

OVERVIEW OF THE ENVIRONMENTAL DISTRIBUTION, RESISTANCE, MORTALITY, AND GENETIC DIVERSITY OF NEW CORONAVIRUS (COVID-19): REVIEW

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Abstract. We have witnessed three outbreaks of the epidemic or pandemic caused by coronaviruses (SARS-CoV, MERS-CoV, SARS-CoV-2 or Covid-19) around the world in the years 2003 to 2020, starting in China and the Middle East (Saudi Arabia). Controversies have been raised on the origins of these viruses from bats or camels. In fact, the main resources of distribution, pathogenicity, transmission methods, genetic relativity and many important issues related to these viruses are still unclear. Various studies have confirmed the genomic and protein similarities in these viruses. However, there are apparently many genetic mutations in various parts of the genome, and their surface proteins, suggesting that the human community is facing a particular pathogenic serotype and needs further studies to control of its infections in the future. In this review, a brief overview is discussed on the so-called coronaviruses resources, resistance to some environmental factors, mutations between serotypes, genomic similarities, and the future infections.

Keywords: Covid-19, SARS-CoV, MERS-CoV, Pathogenicity.

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1. Introduction

According to scientific evidences, it is not yet clear how the new coronaviruses (Covid-19) will spread between the environment, animal and humans. Alternatively, it is not clear how much they are resistant to environmental conditions (Geller *et al.*, 2012; Chan *et al.*, 2011; Shu-Ming *et al.*, 2003). Perhaps a comparison of the genomic sequences of the different viruses in this family (SARS-CoV, MERS-CoV, SARS-nCoV or Covid-19), and their mortality rate (Xiaolu *et al.*, 2020; Ranjit *et al.*, 2020; Sahin *et al.*, 2020) as well as the epidemiological data may help clarify the complexities of the diseases caused by these viruses particularly Covid-19. For this reason, this study has compiled and reviewed some new articles on the spread, resistance to environmental factors, mortality, genetic variation and a series of epidemiological information on these viruses.

2. Covid-19 and other coronaviruses distribution and resistance in environmental conditions

At present, the resistance of Covid-19 virus to ambient temperature and humidity is unknown. However, in the case of the SARS virus, the type specific member of the family, Coronaviridae, has been found to be relatively resistant to cold and moisture (Geller *et al.*, 2012; Chan *et al.*, 2011). The SARS virus is resistant to normal conditions of temperature and humidity (22- 25°C and 40-50% humidity) for up to 5 days, but temperatures more than 38°C and humidity more than 95% can slow its multiplication speed. However, its resistance in low humidity and low temperatures is relatively high, which is the reason that they may spread easily in subtropical areas including China and Hong Kong (Geller *et al.*, 2012). Survival of SARS in human specimens have been reported very high, which indicates its high resistance against harsh environmental conditions, however, fortunately the virus could be killed by UV radiation, temperatures higher than 38, alkaline and acidic pH (Shu-Ming *et al.*, 2020; Darnell *et al.*, 2004). However, what makes Covid-19 surprisingly different from others is its very high speed of spreading and possibly its resistance to environmental factors. In one study, it has been reported that unlike SARS, Covid-19 patients had a higher viral load in the first stage of the disease, which could be attributable to its severity and pandemic rate (Darnell *et al.*, 2020). Therefore, the prevalence of diseases caused by these viruses could be explained in relation to ambient temperature and humidity in different geographic seasons. Also, based on this pattern of resistance and genetic similarity and to some extent the surface polyproteins of Covid-19 and SARS virus, it is likely that after this pandemic, the disease of Covid-19 will be occurred as seasonal epidemics in different geographical areas.

