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Update on Emerging and Re-Emerging Zoonotic Viral Disease

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Abstract

Emerging zoonotic infectious diseases are those infections, in which the incidence of humans and animal have either increased during the last two decades or threaten to increase in the near future. Among diseases emerging in the 21st century, emerging and re-emerging Zoonotic is raising one of the greatest concerns for public health globally. This infectious diseases account for 26% of annual deaths worldwide. There is clearly a need to understand the dynamics of infectious diseases in complex multi host communities in order to mitigate disease threats to public health, livestock economies and wildlife due to emerging and re-emerging zoonotic diseases. This paper was designed with the objectives to provide updated compiled information about emerging and re-emerging viral zoonotic diseases. The viruses that cause emerging and re-emerging diseases are dynamic and ever changing, able to mutate into forms that at times make them more or less virulent, transmissible, and/or resilient. They emerge and re-emerge in a world of rapid advances and ease in international travel and trade, and are carried around the globe in humans and animals. The ability of a pathogen to infect multiple hosts, particularly hosts in other taxonomic orders or wildlife, is also a risk factors for emergence in human and livestock pathogens. Future occurrences of newly emerging and re-emerging diseases are most likely to erupt at these intensifying interfaces. It is inevitable that emergence and re-emergence will continue to occur. Thus, to reduce the impact, a robust public health infrastructure should be maintained or developed to enable rapid detection and response.

Keywords: Emerging Disease, Re-emerging Disease, Viral Diseases, Zoonosis

INTRODUCTION

Emerging zoonotic infectious diseases are those infections, in which the incidence of humans and animal have either increased during the last two decades or threaten to increase in the near future. This term includes newly appearing infections or those spreading to new geographical areas. It also refers to those diseases which were easily controlled previously by antimicrobials but have developed new resistance to different drugs. Re-emerging infectious diseases are those that have reappeared after a significant decline in their incidence .This may include virus (Zika virus, Nipah virus, Ebola virus,West Nile virus,H5N1 Avian influenza, Rift valley fever, etc),bacteria (Typhoid fever, Diphtheria, Hepatits C,. etc) and protozoa(Alula,*et al*, 2012).

A literature survey identified 1,407 species of human pathogens, with 177 (13%) species regarded as emerging or re-emerging. Distribution of these pathogens by groups shows that 37 per cent of emerging and re-emerging are viruses and prions followed by protozoa (25%) (Lonnie, 2004). Viruses with RNA as their genetic material can quickly adapt and exploit these varying conditions because of the high error rates of the virus enzymes (polymerases) that replicate their genomes. This indicates that emerging and re-emerging pathogens are disproportionately viruses. However, a complex interplay of factors can influence disease emergence and re-emergence (Stuart *et al,* 2000).This often follows ecological change caused by human activities such as agricultural changes, urbanization, migration, deforestation and dam building (Pal, 2007). In addition, international travel, breakdown of public health measures and microbial adaptation also led to the emergence of the zoonotic diseases (Dasseberger, 2000;Chug, 2008).

The emerging and re-emerging infectious diseases account for 26 per cent of annual deaths worldwide. Nearly 30 per cent of 1.49 billion disability-adjusted life years (DALYs) are lost every year to diseases of infectious origin (Taylor, et *al.,* 2001; WHO, 2005). The burden of morbidity and mortality associated with infectious diseases falls most heavily on people in developing countries, and particularly on infants and children (about three million children die each year from malaria and diarrhoeal diseases alone) (Fauci,2001) and Future occurrences of newly emerging and re-emerging diseases are most likely to erupt at these intensifying interfaces. In less developed countries, the communities most likely to be affected by such outbreaks are, those that are poor or in less accessible areas. Such community’s frequently rely on inadequate methods of medical surveillance and diagnostics, as well as traditional treatment methods. As the result, it is unfortunately quite likely that an emerging disease with high epidemic potential may only be detected after it has become established in humans or their livestock and has already spread significantly (Westbury and, 2000). There is clearly a need to understand the dynamics of infectious diseases in complex multi host communities in order to mitigate disease threats to public health, livestock economies and wildlife due to emerging and re-emerging zoonotic diseases. Therefore, the aims of this paper were to provide updated compiled information about emerging and re-emerging viral zoonotic diseases. Moreover, the paper reviews the factors responsible for emergencies and re emergences of these diseases and provides information on future challenge and strategy of control and prevention of these diseases.

