

# Chapter 14

## Drivers of Emerging Viral Zoonoses



Sandeep Ghatak, Arockisamy Arun Prince Milton, and Samir Das

**Abstract** Zoonotic viral diseases continue to inflict human mortality and morbidity worldwide. While efforts are on for containment of these diseases, many new viral diseases, especially those of zoonotic origin, were discovered in humans, often in newer geographical areas where diseases were not reported previously. It is now an established fact that with changes in society, demography, climatic patterns, global economy and trade, viral zoonoses have made a comeback. Many factors are responsible for the emergence of viral pathogens worldwide. These factors, known as ‘drivers’, are numerous and are complexly interlinked. Major drivers of the emergence include ecological perturbations caused by changes in agricultural practices, livestock husbandry, and developmental activities; global warming and changes in climatic patterns, various forces of globalization such as international travel, trade and commerce; *human demographic changes augmented by rising population and urbanization, population mobility*; human behavioural changes; microbial adaptation and evolution; changing technology and industrial practices; and deficiencies in public health infrastructure. Emergence of many new viral zoonoses, e.g. Nipah virus infection, severe acute respiratory syndrome, Middle East respiratory syndrome, highly pathogenic avian influenza, Crimean–Congo hemorrhagic fever, Alkhurma hemorrhagic fever, and others is testimony to role of complex set of drivers in predisposing emergence. Though detailed discussions of these drivers of emerging zoonotic infections are beyond the scope of the current discourse, in this chapter an attempt shall be made to discuss the most important causes of emergence of viral zoonoses so that these complex linkages are recognized and acted upon for attaining sustainable health.

**Keywords** Climate · Diseases · Drivers · Ecological · Emergence · Emerging · Factors · Global warming · Globalization · Infectious · Viral · Zoonoses

---

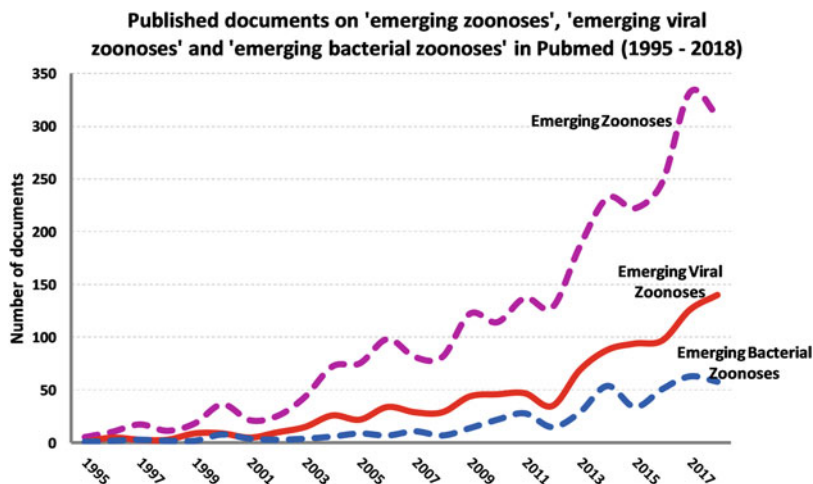
S. Ghatak (✉) · A. A. P. Milton · S. Das  
Division of Animal Health, ICAR Research Complex for NEH Region, Umiam, Meghalaya,  
India

## 14.1 Prologue

Infectious diseases are among the major causes of human mortality and morbidity all over the world. They continue to take a heavy toll on the progress made so far. However, with the advent and successful implementation of many health technologies and interventions, especially in decades around 1950s–1970s, infectious diseases were significantly under control (Fong 2013; Leibovici 2018; Rezza and Ippolito 2017; Semenza et al. 2017; van Doorn 2014; World Health Organization 2014). With changes in society, demography, climatic patterns, global economy and trade, infectious diseases made a comeback. Many new diseases that were hitherto unknown to cause human diseases were identified, new geographical areas where diseases were not reported previously were invaded and old diseases that were once thought to have been controlled reappeared in the populations (Fong 2013; Fong and Drlica 2003; Leibovici 2018; Semenza et al. 2017; van Doorn 2014). These events had a deep impact on our view of infectious diseases, and new concepts of emerging infectious diseases began to take shape. It was observed that many of the emerging infectious diseases originated from the animal world (zoonoses), bringing back emerging zoonoses in the forefront of discussions. Further examination of the newly emerging zoonoses revealed that most of them were caused by viral pathogens indicating the continual risk from the emerging zoonotic viral pathogen. A quick analysis of data obtained from ‘PubMed’ database of National Institute of Health, United States reveals increasing academic interest in emerging viral zoonoses (Fig. 14.1).

Many factors are responsible for such emergence of pathogens worldwide (Table 14.1). These factors (or drivers) are numerous, sometimes subtle yet complex and are often complicatedly interlinked with far-reaching consequences, predisposing emergence of new infections (Fongs 2013, 2017; Fong and Alibek 2007; Fong and Drlica 2003; Jones et al. 2008). Though a detailed discussion of these drivers of emerging zoonotic infections is beyond the scope of the current discourse, in this chapter an attempt shall be made to discuss the most important causes of the emergence of viral zoonoses.

Emerging infectious diseases are broadly described as those infections whose incidence in humans had swelled more than expected in two preceding decades or might pose a threat of increased incidence shortly (Chomel 1998). In a significant study by Jones et al. (2008), it was observed that majority (60%) of the emerging infectious diseases were of animal origin (zoonoses) and almost 72% of them were having their roots traceable to wildlife. Naturally, therefore, the term emerging zoonoses came under intensified discussion and were generally defined as zoonotic infections caused by new agents, or by already known agents, occurring in locations or in host species in which the infection was previously undocumented (Chomel 1998). While the study by Jones and colleagues (Jones et al. 2008) noted that majority of emerging infectious diseases were caused by bacteria, the contribution of emerging viral zoonoses were also significant as was evidenced by recent emergence and outbreaks of many viral infections such as Ebola hemorrhagic



**Fig. 14.1** Academic documents on ‘emerging viral zoonoses’ as available in the PubMed database (1995–2018) (Data source: <https://www.ncbi.nlm.nih.gov/pubmed/>. Accessed on 3 Aug 2019). In order to assess the academic interest in the study of emerging viral zoonoses a search was made in the ‘PubMed’ database using the term ‘emerging viral zoonoses’. To compare the results, searches were also conducted for two comparable topics with search terms of ‘emerging zoonoses’ and ‘emerging bacterial zoonoses’. Results revealed that search for ‘emerging zoonoses’ yielded greatest number of documents, followed by search with ‘emerging viral zoonoses’ and ‘emerging bacterial zoonoses’. This was expected as the latter two terms are subsets of the former search term. However, the results also indicated greater academic interest for ‘emerging viral zoonoses’ compared to ‘emerging bacterial zoonoses’ as evidenced from available records in PubMed database

fever, Nipah virus infection, Zika virus, severe acute respiratory syndrome (SARS), Middle East respiratory syndrome (MERS), highly pathogenic avian influenza, Crimean–Congo hemorrhagic fever (CCHF), West Nile fever (WNV), Alkhurma hemorrhagic fever, Rift Valley fever (RVF), dengue hemorrhagic fever, West Nile virus fever, swine influenza, Usutu virus infection, Oropouche fever, hepatitis E infection, and many more (Al-Tayib 2019; Ambat et al. 2019; Bailey et al. 2018; Blacklaws and Daly 2018; Chu et al. 2019; Clé et al. 2019; Fong 2017; García-Bocanegra et al. 2019; Goneau et al. 2018; Jánová 2019; Sakkas et al. 2018; Sayed et al. 2019; Wang and Cowled 2015). In addition to the ever-expanding list of human viral infections, a recent study estimating the mammalian viral diversity indicated that there might be as many as 10,000 viruses with zoonotic potential (Carlson et al. 2019). This indicated that in times to come zoonotic viral infections will possibly continue to emerge and cause considerable damage to the society.

**Table 14.1** Major drivers for the emergence of zoonotic viral diseases

Host related	Agent associated	Environmental
<ul style="list-style-type: none"> <li>• International travel, trade and commerce</li> </ul>	<ul style="list-style-type: none"> <li>• Microbial adaptation and evolution</li> </ul>	<ul style="list-style-type: none"> <li>• Ecological changes</li> </ul>
<ul style="list-style-type: none"> <li>• International travel</li> </ul>		<ul style="list-style-type: none"> <li>• Changes in agricultural practices</li> </ul>
<ul style="list-style-type: none"> <li>• International trade and commerce</li> </ul>		<ul style="list-style-type: none"> <li>• Changes in livestock husbandry</li> </ul>
		<ul style="list-style-type: none"> <li>• Developmental activities causing ecological perturbations</li> </ul>
<ul style="list-style-type: none"> <li>• Human demographic changes</li> </ul>		<ul style="list-style-type: none"> <li>• Global warming and climate change</li> </ul>
<ul style="list-style-type: none"> <li>• Rising population density and urbanization</li> </ul>		
<ul style="list-style-type: none"> <li>• Population mobility</li> </ul>		
<ul style="list-style-type: none"> <li>• Human behavioural changes</li> </ul>		
<ul style="list-style-type: none"> <li>• Rise in tourism</li> </ul>		
<ul style="list-style-type: none"> <li>• Changing consumer behaviours</li> </ul>		
<ul style="list-style-type: none"> <li>• Changes in technology and industry</li> </ul>		

## 14.2 Drivers for the Emergence of Viral Zoonotic Diseases

### 14.2.1 Ecological Changes

Over the long history of evolution, pathogens including viruses are often acclimated to specific ecological settings (niches) where they perpetuate involving single or many hosts. This well-adapted lifecycle of agents is delicately balanced and depends on several interplaying factors including host abundance, patterns of vegetation, vector availability, the survival of hosts, immune status of the host population, pathogen characteristics, and climatic conditions such as precipitation, temperature, and humidity, etc. Any change(s), subtle or catastrophic, that might happen to such evenly balanced ecosystem, results in altered pattern of disease of pathogen distribution and when human hosts are involved, emergence of a zoonotic infection takes place (Dantas-Torres 2015; Fong 2013; Heffernan 2018; Karesh et al. 2012; Kilpatrick and Randolph 2012; Kock 2014; Semenza et al. 2017). In many instances, the force behind such ecological changes is anthropogenic (McMahon et al. 2018).