3. Genome diversity in Covid-19, SARS, MERS-Cov

Given the Covid-19 as an emerging disease, the results of several studies on the first isolates of the virus is discussed in this section. Perhaps one of the most important studies is the genomic study of 103 isolate in Wuhan, China. In this study, evaluation of 103 strains in the new Wuhan epidemic showed that Covid-19 have indicated a 4% genetic difference with known SARS virus, which was 17% in strains isolated from neutral sites. Results of this study indicates a higher genetic divergence between SARS and Covid-19, particularly in the host binding sites of spike proteins. Researchers also referred to L (more aggressive) and S (less aggressive) types of virus. They proposed that S strains would be dominant due to selective preventive pressures on the control of L strains diseases and in turn would induce immunity in population without severe pathogenic effects in the future (Xiaolu *et al.*, 2020). Other study in Nepal on a 32-year-old patient showed that the new covid-19 virus was highly mutagenic, and within a short time the patient returned from china to Nepal whole-genome sequence analysis of isolated Covid-19 revealed that more than 99.99% was similar to SARS-CoV-2 (covid-19) from Wuhan, China strain. But, in comparison with the Chinas Covid-19, five silent mutations was identified in the serotype isolated from the so-called patients (Ranjit *et al.*, 2020), in other studies also referred to mutations including in the spike genes and related binding capacities of this virus to hosts, which indicates that we have encountered with a highly mutagenic serotype (Ranjit *et al.*, 2020; Sahin *et al.*, 2020). In other study, analysis of genome sequences in three known coronaviruses (Covid-19,

SARS-CoV, and MERS-CoV) indicated that Covid-19 and SARS-CoV have more identities than MERS-CoV. However, amino acid sequences of Covid-19 particularly in the lab polyprotein and s-proteins of surface was different from others, s-proteins have two subunits which conducting the entry of virus to host cells. Nucleocapside proteins of Covid-19 also has about 90% amino acid similarity with SARS-CoV (Kannan *et al.*, 2020; Wu *et al.*, 2020). In fact, comparing the genome sequences of these viruses showed that Covid-19 have about 80% and 50% similarities with Bat-derived severe acute respiratory syndromes (SARS)-like coronaviruses and MERS viruses, respectively (Lu *et al.*, 2020; Geng *et al.*, 2020). In another study by Diego et al (2016) on the mutagenicity and compatibility of both SARS-CoV and MERS-CoV viruses, it was reported that two open reading frames (ORF1a and ORF1b) are responsible for majority of genome translation to polyproteins in beta-coronaviruses. Spreading of these viruses from bats to humans, shifting their host was investigated in this study by analysis of molecular events including the impact of evolution pressure on ORF 1a and ORFb1 transcription. Researchers concluded that non-structural proteins of ORF 1a and ORFb1 undergoing different mutations in the virus biological cycle and evolution in ORF1a may be helping to virus shift its hosts for pathogenicity (Diego *et al.*, 2016; Sahin *et al.*, 2020). Above mentioned facts indicate that Covid-19 most probably was emerged from SARS-CoV, but may have undergone large extent of mutations in the genome and surface proteins particularly in the s-proteins as ligands of host cells. Therefore, the differences in the severity of the virulence and mortalities', using different routes of transmission, and even different signs and symptoms of these viruses was explainable because of different pathogenicity potentials.

4. Comparison of mortality and morbidity in Covid-19, SARS, MERS-Cov

Comparison of mortality and morbidity of three known coronaviruses indicate that Covid-19 was very dangerous than two others (Graziano *et al.*, 2020), and according to the World Health Organization (WHO) statistics, of the 8089 cases of SARS, about 774 patients were died (Graziano *et al.*, 2020). On the other hand, since the outbreak of respiratory diseases in Saudi Arabia in 2012 (Zaki *et al.*, 2012) from 1500 MERS cases only 571 death were reported worldwide (Cotten *et al.*, 2014) indicating that although MERS and SARS have been reported with apparently high mutations and lethality, but, in fact, they are controlled by natural factors such as complicate human or animal immune systems or other preventive controls. Otherwise, it was expected that the human or animal species would become extinct by the thousands of old or emerging microbial agents. What is interesting, firstly, is that there are no statistics of morbidity and mortalities from the SARS or MERS disease in human societies since their initial outbreak (Zaki *et al.*, 2012; Cotten *et al.*, 2014) suggests that the origin of these viruses may be unnatural and handmade. Secondly, Covid-19 may be in decline after this pandemic similar to attributed viruses, despite changes in surface proteins or genomic mutations reported in scientific literature. Of course, the issue of Covid-19 is a bit different, because its death rate is reported to be high. Different reasons including high aged population in the Italy (7.2% death, vs. 2.3% in China) has been attributed to this severity as reported in a recent commentary in JAMA (Graziano *et al.*, 2020).

