Chapter

Mode of Transmission and Viral Shedding of SARS-CoV-2: Emerging New Paradigms

Adamu Ishaku Akyala

Abstract

SAR CoV-2 is an important group of animal and human pathogens that infect respiratory tract, hepatic, gastroenterological, and nervous systems of mouse, bat, bat, humans and other vertebrates. Middle East Respiratory Syndrome (MERS) and severe acute respiratory syndrome (SARS) Outbreaks in 2002–2003 have demonstrated the possibility of human to human transmission, animals to humans transmission of the emerging SARS-CoV-2. The World Health Organization (WHO) On 12 January 2020 renamed novel coronavirus infectious disease (COVID-19) to SARS-CoV-2 In late 2019, the first case of the COVID-19 was reported. A total of 87,137 confirmed cases globally, 79,968 confirmed in China and 7169 outside of China, with 2977 deaths (3.4%) had been reported by WHO in March 1, 2020. Meanwhile, several independent research groups have identified that SARS-CoV-2 belongs to β-coronavirus, with highly identical genome to bat coronavirus, pointing to bat as the natural host and by proxy has a zoonotic propensity. Angiotensin-converting enzyme 2 (ACE2) is the same receptor been used by the novel coronavirus as that of SARS-CoV and largely spreads through the respiratory tract. Currently, there are few specific antiviral strategies, but several potent candidates of antivirals and repurposed drugs are under urgent investigation. In this review, we summarized the latest research progress on the transmission mode dynamics and viral shedding in provide direction for isolation protocol. R0 estimates for SARS have been reported to range between 2 and 5, which is within the range of the mean R0 for COVID-19 found in this review. Due to similarities of both pathogen and region of exposure, this is expected. On the other hand, despite the heightened public awareness and impressively strong interventional response, the COVID-19 is already more widespread than SARS, indicating it may be more transmissible.

Keywords: coronavirus disease 2019 (COVID-19), transmission, clinical characteristics, viral shedding

1. Introduction

In late December, 2019, an epidemic of respiratory disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) began in the city of Wuhan in China which spread to over 30 countries of the world [1]. In the last 25 years, notable highly infectious respiratory viruses with pandemic potentials has emerged and remerged. Notable of which is the influenza virus that issued a

global alert in 1918, 1957, 1968, 2003, and 2019 causing severe acute respiratory diseases [2]. The Novel SARS-CoV-2 outbreak resulted in globally, as of 2:33 pm CEST, 17 May 2020, there have been 4,525,497 confirmed cases of COVID-19, including 307,395 deaths, reported to WHO with substantial economic impact. Since then several other viral respiratory pathogens have emerged including Middle East respiratory syndrome coronavirus (MERS-CoV), adenovirus-14, and virulent strains of influenza viruses. Soon after the discovery of SARS, new coronaviruses NL63 and HKU1 were identified [2, 3]. The emergence of 35 different respiratory viruses underscores the epidemic potential and overall threat to global health security. Severity caused by Novel SARS-CoV-2 has been recognized as a global public health security threat [3]. Many African countries are not prepared for the Novel SARS-CoV-2 outbreak due to poor and weak healthcare system, poor surveillance and response system, as well as inadequate and overstretched health facilities and services established higher risk of Novel SARS-CoV-2 importation from Europe to Africa than china importation, comparing rapid spread of the virus in selected sub-Sahara countries than in European countries. Some African countries have developed capacity to respond to the outbreak as at 11 May, 2020, a total of 13,814 confirmed cases and 747 deaths from Novel SARS-CoV-2 have been documented in Africa [2].

