Review Article

Emerging and Re-Emerging Virus

Dharsan.R[1], R.V.Geetha[2], Lakshmi.T[3]

[1]Research Associate, Dental Research Cell, Saveetha Dental College and Hospitals, [2]Associate Professor, Department of Microbiology, Saveetha Dental College and Hospitals, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai, India, [3]Associate Professor, Department of Pharmacology, Saveetha Dental College, Saveetha University, Chennai, India

Abstract

Infectious diseases remain a major cause of human and animal morbidity and mortality leading to significant healthcare expenditure. However, enormous successes have been obtained against the control of major epidemic diseases, such as malaria, plague, leprosy and cholera, in the past. The vast terrains and extreme geo-climatic differences and uneven population distribution present unique patterns of distribution of viral diseases. Dynamic interplay of biological, socio-cultural and ecological factors, together with novel aspects of human-animal interphase, pose additional challenges with respect to the emergence of infectious diseases. The important challenges faced in the control and prevention of emerging and re-emerging infectious diseases range from understanding the impact of factors that are necessary for the emergence, to development of strengthened surveillance systems that can mitigate human suffering and death. Viral pathogens are known to cause outbreaks that have epidemic and pandemic potential which would result in severe range of mortality and Health care expenditure on a scale depending on the pathogenicity of the virus.

Keywords*: Avian influenza - CCHF - emerging infections - Nipah virus - COVID-19- Respiratory viral infections - re-emerging virus - rotavirus - viral diseases*

Introduction

The emergence of new human pathogens and the re-emergence of several diseases in the current decade are of particular concern.[1] Emerging pathogens may be described at a basic level as those diseases whose occurrence has been shown to have risen in recent decades or that have threatened to increase in the future. Several factors underlie the emergence of such diseases, including population growth, poverty and malnutrition, increased domestic and global connectivity, economic factors leading to population migration, the prevalence of immuno-suppressive diseases in social practices, unplanned urbanization, deforestation and changes in agricultural practices such as mixed agriculture.[2] Genetic variations in infections were also responsible, to some degree, for these outbreaks. It is estimated that about 60% of infectious diseases and 70% of emerging human infections are of zoonotic origin, two-thirds of which arises from wildlife, like COVID-19.[3] Habitat destruction due to unplanned urbanization has placed human at contact with animals and arthropod vectors of viral infection.[4] Such interactions have been one of the major causes for increased human susceptibility to infections by novel pathogens, in the absence of specific immunity in these population.[5]

Respiratory viral infections, arboviral infections and bat-borne viral infections represent three major categories of emerging viral infections.[6] Infection aerosols of the tracheo bronchial tree represent efficient means for spread of viral pathogens affecting the respiratory tract. Pandemic influenza H1N1, highly pathogenic avian influenza (A1) injection (H5NI) and the Middle East respiratory Syndrome coronavirus (MERS-CoV) also

Corresponding author*
R.V.Geetha
Associate Professor, Department of Microbiology
Saveetha Dental College and Hospitals
Saveetha Institute of Medical and Technical Sciences,
Saveetha University, Chennai, India.
Email : geetha@saveetha.com
Phone number: +91- 97104 56203

the COVID-19 pathogen that pose severe threat in this category.[7] Arthropod -borne viruses have constantly been the reason for emerging and re-emerging disease including Crimean - Congo hemorrhagic fever (CCHF), dengu , chikungunya, encephalitis. Severe and major arboviral pathogens of human belong to the three genera of Flavivirus, Alphavirus and Nairovirus.[8]

Several bat-borne viruses have also come into prominent notice, best exemplified by Nipha virus disease, COVID- 19 severe fever with thrombocytopenia virus (SFTV), as well as Ebola virus disease.[9] Theme of re-emergence of the virus is often seen in a more virulent forms following their initial discovery.[10] There have also been cases of discovery of novel pathogens in the country, the example include CHPV, CCHP and KFD virus in the 1950s-196 but their pathogenic and public health significance Remained unexplored for a long time.[9,11] Several of these infections to take a heavy toll on the animal and agricultural industry. [12]The economic costs associated with such infections can be heavy as can be inferred from the high cost of medical and intensive care, days of productive work lost, impact on travel and tourism ban on export of agricultural produce and products from affected regions. The major emerging and re-emerging viral infections of public health importance have been reviewed that have already been included in the Integrated Disease Surveillance Programme so that control and prevention of emerging and re-emerging infectious diseases could be handled through understanding the impact of factors that are necessary for the emergence and to develop and strengthen surveillance systems that can mitigate human suffering and death.

