Principles in Nursing Practice in the Era of COVID-19

Amanda Bergeron
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Linda Holifield
Editors

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Preface

In Wuhan, China, in late 2019, a pneumonia of unknown etiology was identified by Chinese authorities and reported to the World Health Organization (WHO). Later on, the etiology of the pneumonia would be identified as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). This virus spread rapidly, causing a worldwide pandemic of coronavirus disease 2019 (COVID-19). Scientists, researchers, and medical professionals around the world have been working tirelessly since the beginning of the pandemic to develop processes for prevention and treatment modalities to control the highly contagious disease.

Infection prevention and control practices are essential to the provision of safe and high-quality healthcare for patients with COVID-19. Just as transmission-based precautions must be applied in cases of tuberculosis or measles, similar practices must be implemented to prevent the transmission of SARS-CoV-2. Standard precautions, such as hand hygiene, have immense research to support their implementation across all settings in which healthcare is provided. Many studies, early in the pandemic, made it clear that limiting close contact between those infected with the virus and those not is essential to reducing transmission. From that early data, public health entities began recommending symptom screening, testing, and subsequent isolation as methods of isolating cases of infection. The incubation period of SARS-CoV-2, which is defined as the time between exposure to the virus and development of symptoms, is 5–6 days on average, but it can be as long as 14 days. Given that infected people without symptoms can transmit the SARS-CoV-2 virus, it is essential to implement source control measures, such as face masks in public, physical or social distancing, hand hygiene, and adequate ventilation indoors. Along with these general measures, healthcare facilities must supply proper personal protective equipment to their employees, such as face masks, respirators, gowns, and gloves, as the virus is transmitted primarily through respiratory droplets, but can also become aerosolized during certain medical procedures. Testing for screening, diagnosis, and contact tracing is another paramount measure to reducing community infection burden. Finally, there are now vaccinations specific to SARS-CoV-2, which prevent severe COVID-19, thus reducing mortality and relieving strain on local healthcare entities, as fewer cases require hospitalization.

The SARS-CoV-2 virus has revealed itself to have a variety of acute complications, especially in those critically ill with COVID-19. These complications include, but are not limited to, sepsis, acute respiratory distress syndrome, and shock. The guidelines that exist to describe the classification, nature, and treatment of these complications have been derived from various other diseases; however, with some minor changes, they can be applied to the management of severe COVID-19. Management of oxygenation in those with COVID-19 infection is paramount to the treatment of these patients. Survival and morbidity are impacted by oxygenation and ventilation strategies. Hypoxia needs to be accurately assessed and measured, with management strategies targeted to clinical characteristics and patient response. Close monitoring at the bedside, coupled with prompt escalation of care, helps minimize poor outcomes. Once ventilation strategies have been maximized, use of more invasive management techniques, like ECMO, may need to be considered.

Pharmacological management for this disease is an ever-developing field, with new products for treatment and prevention of severe disease becoming available regularly. Because of the varying strength of evidence in case studies and evaluation of real-world results, pharmacological agents used to treat and manage patients with COVID-19 can differ widely in both agents and dose used.

At the start of the COVID-19 pandemic, the focus of medical care and treatment of the disease was in the acute phase of the illness; however, as time progressed, research revealed that various symptoms can persist for 4 or more weeks after the initial infection. Several terms have been coined to describe this syndrome, such as "long-COVID," "chronic COVID syndrome," "post-acute COVID-19 syndrome," or "persistent post-COVID syndrome (PPCS)." In this patient population, symptoms persist, inhibiting the normal activities of daily living of the affected individuals, thus greatly affecting their quality of life. Nurses must also consider those patients who have recovered from severe COVID-19 and who deal with the long-term effects of hospitalization as well as those effects causing chronic organ dysfunction. Nurses should be able to recognize these long-term sequelae and be aware of the impacts on quality of life and mortality, as specialized post-acute care and rehabilitation are needed to assist patients who have recovered from the acute illness.

