A Preliminary Review on Novel Coronavirus Disease: COVID-19

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Abstract: Coronaviruses (CoV) are a large group of viruses that can cause health disorders ranging from the usual cold to most severe diseases like Middle East Respiratory Syndrome (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS-CoV). These viruses are generally found among animals. In atypical circumstances, these viruses can propagate to humans from animals. The spikes protruding from the membrane of the virus look like the sun's corona, hence the name ‘coronavirus’ has been given. Coronaviruses (CoV) belong to the species of Corona with a high mutation rate than the Coronaviridae. The objective of this review article was to investigate good strategies of treatment and preliminary analysis concerning the disease, and prevention in the early stage of the COVID-19 outbreak.

Keywords: Coronavirus, COVID-19, SARS, MERS, SARS CoV, MERS CoV, Influenza, Epidemics.

1. INTRODUCTION

The origin of the virus is mentioned [1]. In February 2020, the World Health Organization (WHO) named the disease due to this novel coronavirus as "COVID-19"[2]. Here "Co" stands for "Corona," "vi" stands for "Virus," and "d" stands for "Disease," and "19" is its year of identification. The Corona epidemic started on December 31, 2019[3]. According to the World Health Organization, the novel coronavirus (nCoV) is the global burden that was not formerly identified in humans. In December 2019, a virulent disease of coronavirus started and killed over 33,389 people and infected over 7,32,222 people until March 30, 2020, throughout the world. This virus has extended to 199 countries in the world so far [4]. Based on the genetic structure and physical appearance, the virus was named to assist diagnostic tests, medications, and vaccines. The International Committee on Taxonomy of Viruses (ICTV) authorizes and organizes the nomenclatures of these viruses, and this particular coronavirus is thought of as SARS-CoV-2[5]. The physical structure of this virus looks like a pleomorphic wrought fragment consisting of single-stranded positive-sense RNA, including a nuclei-protein in a capsid related to protein matrix [6]. The club-shaped glycoprotein projections and envelope with RNA structure is shown in Fig. (1a, 1b and 1c).

The WHO states that “from the probability of communications perspective, the title SARS can have premeditated consequences in terms of making unnecessary anxiety for a few populations, mostly in Asia which was worst suffering from the SARS outbreak in 2003” [7,8]. Hence, to differentiate it from SARS Coronavirus, the name of the novel coronavirus was granted as the “SARS-CoV-2”. The common symptoms of Coronavirus include sickness or illness from the SARS outbreak in 2003” [7,8]. Hence, to differentiate it from SARS Coronavirus, the name of the novel coronavirus was granted as the “SARS-CoV-2”. The common symptoms of Coronavirus include sickness or illness having a mild to moderate upper respiratory tract disease, sort of cold, headache, unusual body temperature, muscle aches, etc. The typical time-period for secondary cases related to limited human-to-human propagation is five days, but it may vary from 2-13 days based on the immune system of the humans. In MERS-CoV patients, the time for disease inception to hospitalization is four days [9,10].

1.1. Literature Survey

On December 12, 2019, the first case of the COVID-19 was registered. The Huanan seafood market of Wuhan city of China was considered as the origin of this novel coronavirus. Later 27 unpredictable pneumonia cases were registered from the same area, among those, seven cases were severe as officially announced on December 31, 2019. On 22nd January 2020, the Chinese government declared that the new virus had generated from wild bats, and it belongs to beta-coronavirus of group-2 that contains SARS-CoV [9,10]. Even though SARS-CoV and SARS-CoV-2 viruses seem to be identical in appearance and belong to the same subgroup of beta coronaviruses, their genome level is matched up to 70% only and severity level is high in SARS-CoV-2 [11].