EMERGING ZOONOTIC VIRAL DISEASES

Zika Virus

Among diseases emerging in the 21st century, *Zika* is raising one of the greatest amounts of concern for public health globally. *Zika virus (ZIKV*) has presented as outbreaks since 2007; however, more recently, it has become the main suspected cause of an unusual and completely unexpected microcephaly epidemic, exposing the urgent needs for knowledge about this disease Zika is a mosquito-transmitted virus that has spread broadly in tropical regions and caused epidemics, especially in the past 8–9 years. In its native range in West Africa and Uganda, Zika virus is maintained in forest cycles between infected tree hole mosquitoes and arboreal primate hosts, with human infections regarded as incidental and medically inconsequential (Kuno,et al.,1998). Zika virus (ZIKV) disease is caused by an arthropod-borne (arbo) virus (Flaviviridae family genus *Flavivirus*, Spondweni serocomplex) consisting of three genetically distinct strains (lineages); one from Asia and two from Africa (Kuno, *et al.*, 1998; Faye et al. 2014.)

The virus was first isolated from Zika Forest of Uganda in 1947 from a sentinel rhesus monkey and named after Zika Forest, where it was first discovered by scientists working at the nearby Yellow Fever Research Institute in Entebbe, Uganda. Initial isolates came not only from the sentinel monkey, caged on a tree platform in this forest, but also from Aedes africanus mosquitoes captured while feeding on humans (Dick *et al.*, 1952). In the invasive range of the virus outside of Africa, the most likely vector of Zika is Aedes aegypti, first recognized as infected in nature in Malaysia (Marchette *et al.*1969). The preference of domestic Aedes aegypti for feeding on human hosts in tropical cities overrides its inefficiency in developing the ZIKV (Diagne *et al.*,2015). The other is Aedes albopictus which has been implicated as a Zika vector in Gabon (Grard *et al.*, 2014) and has expanded its invasive range worldwide. This finding assumes greater importance because both the mosquito and Zika virus are extending their range and thus it is possible that human-feeding populations of this vector species may co-occur with the emergent virus (Duffy *et al.*, 2009). Zika was later identified from multiple countries in West and Central Africa, where it was also believed to persist in forest cycles between arboreal mosquito vectors and simian hosts (Faye *et al.*, 2014). Evidence of Zika in Pakistan, Malaysia, and Indonesia indicated that Zika became established in Asia, perhaps around Island, Micronesia, which resulted in 2007 in the first epidemic attributable to this virus (Duffy ,*et al.*, 2009 and Faye *et al.*, 2014). This Asian lineage was believed to be the source of an introduction of Zika to Yap Island, Micronesia, which resulted in 2007 in the first epidemic attributable to this virus (Duffy, *et al.*, 2009).

A larger outbreak of Zika in French Polynesia during 2013, also derived from the Asian lineage, followed the epidemic in Yap (Cao-Lormeau *et al.*, 2014). An epidemic in north eastern Brazil in early 2015 Campos *et al.*, (2015) is suspected to have begun with the introduction of Zika by a traveler from French Polynesia (Musso, 2015). More than twenty countries in the tropical Americas, as well as the Common wealth of Puerto Rico and the US Virgin Islands, currently recognize active ZIKV transmission (CDC ,2016).

