Review Article

Historical journey of coronavirus to COVID-19 pandemic: An overview

Mandeep Rana, Simran Singla, Priya Jaswal, Gurfateh Singh

Department of Pharmacology, University School of Pharmaceutical Sciences, Rayat Bahra University, Mohali, Punjab, India

Correspondence:
Dr. Gurfateh Singh, University School of Pharmaceutical Sciences, Rayat-Bahra University, Mohali, Punjab, India.
Phone: +91-9216781466.
E-mail: dr_sugga@yahoo.co.in

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ABSTRACT

Human coronaviruses are non-segmented positive-sense RNA viruses enveloped by nucleoproteins with club-shaped glycoprotein's which are responsible for various diseases in our ecosystem. In the 21st century, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) stands with high pathogenicity as compared to SARS-CoV in 2002 and Middle East respiratory syndrome coronavirus in 2012. Coronavirus disease 19 (COVID-19), a flooded event, with its core in Wuhan city has come out as an omnipresent public health emergency of global interest in December 2019 by the World Health Organization. Humans got this virus from the bats through any intermediate source, but still it is unknown. At present, 200$^+$ countries or territories have been affected by SARS-CoV-2, with a universal prevalence of 73,327,817 confirmed cases and 1,630,864 deaths as of December 15, 2020. At present, the COVID-19 cases stand in front of our corona warriors as an asymptomatic carrier platform with respiratory problems which affects all age groups. Droplets or direct contact may be the easiest way of human-to-human transmission of infection with a mean incubation period of 7–14 days. This review enlightened on the epidemiology, history, pathogenesis, and comparative analysis of COVID-19.

Keywords: Asymptomatic, nucleoproteins, pandemic, severe acute respiratory syndrome coronavirus 2

Introduction

Coronaviruses (CoVs) are positive-sense RNA viruses having nucleoprotein envelope (E) with club-like projections which causes numerous diseases in mammals and birds.[1,2] According to serological studies, CoVs are fractioned into three genera normally referred to as groups[3] and this grouping has been confirmed by recent genome sequence analysis.[4] Group I CoVs (animal pathogens) such as TGEV of the pig, feline infectious peritonitis virus, porcine epidemic diarrhea virus, human CoVs HKU1, and HCoV-229E lead to respiratory infections. Group II (veterinary pathogens) such as equine coronavirus, porcine hemagglutinating encephalomyelitis virus, BCoV, or human CoVs NL63 and OC43 also caused respiratory infections just like HCoV-229E.[5,6] Group III (avian CoVs) is pheasant CoVs, turkey CoVs, and IBV.[7] After that, the disastrous journey of CoVs began with the first outbreak of severe acute respiratory syndrome (SARS-CoV) in South China (2002–2003) with 774 deaths, 8096 reported cases and stands with a mortality rate of 9.6%.[8,9] Another highly pathogenic CoVs, Middle East respiratory syndrome coronavirus (MERS-CoV) first emerged in Saudi Arabia in September 2012, with 858 deaths, 2494 confirmed cases and stands with fatality rate 34.4%.[10] Recently in December 2019, SARS-CoV-2, asymptomatic pathogen, knocked the universal door of coronavirus disease 19 (COVID-19) health crisis.[11] SARS-CoV-2 originated in Wuhan City of China in December 2019 and rapidly spread to all over the world.[12] Ancestry of coronavirus predicts that this is the third instance of arrival of coronavirus after SARS-CoV and MERS-CoV.[13,14] The World Health Organization (WHO) entitled novel coronavirus as COVID-19 on February 11, 2020.[15] This pandemic usually has three stages: In Stage one, there is no local spread, cases are reported usually in people who have travel background from an already affected country. Stage two deals with local transmission means the infected carrier with travel history infects the other persons who are in close proximity with them. Stage three confirmed by community spread, the source is untraceable and this is practically uncontrollable stage, accompanied by major clusters of infected people all over the nations.[16] It is noted that CoVs enter a human cell through membrane (M) angiotensin-converting enzyme-2 (ACE2) exopeptidase receptor[17] and comprise symptomatic and

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asymptomatic states that require treatment in the intensive care unit due to infections in multiple organ systems of the human body. This overview showed the connectivity between the SARS-CoV, MERS-CoV, and SARS-CoV-2 which may become a milestone creature about the progression history of COVID-19 globally.

