Factors Contributing to Emergence of infectious viral diseases in India: Issues and Challenges after COVID-19 Pandemic

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Abstract

Emerging and re-emerging viral infections are major cause of morbidity and mortality in humans and animals. India had experienced numerous infectious disease outbreaks and epidemics in past years. However, tremendous strides have been achieved in the past in the fight against serious epidemic diseases. It has been found that a wide range of complex factors, such as pathogen evolution, human invasion, commerce in wild animals, microbial adaptation, changes in the environment and dynamic interactions between humans and animals influence the emergence and transmission of infectious viral diseases. As the COVID-19 pandemic demonstrated, India's secondary and tertiary health-care system is quite advanced. The study of infectious diseases, in particular their pathogenesis, genetic profile and diagnosis has fundamentally changed with the advent of genome sequencing and nucleic acid detection technology. Additionally, advance therapy and vaccination led to best possible patient management and care. Further scientific investigations and research are needed to discover neglected diseases that have the potential to cause epidemics as well as to develop updated vaccines, modern treatment strategy and diagnostics at molecular level. This evaluation will aid for policymakers, academics and researchers to redesign the course of action to combat the deadly emerging pathogenic viruses and also preserve the ecosystem.

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I. Introduction

COVID-19 was latest example of an unexpected, novel, and devastating pandemic viral disease with high mortality rate throughout the globe. The pandemic had far-hitting consequences on individuals, communities, health systems, and economies particularly in low and middle- income countries such as India. It comes up as a major challenge not just for the medical and research community but for the entire world to think about the emerging or re-emerging infections. Our ecosystem specially human and animal health have significantly affected by emerging infections since ancient times. Emerging and/or re-emerging infections can be defined as novel etiological agents that have newly appeared in a geographic range or have existed previously but rapidly increasing in incidence or found to be increased in the future (1,2).

The crisis of COVID-19 pandemic has affected every sector of our society and the public health system underwent many changes during this period. India has developed primary to tertiary level health-care infrastructure and well-managed the overall situation within a short period of time. To control the COVID-19 virus from spreading, other countries and India imposed a series of lockdowns followed by gradual unlock-down cycles which took place nationwide with imposes huge costs on communities, health systems, and economies (3). Middle of the year 2022 onwards life has come to normal though economy and social consequences still under threat. From a public health point of view, it is right time for constructive analysis of countries health scenario and to find out the factors responsible for an outbreak of emerging or re-emerging diseases. This review will help policymakers, healthcare professionals, program implementers, academicians and researchers to redesign the course of action to tackle the deadly emerging pathogenic viruses as well as to save the ecosystem.

As per past studies, 1415 microbial diseases affecting humans including 217 viruses, 538 bacteria and rickettsia, 307 fungi, 66 protozoa, 287 helminths (4). It is estimated that nearly two-thirds of common human

infectious diseases arise from pathogens shared with wild or domestic animals, is called zoonotic infection and up to 75% of it regarded as "emerging" human pathogens (4-6). Domestic animals, poultry, livestock and wildlife are the main souce of zoonotic viral infections. When the pathogen from an infected animal enters a human host, the phenomenon is called zoonotic spillover. This process can take place either directly from a natural reservoir or an intermediate animal host or indirectly from pathogens in the environment (7-9). Most of the cases humans can be called dead-end hosts. The best exemplified by arboviral infections such as Chikungunya, Dengue and Zika outbreaks in tropical and sub-tropical regions and the influenza with SARS, MERS outbreaks across the globe (2,10).

II. Transmission

Human get infected by various modes of contact with an infectious etiological agent. Viruses, bacteria, fungi, protozoa, and helminths are five major infectious agents have been recognized so far (11,12). Transmission process includes a certain level of host pathogen interaction, contact and/or spillover between reservoir specimens with the native host and also through various environmental factors (13,14). Pathogenic viruses go through various stages of adaptation to infect its host. A virus must first enter cells at a body surface of the host, it include the mucosal linings of the respiratory, alimentary, urogenital tracts, conjunctival membranes or cornea (the outer surface of the eye) and the skin. Most common zoonoses happening indirectly, e.g. through insect vectors or, more frequently, via the food system (15). Many living organisms that can transmit infectious pathogens from a reservoir to a host (between humans, or from animals to humans) are called vectors. Vectors are generally from arthropods, and particularly mosquitoes, ticks, sand flies and biting midges that ingest disease-producing pathogens during a blood meal from an infected host (human or animal) and later transmit it into a new host (16). Birds and Bats are also important reservoir hosts of emerging viruses (17). In bats, up to 66 distinct viruses have been identified and some of them can cause severe disease in human (17). As per study, a range of 5 to 31 zoonotic viruses shared with human by domestic animal species whereas wild animal species share a range of 0 to 16 viruses (18).

III. Factors Contributing to Emergence of infectious viral diseases

There are many factors responsible for emergence of pathogens. It includes A) Human factor B) Viral factor and C) etiological or environmental factors.