### 14.2.1.1 Changes in Agricultural Practices

Changes in agricultural practices can bring about local microecological changes prompting the emergence of zoonotic diseases. For example, when grasslands were converted into arable land, and corn cultivation began, they led to a surge in the population of a *Calomys musculus* rodent, perhaps due to abundance in food. This, in turn, resulted in an increased number of cases of Argentinian and Bolivian hemorrhagic fevers caused by Junin and Machupo type *Coronaviruses* (Chomel 1998; Morse 1995). Increase in the incidence of Rift Valley fever in Egypt is believed to be associated with expansion of irrigated areas for agricultural development (Chomel 1998; Fawzy and Helmy 2019; Morse 1995; Morse et al. 2012).

Expansion of new agricultural activities and human habitation may also lead to the emergence of zoonotic viral infections. In the Latin American country of Peru, an outbreak of cases of vampire bat transmitted rabies occurred following sudden changes in the farming practices. It is believed that before the outbreak there was an increase in pig rearing and human settlements created near and inside forested areas. As the pig population grew vampire bats found new prey for bloodsucking. However, when the rising pig population posed threat to traditional crops in the area, many pigs were culled, and the vampire lost their usual prey for blood and turned onto human settlers with poor housing facilities. As vampire bats are among the natural reservoirs of Rabies virus, eventually an outbreak of rabies erupted among people living in the Peruvian jungles (Chomel 1998; Shipley et al. 2019; Wang and Cowled 2015).

### 14.2.1.2 Changes in Livestock Husbandry

Among all agricultural activities, livestock husbandry is considered to be the fastest growing sector worldwide (FAO 2011). With the burgeoning global population, increasing urbanization, and rising income level, the world today is experiencing an unprecedented demand for livestock origin foods (Mottet et al. 2018). In Asian countries, per capita intake of animal proteins per day increased from 7 gm to 25 gm between 1960 and 2013 (Van Boeckel et al. 2015). There was an estimated increase of 725% in poultry meat demand (FAO 2011). The massive rise in demand led to the intensification of livestock production systems and also expansion of extensive systems of rearing livestock, most of which took place in Asian countries (Gilbert et al. 2018). The rapid intensification of animal husbandry practices led to greater potential for spread of livestock diseases within farms due to loss of genetic diversity among farmed animals and also due to proximity of available susceptible hosts (Ostfeld 2009). Along with that with increasing global population numbers and population density, particularly in Asian countries, human–animal contact is becoming more frequent. The plausible link between intensification of livestock farming and subsequent emergence of viral zoonoses is exemplified by the emergence of Nipah virus infection in Malaysia, highly pathogenic avian influenza in Asian

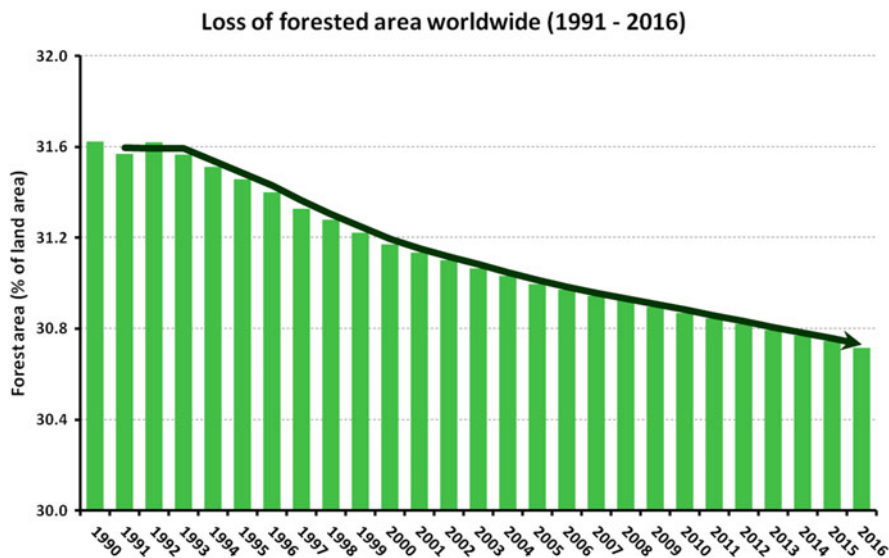
countries. In late 1990s (1997–1999) with booming of piggery in Malaysia, forests were cleared to accommodate new farms. Bats which might have lost their nests started roosting in pig sheds, and pigs contracted the deadly virus (Nipah), eventually spilling over the infection to in-contact persons and then to other people (Ambat et al. 2019; Sayed et al. 2019). Similarly, Influenza A virus, which is maintained in a wild migratory birds, found readily susceptible hosts (intensively farmed chickens in various countries of Asia), when migratory birds nested around water bodies with poultry birds nearby during their annual migration resulting in the emergence of HPAI (H5N1) and subsequent epidemic spread of this viral zoonoses (Bailey et al. 2018; Blacklaws and Daly 2018; Goneau et al. 2018; Lal 2007; Morse et al. 2012; Plowright et al. 2017).

Farming of newer species of livestock and birds also provides newer opportunities for disease emergence. Crimean–Congo hemorrhagic fever is a viral hemorrhagic fever caused by *Nairovirus* of the family *Bunyaviridae* and is transmitted by ticks from animals to humans. Many wild and domestic animals including cattle, sheep, goat act as hosts for the virus. Human to human transmission occurs mostly through direct contact with body fluid (blood and secretions) of the infected person. The disease in humans is usually manifested by fever, muscular pain, body ache, stiffness in the neck, headache, diarrhoea, vomiting, neurological symptoms like the state of confusion, depression, petechial haemorrhage on the skin and mucosal surfaces. Case fatality rates hover around 30% (Bird and Mazet 2017; Chomel 1998; Möhlmann et al. 2018; Spengler et al. 2019).

While many domestic animals are hosts of the virus, birds are usually resistant with notable exceptions of ostriches which are susceptible. In South Africa, Ostriches became popular as new farm birds. An outbreak of Crimean–Congo hemorrhagic fever was reported among persons engaged in an ostrich slaughterhouse indicating the inherent risk of the emergence of viral zoonoses with new farmed animals (Chomel 1998). Similarly, an outbreak of Western equine encephalitis was reported among farmed emus in the United States (Chomel 1998).

### 14.2.1.3 Developmental Activities Leading to Ecological Perturbations

To meet the demand and aspirations of a surging human population, the last few decades have witnessed an unprecedented rush for harnessing various natural resources and energy. Hurried anthropogenic activities resulted in degradation of natural forests, landscape alteration through the expansion of farming and developmental activities such as dam building for hydroelectric power and irrigation, change in natural waterways, unplanned urbanization, environmental pollution, and many more. These factors, in turn, caused—loss of habitats for animals and vectors, thus destabilizing the natural foci of infections; altered the composition of various species; affected the interaction between domestic, peri-domestic, and wild animal. As a result pathogens that were once restricted to the confines of secluded ecosystems gained new opportunities to infect humans and other hosts. Expansion of human habitation into forested areas also offers scope for new infections to emerge.



**Fig. 14.2** The global trend in net deforestation (Data source: <https://data.worldbank.org/indicator/ag.lnd.frst.zs>. Accessed on 14 Aug 2019). During the last three decades (1990–2019) worldwide loss of forested areas amounted to approximately 1.6% of total land area of the earth. This huge loss of forest land caused loss of habitats for a multitude of species of animals and plants resulting in irreversible ecological changes. Ecological perturbations are one of the prime drivers for the emergence of viral zoonotic diseases such as Mayaro fever outbreak in Amazonian basins

There is number of instances where deforestation was linked to the emergence of zoonotic viral infections (Fig. 14.2).

It is believed that deforestation and encroachment of forest lands are key factors for the emergence of Mayaro virus infection (Acosta-Ampudia et al. 2018). Mayaro virus infections are usually restricted in the Amazonian basin area and are maintained in a sylvan cycle involving forest mosquitoes and vertebrates. However, infections were spreading in non-forested areas, possibly due to perturbations in the existing disease ecosystem (Acosta-Ampudia et al. 2018; Mackay and Arden 2016). Encroachment into the forested area has also been implicated in the emergence of Oropouche virus fever. Historically the Oropouche virus and Orthobunya virus were responsible for more than 30 epidemics and more than 500,000 cases in Latin American countries. The virus is maintained in a sylvatic cycle involving biting midges (*Culicoides paraensis*) as the arthropod vector, primates, and birds. However, human ingress into forest areas leads to infection in humans who then triggers the urban cycle of the disease as they return/travel to urban areas. Other factors that incite the disease spread include rising temperature and increased rainfall (Morse and Schluederberg 1990; Sakkas et al. 2018; Walker et al. 2018; Woolhouse et al. 2016). Thus developmental activities leading to anthropogenic influences disturbing natural ecosystem of the diseases are among the potential causes of emergence of many viral zoonoses. The emergence of Nipah virus infection could also be linked to

developmental activities (piggery development) by encroachment of forest lands (Ambat et al. 2019; Sayed et al. 2019).

