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Chapter

Origin and Impact of COVID-19 on Socioeconomic Status

Gaffar Sarwar Zaman and Mesfer Al Shahrani

Abstract

The coronavirus pandemic, known as COVID-19, is an evolving pandemic caused by a coronavirus, the SARS-CoV-2. The virus was first detected in Wuhan, China, in December 2019. In January 2020, the World Health Organization (WHO) notified this upsurge as an international emergency concerning public health. It was declared a pandemic later in March 2020. By May 12, 2021, 160,363,284 cases had been registered, and 3,332,762 deaths have been reported, caused by COVID-19, characterized as a horrific pandemic in the history of humankind. Scientists have reached a consensus about the origin of COVID-19, a zoonotic virus arising from bats or other animals in a natural habitat. The economic impact of this outbreak has left far-reaching repercussions on world business transactions, along with bond, commodity, and stock markets. One of the crucial incidents that popped up was the oil price war among OPEC countries. It caused plummeting oil prices and the collapse of stock markets globally in March 2020, as the OPEC agreement failed. However, COVID-19 plays a crucial role in the economic recession. The monetary deficit impact on the travel and trade industries is likely to be huge, in billions of pounds, increasing daily. Other sectors have also suffered significantly.

Keywords: pandemic, COVID-19, zoonotic virus, economic impact, economic recession

1. Introduction

1.1 Historical background

Coronavirus (CoV) was tracked down in the 1960s. The Coronavirus Study Group, patronized by the International Committee on Taxonomy of Viruses (ICTV), applied the principle of comparative genomics to further evaluate and segregate the reproductive proteins on open reading frames to identify the variables that convert CoV at varying cluster ranks. CoVs are linked to diseases of different magnitudes. SARS (in 2002–2003) and MERS (in 2012) were the most severe types causing far-reaching pandemics.

Recently, people worldwide have been hugely impacted by COVID-19; it holds the fifth rank as a pandemic since its inception following the 1918 Spanish flu. Since late December 2019, there were possible warning signs followed by the flare-up because of unusual pneumonia incidences in the Chinese city of Wuhan. The symptoms of this complex disease in patients suffering from fever, malaise, dry cough, and dyspnea have been identified as viral pneumonia [1, 2], termed by the press, in the first instance, as Wuhan pneumonia, because of its association

with its symptoms. A comprehensive analysis of the entire genomes has concluded that the outbreak has been caused by the novel coronavirus that has earned the 7th rank as a member of the coronavirus family that infects human beings [3]. The WHO temporarily used terminology for this latest virus as 2019-nCoV on January 12, 2020; soon after, this infectious ailment was officially named COVID-19 on February 12, 2020. Based on phylogeny, taxonomy, and established practices, a subsequent designation for this virus has been considered SARS-CoV-2 by the ICTV [4]. Eventually, the people-to-people transmission of COVID-19 in Hong Kong was identified in the clinical data [5]. As COVID-19 first cropped up in a Chinese city, it gradually developed in four months and swiftly flared up to other parts as a worldwide emergency. Finally, on March 11, 2020, the WHO evaluated COVID-19 as a pandemic, followed by the 1918 Spanish flu, 1957 Asian flu, 1968 Hong Kong flu, and 2009 Pandemic flu. All these pandemics exterminated about 55.5 million people collectively (**Figure 1**) [6–9].

2. Structure of COVID-19

Coronaviruses (CoVs) are affiliated with the Coronaviridae family, constituting a group of enveloped, positive-sense, single-stranded RNA viruses [10, 11]. They are named "CoVs" because of their crown-like structure under an electronic microscope [12–15]. Coronaviruses emerge from the Coronaviridae family, of the order of nidovirales. It was called the "coronavirus" due to the crown-like spikes on its periphery. Coronaviruses comprise a single-stranded RNA that is a tiny nucleic particle (65–125 nm in diameter) (**Figure 1**).