A) Human factor: There are many factors where human activities are directly or indirectly responsible for disease emergence.

A. i) Human Encroachment on Wild-Life Habitats

Deforestation due to habitat expansion for humans and mining activities disrupt ecological and environmental conditions, raising the possibility of coming into contact with new emerging pathogen through wild animal. The dramatic increase of human encroachment on wildlife not only associated with emerging pathogens as well as imbalance of ecological and environmental condition. Pathogens may be shared through animal urine and droppings which may be aerosolized and infect susceptible vertebrates including humans. For example, the outbreak of Kyasanur Forest Disease (KFD), a tick-borne flavivirus pathogens mostly prevalent in south west India (19) and Nipah virus encephalitis outbreak reported in Kerala state and some part of West Bengal mainly caused by bats species due to deforestation (10).

A. ii) International Travel and Trade

Global mobility of humans, animals, plants, and various products largely extended in last decade which is one the main source of infectious diseases to cause epidemics. Several emerging or re-emerging infectious diseases were seen beyond their geographic boundaries as in recent years of trade, tourism and migration (especially via air travel) between different countries increased in a high volume (20).Vector-borne infections, including arthropod-borne viruses (arboviruses) and air borne respiratory viruses are main cause of outbreak in new geographical location. Best example is COVID-19 pandemic in recent times which originated from China, though is spread throughout the globe within a short period of time. We have also witnessed spread of Zika virus, Middle Eastern respiratory syndrome coronavirus (MERS-CoV), and Influenza H1N1 novel pathogens to far distant countries (20). Rapid global spread 2009 H1N1 pandemic influenza influenced by Aedes albopictus (Asian tiger mosquito) and the world-wide spread of hantaviruses by rats was also noticed (21,22).

A. iii) Changes in Agricultural Practices

To produce more varieties of grains throughout the year, the agricultural practices have changed a lot. The development of new farmland by removing of forests and exposure to disease-carrying arthropods and rodents by farmers, one of the reasons of emerging viral diseases. Numerous dam construction projects are being undertaken in rivers in order to boost agricultural productivity and flood control. The chemical, physical, and biological changes of river ecosystems are seen after dam construction which is also reason for disease

emergence. For exemple, Japanese encephalitis (JE) virus outbreak in India was documented in the area where dams and canals were built to bring in water for cultivation and large pig population in those areas is conducive for outbreaks (23). The chikungunya outbreak by Aedes albopictus mosquitoes in Kerala in the year 2007 was reported due to modified agricultural practices in the rubber plantation field (24).

A. iv) Wild-Life Trade/Ecotourism

Wild-life trade and translocation for ecotourism, access to petting zoos, consumption of exotic wild animal and bushmeat has increased a large scale which indirectly contribute to emergence of pathogenic viruses (19). To meet the high demand for animal proteins such as civets, and many varieties of wild mammals are put in the in overcrowded cages before slaughtering or butchering. The animals fought or were bitten inside the cage when they were in close proximity, the chance of virus transmission through bloody wounds or close contact is high. The other chance of transfer of infection from excreted material of different animals within close contact. The chance of cross-species pathogen transmission can also happen due to different animals are kept in same cage. Outbreaks of Marburg and Ebola and novel SARS coronavirus have been associated with wild -life trade related disease transmission (25).

A.v) Increase in population density, poverty

Increase in population density is indirectly correlated with disease transmission. The dramatic increase in the human population in last decade force to encroach into virgin forests which indirectly affect the virus reservoirs and the increase chance of viral transmission from animals to humans. A large section of people under poverty level due to increase human population which also favors the spread and perpetuation of diseases.

A. vi) Urbanization

Rapid growth of urban cities with poor urban planning and little capacity to meet the needs of a rapidly growing population often leads to the development of slums and shantytowns which indirectly leads to the spread of viral diseases. Rate of any viral pathogenic transmission is more in densely populated urban cities than rural area of any geographical location. Environmental pollutants in industrialized centers in the more and less developed nations have a deleterious impact on human health specially pulmonary and gastrointestinal infections (26). Dengue Virus spread by *Ae aegypti* to thrive in intimate association with large and crowded human populations in tropical or urban cities, creating conditions that are ideal for epidemic dengue transmission.

A. vii) Hunting

In Africa and few parts of Asia, tribal people have traditional culture of hunting wild animals for food. The chance of pathogenic virus transmission in humans occurs through blood or body fluids as they slaughter the animals unscientifically and eat raw or with minimum cooking. It was reported that the simian immunodeficiency virus (SIV) a cross-species transmission from nonhuman primates to human beings happened several decades earlier (27,28). SIVs might enter man by direct exposure to monkey (reservoir for SIV) bodily fluids or eating raw monkey meat or drinking monkey blood (26).

