Emerging Zoonotic Diseases - A Potential Risk to Human and Animal Health

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The history of infectious diseases occurrence in human and animal population is very well scripted in epics and olden literatures. The Zoonotic diseases transmitted between human and animals is not a new phenomenon, but the depth of knowledge on common diseases of animals and human beings might have been lesser than the modern understanding but evidence depicts some of the diseases shared between human and animals were found in 3000-year-old Egyptian mummies.

The impact of globalisation, World trade and development, industrialisation, restructuring of agricultural and animal husbandry sector and level of consumer's preference made several changes in the global policies. Developmental changes to cater the needs of global population is essential and as well accepting that the modernization paved up way for emergence or re-emergence of infectious and Zoonotic diseases worldwide.

An emerging disease is defined as a new infection resulting from the evolution or change of an existing pathogen or parasite resulting in a change of host range, vector, pathogenicity or strain; or the occurrence of a previously unrecognised infection or disease. A re-emerging disease is considered an already known disease that either shifts its geographical setting or expands its host range, or significantly increases its prevalence.

The rapid detection and response to an emerging or re-emerging disease is crucial. The rapid detection of such a new epidemiological event is therefore a key element for all policies to be developed. It is often the case that the disease will have spread undetected for a significant period of time before it is detected and reported. Till now rapid detection of emerging diseases is not achieved in many developing countries and some developed countries where there are possible deficiencies in the veterinary infrastructure, expertise, diagnostic laboratories and in surveillance capabilities as a whole especially for new diseases. The preparedness and response capability of a country towards an emerging disease largely depend on the availability of such facilities and it is therefore not surprising that methods to control emerging diseases in some developing countries are less effective. Most of the recent emerging diseases have an animal origin, and almost all of them have zoonotic potential.

These diseases must therefore be addressed through coordinated actions between animal and public health authorities (OIE, 2018).

Zoonoses - a Public Health Concern

Zoonoses are a threat to public health for a number of reasons.

- The number and types of zoonotic diseases are increasing as people, animals, and vectors can travel the globe in less time than it takes for disease symptoms to develop after exposure (incubation period).
- Human manipulation of the environment (e.g., climate change) is helping some zoonotic disease vectors thrive.
- Overuse of antibiotics has made some of these diseases harder to treat (antibiotic resistance).
- Some organisms that cause zoonoses could be used for bioterrorism.
- Vaccines are not available to protect humans against many zoonotic diseases.
- Treatments may not exist or be readily available for people infected with some zoonoses.
- Some zoonoses may take a different, or more deadly, form in people than in animals

Emerging Zoonotic Diseases - a Threat

Emerging disease are those diseases that are newly recognized or newly evolved, or those have occurred previously but shows an increase in incidence or expansion in geographical, host or vector range.

These diseases are of serious impact on the public health concern as well as on the economy. A large number of infectious diseases have been identified in the last few decades this could be due to the recent advances in the diagnostic techniques with improved sensitivity along with use of molecular methods. But, many diseases have actually emerged due to the changes in environmental conditions, ecological disturbances and damages caused by human activities, human and animal population dynamics and their interaction, changes in agriculture practices, increased and rapid mode of transportation facilities and movement of people and goods, and others (Wang and Crameri 2014). This could result in emergence of a disease in any part of the world. Thus, these diseases should be considered as a threat to the global public health as they do not recognize any political boundaries (Hallaj, 2010).

Among the long list of infectious agents known to infect humans, 60 per cent are zoonotic in nature and 75 per cent of these zoonotic pathogens are considered as emerging pathogens (van Doorn, 2017). These pathogens not only emerge from animal reservoirs, they also emerge due to their ability to acquire resistance against antibiotics such as the MRSA and multidrug resistant salmonella. The increased and unjustified use of antimicrobials in animal production system also favors their emergence and further spread to human beings (van Doorn, 2017).