Four subcategories of coronaviruses—(a) alpha, (b) beta, (c) gamma, and (d) delta coronavirus—exist. These viruses were considered the agents of infections only in animals until an upsurge of SARS-CoV was identified in Guangdong, China,

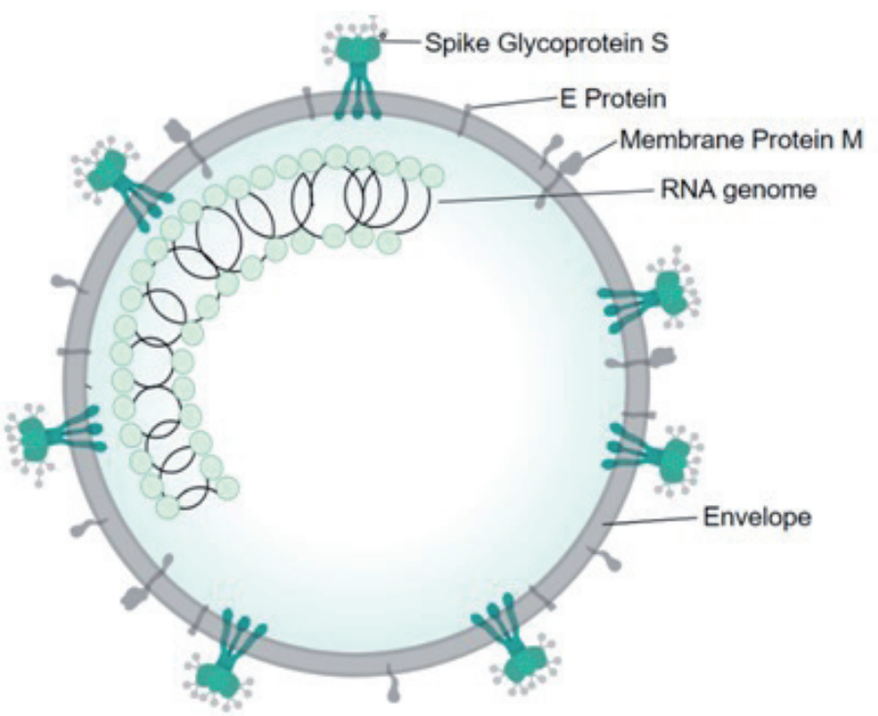


Figure 1.
Construction of respiratory syndrome that generates coronavirus in humans. [This file is licensed under the Creative Commons Attribution-Share Alike 4.0 International license; https://en.wikipedia.org/wiki/COVID-19].

in 2002 [14]. MERS-CoV, another pathogenic coronavirus, caused an endemic in the Middle East countries within ten years [15]. Around December 2019, Wuhan, a burgeoning business point of China, had experienced a flare-up of an unusual coronavirus, causing deaths of an estimated eighteen hundred people and infecting seventy thousand citizens in a fortnight of the outbreak. A formal notification announced that this virus was a member of the beta-type coronaviruses.

According to the ICTV, the main reason for COVID-19 is SARS-CoV-2; Chinese researchers have labeled this extraordinary virus as 2019-nCov or Wuhan coronavirus [16–18]. Statistically, 8098 individuals were infected by SRAS-CoV (2003), causing several deaths; the mortality rate reached 9% in 26 countries, whereas the novel coronavirus (2019) affected 120,000 individuals. In 109 nations, the infection caused a huge human loss, leaving a 2.9% mortality rate when this paper was published. Regarding communicability, SARS-CoV-2 is more intense than SRAS-CoV. The fundamental basis of the transmission was genetic rearrangements of the spike protein in the receptor-binding domain (RBD) of SARS-CoV-2, expected to have developed its transferability. In this review article, the source of human coronaviruses has been discussed as precisely as possible. The correlated infectivity and biological characteristics of MERS and SARS have been discussed with exceptional attention on COVID-19.