A. viii) Unplanned migration of human

Unplanned migration of large number of people in a small area due to civic war or natural disasters or in search of work/economic opportunities can play a relevant role in the spread of infectious diseases within hosting locations. Refugee camps and resettlement areas are often characterized by crowded living conditions with limited access to health services, poor vaccinated status and insufficient supplies to meet their basic needs are also responsible for disease outbreak. For example, in mid-2000, outbreaks of measles occurred in refugee camps in Tanzania (29). Viral hepatitis and virus responsible to respiratory illness are common outbreak found in different refugee camps (30).

A. ix) Migradatory birds

Out of all the terrestrial vertebrates, only birds have the ability to transcend national and intercontinental borders. Wild birds are capable of traveling long distances in a matter of hours. Migratory Birds carry pathogens that can be shared by different species at the time of breeding, wintering, and stopping sites. For example-West Nile and Avian Influenza viruses are common infection shared by migratory birds (17).

A. x) Pasturage practices

For the purpose of raising productivity to meet the consumption of meat requirement of livestock and poultry, monocultures of genetically identical individuals are main technical way which promotes susceptibility to infection. Pasturage practices are the cause of the proximity of animals to humans, source of viral transmission. Zoonotic viruses can be transmitted from reservoir animals to other animals or humans by the direct contact of blood, bodily fluids. For example, SARS-CoV crossinfection during pasturage procedure is very common in wild animal markets in China (26).

A. xi) Research work and Bio-Terrorism

Throughout the globe, many research institutes are working on pathogenic microorganisms. There are chance to spread new variant of pathogen from a research laboratory due to lapses in biosafety and biosecurity protocol or any other laboratory accidents. Even though these instances are rare, the need for the necessity of strictly adhering to good laboratory practices while doing research with viral agents speacially highly contagious diseases. Potential viruses with high morbidity and mortality can be use as weapons of bio-terrorism. Genetically modified viruses with enhanced virulence are also a possible way to use as weapons to a new geographical site. Past history showed that anthrax, smallpox, ebola, marburg, venezuelan equine encephalitis virus, eastern equine encephalitis virus et used as bioweapons (1).

A. xii) Modern medicine and unsafe practices

Nowadays, modern medicine and its practices impact millions of individuals globally. Poor nations frequently use antiviral medications carelessly, which speeds up the emergence of resistance strains. Different country or geographical region has their own medical protocol and practices, which partially influence the drug response to that particular disease. Unintentionally, subpar healthcare procedures contribute to the spread of illness. In rural area of a underdeveloped nations, only few hospitals have access to single-use needles and syringes. Proper biosafety and sterilization procedures are also not properly maintained. There is a chance to get infected by many bloods borne infection including HBV, HCV and HIV etc. Now a days good laboratory practices and strict surveillance have minimized the infection rate.

A. xiii) Blood transfusions and selling blood

Blood-borne viruses can spread quite effectively through transfusions. In underdeveloped nations, proper blood transfusions protocol not followed at blood banks and also using non-sterilized equipment which responsible to get infected by blood borne infections. Some traditional cultural concept also promote these, for example- blood loss is dangerous in Chinese cultural, as a result, blood was frequently drawn from many donors simultaneously. The blood centers pooled the blood, kept the plasma, and reinfused the leftover red blood cells back into the blood donors. For a result, at least 250,000 blood donors get infected by HIV and many received contaminated blood in 1900s (26). Now days, positivity rate of post transfusion transmitted infections became low due to all blood banks and transfusion centers are strictly following the standard transfusion protocol.

A. xiv) Organ or bone marrow transplantation

Immunosuppressive medications reduce immune system function and promote opportunistic infections in organ or bone marrow transplant recipients, chemotherapy patients, renal dialysis patients, and long-term corticosteroid users. Transplant patients most frequently get infected by herpes simplex virus-1 &2 (HSV-1&2), Epsteine Barr virus (EBV), human cytomegalovirus (HCMV), varicella-zoster virus (VZV), human herpesvirus-6 (HHV-6) and -7 (HHV-7), human papillomavirus (HPV), adenovirus, respiratory syncytial virus (RSV), parvovirus B-19, viral hepatitis and many other air borne pathogens (26).

Direct animal virus introduction into humans is made more likely by the use of animal organs for transplantation, or xenotransplantation. M.G. Michaels and coworkers identified that baboon cytomegalovirus (BCMV) DNA was found in a recipient's liver after xenotransplantation (31).

A. xv) Civil strife

Civil strife and war also responsible for disease emergence. Water-borne, rodent-related diseases, respiratory and others diseases are prevalent during these periods due to economic collapse and lack of public disease control measures.

A. xvi) Mass Gathering

There are serious public health concerns raised by the any socio-cultural, political, religion and sports event that draws a sizeable crowd. These chances give rise to circumstances in which people are in close proximity to one another, a key concern is the transmission of gastrointestinal and respiratory viral diseases.