Epidemiology

COVID-19 is a remarkable pandemic that has already reached over 73 million confirmed cases globally with at least 1,630,864 deaths and India have 9,906,507 cases with 143,746 deaths as reported by the WHO as of December 15, 2020.[18] It is observed that the exposure to the virus leads to COVID-19 infection that affects both the immunosuppressed and normal population.[19,20] According to the last guidelines from Chinese health authorities, the mean incubation period of COVID-19 is of 7 days ranging from 2 to 14 days.[21] COVID-19 incubation period remains commensurate to other recent epidemic viral diseases–SARS-CoV (2–7 days) and MERS-CoV (2–14 days) but it is somewhat longer than swine flu (1–4 days) and seasonal influenza (1–4 days).[22,23] According to the WHO, COVID-19 is a highly infectious disease, with a reproductive number (R_0) estimates ranging from 1.4 to 3.5.[24] The risk of spreadability of COVID-19 is much more than the SARS-CoV due to the higher effective R_0 of COVID-19, that is, 2.9 as compared to the SARS reported R_0, that is, 1.77.[25] Based on preliminary information of SARS-CoV-2, the duration of virus stay on various surfaces depends on the different environmental conditions.[26]

Corona Virology from SARS to MERS

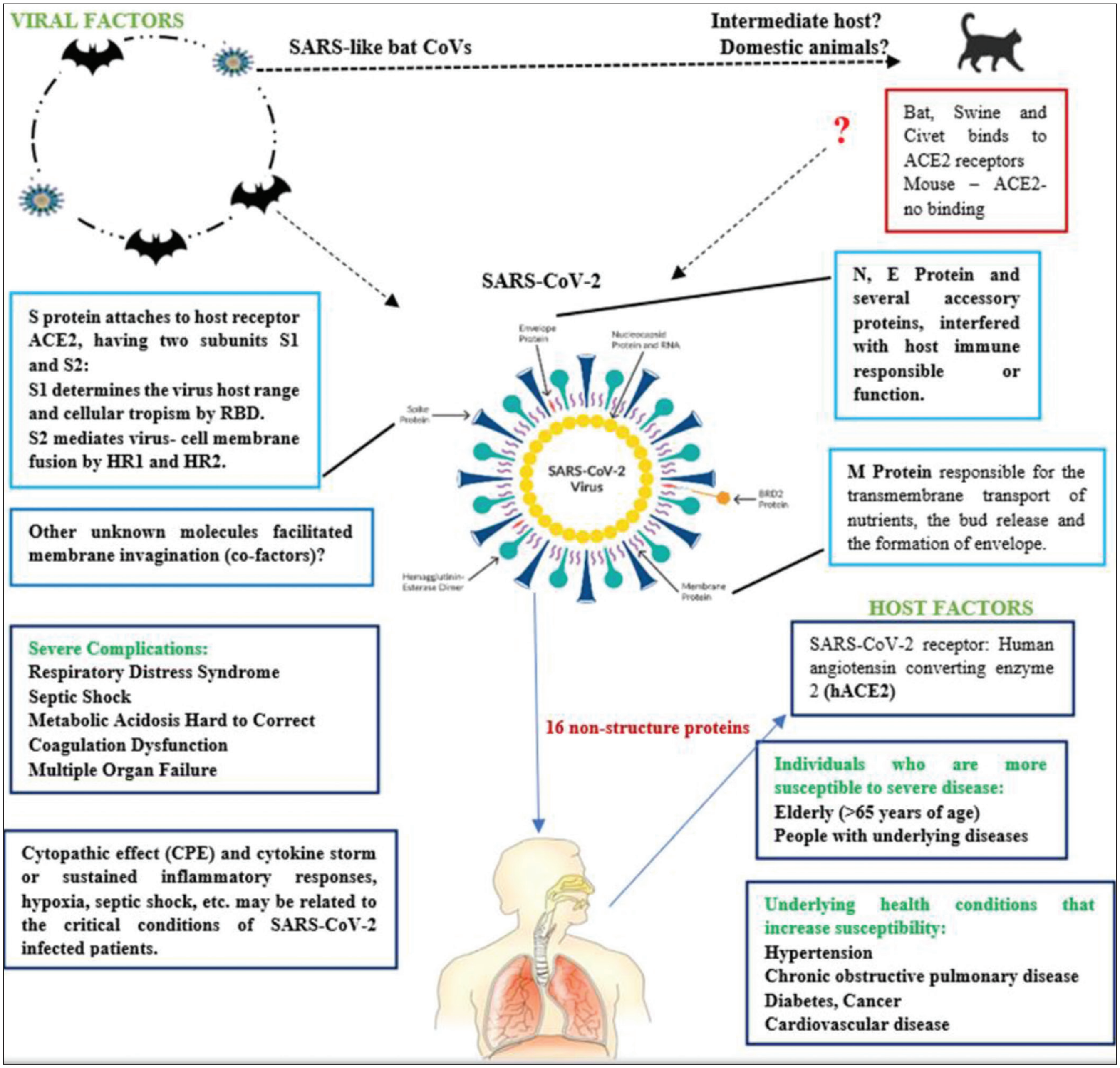
The term "CoV" was coined in 1968, derived from the "corona"-like or crown-like morphology,[27] and is categorized into four categories: α-CoV, β-CoV, δ-CoV, and γ-CoV.[28] Formerly, CoVs causing human infection are of six types, categorized into high and low pathogenic CoVs.[1,2] The highly pathogenic coronavirus, that is, SARS and MERS chiefly affects the lower respiratory tract and causes virulent pneumonia,[1,29] while in contrast, the low pathogenic CoVs such as OC43, HKU1, 229E, and NL63 also report upper respiratory tract infections associated with mild respiratory diseases.[2,30] The SARS-CoV-2 is enveloped, single positive-stranded RNA virus with genome ranging from 26 to 32 kilo bases in length.[1,31] SARS-CoV-2 is closely linked with two bat-derived SARS-like CoVs species, namely, bat-SL-CoVZXC21 and bat-SL-CoVZC45 show 88–89% similarity, but it varies from SARS-CoV and MERS-CoV with ~79% and ~50% similarity, respectively.[32,33] From symptomatic to asymptomatic states of SARS-CoV-2 infection, the clinical symptoms vary extensively that includes fatal complications such as acute respiratory distress syndrome and multisystem organ failure followed by death.[34,35] The severity of SARS-CoV-2 is more than SARS-CoVs, the first highly pathogenic human CoV (2003)[36] because of elongated S proteins of SARS-CoV-2, therefore, its receptor-binding affinity is much more than SARS-CoV.[32] Moreover, the nucleocapsid (N) proteins of SARS-CoV help to neutralize the defense criteria of the host by antagonizing the action of interferon-gamma, a cytokine that activates macrophages but it is still unclear that SARS-CoV-2 N protein has similar quality or not.[1] Second, the R_0 (R through) of SARS-CoV-2 is 2–3 times higher than SARS-CoV, as higher the R_0 (R through) higher will be the diffusible action of virus, at the same time showing the long incubation period accompanied by mild-to-moderate symptoms or suppressed infection and low mortality rate.[37] Both SARS-CoV and MERS-CoV are zoonotic virus with possible origin in bats and camels.[38,39] In SARS-CoV, young people were more prone to it while in MERS-CoV people above 50 years of age came under this category, however, COVID-19 all age groups are vulnerable to it[40] [Figure 1].

