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Emergent Infectious Disease: Coronavirus COVID-19: The present foe

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Abstract: It wasDecember 31, 2019, when a cluster of patients was observed having pneumonia like symptoms and China informed the World Health Organization of anovel viralpneumoniain sea food market of Wuhan city, in Hubei Province. This pathogenic agent exhibited its high emerging ability and blowout all over the world in a very sort span of time. This newly emerging virus displayed influenza like symptoms along with severe chest pain and sore throat etc. The etiology of these infectionswas a novel coronavirus (2019-nCoV), possibly connectedto zoonotic or environmental exposure from the seafood market in Wuhan. Humantohuman transmission has accounted for most of the infections, including among health care workers.In this review we compared the clinical characteristic, management, outcomes, and infection control practices for patients infected with novel coronavirus (SARS-CoV-2).

Keywords: COVID−19; Pandemic; Therapy; Vaccines

Introduction

Coronavirus(SARS)-CoV2seems to be an emerging pathogen now a days which majorly targets the human respiratory system. Previous versions of coronaviruses (CoVs) known as the severe acute respiratory syndrome (SARS)-CoV and the Middle East respiratory syndrome (MERS)-CoV which have been formerlyreported as a threat to public health(Wu et al., 2020). Initiation, of emergence was from late December 2019, when a cluster of patients was admitted to hospitals suffering from pneumonia like symptoms caused from an unknown agent. These patients were epidemiologically linked to a seafood and wet animal wholesale market in Wuhan, Hubei Province, China. On 11, 2020 world health organization (WHO) informed the world about the onset of a potential Coronavirus outbreak given the estimate of a reproduction number and identified as Novel (New) Coronavirus (COVID-19) (Wit et al., 2020).

Genetic analysis revealed the fact that the virus was closely related to the coronaviruses that had been isolated from bats, but distinct from, severe acute respiratory syndrome coronavirus (SARS-CoV)(Huang et al., 2020). On 2nd January 2020 WHO, announce the health recommendation basses on the knowledge occupying from the previous outbreaks of corona caused by the SARS-CoV and Middle East respiratory syndrome coronavirus (MERS-CoV) (WHO, 2020). Moreover, researches conducted in the past several months suggested major differences between the outbreaks and characteristics of COVID-19 compared with those of SARS-CoV.It is difficult to estimate the case fatality ratio as at initial times symptomsincluded severe pneumonia but its now adjusted tomild clinical presentation as well as asymptomatic in most of the cases. The fatility rate of SARS CoV2 is lower than that for SARS (10%) and MERS (Peng et al., 2020). The actual case fatalityratio of infection with COVID-19 will eventually bebased on all clinical illness and at the time of writinginformation on subclinical infection is not availableand awaits the development of serological tests andsero-surveys.At present, emergence of COVID-19 seems to spread through contact from person to person using the exact mechanism as found during common cold or influenza viruses—for instance, sneezeing or coughing, face to face contact, larval secretionsof infected patients (Chen et al., 2020).

However, worldwide lock-down creates a positive impact and slowed international spread of COVID-19,but, the effect is expected to be short-lived (WHO modelling group). Efforts are currently underway all over the world to control the spreading of corona to interrupt potential transmission chain including banned on public transports, gathering and traveling modes to reduce the risk of infection (WHO,2020; Benvenuto et al., 2020).In this manuscript we first compared the clinical characteristics and symptoms of patients infected with coronavirus (SARS, MERS and SARS CoV2) (Table 1). We subsequently reviewed our current understanding of the risk factors, diagnosis, infection control practices, and management of patients with CoV2 due to endemic HCoVs and the 2019-nCoV or SARS-CoV-2.

Table 1. Comparison among outbreaks of severe acute respiratory syndrome (SARS), Middle East respiratory syndrome (MERS) and COVID−19, causing respiratory syndrome.