A. xvii) Lack of surveillance

The nature of the infectious disease outbreak necessitates immediate management and ongoing surveillance. In addition to the need for continued research for effective countermeasures as wide distribution of zoonotic diseases, some of which are not yet fully understood or described. Effective surveillance helps to create and

successfully deploy vaccinations and medications where they are needed. It also directs to develop the infrastructure and other associated requirements to enable quick diagnosis.

B) **Viral factor:** By mutating its genome, virus evolves into new strains which are responsible for emergence of diseases.

B. i) Microbial Adaptation

All species including microbes are constantly evolving to adapt to the ecosystem. Study showed that many viruses specially RNA viruses show a high mutation rate and rapidly evolve into new variants or strains by mutating its genome (32). As a result, a new variant may show new manifestation of pathogenesis with altered virulence. The immune system fails to identify the new variant as a result vaccine against existing variant are ineffective. The common adaptation strategies for virus evolution are point mutation, recombination, and gene reassortment. It was documented that viral mutation rates roughly range between 10^{-8} and 10^{-4} substitutions per nucleotide per cell infection (s/n/c), in case of RNA viruses is approximately 10^{-6} to 10^{-4} , whereas in DNA viruses it is 10⁻⁸ to 10⁻⁶ (32). It was estimated that the mutation rate of the SARS-CoV during the 2002-2003 epidemic to be 8.26 x 10⁻⁶ nt per day (i.e.3 mutations per RNA in every round of replication) (33). Through the process of recombination, two copies of genetic material can exchange to create a new "mixed" or "hybrid" genome molecule. A typical example of recombination is SARS-CoV, here two RNA molecules to cross over when two CoVs infect the same cell (a process known as "co-infection"). Phylogenetic analyses confirmed that the existence of previous recombination events between mammalian-like and avian-like parent viruses in the evolution of SARS-CoV. Gene reassortment is the third way by which viruses get mutated. When numerous segmented viruses co-infect the same cell in the same host, a process known as gene reassortment takes place. This results in the progeny virus carrying a genome set that was generated from each of the multiple parent viruses. For instance, the characteristic that makes the influenza A virus's genome is made up of eight ssRNA segments. Reassortment among viruses is referred to as a "genetic shift". When two distinct influenza strains of influenza A viruses co-infect the same cell, their offspring viruses may inherit sets of RNA segments that combine sequences from both parent viruses. Widely divergent sequences can therefore arise by recombination or reassortment when many viral strains co-infect the same cell in the host animal (26).

B. ii) Anti Viral Resistance/ Drug resistance microbes

Viruses by natural selection are known to rapidly undergo genome mutations with successive replications which result in emergence of antiviral drug-resistant strains (34). Antiviral drugs mainly target a specific site found on that virus and destroy the virus. When virus mutated its genome, the antiviral drugs do not recognize the targeted site, as a result antiviral drug show reduced action and virus get resistant to that particular drug. To date, antiviral drug resistance has been reported for human viral diseases including hepatitis B and C, herpes, and influenza (35). Study showed that by exposure of animal reservoirs to environmental waters containing antiviral drugs accelerated the antiviral drug resistance (36,37,38). It was found that water fowls, such as ducks (natural reservoirs of influenza virus) may ingest anti-influenza drugs in environmental waters during influenza outbreak which partially involve emergence of anti viral resistance strains (35).

C) Etiological or environmental factors: Climate and environment are typically interrelated, changes in the climate have an unplanned impact on the environment and environmental changes have an impact on the pathogen emergence.

C. i) Environment ,Climate Change and natural disaster

The diseases can be affected by climate change directly through changes to pathogens life cycle, reprod uction, and survival, or indirectly through changes to their habitats and surrounding ecosystems. Climate change particularly temperature and moisture variations could influence the disease emergence and its transmission. Vector-borne infectious diseases will lead to a surge in the spread of Dengue, Chikungunya mainly in tropical countries as temperature and humidity plays an important role in the transmission and incubation of arboviruses (39). Influenza virus and several other respiratory pathogens, are more highly seasonal in temperate climates though their existence seen greater year-round due to climate change (39). Natural disaster like extreme rainfall, flood, cyclone and drought also responsible for emergence of pathogens. Waterborne pathogen concentration rises by droughts and reduced at the time of rainfall. While following a drought, heavy rains and floods can spread the disease as floodwaters are tainted with human and animal waste, increasing the risk of fecal-oral transfer of diseases.

C. ii) Global warming

The effects of global warming are often ignored as global temperatures have been rising faster since 1950s. By the end of this century, they are predicted to have increased from 1.8 to 5.8° C (39). The pathogen, host and vector, all play a significant role in the transmission of infectious diseases, and all three rely heavily on temperature variation.

According tostudies, temperature variations, for instance, have a considerable impact on the dengue vir us, causing it to fly farther, be active for longer periods of time, and require less time for extrinsic incubation (40). Since we are currently experiencing the highest level of global warming, it is regrettable to say that there is a demonstrated correlation between rising infectious illness rates and climate change by global warming (39,41).