Similarly, On November 16, 2003, the virus Severe Acute Respiratory Syndrome (SARS) started near Hongkong border, China's Guangdong province, where the farmer from the Foshan of Shunde district was the first case of infection [12]. Similarly, in earlier 2012, a new type of Coronavirus...
was recognized in China as Middle East Respiratory Syndrome coronavirus (MERS-CoV). On May 12, 2013, the social affairs and health department of the French ministry confirmed the first case of propagation from human-to-human, and the second case was confirmed and reported by the ministry of health in Tunisia [12]. In these two cases, the person who was reported to contain the viral disease got infected from his father in the first case, and the person in the second case got infected when visited Qatar and Saudi Arabia. The pictorial representation of the origin of novel coronavirus is shown in Fig. (2).

Fig. (1). Structure of Coronavirus (a) outer appearance (b) Internal structure (c) positive sense RNA. (Source: https://en.wikipedia.org/wiki/Coronavirus).

Fig. (2). Origin of novel coronavirus SARS-CoV-2.

2. EPIDEMICS OF CORONAVIRUS (FROM DECEMBER 31, 2019 TO MARCH 30, 2020):

From the statistical modeling performance of COVID-19 cases (live World meter data) as shown in (Fig. 3) and information observed in SARS-CoV (2003) epidemics, the time-to-time diagnosis for Integrated Intervention and Quarantine (IIQ) appears to be necessary to control the outbreak [13]. The present growth factor of COVID-19 indicates that the number of registered cases and the number of deaths is approximately 4.5% (with the reference of China and Italy), and the number of infected people versus recovered is about 73%.

If the current situation continues, the number of virus-infected people and deaths is expected to reach a peak value at the beginning of April 2020 [14]. The analysis is observed from Fig. (3a, 3b and 3c) with an exponential trend line.

The typical mean gap between the inception of symptoms and separation is about 5 to 6 days, and it projected a day-wise decrement in peak population by 72-85% and collective infected individuals and deaths by 55-70% [15]. It is expected that by maintaining self-disciplinary and precautionary programs like "Janatha Curfew" (Stay within the home at least 14 hours in a day) which started on March 23, 2020 and integrated interventions like quarantine, promoting face masks and restricted traveling may reduce 10% of propagation rate in virus spread. Hence, the range of peak population will be diminished to 20-47%, and infection rate and death rates will be diminished by 23-49% [16].

2.1. Growth Factor of Novel Registered Cases

The growth factor (GF) is the feature by which a measure multiplies itself along with time. The principal method used here is "every day's up-to-the-minute new cases on the previous day". For instance, action rising by 7% every period (in the above case daily) features a growth factor of 1.07. A growth factor higher than 1 indicates an increase, whereas the one which lies in between 0 and 1 is an indication of turn down, with the number ultimately approaching zero. If the growth factor consistently shows value above 1, it could be a signal of an exponential improvement in coronavirus effect [17,18]. Fig. (4a) and (4b) shows growth factor and day to day registered cases.

3. SARS-CoV-2 VS. INFLUENZA (FLU)

COVID-19 is a disease caused by the SARS-CoV-2 novel virus, which appeared recently in December 2019.
Therefore, medical health professionals are still searching for its mode of propagation, characteristics, and severity. The influenza virus is the common cold that appeared 2400 years ago, but its real evidence was reported in 1580. The symptoms of common flu are more likely to come out with the rapid commencement of illness, normal fever, headache, sore throat, body aches [19]. In comparison with flu, novel coronavirus appears with an initial mild health disorder, headache and muscle aches, and light body temperature. SARS-CoV-2 and Influenza both are spreading viruses that can cause the most common respiratory problems. The best way to avoid the spread of these viruses is to practice precautionary measures like maintaining hygiene, frequent handwashing with good anti-bacterial soap, the use of sanitizers, avoiding touching mouth, eyes, nose, and isolation at home or hospital during sickness, etc. [20, 21]. The critical symptoms of flu and COVID-19 are respiratory illnesses that infect the lungs, nose, and throat. More frequently, the old age people, younger children, and people with chronic disorders like asthma, diabetes, cardiovascular diseases, including pneumonia are at risk due to the effects of these viruses [22]. People infected with these viruses are most expansive in the
first four days of illness. However, healthy people may take 7-14 days to show the symptoms of the illness. The annual vaccination can take two weeks for developing antibodies [23]. However, no vaccination has been developed so far for SARS-CoV-2 and worldwide scientists and researchers are working on it. The vaccination for influenza was developed in early 1940. As COVID-19 vaccination is under development, therefore, people must take precautionary measures [24, 25].

