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# A comprehensive review on genomic diversity and epidemiology of COVID-19

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## Abstract

A respiratory outbreak of COVID-19 started from Wuhan, China and on 30 January 2020, WHO declared this infection to be epidemic, implementing public health emergency worldwide. On 11th March 2020, observing its prevalence in the whole world and WHO declared as a pandemic. Many countries completely collapse in the grip of this pandemic, as there are no effective treatments available, the precaution is the sole remedy to minimize this infection. The emergence and pandemic of SARSCoV-2 (since the SARS-CoV in 2002 and MERS-CoV in 2012] manifest the third time outline of highly contagious and pathogenic infection with infect-ability to spread globally in the twentieth-first century. The SARS CoV-2 genome is highly identical to bat coronavirus which is considered to be the perfect natural host. This coronavirus even utilizes the same ACE2 receptor as SARS-CoV and mainly spread the infection to the respiratory tract, which evidently showed that transmission of this virus through interactions and exposures. The death toll of these infected patients is increasing day by day especially when they have prehistory fatal diseases like cardiovascular, diabetics, and respiratory diseases. In this review, we summarized and explained the research progressed and available data on epidemiology, COVID-19 phylogenetic relation and its impact of different fatal disease and their relation and discuss the precautionary methods to combat this pandemic. Moreover, the pieces of evidence of spreading the virus through pets and prevention of being spreading by copper metal endorsement.

## Biography

Zeshan Haider Raza has completed his Masters at the age of 25 years from University of Veterinary and Anima Sciences, Lahore, Pakistan. He is a Research Associate in a Research Project at the Institute of Biochemistry and Biotechnology, UVAS, Lahore, Pakistan.

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