Year	Pathogenic diseases	Place	Condition
1918-1919	Influenza	It began in Mumbai and then spread to northern India	Pandemic
1974	Small Pox	West Bengal, Bihar and Odissa	Epidemic
1970 to 1990	Polio	Uttar Pradesh and other parts of India	Epidemic
1994 and 2003	Plague	Surat, Gujarat (1994) Shimla,Himachal Pradesh (2003)	Epidemic
2003, 2006 2022	Dengue*	Delhi and spread to nearby states (2003, 2006) All over India, Northern part is mostly affected (2022)	Epidemic
2003	SARS:Severe Acute Respira tory Syndrome	Northern parts of India	Epidemic
2006	Chikungunya*	Ahmedabad and South India	Outbreak
2009 and 2015	H1N1 Flu	All over India. Rajasthan, Maharastra, and Gujarat were the badly affected states	Pandemic
2001, 2007, 2018, 2023	Nipah Virus	Kerala (2018,2023)and West Bengal (2001, 2007)	Outbreak
2019-2021	SARS-CoV-2 (COVID-19)	All over India	Pandemic
1957,2012	Kyasanur forest disease (KFD)	Karnataka (1957) Kerala, Tamil Nadu, Goa and Maharashtra (2012)	Outbreak
2011	Crimean-Congo haemorrhagic fever (CCHF)	Gujarat and Rajasthan	Outbreak
2004	Hand, foot and mouth disease (HFMD)	Eastern parts of India	Outbreak
2007	Sapovirus	Vellore in south India	Outbreak
1999	Norovirus (NoV)	Delhi	Outbreak
2007	Chandipura virus	Maharashtra	Outbreak

IV.	Viral	disease	outbreak s	since 20th	Century	v in India
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* Dengue and Chikungunya outbreak in rainy season in various part of India is very common. Increasing numbers of dengue cases and fatalities are being reported in multiple urban and rural healthcare settings in India (Source Ref: 10, 42-44).

V. Disease Surveillance network in India

The Integrated Disease Surveillance Project (IDSP), initiated in 2004 by the Union Ministry of Health and Family Welfare, Govt. of India, aims to establish a network connecting to every state-run medical institutions and district hospitals for the purpose of disease trend monitoring, health professional training and tele-education. With the aid of information and communication technology, the project is carried out by the Central Surveillance Unit of the National Centre for Disease Control (NCDC) under Govt. of India, New Delhi. Its objectives are to identify early warning signs of impending disease outbreaks and to launch prompt and efficient health actions at national. state. and district levels throughout the country. India has made significant strides and continues to show a strong commitment to building and running a disease monitoring program with the WHO's adoption of the International Health Regulations (IHR), 2005.

In order to build infrastructure for the timely identification of viruses causing outbreaks or linked to significant morbidity/mortality and prompt diagnosis at molecular level, the Department of Health Research (DHR), under Ministry of Health & Family Welfare, Govt. of India, established a network of Virus Research and Diagnostic Laboratory (VRDLN). It also will aid in the collection of surveillance data on common viral infections across the nation and provide necessary information to health department. The National Vector Borne Disease Control Programme (NVBDCP) is responsible for conducting nationwide surveillance and prevention for vector-borne diseases namely lymphatic filariasis, Japanese encephalitis, kala-azar, dengue, malaria, and chikungunya (1, 45). To combat viral hepatitis, National Viral Hepatitis Control Program (NVHCP) initiated under National Health Mission (NHM), Govt. of India. This is a thorough approach that addresses all aspect of viral hepatitis A, B, C, D, and E, including prevention, detection and therapeutic management of the infected patients.

VI. One Health Approach

The phrase "One Health" was first coined at a Wildlife Conservation Society meeting in 2004 and explicitly acknowledged the connection between human and animal health and the risks that diseases pose to ecosystem (46,47). These approach was a significant step toward acknowledging the vital importance to balance and optimize the health of people, animals, and the larger environment, including ecosystems in a sustainable manner. One Health is an integrated, all-encompassing strategy working at the regional, national, and global levels which acknowledges the collaborative approaches for responding to disease that are emerging or that are resurrecting. It also including wildlife health as a crucial element of global disease prevention, surveillance, control and mitigation (46-48).

One Health approach gained importance after the pandemic of the novel zoonotic coronavirus disease (COVID-19). The potential risk of many more emerging and re-emerging zoonotic infectious disease, the growing antimicrobial resistance (AMR) and food-borne diseases transmission has attracted global concerns. These days, the One Health method is used to address complicated health issues and has gained acceptance among scientists, public health professionals, and international communities. We anticipate more affordable and cost benefit models will develop to illustrate how the One Health approach may actually work to romote sustainability and wellbeing in various socioecological contexts throughout the world. Consequently, "One world -One health" approach also supported by the World Health Organization (WHO), World Organization for Animal Health (WOAH), Food and Agriculture Organization (FAO), and United Nations Environment Programme (UNEP) to make a healthy world (49).