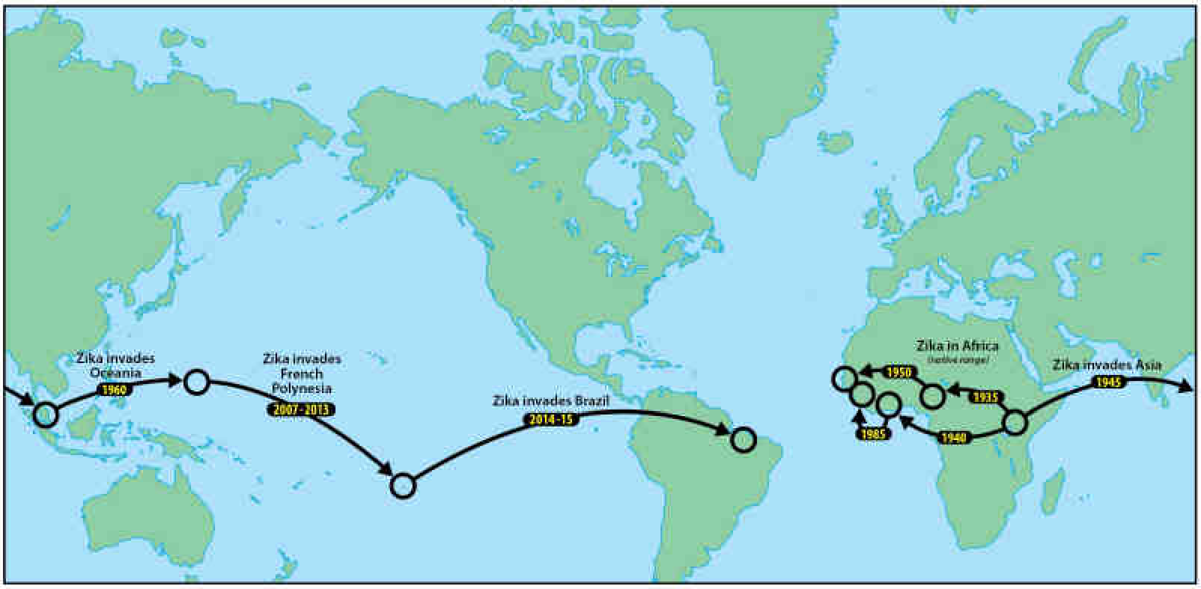

Figure 2. Proposed directional movement of Zika virus within Africa and through its invasive ranges Source: (Faye *et al.*, 2014). .

Until recently illnesses from ZIKV have been classified as clinically mild with symptoms lasting several days to a week, with many infected individuals being asymptomatic (80%) (CDC, 2016). Hospitalizations and fatalities were uncommon. However, the 2013 ZIKV outbreak in French Polynesia implicated ZIKV in neurological complications resulting in Guillain-Barré syndrome, and the recent ZIKV outbreak in Brazil is associated with an increase in the number of babies born with micro cephaly (ECDC 2015; PAHO/WHO 2015, 2016).

Avian Influenza

The emergence and re-emergence of influenza viruses with pandemic potential for both human and veterinary public health is of great concern to humans globally. The convergence of factors affecting contemporary human and animal health issues has led to changing roles for veterinarians and public health officials worldwide (Webster *et al.*, 2004). Avian influenza or bird flu, caused by the highly pathogenic H5N1 influenza virus has affected at least eight countries in Asia leading to outbreaks of severe disease, mass deaths and destruction of chickens. The virus that caused such destruction is known to have the capacity to be transmitted from infected chickens to cause severe disease and high mortality in humans (Obi *et al* ., 2010).

The evolution of influenza is a continuing process and the increasing of emergence of the highly pathogenic and the increasing of emergence of the highly pathogenic to both veterinary and human public health officials. Highly concentrated poultry and pig farming in conjunction with traditional live animal provide optimal condition for increased mutation, re assortement and recombination of influenza virus. Strategies to reduce the evolution of influenza and emergence of pandemics include the separation of species, increased biosecurity and the development of new vaccine strategies and better basic knowledge of the virus (Webster *et al*., 2004).
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Ebola Virus

Ebola virus, the cause of Ebola viral disease, has drawn international attention after a recent outbreak in West Africa. Ebola virus belongs to the family of filoviruses.(Feldmann,2014) Ebola and Marburg viruses, along with the family of arena viruses (Lassa and New World arenaviruses), bunyaviruses, and flaviviruses (eg, yellow fever), cause a viral hemorrhagic fever (Pigott, 2005) . Ebola was first recognized in 1976 when 2 unrelated outbreaks occurred in southern Sudan and the Democratic Republic of the Congo. The virus was given the name Ebola after a small river near the epicenter of the Democratic Republic of the Congo outbreak (Muyembe *et al* .,2012).Including the present epidemic, there have been approximately 20 recognized outbreaks of Ebola, all occurring in Africa, with fatality rates of 25% to 90%.(WHO, 2014)

The current Ebola outbreak that began in March 2014, initially announced by the Centers for Disease Control and Prevention (CDC) on March 25th, is the largest in history (CDC, 2014). It is associated with a new strain of Zaire species, the most deadly of the 5 Ebola species, with a reported case fatality rate of approximately 55% (Gostin *et al*., 2014). According to the CDC, as of September 30, 2014 (the most recent information available at this article's writing), there have been 6,574 total cases (3,626 were laboratory confirmed) across 5 countries (Guinea, Liberia, Nigeria, Senegal, and Sierra Leone) and 3,091 suspected case deaths (CDC.2014). Figure 1 shows a map of the West African countries affected by the outbreak (CDC, 2014).

Figure 1. Centers for Disease Control and Prevention map of 2014 Ebola outbreak in West Africa outbreak distribution map,updated September 17, 2014.