The pathogens jumps from the animal species to human and tries to establish itself in-fact it is now accepted that most of the infectious diseases of human, have had their origin in animal population (van Doorn, 2017). This species jump occurs due to unusual contact between man and animals due to their social, cultural and behavioral changes (van Doorn, 2017).

Disasters and disease risk

During natural disasters, the risk of occurrence of infectious diseases although is less compared to other losses. But the rate of spread of the infectious diseases in the post disaster phase as people are displaced, they begin to migrate and congregate at few spots, the sanitation becomes poor, and availability of safe water supplies, becomes limited. All these factors create an ideal condition for the emergence of new diseases which were previously unknown to occur in the population.

The relationship between natural disasters and communicable diseases is frequently misconstrued. The risk for outbreaks is often presumed to be very high in the chaos that follows natural disasters, a fear likely derived from a perceived association between dead bodies and epidemics. However, the risk factors for outbreaks after disasters are associated primarily with population displacement. The availability of safe water and sanitation facilities, the degree of crowding, the underlying health status of the population, and the availability of healthcare services all interact within the context of the local disease ecology to influence the risk for communicable diseases and death in the affected population (John *et al*, 2007).

In the definition given by CDC it is mentioned that "emerging diseases are those whose incidence in humans has increased in the past two decades or threaten to increase in the near future". Going by this definition, let us consider only those zoonotic diseases that have emerged in India and around the world in the period between 1999 to 2018.

Year	Zoonotic agent / diseases
1999	Nipah
2003	Severe acute respiratory syndrome (SARS), H5N1 influenza virus
2009	H1N1 Pandemic influenza virus
2011	Crimean Congo hemorrhagic fever (CCHF) in India
2012	Middle East Respiratory Syndrome (MERS)
2013	H7N9 Influenza virus
2014	Ebola haemorrhagic fever

Nipah Virus Infection

Nipah virus is an important zoonotic viral disease first reported in Asia during 1998 at Malaysia transmitted through contaminated food or directly between people. In the infected people, it causes a range of severe illnesses from asymptomatic (subclinical) infection to acute respiratory illness and fatal encephalitis. The virus can also cause severe disease in animals such as pigs, resulting in significant economic losses to the farmers. Although, Nipah virus has caused only a few known outbreaks in Asia, it infects a wide range of animals and causes severe disease and death in people, making it a public health concern during 1998 and 1999.

The Nipah virus belongs to the genus *Henipa virus* of the *Paramyxoviridae* family. Fruit bats belonging to the *Pteropus* sp. act as reservoir and vectors of the virus. Virus is present in the urine and saliva of bats. Transmission can occur directly from bat to man following consumption of fresh palm sap or its fermented product contaminated by bat secretions or by close contact with secretions of other infected animals (pigs) or fomites. Even food-borne transmission via ingestion of meat is possible as reported in Philippines. Nosocomial transmission can occur by close contact with infected patients or their secretions which is very much worrisome. The Mortality rate may be 40-70 per cent but can be up to 100 per cent.

Epidemiology: Nipah viral disease was first recognized in 1998 in Malaysia where it caused acute encephalitis and respiratory distress in pigs and encephalitis among pig farmers and slaughterhouse workers. In this outbreak, people got infected following exposure to infected pig (Chadha et al. 2006). The disease also occurred in Singapore when pigs or pork meat exported from Malaysia acted as source of infection. In both these outbreaks a total of 276 people got infected (Luby *et al.,* 2009) and in an effort to control the infection around 9,00,000 pigs were culled (Luby *et al.,* 2009). In 2001, NiV outbreaks occurred in Bangladesh where the virus was found to be directly transmitted between bats and man without involvement of intermediate host. A total of eight outbreaks occurred in Bangladesh till 2008 with 135 cases and 98 mortalities.

