetes, cardiovascular diseases, chronic obstructive pulmonary disease, hepatitis B, cancer, and chronic kidney diseases) had 79% higher chances of needing a respirator or intensive care or both or even death (Begley, 2020).

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people is considered high given the growing number of cases.

COVID-19 poses a significant threat to health, and the situation is changing every day. The danger may vary within and within communities; however, the risk to Canadians is considered high given the growing number of cases. It doesn't mean the disease can get to all Canadians. It means that our health-care system already has a considerable effect. If we don't flatten the disease curve now, the rise in COVID-19 cases may affect the services available to people in health care. For such conditions like cruise ships populated areas (including public transport and malls) crowds (religious as well as cultural situations, movie theaters, sports venues, festivals and symposiums), the risk for COVID-19 may be increased.

Risk factors for COVID-19 seem to include; frequent travel or residence in a region with widespread COVID-19 population spread as determined by CDC or WHO and Frequent contact (within 6 feet or 2 meters) with anyone who has COVID-19 and who might be coughed or sneezed by an infected individual.

11 Coronavirus and COVID-19: Who bears a higher risk?

Some people have a high chance of developing a severe infection if they develop COVID-19, the disease due to the new coronavirus, particularly those over the age of 85 and patients with chronic illness, lung disease or diabetes.

12 The Elderly and the COVID-19

- Elderly people are more prone to have long-term health concerns that may place them at risk.
- Everyone's immune systems appear to weaken with the time of life, which makes it harder for elderly people to fight viruses
- With time, lung tissue becomes less elastic, rendering respiratory disorders like COVID-19 a significant concern for elderly people.
- The inflammatory response might be more severe in older people, causing damage to the organs.

13 COVID-19 and cardiac disease

Though, COVID-19 often influences the airways and lungs, all such organs work with the heart to pass oxygen into the tissues of the body. The heart has to work harder when the lungs are overburdened due to illness, which produces obstacles for people who live with heart disease.

The American Heart Association states that COVID-19-like viral illnesses will raise the risk of a heart attack in people with plaque accumulation in their blood vessels. Research indicates that viral disease will increase the risk of a piece of plaque lining the arteries breaking off and preventing blood flow to the heart.

14 Lung Disease and COVID-19

Chronic airway and pulmonary diseases, including chronic obstructive pulmonary disease (or COPD, such as emphysema), asthma, pulmonary fibrosis and interstitial lung disease, may set the stage for more severe infection with the new coronavirus due to scarring, inflammation or lung injury.

Working with the physicians and ensuring they have sufficient quantities of repair and rescue medicines on hand is very necessary for people with these conditions.

15 Diabetes as a COVID risk factor-19

People who are living with diabetes are more likely to get sick from the current coronavirus. Type 1 and Type 2 diabetes can cause elevated blood sugar. Poorly regulated sugar in the blood can make viral diseases more harmful, like COVID-19, probably because higher blood sugar can create an atmosphere whereby viruses are likely to grow.

Additionally, diabetes enhances inflammatory responses and reduces the immune response, making it more difficult for people living with the condition to eventually fight off diseases. Anyone living with diabetes should stick to their prescription regimens and do whatever they can to keep their blood sugar in check. Getting a good supply of medicines and

keeping in close contact with the doctor will lead to peace of mind.

16 Association between genetic polymorphisms and severity of COVID-19 infection among populations

Researchers have identified gene polymorphisms of the mannose-binding lectin, that occurs due to antigen presentation, increases the risk of humans contracting an infection or acute infection of the COVID-19, which varies from one population to another (Li *et al.*, 2020). The human immune systems are innate and responsible for fighting diseases such as viral infection in the body by inhibiting the spread of the diseases and developing adaptive responses by establishing an antiviral state, which is crucial in fighting viruses such as the SARS-CoV-2 virus (Kikkert, 2019; Li *et al.*, 2020).

Furthermore, cases of ACE2 polymorphisms, which is prevalent in some Asian populations is known to increase cases of SARS-CoV-2 not to mention causing other infection such as diabetes and hypertension (Fang *et al.*, 2020b). Because SARS-CoV-2 relies on the ACE2 receptors to invade target cells gene polymorphisms that relate to the increase in the number of ACE2 in the body is thought to be a contributor in the susceptibility of some people to the SARS-CoV-2 virus as compared to other population (Cao *et al.*, 2020; Fang *et al.*, 2020b).

17 Pregnancy

At the beginning of February, a Chinese state media documented an infected woman who gave birth to a positive baby. Newborn babies may be infected due to proximity with patients, like any person. However, the case increased fears that pregnant women may transmit the viruses to their fetus through the placenta (Begley, 2020). Only one study has examined such "vertical transmission". Additionally, scientists in Wuhan University concluded that, of 9 pregnant infected patients, (all had cesarean sections) during their trimester three, none appeared to pass viruses to their newborns, all of them scored highly at the

Apgar scale on newborns' health. "COVID-19 has not been severe to pregnant women based on the few in this research," wrote the scientists. That was surprising because pregnancies suppress the system of immunity (so it does not affect the fetus). Pregnant females are susceptible to respiratory pathogens compared to non-pregnant females.