Of the 5 species of Ebola virus, only 3 are of human significance and have also been implicated in large outbreaks: Zaire, Sudan, and Bundibugyo. Bundibugyo and Sudan have a fatality rate of approximately 25% and 50%, respectively (Pigott, 2005). A fourth species, Côte d'Ivoire virus, was responsible for a single case in 1994 in Côte (Feldmann and Geisbert ,2011). The fifth species, Reston virus, was found in the Philippines and the United States (Preston, 1995) but is not responsible for any symptomatic disease in humans to date (Barrette *et al.*, 2014).

Transmission of Ebola viral disease occurs by direct contact through broken skin or mucous membranes or by objects such as needles. Bodily fluids, including saliva, blood, vomit, diarrhea, and semen, appear to be infectious (CDC, 2014). Transmission has also occurred from deceased Ebola victims to family members who performed ritualistic washing of the corpse at the burial, through direct contact with infected animals, especially handling animal carcasses or consuming bush meat (Francesconi, 2003).

In general, Ebola is not thought to be spread by droplets or airborne transmission, although the role of airborne transmission during recent outbreaks has not been entirely excluded (Francesconi, 2003). Ebola infection is characterized by an initial nonspecific viral syndrome that is further complicated by septic shock and disseminated intravascular coagulation. Incubation time for humans ranges from 2 to 21 days. Most patients become symptomatic after 8 to 9 days, and once symptoms are present, the infection is contagious (Glatter,2014)

Niphah Virus

NIpah virus is an emerging zoonotic virus closely related to Hendra virus. Both are members of the genus Henipa virus, a new class of virus in the Paramyxo viridae family,both viruses are public concern for their wide host range, ability to jump species barrier, high mortality they cause (Brooks, et al.,2010). Fruit bats of the family Pteropodidae – particularly species belonging to the Pteropus genus are the natural hosts for Nipah virus. These bats are migratory, and there is no apparent disease in fruit bats (Chowdhury, 2011).

Nipah virus was first identified and confirmed in Malaysia in 1999 when the virus crossed the species barrier from bats to pigs and then infected humans, inducing encephalitis with up to 40% mortality. The survivors were inflicted with residual neurological problems (Mudie, 2011). The virus itself was named after a town in Malaysia. The outbreak was attributed to pigs consuming fruits partially eaten by fruit bats, and transmission of infection to humans. Most of the affected pigs had severe lung lesions with varying degree of lung and trachea with or without blood.

Nipah virus emerged as a new human pathogen under changing ecological conditions that point to acomplex inter play of human activities as the ultimate cause of this disease emergence (Webster *et al* ,2004). Infected people initially develop influenza-like symptoms of fever,headaches, myalgia, vomiting and sore throat.This can be followed by dizziness, drowsiness,altered consciousness (Goh et al,2000) and neurological signs that indicate acute encephalitis. In the long term, persistent neurological dysfunctions are observed in more than 15% of people and the case fatality rate is estimated at 40% to 75%; however, this rate can vary by outbreak depending on local capabilities for surveillance investigations, (Colledge et al, 2010).

REEMERGING ZOONOTIC VIRAL DISEASES

Rift Valley Fever

Rift Valley fever (RVF) is an important, neglected, zoonotic, mosquito-borne viral disease that causes severe human illness and death, as well as significant economic losses in the livestock industry. The disease is caused by RVF virus (RVFV), an arbovirus of the Bunyaviridae family (WHO, 2001). The virus is known to infect different animal hosts, particularly sheep, cattle, and goats.2 Infection by RVFV usually spreads in animals first via mosquito bites (WHO, 2016). From animals, the virus is transmitted to humans through direct contact, such as contact with the raw products or secretions of infected animals (Acha,and Szyfres ,1987; Seufi ,and Galal ,2010).

The virus can also be transmitted by aerosols from blood and other infected body fluids, and infections are frequent among virologists, veterinarians, and slaughterhouse workers (Turkistany *et al*., 2001; Antonis *et al.*, 2013). *Aedes* mosquitoes are considered to be the major maintenance host and source of RVFV outbreaks (Linthicum *et al.*, 1999; O'Malley ,1990; Crabtree *et al.*, 2012). It has been confirmed that RVFV is carried in *Aedes* mosquito eggs, which can survive in dried mud for several years (Davies *et al.*, 1985). Transovarial transmission of RVFV depends on certain ecological conditions that enable the virus to survive in water while infected eggs hatch to become adult mosquitoes (Sang *et al*.,2010). However, these ecological conditions cannot fully explain why RVFV outbreaks do not occur at random but rather show a close association with heavy rainfall, mainly the El Niño–Southern Oscillation, as well as sea surface temperature anomalies in the Indian and Pacific Oceans (Kahlon,*et al.,* 2010). Whereas the role of the *Aedes* mosquito in outbreak initiation is fundamental, virus amplification and circulation can also occur via *Culex* and *Anopheles* mosquitoes. In East Africa, the complexity of the epidemiological pattern of the disease is owing to the fact that different mosquito species can serve as epidemic/epizootic vectors of RVFV (Kebede *et al.*, 2010).

