

## A Comprehensive Review on Emerging and Re-emerging Zoonotic Viral Diseases: A Major Threat to Human Beings

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### Abstract

A zoonotic disease is an infectious disease caused by pathogens such as bacteria, virus, rickettsia, fungi, parasite or prion that has been transmitted from an animal, especially a vertebrate to human beings. Usually, the first infected human transmits the infectious agent to other humans very rapidly; it is one of the important concerns of zoonoses. The World Health Organization (WHO) currently list the Emerging infectious diseases (EID) of epidemic issues in their research and development blueprint as COVID-19 (Corona viruses), Middle East Respiratory Syndrome (MERS), Severe Acute Respiratory Syndrome (SARS), Ebola and Marburg viruses (Filovirus), Crimean Congo haemorrhagic fever (Nairo virus), Lassa Fever (Lassa virus), Nipah (Henipa virus), Rift Valley fever (Phlebo virus) and Zika (Flavi virus). Due to the deadly pandemics facing by the globe, it is essential to understand the way of transmission of emerging viruses, its mode of infection and important measures to eliminate or control them from the world is essential. However, mankind overcomes so many deadly viruses with the help of scientific knowledge, through vaccination, new therapies, drugs etc. Nowadays, viral zoonoses like rabies (Lyssa virus) are 100% preventable through vaccination and medication even though, humans face lots of new threats especially emerging zoonosis diseases like Covid19. This review summarized the major zoonotic viruses affecting human beings, their source, pathogenicity and its important ways to overcome the transmission of microbes from animal to humankind.

**Keywords:** Zoonoses, pandemic, COVID19, influenza, emerging infectious diseases, vaccination.

### Introduction

Currently many emerging and re-emerging viral diseases, especially zoonotic diseases are reported frequently in the different parts of the world and their impact on human health is increasing day by day. It is not limited to human beings, the occurrences of viruses in domestic and wild animal reservoirs and arthropod vectors in disease transmission makes a great challenge to control or eradicate these viruses. The increasing human population also one of the major challenging task to control the spread of zoonotic diseases. Some virus is categorized under dreadful emerging and re-emerging viral diseases such as coronavirus- severe acute respiratory syndrome, Nipah, Avian influenza, Pandemic influenza, Ebola, Chikungunya virus etc. These deadly viruses not only affect human and animal health it also affects and leads to a significant burden on global economy. Zoonoses include a huge percentage of all newly identified infectious diseases as well as prevailing diseases in human beings.

Nearly 1,415 pathogens known to infect humans and among this 61% were zoonotic that is from animals to humans (Taylor *et al.*, 2001). The reservoirs/amplifying hosts for viral zoonoses are mammals, birds, reptiles, and perhaps amphibians. Mostly, these viruses exhibit mild or no disease to their nonhuman vertebrate hosts. However, some viruses possess a very limited host range and others have a wide range of vertebrate host (Reed, 2018). The current scenario in India recommends the need to look seriously into several vital aspects of this zoonotic disease, which includes diagnosis, intervention, patient management and control measures. Zoonotic pathogens can transmit to humans through any contact point with domestic or wild animals. The markets vending the wild animal's meat or its by-products are at high risk due to the huge number of novel or unidentified pathogens known to be in some wild animal populations. People living nearer to wilderness zones or in semi-urban areas with more contact of wild animals are at high risk of getting diseases from animals such as rodents, rats, foxes, monkeys etc.

Natural habitat destruction and urbanization upsurge the risk of zoonotic diseases by increasing the contact between wild animals and humans. Pandemics are unpredictable due to arise of zoonotic viruses, but its periodic outbreaks can cause health issues, economic losses and various social concerns worldwide. With the increase of global travel, a pandemic can spread rapidly within less time period. Ongoing circulation of some zoonosis viruses in poultries, such as A (H5) and A (H7) viruses, is of public health concern as these types of viruses cause severe disease in human beings and it have an ability to undergo mutation and increases the viral spread among humans. While, it is essential to hurry up the steps to producing effective vaccines and therapies for the control and treatment of zoonosis virus. At present public health prophylaxis is the most significant issue to control the transmission of the diseases.