Not only has the COVID-19 pandemic left lasting effects on the individuals who have contracted the disease, but it has also severely affected the mental health of both healthcare workers and the general public. Healthcare practitioners have been at the forefront of preventing and treating this disease while also living under the same social constraints as the public, which has led to increased burnout rates and decreased job satisfaction. Mandates, such as social quarantine, have had a significant psychological impact on the public, and compliance to preventative federal mandates varies in the general population. Along with this, social disparities in society and healthcare have become highly relevant during this pandemic. Populations with poor access to healthcare, and those distrustful of the systems in place, have been disproportionately affected by the disease and have decreased access to preventative vaccination and other prevention strategies.

This book aims to provide a generalized overview of COVID-19 as it applies to the lives and professional practice of nurses. Because research on the disease is still very active, recommendations for prevention, treatment, and general considerations are apt to change rapidly. As with management guidelines for any disease, time and further scientific studies often reveal new strategies in treatment approach, problems with previous management methods, and considerations that were previously unconsidered. It is up to the educated consumer of these studies to determine their relevance to current disease management guidelines.

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1 History and Epidemiology

Linda Holifield

1.1 History and Epidemiology

In the year 2020, the world was stunned by the emergence of a novel coronavirus which quickly spread across the globe to become the most significant pandemic of the twenty-first century. The international committee of taxonomy of viruses named this novel virus SARS-CoV-2 and the disease that it causes is COVID-19. The COVID-19 pandemic has impacted a multitude of countries on every continent, causing a strain on healthcare systems and on the global economy. However, COVID-19 is not the only epidemic caused by a coronavirus, nor is it the only pandemic of this century. Viral infections are common sources of infectious disease and are the common culprits in major biological outbreaks [1]. Prior to the outbreak of COVID-19, there had been other viral epidemics. A disease epidemic occurs when there is an increase in the number of cases of a disease than what is normally expected in the population. A pandemic occurs when an epidemic spreads over multiple countries and continents. Other modern pandemics include the HIV/AIDS, H1N1, and Zika virus. This chapter will discuss the epidemiology of SARS-CoV-2, provide a timeline of events, and will discuss coronavirus virology based on what is currently known.

1.2 Timeline of Events

In late December 2019, a group of patients with pneumonia-like symptoms of unknown etiology were reported from Wuhan, Hubei Province, China [2]. The common link among these cases was that most of the patients either worked or lived in

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and around the local Huanan seafood wholesale wet market [2]. While the initial cause for the outbreak was unknown, the market was shut down and an investigation was initiated. At that time, there were 44 cases of pneumonia requiring hospitalization and the outbreak was limited to Wuhan city. Despite closing the wet markets in China, the virus continued to spread suggesting person-to-person transmission. Investigators ruled out a number of respiratory pathogens as the potential cause. By January 7, 2020, investigators had isolated the responsible virus and identified it as a novel coronavirus, a strain of coronavirus never before isolated in the population and thus with no existing immunity [3, 4]. The virus was tentatively named 2019 novel coronavirus (2019-n-CoV). On January 12, 2020, a Chinese laboratory announced that the complete genetic sequencing of SARS-CoV-2 was complete and the information made available to the WHO [3, 5]. On January 15th, the first case of COVID-19 was identified in the United States in Washington State in a gentleman with recent travel to Wuhan China. By January 30th, 2020, the WHO declared the COVID-19 epidemic as a public health emergency of international concern [5]. A Public Health Emergency of International concern (PHEIC) is defined as an extraordinary event with a public health risk to other countries through international spread of disease and requires a coordinated international response [6]. At that point, the WHO issued a number of requirements for all countries with regard to disease reporting, but it was especially noted that countries should be prepared to handle the containment of the disease; specifically, to anticipate the need for active surveillance, early detection, isolation, case management, contact tracing, and the prevention of further spread [7]. As SARS-CoV-2 continued to spread across the globe, the WHO continued to work with Chinese health officials and other international health agencies to establish research priorities and surveillance systems. On March 11, 2020, the WHO Director-General issued a statement declaring COVID-19 a pandemic [8]. At that time, the virus had spread to 114 countries across the globe. The Director-General called on all nations to prepare and be ready and to activate and scale up response mechanisms [9]. Just 2 days later, United States President Donald Trump declared a nationwide emergency. Shortly thereafter, on March 17th, the first human trial of the vaccine in the United States began [10]. April 9, 2020 signified the hundred-day mark since the beginning of the pandemic; there were over a million cases worldwide. As countries enacted shutdowns and travel restrictions, teams across the globe continued to work to learn more about the virus and discover methods of containment and treatment. In May of 2020, the WHO released a preliminary case definition for multisystem inflammatory syndrome in children after clusters of Kawasaki-like sequelae were seen in children [11]. In September of 2020, The United Nations opened the 75th session of the General Assembly, held virtually. At the forefront of the assembly was discussion of the Coronavirus pandemic and it's sweeping effect on the well-being of the Nations. The WHO in conjunction with a number of international organizations described the harmful impact of the "infodemic", the excessive amount of information available via a variety of media containing information about the pandemic which may or may not be accurate. International leaders called on civil leaders, media outlets, and social media platforms to take action against the spread of misinformation [12]. On December 11, 2020, the Food and Drug administration approved the first vaccine for distribution to individuals aged 16 and over in the United States [13]. Shortly thereafter, the first doses were administered to healthcare workers across the country.