Recent RVF outbreaks have been characterized by severe infection and death in humans, with a high case-fatality rate (CFR) of 50% for the hemorrhagic syndrome form (Clements, 2007). This outbreaks in East African (Tanzania, Kenya, and Somalia) caused 478 human deaths in 1998 and 309 in 2007 (who 2007;WHO, 2008;Mohamed *et al*., 2010). In Saudi Arabia, the first recorded outbreak occurred in 2000, resulting in 883 human cases with 124 deaths (CFR 14%) in that country22 and 1,328 human cases and 166 deaths in neigh boring north western Yemen.23–25 During the 2007 outbreak in Sudan, 698 cases and 222 deaths were recorded. It is clear that the epidemiological pattern of recent RVFV outbreaks has changed to resulting in more severe illness and high fatality rates among humans (Adam *et al*., 2010).In addition, the disease can result in negative consequences to the livestock, and other sectors of the economy. For example, the 2006/2007 RVFV outbreak resulted in losses of over 60 million USD, equivalent to the annual value of livestock trade between East African countries. The 2007 outbreak in Sudan led to bans on livestock exports to Saudi Arabia, which had a massive economic impact on trade between the two countries (Adam, 2016).

West Nile Virus

West Nile Virus (WNV) is re emerging pathogen whose ecology and epidemiology span the multidimensional interface between viral pathogen, invasive arthropod disease vectors, wildlife, domestic animals and human beings (Suthar *et al.,* 2013). It is a neurotropic flavivirus that is endemic in many parts of the world. As an arbovirus, WNV is transmitted by mosquitoes between birds and mammals. More than 100 different mammalian species, including many species of bats, have been shown to be susceptible to WNV infection (Root ,2013),and further increasing the risk of emergence via the close proximity of animal and human populations. It is First isolated from a febrile patient in Uganda in 1937, and was introduced into North America in 1999, resulting in a large outbreak and rapid spread from the East Coast to the West Coast in a very short period. Although most (~80%) human infections are subclinical, symptomatic infections range from a self limiting fever to severe neurological disease, long-term sequelae and death (Suthar *et al.*, 2013). The year 2012 saw a new wave of WNV outbreaks in the USA, with the second-highest number of WNV cases on record (Arnold, 2012). High numbers of WNV cases were also reported in Europe in the same year, with 224 cases in the European Union and 538 additional cases in neighbouring countries (Arnold, 2012). Epidemiologists suspect that a combination of the presence of wild birds, increased mosquito populations and favourable weather conditions in the USA and Europe are the key drivers for these outbreaks (Arnold, 2012).

FACTAR OF EMERGENCE AND RE EMERGANCE

The complex interaction between environment/ecology, social, health care, human demographics and behavior influences the emergence and re emergence of zoonotic viral diseases (Venkatesan, 2010). The critical factors consist of microbial adaptation and change; host susceptibility; climate and weather; changing ecosystems, demographics and populations, including issues of wildlife and exotic animals; economic development and land use; international trade and travel; technology and industry; reduction in animal and public health services or infrastructure; poverty and social inequity;war and dislocation;lack of political will;and intent to harm (Hamburgm, and Lederberg,2003). However, the questionnaire response from different countries officials identified microbial adaptation, climatic conditions, international travel and globalization and trade as the most common events that were contributing to the emergence and re-emergence of zoonotic diseases (Lonnie, 2004).