Fig. (6) shows the protein structure of the novel coronavirus.

3.1. Genome Structure of Coronavirus

Coronaviruses come under the classification of the coronaviridae family of viruses. These coronaviruses are enclosed with 120 to 160-nanometer specks and have an ingeminated genome of positive sensed mono-stranded RNA of 27–32kb [25]. This huge, positive-stranded RNA gene is associated with the protein of n-type to hide a helical shaped nucleocapsid. The diameter of the helical-nucleocapsid is almost 9 –11nm. There are 20nm lengthy flower-shaped leaves uniformly distributed on the external envelope surface to give the look of a solar corona as shown in Fig. (6). This structural protein contains a 50–60kda phosphorylated nucleocapsid (n), membrane (m), and glycoprotein of 20–30kda. This is surrounded by a protein substance encapsulated within the lipid bilayer and interacts with the nucleocapsid. Therefore, the spike(s) of 180–220kda glycoprotein formed the leaflet-shaped plenomers. The various types of viruses, including human Coronavirus OC43 (HCoV-OC43), contain 3-glycoproteins (HE; 65kda), which causes hemagglutination and has acetyl esterase activity [25]. The genome structure of coronavirus contains positive-sense monoparitite, single-stranded, polyadenylated, and capped RNAs that range within the order of 27 to 32 kb. The 5′ end within the order of 20 to 22kb carries the replicated gene, which encodes different enzymatic activities [26].

The replicated gene yields are contemplated in two extensive, precise comprehension molds, ORFs 1a and 1b, as shown in Fig. (7). The organization of the genes indoctrinates polymerase viral RNA and dependent RNA, 4- structural proteins- spike (S), membrane (M), envelope (E), and nucleocapsid (N) proteins is shown as Pol-S-E-M-N in Fig. (6). CoV genomes too incorporate a variety of external open reading frames (ORFs) that predetermine 2-4 non-structural (NS) proteins of anonymous functions. Within the genome structure, an intergenic sequence (IS) of about seven bases can be observed at the 5′ end of each gene. The intergenic sequence is necessary for the configuration of subgenomic RNAs [9]. CoV-contaminated cells consist of several superimposed capped subgenomic, and polyadenylated mRNAs with a regular 3′ end. Every subgenomic mRNA and viral genomic RNA also is an mRNA, which is translated to acquire the protein prearranged by the 5′ gene on the mRNA [14].

Several scientists from China have already sequenced the genome structure of SARS-CoV-2 and made the information accessible to worldwide researchers [27]. The genomic sequence shows that China authorities quickly identify the epidemic; COVID-19 registered cases have been rising because of human-to-human transmission after a distinct debut into the human population. The scientists Andersen and his collaborators at numerous further research institutes used this sequence data to analyze the root cause and progression of SARS-CoV-2 by concentrating on several tell-tale countenances of the virus [28].

3.2. Coronavirus Pathogenesis

The most important way of communication of human Coronaviruses by the use of the respiratory tract possibly extends by large droplets by aerosols (e.g., sneezes). The health sickness starts with the ordinary-cold to malfunctioning of ciliary action (ciliostasis) and retrogressive changes disturbing the cilia of epithelial cells of the tract. Infection remains confined to a tiny lower area to the upper respiratory tract because the best possible temperature for viral development is 33° C to 35°C. HCoV-OC43 generally causes placid upper respiratory tract infections, although it has also been reported to possess neuro-invasive properties [28].