3. The virus (COVID-19)

From a pneumonia patient with an unidentified etiology, three specimens of bronchoalveolar washing were extracted on December 30, 2019, in Wuhan Jinyintan Hospital. However, close observation was established regarding this etiology due to the SARS outbreak that flared up in 2000–2003. The polymerase chain reaction (PCR) (reverse transcription-polymerase chain reaction RT-PCR) assessment of these specimens was positive for the entire beta coronaviruses. For the procurement of the whole genome sequences of the virus, Illumina and nanopore sequencing were used only to establish that the characteristics of the virus are identical to those of the coronavirus family. It was also proven that the virus belonged to the Beta-coronavirus 2 B lineage, designated by bioinformatics analyses. Arrangement of genome size of the COVID-19 virus and existing Beta-coronavirus depicted the nearest interrelation with the strains of Bat-Cov RaTG13 with 96% similarity. Virus segregation was carried out by commonly used cell lines—such as Vero E6, Huh-7, and human airway epithelial cells; simultaneously, cytopathic effects (CPE) were put in surveillance for 96 hours after vaccination. Typical crown-shaped flecks were observed under a transmission electron microscope (TEM) with negative staining. Sera extracted from convalescent patients have the potential to neutralize the cellular infection of the isolated virus completely. Interstitial hyperplasia-induced multifocal pneumonia was isolated from ACE2 Rhesus monkeys and mice intranasally challenged with the same virus. One hundred and four strains of the virus were separated from COVID-19 patients in different locations. The observation started at the end of December 2019 and lasted until mid-February 2020 for genome arrangement analysis; it exhibited 99.9 percent homogeneity lacking transformation (**Figure 1**).

At the outset of the outbreak, the WHO announced the name of the interim virus as 2019-nCoV for COVID-19. For histological examination, post-mortem samples were collected from the liver, lungs, and heart of a 50-year-old male. The analysis made it clear that there was bilateral alveolar disruption with cellular fibromyxiod exudation. The lung is the organ where a desquamation of pneumocytes and a hyaline membrane is formed, indicating acute respiratory distress syndrome

[ARDS]. These tissues in the lungs also exhibited cellular and fibromyxoid excretion, pneumocyte exfoliation, and lung congestion. In addition to both lungs, the domination of lymphocytes was also detected in interstitial mononuclear inflammatory infiltrates. Polynuclear syncytial cells with unusually expanded pneumocytes featuring stretched nuclei, prominent nucleoli, acidic and basic granular cytoplasm were deciphered within alveolus areas with an exhibition of cytopathic effects, leaving no evidence of intranuclear inclusions.

4. Most likely ecological pool and source of coronavirus

It is important to be acquainted with its origin and transmission to develop preventive measures and to inhibit the spread of infection. As far as the occurrence of SARS-CoV, surveyors primarily concentrate on palm civets and raccoon dogs as the main storehouse of infection. Only the specimens excluded from the civets demonstrated positive outcomes for viral RNA identification in the food market, suggesting that the secondary host might be the civet palm [19]. In 2001, the samples obtained from sound people of Hong Kong were isolated, and the molecular analyses were conducted; the result showed 2.5 percent of antibodies developed against SARS-coronavirus. This implied that SARS-coronavirus might have circulated in humans before giving rise to the outbreak in 2003 [20]. Subsequently, Rhinolophus bats were also discovered to develop antibodies against SARS-CoV, suggesting that bats were a source for viral reproduction [21]. For the first time, MERS-coronavirus evolved in the Kingdom of Saudi Arabia in 2012 [22]. MERS-coronavirus, known as beta-coronavirus, had camels as a primary host for the zoonotic disease [23]. In a recent study, MERS-coronavirus is believed to be spotted in Perimyotisbats and Pipistrellus [24], implying that bats are the virus' primary source and transmission mode [25, 26]. At the outset, a group of researchers believed that snakes were the probable origin; however, genomic analysis for similarity measures explains that novel coronaviruses and SARS viruses support the assertion that snakes were not the central storehouse, however, bats were [27, 28]. Further analyses of homologous rearrangement showed that SARS-CoV (CoVZXC21) generated receptor binding and the prim of the spike glycoprotein of novel coronaviruses (as shown in **Figure 1**). The construction of respiratory syndrome generating human coronavirus CoVZC45 is an unknown Beta-CoV [29].