### 14.2.2 *Global Warming and Climate Change*

Climate change is one of the greatest challenges faced by humanity affecting all spheres of life, including health. Current projection of climate change events predict 1–3.7 °C rise in global temperature with profound effect on biological systems (Afrough et al. 2019; Anderson et al. 2016; Dantas-Torres 2015; Glennon et al. 2018; Houghton 2019; Li and Du 2019; Mackay and Arden 2016; Rohr et al. 2019). In addition to warming events, climatic models also predict the increased frequency of extreme weather events, more precipitation in higher latitudes, desertification of lower latitude areas, among others. Effects of these weather events often lead to flooding and inundation of urban areas, untimely rainfall, higher winter temperature, etc. (Gould et al. 2017; Grubaugh et al. 2019; Jones et al. 2008; Ostfeld 2009; Petersen et al. 2018; Saker et al. 2004). In the realm of emerging viral zoonoses, all these effects indirectly help survival of viral pathogens and their arthropod vectors with increased insect vector activity and propensity (Dash et al. 2013; Fong 2017; Gould et al. 2017; Grubaugh et al. 2019; Ostfeld 2009; Petersen et al. 2018; Rezza and Ippolito 2017; Semenza et al. 2016). Some arthropod-borne zoonotic viruses have emerged as a major health problem all around the world. Expansion of vector ranges both spatially and temporally is causing the zoonotic viruses to emerge in new areas and to eventually linger in the population. For example, recent emergence of Zika virus since 2015 in American continents and Caribbean region (Blacklaws and Daly 2018; Gould et al. 2017; Heinz and Stiasny 2017; Higuera and Ramirez 2019; Manore et al. 2017). The virus is primarily spread by *Aedes aegypti* mosquitoes which appear to have expanded its range causing infections in new areas. Similar to Zika virus, other arboviruses such as Chikungunya virus and Dengue virus also emerged in recent years in many new areas or have reemerged with enhanced ferocity in endemic areas. It is estimated that in American continents infection with Chikungunya virus results in approximately 1.2 million cases (Fong 2017; Fong and Alibek 2007). Dengue virus infection is known to have caused multiple outbreaks in Asia and Africa with an urban and sylvatic cycle, which are usually separately maintained. However, recent resurgence in urban outbreaks of Dengue virus in many parts of the world is perhaps due to enhanced vector activity and failure of appropriate public health measures (Fong 2017; Fong and Alibek 2007; Fong and Drlica 2003). Apart from general warming of climate, extreme weather events also pose risks. Effects of extreme weather events may be on two fronts. First, these events may lead to earlier appearance of a seasonal infectious agent in an area or may introduce an agent in a new area as was observed for Rift Valley fever in Africa. In 1997–1998 following extremely heavy rainfall, almost 90,000 cases and 1000 deaths due to Rift Valley fever were recorded in the countries lining Horn of Africa (Saker et al. 2004). Second, existing public health services are



often overwhelmed during extreme weather events causing under-control diseases to flare up, e.g. urban settlements of developing countries usually experience outbreaks of dengue fever, chikungunya infections following extreme rainfall and waterlogging inside cities. During 1987–1992 in the USA, prolonged drought was followed by heavy rainfall in 1993, causing a sudden rise in rodent population as most of the rodent predators were killed during the preceding draught. Booming rodent population subsequently caused the emergence of Hantavirus pulmonary syndrome (Grubaugh et al. 2019; Nickerson and Schurr 2006; Saker et al. 2004).

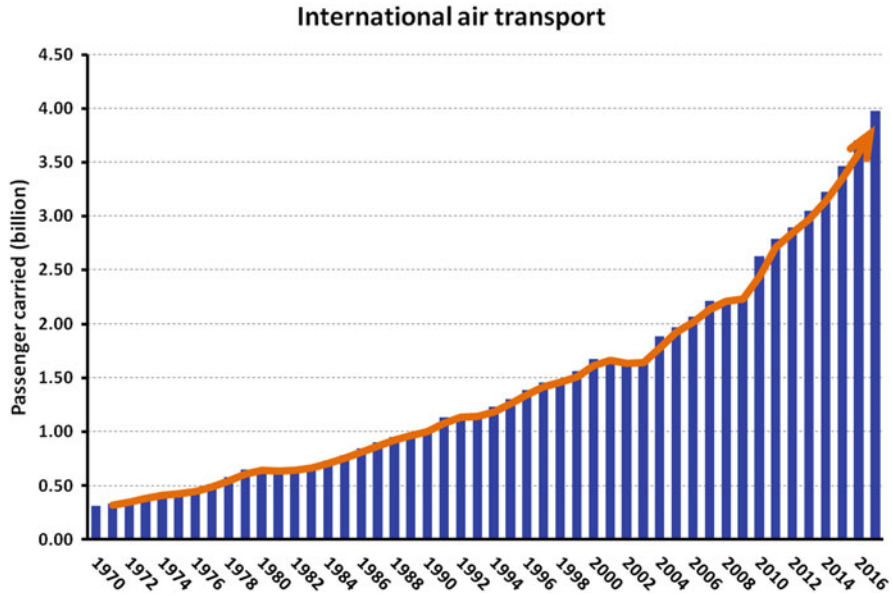
### ***14.2.3 International Travel, Trade and Commerce***

#### **14.2.3.1 International Travel**

Dissemination of infectious diseases, including that of zoonotic diseases of viral aetiology, had historically been associated with human movements. History of zoonotic diseases reveals that many infections such as plague, yellow fever spread all over the world following human movement across countries and continents. However, in recent times the risks of spread of infections have dramatically increased in contrast to ancient times. With the advent of cheaper air travel and economic improvements, human movements across international borders have increased by an enormous scale with miraculous speed and invasive reach (Fig. 14.3).

These days, it is not impossible for any person to reach any place on earth within 24–48 h. Increased magnitude of high-speed travel to remote locations enabled many zoonotic diseases to establish a new focus of infections in distant places. There is number of instances where spread of viral zoonotic diseases has been exacerbated by air travel.

Influenza A virus is a highly infectious agent responsible for epidemics of influenza throughout the world, causing 300–600 thousand deaths globally. In addition to human infection, the virus causes infection in a wide range of hosts and is maintained in nature among wild birds, especially migratory water birds. Usually, strains of Influenza A virus infect their respective hosts, but domestic animals such as pigs may be infected by both avian and human strains of the virus. Due to segmented genomic structure of the virus, mixed infection of the pigs with avian and human type of the virus may give rise to recombinant strain with new antigenic structure which may potentially cause pandemic across the world and caused multiple pandemics in the past resulting in deaths in millions in the past. International air travel further aids in dissemination of the virus, allowing rapid global mobility of incubating hosts (humans). Recently in 2009, a novel strain of influenza virus emerged in a Mexican pig farm. With the help of international air travel the virus rapidly spreads throughout the world and caused about 123–200 thousand deaths worldwide (Findlater and Bogoch 2018; Houghton 2019; Mangili et al. 2015).



**Fig. 14.3** International air travel trend (Data source: <https://data.worldbank.org/indicator/IS.AIR.PSGR>. Accessed on 14 Aug 2019). International air transport (passenger carried) includes both domestic and international aircraft passengers of air carriers registered in the country. From 1970 onwards there was a rapid increment in international air travel. In the year 2016, as many as nine times the people travelled through international air as compared to 1970. Such a rapid rise in air travel aggravates the transport of zoonotic viral infections throughout the world as was evidenced in case of outbreak of severe acute respiratory syndrome

Similar to Influenza A virus, in case of a global outbreak of severe acute respiratory syndrome (SARS) also, air travel played a key role in the dissemination of the infection. SARS is caused by a Coronavirus which is believed to have originated in horseshoe bats. From horseshoe bats, the virus was transmitted to civet cats from which the virus eventually was spread to humans and finally human-to-human transmission led to the epidemic spread of the disease. In February of 2003, SARS was reported for the first time from the Guangdong province in China. In about 8 months of the SARS epidemic, the disease caused more than 8000 cases and approximately 750 deaths (Findlater and Bogoch 2018; Mangili et al. 2015; Mourya et al. 2019). The disease was characterized by fever, sore throat, dry cough, respiratory difficulties, myalgia and malaise, sometimes rash and diarrhoea. Case fatality rates of SARS were about 10%. After the initial detection of these emerging viral zoonoses, the disease spread to more than 12 countries, including Taiwan, Hong Kong, Vietnam, Singapore, Philippines, and Canada mostly facilitated by international air travel and mobility of the infected incubating individuals. Rapid global spread led to international panic and loss in tourism and trade. Estimates of economic loss due to SARS indicated a cost of USD 11 billion worldwide which included costs of various public health measures for containing the spread,

treatment, public awareness, and additional screening at airports for SARS. SARS had brought about changes in International Health Regulations practices and adoption (Findlater and Bogoch 2018; Fong and Drlica 2003; Grubaugh et al. 2019; Vonesch et al. 2019).

In 2012, the zoonotic potential of the Coronaviruses caused the emergence of another viral disease named Middle East respiratory syndrome (MERS) in Saudi Arabia. Domesticated camel is believed to be the reservoir of the MERS Coronavirus. In humans, the infection causes flu-like symptoms characterized by fever with occasional chills, cough, breathing trouble, sore throat, myalgia, and abdominal tenderness. However, vomiting and diarrhoea are also noticed. Case fatality rates may reach as high as 35%. Human-to-human transmission occurs through close contact with infected individuals. Since its first report in 2012, the disease spreads to 27 countries in four continents (Asia—Saudi Arabia, Bahrain, Iran, Jordan, Lebanon, Kuwait, Oman, Qatar, United Arab Emirates, China, Malaysia, Republic of Korea, Thailand, Philippines; Africa—Tunisia, Yemen, Algeria, Egypt; Europe—Austria, France, Germany, Greece, Italy, the Netherlands, Turkey, United Kingdom; and North America—United States) with more than 2000 cases. Since Saudi Arabia is an important tourist destination with considerable air connectivity, many more people from various countries are at risk of contracting the disease. In addition, international Hajj festival with huge inflow of tourists from all over the world over a short period of time also offers opportunity for potential spread of MERS Coronavirus (Bailey et al. 2018; Findlater and Bogoch 2018; Grubaugh et al. 2019; Li and Du 2019; World Health Organization 2014).