Material and Methods

Article collection for this systematic review was collected and analysed from the PMC database, Mediline embrace Cochrane. Necessary articles selected based on this importance to this review article on emerging and re-emerging viral threat. From which 30 articles were reviewed and selected using scholarly search engines of PubMED & Google,Inc.

Emerging Viral infections identified as public health threats

Viral pathogens are known to cause outbreaks that have epidemic and pandemic potential. [13,14]Integrated Disease Surveillance Programme (IDSP) is a laboratory-based, IT enabled system in the country for Surveillance of epidemic prone disease. During 2017, the IDSP showed a total of 1683 outbreaks of such disease of which 71 % of those outbreaks were caused by viral pathogens while the rest 29 % were non-viral. Subclinical and sporadic infection as well as those not identified by the health facility are often missed by the surveillance system.[4,13]

Impact of Mass gatherings and emerging viral infections

Mass gathering opportunities create situations for human proximity within very close distances and the challenges they present to the maintenance of sanitation, a considerable public health concern. Transmission of respiratory and gastrointestinal infection remains a major concern during several large-scale assemblies, for example outbreak of cholera at Kumbh Mela festival in 1817. [15]Large scale gatherings provide platforms for exchange of genomic material and thereby evolution of pathogens, including viruses.[1617]

Nosocomial Transmission and Emerging infection

Institutional care of vulnerable people with compromised immune systems may present opportunities for transmission of viral infection.[16,18] Appreciable risks also exist at dental clinics, haemodialysis units etc. where sterilization/disinfection practices for patient care instruments are not followed stringently. Hospital-associated transmission of infection was a prominent finding during the outbreak of Nipah infection in Bengal and Kerala, where several health care staff fell victims to the infections.[19]

Laboratory Accidents/Lapses in Biosafety practices

There is a current investigation going on at WHO regarding the outbreak of COVID-19 at Wuhan, China. Several experts believe that the initial outbreak of COVID-19 is from the Wuhan Institute of Virology, a microbiology laboratory under the Chinese Academy Science and investigations are ongoing.[20,21] Neglect of laboratory biosafety requirements as well as laboratory accidents may also lead to the occurrences of emerging/ re-emerging infections. Recently there was a report on the development of buffalopox (BPX) lesions on the

palm of a biomedical researcher following a shrapnel injury, warranting surgical treatment and leading to delayed healing.[22] Such reports, through infrequent emphasize the need for stringent adherence to biosafety guidelines to be observed in research involving viral agents with human pathogenic potential.[23]

Current Scenario of Emerging Viral Infections

Despite an elaborate armamentarium to tackle microbes, emerging infectious diseases remain a crucial global challenge. Emerging infections can have a significant impact on human well being and can cause gigantic monetary misfortunes. Expanded checking and reconnaissance by associations, for example, the U.S. Centers for Disease Control and Prevention(CDC)and the World Health Organization (WHO), and a few other distributed reports of cases, outbreaks and pandemics have identified numerous unrecognized viral pathogens developing globally with increasing frequency. Historically, Asia is believed to be the epicentre of several emerging viral diseases, (2 influenza pandemics in the previous millennium, SARS in China, avian influenza in Hong Kong etc.) that are of significant global public health importance. Acute respiratory disease claims over four million deaths every year and causes millions of hospitalization in developing countries every year. Over 200 viral pathogens, belonging to the families Orthomyxoviridae, Paramyxoviridae, Picornaviridae, Coronaviridae, Adenoviridae and Herpesviridae cause respiratory infections in humans. Influenza, parainfluenza, respiratory syncytial virus (RSV) and adenoviruses remain important respiratory pathogens. Human meta pneumovirus has been recognised worldwide as a pathogen of significance.[24]

COVID-19:

Coronavirus disease 2019 (COVID-19) is characterized as illness caused by a novel coronavirus now called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; once in the past called 2019-nCoV), which was first distinguished amid an outbreak of respiratory illness cases in Wuhan City, Hubei Province, China. It was initially reported to the WHO on December 31, 2019. On January 30, 2020, the WHO declared the COVID-19 outbreak a global health crisis. On March 11, 2020, the WHO declared COVID-19 a global pandemic, its first such designation since declaring H1N1 influenza a pandemic in 2009. [25] [26]

Illness caused by SARS-CoV-2 was named COVID-19 by the WHO, the acronym got from "coronavirus disease 2019. " The name was picked to avoid stigmatizing the infection's causes as far as populations, geography, or animal associations. [20]