5. Transmission of COVID-19

It is universally acknowledged that people-to-people transmission of SARS-CoV-2 occurs in the community, family settings, and health care. Substantial dissemination methods involve droplets from the respiratory duct and indirectly through fomites and aerosols. Some circumstantial evidence shows that PCR and culture are two important laboratory tests used to separate the virus from saliva and identify its feces [30–33]. It has also been observed that the virus appears differently in both blood and urine [34, 35]. If the COVID-19 is mild, the virus shedding in respiratory samples remains for a long period in the case of children; the virus having RNA is obtained in higher magnitude (83.3%) in feces with lasting shedding for a fortnight, whereas it lasts for more than one month in children [27]. Diverse research suggests that the spread of the virus can be seen during incubation on the day or the day before the signs are set forth and spread from very mild asymptomatic infections [36–40]. From the day of his admission, positive samples were collected from the nasopharynx of a half-year-old baby with a high viral load;

these specimens were positive for several days [41]. Therefore, multiple instances may remain undetected and pose a sustainable challenge for virus transmission [42]. The replication number (Ro) is usually considered to be in the range of 2.0 and 2.8 [37–40]; in case higher multiplication numbers are recommended, the serial interlude remains within a span of 5 to 7 days [43–45]. The mean incubation period is between 4.75 and 7 days [46, 47], ranging from 3 to 14 days. Information about the virus load is increasing simultaneously with an increase in our understanding of the virus. In another instance, patients with higher viral loads were identified; the viral droplets in the nose were higher than those in the throat. The intensity of viral droplets was alike in the case of a single symptomatic patient and an asymptomatic patient [32]. On another occasion, for a comprehensive study, the assessment of the virus load was conducted in a pair of patients with a series of samples collected from swabs, throat, urine, stool, and sputum over consecutive days from admission to hospitalization. The viral loads peaked with 104 to107 copies/mL at approximately 5 to 6 days after the onset of symptoms. Similar samples of viral droplets from other patients were examined by the writers, who found the viral loads to be nearly 1011 copies/mL in the throat sample, but the sputum samples had a median of 7.99 × 194, 7.52 ×105. Additionally, the virus was examined using RT-PCR in feces from 9 out of 17 established studies [24]. An examination of nine pregnant women infected with the virus did not provide substantial proof of ureteral transmission to the fetus [48].

As a positive-stranded RNA virus, SARS-CoV-2 was discovered, which is said to belong to the genus beta coronavirus, having a crown-like spike composed of glycoproteins enveloping the surface (**Figure 2**) [18]. There are six categories of coronaviruses found in human beings along with SARS-CoV-2; they are MERS-CoV, HCoV-HKU1, HCoV-OC43, HCoV-229E, SARS-CoV, and HCoV-NL63 [22]. Evaluation of phylogenetics demonstrated that ARS-CoV-2 was nearly related to SARS, with 88–89% similarity; it is also deemed to be derived from bat-SL-CoVZXC21 (unique identifier: MG772934.1) and bat-SL-CoVZC45 (unique identifier: MG772933.1); however, it has a comparatively distant relationship with SARS-CoV and MERS-CoV being 79% and 50% similar, respectively [23–25]. SARS-CoV-2 is covered with a wrapper; it is circular, elliptic, and often