In India, NiV emerged in Siliguri, West Bengal simultaneously during the 2001 Bangladesh outbreak. Here, cases were identified by retrospective investigation of sample collected during the outbreak by serological and by detection of NiV RNA in the urine samples of patients. The virus was found to be genetically more closely related to Bangladesh isolates (Chadha et al. 2006). Later, another outbreak occurred in Nadia district in 2007. Both Siliguri and Nadia are near Bangladesh border (Luby et al. 2009). Evidences of virus, has been detected among bats in Madagascar, Cambodia, Thailand, Indonesia, Ghana, Papua New Guinea, Philippines and Australia. Recently in Kozhikode, Kerala 2018 the virus has emerged and it has claimed 12 lives including a nosocomial infection.

Prevention and control: Controlling natural cycle is practically impossible as the infected bats can migrate for long distances and spread the infection. Early recognition by targeted surveillance for virus among bats and livestock population would be useful. Culling of infected and in-contact animals is effective in controlling further spread of disease. Controlling movement of animals including export during outbreak from infected areas. Avoid drinking of date palm sap or contaminated fruits from bat infested areas. Isolating the patients especially from family members is important. Community involvement is very much essential and further the healthcare workers must adopt proper prevention and control practices without any deviation in the recommendations.

Crimean Congo hemorrhagic fever (CCHF)

It is a tick borne viral zoonotic disease caused by *Nairovirus* of *Buniyaviridiae*. It is a viral hemorrhagic fever with signs of bleeding disorders like rashes, melena, epistaxis, petechiae, hemoptysis, hematuria and multiple organ failure can occur. The disease was first reported in Crimea in USSR and was called as Crimean Hemorrhagic fever. Later, another outbreak occurred in Congo in 1956 and in 1969 both the diseases were found to be caused by same pathogen there the name Crimean Congo hemorrhagic fever was adopted. In CCHF case fatality can be very high (10-40 per cent) (NHP, 2018). The virus typically infects cattle and small ruminants by the bite of infected ticks, but the infected animals do not show any clinical signs of the disease. Human acquire the infection by bite of infected ticks and through contact with blood and other body fluids of infected patients (nosocomial) or animals (WHO-SEARO, 2018). The virus can be transmitted by a number of ticks but the most important one is *Hyalomma.*

Epidemiology: The disease occurs in many parts of the Eastern Europe, former Soviet Union, the Mediterranean, in north western China, central Asia, southern Europe, Africa, the Middle East, and in the Indian subcontinent (WHO-SEARO, 2018). In India, the disease was recorded in 2011 as a nosocomial outbreak in Ahmedabad, Gujarat in this epidemic, three patients died due to multiple organ failure, one confirmed case and two suspected case. The reason for this sudden emergence of the disease was suggested to be the changes in land use pattern and encroachment into forest areas. CCHF cases were documented from 6 districts of Gujarat (Ahmedabad, Amreli, Patan, Surendranagar, Kutch, and Aravalli) and 3 districts of Rajasthan (Sirohi, Jodhpur, and Jaisalmer). Recently, a CCHF case was reported from Uttar Pradesh state (NHP, 2018) NIV has conducted sero surveillance and detected antibodies against CCHF in sheep, goats and cattle in Gujarat (15 districts) and Rajasthan (Mourya *et al.*, 2015); ProMED-mail, 2018a). In a cross-sectional seroprevalence study covering 22 states and 1 union territory, a total of 5636 serum samples cattle, sheep, and goats were screened and this 354 samples turned positive from all the states indicating a nationwide prevalence of the disease (Mourya *et al.*, 2015)

Prevention and control: The introduction of the disease can be avoided by avoiding tick bites by avoiding infested areas and by the use of protective clothing and repellents. Avoid encroachment in to forest areas. In the hospitals as the virus can spread by nosocomial infections, proper infection control measures should be adopted and the patients should be kept under strict isolation and samples should be collected with utmost care.