Influenza:

Influenza infections having a place with the orthomyxoviridae family are the incessant causes of epidemics and pandemics affecting humans. Influenza pandemics have happened earlier in 1918 swine influenza 1957 Asian flu 1968 Hong Kong flu 1977 Russian flu and the recent pandemic of 2009 pandemic influenza a H1N1 influenza infection type an is exceptionally variable shows consistent antigenic variation and is a major cause of pestilences and pandemics. The surface antigenic glycoproteins undergo two major kinds of antigenic variation viz. Antigenic shift and antigenic drift. Antigenic shift is the consequence of major changes in one or both the surface antigens [haemagglutinin ha and neuraminidase na] causes occasional pandemics. Three mechanisms may be operative in the antigenic shift leading to development of pandemic influenza strains viz. Genetic reassortment direct transfer from avian/mammalian host to humans and virus recycling. Antigenic drift results because of minor changes in HA or NA and causes frequent epidemics. influenza infections are constantly developing and show universal dispersion in nature animals and humans.[27]

Severe acute respiratory syndrome-associated coronavirus (SARS-CoV):

SARS was first reported in the Guangdong territory of China in February 2003 demonstrating human-to-human transmission. The disease caused an estimated 8000 cases and in excess of 750 deaths in more than 12 countries. The WHO gave a global alert about the disease on March 13, 2003. Although the cases generally remained restricted to China, a couple of cases were accounted for from North and South America, Europe and Asia. No case, be that as it may, has been accounted for from India.[28]

MERS-CoV:

MERS-CoV is a zoonotic viral illness causing respiratory contamination which was first revealed in Saudi Arabia in 2012 and has since spread to 26 unique nations. More than 2207 laboratory-affirmed cases and 787 deaths have happened because of MERS-CoV disease globally, since 2012. The clinical range of illness associated with MERS-CoV ranges from asymptomatic contaminations to acute respiratory distress syndrome, coming about in multi-organ failure and death. The case-fatality rates (CFRs) have remained high at 3-4 for every 10 cases. Limited information as of now exists about the transmission dynamics of this infection, and complete treatment and a prophylactic vaccination remain unavailable till date. Proof for secondary, tertiary and quaternary cases of MERS following from a solitary contaminated patient also exists, even in the absence of mutations conferring hyper-virulence. No case of contamination with this infection has been identified in India up until now. Bats are believed to be the natural supply of this infection, and many patients built up the illness after contact with camels. India is home to a great decent variety of bat species and has a substantial camel population. The nation also reports heavy passenger traffic from the Center East, as part of pilgrimage, work, the travel industry and trade. These facts call for preparedness and surveillance against this infection in the country.[29]

RSV:

RSV is an important pathogen causing acute lower respiratory tract contamination (ALRTI) in small kids. It can also affect more older adults and immuno-compromised individuals. Estimates indicate an annual frequency of approximately 34 million scenes of ALRTI associated with RSV disease in kids aged five years or less.[26] RSV contaminations also lead to about 3,000,000 cases of hospitalization and about 66,000-199,000 deaths, with more than 99 percent of the deaths detailed from growing nation. Considering the general health significance, the WHO has started a pilot venture for RSV surveillance in its six locales, using the entrenched platform of Global Influenza Surveillance and Reaction System. The exact weight and impact of RSV diseases in the nation should be concentrated in depth. [30,31]

Nipah virus: Nipah virus (NiV) and Hendra virus (HeV) are closely related members of the family Paramyxoviridae and are included in a new genus, Henipavirus. Nipah virus, a zoonotic paramyxovirus, is an emerging virus endemic in Southeast Asia. Beginning in September 1998 a major outbreak of disease in pigs and human beings appeared in the northern part of peninsular Malaysia, resulting in 265 infected individuals and 105 deaths, most of whom were farmers or abattoir workers who had come in close contact with infected pigs. Nipah virus associated encephalitis outbreaks with a high mortality occurred in Bangladesh between 2001 and 2007. A similar outbreak which was retrospectively identified to be due to Nipah virus was reported in 2001 from Siliguri, West Bengal, not far from Bangladesh. It has a unique genetic signature and may have co-evolved within local natural reservoirs. Patients usually present with fever, malaise, headache, myalgia, sore throat, nausea and vomiting, sometimes accompanied by vertigo and disorientation. Severe cases progress to encephalitis, which may be complicated by seizures and coma. Procedures for the laboratory diagnosis of Nipah virus include serology, histopathology, PCR and virus isolation.