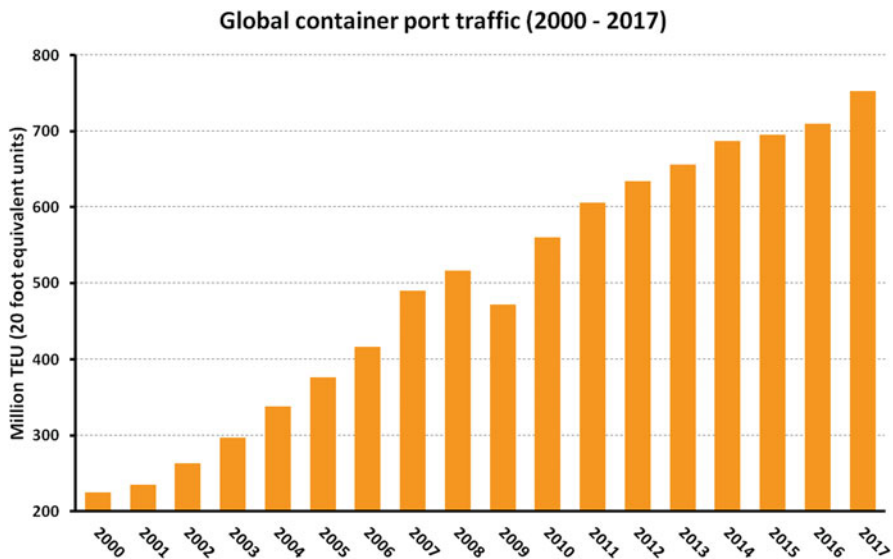
The global spread of other zoonotic viruses was also accelerated by international air travel. In western Africa in 2014, the epidemic of Ebola virus disease broke out. Though the virus was first discovered in 1976, the West African outbreak was perhaps the largest. Natural hosts of the virus are believed to be Fruit bats (*Pteropus*). Humans acquire Ebola virus infection from close contacts with bats and their body fluids. However, other animals and their body fluids have also been implicated in the spread of the disease to humans. Human-to-human transmission occurs similarly through close contact and their bodily secretions and fluids. Fomites and objects that had been contaminated by infected persons also play an important role in the transmission of the disease. Highly infectious nature of the disease contributes to rapid human-to-human spread, and in many cases, health workers fell victim to Ebola infection while attending to infected people. In humans, Ebola virus disease is characterized by fever, sore throat, headache, myalgia followed by vomiting, diarrhoea, and typical rashes. Eventually the disease causes multi-organ failure leading to death in many cases. Hemorrhagic signs such as gingival bleeding and blood in stool are also reported. Case fatality rates of Ebola virus disease are very high and vary between 25 and 90% with average being around 50%. The spread of the 2014 epidemic of Ebola virus disease was facilitated initially through road travel and the disease clawed out from Sierra Leone to neighbouring Guinea and Liberia. Subsequently, the disease leaped out of these countries through international air travel to several other faraway countries including the USA, Italy, United Kingdom, Spain, and Nigeria. Over 2 years the deadly epidemic caused approximately 22,000 cases

with more than 11,000 deaths. Outbreaks of the disease are continuing in various areas of African continent with huge potential for global spread (Beeching et al. 2014; Broadhurst et al. 2016; Findlater and Bogoch 2018; Malvy et al. 2019). In effect the air travel, especially the international routes, enabled many viral zoonotic diseases to leap out of its initial foci with relative ease and made the job of epidemiologists more difficult who can no longer rely on the classical parameter of geographic contiguity of disease dissemination.

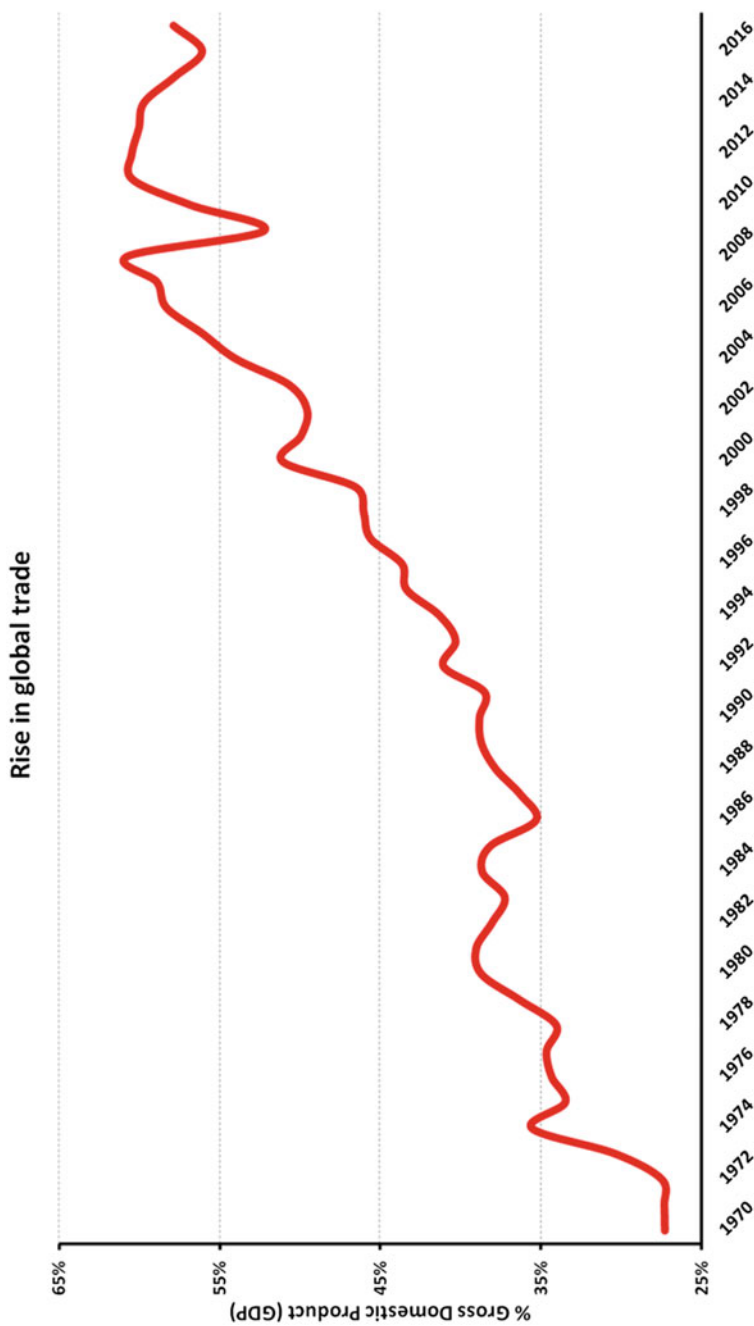
### 14.2.3.2 International Trade and Commerce

With increasing globalization, the volume of trade within and across national borders has also increased significantly. Data from the shipping industry reveal a phenomenal increase in container cargo in various seaports during the last two decades (Fig. 14.4).

Not only did the volume of trade increased in the last decades, there was also rise in varieties of materials traded. Moreover, trading activities became more and more important in the economic output of countries, which is evident when measured against country GDPs (Fig. 14.5).



**Fig. 14.4** A global upsurge in shipping activities (Data source: <https://data.worldbank.org/indicator/IS.SHP.GOOD.TU>. Accessed 14 Aug 2019). As per data of the World Bank, the volume of container traffic through various shipping routes increased from about 225 million TEU to more than 75 million TEU indicating a 3.5-fold increase in just 17 years. A large volume of trade in many instances facilitates spread of zoonotic infections, including viral diseases across international borders and continents



**Fig. 14.5** The worldwide increase in trade volumes (Data source: <https://data.worldbank.org/indicator/NE.TRD.GNFS.ZS>, Accessed 14 Aug 2019). Despite occasional instability, from 1970 onwards there had been a steady rise in global trade. The rise in trade was not only in quantum of goods and services traded, the contribution of trading activities in the economies of the nations also increased. This indicated that if the current trend continues, the global economy will largely be driven by trading activities. As majority of these trading activities are across international borders, they may facilitate the emergence of viral zoonotic diseases as has been observed in the past centuries when diseases spread along the trade routes

Historically zoonotic diseases, including viral zoonosis, were disseminated along the trade routes. The plague reached the western hemisphere following the ancient trade routes. Yellow fever, an important viral zoonotic disease, is believed to have spread from Africa to America following the shipping routes (Chomel 1998; Dash et al. 2013; Esser et al. 2019; Findlater and Bogoch 2018; Higuera and Ramirez 2019; Muzemil et al. 2018; Saker et al. 2004; Tagliapietra et al. 2018).

While trades in goods and services are a general facilitator of spread of zoonotic diseases, trading in wildlife and products is another important avenue for dissemination of zoonoses. Wildlife meat is traditionally savoured by many tribal populations around the world. However, meat from wildlife has been implicated in the emergence and dissemination of Nipah virus, Ebola virus, Monkeypox virus (Ambat et al. 2019; Beeching et al. 2014; Broadhurst et al. 2016; Karesh et al. 2012; Malvy et al. 2019; Mazzola and Kelly-Cirino 2019; Muzemil et al. 2018; Petersen et al. 2018; Sayed et al. 2019). In recent years, the role of civet cats used as human food came into increasing attention following SARS epidemic. The causative agent of SARS (SARS-CoV) thrives naturally in bats, and civet cats might have picked up infection occasionally from them. However, when meats from civet cats found their way into the market, the SARS-CoV spilled over to new hosts, humans; and a new viral zoonosis, SARS emerged (de Wit et al. 2016; Parashar and Anderson 2004). Apart from meat from wildlife, various other body parts of animals are used in traditional medicines (Chomel et al. 2007). Trading of pets such as psittacine birds and rodents has become increasingly common and also might play roles in the emergence and spread of viral zoonoses (Chomel et al. 2007). The importation of Monkeypox infected pet rodents in to the USA indicated the potentials of trade in wildlife as a driver for the emergence of viral zoonoses (Chomel 1998; Petersen et al. 2019; Sklenovská and Van Ranst 2018). An increasing trend of adopting more and more exotic pets may also serve as source for spread of new viral zoonoses. In the USA and Germany, outbreak of chorio-lympho-meningitis was reported among pet owners following adoption of hamsters (Chomel 1998).

#### ***14.2.4 Human Demographic Changes***

Over the last couple of decades, the world has witnessed an explosive rise in the human population with associated changes in demographic patterns. Cultural and behavioural changes were also pronounced. World population projections indicate that by the year 2050 the global population is expected to reach 9.7 billion with most of the growth in developing regions of the world (<https://www.un.org/development/desa/en/about/desa-divisions/population.html>). It is projected that with the rise in population, there will be even denser spatial clustering of populations in the cities of the world. Though cities usually provide better economic opportunities and better livelihood options, often the public service infrastructures including health and sanitation measures are stretched beyond limits. These situations provide fertile grounds for zoonotic diseases to spread, especially vector-borne viral zoonoses.

#### 14.2.4.1 Rising Population Density and Urbanization

Increasing population and concentration of economic activities in selected areas have resulted in massive urbanization and increased population density all over the world including in urban areas. While the quantum of urban areas remained almost unchanged, number of people living in cities has increased steadily over the years. Almost 55% of the global population today lives in cities. At the same time, global population density rose from about 28 persons/sq. km in the 1970s to more than 59 persons/sq. km in 2019 (Fig. 14.6).