Genome sequence associated with Middle East respiratory syndrome (MERS) and human severe acute respiratory syndrome (SARS) has been systematically analyzed to be linked to beta bat coronavirus [4], WHO officially named the virus "SARS-CoV-2" although its origin is still been investigated which suggests human to human transmission could be through wild animals been sold illegally at a wholesale seafood market in Wuhan [5]. In this review, we summarized the latest research progress on the transmission mode dynamics and viral shedding in provide direction for Isolation protocol. The transmissibility of SARS-CoV-2 is represented by the reproduction number (R0) which is the average number of new infections generated by an infectious person in a totally naïve population [6].

2. SARS CoV-2 viral genome and key virulence factors

A 29.9 kb weight of genome structure which are key virulence factors where profile from SARS CoV-2 patients in Wuhan market in China [7]. While SARS-CoV and MERS-CoV have positive-sense RNA genomes of 27.9 and 30.1 kb, respectively [8]. MERS-CoV and SARS-CoV 2 are made up of 27.9 and 30.1 kb RNA genomes positive-sense with 6–11 variable opening frame (ORFs) [9]. The first ORF (ORF1a/b) location translate pp1a and pp1ab polyprotein which is made up of two-third RNA viral genome encoded in the 16 non-structural proteins (NSP) while other encasement are of structural and accessory protein ORFs. Other essential viral structural proteins include; nucleocapsid (N) protein, matrix (M) protein, small envelope (E) protein and spike (S) glycoprotein [10], It was established by Wu et al. that several accessory proteins interfere with innate immune response of the host [7].

3. Epidemiology—origin, Reservoirs and transmission dynamics of SARS-CoV-2

The SARS-CoV-2 is positive-sense RNA virus from the family of β-coronavirus with a non-segmented envelope belonging to the subfamily of Orthocoronavirinae

and sarbecovirus subgenus [4]. α–/β–/γ–/δ-CoV. α- and β-CoV are the four genera of coronavirus that infect mammals. Birds are infected by γ- and δ-CoV genera. Six genera have been identified to cause mild respiratory tract infection in humans, they include; HCoV-OC43, β-CoVs HCoV-HKU1, HCoV-NL63 and HCoV-229E while fatal respiratory tract infection in human is caused by SARS-CoV, β-CoVs and MERS-CoV. There is similarity in homology genome sequence between SARS-CoV-2 and bat CoV RaTG13 with 96.2% identity. Evolutionary analysis suggest SARS CoV-2 is transmitted to humans from bat as intermediate host with special viral tropism to angiotensin-converting enzyme 2 (ACE2) receptors. On December 12, 2019, an epidemic of unknown origin broke out in Wuhan province of China causing acute respiratory tract infection in human population. Source of infection was traced to seafood market. Studies suggest Bat might be the reservoir host of SARS-CoV-2 [6, 11]. Phylogenetic analysis of protein sequence alignment reveals intermediate host such as turtles and pangolin as sources of human to human transmission and also implicated in nosocomial transmission seen within health care workers as revealed on 14 February 2020 by National Health Commission of China [12].

4. Detection of SARS-CoV-2 in different types of clinical Specimens

Reveals SARS-CoV-2 was detected in 205 patients at multiple sites with lower respiratory tract samples, importantly the RNA virus has been detected in feces which imply SARS-CoV-2 may be transmitted by the fecal route. A small percentage of blood samples had positive PCR test results, suggesting that infection sometimes may be systemic. Transmission of the virus by respiratory and extra respiratory routes may help explain the rapid spread of disease. In addition, testing of specimens from multiple sites may improve the sensitivity and reduce false-negative test results. Two smaller studies reported the presence of SARS-CoV-2 in anal or oral swabs and blood from 16 patients in Hubei Province, 3 and viral load in throat swabs and sputum from17 confirmed cases.