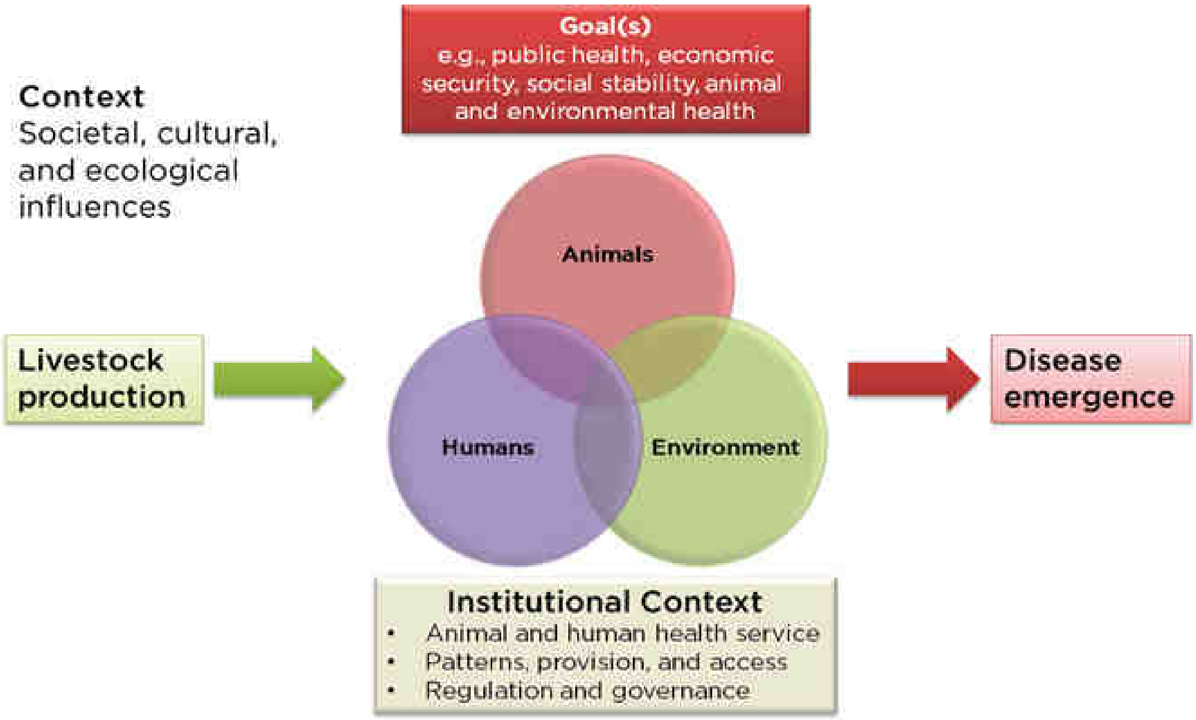

Figure 3: a systems perspective on disease emergence

Change of ecosystems and global warming

Change of ecosystems is a wide concept that includes many different drivers, where of one of the most frequently mentioned is changed land use. It has been shown that since the 1940s, almost 50% of the events of zoonotic pathogen emergence have resulted from changes in land use (Keesing *et al*, 2010). This concept includes for example deforestation, agriculture, modification of wetlands, dam construction etc. (Institute of Medicine, 1992). These drivers are believed to act by placing humans, reservoirs and vectors in increased proximity to one another (Institute of Medicine, 1992; Patz *et al.*, 2004). Some may also affect wildlife habitats, which in turn will increase contact frequency between humans and wildlife pathogens (Patz *et al.*, 1994). The fact that since the 1940s almost 75% of emerging zoonotic pathogens originated in wildlife, and that this trend appears to be significantly increasing over time, supports the hypothesis that human activities that increases contact with pathogens of wildlife, are substantial risk factors for disease emergence (Jones *et al.*, 2008). Processes such as damming and irrigation water in agriculture, are likely to promote vector-borne disease agents since many vectors breed in standing water (Morse, 1995). Also, recent information suggests that activities that contribute to reducing biodiversity in flora and fauna also may increase transmission of infectious pathogens via different mechanisms (Keesing *et al*, 2010).

The influences of global warming on the emergence of infectious diseases have yet to be fully elucidated. The survival of pathogens outside their hosts, as well as the seasonality of viruses such as Influenza A, is likely to be affected by climate change. Pathogens transmitted by vectors are also expected to be affected in different ways. First of all, higher global temperatures may increase the areas of habitats suitable for breeding. Secondly, an increased precipitation and a subsequent rise in sea level may positively affect vectors that are dependent on water to complete their life cycles (Institute of Medicine, 1992). The fact that a significant increase in the importance of vector borne transmission has been observed, and that it has been correlated to climate anomalies, may be regarded as supports to this hypothesis (Jones *et al*, 2008).Example Influenza A, Hantavirus, Rift Valley Fever virus, Nipah virus etc *(Chua et al.,2002).*

Human behavior

Human behavior is a vital component for emergence of many infectious diseases, and therefore changing patterns of human activities is often important to halt epidemics (Institute of Medicine, 1992; Morse *et al.*, 2012). Human consumption of bush meat is believed to constitute an important factor in the emergence of several infectious diseases. It places humans in close contact with not only live animals and vectors, but also with body fluids during butchering of the carcasses (Karesh *et al.*, 2009 and Wolfe *et al.*, 2005). Also, transportation, sale and consumption may put humans at additional risk .Example Simian foamy virus, Ebola virus, HIV, SARS etc. (*Wolfe et al., 2005)*

