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Editorial

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Emerging COVID-19: Brief Focus on its Zoonotic Potential and Prevention

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Editorial Note

From history the world had experienced several devastating pandemic emerging infectious diseases where the vast majority of them being viral diseases. The Spanish flu and influenza of different strains, Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS) can be mentioned as typical examples. Surprisingly, most of those viral diseases were traced back to zoonotic origin. Nowadays the world has been under emergence condition due to a strange viral disease finally identified to be SARS-CoV-2 causing pneumonia like disease [1]. After its first appearance from China of Wuhan City by December 2019, within three to four months almost all countries in the world have reported causalities. This review attempts to examine a brief history, biology, clinical features, and diagnosis and disease management of COVID-19. It emphasizes on origin and possible zoonotic transmission of the current pandemic. Furthermore, our review focuses on the most up-to-date scientific information for effective prevention and management of COVID-19 in the world.

According to some literatures, the oldest common ancestor of coronavirus (CoV) has been dated as far back as the 9th BC. The name 'coronavirus' originates from the Latin word corona, meaning "crown" or "halo", due to its characteristic appearance under twodimensional transmission electron microscopy [2]. Hence, the name corona refers to the characteristic appearance of the virion. First discovered in the 1960s, coronaviruses are a family of enveloped positive-sense single-stranded Ribonucleic Acid (RNA).

In comparison to human pathogenic subtypes of CoV associated with mild clinical symptoms, Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrome Coronavirus (MERS-CoV) were associated with severe forms of respiratory disease. In 2002, a subtype of the beta-CoV which rapidly spread across Guangdong, China resulted in 8,000 infections and 774 fatalities in 37 countries while MERS-CoV accounted for 2,494 confirmed cases and 858 fatalities after first detected in Saudi Arabia in 2012.

In late December 2019, a cluster of atypical pneumonia cases started in Wuhan City, China. Genetic sequencing studies have revealed the cause as a new strain of CoV which was initially designated as the novel coronavirus-2019 (2019-nCoV). Nonetheless,

the International Committee on Taxonomy of Viruses designated it as the SARS-CoV-2 virus and the disease caused by the novel virus called coronavirus disease-2019 was renamed as COVID-19 by the World Health Organization (WHO) [3-5]. This outbreak of an emerging disease caused by SARS-CoV-2 was later known as COVID-19. After the first known case recorded on December 1, 2019 in Wuhan City it was reported to have rapidly spread in China and outside.

Although some reports indicate early rapid spread with cases doubling every 7.5 days yet in less than three months of its first report, the outbreak has been reported to stretch to every corners of the world. After deep analysis of the issue, World Health Organization (WHO) declared the epidemic of COVID-19 as a pandemic on 11th March 2020 (WHO, 2020). From the daily mainstream media reports, the world is facing the COVID-19 wave with more than 1.3 million confirmed cases, and 75,000 deaths as of 7th of April 2020 approximately after four months of the disease surge since December 2019.

Coronaviruses are medium-sized viruses with an average size of 125 nm. The nucleocapsid of the viruses has a helical shape which is uncommon for positive sense RNA viruses (Fehr and Perlman, 2015). The vision shape is spherical, with an average size of 125 nm. Despite some variation in size, shape of coronaviruses looks relatively uniform [6].

Coronaviruses are enveloped viruses with club-shaped spike peplomers covering their surfaces. The genome size of this viral group ranges between 27 kielbasas and 34 kielbasas, which is larger than most other RNA viruses. The genome encodes the following five Structural proteins namely Spike (S), Membrane protein (M), Nucleocapsid protein (N), Hem agglutinin-Esterase glycoprotein (HE), and small Envelope (E). Under the electron microscope the spike glycoproteins project through the viral envelope and forms the characteristic spikes in the coronavirus "crown.", imparting a crownlike appearance. It mediates receptor binding and fusion with the host cell membrane and with major antigens stimulating neutralizing antibody, and also targets of cytotoxic lymphocytes. The M protein plays an important role in viral assembly [7]. The nucleocapsid protein may be involved in the regulation of viral RNA synthesis and may interact with M protein during virus budding. The hem agglutinin moiety binds to neuraminic acid on the host cell surface, possibly permitting initial adsorption of the virus to the membrane.

Zoonotic Potential of COVID-19

The term zoonosis is defined as disease and infection which are naturally transmitted between vertebrate animals and man. There are two types of zoonotic diseases namely obligate zoonotic diseases that are transmitted only from animal to human and facultative zoonotic diseases which are mostly transmitted among humans [8].

Emerging viral diseases are those diseases in a process of adapting to new host and vice versa. They originate in one organism and then pass to another thereby causing disease. For further identification, they can be classified as suddenly appearing or suddenly come to the attention of medical scientists.

Although socio-economic, environmental and ecological factors are among the driving forces of emerging and re-emerging infectious diseases, studies showed that emerging or newly discovered pathogens



are three times more likely to be zoonotic. In other words, two-third of emerging infections originates from animals, the majority being from wildlife. In a similar fashion, several human viruses have their origin of animals implying that they may jump the species boundary. Sometimes the pathogens that infect animals can evolve and infect people and become new human pathogens. Other scientific reports indicated that some modern viruses were associated with the earliest precursors of mammals and coevolved with humans [9].

As of today, there have been conflicting dilemmas on the origin of human coronavirus. Some scholars speculate that the virus might originate from animals and human acquire from food source while others propose that the viruses undergone mutation and evolve as new infectious agent. Recent reports of COVID-19 outbreak from Wuhan City, China showed that the majority of patients diagnosed with the disease had links to the Huanan Seafood Market, implying a zoonotic origin [10]. Further studies from gene characterization showed that bats and rodents are the gene source of alpha-CoV and beta-CoV. On the other hand, avian species are deemed as genetic sources of delta-CoV and gamma-CoV. Similar studies of genomic characterization revealed a nucleotide match of 89% between SARS-CoV-2 and bat SARS-like CoVZXC21. Moreover, the virus was isolated from different animal species including camels, masked palm civets, mice, dogs, and cats. The repeated emergence and outbreaks of CoVs indicate a public health threat. This suggests the possibility of animalto-human and human-to-human transmission of newly emerging CoVs. The ongoing changes in ecology and climate make future emergence of such infections more likely.

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