Severe acute respiratory syndrome (SARS)

SARS as the name indicates it is a viral respiratory disease SARS-Coronavirus. The virus is detected in the respiratory secretions, feces, urine, and tissue specimens from lung biopsy of patients indicating that it is not particularly confined to the respiratory tract alone (Peiris *et al.,* 2003). The zoonotic link of the agent was suggested based on the fact that the disease initially occurred among those who were occupationally exposed to live, caged exotic animals used as 'game food' and the virus was isolated from Himalayan palm civets and from a raccoon dog, there (Peiris *et al.*, 2003). But late the source of the virus was traced back to the horseshoe bats (*Rhinolophus sinicus*) present in a remote cave in Yunnan province, thus civet just acted a medium through which the virus spread (Hu *et al.,* 2017). The virus is transmitted by inhalation of respiratory droplets and by contact with mucous membranes. The disease presented with flu like illness with fever being the common sign, respiratory distress and pneumonia and secondary bacterial complications (Peiris *et al.*, 2003; Skowronski *et al.*, 2005). Although, the diseases occurred and as pandemic and caused huge havoc in 2003, no further cases were reported since 2004.

Epidemiology: It occurred as the first pandemic in the present century occurring between November, 2002 and July, 2003 affecting a total of 8,098 individuals with 774 case fatalities. The disease first emerged in the Guangdong Province of China, then spread rapidly to Hong Kong and then to Vietnam, Singapore, Canada and others affecting a total of 37 countries mainly through patients travelling through flights.

Prevention and control: As the virus spreads rapidly through aerosols strict isolation of infected patients is important and during the pandemic many health care professionals also succumbed to it, adoption of proper infection control practices is must. Wearing facemask, proper hand washing, disinfection of cloth and fomites that have come in contact with the patients plays important role. Surveillance of all the passengers at the airport and quarantining the suspected individuals during the pandemic played major role in controlling further spread of the virus. Thus early recognition of the patients, isolation, and contact tracing plays important role along with creation of public awareness (Peiris et al., 2003).

Middle East Respiratory Syndrome (MERS)

Commonly known as camel flu is another viral respiratory disease caused by MERS-Coronavirus (*Betacoronavirus*). Here also the signs of respiratory distress, fever and diarrhea are observed. Asymptomatic infection is also reported in laboratory confirmed cases is also known to occur. The case fatality rate may reach 35 per cent (WHO, 2018). Camels are involved in transmission of the virus to humans either directly or indirectly but the exact mechanism still remains unclear. Camel carries antibodies against the virus and are considered as major reservoirs of the agent (WHO, 2018). The virus is considered to have originated from bats and subsequently spread to camels. The virus can spread from person to person by close contact especially in health care settings when the cases are handled.

Epidemiology: The disease was first described and the virus was first isolated in Saudi Arabia 2012 and isolation was done in Jeddah, Saudi Arabia from a patient who died of severe respiratory illness. Since then it has been reported from 27 other countries like Algeria, Austria, Bahrain, China, Egypt, France, Germany, Greece, Islamic Republic of Iran, Italy, Jordan, Kuwait, Lebanon, Malaysia, the Netherlands, Oman, Philippines, Qatar, Republic of Korea, Thailand, Tunisia, Turkey, United Arab Emirates, United Kingdom, United States, and Yemen. Although most of the cases were from Saudi Arabia and those cases reported from outside Middle East had the history of travelling to Middle East (WHO, 2018). A total of 1832 confirmed cases with 741 fatalities have been noted till date (ProMED-mail, 2018 b). No confirmed case has been recorded in India and the Ministry of Health and Family Welfare, Govt. of India has issued guidelines to report any suspected cases among travellers returning from Middle East (Kumar et al., 2015)

Prevention and control: General hygienic measures like hand washing, avoiding contact with sick animals, must be adopted by those who visit or work with camels. Avoid consuming raw or under cooked milk and meat products originating from camels. Proper infection control practices must be adopted while treating or handling samples originating infected patients.