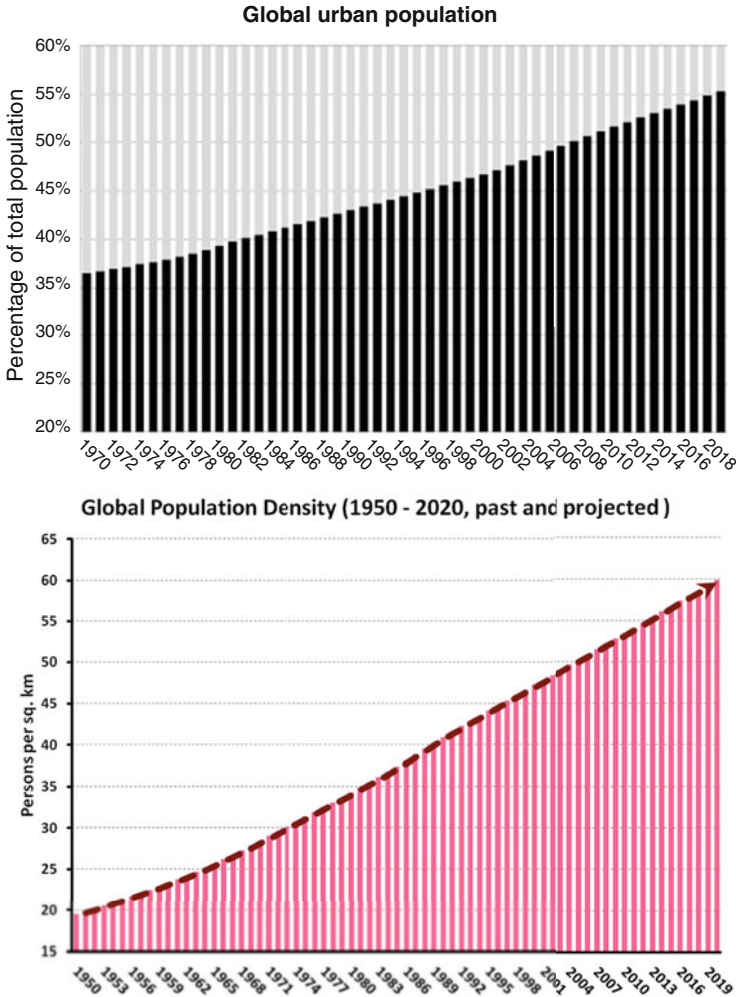
Increased population density allows more frequent contacts between infected hosts and susceptible individuals. Host population density also affects the efficiency of the vectors for transmission of the diseases. Studies have shown that increased population density does enhance the likelihood of a sustained outbreak of diseases (Tarwater and Martin 2001). Many cities in Asia have become almost endemic for several viral zoonotic diseases such as dengue, chikungunya, etc. (Dash et al. 2013; Lal 2007; Mackenzie 2005). With the rise in global temperature and the heat island effects, cities around the world provide an ambience of high host density, warmer temperature, ample breeding grounds for mosquito vectors, e.g. discarded tires accumulated water, plastic pouches with a small puddle of rainwater, clogged drainage due to choking by disposable plastic bags, etc. As a result, there is a consequent rise in the vector-borne zoonotic viruses all around the world. Recent studies on Zika and Chikungunya virus transmission also substantiate these phenomena (Chua et al. 2016; Manore et al. 2017).

#### 14.2.4.2 Population Mobility

Movement of the population across regions had always been associated with the movement of diseases from one place to another. Migration of people occurs due to many factors and due to various reasons. The movement happens within the countries and also across international borders. In the last two decades, the number of refugee population has increased significantly after a steady fall over the preceding decades (Fig. 14.7).

Current estimates reveal that more than 25 million people are living today with refugee status. Moreover, available data from World Bank estimates that the number of international migrants has also increased significantly in 1995. Today more than 3.3% of the global population is international migrants.

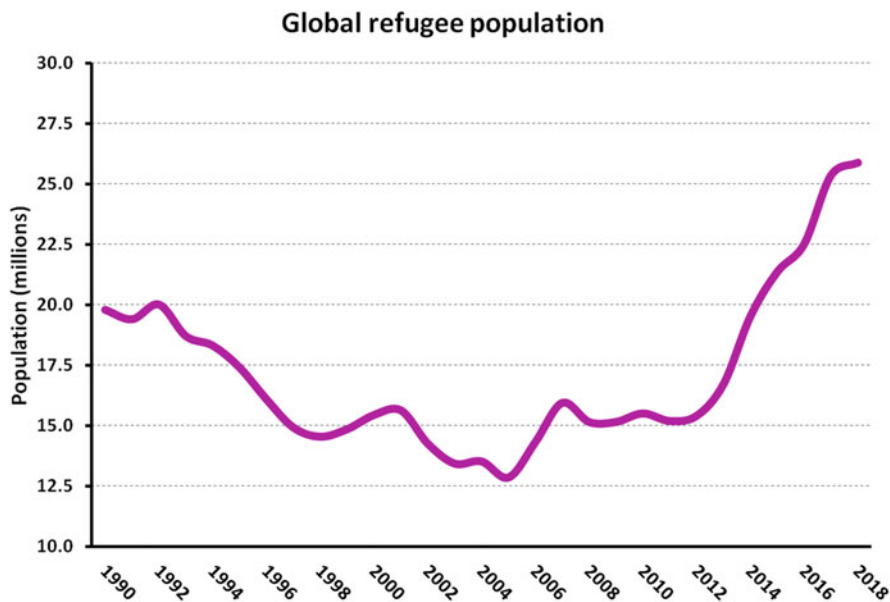
While economic opportunities had traditionally been a major force behind the trans-border movement of people, other factors such as war, border conflicts, ethnic fights, and natural calamities such as drought, flood, desertification, rising sea level, etc. also contribute towards migration of people en masse. Migration of human population comes along with consequent ghettoization of the displaced population with the considerable downside of sanitation, hygiene, water quality, and overall public health infrastructure in the area. All these factors encourage diseases, including vector-borne zoonotic viral diseases to break out. The current crisis of



**Fig. 14.6** Urbanization and population density trends (Data source: <https://data.worldbank.org/indicator/sp.urb.totl.in.zs>. Accessed 14 Aug 2019. <https://data.worldbank.org/indicator/EN.POP.DNST>. Accessed 14 Aug 2019). All over the world, there had been a steady increase in urban population. In the 1970s, about 35% of global population was urban which rose to 50% in the preceding decade. As per available data in 2018 more than half of world population lives in cities creating more stress on urban infrastructures. Global population density, on the other hand, saw meteoric surge. On every square kilometre of land, almost three times the people live today (2019) as compared to 1950. Higher population density exerts pressure on available natural resources and poses challenges to available economic opportunities

displacement of Rohingya population in Southeast Asia is an example of these. Several researchers have expressed concerns about the possibility of outbreak of diseases among these displaced peoples (Cousins 2018; Islam and Nuzhath 2018). Similar situations may also be observed in many places in Africa (Castelli and Sulis 2017; Rote and Markides 2015).





**Fig. 14.7** Global refugee population (Data source: <https://data.worldbank.org/indicator/sm.pop.refg>. Accessed 14 Aug 2019). ‘Refugees are persons who are outside their country of origin for reasons of feared persecution, conflict, generalized violence, or other circumstances that have seriously disturbed public order and, as a result, require international protection’ (United Nations, 2019). From 1990 to 2004, there was a steady decline in number of refugee population worldwide. This was followed by a sharp rise in refugee population till 2018. These sections of population are considerably deprived of health care and other amenities, including sanitation and hygiene. Zoonotic infections are known to disproportionately affect such vulnerable population leading to the emergence of zoonotic infections

## 14.2.5 Human Behavioural Changes

With the increasing globalization of trade in goods and services accompanied by rising incomes, especially in developing countries, there had been a considerable shift in consumer behaviour and lifestyle of the people. These changes, in some cases, provide suitable stimuli for new zoonotic diseases to emerge.

### 14.2.5.1 Rise in Tourism

Throughout history, touring places had been an important pleasure activity of the people with surplus earnings. However, during the last two decades, there has been a phenomenal rise in international tourism throughout the world. Available data indicate that between 1995 and 2017, number of international tourists arrivals have swelled from about 524 million to more than 1.3 billion worldwide (Fig. 14.8). Not only did the quantum of tourists increased, the type of tourism also changed with more exotic destinations added to the lists of places to be visited.



**Fig. 14.8** A global rise in international tourism (Data source: <https://data.worldbank.org/indicator/ST.INT.ARVL>. Accessed 14 Aug 2019). There has been a phenomenal rise in international tourists. According to available World Bank data the number of international tourists more than doubled during the period between 1995 and 2017

Today people are keenly interested in wildlife tourism, eco-tourism, adventure tourism, and others, which expose the non-native population to remote and/or pristine ecosystems. While the revenue earned is arguably for the preservation of these ecosystems and associated people, there are concerns for encroachment, unnecessary commercialization of forest resources, perturbation to delicate ecosystems, and potential scope for the emergence of new zoonotic diseases including viral diseases. Herpes B virus, also known as Cercopithecine Herpesvirus 1, causes zoonotic infection in humans. Natural hosts of the virus are Macaques. In humans, the disease causes fulminant encephalomyelitis with severe neurological dysfunction with high fatality rates. It has been observed that Asian macaques in Balinese temples were able to transmit Herpes B virus through direct contact. As many Asian temples are important tourist destinations and macaques thrive in the temple and adjacent territory, such contact does pose a significant threat of transmission of viral zoonoses (Chomel et al. 2007). Though, it is difficult to specifically identify the transmission of zoonotic diseases from wildlife to tourists, a recent study by Carne et al. (2017) identified possible risk factors for transmission of zoonotic infections from macaques to tourist. The authors observed that proximity between tourists and visibly diseased macaques, which were coughing and sneezing, posed particular risk and advised appropriate use of personal protective gears for preventing possible new infections.

Though most of the studies document the transmission of zoonosis from wildlife to humans, a few studies documented the occurrences of zoonoses (reverse zoonoses). A review by Messenger et al. (2014) analysed cases of reverse

transmission and found that such incidents were reported from all continents except Antarctica. However, a recent report identified anthropogenic transmission of zoonotic agents to penguins of Antarctica too, thus highlighting the impacts of tourism on uninhabited natural ecosystems (Bolevich 2018).