### Mode of transmission

Zoonotic disease has various modes of transmission and some newly transmitted diseases are not well studied. The transmission of these viruses maybe occurs in various ways. The persons having direct contact with animals are more susceptible to zoonoses, it includes farmers, veterinarians, slaughterers/butchers, researchers, pet owners and animals used for food (meat and eggs) (Jain *et al.*, 2020). Commonly in direct zoonosis the disease is directly transmitted from animals to humans through different media such as air (Corona and influenza), through bites and saliva (rabies) by way of contact with rodent excreta (Hanta virus). The vector (tick bite, and insects like mosquitoes or flea) or arthropod based transmission also observed which carry the infectious agents without getting sick and transmit it to human beings (Dengue, Chikungunya, yellow fever virus, West Nile Virus). Huet *et al.* (1990) described that the HIV (Human Immunodeficiency Virus) was a zoonotic diseases transmitted from chimpanzees to humans in the early 20<sup>th</sup> century, now it is mutated to a separate human-only virus. The migration of birds, also a main mode of transmission of new endemic foci of disease at great distances from disease originated site (avian influenza). Host genetics plays a vital role in determining which animal viruses can able to replicate themselves in the human body. Deadly animal viruses need few mutations to start replicating themselves in human cells. These mutated viruses are dangerous and it required combinations of mutations which might be randomly raised in the natural reservoir (Warren *et al.*, 2019).

### Contributing factors of emerging diseases

There are various mechanisms involved in the emergence of novel diseases into the environment (Smolinski *et al.*, 2003):

- Microbial mutation and adaptation (genetic drift and genetic shift).

- Human vulnerability to infection (immune-suppressive disease like AIDS).
- Climate and weather condition (diseases transmitted by animal vectors such as mosquitoes).
- Changing ecosystems (SARS related coronaviruses).
- Urbanization
- Economic development (over usage of antibiotics to surge meat yield of farmed cow's cause's antibiotic resistance).
- Cessation of public health measures.
- Social inequality and poverty (tuberculosis (TB) is a problem in low income areas).
- War and scarcity.
- Intent to harm (Bioterrorism Anthrax attacks 2001).

Table 1. The following table summarizes the major outbreaks of zoonoses infectious diseases (Fauci, 2005).

Disease	Country or region	Year of start of outbreak
Nipah virus	Malaysia	1998
West Nile virus	USA	1999
Rift Valley fever	Saudi Arabia and Yemen	2000
Influenza A virus subtype H7N2	-	2002
Monkeypox	USA	2003
Melaka virus	Malaysia	2006
Heartland virus	USA	2009
Lassa fever	Mali	2009
Pandemic H1N1/09 virus	Global pandemic	2009
H3N2v	-	2011
MERS-CoV	-	2012
Mojiang paramyxovirus	-	2012
Chikungunya	Caribbean	2013
Ebola virus disease	West Africa	2014
H7N4	-	2018
Monkeypox	Liberia, UK	2018
Nipah virus	India	2018
SARS-CoV-2	Global pandemic	2019-present

### Coronavirus

Coronaviruses (CoVs) are enveloped, single-stranded RNA virus coming under the family Coronaviridae (Lai, 2007). Coronavirus was divided into four types: alpha coronavirus, beta coronavirus, gamma coronavirus and delta coronavirus. Till now six variant of HCoV (human coronaviruses) has been identified, such as alpha-CoV (HCoV-NL63, HCoV-229E) and the beta-CoV (HCoV-OC43, HCoV-HKU1, SARS-CoV and MERS-CoV) (Drosten *et al.*, 2003; Yang and Leibowitz, 2015).