Influenza Pandemic

One of the oldest and a threat to mankind in all time is Influenza virus infection- a common respiratory pathogen. Though several groups of flu viruses proved to be the causes of respiratory tract infection worldwide in animals and human beings, the new atypical influenza virus could be the future cause of new worldwide pandemics.

India is concerned about the highly pathogenic avian influenza (HPAI) H5N1 virus first reported in domestic geese. The upsurge of HPAI H5N1 epizootic waves linked to changes in agricultural practices, intensification of the poultry sector, and globalisation of trade in live poultry and poultry products.

Epidemiology: Highly pathogenic avian influenza viruses of the subtype H5N1 (HPAIV-H5N1) have circulated continuously in Asia, Europe, and Africa since 2003. In the year 2006, fourteen Indian states were affected with H5N1 Avian Influenza outbreaks and most of the H5N1 Avian Influenza outbreaks were reported in 2008 and was restricted to Eastern and North Eastern states of India. Apart from H5N1, H9N2, H4N6, H11N1, H4N2, H9N3, H2N2, H3N2 viruses isolated from different bird species / ducks from different places in India. Isolation from wild water/migratory birds indicates they may be the reservoir without any symptoms and may act as source of infection for other species (Sridevi *et al.,* 2014).

Many such historical outbreaks due to emerging of new atypical influenza viruses have been reported worldwide within the past decades, there are several new epidemics due to new atypical respiratory viruses such as H5N1 bird flu (Trampuz *et al.,* 2004) and H1N1 swine flu. (Vincent *et al.,* 2008). H7N9 bird flu is the newest atypical influenza virus infection that has just been reported since early 2013.

Due to the nature of a new emerging infection, there are limited data on the natural history of H7N9 influenza infection. Hence, diagnosis and treatment are difficult. Bird flu is not a new thing. Bird flu usually means the influenza infection in avian. However, the case that human beings get the avian type influenza virus infection is usually problematic, and the atypical influenza virus infection can be the result. The new virus is considered to be the result from the genetic mutated classical avian H7N9 influenza virus and has high potential to cause mammal infection (Kageyama *et al.,* 2013), shortly the HA gene was derived from duck origin, and the NA gene derived from migratory birds infected with avian influenza viruses.

	January 2005-December 2012	January 2013-January 2018	January 2018
Number of countries and territories affected by HPAI in domestic birds	65	68	8
Number of outbreaks reported in domestic birds	8345	6895	18
Number of subtypes reported in Domestic birds	4	12	3

(Courtesy: OIE Situation Report of Avian Influenza -25.01.2018)

During the period 2013 – 2017, 12 different influenza A subtypes were reported, as shown in Table, Europe reported the highest virus diversity (7 subtypes), followed by Asia and the Americas (6 subtypes each), Africa (3 subtypes), and Oceania (1 subtype). Subtypes H5N1, H5N2 and H5N8 were the most geographically widespread and commonly reported in four out of five regions.

In 2018, outbreaks of HPAI of subtype H5N6 were confirmed in poultry in the Netherlands and Germany and in captive birds in the Netherlands and Sweden up to March. HPAI outbreaks of subtype H5N8 occurred in poultry in Italy during March, 2018 while outbreaks continued to be detected in Bulgaria until July, 2018.

Prevention and control: Currently, the best way to prevent infection with avian influenza A viruses is to avoid source of exposure whenever possible. Infected birds shed avian influenza virus in their saliva, mucous and faeces. Human infections with bird flu viruses can happen when enough viruses get into a person's eyes, nose or mouth, or is inhaled. A flu pandemic would put at risk the health of millions and have serious economic consequences. A flu pandemic could be substantially more damaging in both human and economic terms.

Following general measures could help in controlling the spread of disease in a region or at country level.

1. Stringent application of Export and Import regulations.
2. Science-based restricted trade with affected countries.
3. Continuous Surveillance at entry points.
4. Promote international capacity building.