Eugenic Pillars Along with Life Journey of COVID-19

COVID-19 resides in genealogy B β-COVs, subgenus sarbecovirus, having positive-sense RNA associated with nucleoprotein.[32,41] The SARS-CoV-2 genome contains round about 10 open reading frames (ORFs). The first ORFs (ORF1a/b) are two-third of viral RNA and its translation yields two polyproteins while leftover ORFs of SARS-CoV-2 encode four main structural proteins: N, E, spike (S), and M proteins along with accessory proteins whose functions are undiscovered.[42] The ORF1 of coronaviruses contains definite genes in the downstream region whose function is to import proteins for S formation, N, and viral replication.[43] It was observed that S proteins are the determinant of virus entry into the host. SARS-CoV-2 S glycoprotein binds with ACE2 and enters into target cells through an endosomal pathway that results in the formation of ACE2 virus complex.[44-46] This complex is translocated to endosomes, where endosomal acid proteases (cathepsin L) separate the S proteins so that its fusion activity is initiated.[47] The viral replicase polyproteins (pp1a and pp1ab) are translocated from viral genome and by the action of viral proteinases, they are converted into small products. The discontinuous transcription on the plus-strand genome leads to the synthesis of subgenomic negative strand template which acts as templates for mRNA synthesis.[48] The full-length negative-strand cut as a template for genomic RNA which helps in assembling of N proteins and the viral N into the cytoplasm, which is accompanied by budding into the lumen of the endoplasmic reticulum-Golgi intermediate compartment and finally with the help of exocytosis virions is released from the cell [Figure 2].[49]