It causes highly transmissible diseases, it infect humans and animals and initiating mild to severe diseases. CoV is considered as a Zoonotic disease (Coleman and Frieman, 2014; Reusken *et al.*, 2014), due to its capability to infect different species. This leads to host jumps; it allows the emergence of new coronaviruses such as SARS-CoV, MERS-CoV and SARS-CoV-2 (Andersen *et al.*, 2020). It was identified that CoV is also transmitted through faecal-oral route of animals (Kipar *et al.*, 2010).

### Severe acute respiratory syndrome (SARS)

Severe Acute Respiratory Syndrome (SARS) causes severe respiratory disease and it was first reported in Hong Kong, and China in 2002-2003 (Jain *et al.*, 2020). The causative agent of SARS was identified as a novel coronavirus (SARS-CoV) was reported by Zhong *et al.* (2003). The symptom of SARS starts with an influenza-like illness that was followed by fever, headache, myalgia and is often accompanied by acute atypical pneumonia, respiratory failure and finally leads to death. It was transmitted from an infected person to uninfected persons, through direct contact with infectious droplets and fomites. Yu *et al.* (2004) reported that the sudden outbreak of this disease spread rapidly within a short period of time to Hong Kong, Canada, Singapore, Taiwan, Vietnam, the United States and several European countries. Guan *et al.* (2003) described two animal reservoirs of SARS such as the Himalayan palm civets (*Paguma larvata*) and racoon dogs (*Nyctereutes procyonoides*) which harboured virus which was highly similar to SARS virus. Lau *et al.* (2005) reported that the horseshoe bats (*Rhinolophus* sp) of three species found in China are probably to be the wildlife reservoirs of the SARS virus.

### Middle East respiratory syndrome (MERS)

Middle East Respiratory Syndrome (MERS) is an emerging zoonosis infectious disease, caused by Middle East Respiratory Syndrome Coronavirus (MERS-CoV). It belongs to the family *Coronaviridae*, order *Nidovirales* comes under RNA virus. MERS virus was first reported in 2012, September in Saudi Arabia. The origin of the MERS virus is not completely implicit but, based on the analysis of different genomes of the virus, it is supposed that bats are the reservoirs of the virus and it was transmitted to camels. Corman *et al.* (2014) explained that the MERS-CoV virus appears to have originated in bats. MERS virus is found to be closely related to the *Tylosycteris* bat coronavirus HKU4 and *Pipistrellus* bat coronavirus HKU5, was reported by Wang *et al.* (2014). The transmission of virus from bat to camel was observed in 1990s and its infection transmission was found in human during the year, 2010 (Cotton *et al.*, 2014). The Countries such as Saudi Arabia and the United Arab Emirates grow and consume large amounts of camel meat and the imported camels from these regions might

have carried the virus to the Middle East. It has been observed in camel milk, meat, organs and also urine but infected camels may not show any illness. More evidence given by Reusken *et al.* (2014) proved that the antibodies against MERS in the serum of 100 % of aged racing camels from Oman and 14 % of camels from Spain. It is a contagious disease and sometimes it may be fatal causing respiratory illness. Symptoms of MERS-CoV include fever, dry cough and shortness of breath and occasionally it may include vomiting, nausea, and diarrhoea. The incubation period of MERS-CoV is 2 to 14 days.

### SARS-CoV-2

The 2019-nCoV is officially called SARS-CoV-2 comes under the RNA virus, and the disease is named COVID-19. It was first reported in Huanan Seafood Wholesale (Wet) Market, Wuhan city, China in December 2019 (Huang *et al.*, 2020). This virus spread worldwide and causes a major pandemic. Lai *et al.* (2020) reported the phylogenetic analysis of SARS-CoV-2 was reported within bat SARS related coronaviruses, it suggested the way of transmission from animal market to humans. Boni *et al.* (2020) detailed that the SARS-CoV-2 virus shows 96% identical whole-genome level of coronavirus, which was isolated from *Rhinolophus affinis* (horseshoe bats) in Yunnan province, China. It was identified that the human pneumonia outbreak related to a new coronavirus is probable a bat origin. Lam *et al.* (2020) reported that the 91% similarity of coronavirus identified in *Manis javanica* (Malayan pangolin) with SARS-CoV-2 virus isolated from human. A symptom of COVID 19 can range from no symptoms (asymptomatic) to severe pneumonia and death. During the onset of infection, most common symptoms were found such as fever, cough, fatigue or myalgia and some atypical symptoms included headache, diarrhoea and hemoptysis. Fifty percent of patients had suffered from Lymphocytopenia, dyspnea and pneumonia. The incubation period of CoVID-19 is 2 to 14 days (Wang *et al.*, 2020).

