SARS-CoV-2: Brief History and Molecular Biology*

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Abstract

The COVID-19 pandemic started in early December 2019. It appeared first time in People Republic of China and spread worldwide infecting more than 50 million people till today. The disease caused more than one million deaths worldwide and still the threat is present. The acute pneumonia resulting in severe respiratory syndromes are typical symptoms of novel coronavirus. End of the COVID-19 pandemic is unpredictable. In this project, development of vaccine and early diagnosis of the disease is proposed. Currently, there is no proper vaccine for this disease. However, preventive measures are the only solutions for this typical disease. The origin of COVID-19 can be traced back to bat coronavirus, where it is almost to 97% identical to existing strains. However, due to unique furin cleavage site the novel human coronavirus is spreading at alarming rate. This article is discusses the history, classification, characterization and epidemics of viruses especially the coronaviruses.

Keywords: Pandemic; Vaccine; Furin Cleavage; Coronavirus; COVID-19

1 Introduction

An outbreak of mystery illness/disease possibly around the end of October 2019 and the start of December 2019, has been drawing tremendous attention around the world. The disease is now globally known as COVID-19 (Coronavirus disease for the year 2019). The coronavirus disease 19

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(COVID-19) is a highly transmittable and pathogenic viral infection caused by severe acute respiratory syndrome novel coronavirus (nCoV), which emerged in Wuhan city of Hubei province in China and spread around the world. Coronaviruses are a group of family-based viruses containing strains that roots potential diseases in birds and mammals. The zoonotic SARS-nCoV, believed to have originated from infected bats, is the seventh member of enveloped RNA coronavirus. However, the original source of novel coronavirus is unclear. Based on its phylogenetic relationships and genomic structures the novel coronavirus belongs to genera Betacoronavirus which has a close similarity to that of severe acute respiratory syndrome-related coronaviruses (SARS-CoV) and the virus uses ACE2 as the entry receptor like SARS-CoV. These similarities of the SAR-nCoV to the one that caused the SARS outbreak (SARS-CoVs) the Coronavirus Study Group of the International Committee on Taxonomy of Viruses termed the virus as SARS-CoV-2. The understanding of the genetic and phenotypic structure of SARS-CoV-2 in pathogenesis is important for the production of drugs and vaccines. At present, there is no clinically approved antiviral drug or vaccine available to be used against COVID-19. However, few broad-spectrum antiviral drugs have been evaluated against COVID-19 in clinical trials, resulted in clinical recovery.

2 Viruses

Viruses are an emerging threat to human being. They are obligate intracellular parasites, which may or may not cause a disease. For several years, viruses were considered as a piece of nucleic acids. There was a debate among scientists that whether viruses are living or non-living. However, with the current evidences, viruses are considered living once they live inside a host and non-living when they are outside the hosts' body. If a line is drawn between the living and non-living, it lies in the border [1]. However, the peculiar characteristic of virus is that it can be living after entering to the body of a living organism, causing harmful effects. They behave like a particle outside of our body. Most of the times, viruses may cause lethal cellular infections, which can result in the death of the host. The viruses infect almost all the kingdoms of life. Their greater diversity and highly pathogenic activities made their reputation as a serious threat to all mankind. Scientists agree that viruses cannot be related to a single common ancestor; rather they present a complex phenomenon of nucleotides evolution.

3 Naming and Classifying Rules for the Viruses

Initially, the viruses were considered as non-living creatures. But with the discovery of DNA as a genetic material during 1950s, the viruses were placed among living organisms. For the first 60 years of virus discovery, there was no system for classifying viruses. Consequently, viruses were given names haphazardly, a practice that continues today. Vertebrate viruses may be named according to the associated diseases (poliovirus, rabies), the type of disease caused (murine leukemia virus), or the sites in the body affected or from which the virus was first isolated (rhinovirus, adenovirus). Some viruses are named for where they were first isolated (Sendai virus, Coxsackievirus), for the scientists who discovered them (Epstein-Barr virus), or for the way people imagined they were contracted (dengue = 'evil spirit'; influenza = 'influence' of bad air).

The characterization of viruses started with the discovery of electron microscope. By the early 1960s, new viruses were discovered and studied with electron microscopy. They were identified