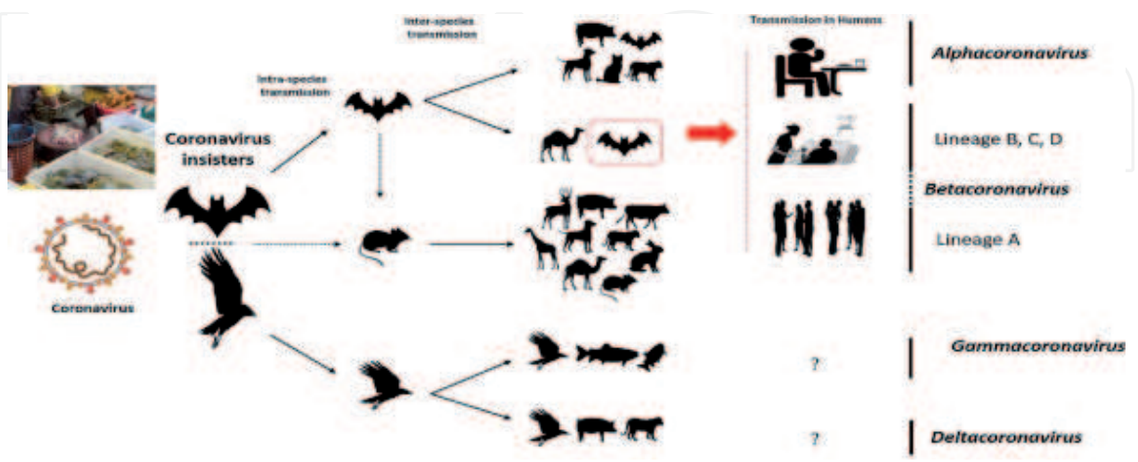


Figure 2.
The main stockpile and medium of transmission of coronaviruses (presumed stocks of SARS-CoV-2 are circled red); the alpha and beta members of coronaviruses have the potential to afflict human beings; the devouring of animals, infected with the virus as an origin of food, is the prime reason of virus spreading from beasts to human beings. Owing to being in contact with a virus-infected person, finally, the virus spread to sound individuals. Arrow with dotted black lines demonstrates the likelihood of virus spread from the bat, whereas the arrow with solid black lines represents the accurate transferal. Reference: [49]. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

polymorphic elements have a radius ranging between 30 nm and 70 nm [26]. The phylogenetic reports and additional research on entire genome sequencing have shown that COVID-19 is inconsistent with SARS-CoV. It can thus be considered the latest beta-coronavirus damaging human organs [27]. The genesis of the 2019-nCoV has been mysterious ever since, but the rising surge is deemed to be connected to the Seafood Market of Huanan in South China [28]. Researchers have been striving to discover the sources in animals to do away with the spread of this novel coronavirus, but none are certain until now. The maximum number of hosts is consistent with the prospective sources of the 2019-nCoV that it belongs to seafood, pangolins, or even bats [3, 4, 26]. The immediate work is to track down the transitory source instrumental in transmitting the coronavirus to human beings. Therefore, determining the source of the virus must bear the potential to help discover the zoonotic transmission method [26]. SARS-CoV-2 demonstrates the risk of high pathogenicity and communicability [29]. It is likely to be transferred from one person to another by the viral loads of infected persons who are directly in contact with the surfaces already contaminated by the respiratory droplets through sneezing, coughing, and physical contact with infected patients [29]. According to several reports, symptomatic individuals are the most recurring sources of COVID-19 escalation [27]. Furthermore, there are opinions that asymptomatic individuals can also transmit the virus as intensely as symptomatic individuals. Besides, more studies are required to understand and explain the durability of infectiveness, the procedures of transmission, and the incubation period of the virus. As HCoV-19 is the latest phenomenon among human beings, much effort is needed to be acquainted with the sources of this virus. Based on a twisted explanation or inappropriate delineation of the early released and restricted amount of data on the HCoV-19 genome, different suppositions or hypotheses are prevalent in that HCoV-19 was artificially produced in mysterious circumstances [50, 51] Specifically, the installation of a polybasic (furin) at the cleavage site of the spike protein was discovered in beta-coronaviruses for the first time (48). Based on the comprehension and information collected from the MERS-CoV and SARS-CoV outbreaks, SARS (Bat-CoVRaTG13) in *Rhinolophus* affinis was successfully detected and separated; it was 95% similar to HCoV-19. It could be propounded that the COVID-19 virus possibly belongs to bats with a higher degree of conviction [52]. Additionally, phenylacetic acid amide on the cleavage region of S1 and S2 has recently been observed in the coronavirus genetic arrangement detected in a different *Rhinolophus malayanus* [52]. These outcomes imply that there are nearly two bat types: *Rhinolophus malayanus* and *Rhinolophus* affinis. They are presumed to be the native sources of HCoV-19. Bats are believed to be a possible animal pool for HCoV-19- and SARS-like [53] coronaviruses. Presently, non-comprehensive evidence is found to show the bats responsible for directly spreading HCoV-19-like coronaviruses to human beings. Recent research shows that the Malayan pangolin (Manisjavanica) has been considered a potential natural storehouse or transitional source of HCoV-19 [54–56]. In another study, community genomic sequencing of blood, intestine, and lung samples from Malayan pangolins was examined by Lam et al. [54, 57]. They detected virus sequences with a connection with a pair of subcategories of HCoV-19 like coronaviruses. Specifically, five analytical remnants of the pangolin virus, which play a significant role in human receptor binding, are similar in every detail to HCoV-19 [57]. Based on a re-evaluation conducted on a formerly announced virus metagenomics dataset of Malayan pangolins [58], it is recommended that there is a prospective pangolin origin of HCoV-19 [59]. The all-inclusive feature of HCoV-19 concerning Pangolin-CoV in pangolins has repeatedly suggested that Malayan pangolin could be a prospective transitional source for HCoV-19 [55]. It is believed that HCoV-19 could spring from a probable intermingling of the aforementioned