### Crimean-Congo hemorrhagic fever (CCHF)

Crimean-Congo hemorrhagic fever (CCHF) is a zoonotic viral disease that belongs to the genus *Nairovirus* of the *Bunyaviridae*, which shows no disease symptoms in infected livestock but it causes a severe threat to humans with a high mortality rate (50%). It is a segmented, negative-stranded RNA virus belonging to the family *Bunyaviridae*, genus *Nairovirus* (Drosten *et al.*, 2002). The virus (CCHFV) is frequently spread by ticks, livestock to human and human to other humans. It was commonly seen in Africa, Asia, and Eastern Europe (Camicas *et al.*, 1994). Chinikar *et al.* (2008) reported that the main source of virus to humans through the bite of Ixodid ticks (*Hyalomma*) having contact with blood or tissues of infected livestock (cattle, goats, sheep and other mammals).

Vertical transmission is also occurring, by means of tick eggs. It was reported that Ixodid ticks have been found on migrating birds, between Europe and Africa, it may be the way for long-distance dispersal of these viruses. The National Institute of Virology, Pune detected Crimean-Congo hemorrhagic fever virus-specific IgG antibodies in livestock serum samples from Gujarat and Rajasthan states during December 2010. The disease shows mainly four stages that is incubation, prehemorrhagic, hemorrhagic and convalescence and the incubation period takes 3 to 7 days. Symptoms include fever, headache, myalgia, and dizziness. Conjunctivitis, facial hyperemia and occasionally diarrhoea are also observed. During the hemorrhagic period the most common bleeding sites are in the nose, the gastrointestinal tract, the genitourinary tract, and the respiratory tract (Ulrich *et al.*, 2013).

### Ebola and Marburg viruses

Ebola virus (EBOV) and Marburg virus (MARV) are zoonotic agents comes under filoviruses have negative-sense RNA strand and have a covering or envelope. Marburg virus was reported in 1967 in the German city of Marburg. It causes a severe form of hemorrhagic fever with a fatality rate of more than 25% (Sanchez *et al.*, 2007). It was first reported in laboratory workers, having contact with the organs, blood or cell cultures from a batch of African green monkeys (*Chlorocebus aethiops*) which was imported from north western Uganda. The natural reservoir of these viruses has not been certainly identified, but some species of bats were suspected. Marburg virus in the Egyptian fruit bat *Rousettus aegypticus* was isolated from Kenya, it indicates that Chiroptera (bats) play an important role in the natural life-cycle of the filoviruses. The Ebola virus first outbreak was recognised in 1976, near the Ebola River in Zaire, now it is known as the Democratic Republic of Congo, (DRC). More than 20 outbreaks were reported in and around Africa, but most known outbreaks occur during last past 20 years (Bell *et al.*, 2016). In, December 2013, a huge Ebola virus outbreak started in rural Guinea of West Africa, and then spread rapidly to neighbouring Liberia and Sierra Leone. It was first predictable in March 2014, even though it infects thousands of people and had a fatality rate of about 59% was reported. Meanwhile, the infected travellers have spread the Ebola virus to Nigeria, Europe, and also to North America. The source of the Ebola virus has been linked to the consumption of wild animal meat in affected areas (bushmeat) or soup made from bats was observed. Filoviruses are extremely contagious. The transmission of the virus from human to human occurs *via* skin and mucous membrane contact with body fluids such as blood, breast milk, saliva, vomit, stool, sweat, semen, urine of an infected person. Symptoms of Marburg and the Ebola virus infection are very similar.

