

Review: COVID- 19, Again Zoonotic Disease Emerging!

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ABSTRACT

Zoonotic, animal sources of diseases and animal are also benefits to people like food, fiber, livelihoods, travel, sport, companionship. Pandemics of various infectious diseases sources are virus based. Ebola virus (EBOV) belongs to the family Filoviridae. Severe Acute Respiratory Syndrome (SARS), On March 30, 2013, a novel avian influenza A H7N9 virus causing human infections was identified in China, Nipah virus-like severe acute respiratory syndrome coronavirus, HIV, and highly pathogenic avian influenza. Currently COVID-19 disease emerging.

KEYWORDS : Zoonotic, Pandemics, Evola, Severe Acute Respiratory Syndrome (SARS), Avian influenza, Nipah.

INTRODUCTION

Animals provide many benefits to people like food, fiber, livelihoods, travel, sport, companionship, and education for people across the globe. Millions of peoples of world have one or more pets. We might come into contact with animals in either urban or rural settings, during travel, while visiting animal exhibits, or while enjoying outdoor activities. However, animals can sometimes carry harmful germs that can spread to people and cause illness - these are known as zoonotic diseases or zoonoses. Zoonotic diseases are caused by harmful germs like viruses, bacteria, parasites, and fungi. These germs can cause many different types of illnesses in people and animals, ranging from mild to serious illness and even death.

Pandemics of various infectious diseases with millions dying have been recorded in the history for the past several centuries. The most well known in the history have been pandemic due to plague^[1] in Asia and several pandemics of influenza that killed millions of people^[2].

The first time a human influenza virus was isolated was in 1934, this virus was given the subtype designation H0N1 (where H is hemagglutinin and N is neuraminidase). The H0N1 subtype persisted until 1947, when a major antigenic shift generated a new

subtype, H1N1, which replaced the previous subtype and became prevalent worldwide until 1957, when H2N2 emerged. The H2N2 subtype prevailed for the next decade and was replaced in 1968 by H3N2. Antigenic shift in 1977 saw the re-emergence of H1N1. The most recent antigenic shift, in 1989, brought the re-emergence of H3N2, which remained dominant throughout the next several years. However, an H1N1 strain re-emerged in Texas in 1995, and current influenza vaccines contain both H3N2 and H1N1 strains. [www.whfreeman.com/immunology]

There are so many epidemic zoonotic diseases are transmitted to the world time to time like Ebola, SARS, MERS, influenza and Nipah.

EBOLA

Ebola virus (EBOV) belongs to the family Filoviridae, the genus Ebolavirus, and frequently causes fatal infection in humans^[3]. EBOV disease (EVD) may show multiple, serial, and nonspecific-disease symptoms including high fever, headache, vomiting, anorexia, diarrhea, and aching muscles^[3-6]. Unexplained bleeding in the eyes, nose, gums, and gut occurs in the advanced stages^[3-6]. The first outbreak of EVD was reported in 1976 in the Democratic Republic of the Congo^[7]. Since then, there have been reports of small EVD outbreaks in some countries in Central Africa, including Sudan and Uganda^[3,8], with an estimated 2350 cases of EVD occurring between the 1970s and 2013. The disease can therefore be regarded as endemic to some areas of Central Africa.

In March 2014, an outbreak of EVD was reported for the first time in West Africa, in Guinea, and it spread rapidly to neighboring countries including Liberia and Sierra Leone, creating a serious epidemic^[9]. This has caused major health concerns both in and beyond the region, with the World Health Organization (WHO) and numerous countries initiating health monitoring and containment measures^[10, 11].

Ebola virus (EBOV) and Marburg virus (MARV), are known as emerging and re-emerging zoonotic pathogens causing acute hemorrhagic fever with a high case-fatality rate in humans (up to 90%)^[12]. Ebola hemorrhagic fever (EHF) was first reported in 1976 during the Ebola outbreak in the Democratic Republic of the Congo (formerly Zaire), and the virus is named after the Ebola River where it was discovered. Uganda in 2000-2001 caused by Sudan virus (SUDV). This outbreak resulted in 425 cases, of which 216 were laboratory confirmed, and the overall case fatality rate was 53%^[13]. Historically, this strain has caused the highest mortality (90%), while the current estimate of case fatality rate is less than 60%^[14].

The majority of cases are between 15 to 44 years old (49.9% male). In terms of reported morbidity and mortality, the EVD epidemic is much greater than all previous outbreaks combined. The real number of those who have been infected and died is likely much higher^[15].

SEVERE ACUTE RESPIRATORY SYNDROME (SARS)

On 11 February 2003, an unidentified agent had caused some 300 cases of pneumonia in persons in the south of China. On 12 March 2003, the World Health Organization (WHO) issued a global alert regarding these and similar cases in Hong Kong and Vietnam. This clinical syndrome subsequently became known as "severe acute respiratory syndrome" (SARS). Since then, 8098 people in 26 countries have had probable SARS diagnosed, 774 of whom have died, yielding a global case-fatality rate of ~10%^[16, 17]. On 5 July 2003, the WHO reported that the last known human chain of transmission of SARS had been broken^[18].