5. Continual Surveillance for rapid detection upon introduction to prove freedom from disease to our trading partners.
6. Air surveillance in wild, migratory birds for the early detection of HPAI H5N1 virus is in place to pace to detect a possible disease incursion.
7. National Veterinary Stockpile.
8. National Animal Health Laboratory Network.
9. National Animal Health Emergency Response Corps.

Ebola Haemorrhagic fever

Ebola Virus Disease (EVD), formerly known as Ebola haemorrhagic fever, is a severe, often fatal illness in humans. The virus is transmitted to people from wild animals and spreads in the human population through human-to-human transmission. Both the World Health Organization and recent reports have suggested that the 2014 outbreak of Ebola can be traced to fruit bats in the West Africa region. Guinea, where bat soup is a local delicacy, has reportedly banned the sale and consumption of bat meat since the start of the outbreak. Non-human primates, like monkeys, are also suspected carriers of the disease and, as in humans; the Ebola virus can kill them. Research has shown that gorillas and chimpanzees suffer massive population declines during Ebola outbreaks, with the virus killing an estimated 5,000 gorillas in Gabon and the Republic of the Congo from 2002—2003. The average EVD case fatality rate is around 50 per cent. Case fatality rates have varied from 25 per cent to 90 per cent in past outbreaks. The first EVD outbreaks occurred in remote villages in Central Africa, near tropical rainforests in the year 1976.But the disease occurrence was accelerated in a new phase and several deaths were reported in the 2014–2016 outbreak in West Africa involved major urban areas as well as rural ones. Early supportive care with rehydration, symptomatic treatment improves survival. There is as yet no licensed treatment proven to neutralize the virus but a range of blood, immunological and drug therapies are under development.

Epidemiology: The first cases of Ebola virus infection were reported in Zaire (now known as the Democratic Republic of the Congo) in 1976. There were 318 cases and 280 deaths, an 88 per cent case fatality rate. Transmission in this outbreak was traced back to the use of contaminated needles in an outpatient clinic at Yambuku Mission Hospital. Since then, frequent outbreaks have occurred in Central and Western Africa. The most common species of Ebola virus responsible for outbreaks is the *Zaire ebolavirus* , the second most common species being the *Sudan ebolavirus* (Peterson *et al.*, 2004).

The *Zaire ebolavirus* was responsible for the outbreak that started in West Africa in 2014. It was first reported in March 2014, and was the largest outbreak since the virus was first discovered in 1976. Genetic sequencing has shown that the virus isolated from infected patients in the 2014 outbreak is 97 per cent similar to the virus that first emerged in 1976. Over 28,000 cases (confirmed, probable, and suspected) were reported in this outbreak, with over 11,000 deaths. A new outbreak was announced in the Democratic Republic of the Congo (DRC) in August 2018. As of 29 August 2018, 116 cases (86 confirmed, 30 probable), including 77 deaths, have been reported in the North Kivu and Ituri provinces of the DRC (WHO, 2018).

Prevention and Control

The WHO Ebola Viral disease monitoring group recommends the following measures to control outbreaks, namely case management, surveillance and contact tracing, a good laboratory service, safe burials and social mobilisation. Further it advises that Community engagement is the key to successfully controlling outbreaks through creation of awareness among the risky population on risk factors and protective measures (including vaccination). Ebola viral transmission could be contented with the following:

- **Reducing the risk of wildlife-to-human transmission** from contact with infected fruit bats or monkeys / apes and the consumption of their raw meat.
- **Reducing the risk of human-to-human transmission** from direct or close contact with people with Ebola symptoms, particularly with their bodily fluids.
- **Reducing the risk of possible sexual transmission,** WHO Advisory Group on the EVD Response, recommends that male survivors of EVD practice safe sex and hygiene for 12 months from onset of symptoms or until their semen tests negative twice for Ebola virus.
- **Outbreak containment measures,** including prompt and safe burial of the dead animals and human beings of suspected EVD. Close monitoring of person in contact for their health for 21 days.

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