1.3 Coronavirus Virology

The Coronaviruses (COVs) have been cited as the source organism in three major epidemics. Coronaviruses were first described in the 1960s as a virus with the ability to cause disease in humans. In November of 2002, there was an emergence of atypical pneumonia in the Guangdong Province of China. The responsible agent was identified as a novel coronavirus named SARS-CoV for the severe acute respiratory syndrome (SARS) that was associated with the infection. Over 8000 people were infected with a case fatality rate of 7% and the virus had spread to 29 countries [14, 15]. The epidemic of SARS was considered contained by July 2003 [14]. In 2012, another outbreak of a novel coronavirus was reported. The outbreak of acute respiratory syndrome originated in Saudi Arabia and spread rapidly throughout the Middle East. The virus was initially called novel coronavirus but was given the name Middle East respiratory syndrome coronavirus (MERS-CoV) [16]. Over 2000 people were infected with MERS-CoV with a case fatality rate of 34.4% and the virus had spread to 27 countries [14].

Coronaviruses are a large family of single-stranded RNA viruses [8]. Their name is derived from the crown-shaped spikes present on the surface which is seen on electron microscopy [2]. There are four main genera of coronavirus: alpha, beta, delta, and gamma. These are subclasses of virus and should not be confused with coronavirus variants which will be discussed later. In the Coronavirus family, there are seven common strains of virus that have been identified in human infections [17]. Of the seven strains of coronavirus, three have been identified as the source of epidemic level disease outbreaks among humans. These are: Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV), Middle East Respiratory Syndrome (MERS-CoV), and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). The other common human coronaviruses are 229E, NL63, OC43, and HKU1. Among these strains, 229E and NL63 are alpha-coronavirus and OC43 and HKU1 along with SARS-CoV/MERSCoV/SARS-CoV-2 are all beta-coronaviruses. When comparing the genetic sequencing among the coronaviruses, SARS-CoV-2 is 50% identical to MERS-CoV and 80% identical to SARS-CoV [2, 5]. However, there are seven domains in the genetic sequence that are used to identify a virus as a coronavirus, and along those domains, SARS-CoV and SARS-CoV-2 are 94.4% identical [5].

Coronaviruses are found in both animals and humans. They can cause zoonotic diseases which means that animals act as a vector or carrier for the virus and can spread virus from animals to humans ultimately causing disease in humans [17]. The SARS-CoV and MERS-CoV viruses are believed to have their origins in bats.

These viruses spread to an intermediate host animal which were then transmitted to humans. In the case of SARS-CoV, the intermediate host was a palm civet (palm cat), and in MERS-CoV, a dromedary camel. In a similar manner, genetic sequencing has demonstrated that SARS-COV-2 has 96.2% similarity to bat coronaviruses which has led experts to believe that the SARS-CoV-2 has its origin in bats via an unknown intermediate host [18]. The belief in an intermediary host is based on two factors: first, the differences in sequences do not fit the timeline for the estimated mutation rate that the virus would need to undergo to arrive at its present coding, and two, there are genetic differences with the code for the spike protein which the virus needs to enter human cells [19]. Early in the pandemic, it was thought that Pangolins might have been the intermediate host based on the finding of coronaviruses in Malayan pangolins which had very similar genetic sequences at the spike protein, but that was ruled out as the intermediate host due to wider variation in the genetic sequencing [20]. Scientists continue to search for the intermediary host by doing retrospective sequencing of animal surveillance samples from China [21].