The National One Health Programme for Prevention and Control of Zoonoses (NOHP-PCZ) is being implemented by the National Center for Disease Control (NCDC) under the Ministry of Health & Family Welfare (MoHFW), Govt. of India. One of the main goals of the program is to "Strengthen the surveillance and diagnostic capacity of zoonoses" at the national, state, and district levels by creating a network of Sentinel Surveillance Sites on Zoonoses (50).

VII. Post Pandemic Issues and Challenges

India had experienced to address a number of important health challenges in past years. During the last pandemic, COVID-19 received all of the attention as a result many other crucial health issues received insufficient attention. There are numerous additional communicable diseases including leprosy, malaria, and tuberculosis and noncommunicable diseases like cancer, diabetes, and hypertension are also becoming a bigger problem now a days. Simultaneous attention is needed for other significant public health challenges such as mental health, malnutrition, elderly health, and mother/child health.

In India, health care infrastructure in rural and urban areas is varied a lot till date. The government and private health sector also differs a lot in account of infrastructure, disease management, time bound treatment, cost of treatment and availability of doctors/paramedical staffs. There is a great deal of disparity in the accessibility, price, and availability of health services for poor family. The commercial health sector is still taking advantage of the circumstances for its own gain, as it was seen during the pandemic. Due to huge number of patients, there is a vicious cycle after greater out-of-pocket expenses and an increasing or forced reliance on the private health sector. In tribal, remote, and difficult-to-reach urban and rural areas, health services and infrastructure remain inadequate and neglected till date. Due to modern facilities and communication, doctors and health care professionals are hesitate to work and stay in those areas. Instead of focusing more on prevention, we still prioritize the curative components. Significant problems with the health care infrastructure include under qualified and overworked personnel. In the government health system, there are numerous openings though manpower shortage is there as administrative process and financial approval is still big concern.

Human civilization is undergoing a rapid progress as a result of the acceleration of globalization and dramatically increased dynamics and growth of the population. To combat highly infectious diseases in highly populated country like us is very challenging. Health authorities and law makers have to plan accordingly and implement the same to all concern departments.

VIII. Key Positive Features

India's secondary and tertiary health-care infrastructure is well-developed, as the two-year COVID-19 epidemic showed. In addition, the Indian health system demonstrated its ability to provide a swift, well-coordinated national response to highly populated country like us in accordance with the circumstances. Additionally, the Indian manufacturing sector showed the ability to boost output of pharmaceuticals, medical devices, diagnostic/preventive kits, and other items as needed. Many Indian pharmaceutical companies also extended their hand to develop life saving vaccines with other foreign companies. The government of India and all state government also worked together and prepared various health related plan to overcome this situation. Other than clinician and professionals involved in laboratory COVID-19 diagnosis, other warriors including

sanitation work, emergency service, maintaining law and order have done tremendous work to maintain all needs of a society. Social media and information technology were very helpful in addressing the demands, particularly in raising community awareness. The healthcare workforce and volunteers also showed a strong desire to work in the face of difficulty and eagerness to volunteer many healthcare associated issues.

The development of nucleic acid detection and genome sequencing technologies profoundly transformed the study of infectious diseases, particularly their pathophysiology, genetic profile and diagnosis. Advance therapy also led the best possible patient care and management. In comparison to conventional approaches, a variety of molecular assays with improved sensitivity and specificity have been developed for the faster detection, characterization, and quantification of the growing number of infectious and other diseases.

The successful development of drugs and vaccines against the majority of infectious disease pathogens has been facilitated by the accumulation of genomic and proteomic data. These data also have made it easier to better understand the known infections and find novel or previously undiscovered information about various diseases.

IX). Conclusion

A true threat to public health is posed by emerging and neglected infectious diseases and its epidemics can have detrimental social, political, and economic effects. The understanding of disease aetiology, pathogenesis, and molecular epidemiology has improved due to advances in basic science research, development of molecular technologyin diagnostics and treatment. These developments have also made it possible to rationally design vaccines, which have helped to successfully eradicate some diseases. With concerns of continued global expansion; pandemic preparedness however remains a major global challenge especially densely populated and economically poor countries. Infectious disease emergence and transmission have been discovered to be influenced by a wide range of complicated factors, including pathogen evolution, human encroachment, wild life trade, microbial adaption, changes in the environment, dynamic human-animal interactions and poverty. More number of scientific study and research is required in order to vaccine development, treatments, and diagnostics, as well as to potentially identify diseases with its ability to spread epidemics. Addressing new and emerging infectious viral diseases, effective interagency between research collaborations, networking among national/international organizations, enough financial support for the public health infrastructure, and poverty reduction is earnestly required.