5. Simple epidemiologic reasons for animal origin of Covid-19 virus

According to various scientific resources, the Covid-19 reservoir is a type of zoonotic disease (derived from Bat). Diseases of animal origin usually have diverse clinical symptoms and different ways of transmission. *Francisella tularensis* and *Salmonella* spp. are from zoonotic diseases examples, which have been transmitted to humans with different ways (Hilde *et al.*, 2004). Unpublished data on its high mortality, especially among physicians and nurses, as well as the uncertainty of Covid-19 sources and reservoirs, and intricate transmission behavior between environment, animal, and human hosts (Zhou *et al.*, 2020; Ji *et al.*, 2020; Guo *et al.*, 2020) indicate that the international community is facing an emerging new strain of the virus. That changes its genetic diversity every time between the different host's transmissions. The rapid outbreak of Covid-19 diseases and in turn its relatively fast and partially unknown contagiousness, long duration of stay on environmental surfaces and fomites, and high mortality rate particularly among physicians and nurses as the first line of control in some countries, indicate that such agents are at least should be classified in the Biosafety level-3 agents. In addition, it seems that a combination of aerosol, infectious respiratory droplets, and close contacts may play a role in their transmission between humans. (Wu *et al.*, 2020; Neeltje *et al.*, 2020; Cai *et al.*, 2020) Depending on the different methods of transmission, the signs and symptoms of Covid-19 are also unique. So, a wide range of symptoms including fever, cough, fatigue, sputum production, headache, diarrhea, dyspnea, lymphopenia, cardiac injury, and abnormal CT scan x-ray opacities have been reported in patients with the virus (Ren *et al.*, 2020; Huang *et al.*, 2020; Wang *et al.*, 2020; Carlos *et al.*, 2020; Lei *et al.*, 2020), which all indicate its wild origin.

6. Conclusion

Covid-19 has infected very rapidly large numbers of people in most countries around the world. The route of its transmission is almost obscure and has a very highly and intricate transmission rate. However, the likelihood of its becoming a dangerous pandemic such as AIDS or pandemics of the last century is very low. On the other hand, because of its high transmission speed, it does not allow countries to use known preventive methods such as quarantine or basic health principles. Therefore, it seems that natural phenomena such as herd immunity due to repeated passages of virus in the human immune system will soon modulate its pathogenicity and become a compatible strain in the human population. Comparison of the mortality and the distribution of the disease caused by these three viruses indicates that Covid-19 is much more invasive than the two preceding's, and mutagenicity studies, especially in Covid-19 surface proteins, are due to the high mutagenic potential of this virus. Therefore, one other possible hypothesis is that the virus will be rapidly suppressed in the human population by adaptation or phenomena such as genetic drift, activation and silencing of genes (Bell *et al.* 2004), but given the mutational power that it has in particular to modifying surface binding proteins, it may also will soon be able to mutate into a more aggressive strains. For this reason, the virus may reach an adaptation after infecting a very high percentage of the population. The issue of the Covid-19 outbreak reminds all countries around the world and health care decision makers that more attention must be paid to health infrastructures. In the meantime, it has again shown to the world that despite many

claims of scientific advancement, there are often still many shortages in the early detection of advertent or inadvertently events. Recalling the need for advanced diagnostic and reference molecular laboratories for monitoring of the infectious diseases in all countries.

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