1.3.1 Variants of Concern

The coronavirus, like all viruses, accumulates mutations in the nucleotide sequence over time. These mutations form variant strains of the virus. While most variants will have no impact on viral behavior or expression (phenotype), some mutations may cause changes to the way that the virus behaves in the form of increased transmissibility, atypical clinical course, decreased effectiveness of vaccine immunity or acquired immunity, decreased responsiveness to therapy, and failure of laboratory tests to detect virus [22]. Scientists and epidemiologists have been conducting genome sequencing and monitoring to identify any mutations to the virus since the initial sequencing of SARS-CoV-2 was completed. The reason for this surveillance is because the development of new variants is an expected phenomenon, and it is important to monitor for the mutations whose expression may lead to a more virulent strain than the original or wild-type strain.

The World Health Organization (WHO) classifies the more concerning variants as either variants of interest (VOI) or variants of concern (VOC) [23]. In the United States, the Department of Health and Human Services established a SARS-CoV-2 Interagency Group (SIG) to monitor variant surveillance and they have further classified variants as: Variant Being Monitored (VBM), Variant of Interest (VOI), Variant of Concern (VOC), and Variant of High Consequence (VOHC) [41]. In addition to the scientific name given to each variant, the WHO has assigned Greek alphabet labels for variants of interest and concern to assist public discussion of the variant strains. A Variant of Interest is a variant that is suspected to have higher transmissibility, cause a more severe illness, bypass the immune response developed from either previous COVID-19 infection or vaccination (a phenomenon known as viral escape), or may evade traditional diagnostic testing [24]. When evidence accumulates that these are being observed in the population, then a variant becomes a Variant of Concern.

Surveillance of variants can be done through genomic surveillance as well as through the detection of epidemiological signals and unexpected trends. Examples of surveillance indicators or alerts would be an increase or change in trends in number of cases (especially if skewed toward a group with specific shared characteristics such as age or gender), an increase in cases among health care workers, evidence of more severe illness than previously observed in the population, or an increase in hospitalizations or intensive care unit admissions [22]. Unexpected trends discovered during routine surveillance can indicate that something has changed in the behavior of the virus and should trigger an alert of variant behavior.

As of 2021, the WHO has identified a number of Variants of Concern. A brief synopsis is given below of the most significant variants to date.

1.3.1.1 B.1.1.7 (Alpha)

In December 2020, there was an unexpectant rise in cases in the United Kingdom which was attributed to the variant B.1.1.7, also known as the Alpha variant [25]. It has since spread to over 80 countries. The transmissibility rate is reported to be 43–90% higher in this strain than in the wild type [26]. The variant contains multiple mutations in its genome. Some of these mutations are in the spike protein which is the basis of some COVID-19 vaccines [27]. While there is some reduced efficacy of the vaccine and of monoclonal antibody therapy, the response to both has been generally effective in neutralizing the variant strain [28].

1.3.1.2 B1.351 (Beta)

The beta variant was detected in December of 2020 from the Republic of South Africa. Within a month of the variant's identification, it became the dominant strain in South Africa [26]. It has now been found in over 40 countries. It is known to have a transmissibility rate that is 1.5 times higher than the original strain [28]. The risks for ICU admission and death have not been found to be significantly higher compared to non-variant cases [29]. With regard to treatment, there is some degree of escape from monoclonal antibodies [28]. With regard to the vaccine, the mRNA vaccines show some degree of protection after the second booster [29].

1.3.1.3 P.1 (Gamma)

The P.1 or Gamma variant has been circulating since 2020 when it was first identified from Brazilian passengers traveling to Japan [30]. This variant is extremely infections and is responsible for a surge of infections that struck the Brazilian Amazon, plunging the country into crisis [27]. The gamma variant is relatively refractory to monoclonal antibody treatments [29]. With regard to vaccines, there is reduced efficacy of the vaccine compared to the original strain, but still effective enough to provide protection in most vaccinated individuals [29].