International Travel

The ever increasing world population and migration of masses in search of job to urban areas, lead to overcrowding, inadequate sanitation and hygiene, which provide an ideal breeding ground for infectious agents. Increased international travel,especially without taking appropriate vaccine and other protective measures, lead to increased infection in travelers, who subsequently bring the infection back own homes on their return (Obi, 2010). In addition to human movements, increased cross-border trade of livestock and wildlife is also a concern. Trading centers, for example,can act as mixing bowls for “humans and dozens of other species before they are shipped to other markets, sold locally, or even freed and sent back into the wild” (Richard *et al.*,2011).

Globalization and Trade

The phenomenon of globalization has been one of the most remarkable changes in our lives over the last quarter of a century. Globalization has been the driving force that has profoundly impacted international trade, economics and cultural interactions. The spatial mobility of the average human has increased more than 1,000 folds since 1800. At the turn of this century almost 700 million people travelled internationally and this number is expected to reach 1 billion by 2010 (Eberharp, 2000) .Not only are more people travelling, but travel is faster and more culturally widespread and permeates into areas of the world not readily accessible in the past. People, animals and products can circumvent the globe faster than the incubation period of almost every pathogen known today (Lonnie, 2004).

Microbial Adaptation

In addition to the climatic conditions, international travel and globalization and trade of demographic and environmental factors, which can drive the emergence of novel diseases and increase the incidence, prevalence, or geographic scope of existing ones, the importance of public health system factors as influences, in particular for the emergence of newly resistant strains, should not be underestimated (Richard *etal.*,2011).Microbes are especially competent at adaptation and change under selective pressures for survival and replication. The remarkable adaptation of microbes to become resistant to antimicrobial products is seen in both human and animal populations and is linked between the two (Lonnie,2004).

FUTURE CHALLENG OF EMRGING AND RE EMERGING ZOONOTIC VIRUS

Emerging and re-emerging zoonotic diseases are responsible for profound political, social, and economic impacts on society. Despite extraordinary progress during the past two decades, infectious diseases still kill 15 million people each year, and deadly new diseases continue to emerge and re-emerge (Graham *et al*., 2010 and Woolhouse *et al.*,2012) .We have recently entered a new epidemiologic era in which these diseases are showing an upward trend and their global effect is unprecedented. In relation with this approximately 75% of the new infectious diseases in humans are zoonotic; thus, the veterinary profession and animal health officials are faced with immense challenges, from this zoonosis A literature survey identified 1,407 species of human pathogens, with 177 (13%) species regarded as emerging or re-emerging. (Hamburg *et al.*, 2003)

The world in which we live and work is growing progressively interdependent and complex. Unfortunately, this interdependence and complexity is also creating new factors to ensure that emerging and re-emerging diseases will continue to have significant effects on animal health well into this century. The OIE and animal health officials worldwide are experiencing the impact of emerging zoonoses and clearly believe that these diseases and countries' responses will be a much more important part of the future (Hamburg *et al.*,2003).

The emergence and re-emergence of zoonotic diseases are challenges to all professionals concerned with public health. Some of the emerging and re-emerging zoonoses such as Nipah virus,Zika virus, West Nile fever, monkey pox, avian influenza, SARS and swine flu (Brown, 1997;Chomel, 1998; Hubalek and Halouzka, 1999; Giulio and Eckburg 2004; Caceres and Ottle,2009; Pal and Abdo,2012) drew experts on veterinary medicine, public health, microbiology, ecology, conservation, disease modelling and forecasting from around the world. So the impact of global warming and changes in food chain will continue to create opportunities for the emergence of new diseases and re-emergence of old diseases (Eckburg, 2004).

The World Health Organization has warned that the source of the next human pandemic is likely to be zoonotic and that wild life is aprime culprit (WHO). While the current list of known EIDs is a major concern, it is the unknown EIDs out there, with a potential for efficient human-to-human transmission, that may pose the biggest threat. Over the past decade there have been a number of epidemics, raising the concern that they are precursors to a pandemic. Over the past century, humanity has witnessed the emergence of numerous zoonotic infections that have resulted in varying degrees of human fatalities. For instance Influenza viruses originating from birds account for an important portion of these deaths and recently many new zoonotic viruses originating in bats, such as Hendra virus, Nipah virus, and severe acute respiratory syndrome coronavirus (SARS-CoV), have caused outbreaks with high mortality rates.