An incubation period of 2 to 20 days was seen in these infections, fever, myalgia, and headache occur, and often with abdominal pain, nausea, and upper respiratory symptoms such as cough, chest pain, pharyngitis observed. Photophobia, conjunctivitis, jaundice and lymphadenopathy also reported. Vomiting and diarrhoea may also be observed (WHO, 2018).

### Lassa fever

Lassa fever is caused by the Lassa virus; it is a single-stranded RNA hemorrhagic fever virus from the family *Arenaviridae*. It was first discovered in 1969 and has been named after the first report of a case in Nigeria. It is endemic in most parts of West Africa including Liberia, Sierra Leone, Guinea and Nigeria. The animal vector for the Lassa virus was found to be the "multimammate rat" (*Mastomys natalensis*). Lassa virus transmitted through contact with household items, water, food or air contaminated with the droppings or urine of infected rats. It causes hemorrhagic fever like Ebola or Marburg hemorrhagic fever viruses. It was followed by acute hemorrhagic fever characterized by fever, muscle aches, sore throat, nausea, vomiting, diarrhoea and often chest and abdominal pain. The incubation period for this virus is variable; it may be from six days to three weeks (El-Bahnasawy *et al.*, 2015).

### Zika Virus

Zika virus was discovered in the Zika forest, Uganda in 1947. It comes under the *Flaviviridae* family mostly found in arthropods, primarily in ticks and mosquitoes. It possesses an unsegmented, single-stranded, and has positive-sense RNA genome. Zika virus was maintained in nature through a mosquito-monkey-mosquito transmission cycle. *Aedes mosquito (A. aegypti and A. albopictus)* act as a vector to transmit the virus, while mosquito feeding on human and the virus passes inside the cells and they use host machinery and finally establish infection. In 2015, Zika disease outbreak was reported in Brazil, and the disease spread rapidly across South and Central America and Mexico regions (Zanluca *et al.*, 2015; Summers *et al.*, 2015) Another outbreak was observed during 30<sup>th</sup> March 2016, autochthonous cases of Zika virus infection have been reported from 61 countries or territories worldwide (Calvet *et al.*, 2016). The clinical symptoms include fever, macula-papular skin rashes, asthenia, non-purulent conjunctivitis, myalgia, arthralgia, headache, edema of hand and feet are commonly found (Singh *et al.*, 2016). The incubation period of Zika virus is 3-12 days. Sexual transmission of the Zika virus was also identified in recent studies. It indicates that men infected with the Zika virus can have a viable virus that can present in their semen for up to 6 months or more.

And one of the major complications of the Zika virus infection is vertical transmission from mothers to infants either in utero or during delivery was also reported (Baselar et al., 2017).

### Nipah virus

Nipah virus is a zoonotic disease caused by Nipah virus (NiV), a paramyxovirus belonging to the genus *Henipavirus* of the family *Paramyxoviridae*. It is a non-segmented negative-stranded RNA genome with helical nucleocapsids encased in an envelope forming spherical to filamentous, pleomorphic virus particles (Harcourt et al., 2001). It was first reported in Kampung Sungai Nipah village of Malaysia in 1998. NiV is transmitted from specific types of fruit bats (flying foxes), mainly *Pteropus* sp. which is natural reservoir host. The infected fruit bats can able to spread the disease to other animals or to humans. Pigs act as intermediate as well as amplifying hosts in the spreading of NiV. The close contact of humans with infected animals or their body fluids (saliva, urine) can become infected. It has a broad range of mammalian host and highly pathogenic. The rapid transmission of disease from person to person was observed and it is included in the pandemic list (Raj et al., 2019). In India, there was a large outbreak of NiV in Siliguri, West Bengal in 2001, another smaller outbreak in 2007 in Nadia district, West Bengal and in 2018 sudden outbreak in Kozhikode, Kerala was reported (Hutin et al., 2018). In NiV infected person, it causes a range of illnesses from asymptomatic infection to acute respiratory illness and fatal encephalitis. The common symptoms observed are fever, cough, sore throat, headache, vomiting and difficulty breathing. The severe symptoms may include disorientation, drowsiness, or confusion, seizures, coma and encephalitis. The incubation period of the Nipah virus is 4 to 21 days.