1.3.1.4 B.1.617.2 (Delta)

Several variants emerged in India in December 2020 which led to a huge spike in the number of cases. Among those variants was B.1.617.2, also known as the Delta variant, which became rapidly dominant. It has spread to at least 124 countries and, at one point, was responsible for 90% of the new cases in France [25]. The Delta variant is reported to be more transmissible and have a higher risk for hospitalization and mortality than other variants of concern [26]. The variant did demonstrate escape from the activity of monoclonal antibody and convalescent plasma therapy [26]. However, the mRNA vaccine does show some degree of protection against the Delta variant [31].

As previously stated, the development of mutations is a natural part of viral evolution. Therefore, it is vital to continue close monitoring of the population for new variants and to monitor the spread of existing variants. The current vaccines available on the market show some protection against the current variants [30]. Increasing vaccination efforts across the world will also contribute to controlling the spread of the virus and therefore the pandemic.

1.4 Case Definition

The hallmark of every outbreak investigation is the case definition. This is a standardized definition used for public health surveillance in the identification of infected individuals. For COVID-19, the WHO has established three categories with criteria for suspected, probable, and confirmed cases of SARS-CoV-2 infection which are delineated below [32].

The clinical criteria are acute onset of fever and cough or acute onset of any three of the following: fever, cough, general weakness/fatigue, headache myalgia, sore throat, coryza, dyspnea, anorexia/nausea/vomiting, diarrhea, altered mental status.

A suspected case of SARS-CoV-2 infection:

1. A patient who meets the clinical and epidemiological criteria.
2. A patient with severe acute respiratory illness (with history of fever and cough with onset in last 10 days and requiring hospitalization).
3. Asymptomatic person not meeting epidemiologic criteria with a positive SARS-CoV-2 Antigen-rapid detection test.

A probable case of SARS-CoV-2 infection:

1. A patient who meets clinical criteria and has either come into contact with a probable or confirmed case or is linked to a COVID-19 cluster.
2. A suspected case with chest imaging (radiography, CT, lung ultrasound) showing finding suggestive of COVID-19 disease.
3. A person with recent onset of loss of smell or loss of taste and the absence of any other identified cause.
4. Death in an adult with respiratory distress with no other identifiable cause. The patient was also a contact of a probable or confirmed case or linked to a COVID-19 cluster.

A confirmed case of SARS-CoV-2 infection:

1. A person with a positive nucleic acid amplification test (NAAT).
2. A person with a positive SARS-CoV-2 Antigen RDT and meeting either the probable or suspect case criteria listed above.
3. An asymptomatic person with positive SARS-CoV-2 antigen-rapid detection test who is a contact of a probable or confirmed case.

1.5 Transmission

The ability to understand and quantify disease transmission is vital in controlling the spread of a disease. Transmissibility is the ability of a disease to be passed from one person or organism to another. When discussing the transmissibility of an infectious agent, a common term utilized is the reproduction number, R0, pronounced "R naught". The reproduction number (R0) is a measure of infectivity that represents the number of people who can be infected by coming into contact with one sick person in a population that is neither immune nor vaccinated [18, 33]. If a disease outbreak has a reproduction number greater than 1, then it is expected that the spread will continue exponentially, whereas a disease with a reproduction number less than 1 is not expected to continue [33, 34]. The reproduction number is meant to estimate contagiousness based on complex mathematical modeling, which involves the infectious period, the mode of transmission, and the contact rate. In other words, the reproduction number is an estimate of contagiousness which takes into account both the biology of the virus and the patterns of human behavior that contribute to spread. Patterns of behavior vary widely among different countries. Therefore, the estimated value of the reproduction number in China or Europe may not accurately reflect the reproduction value in the United States. It is also not valid to compare reproduction number values among historic or emerging infections without recalculating this using the same modeling assumptions [35]. There has been much discussion in modern media about the reproduction number in relationship to COVID-19 in an attempt to anticipate the severity of the pandemic. It is very easy to misinterpret and misapply the reproduction number so that the true interpretation of the metric is distorted [35]. For example, obtaining an accurate count of the number of cases during an active outbreak is difficult under the best of circumstances. Even in modern times, there is rarely sufficient data collection systems in place to capture the early stages of an outbreak. As a result, the reproduction number is often estimated retrospectively. Determining the reproduction number for COVID-19 is particularly limited by asymptomatic spread [34]. Despite these limitations, the reproduction number of COVID-19 has still been used in common discussion and it is important to have a basic understanding of what it is and how it is used in discussions of epidemiology.