Retrospectively identified a convenience sample of patients admitted to Beijing Ditan Hospital, Capital Medical University, with a diagnosis of COVID-19 and paired RT-qPCR testing of pharyngeal swabs with either sputum or feces samples. A diagnosis of COVID-19 required at least 2 RT-qPCR–positive pharyngeal swabs, and patients underwent treatments as well as initial and follow-up testing of pharyngeal, sputum, or fecal samples at the discretion of treating clinicians. Hospital discharge required meeting four criteria: afebrile for more than 3 days, resolution of respiratory symptoms, substantial improvement of chest computed tomographic findings, and two consecutive negative RTqPCR tests for SARS-CoV-2 in respiratory samples obtained at least 24 hours apart [13]. We report the findings of patients with at least one initial or follow-up RT-qPCR positive sputum or fecal sample obtained within 24 hours of a follow-up negative. RT-qPCR pharyngeal sample. The RT-qPCR assay targeted the open reading frame 1ab (ORF1ab) region and nucleoprotein (N) gene with a negative control. A cycle threshold value of 37 or less was interpreted as positive for SARS-CoV-2, according to Chinese national guidelines. Among 133 patients admitted with COVID-19 from 20 January to 27 February 2020, we identified 22 with an initial or follow-up positive sputum or fecal samples paired with a follow-up negative pharyngeal sample. Of these patients, 18 were aged 15–65 years, and 4 were children; 14 were male; and 11 had a history of either travel to or exposure to an individual returning from Hubei Province in the past month. Fever was the most common initial onset symptom.

5. Clinical characteristics, complications and clinical outcomes

Direct contact, respiratory secretions and droplets from respiratory tract are emerging rout of SARS-CoV-2 spread [10]; SARS-CoV-2 was isolated from fecal samples of severe pneumonia patients at Sun Yat-Sen University, Guangdong, China on February 2020, Zhang et al. [14]. ACE2 protein abundance on lung alveolar epithelial cells and enterocytes of small intestine has been discovered [15], which may reveal broad understanding of the routes of infection and disease. Epidemiological investigation reveals signs and symptoms to SARS-CoV-2 becomes manifest between 1 and 14 days, mostly 3–7 days suggesting SARS-CoV-2 can be contagious during a latency period. Elderly and individuals with underlying diseases are at risk of acquiring SARS-CoV-2. A median age of 47–59 years and 41.9–45.7% of patients were females [10, 12, 16]. Comorbidities associated with SARS-CoV-2 in adult might lead to flu like symptoms, malaise, cough which might lead to respiratory failure, distress syndrome and even dead. SAR-CoV-2 patients had good clinical outcome except for few that have associated comorbidities. As at March 1st 2020, there are 79,968 confirmed cases with severe cases totaling 14,475 (18.1%) and 2873 deaths (3.5%) from the China mainland as reported by the WHO [2]. liver dysfunction, acute cardiac injury, Arrhythmia, acute respiratory distress syndrome (ARDS), acute kidney injury are among associated complication [16]. The severity of the disease is associated with poor clinical outcome mostly seen among the elderly which progress faster with dead mostly seen among people aged 65 years [16, 17].

6. Conclusion

The global outbreak of SARS-CoV-2 is across 85 countries. Our study revealed that person to person transmission within family cluster or Nosocomial infection is possible in setting where precautions such as personal hygiene, social distancing and the use of personal protective equipment are not adhered to. Clinicians should be aware of clinical history of contact patients to enable them promptly identify in order to curb further spreading in hospital and family cluster.

Our recommendation will be for adoption of National Guideline that will reveal epidemiological exposure history as an important reference point for identifying the source of infection and strengthened protection, and isolation measures. Close contacts to confirm Cases should be included highly Suspected Cases during Incubation period of Confirmed Cases. Availability of high sensitive rapid diagnostic reagents for Novel SARS-CoV-2 should be accelerated in order to facilitate community testing.

DOI: http://dx.doi.org/10.5772/intechopen.93187

Author details

Adamu Ishaku Akyala
Department of Microbiology, Faculty of Natural and Applied Sciences,
Nasarawa State University, Keffi, Nasarawa State, Nigeria

*Address all correspondence to: i.adamu@erasmusmc.nl

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