### Rift Valley fever (RVF)

The disease is caused by the Rift Valley Fever Virus (RVFV), is negative-stranded RNA virus under the family *Bunyaviridae* and the genus *Phlebovirus*. RVFV is transmitted by mosquitoes and this virus replication occurs in domestic ruminant. It inflicts significant damage to livestock. It is an emerging zoonotic disease distributed in sub-Saharan African countries and also caused major outbreaks in several countries including Kenya, Tanzania, Somalia, South Africa, Madagascar, Egypt, Sudan, Mauritania, Senegal, Saudi Arabia, and Yemen (Bird et al., 2009). Some species of *Culex*, *Aedes* or *Anopheles* mosquito plays a major role in amplifying RVFV among mosquitoes, ruminants and humans (Turell et al., 1984; Turell et al., 1988). *Culex tritaeniorhynchus* and *Aedes vexans* are major mosquito vectors. Other possible vectors include *Aedes mcintosh*, *A. ochraceus*, *A. caspius*, *Culex antennatus*, *C. pipiens*, *C. zombaensis*, *C. perexiguus* and

*C. quinquefasciatus* (Turell et al., 2007) a play major role in disease transmission. It may also spread by contact with infected animal blood, raw milk or the infected mosquitoes bite. Animals such as sheep, goats, cows and camels may be infected by RVF, mainly from mosquitoes. RVFV infection in humans usually starts with mild illness such as fever, weakness, back pain and dizziness. In some cases, it developed into neurological disorders, partial or complete blindness, hemorrhagic fever, or thrombosis (Ikegami and Makino, 2011). The incubation period of the virus is 2 to 6 days.

### Prevention and control of zoonosis

The Preventive measures to control zoonotic diseases differ from each pathogen. The major routes of transmission of zoonotic viruses are direct or indirect contact, aerosol or through vectors. Currently, there has been an increase in the frequency of occurrence of new zoonotic diseases. The elementary principles of zoonotic disease prevention and control contain reservoir neutralization, reducing contacts and increasing host resistance (Haregua, 2019). Here some important strategies to manage various zoonotic diseases were discussed below.

1. Proper handling and proper guidelines for animal care in the agricultural sector assist to decrease the spread of foodborne zoonotic diseases through eggs, meat, dairy or maybe through some vegetables (WHO, 2020).
2. Should set proper standards to avoid contamination of drinking water with urine or faeces of rat/rodent. The protections of surface water in the natural environment from any mode of contamination are very important to decrease the spread of zoonotic diseases.
3. Appropriate handling of poultry and poultry waste is essential to reduce some types of zoonosis such as H5N1, which is generally spread by domestic poultry, by means of transmission from infected birds to healthy birds. The infected poultry products and the use of infected poultry manure as fertilizer in agricultural fields also involved in the spread of zoonosis diseases. (WHO, 2008).
4. By continues monitoring of animal health management such as routine vaccinations, immune stimulants, pre and probiotic feed additives will contribute to ideal increases in animal health and decrease the spread of zoonotic diseases.
5. Taking appropriate precautions such as proper hand-washing after contact with field animals and other behavioural adjustments can able to decrease the community spread of zoonotic diseases.
6. Proper rules should be manipulated to stop deforestation. In the case of wildlife, they act as a major reservoir for dreadful viruses. Mainly the destruction of forest, lead to habitat loss for many wild animals and

they start entering into villages may be the source of dreadful viruses to humans.