	SARS	**MERS**	**NOVEL CORONA**	**Reference**

Global Impact	26 countries	27 countries	168 countries*	(Peng et al., 2020)
Origin	Guangdong, China	Jeddah, Saudi Arabia	Wuhan, China	(WHO, 2003,2015,2020)
Group	*Beta*	*Beta*	*Beta*	(Peng et al., 2020)
Confirmed cases/Fatality rate (%)	8096/10%	2494/ 37%	266079*/ 4.20%*	(WHO, 2003,2015,2020)
Incubation period	2-11 Days	2-13 Days	2-14 Days	(Su et al., 2016)
Transmission	Bat→Palmcivet cat →human	Bat→Camel→human	Unknown	(Su et al., 2016)
Symptoms	Fever, myalgia, Headache , chills, dyspnea, malaise, non-productive cough, respiratory distress, diarrhea	Fever, cough, chills, Sore throat, myalgia, arthralgia, diarrhea, pneumonia, vomiting, acute renal impairment	Fever, common cold, myalgia, fatigue headshake, nausea, vomiting, diarrhea	(Peng et al., 2020)

* Number will most likely continue to change until all infected persons recover.

Structural difference between COVID−19 and other human coronavirus

According to the Chinese Center for Disease Control and Prevention, the structural similarities and dissimilarities in novel coronavirus (COVID−19) genomes have been detected by the researchers as compared to the genomes or other known viruses including SARS-

coronavirus(Chu et al., 2020). The researchers identified the differences in the genome of 29,800 nucleotides sequences which differ by 5 nucleotides. Fourteen open reading frames have also been detected which possibly encode 27 proteins. Previous literature suggested that the difference between four structural and eight accessory proteins might be responsible for the pathogenicity of novel coronavirus(Gorbalenya et al., 2020; Hoek et al., 2004). Wu et al., 2020describedthe relatedness between highly conserved proteins of all coronaviruses, while, accessory proteins are generally unique to each specific group of coronaviruses. The sequence of amino acidsdemonstrated the possible connection of COVID−19 to the SARS-like coronaviruses and more distant relation to SARS coronavirus'. The scientific community stated that the structure of COVID−19 is most closely resembled to bat SARS-like coronaviruses from which SARS-CoV evolved. However reported sequence results indicated the fact that present COVID-19 is not structurally related to MERS coronaviruses. Since the information of COVID−19 is limited, it is difficult to infer the functional significance of the amino acid substitutions between COVID−19 and the SARS as well as SARS-like CoVs. The researcher community fails to find a single bat SARS-like coronavirus which exactly have the same sequence of accessory proteins similar to new coronavirus. Instead, some COVID−19 proteins are more like those of bat SARS-like Coronaviruses. However, accessory proteins (3a and 8b) are analogous to SARS-CoVs. Nonetheless, the systems on how the novel Coronaviruses has changed and adjusted its characters over its short history in people are the focal point of future examination(Huang et al., 2020).

Pandemiology of COVID−19 outbreak

Some of the confirmed cases have no epidemiological link to wet markets, suggesting the possibility of human-to-human transmissions and/or multiple spill-over events in different settings(Chu et al., 2020), resulting in the prevalence of outbreak i.e. more relative studies with bigger population have been reported(Li et al., 2020b). Indeed the major dispersion of COVID−19 outbreak has recalled the reminiscences of the severe acute respiratory syndrome (SARS)–coronavirus (CoV) outbreak, which started 17 years ago(Zhong et al., 2003; N. Zhu et al., 2020). The epidemic of 2019 novel coronavirus (now called SARSCoV-2, causing the 'coronavirus disease 2019', i.e. COVID−19) has expanded from Wuhan (China) and later on

exported to about 200 countries, some of which have seen onward transmission. Early in an epidemic, counting the total number of confirmed cases, comprising mild cases, is required to standardize the epidemic response. On the other hand, case fatality and hospitalization ratios are often used to assess impact with some cautions (Figure.1). These measures should be interpreted carefully, as patients may take time to developed serious symptoms, or could die (WHO, 2020). Therefore, it may not be possible to exactly estimate the ratio of infected cases in order to calculate those ratios. The first confirmed case of COVID−19 to be observed in China were severe enough to come to medical attention and result in testing, but the total number of people infected has been elusive due tolack of severe disease manifestations as many infected people remain asymptomatic or mildly symptomatic, which consequently affects the ability to identify the chains of transmission and subsequent contacts.The projected case mortality ratio among medically attended patients thus far is varying from region to region (Figure 2). The quantification of persons infected can be deceptive pointers of the epidemic's trajectory if these counts are limited by problems in access to care or bottlenecks in laboratory testing, or if only patients with severe cases are tested.