Conflict of Interest:

The authors declare they have no conflict of interest. \Box

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References

- Mani S Reeta, Ravi V, Desai A, Madhusudana SN. Emerging Viral Infections in India. Proc. Natl. Acad. Sci. Sect B. Biol. Sci.2012;82(1):5-21.
- [2]. Parvez MK, Shama P. Evolution and Emergence of Pathogenic Viruses: Past, Present, and Future. Intervirology. 2017; 60:1-7.
- [3]. Gupta V, Santosh KC, Arora R, Ciano T, Kalid KS, Mohan S. Socioeconomic impact due to COVID-19: An empirical assessment. Information Processing and Management.2022. 59;102810:1-20.
- [4]. Taylor LH, Latham SM, Woolhouse MEJ. Risk factors for human disease emergence. Phil Trans R Soc Lond B .2001;356:983-989.
- [5]. Woolhouse MEJ, Gowtage-Sequeria S. Host range and emerging and re-emerging pathogens. Emerg Infect Dis. 2005;11:1842-1847.
- [6]. Kilpatrick AM, Randolph SE. Drivers, dynamics, and control of emerging vectorborne zoonotic diseases. Lancet.2012;380:1946-1955.
- [7]. Wang LF, Crameri G. Emerging zoonotic viral diseases. Rev. Sci. Tech.2014;33:569-581.
- [8]. Plowright RK, Parrish CR, McCallum H, Hudson PJ, Ko AI, Graham AL, Et al. Pathways to zoonotic spillover. Nat. Rev. Microbiol.2017;15:502-510.

[9]. Parrish CR, Holmes EC, Morens DM, Park E, Burke DD, Calisher CH, Et al. Cross-species virus transmission and the emergence of new epidemic diseases. Microbiol. Mol. Biol. Rev.2008;72:457-470.

- [10]. Mourya DT, Yadav PD, Ullas PT, Bhardwaj SD, Sahay RR, Chadha MS, Et al. Emerging/re-emerging viral diseases & new viruses on the Indian horizon. Indian J Med Res.2019;149:447-467.
- [11]. Barber NC and Stark LA. Online resources for understanding outbreaks and infectious diseases. CBE Life Sci Educa.2015;14:1-5.
- [12]. "Globalization and infectious diseases: a review of the linkages. Saker L, Lee K, Cannito B, Gilmore A, Campbell-Lendrum D. http://www.who.int/tdr/publications/documents/seb topic3.pdf.
- [13]. Tibayrenc M. Encyclopedia of Infectious Diseases: Modern Methodologies, John Wiley & Sons, 2007.
- [14]. Carruthers VB, Cotter PA, and Kumamoto CA. Microbial pathogenesis: mechanisms of infectious disease. Cell Host and Microbe.2007; 2(4):214-219.
- [15]. Grace D.Infectious Diseases and Agriculture. Encyclopedia of Food Security and Sustainability. 2019;3:439-447.
- [16]. Mackenzie SJ, Jeggo M. The One Health Approach-Why Is It So Important? Trop Medi and Infec Disease. 2019;4:88.
- [17]. Artikaa MI, Wiyatnoc A, Ma'roef NC. Pathogenic viruses: Molecular detection and characterization. Infect, Genet and Evolut.2020;104215.