#### **14.2.5.2 Changing Consumer Behaviours**

The global rise of the consumer-driven market economy led to fundamental changes in the ways goods and merchandises are traded today. The effect is more pronouncedly perceived in the food and agriculture sector than any other areas. Consumers today increasingly demand quality products with better safety. Moreover, exposure to international media and market information led to a rise in taste for exotic products resulting in trans-border movement of food and food products. As most of the consumers with disposable incomes are located in urban areas, there is increasing demand for foods, especially that of animal origins, in urban areas prompting development of peri-urban livestock farming. Peri-urban farming comes with its own set of problems, e.g. environmental pollution, creating a putative focus of zoonotic diseases that may emerge and spread to urban population nearby, providing vector breeding opportunities, etc. These factors along with others are among the inciting causes for the emergence of viral zoonoses, particularly, vector-borne zoonotic infections. In developing countries, surging demand for livestock proteins also results in cropping up of wet markets that are under-regulated. Wet markets provide ample scope for spread of new agents of viral zoonoses to new hosts (humans) resulting in the emergence of novel viral zoonoses. SARS is a prime example of such emergence as described previously (Bailey et al. 2018; de Wit et al. 2016; Lal 2007; Parashar and Anderson 2004; Wang and Anderson 2019).

#### **14.2.6 Microbial Adaptation and Evolution**

To survive in a harsh and changing world, the agents of zoonotic viral infections need to adapt themselves and evolve too with better fitness. Viruses adopt multiple strategies for their survival. The measures range from a mutation in the genome resulting in antigenic variation to evade host immune response to acquiring the ability to overwinter in hosts for a longer period. Even strategies for acquiring new host specificity (or a loss thereof) are also adopted. Thus adaptation and evolution of viral agents provide newer avenues for the emergence of new zoonotic infections. Interestingly, most of the mutational changes in viruses occur in RNA viruses, which are presumably due to lack of proofreading capacity of RNA polymerase enzyme involved in viral replications.

Influenza A virus undergoes antigenic shifts and drifts, which allows the virus to evade existing host immune response. The genome of the Influenza virus is segmented. When a particular cell is affected by two different types of virus, during

replication stage, a recombinant virus may emerge, combining genomic segments from two different strains. The resulting strain bears a new antigenic structure against which hosts do not have any immunologic memory, thus initiating a possible new pandemic (Bailey et al. 2018; Goneau et al. 2018; Lloyd-Smith et al. 2009; Morse et al. 2012). Mechanism of immune evasion through antigenic variation is employed by many flaviviruses too (Heinz and Stiasny 2017; Ye et al. 2013). Mutations in the genome of West Nile virus is known to cause variation in the expression of neutralizing epitopes (Li et al. 2005).

Similarly, antigenic variation among various genotypes of Chikungunya viruses affects cross-protection by neutralizing sera (Chua et al. 2016). Dengue virus, the causative agent of dengue hemorrhagic fever, is also known for antigenic variation for evading host immune barriers (Bell et al. 2019). In addition to short-term adaptation of viruses relatively ancient recombination events are also believed to have contributed towards the emergence of new viral zoonotic agents. It is thought that recombination events involving the Sindbis-like virus and Eastern equine encephalitis viruses led to the emergence of Western equine encephalitis virus (Chomel 1998).

### ***14.2.7 Technology and Industry***

Technology has always been crucial in shaping the history of humans. Since the time of the industrial revolution, the impact of technology on human health and infectious diseases had been immense. Technological advances affected almost all facet of human lives—including change in agricultural production systems, intensification of livestock farming, mechanization and centralization of food processing transport and marketing, organized health care and public health, enhanced communication including shortening of travel times, closed area ventilation systems, creation of new range inanimate objects and fomites harbouring infectious agents (e.g. automated teller machines, public telephones, surfaces of public transport systems, etc.), integrated water supply systems, mechanically controlled sanitation systems, and many more. One of the most current threats from evolving medical technology involves risks of acquiring zoonotic viruses following xeno-transplantation. Concerns have been raised regarding the transfer of porcine endogenous retroviruses to humans following organ transplantation (Prabha and Verghese 2012). Moreover, blood transfusion also poses risk of acquiring hidden viral infection by the recipient, and usually strict vigil is necessary.

Changes in the water supply systems worldwide definitely provided safer water to a large number of population, but at the same time centralization of the water supply system of the cities up the risks of common source epidemics due to viral hepatitis (Bloch et al. 1990; Gall et al. 2015). Similar is the risk associated with centralized processing of food products that are marketed globally (Henchion et al. 2017; Rohr et al. 2019).

### ***14.2.8 Public Health Deficiencies***

Breakdown of public health infrastructure that is supposed to prevent and preempt the spread of infections may also encourage the emergence of new zoonotic infections. Various factors contribute to deficiencies in public health infrastructures worldwide. Among the major factors include political disturbances, wars, border conflicts, ethnic struggles, insufficient investments in public health, and lack of political wills in policymakers. It has been observed that coverage of vaccinations was lower in politically troubled territories leading to an increase in the prevalence of infectious and zoonotic diseases such as yellow fever (Chomel 1998). Overpopulation, unplanned urbanization, migration, and social upheavals may also overwhelm the existing public health infrastructure leading to outbreak of diseases in peri-urban and urban areas as is witnessed by many Asian cities with almost endemic prevalence of mosquito-borne zoonotic viruses. Inadequacy of public health may also lead to spread of HIV infections, which in turn create a buildup of immuno-compromised population susceptible to many emerging and reemerging viral zoonoses, often with fatal outcomes.

## **14.3 Epilogue**

Infectious diseases with its subset of viral zoonotic diseases had always been important in influencing the courses of human development and history. The events of biological and cultural evolutions of *Homo sapiens* are a history of co-evolution with infectious diseases, many of which were shared with animals. Infectious diseases and zoonoses, in particular, perpetuate in the nature within complex yet delicately balanced ecosystems which when perturbed spills out the infections to unnatural hosts, mostly humans. This understanding of zoonotic diseases ecology is central to disease emergence. With rising population, expanding globalization of trade, commerce, agricultural activities, changing the climate, declining forest covers, the root drivers for the emergence of zoonotic diseases, which are often of viral origin, sometimes become obscured. Recognizing these linkages that drive the emergence of viral diseases is crucial to our understanding of complex disease biology and attaining sustainable health for all. As highlighted in this chapter before, increasing academic interest in the study of 'emerging viral zoonoses' is a positive indication which needs to be followed by actionable information, judicious execution, and creation of a policy framework for effective handling of contingencies arising out of the emergence of viral zoonotic diseases.

**Acknowledgements** All the authors of the manuscript thank and acknowledge their respective Institutes/Organizations.

**Conflict of Interest** There is no conflict of interest.

## References

- Acosta-Ampudia Y, Monsalve DM, Rodríguez Y, Pacheco Y, Anaya JM, Ramírez-Santana C (2018) Mayaro: an emerging viral threat? *Emerg Microbes Infect* 7:1–11. <https://doi.org/10.1038/s41426-018-0163-5>
- Afrough B, Dowall S, Hewson R (2019) Emerging viruses and current strategies for vaccine intervention. *Clin Exp Immunol* 196:157–166. <https://doi.org/10.1111/cei.13295>
- Al-Tayib O (2019) An overview of the most significant zoonotic viral pathogens transmitted from animal to human in Saudi Arabia. *Pathogens* 8:25. <https://doi.org/10.3390/pathogens8010025>
- Ambat AS, Zubair SM, Prasad N, Pundir P, Rajwar E, Patil DS, Mangad P (2019) Nipah virus: a review on epidemiological characteristics and outbreaks to inform public health decision making. *J Infect Public Health* 12:634. <https://doi.org/10.1016/j.jiph.2019.02.013>
- Anderson TR, Hawkins E, Jones PD (2016) CO<sub>2</sub>, the greenhouse effect and global warming: from the pioneering work of Arrhenius and Callendar to today's Earth System Models. *Endeavour* 40:178–187. <https://doi.org/10.1016/j.endeavour.2016.07.002>
- Bailey ES, Fieldhouse JK, Choi JY, Gray GC (2018) A mini review of the zoonotic threat potential of influenza viruses, coronaviruses, adenoviruses, and enteroviruses. *Front Public Health* 6:1–7. <https://doi.org/10.3389/fpubh.2018.00104>
- Beeching NJ, Fenech M, Houlihan CF (2014) Ebola virus disease. *Br Med J* 349:g7348. <https://doi.org/10.1136/bmj.g7348>
- Bell SM, Katzelnick L, Bedford T (2019) Dengue genetic divergence generates within-serotype antigenic variation, but serotypes dominate evolutionary dynamics. *eLIFE* 8. <https://doi.org/10.7554/eLife.42496>
- Bird BH, Mazet JAK (2017) Detection of emerging zoonotic pathogens: an integrated one health approach. *Annu Rev Anim Biosci* 6:121–139. <https://doi.org/10.1146/annurev-animal-030117-014628>
- Blacklaws BA, Daly JM (2018) Emerging viruses of zoonotic and veterinary importance. *Vet J* 233:1–2. <https://doi.org/10.1016/j.tvjl.2017.12.022>
- Bloch AB, Stramer SL, Smith JD, Margolis HS, Fields HA, McKinley TW, Gerba CP, Maynard JE, Sikes RK (1990) Recovery of hepatitis A virus from a water supply responsible for a common source outbreak of hepatitis A. *Am J Public Health* 80:428–430. <https://doi.org/10.2105/ajph.80.4.428>
- Bolevich M (2018) Tourists may be making Antarctica's penguins sick [WWW Document]. *Science* (80). <https://doi.org/10.1126/science.aaw3749>
- Broadhurst MJ, Brooks TJG, Pollock NR (2016) Diagnosis of Ebola virus disease: past, present, and future. *Clin Microbiol Rev* 29:773 LP–773793. <https://doi.org/10.1128/CMR.00003-16>
- Carlson CJ, Zipfel CM, Garnier R, Bansal S (2019) Global estimates of mammalian viral diversity accounting for host sharing. *Nat Ecol Evol* 3:1070–1075. <https://doi.org/10.1038/s41559-019-0910-6>
- Carne C, Semple S, MacLarnon A, Majolo B, Maréchal L (2017) Implications of tourist–macaque interactions for disease transmission. *EcoHealth* 14:704–717. <https://doi.org/10.1007/s10393-017-1284-3>
- Castelli F, Sulis G (2017) Migration and infectious diseases. *Clin Microbiol Infect* 23:283–289. <https://doi.org/10.1016/j.cmi.2017.03.012>
- Chomel BB (1998) New emerging zoonoses, a challenge and an opportunity for the veterinary profession. *Comp Immunol Microbiol Infect Dis* 21:1–14. [https://doi.org/10.1016/S0147-9571\(97\)00018-0](https://doi.org/10.1016/S0147-9571(97)00018-0)