3.3. Medical Manifestation of Coronavirus

The general medical manifestation of novel coronavirus nCoV [27, 28, 29]

- The lower tract is not often concerned, even supposing pneumonia may take place.
- Asthmatic kids may experience panting castigate, and respiratory signs could be exacerbating in old age persons with the unceasing pulmonic illness.
- HCoV-OC43 can transmit a disease to neurons and cause encephalitis.
- 229E and OC43-related serogroups from HCoV show upper respiratory signs and symptoms in Higher and Lower aged persons which differ in rate and relentlessness.
- HCoVs roots tract illnesses like bronchoalveolar and pneumonia, nevertheless intestinal flu and neurological diseases may also manifest.
- The HCoV may end up in "common colds" typically afibrile, in old age people.
- The signs are nasal discharge, malaise, chills, runny nose, headache, and cough.
- The minimum and maximum incubation phase is from 2 to 5 days.
- The significant symptoms last for seven days, with a minimum and maximum range of 3 to 18 days.
- The virus affected person with indicative corona infection presents an increase in neutralizing and accompanying complex immunoglobulin titers in the blood after immunization that wane after a few days [29].

3.4. Precautionary Measures to Control the Propagation

The following precautionary measures must be maintained to minimize the viral propagation from human to human. The secondary propagation medium of the SARS-CoV-2 source and its disinfection methods are depicted in Table 1.
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Fig. (4). (a) Growth factor of novel coronavirus (b) 2019-nCoV outbreak between January to March 30, 2020. (Source: https://www.worldometers.info/coronavirus/coronavirus-cases/#case-growth-outchina).

Fig. (5). The structural difference between Influenza and Coronavirus. (Source: https://www.hopkinsmedicine.org/health/conditions-and-diseases/coronavirus/coronavirus-disease-2019-vs-the-flu).
Fig. (6). Protein structure of Coronavirus. 
(Source: https://en.wikipedia.org/wiki/Coronavirus).

Fig. (7). Genome structure of Coronavirus. 
(Source:https://geneticeducation.co.in/novel-coronavirus-covid-19).

Table 1. Precautionary measures [1].

| S. No. | Precautionary Measures to Control |
|-------|----------------------------------|
| 1     | Altogether avoid closed contact with anyone showing signs of respiratory disease |
| 2     | Wash cloves – change them Frequently |
| 3     | Wash your Hands – use sanitizer |
| 4     | Wash your towels if they need to be touched your hands |
| 5     | Should cover your face especially Nose and mouth once you cough or sneeze |
| 6     | Must maintain and wear the surgical mask |
| 7     | Avoid touching doorknobs and banisters |
| 8     | Cook food thoroughly |
3.5. Laboratory Diagnosis of Coronavirus:

The following are the ways of diagnosis of nCoV and (Fig. 8) shows the step by step diagnosis approach [30]:

- Virus segregation - The individual HUH7 used as a prime isolator for 229E, OC43and HKU-1 viruses from therapeutic specimens, and NL63 cloistered in LLC-MK2 and Vero B4 cells.
- Using RT-PCR for the Recognition of viral RNA.
- For the identification of enteric coronaviruses, e-microscopy is useful.
- For serological diagnosis ELISA assays, immune fluorescence tests are used.
- The infections with strain 229E are feasible, employing a passive hemagglutination test, within which red cells coated with coronavirus antigen reacted with antibody-containing sera.
- The virions related to HCoV-OC43 express HE glycoprotein on the surface of the viral envelope that is detected by hemagglutination and acetyesterase assays.

CONCLUSION

SARS-CoV-2 is a naturally originated virus first reported in Wuhan, China, on December 12 but it was officially announced on December 31, 2019, as an epidemic. Now it has spread to 199 countries and considered a pandemic. So far no exact medicine has been discovered. This virus severely affects elderly persons with co-morbidities. It spreads mainly due to respiratory droplets, and the most common symptoms are dry cough and pneumonia. The mortality rate of severe cases ranges from 2.3 to 5%.

CONSENT FOR PUBLICATION

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CONFLICT OF INTEREST
The authors declare no conflict of interest, financial or otherwise.

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