- [18]. Johnson CK, Hitchens PL, Pandit PS, Rushmore J, Evans TS, Young CWC. Global shifts in mammalian population trends reveal key predictors of virus spillover risk. Proceedings of the Royal Society B: Biological Sciences.2020;287(1924):20192736.
- [19]. Chomel BB, Belotto A, Meslin FX. Wildlife, exotic pets, and emerging zoonoses. Emerg Infect Dis.2007;13:6-11.
- [20]. Tatem, AJ, Rogers DJ, Hay SI. Global transport networks and infectious disease spread. Adv Parasitol. 2006; 62:293-343.
- [21]. Centers for Disease Control (CDC). Aedes albopictus introduction into continental Africa. MMWR Morb Mortal Wkly Rep. 1991;40:836-838.
- [22]. LeDuc JW, Childs JE, Glass GE. The Hantaviruses, etiologic agents of hemorrhagic fever with renal syndrome: a possible cause of hypertension and chronic renal disease in the United States. Annu Rev Public Health. 1992; 13:79-98.
- [23]. Banerjee K. Emerging viral infections with special reference to India. Indian Indian J Med Res. 1996;103:177-200.
- [24]. Kumar NP, Joseph R, Kamaraj T, Jambulingam P. A226 V mutation in virus during the 2007 chikungunya outbreak in Kerala, India. J Gen Virol.2008;89:1945-1948.
- [25]. Woo PC, Lau SK, Yuen KY. Infectious diseases emerging from Chinese wet-markets: zoonotic origins of severe respiratory viral infections. Curr Opin Infect. Dis.2006;19:401-407.
- [26]. Hui Wai EK. Reasons for the increase in emerging and re-emerging viral infectious diseases. Microbes and Infection.2006;8(3):905-916.
- [27]. Hahn BH, Shaw GM, De Cock KM, Sharp PM. AIDS as a zoonosis: scientific and public health implications, Science.2000;287(5453):607-614.
- [28]. Korber B, Muldoon M, Theiler J, Gao F, Gupta R, Lapedes A, Et al. Timing the ancestor of the HIV-1 pandemic strains.Science.2000;288(5472):1789-1796.
- [29]. Kamugisha C, Cairns KL, Akim C. An outbreak of measles in Tanzanian refugee camps. J. Infect. Dis.2003; 187:58-62.
- [30]. Chironna M, Germinario C, Lopalco PL, Carrozzini F, Barbuti S, Quarto M. Prevalence rates of viral hepatitis infections in refugee Kurds from Iraq and Turkey. Infection.2003;31:70-74.
- [31]. Michaels MG, Jenkins FJ, George KS, Nalesnil MA, Starzl TE, Rinaldo CRJ. Detection of infectious baboon cytomegalovirus after baboon-to-human liver xenotransplantation. J. Virol.2001;75:2825-2828.
- [32]. Sanjuan R, Domingo-Calap P. Mechanisms of viral mutation. Cell. Mol. Life Sci. 2016;73:4433-4448.
- [33]. Molecular evolution of the SARS coronavirus during the course of the SARS epidemic in China. Chinese SARS Molecular Epidemiology Consortium. Science.2004;303:1666-1669.
- [34]. Richman DD. Antiviral drug resistance. Antiviral Res. 2006;71:117-121.
- [35]. Kumar M, Kuroda K, Dhangar K, Mazumder P, Sonne C, Rinklebe J, Et al. Potential Emergence of Antiviral-Resistant Pandemic Viruses via Environmental Drug Exposure of Animal Reservoirs. Environ. Sci. Technol. 2020; 54:8503-8505.
- [36]. Nannou C, Ofrydopoulou A, Evgenidou E, Heath D, Heath E, Lambropoulou D. Antiviral drugs in aquatic environment and wastewater treatment plants: A review on occurrence, fate, removal and ecotoxicity. Sci. Total Environ. 2020;699:134322.
- [37]. Singer AC, Howard BM, Johnson AC, Knowles CJ, Jackman S, Accinelli C, Et al. Meeting report: risk assessment of Tamiflu use under pandemic conditions. Environ. Health Perspect.2008;116(11):1563-1567.
- [38]. The race against COVID-19. Nat. Nanotechnol. 2020;15:239-240.
- [39]. Uwishema O, Masunga DS, Naisikye KM, Bhanji FG, Rapheal AJ, Mbwana R,Et al. Impacts of environmental and climatic changes on future infectious diseases. Intl J of Surgery.2023;109:167-170.
- [40]. Robert MA, Stewart-Ibarra AM, Estallo EL. Climate change and viral emergence: evidence from Aedes-borne arboviruses. Curr Opin in Virol. 2020;40:41-47.
- [41]. Hii YL, Zaki RA, Aghamohammadi N, Rocklov J. Research on climate and dengue in Malaysia: a systematic review. Curr Environ Health Rep.2016;3:81-90.
- [42]. Dangore-Khasbage S, Meshram M, Juneja S. Epidemics and Pandemics in India Since 20th Century A Brief Review. J Evolution Med Dent Sci.2021;10(33):2278-4802.
- [43]. Sarma N. Hand, foot, and mouth disease: current scenario and Indian perspective. Indi J Dermatol Venereol Leprol.2013;79(2):165-175.
- [44]. 2007, Gurav YK, Tandale BV, Jadi RS, Gunjikar RS,; Tikute, SS.; Jamgaonkar AV, Et al. Chandipura virus encephalitis outbreak among children in Nagpur division, Maharashtra. Indi J of Med Reser.2010;132(4):395-399.
- [45]. Integrated Disease Surveillance Programme, Ministry of Health & Family Welfare, Government of India. Available from: http://idsp.nic.in/index4. php?lang=1&level=0&linkid=406&lid=3689, accessed on June 5, 2018.
- [46]. Mackenzie JS, Jeggo M. The One Health Approach-Why Is It So Important? Trop. Med. Infect. Dis. 2019;4: 88.
- [47]. Wildlife Conservation Society. OneWorld-One Health: Building Interdisciplinary Bridges. 2004. Available online: http://www.oneworldonehealth.org/sept2004/owoh_sept04.html (accessed on 22 May 2019).
- [48]. Nii-Trebi NI. Emerging and Neglected Infectious Diseases: Insights, Advances, and Challenges. BioMed Reser Inter.2017;5245021:1-15.
- [49]. Zhou XN, Tanner M. Science in One Health: A new journal with a new approach. Sci in One Health. 2022;1: 100001.
- [50]. Operational Guidelines For Sentinel Surveillance Sites On Zoonoses (SSSZ)-2023. National One Health Programme For Prevention And Control Of Zoonoses Division Of Zoonotic Diseases Programmes. National Center for Disease Control, Directorate General Of Health Services Ministry Of Health And Family Welfare, Government Of India.