- Chomel BB, Belotto A, Meslin FX (2007) Wildlife, exotic pets, and emerging zoonoses. *Emerg Infect Dis* 13:6–11. <https://doi.org/10.3201/eid1301.060480>
- Chu DT, Ngoc TU, Chu-Dinh T, Ngoc VTN, Van Nhon B, Pham VH, Nghia LL, Anh LQ, Van Pham TH, Truong ND (2019) The possible zoonotic diseases transferring from pig to human in Vietnam. *Eur J Clin Microbiol Infect Dis* 38:1003–1014. <https://doi.org/10.1007/s10096-018-03466-y>
- Chua CL, Sam IC, Merits A, Chan YF (2016) Antigenic variation of East/Central/South African and Asian chikungunya virus genotypes in neutralization by immune sera. *PLoS Negl Trop Dis* 10:1–22. <https://doi.org/10.1371/journal.pntd.0004960>
- Clé M, Beck C, Salinas S, Lecollinet S, Gutierrez S, Van de Perre P, Baldet T, Foulongne V, Simonin Y (2019) Usutu virus: a new threat? *Epidemiol Infect* 147:e232. <https://doi.org/10.1017/S0950268819001213>
- Cousins S (2018) Rohingya threatened by infectious diseases. *Lancet Infect Dis* 18:609–610. [https://doi.org/10.1016/s1473-3099\(18\)30304-9](https://doi.org/10.1016/s1473-3099(18)30304-9)
- Dantas-Torres F (2015) Climate change, biodiversity, ticks and tick-borne diseases: the butterfly effect. *Int J Parasitol Parasites Wildl* 4:452–461. <https://doi.org/10.1016/j.ijppaw.2015.07.001>
- Dash AP, Bhatia R, Sunyoto T, Mourya DT (2013) Emerging and re-emerging arboviral diseases in Southeast Asia. *J Vector Borne Dis* 50:77–84
- de Wit E, van Doremalen N, Falzarano D, Munster VJ (2016) SARS and MERS: recent insights into emerging coronaviruses. *Nat Rev Microbiol* 14:523
- Esser HJ, Mögling R, Cleton NB, Van Der Jeugd H, Sprong H, Stroo A, Koopmans MPG, De Boer WF, Reusken CBEM (2019) Risk factors associated with sustained circulation of six zoonotic arboviruses: a systematic review for selection of surveillance sites in non-endemic areas. *Parasit Vectors* 12:1–17. <https://doi.org/10.1186/s13071-019-3515-7>
- FAO (2011) Mapping supply and demand for animal-source foods to 2030. In: Robinson TP, Pozzi F (eds) *Animal Production and Health Working Paper*. No. 2. <https://doi.org/10.1287/opre.1080.0628>
- Fawzy M, Helmy YA (2019) The one health approach is necessary for the control of Rift Valley fever infections in Egypt: a comprehensive review. *Viruses* 11:1–24. <https://doi.org/10.3390/v11020139>
- Findlater A, Bogoch II (2018) Human mobility and the global spread of infectious diseases: a focus on air travel. *Trends Parasitol* 34:772–783. <https://doi.org/10.1016/j.pt.2018.07.004>
- Fong IW (ed) (2013) *Challenges in infectious diseases*, 1st edn. Springer Science and Business Media, New York
- Fong IW (2017) *Emerging zoonoses : a worldwide perspective*, 1st edn. Springer International Publishing AG, Gewerbestrasse
- Fong IW, Alibek K (eds) (2007) *New and evolving infections of the 21st century*. Springer Science & Business Media, LLC, New York
- Fong IW, Drlica K (eds) (2003) *Reemergence of established pathogens in the 21st century*, 1st edn. Kluwer Academic Publisher, New York
- Gall AM, Mariñas BJ, Lu Y, Shisler JL (2015) Waterborne viruses: a barrier to safe drinking water. *PLoS Pathog* 11:1–7. <https://doi.org/10.1371/journal.ppat.1004867>
- García-Bocanegra I, Rivero A, Caballero-Gómez J, López-López P, Cano-Terriza D, Frías M, Jiménez-Ruiz S, Risalde MA, Gómez-Villamandos JC, Rivero-Juarez A (2019) Hepatitis E virus infection in equines in Spain. *Transbound Emerg Dis* 66:66–71. <https://doi.org/10.1111/tbed.12962>
- Gilbert M, Conchedda G, Van Boeckel TP, Cinardi G, Linard C, Nicolas G, Thanapongtharm W, D’Aielli L, Wint GRW, Newman SH, Robinson TP (2018) Global distribution of chickens and pigs raised in extensive, semi-intensive and intensive systems in 2010 (5 minutes of arc). <https://doi.org/10.7910/DVN/A7GQXG>
- Glennon EE, Restif O, Sbarbaro SR, Garnier R, Cunningham AA, Suu-Ire RD, Osei-Amponsah R, Wood JLN, Peel AJ (2018) Domesticated animals as hosts of henipaviruses and filoviruses: a systematic review. *Vet J* 233:25–34. <https://doi.org/10.1016/j.tvjl.2017.12.024>

- Goneau LW, Mehta K, Wong J, L'Huillier AG, Gubbay JB (2018) Zoonotic influenza and human health—part 1: virology and epidemiology of zoonotic influenzas. *Curr Infect Dis Rep* 20:37. <https://doi.org/10.1007/s11908-018-0642-9>
- Gould E, Pettersson J, Higgs S, Charrel R, de Lamballerie X (2017) Emerging arboviruses: why today? *One Heal* 4:1–13. <https://doi.org/10.1016/j.onehlt.2017.06.001>
- Grubaugh ND, Ladner JT, Lemey P, Pybus OG, Rambaut A, Holmes EC, Andersen KG (2019) Tracking virus outbreaks in the twenty-first century. *Nat Microbiol* 4:10–19. <https://doi.org/10.1038/s41564-018-0296-2>
- Heffernan C (2018) Climate change and multiple emerging infectious diseases. *Vet J* 234:43–47. <https://doi.org/10.1016/j.tvjl.2017.12.021>
- Heinz FX, Stiasny K (2017) The antigenic structure of Zika virus and its relation to other flaviviruses: implications for infection and immunoprophylaxis. *Microbiol Mol Biol Rev* 81:1–27. <https://doi.org/10.1128/membr.00055-16>
- Henchion M, Hayes M, Mullen A, Fenelon M, Tiwari B (2017) Future protein supply and demand: strategies and factors influencing a sustainable equilibrium. *Foods* 6:53. <https://doi.org/10.3390/foods6070053>
- Higuera A, Ramirez JD (2019) Molecular epidemiology of dengue, yellow fever, Zika and chikungunya arboviruses: an update. *Acta Trop* 190:99–111. <https://doi.org/10.1016/j.actatropica.2018.11.010>
- Houghton F (2019) Geography, global pandemics & air travel: faster, fuller, further & more frequent. *J Infect Public Health* 12:448–449. <https://doi.org/10.1016/j.jiph.2019.02.020>
- Islam MM, Nuzhath T (2018) Health risks of Rohingya refugee population in Bangladesh: a call for global attention. *J Glob Health* 8:20309. <https://doi.org/10.7189/jogh.08.020309>
- Jánová E (2019) Emerging and threatening vector-borne zoonoses in the world and in Europe: a brief update. *Pathog Glob Health* 113:49–57. <https://doi.org/10.1080/20477724.2019.1598127>
- Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, Daszak P (2008) Global trends in emerging infectious diseases. *Nature* 451:990–993. <https://doi.org/10.1038/nature06536>
- Karesh WB, Dobson A, Lloyd-Smith JO, Lubroth J, Dixon MA, Bennett M, Aldrich S, Harrington T, Formenty P, Loh EH, MacHalaba CC, Thomas MJ, Heymann DL (2012) Ecology of zoonoses: natural and unnatural histories. *Lancet* 380:1936–1945. [https://doi.org/10.1016/S0140-6736\(12\)61678-X](https://doi.org/10.1016/S0140-6736(12)61678-X)
- Kilpatrick AM, Randolph SE (2012) Drivers, dynamics, and control of emerging vector-borne zoonotic diseases. *Lancet* 380:1946–1955. [https://doi.org/10.1016/S0140-6736\(12\)61151-9](https://doi.org/10.1016/S0140-6736(12)61151-9)
- Kock R (2014) Drivers of disease emergence and spread: is wildlife to blame? *Onderstepoort J Vet Res* 81:4–7. <https://doi.org/10.4102/ojvr.v8i12.739>
- Lal SK (2007) Emerging viral diseases of Southeast Asia. Karger, New York
- Leibovici L (2018) Emerging infections in CMI. *Clin Microbiol Infect* 24:327. <https://doi.org/10.1016/j.cmi.2017.12.014>
- Li F, Du L (2019) MERS coronavirus: an emerging zoonotic virus. *Viruses* 11:663. <https://doi.org/10.3390/v11070663>
- Li L, Barrett ADT, Beasley DWC (2005) Differential expression of domain III neutralizing epitopes on the envelope proteins of West Nile virus strains. *Virology* 335:99–105. <https://doi.org/10.1016/j.virol.2005.02.011>
- Lloyd-Smith JO, George D, Pepin KM, Pitzer VE, Pulliam JRC, Dobson AP, Hudson PJ, Grenfell BT (2009) Epidemic dynamics at the human-animal interface. *Science* 326:1362–1367. <https://doi.org/10.1126/science.1177345>
- Mackay IM, Arden KE (2016) Mayaro virus: a forest virus primed for a trip to the city? *Microbes Infect* 18:724–734. <https://doi.org/10.1016/j.micinf.2016.10.007>
- Mackenzie JS (2005) Emerging zoonotic encephalitis viruses: lessons from Southeast Asia and Oceania. *J Neurovirol* 11:434–440. <https://doi.org/10.1080/13550280591002487>
- Malvy D, McElroy AK, de Clerck H, Günther S, van Griensven J (2019) Ebola virus disease. *Lancet* 393:936–948. [https://doi.org/10.1016/S0140-6736\(18\)33132-5](https://doi.org/10.1016/S0140-6736(18)33132-5)
- Mangili A, Vindenes T, Gendreau M (2015) Infectious risks of air travel. *Microbiol Spectr* 3. <https://doi.org/10.1128/microbiolspec.IOL5-0009-2015>