Hantavirus:

The occurrence of 'hantavirus pulmonary syndrome' in 1993 in the Southwestern United States due to the emergence of a disease caused by viruses known for decades, was attributed to the relatively abrupt and short-lived weather changes due to the El Nino effect. The El Nino effect provoked heavy rainfall across the southern states in the US, leading to proliferation of vegetation and consequently the rodent population, the natural hantavirus hosts which are asymptomatic carriers of the virus. As the population of rodents, especially deer mice (Peromyscus maniculatus) exploded and they sought food and shelter in human dwellings, people were exposed to the aerosolized animal droppings, urine and saliva, which lead to the infection. The outbreak has continued since and by December 1, 2009, a total of 534 cases of hantavirus pulmonary syndrome with 36% mortality have been reported in the United States. Hantaviruses are the most widely distributed zoonotic rodent borne viruses known to cause two significant clinical syndromes-haemorrhagic fever with renal syndrome (HFRS) and Hantavirus pulmonary syndrome

(HPS), also referred to as Hantavirus cardiopulmonary syndrome (HCPS). Hantaviruses belonging to the family Bunyaviridae, genus Hantavirus are enveloped RNA viruses and currently up to 22 species and more than 30 genotypes have been Described. There are no specific antiviral drugs for treatment of all hantavirus infections. Ribavirin used in clinical trials in China for HFRS has been reported to cause significant reduction in fatality. Prevention of exposure to rodent excreta is the best preventive strategy

Ebola:

Ebola hemorrhagic fever is a viral disease caused by Ebola virus (a member of the Filoviridae family or filoviruses) that results in nonspecific symptoms (see symptom section of this article) early in the disease and often causes internal and external hemorrhage (bleeding) as the disease progresses. Ebola hemorrhagic fever is one of the most life-threatening viral infections; the mortality rate (death rate) may be very high during outbreaks (reports of outbreaks range from about 25%-100% of people infected, depending on the Ebola strain). Because most outbreaks occur in areas where high-level intensive care supportive public health services are not available, survival rates are difficult to translate to potential outbreaks in Ebola-affected areas with more resources. Ebola viruses are highly contagious once early symptoms such as fever develop. The infected patient sheds infectious viruses in all body secretions (bodily fluids); direct contact with any of these secretions may cause the virus transmission to uninfected individuals. Definitive pathogenesis of EVD is still unknown due to the lethal nature of the virus and rarity of human studies. Concurrent transmission of EVD occurs through two main routes; animal-to-human and human-to-human contacts. The early clinical diagnosis of EVD is challenging due to the vague presentation that usually overlaps with multiple differential diagnoses, including malaria, dengue fever, typhoid fever, meningococcemia, and other bacterial infections.[32]

Management of viral infection

Many viral infections resolve on their own without treatment. Other times, treatment of viral infections focuses on symptom relief, not fighting the virus. For example, cold medicine helps alleviate the pain and congestion associated with the cold, but it doesn't act directly on the cold virus.

There are some medications that work directly on viruses. These are called antiviral medications. They work by inhibiting the production of virus particles. Some interfere with the production of viral DNA. Others prevent viruses from entering host cells. There are other ways in which these medications work. In general, antiviral medications are most effective when they are taken early on in the course of an initial viral infection or a recurrent outbreak. Different kinds of antiviral medications may be used to treat chickenpox, shingles, herpes simplex virus-1 (HSV-1), herpes simplex virus-2 (HSV-2), HIV, hepatitis B, Hepatitis C and Influenza.[33]

Vaccines can reduce the risk of acquiring some viral illnesses. Vaccines are available to help protect against the flu, hepatitis A, hepatitis B, chickenpox, herpes zoster (shingles), cancer-causing strains of human papillomavirus (HPV), measles/mumps/rubella (MMR), polio, rabies, rotavirus, and other viruses. Vaccines vary in effectiveness and in the number of doses required to confer protection. Some vaccines require booster shots to maintain immunity.

Conclusion

The earth of extreme geo-climatic diversity, faces a constant threat of emerging and re- emerging viral pathogens of public health importance. There is a need for strengthening disease surveillance in the world focusing on the epidemiology and disease burden. There is also a pressing need to gain detailed insight into disease biomics, including vector biology and environmental factors influencing the diseases. It is also important to strengthen the emergency preparedness for these diseases and response by focusing on 'one health' approach.

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