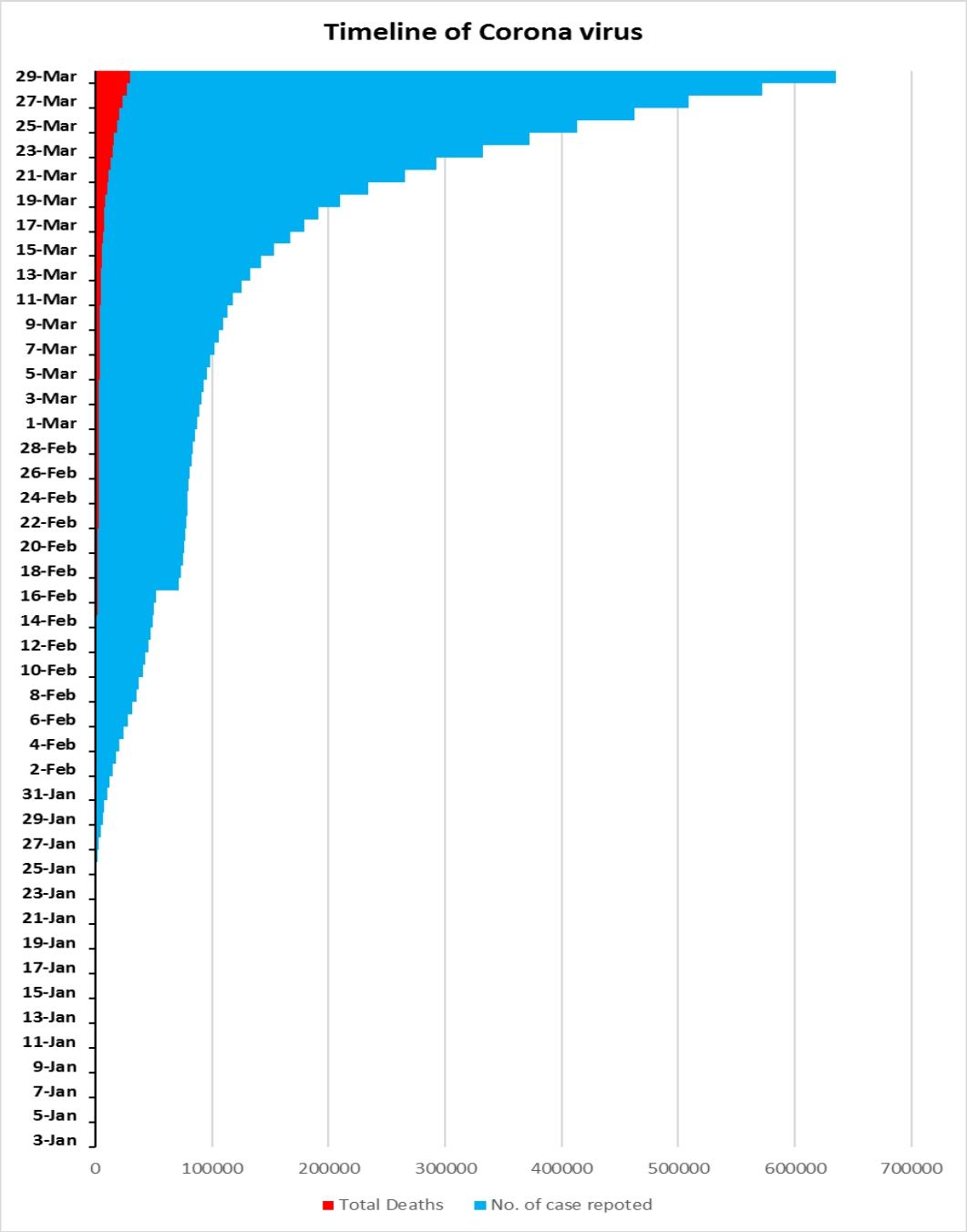

Figure 1: Date wise baseline of COVID−19 all over the world with confirmed cases and number of deaths.

