

Current Scenario of Covid-19 in Translational Medicine

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Citation: Hollis G J (2021) Current Scenario of Covid-19 in Translational Medicine. *Transl Biomed.* Vol.12 No.5:173

Received date: May 8, 2021; Accepted date: May 22, 2021; Published date: May 29, 2021

Abstract

The COVID-19 epidemic caused by the SARS-CoV-2 virus has reached pandemic proportions and caused worldwide instability. With limited ICU beds and insufficient respiratory support, healthcare systems were unprepared to treat patients who progressed to a severe acute respiratory syndrome, the dire sort of the COVID-19 disease. Current antiviral candidates tested or approved for COVID-19 are compounds that are repositioned from other indications. Generally, drugs are often repositioned for the treatment of the SARS-CoV-2 infection if they need evidence of in vitro inhibition against human coronaviruses (CoV). For instance, remdesivir, which was originally intended for treating Ebola, has been recently approved for the treatment of COVID-19 requiring hospitalization; the anti-malaria drug chloroquine is additionally being evaluated for COVID-19 treatment; the anti-HIV drug combination lopinavir-ritonavir is employed off-label in many lower-income countries against COVID-19. Antivirals, however, may come short in severely ill COVID-19 patients. The “novel” coronavirus disease 2019 (abbreviated “COVID-19”) is that the third coronavirus outbreak emerging during the past 20 years. This communicable disease, sustained by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), has been recently declared a worldwide pandemic by the planet Health Organization.

Supported the knowledge garnered to-date on COVID-19, the outbreak caused by SARS-CoV-2 might be reasonably defined as a sort of perfect storm (i.e., the “wrong virus” at the “wrong time”), for a mixture of reasons. For these reasons, COVID-19 will cause dramatic healthcare challenges and environmental contamination. Last but not least, although the foremost recent WHO statistics would presume us to conclude that the death rate of COVID-19 remains not as high as that of SARS or MERS, the extraordinary number of individuals which will be infected by SARS-CoV-2 compared to both former coronaviruses outbreaks sustained by SARS-CoV and MERS-CoV, would make COVID-19 the foremost deadly of such infections.

From phylogenetic evidence, it can now be reasonably concluded that SARS-CoV-2 presumably derives from a bat coronavirus, after undergoing some level of recombination that boosted its virulence in humans. One important aspect that has been recently highlighted, which can partially explain the heterogeneous development of signs and symptoms also because the almost unpredictable clinical progression in infected individuals, is that the possibility of intra-individual active recombination of SARS-CoV-2.

Beyond the important problem of SARS-COV-2 transmission during the incubation phase, the likelihood of transmission by totally or mildly symptomatic COVID-19 cases must be considered. Although no definitive data are available on this matter, Mizumoto et al. administered an easy analysis on all passengers of the Diamond Princess cruise liner.

Introduction

The “novel” coronavirus disease 2019 (abbreviated “COVID-19”) is that the third coronavirus outbreak to possess emerged within the past twenty years, after Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS). This disease is caused by a member of the Coronaviridae family, which has been defined as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) by the International Committee on Taxonomy of Viruses.

Conclusion

Last but not least, the mixture of the present case deathrate with the extraordinary number of individuals that would be potentially infected by SARS-CoV-2 would permit to estimate that the worldwide deaths for COVID-19 may even approximate those recorded during war II if appropriate restrictive measures for preventing human-to-human transmission aren't readily undertaken.