Bat-CoV-RaTG13-like virus [52] and Pangolin-CoV-like virus [55]. Malayan pangolins are reported to have been spotted in the natural habitat across Southeast Asia. However, it has never been considered to belong to China, where HCoV-19 was confirmed for the first time [3, 27, 45, 52] because it was significant as an origin of food and herbal treatment.

Irrespective of its whereabouts still not being identified, multiple cases of COVID-19 have been referred to those who have visited the Seafood Wholesale Market of Huanan, situated in the city of Wuhan, China. On February 11, 2020, the WHO came up with COVID-19, a shortened form for COVID 2019. The virus responsible for this flare-up is recognized as SARS-CoV-2; recently, it has been unearthed and is closely related to bat coronaviruses, SARS-Cov, and pangolin coronaviruses.

6. Spread of the virus

With highly changeable symptoms, COVID-19 ranges from none to fatal ailments. The virus of this illness is said to travel through the air from person to person nearby. Once an infected person coughs, breathes, or speaks, the virus is released and attacks the person next to him. It is also very likely to spread through surfaces already contaminated by virus-affected patients. The duration of this virus is at least 14 days, and it has the potential to spread asymptomatically as well (**Figure 3**).

7. Economic impact

The stock market collapse of 2020 was a serious and unprecedented global phenomenon that started on February 20, 2020 and lasted until April 7, 2020 (**Figure 4**).

A transitional bear was experienced in the market due to the COVID-19 disaster, but the bull returned by April 2020; it went on through December 2020

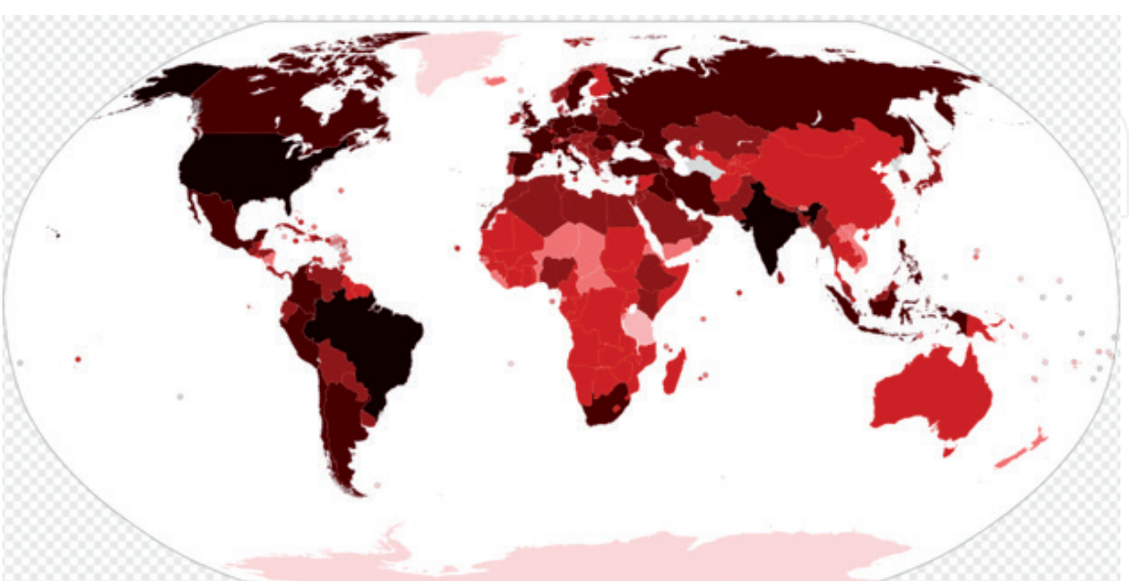


Figure 3.
Total confirmed cases per country as of 10 May 2021. 10,000,000+ 1,000,000–9,999,999 100,000–999,999 10,000–99,999 1,000–9,999 100–999 1–99 0 [this file is licensed under the Creative Commons Attribution-Share Alike 4.0 International license. https://en.wikipedia.org/wiki/COVID-19_pandemic#/media/File:COVID 19_Outbreak_World_Map.Svg.