World Health Organization (WHO) to facilitate the identification of the causative agent of SARS. Pathogen of SARS has been identified, by experimental proof and by Koch's postulates, as a new coronavirus, a single positivestrand RNA virus^[19-21]. The whole genome of SARS coronavirus was first sequenced by the British Columbia Centre for Disease Control (CDC) in Canada on 23, April 2003^[22], and subsequently a total of 16 SARS coronavirus strains isolated from Hanoi, China, Hong Kong, Singapore, and Taiwan were sequenced within short time^[23, 24]. Phylogenetic analysis and comparative genomic studies based on these genomic sequences indicate that the SARS coronavirus is distinct from any of the previously characterized coronaviruses^[25].

AVIAN INFLUENZA

On March 30, 2013, a novel avian influenza A H7N9 virus causing human infections was identified in China^[26]. As of April 18, 2013, the virus had spread to six provinces and municipal cities, likes Shanghai, Anhui, Jiangsu, Zhejiang, Beijing, and Henan. To our knowledge, this outbreak represents the first time that the H7N9 subtype has infected people and caused fatal cases (as of April 18, 2013, 87 people have been infected and 17 have died). In modern times, H7 subtype avian influenza viruses, including H7N1, H7N2, H7N3 and H7N7, have caused more than 100 human infections, including a fatal case in the Netherlands^[27-29]. In wild birds, H7 and N9 avian influenza viruses have evolved to American, Oceanian, and Eurasian lineages^[30, 31].

Emerging infectious diseases (EIDs) are a significant threat to public health globally^[33]. Of those diseases considered to be emerging, approximately 75% are zoonotic (ie, are able to naturally be transmitted between animals and humans)^[34]. Zoonotic EIDs, anthropogenic land use changes and other factors that affect the contact between animals and humans are particularly important^[38, 39]. Deforestation, agricultural expansion, global travel, trade in wildlife, and other anthropogenic factors can lead to increased interaction among humans, domestic animals, and wildlife, increasing the opportunities for pathogens to be exchanged among these groups^[40]. Because of this close connection among the

environment, humans, domestic animals, wildlife and their pathogens, a broad ecologic perspective is useful to understand the reasons for zoonotic disease emergence.

NIPAH VIRUS

Nipah virus-like severe acute respiratory syndrome coronavirus, HIV, and highly pathogenic avian influenza-is a salient example of a wildlife pathogen that emerged in human populations causing a lethal disease. Nipah virus is a recently discovered paramyxovirus belonging to a new genus (Henipavirus) within the family Paramyxoviridae (Order: Mononegavirales, subfamily Paramyxovirinae)^[41]. The first member of this genus to emerge was Hendra virus in 1994 in Australia^[42]. Nipah virus caused a large outbreak in humans in Malaysia during 1998 to 1999 and is responsible for five subsequent outbreaks in Bangladesh between 2001 and 2005^[43, 44, 45]. Both viruses appear to have fruit bat (*Pteropus* species) reservoirs^[46, 47], and both initially emerged via domestic animal amplifier hosts (horses for Hendra virus; pigs for Nipah virus), although some of the recent outbreaks in Bangladesh may have involved direct transmission between bats and humans.

SARS CoV-2 (COVID-19)

Currently transmitting COVID -19 to whole of the world from Wuhan. The most developed country like US, UK, Germany, Italy, France and developing country India also affected with this nCoV (new coronavirus), COVID-19.

Wuhan, city of glove where a lots of pneumonia cases found. After examination, doctor's examined that patients caused by a newly identified Coronavirus on 31December 2019. This coronavirus, was initially named as the 2019-novel coronavirus (2019-nCoV) on 12 January 2020 by World Health Organization (WHO). WHO officially named the disease as coronavirus disease 2019 (COVID-19) and Coronavirus Study Group (CSG) of the International Committee recommended name the new Coronavirus as SARS-CoV-2. The scientists of China quickly isolated a SARS-CoV-2 from a patient within a short period of time on 7 January 2020 and done sequencing of the genome of SARS-CoV-2^[48]. At present, as of 13 April 2020, a total of 1872916, cases of COVID-19 have been confirmed in all over World including 116037cases of death, time 17:58:12 IST and in India a total confirmed cases is 9352 and 324 death cases (ministry of health India) at 7 April 2020 17:58:12 IST.^[49].The epidemic COVID-19 steadily spreading by human-to-human transmission but it is Zoonotic.

The genomic sequence reveled that SARS-CoV-2 is 96.2% identical to a bat CoV RaTG13, shares 79.5% identity to SARS-CoV. On the basis of sequencing results and evolutionary analysis, bat has been suspected as natural host of virus origin, and SARS CoV-2 might be transmitted from bats via unknown intermediate hosts to infect humans. It

is clear now that SARS-CoV-2 could use angiotensin-converting enzyme 2 (ACE2), the same receptor as SARS-CoV^[50], to infect humans.

Human-to-human transmission of SARS-CoV-2 occurs mainly between family members, including relatives and friends who intimately contacted with patients or incubation carriers. It is reported that 31.3% of patients recent travelled to Wuhan and 72.3% of patients contacting with people from Wuhan among the patients of nonresidents of Wuhan. Transmission between healthcare workers occurred in 3.8% of COVID-19 patients, issued by the National Health Commission of China on 14 February 2020. By contrast, the transmission of SARS-CoV and MERS-CoV is reported to occur mainly through nosocomial transmission. Infections of healthcare workers in 33-42% of SARS cases and transmission between patients (62-79%) was the most common route of infection in MERS-CoV cases. Direct contact with intermediate host animals or consumption of wild animals was suspected to be the main route of SARS-CoV-2 transmission. However, the source(s) and transmission routine(s) of SARS-CoV-2 remain unclear.

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