- Manore CA, Ostfeld RS, Agosto FB, Gaff H, LaDeau SL (2017) Defining the risk of Zika and chikungunya virus transmission in human population centers of the eastern United States. *PLoS Negl Trop Dis* 11:1–19. <https://doi.org/10.1371/journal.pntd.0005255>
- Mazzola LT, Kelly-Cirino C (2019) Diagnostics for Nipah virus: a zoonotic pathogen endemic to Southeast Asia. *BMJ Glob Health* 4:e001118. <https://doi.org/10.1136/bmjgh-2018-001118>
- McMahon BJ, Morand S, Gray JS (2018) Ecosystem change and zoonoses in the Anthropocene. *Zoonoses Public Health* 65:755–765. <https://doi.org/10.1111/zph.12489>
- Messenger AM, Barnes AN, Gray GC (2014) Reverse zoonotic disease transmission (Zooanthroponosis): a systematic review of seldom-documented human biological threats to animals. *PLoS One* 9:1–9. <https://doi.org/10.1371/journal.pone.0089055>
- Möhlmann TWR, Koenraadt CJM, Vogels CBF, Oymans J, Wichgers Schreur PJ, Kortekaas J (2018) Vector competence of biting midges and mosquitoes for Shuni virus. *PLoS Negl Trop Dis* 12:1–13. <https://doi.org/10.1371/journal.pntd.0006609>
- Morse SS (1995) Factors in the emergence of infectious diseases. *Emerg Infect Dis* 1:7–15. <https://doi.org/10.3201/eid0101.950102>
- Morse SS, Schluenderberg A (1990) Emerging viruses: the evolution of viruses and viral diseases. *J Infect Dis* 162:1–7. <https://doi.org/10.1093/infdis/162.1.1>
- Morse SS, Mazet JAK, Woolhouse M, Parrish CR, Carroll D, Karesh WB, Zambrana-Torrel C, Lipkin WI, Daszak P (2012) Prediction and prevention of the next pandemic zoonosis. *Lancet* 380:1956–1965. [https://doi.org/10.1016/S0140-6736\(12\)61684-5](https://doi.org/10.1016/S0140-6736(12)61684-5)
- Mottet A, Teillard F, Boettcher P, De Besi G, Besbes B (2018) Review: domestic herbivores and food security: current contribution, trends and challenges for a sustainable development. *Animal* 12:S188–S198. <https://doi.org/10.1017/S1751731118002215>
- Mourya D, Yadav P, Ullas P, Bhardwaj S, Sahay R, Chadha M, Shete A, Jadhav S, Gupta N, Gangakhedkar R, Khasnobis P, Singh S (2019) Emerging/re-emerging viral diseases & new viruses on the Indian horizon. *Indian J Med Res* 149:447–467. [https://doi.org/10.4103/ijmr.IJMR\\_1239\\_18](https://doi.org/10.4103/ijmr.IJMR_1239_18)
- Muzemil A, Fasanmi OG, Fasina FO (2018) African perspectives: modern complexities of emerging, re-emerging, and endemic zoonoses. *J Glob Health* 8:1–6. <https://doi.org/10.7189/jogh.08.020310>
- Nickerson CA, Schurr MJ (eds) (2006) *Molecular paradigms of infectious disease: a bacterial perspective*, 1st edn. Springer Science & Business Media, LLC, New York
- Ostfeld RS (2009) Biodiversity loss and the rise of zoonotic pathogens. *Clin Microbiol Infect* 15:40–43. <https://doi.org/10.1111/j.1469-0691.2008.02691.x>
- Parashar UD, Anderson LJ (2004) Severe acute respiratory syndrome: review and lessons of the 2003 outbreak. *Int J Epidemiol* 33:628–634. <https://doi.org/10.1093/ije/dyh198>
- Petersen E, Petrosillo N, Koopmans M, Beeching N, Di Caro A, Gkrania-Klotsas E, Kantele A, Kohlmann R, Koopmans M, Lim PL, Markotic A, López-Vélez R, Poirel L, Rossen JWA, Stienstra Y, Storgaard M (2018) Emerging infections—an increasingly important topic: review by the emerging infections task force. *Clin Microbiol Infect* 24:369–375. <https://doi.org/10.1016/j.cmi.2017.10.035>
- Petersen E, Abubakar I, Ihekweazu C, Heymann D, Ntoumi F, Blumberg L, Asogun D, Mukonka V, Lule SA, Bates M, Honeyborne I, Mfinanga S, Mwaba P, Dar O, Vairo F, Mukhtar M, Kock R, McHugh TD, Ippolito G, Zumla A (2019) Monkeypox - enhancing public health preparedness for an emerging lethal human zoonotic epidemic threat in the wake of the smallpox post-eradication era. *Int J Infect Dis* 78:78–84. <https://doi.org/10.1016/j.ijid.2018.11.008>
- Plowright RK, Parrish CR, McCallum H, Hudson PJ, Ko AI, Graham AL, Lloyd-Smith JO (2017) Pathways to zoonotic spillover. *Nat Rev Microbiol* 15:502–510. <https://doi.org/10.1038/nrmicro.2017.45>
- Prabha S, Verghese S (2012) Transmission of zoonoses in xenotransplantation: porcine endogenous retroviruses from an immunological and molecular point of view. *Indian J Med Sci* 66:199. <https://doi.org/10.4103/0019-5359.115210>
- Rezza G, Ippolito G (eds) (2017) *Emerging and re-emerging viral infections*. Springer International Publishing AG, Gewerbestrasse

- Rohr JR, Barrett CB, Civitello DJ, Craft ME, Delius B, DeLeo GA, Hudson PJ, Jouanard N, Nguyen KH, Ostfeld RS, Remais JV, Riveau G, Sokolow SH, Tilman D (2019) Emerging human infectious diseases and the links to global food production. *Nat Sustain* 2:445–456. <https://doi.org/10.1038/s41893-019-0293-3>
- Rote S, Markides K (2015) Migration and health. *Int Encycl Soc Behav Sci Second Ed* 16:407–410. <https://doi.org/10.1016/B978-0-08-097086-8.14024-3>
- Saker L, Lee K, Cannito B, Gilmore A, Campbell-Lendrum D (2004) Globalization and infectious diseases : a review of the linkages. World Health Organization, Geneva
- Sakkas H, Bozidis P, Franks A, Papadopoulou C (2018) Oropouche fever: a review. *Viruses* 10:1–16. <https://doi.org/10.3390/v10040175>
- Sayed A, Bottu A, Qaisar M, Mane MP, Acharya Y (2019) Nipah virus: a narrative review of viral characteristics and epidemiological determinants. *Public Health* 173:97–104. <https://doi.org/10.1016/j.puhe.2019.05.019>
- Semenza JC, Rocklöv J, Penttinen P, Lindgren E (2016) Observed and projected drivers of emerging infectious diseases in Europe. *Ann N Y Acad Sci* 1382:73–83. <https://doi.org/10.1111/nyas.13132>
- Semenza J, Lindgren E, Espinosa L, Svendotter M, Penttinen P, Rocklöv J (2017) Determinants and drivers of infectious disease threats in Europe. *Eur J Pub Health* 25:581–589. <https://doi.org/10.1093/eurpub/ckv167.037>
- ShIPLEY R, Wright E, Selden D, Wu G, Aegerter J, Fooks AR, Banyard AC (2019) Bats and viruses: emergence of novel lyssaviruses and association of bats with viral zoonoses in the EU. *Trop Med Infect Dis* 4:31. <https://doi.org/10.3390/tropicalmed4010031>
- Sklenovská N, Van Ranst M (2018) Emergence of Monkeypox as the most important orthopoxvirus infection in humans. *Front Public Health* 6:1–12. <https://doi.org/10.3389/fpubh.2018.00241>
- Spengler JR, Bergeron É, Spiropoulou CF (2019) Crimean-Congo hemorrhagic fever and expansion from endemic regions. *Curr Opin Virol* 34:70–78. <https://doi.org/10.1016/j.coviro.2018.12.002>
- Tagliapietra V, Rosà R, Rossi C, Rosso F, Hauffe HC, Tommasini M, Versini W, Cristallo AF, Rizzoli A (2018) Emerging rodent-borne viral Zoonoses in Trento, Italy. *EcoHealth* 15:695–704. <https://doi.org/10.1007/s10393-018-1335-4>
- Tarwater PM, Martin CF (2001) Effects of population density on the spread of disease. *Complexity* 6:29–36. <https://doi.org/10.1002/cplx.10003>
- Van Boeckel TP, Brower C, Gilbert M, Grenfell BT, Levin SA, Robinson TP, Teillant A, Laxminarayan R (2015) Global trends in antimicrobial use in food animals. *Proc Natl Acad Sci* 112:5649–5654. <https://doi.org/10.1073/pnas.1503141112>
- van Doorn HR (2014) Emerging infectious diseases. *Medicine (Abingdon)* 42:60–63. <https://doi.org/10.1016/j.mpmed.2013.10.014>
- Vonesch N, Binazzi A, Bonafede M, Melis P, Ruggieri A, Iavicoli S, Tomao P (2019) Emerging zoonotic viral infections of occupational health importance. *Pathog Dis* 77:ftz018. <https://doi.org/10.1093/femspd/ftz018>
- Walker JW, Han BA, Ott IM, Drake JM (2018) Transmissibility of emerging viral zoonoses. *PLoS One* 13:1–12. <https://doi.org/10.1371/journal.pone.0206926>
- Wang LF, Anderson DE (2019) Viruses in bats and potential spillover to animals and humans. *Curr Opin Virol* 34:79–89. <https://doi.org/10.1016/j.coviro.2018.12.007>
- Wang L, Cowled C (eds) (2015) Bats and viruses: a new frontier of emerging infectious diseases. Wiley, Hoboken
- Woolhouse MEJ, Brierley L, McCaffery C, Lycett S (2016) Assessing the epidemic potential of RNA and DNA viruses. *Emerg Infect Dis* 22:2037–2044. <https://doi.org/10.3201/eid2212.160123>
- World Health Organization, R.O. for S.-E.A (2014) A brief guide to emerging infectious diseases and zoonoses, 1st edn. WHO Regional Office for South-East Asia, New Delhi
- Ye J, Zhu B, Fu ZF, Chen H, Cao S (2013) Immune evasion strategies of flaviviruses. *Vaccine* 31:461–471. <https://doi.org/10.1016/j.vaccine.2012.11.015>