Figure 4.
Movement of WTI (West Texas intermediate) price of crude oil from 2019. The collapse began on February 20, 2020. For the first time, on April 20, 2020, the prices went down to minus digits in petroleum history. Reference: Sheppard, David; McCormick, Myles; Brower, Derek; Lockett, Hudson (April 20, 2020). "US oil price below zero for first time in history." financial times. Retrieved April 20, 2020.



Figure 5.
Retail experienced a 40–60% plummet in footfall in Mar 2020. Reference: Inc., Aislelabs (April 2, 2020), how retailers globally are responding to coronavirus by Aislelabs, retrieved June 2, 2020.

despite the inability of the US markets to return to the levels of January 2020. This downturn remained until November 2020 because of a slowdown due to COVID-19 (**Figure 5**) [60–64].

The unexpected economic downturn due to COVID-19 trailed economic development and continued growth following the revival of a global monetary setback in 2009. Human history has given rise to unprecedented worldwide joblessness, an all-time low, while the quality of life has gradually settled to a better position worldwide. Over time, the 2020 COVID-19 outbreak—the most menacing upsurge since the Spanish flu of 1918—set out to eradicate the entire economy. The slowdown of the global economy occurred due to the pandemic and the panic caused by it; the equilibrium of demand and supply disrupted the market beyond measure. There is no denying that the International Monetary Fund (IMF) also spotted other diminishing variables before COVID-19, like a global synchronized slowdown in 2019, suggesting the already vulnerable condition of the market [65–70].

Although the collapse started on February 20, 2020, there was a considerable boost in sales in the first fortnight of March 2020. The collapse witnessed many serious daily falls in the stock market worldwide, the largest fall being on March 16; it was termed as 'Black Monday II' as there was a 12–13% fall in most of the business worldwide [71–73]. Two more important collapse dates became obvious: March 9, termed 'Black Monday I' [74–76], and March 12, termed 'Black Thursday' [77]. Banks and reserves worldwide lowered their cash flow and interest rates to manage the stock; furthermore, they offered the markets and investors extraordinary assistance to cope with the situation [78–80].

8. Recession during COVID-19

The slowdown due to COVID-19 is a serious worldwide economic catastrophe that has generated a downturn in many countries and depression in others. It has been considered the worst world economic disaster since the Great Depression [81]. The disaster began because of different government regulations against the production created to inhibit the ongoing outbreak. Significant slowdown symptoms in the collapse of stock markets appeared in late February 2020 and lasted until March 2020 [82–87]. However, the stock market devastation was transitory, and many market indices worldwide revived or established new records by the northern autumn of 2020. By September 2020, every developed economy experienced recession or depression, while all emerging economies were in recession [88–90]. According to the World Bank's anticipation, returning to normalcy would not be accomplished in many countries even by 2025 [91–94].

Due to the COVID-19 pandemic, half of the world population came to a halt to inhibit the spread of COVID-19 [95]. It has caused serious consequences on economies worldwide [96] just after the 2019 world economic slowdown that witnessed the inertia of higher magnitude in the stock markets and consumer activities globally [97, 98].

The slowdown due to the pandemic has caused massive unemployment, inability to sustain unemployment insurance, crashing computer systems, and struggling slow claims processing of the applications [99, 100]. More than 10 million unemployed people were registered in the US by October 2020 [101]. According to the UN forecast conducted in April 2020, the world would see more unemployed people, reducing working hours by nearly seven percent. It has been estimated that nearly 195 million full-time workers lost their jobs [102]. Unemployment, in some countries, was anticipated to reach ten percent; the countries seriously impacted by the COVID-19 outbreak had higher unemployment than before [103–105]. Regarding remittals, even developing countries were not unaffected [106], which exacerbated the global food crisis [107].

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