Despite the limitations in determining the reproduction number, it has been repeatedly shown that the virus is highly transmissible, and the Centers for Disease

Control consider the R0 of SARS-CoV-2 to be greater than 1 though the estimated value varies widely in the literature [36]. While initially associated with wet markets in China, several cases were quickly identified as having had no association with the wet markets [37]. This suggested that there must be an element of person-to-person transmission.

The pathophysiology behind the transmission of the virus is that SARS-CoV-2 uses an enzyme, angiotensin-converting enzyme 2 (ACE2), as an entry point into the body as a cellular entry receptor [18]. The ACE2 enzyme is highly expressed in the epithelial cells of the alveoli, trachea, and bronchi [18]. It is also highly expressed along the glandular cells of gastric, duodenal, and rectal epithelia [8]. SARS-CoV-2 binds to ACE2 with high affinity and acts as an entry receptor for the virus [8]. The spike protein on the virus merges with the viral envelope with the host cell membrane [18].

There have been several mechanisms of disease transmission that have been discussed and theorized to control the spread of the disease. The most discussed are mentioned below.

1.5.1 Animal Transmission

Coronaviruses are zoonotic and can be transmitted from animal to human [1]. The initial cases of COVID-19 were associated with wet markets. Wet markets are open air markets that sell fresh meats and vegetables and may have live wild animals that are butchered on site [38]. To mitigate the spread of the virus, closing the wet markets in Wuhan was one of the very first interventions by the Chinese government. The origin of SARS-CoV-2 is believed to be bats, but the intermediate host has never been identified. In addition to the original animal host, there have been cases of infected Minks spreading the virus to humans [39]. There were two mink farms in the Netherlands that had infected workers, of which at least one was identified as developing the virus from the Minks [39, 40]. The virus is highly transmissible among the Mink population and several variants were identified from the samples taken [39]. One variant is responsible for a number of human infections in the Netherlands and Denmark [39].

Conversely, there is a risk of transmission from humans to animals. Coronaviruses are known to infect animals and while animals may act as a host to the virus, few of them will develop severe infection [41]. The pathophysiology of the viral infection is similar to animals in that the virus binds to the ACE2 receptors in animals [39]. Experimental inoculation has demonstrated that the virus does not replicate well in dogs and did not replicate at all in pigs, chickens, and ducks [39, 42]. It did, however, replicate efficiently in ferrets and cats [41, 42]. In April 2020, there was an outbreak of COVID-19 at the Bronx Zoo in New York City when eight big cats were infected with COVID-19. These cases were linked to a COVID-19 positive zookeeper [40]. Another notable zoo outbreak occurred at the San Diego Zoo where several western lowland gorillas tested positive for SARS-CoV-2 after they developed respiratory symptoms. It is thought that these animals were infected by a zoo staff member [39].

While closing the wet markets in Wuhan was an important step in limiting exposure, future efforts and disease spread should be targeted toward regulating the markets and exotic animal farming rather than a complete ban as it will only encourage black market or illegal sales of wild animals [41].

1.5.2 Person-to-Person

Person-to-person transmission is the predominate method of viral spread. This occurs through droplet particles carrying the virus. The symptomatic COVID-19 patient will experience cough and sneezing. This generates a viral cloud of thousands of viral droplets that range in sizes between 0.6 and 100 μm [43]. The droplet particles have the potential to evaporate and form smaller droplet nuclei depending on the temperature and humidity level of the environment. Warm moist air in the environment helps the viral cloud to remain airborne longer and extends the lifetime of the droplet rather than aid in its evaporation [43]. Droplet transmission occurs when a person comes in close contact (within 6 ft for at least 15 min) with an infected individual and is at risk for having their mucosae exposed to viral droplets [44, 45]. The smaller droplet nuclei contain lighter viral particles that may remain suspended in the air for a longer period and have the ability to cause airborne transmission. Studies have shown that transmission occurs through respiratory droplets and contact. However, airborne transmission is shown to be possible with aerosolizing procedures such as endotracheal intubation, bronchoscopy, administering nebulizers, to name a few [44].