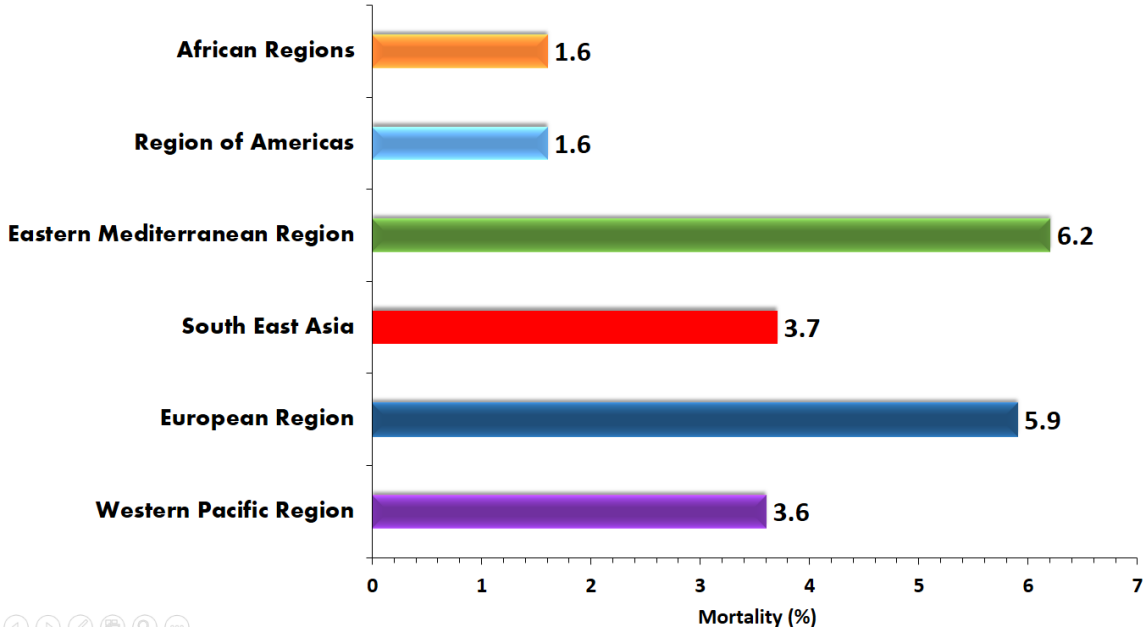

Figure 2: Mortality by COVID−19 in various regions of the world (WHO, 2020). The data represents the value of death percentage till March 29, 2020. The average percent of the regions may increase with an increase in time due to the huge emergence of Covid-19

Therapy/Treatment option

At the early age of infection, the majority of the proposed therapies for Covid-19 was based on the knowledge from the outbreaks of SARS-CoV and MERS-CoV in 2003 and 2012, respectively. Popular treatment options available to treat the disease includes antiretroviral therapy along with antibiotics such as ribavirin, lopinavir/ritonavir, steroids, interferon, and macrolides. As per the emergence increased antiviral therapy refused to give desirable results. Howerver, Remdesivir is a novel nucleotide analogue with activity against SARS and MERS-CoV in vitro and in animal studies and utilized as a compassionate use investigational drug in the first described US case of 2019-nCoV in January 2020. The patient who had mild symptoms showed rapid improvement after treatment with remdesivir. On the other hand, hydrochloroquine was also used on worldwide scale for the treatment of corona virus. However, world scie Investigators from the National Institute of Allergy and Infectious Diseases (NIAID) are preparing to test remdesivir, as well as lopinavir/ ritonavir (Kaletra), and interferon-beta for their activity against 2019-nCoV. However, the success rate is not satisfactory yet. Scientist all over

the world are busy to serach vaccine/treatment option for corona virus. The experimental experimental vaccine will be ready for testing in a phase 3 trial in the coming months to introduced vaccines in the market.

Conclusion

Epidemiologic data on the pathogenicity and contagiousness of this infection got by methods of molecular recognition. Additionally, the penchant of novel Covids to spread in medical care places shows a requirement for fringe medical care offices to be on reserve to distinguish likely cases too. Furthermore, expanded readiness is required at animal markets and other places, while the conceivable source of this arising infection is being explored. In the event that we are proactive in these manners, maybe we will never need to find the genuine pestilence or pandemic capability of 2019-nCoV. However, optimal implementation of controlling practices is a prerequisite requirement for present time to control the emergence in the community and hospital setting.

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