7. The hunting and caging of wild animals (monkeys, bats etc.) to the markets bring humans into close contact with those animals that harbour these viruses, may be the major reason for zoonotic diseases that we are facing now. So complete banning of wildlife hunting may help to reduce the spread of zoonosis.
8. Other factors such as human migration, change in land use pattern, mining (disturbance of ecosystem), coastal land degradation, wetland modification, construction of buildings, habitat fragmentation, deforestation, expansion of agents host range, human intervention in wildlife resources like hiking, camping, and hunting also influence on acquiring zoonotic infections from wildlife to human beings.
9. People living adjacent to wilderness areas or in semi-urban areas with higher numbers of wild animals are at high risk of disease from animals such as rats, bats, foxes or raccoons. Urbanization and the demolition of natural environments raise the risk of zoonotic diseases spreading by increasing interaction between humans and wild animals.
10. The spreading of Nipah virus infection is through the body fluid of bats such as saliva, urine and faeces. So to prevent the infection, avoid the intake of raw fruits or vegetables without proper washing and totally avoid bat bitten fruits, which may be contaminated by an infected bats.
11. Those who are working with animal models in research laboratories should take proper precautions to avoid the potential risk of these viruses to the persons working with non-human primates as laboratory animals.
12. Chemical control of virus spreading vectors such as mosquitoes, ticks etc. should be done by using insect repellents and insecticides.
13. Mechanical control methods involved in the destruction of mosquitoes should be strictly followed by the removal of any objects that can aid in unwanted storage of water in the locations that serve as a breeding point for female mosquitoes. Removal of those objects like unused tyres, plastic bags, unused containers, bottles, and also closing water tanks with lids can prevent breeding areas of the mosquitoes.
14. Preventing infection is ideal, but in many instances, increasing host resistance may only lessen the severity of the disease (Martinma, 2007). Two important methods of increasing resistances are chemoprophylaxis and immunization.
15. Apart from antiviral treatment, public health management includes personal protective measures to prevent the transmission of infection such as:

- Regular hand washing, wearing masks and social distancing.
- Good respiratory hygiene—covering mouth and nose when coughing or sneezing
- Using tissues and disposing of them correctly
- Early self-isolation of those feeling unwell, feverish and having other symptoms
- Avoiding close contact with sick people are essential steps to be followed.

## Conclusion

Zoonotic viral diseases are unpredictable due to the emerging novel viruses, but recurrent events can cause health, economic, and social concerns globally. Zoonotic pathogens can spread to humans through any contact point with domestic or wild animals. Wild animal selling markets for meat or by-products of wild animals are predominantly at high risk due to the huge number of novel or undocumented pathogens known to exist in some wild animal populations. A pandemic situation occurs when a novel virus arises with the capability of continuous transmission of virus from animal to human or from human to human. It was observed that human population has no immunity against the novel viruses. With the increase of worldwide travel, a pandemic can transmit quickly throughout the world. The current spreading of some zoonotic virus is of a public health concern and these types of viruses is the major reason for severe disease in human beings, as well as the virus, have the ability to mutate and increase its transmissibility among human beings. Mutations are more common in RNA viruses (corona, Influenza) than DNA viruses (Pox) the common mutations found were point (insertion/deletion), drift (minor), and shift (major). This is the major problem we are facing in our health sector, no effective treatments for these emerging viruses lead to huge mortality. The present scenario in India suggests the need to look seriously into various important aspects of emerging and re-emerging zoonotic disease, which includes diagnosis, intervention, patient management, control measures. The setting of a national strategy to predict, prevent and manage emerging zoonosis is of very essential one. This could be implemented by improved clinical awareness, advance in using sensitive diagnostic tests, research on the unknown reservoirs and changes in climatic condition. Still, we need more efforts to hasten the development of active therapies and vaccinations. Extreme awareness, vigilance and surveillance are highly desired to prevent these life-threatening viral illnesses.

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