According to studies, the viral load of SARS-CoV-2 is highest surrounding symptom onset and gradually declines [46]. Within 10 days of symptom onset, it is unlikely to recover viral samples capable of replication from patients with mild cases of COVID-19 [47]. People who have recovered from COVID-19 may have prolonged detection of viral RNA. In one investigation, researchers failed to isolate replication-competent virus from adults who persistently tested positive for COVID-19. In contrast, patients who are immunocompromised or who develop severe COVID-19 infection can demonstrate prolonged periods of infectivity from the virus [46].

Given these findings, infection control should rely on early detection and isolation. In addition, all preventative measures should be taken to prevent the spread of potentially infectious droplets.

1.5.3 Asymptomatic/Presymptomatic Transmission

The incubation period is the time that it takes to develop disease after exposure to the virus. The mean incubation period is 5–6 days, but has been reported in the literature to have a range of 1–14 days after exposure [4]. Presymptomatic patients are individuals who are infectious before developing symptoms, while asymptomatic patients are individuals who are never symptomatic. These patients can generate large quantities of droplets through normal breathing patterns which can be very small in size [43]. The virus may be found in the respiratory tract anywhere from 1 to 3 days prior to symptom onset [48]. This method of spread is difficult to quantify because of the challenge of testing patients with no symptoms. There have been studies done which involve estimating infectious time based on exposures and there are studies done testing household contacts [48]. The transmission of the virus from asymptomatic and presymptomatic individuals is well-documented in the literature [48–50]. These studies have important implications as they highlight the importance of prevention in the form of social distancing and in taking added precautions for individuals with known exposures [48].

1.5.4 Vertical Transmission

Vertical transmission refers to the transmission of a pathogen from a mother to her baby either before or immediately after birth. Maternal pneumonias are associated with severe adverse obstetrical outcomes and viral pneumonia is a cause of morbidity and mortality in pregnant women [51]. It is known from previous coronavirus epidemics that pregnant women are at a higher risk for severe illness, morbidity, and mortality [51]. During the COVID-19 pandemic, there have been case reports of pregnant women with viral infection and inflammation of the placenta [52]. The mechanism of transmission is less clear. There have been documented cases of high SARS-CoV-2 viral load in the placenta which could be explained by the expression of ACE2 receptors (the entry point for the virus) expressed in the placenta [53, 54]. However, placental transmission remains speculative and more clinical research needs to be performed [53].

Maternal COVID-19 infection is believed to be at low risk for transmission to the baby [45, 55]. Multiple review articles have noted that the incidence of vertical transmission from mother to baby was minimal and the neonatal outcomes generally favorable [51, 56–62]. In cases with evidence of vertical transmission, transmission does not appear to coincide with the severity of maternal illness [55, 62].

Another speculated form of transmission is through breast milk or while breastfeeding. In one review out of China, there was no evidence of viral particles found in the breast milk of an infected mother [56]. Current guidelines from the Centers of Disease Control are in support of breastfeeding and recommend that breastfeeding parents use hand hygiene before touching their child and expressing mild. If the lactating parent is suspected of having or is positive for COVID-19, the lactating parent should wear a mask anytime they are less than 6 ft from the child. A child who is being breastfed by someone with suspected or confirmed COVID-19 infection should be considered as a close contact and be quarantined for the duration of time prescribed for the lactating parent's quarantine and their own time thereafter [63].

In summation, the majority of studies reviewed indicate low risk of vertical transmission, though all studies highlight the need to continue further research and to take all measures to protect this vulnerable population.

1.6 Conclusion

Understanding the epidemiology of a pathogen is key to limiting the spread of an illness, especially in the setting of a novel pathogen in which no innate immunity or vaccination exists. The critical first step towards this understanding is establishing the case definition which allows for uniformity in data collection. Once that is elucidated, an investigation can begin to determine the nature of disease transmission to control the spread of the pathogen. Finally, continued disease surveillance and monitoring for changes in the nature of the pandemic is vital until a treatment or vaccine can be developed. During the COVID-19 pandemic, identification and isolation of infected individuals and social distancing provided a crucial stopgap in limiting the spread of the virus. This was achieved through the coordinated efforts of public health officials, scientists, health care providers, veterinarians, and wildlife researchers around the globe. Coordinated epidemiological investigations provided the information needed to slow the spread so that scientists had time to study the disease and develop treatments and vaccinations.

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