STRATAGY FORPREVENTION AND CONTROL

In order to prevent and control emerging zoonoses, several major steps need to be taken, including recognition, investigation, and collaboration, the development of advanced structures for diagnosis and surveillance, international and interdisciplinary interventions, applied epidemiological and ecological research, education (training and technology transfer),and information/communication (CDC,1998)

Recognition

Emerging zoonoses need first to be identified. Usually, identification follows recognition of a health problem in the human population and too often only later in the domestic animal or wildlife population, despite the fact that clinical manifestations may have occurred first in the animal reservoir, as illustrated by recent outbreaks of Rift Valley fever,Q fever. A new approach should be toinvestigate health problems concomitantly in animals and humans or to identify health problems in animals that could be associated with human disease. The recent outbreaks and spread of West Nile virus in Europe and Northern America fully support such a strategy. Furthermore, we need to start an inventory of potential pathogens harbored by free-ranging wildlife. Investigation of Hendra virus outbreaks indirectly led to the identification of a rabies virus variant in Australian pteropid bats (CDC, 1998)

Investigation and Collaboration

The collaborative fieldwork of multidisciplinary teams with the support of expert staff scientists and laboratories with advanced molecular biology and immunology techniques is essential to conduct investigations of new and emerging zoonoses. However, initial work is still heavily dependent on field recognition of health problems in animals and/or the human population. Well-trained field epidemiologists, ecologists, and environmentalists, especially those with a veterinary background, will be key players in such an endeavour. There is a strong need for interdisciplinary collaborations in identifying new zoonotic agents. Such collaborative efforts led to the identification of new arena viruses in North America (Fulhorst CF, *etal* 1996). Identification of main risk factors and potential reservoirs is a leading priority, as control measures must be very limited until such factors are identified. Identification of the deer mouse as the main reservoir of the Sin Nombre virus has been essential to reducing human exposure. Similarly, identification of a common exposure to domestic pigs was a key factor in controlling the Nipah virus outbreak in Malaysia. A new approach to investigating new or emerging zoonotic agents is to conduct an inventory of pathogens carried by various wildlife species, especially those that encroach on human habitat. Collaboration at the local level among different institutions or organizations concerned with human health, animal health, and wildlife health is also a key factor for investigating and identifying emerging zoonoses (CDC, 1998)

Advanced Structures for Diagnosis and Surveillance

The prevention and control of emerging zoonoses require even more sophisticated diagnostic tools than before. Investigators at the local level need to have access to reference laboratories fully equipped with molecular biology tools. In a not-so-distant future, one can hope that microchip kits will allow for instantaneous diagnosis of several organisms at the site of investigation. Such progress will be essential for timely surveillance and detection of outbreaks in animal and human populations. Such a technology cannot be developed without major international collaboration, especially between developed countries that have the resources and the know-how, on the one hand, and developing countries, where many of these emerging pathogens are endemic, on the other. It is in the interest of developed countries to protect themselves by investigating possible sources of infection in their natural environment and where human exposure might be at the highest level (CDC ,1998).

Education and Training

The need for training of professionals in the field of zoonotic diseases is an emergency. Medical knowledge has to be extended to those who may see the first animal or human cases of zoo noses. Similarly, training in molecular epidemiology will allow us to better understand the diversity of the pathogens involved and the specificity of their reservoirs and to enhance our ability to control these infections (CDC, 1998).

Communication/Information

Finally, a proper strategy for prevention and control relies on accurate and timely dissemination of information concerning new emerging diseases. Specialized sites on the Internet system are other very important communication and information tools that has been developed in recent years. They will be very useful for the dissemination of prevention and control measures, as is illustrated by the Centers for Disease Control Web site (www.cdc.gov), where all control measures for hantavirus infection control are fully access able to the public (CDC,1998)

CONCLUSION

Conclusively, it is inevitable that emergence and re-emergence will continue to occur. To reduce the impact, robust public health infrastructure must be maintained or developed to enable rapid detection and response. Changes in pathogens and/or their vectors appear to have expanded their geographic or host range as a result of global warming and other associated climatic changes. Globalization, trade, international travel, human demographics and behavior influences the emergence and re-emergence of zoonotic viral disease. The ability of a pathogen to infect multiple hosts, particularly hosts in other taxonomic orders or wildlife, were also risk factors for emergence in human and livestock pathogens. Therefore, the public health system must be prepared for the unexpected agent since no one knows what new diseases will emerge and what old ones will re- emerge. Training should be provided on clinical management, diagnosis and vector control including through a number of WHO collaborating countries. The surveillance of emerging and re-emerging zoonosis virus and potential complication should be enhanced.

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