COVID-19: Emergence

December 31, 2019: First, the Wuhan, China, Municipal Health Commission identified the new reports of patients with an unknown pneumonia due to COVID-19, therefore, seafood market was closed and decontaminated on January 1, 2020.[50] On January 9, 2020, the confirmation of the existence of novel CoV (nCoV) was reported in the Wall Street Journal by Centre for Disease Control and Prevention.[51] January 11, 2020: Various research institutes find out five additional novel coronavirus sequence and submitted the data in GSAID database and this allows the researchers across the world to start working on novel coronavirus.[52] On January 17, 2020, 62 cases were confirmed in China while three were diagnosed in Thailand and Japan with travel history from China.[53] Subsequently, diagnostic tests were developed and carried out in the suspected cases identified in Vietnam, Singapore, and Hong Kong.[54] January 19, 2020: The situation starts worsening with a total count of 198 infected patients in Wuhan.[55] January 20, 2020: Now, the COVID-19



Bat, Swine and Civet binds to ACE2 receptors
Mouse – ACE2-no binding

S protein attaches to host receptor ACE2, having two subunits S1 and S2:
S1 determines the virus host range and cellular tropism by RBD.
S2 mediates virus- cell membrane fusion by HR1 and HR2.

N, E Protein and several accessory proteins, interfered with host immune responsible or function.

M Protein responsible for the transmembrane transport of nutrients, the bud release and the formation of envelope.

Other unknown molecules facilitated membrane invagination (co-factors)?

Severe Complications:
Respiratory Distress Syndrome
Septic Shock
Metabolic Acidosis Hard to Correct
Coagulation Dysfunction
Multiple Organ Failure

SARS-CoV-2 receptor: Human angiotensin converting enzyme 2 (hACE2)

Individuals who are more susceptible to severe disease:
Elderly (>65 years of age)
People with underlying diseases

Cytopathic effect (CPE) and cytokine storm or sustained inflammatory responses, hypoxia, septic shock, etc. may be related to the critical conditions of SARS-CoV-2 infected patients.

Underlying health conditions that increase susceptibility:
Hypertension
Chronic obstructive pulmonary disease
Diabetes, Cancer
Cardiovascular disease

Figure 1: Viral and host factors of SARS-CoV-2

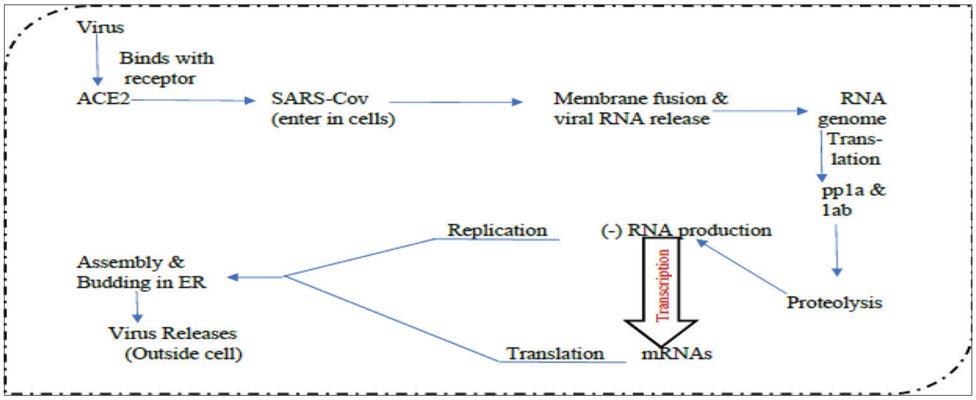


Figure 2: Pathogenesis of COVID-19

starts crossing the boundaries both nationally and internationally. As of January 24, there were 870 total confirmed cases with 26 reported deaths across China and 19 cases in 10 the adjacent countries[56] [Figure 3].[11] January 30, 2020: India's first case was reported in Kerala with travel history to corona affected country and, in few months, it has spread to almost all over India [Figure 4].[11]