Nonetheless, none of these 9 women had severe COVID-19 pneumonia (Begley, 2020). It can be that the immuno-suppression helps. Some severe COVID-19 symptoms are as a result of the immune systems on the rampage as opposed to the lethargic one. The Chinese scientists concluded: An extreme immunity response known as a cytokine storm, the flood of immunity cells and biochemical they manufacture, tears through the lung's tissue (Randy and Winn, 2020).

Since COVID-19 is a new disease, we continue learning how everything affects women who are pregnant. There seems to be no evidence at this time to indicate that expectant mothers are at a higher risk for more severe COVID-19-related outcomes or that COVID-19 may adversely impact their developing child.

18 Diagnosis

A reliable clinical technique to differentiate coronaviruses colds from other colds from less common causative agents or rhinoviruses lacks. For study purposes, viruses may be cultured from the washings through inoculating organs' culture of human beings' nasal tracheal epithelium or fetal and nasal swabs. The viruses in the cultures are detected through electron microscopy and other methods (Samantha *et al.*, 2013). Collecting paired sera (obtained from the convalescent and acute phases of this disease) and testing through ELISA for an increase in antibodies towards 229E and OC43 is a beneficial laboratory diagnosis method. Complement fixation testing may be insensitive while other tests may be inconvenient and may be utilized for only one serotype. Direct polymerase chain reactions and hybridization tests of viral nucleic acids have been created and, especially with the former, are very sensitive assays available for the detection of viruses (Jacobs *et al.*, 2013).

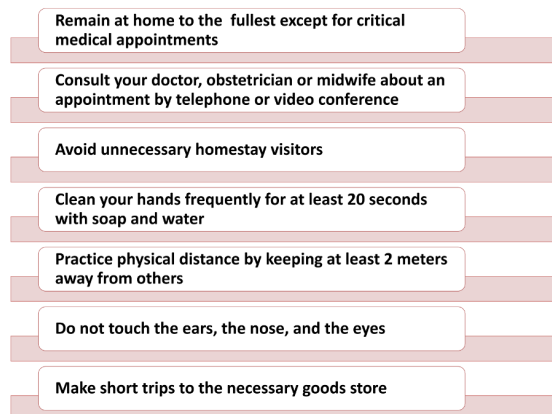


Figure 3. Measures can be taken to minimize the risk of infection.

19 Current prevention and treatment strategies

Since no vaccine is available to avoid COVID-19, measures can be taken to minimize the risk of infection. Following these precautions, the WHO and the CDC suggest stopping COVID-19. By taking the following steps, you can prevent yourself from getting ill (Figure 3).

Although antiviral therapies have been tried, the coronavirus' colds treatments remain symptomatic. The probability of transmission may be minimized through practicing hygienic practices; shun unprotected contacts with wild animals or farm. Individuals having symptoms of acute airways infections should maintain their distances, covering sneezes or coughs with disposable clothes or tissues and clean their hands. Besides, immune compromised people should shun public gatherings and public exposure (The World Health Organization, 2020). If immune compromised individuals must stay in closed spaces with multiple people present, such meetings in small rooms, gloves, masks, and individual hygiene with antiseptic soaps should be done by those in contact with those individuals.

Furthermore, prior room cleaning by antiseptic agents is imperative before exposure. Nevertheless, considering the dangers posed by these persons, exposure should be shunned unless meetings, group events, etc. are emergencies. Strict individual hygiene measures are imperative to ensure the control and prevention of the infection (Cascella *et al.*, 2020). Wang *et al* (2020), reported that a human monoclonal

antibody neutralizes SARS-CoV-2 (and SARS-CoV) in cell culture (Chunyan *et al.*, 2020). This cross-neutralizing antibody targets a communal epitope on these viruses and may offer potential for prevention and treatment of COVID-19 (Bao *et al.*, 2020; 2020; Weingartl *et al.*, 2004). FDA is a fast-tracking malaria drug to possibly treat coronavirus Chloroquine or hydroxychloroquine, used to treat malaria, severe cases of arthritis (Ross and Magwere, 2007).

Some researchers have hypothesized that angiotensin-converting enzyme 2 (ACE2) can be used as a treatment of COVID-19 because the SARS-CoV-2 virus binds itself to its host through the ACE (Fang *et al.*, 2020; Perico *et al.*, 2020; Tignanelli *et al.*, 2020). The severe acute respiratory syndrome coronavirus-2 binds itself via the ACE2 receptor for the intracellular invasion of the host (human) and is the main reason why Fang *et al.*, (2020) postulate that ACE2 receptors inhibitors could serve as a treatment. Because of the critical role of the ACE2 in the spread of coronavirus such as COVID-19, treatment with ACE2 receptors inhibitors require additional exploration since some researchers have raised concern about the safety of this treatment option as it leads to more expression of ACE2 receptors (Kayvon *et al.*, 2019; Danser *et al.*, 2020; Kuster *et al.*, 2020).

Conclusion

Since the outbreak of (COVID-19) disease in China, the illness is spreading very quickly across the globe. There was no evidence showing that the viruses were manufactured in laboratories or engineered. Extensive lab work on the mechanisms of infection and genetic factors such as polymorphism that may play an essential role in disease is needed urgently. However, persons with advanced ages as well as those who are immune compromised have higher risks of contracting the disease. Health care staff should comprehend the disease's presentation, supportive care, and workup. Furthermore, health care experts should know the precautions needed to shun contraction and escalation of this disease.

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