Figure 3: Spreading history of COVID-19 worldwide

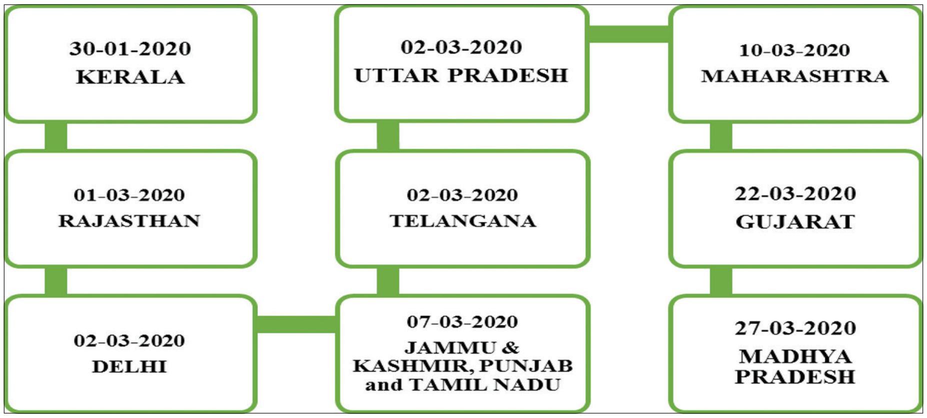


Figure 4: Spreading history of COVID-19 in India

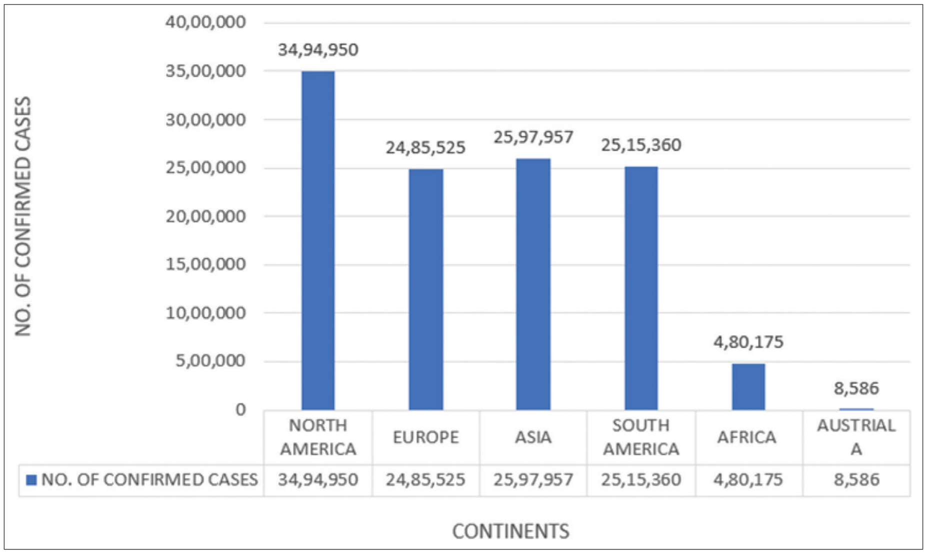


Figure 5: Confirmed cases of COVID-19 worldwide

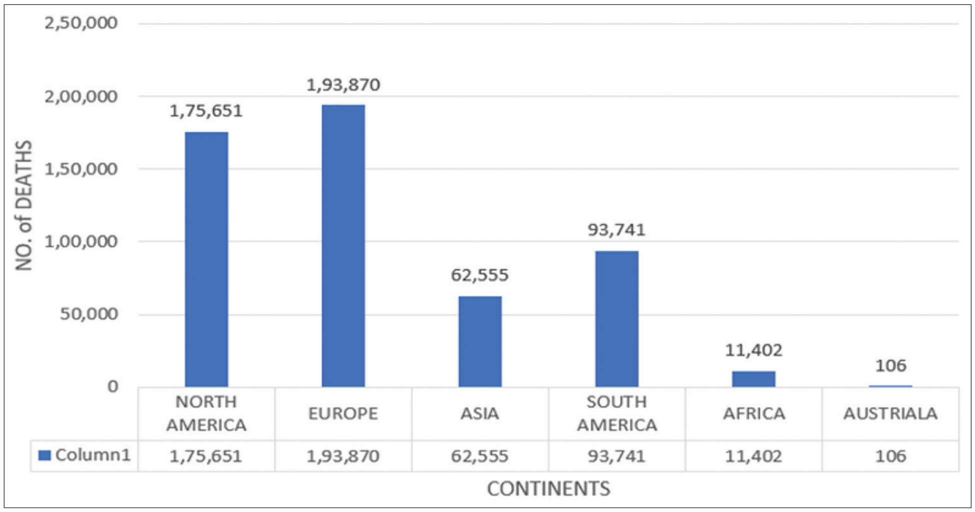


Figure 6: Death cases of COVID-19 worldwide

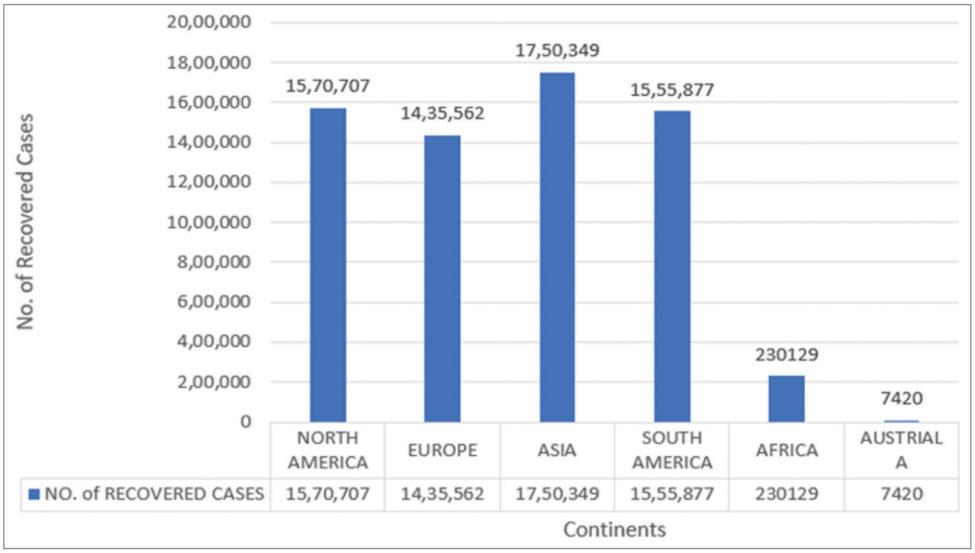


Figure 7: COVID-19 recovered cases worldwide

Severity Scale of COVID-19

Global perspective

Among all the continents, North America is severely affected by the COVID-19 followed by Europe, Asia, South America, Africa, and Australia. Australia reports the least number of COVID-19 cases as of now, that is, 8586 only with least number of deaths and recovery rate is exemplary in Australia [Figures 5-7].[11]

India's perspective

India stands at 2rd position in the tally of COVID-19 affected country with total confirmed cases 9,906,507 and 1.4% fatality rate but the recovery rate is excellent with 93.6%. Maharashtra being the most affected state followed by Tamil Nadu, Delhi, Gujarat, and Uttar Pradesh [Figure 8].[11]

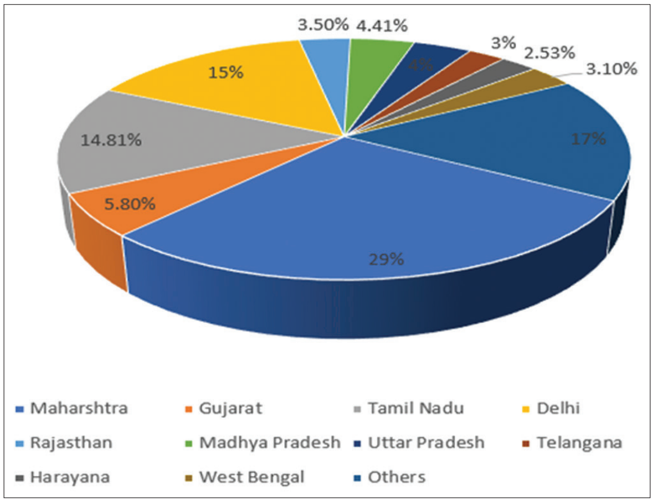


Figure 8: Severity rate of COVID-19

Conclusion

COVID-19, a pandemic, has become a clinical intimation to the general public and also to the frontline warriors all over the world. It is a zoonotic disease which is highly infectious becoming a threat to almost all age groups and spreading worldwide across 200^{+} countries and territories. This COVID-19 storm has challenged every sector of underdeveloped and developed countries such as medical facilities and socioeconomic status. This present review enlightens on the lifetime journey of coronavirus from SARS-CoV (2002) to SARS-CoV-2 (2019). Studies demonstrated that clinically the SARS-CoV and MERS-CoV may have similar pathogenesis and it is also observed that SARS-CoV-2 had the genomic alikeness with MERS CoV. Therefore, it is very interesting to learn more about the homogeneity among SARS-CoV, MERS-CoV, and SARS-CoV-2 that may become a milestone for the future developing drug regimen and vaccines. In this review, the authors expressed the current state of severity of SARS-CoV-2 in India and worldwide scenario along with its pharmacological and non-pharmacological approaches. Moreover, the present study describes the active, recovered, and death cases of COVID-19 in India and worldwide.

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Authors' Contributions

All the authors have contributed equally.

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