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Review article

Emerging and reemerging viral infections in globe with special emphasis in India - A review

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ABSTRACT

It has long been recognized that pathogens, such as viruses, parasites, and other microorganisms, emerge and change over time. Viruses are powerful infectious agents that have co-evolved with humans and are responsible for several serious illnesses in people. There is no herd immunity for most humans, making emerging viruses, particularly the RNA viruses, more dangerous. The high mistake rate of the polymerases that copy the RNA viruses' genomes gives them the ability to adapt to the quickly changing local and global environments. Through mutation (as in the case of Dengue viruses), reassortment (as in the case of influenza viruses), and recombination, they can evolve at a rapid rate (polioviruses). The influenza A viruses (such as H1N1 and H5N1), which have caused numerous outbreaks, epidemics, and pandemics around the world, are the finest example of viruses emerging and reemerging. The complex host-pathogen ecology and the co-evolution of microbes with their hosts are linked to the emergence and reemergence of novel diseases. Human viral illness emergence and reemergence is an ongoing problem that affects a nation's social and economic growth.

Keywords: Emergence; reemergence; human viral diseases; tomato flu; monkeypox virus.

INTRODUCTION

A disease brought on by a pathogen that has not previously been noticed within a population or geographical area is known as an emerging infectious disease (EID). Comparably, an established pathogen that manifests in a new region or that was once under control but now occurs more frequently causes a reemerging infectious illness (1). Viral infections make up a sizable portion of newly and reemerging infectious diseases, and they are becoming increasingly prevalent. The human immunodeficiency virus (HIV), the West African Ebola virus outbreak that lasted from 2014 to 2016, as well as earlier outbreaks of the yellow fever, West Nile, and Nipah viruses, among others, highlight how dangerous newly and reemerging viral diseases may be for global public health. Particularly concerning in the current decade are the appearance of novel human infections and the resurgence of several diseases. Emerging infections are essentially illnesses whose prevalence has been observed to have increased in recent decades or has threatened to increase in the future. Such emergencies frequently result from the discovery or dissemination of pathogens in more recent locations, the acknowledgment of diseases that have long been prevalent in a community but were unrecognized entities, or the discovery of an infectious etiology in previously well-established diseases. Increased domestic and international connectivity, poverty and malnutrition, social practices, immunosuppressive diseases are common, uncontrolled urbanization, deforestation, and changes in agricultural techniques like mixed farming are all causes of these diseases (2). Such outbreaks have also, in large part, been caused by genetic changes in viruses (3).

Factors responsible for the emergence of viral infections

Viral illness emergence or reemergence is influenced by a variety of factors like human factors, natural factors, and viral factors that alter how people are exposed to the organisms. The majority of newly discovered or rediscovered infectious diseases are zoonoses, which are infectious illnesses spread from animals to people. Most zoonotic diseases originate in nature, though they can also come from domesticated animals or be spread by insects like mosquitoes and ticks. Viral diseases like measles are reemerging due to decreased immunization rates and modification of sensitivity of the human population to the virus.

Human factors

Numerous factors relating to social systems and human behavior have an impact on the onset or

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reemergence of viral diseases. Denser populations result from increased urbanization, which is the process of shifting people from rural to urban regions, making them more vulnerable to the spread of infectious diseases. This is especially true in urban areas that are overpopulated and don't have enough sanitary facilities or clean water sources. The spread of economies, populations, and companies around the world is referred to as globalization. Through trade and travel, infectious diseases are now more easily spread between nations. Increased global trade can contribute to the spread of infectious diseases, especially those found in food or animal products (4). Illegal activities, including the trading in bushmeat, can help contagious diseases proliferate. As an illustration, the USGS discovered that bushmeat that was seized at US borders included unique herpesviruses and retroviruses. One of the reasons for transmission of zoonotic infection is illegal transboundary movement of bushmeat. In actuality, the consumption of bushmeat tainted with simian immunodeficiency viruses may have set off the HIV pandemic. Humans' ability to fly between far-off countries rapidly and conveniently has made a significant contribution to globalization. An individual travelling across countries can do this and spread infectious diseases, as was the case with the 2003 outbreak of the severe acute respiratory syndrome (SARS), which was characterized by severe lower respiratory symptoms, pneumonia, and fever. A new coronavirus known as SARS-associated coronavirus was eventually found to be the culprit behind SARS CoV. In this instance, the virus was first seen in Guangdong Province, China, in November 2002 and was quickly disseminated by visitors to more than 30 nations in Europe and North America, as well as other parts of China and Asia. Additionally, SARS-CoV was discovered in civet meat from a restaurant where a staff member who had previously contracted SARS worked (5). Viruses can also be introduced into new ecosystems by importing insects and animals. West Nile virus which belongs to the flavi group of arbo viruses transmitted through culex mosquitoes first reported in Uganda in 1937 and subsequently in other areas of Asia, Africa, Europe, and middle east. Although most infected people are asymptomatic, about20% of them experience fever, body pain, pain in the joints, rash, vomiting and diarrhea. Central Nervous system infection affects less than 1% of infected people overall, but 10% of those who get these neurological side effects pass away. In New York City in October 1999, there was an outbreak of WNV that affected both humans and birds. The child can acquire WNV from the mother during pregnancy, delivery, or breast feeding. West Nile Virus testing of the blood with nucleic acids started in 2003.An infectious disease that is spread from humans to other animals is known as an anthroponosis or an anthroponotic sickness. The emergence, reemergence, and transmission of viral infections are also influenced by various social factors like political unrest or conflicts that uproot thousands of people, resulting in overcrowded refugee populations without access to basic needs like medical treatments, clean water supply, immunizations, poor health infrastructure and reduced immunization policies (6). Human ways of behaving additionally impact the spread of arising and reappearing irresistible illnesses. The fame of eateries and, to some extent, arranged food varieties gives a way to spread food borne infections like hepatitis. An infection, while bringing in natural products, vegetables, and nuts from different nations, can prompt the broad conveyance of an infection. Blood borne infections like HIV or Hepatitis can spread by sexual contacts, sexual exercises, tattoos, piercings, and intravenous medications (7). Thus, the transmission of infections is influenced by Strict and profound practices (8). The episodes of measles can occur in people who stay away from immunizations. In order for the infection to occur, the host should have intracellular elements and receptors for the infections. Organisms that are effortlessly resisted by the host's powerful framework will be killed immediately, while infections that elicit an inward "cytokine storm" by invulnerable framework cells are probably going to impel extreme pathology. Immunocompromised individuals, pregnant women, undernourished people, elderly, and extremely young are mainly more susceptible to infections because of their more weakened immune systems.

Natural and ecological factors

Practically every emerging viral illness can be related to a natural or environmental event. The emergence of probable zoonotic infections can result from urbanization, globalization, deforestation, change in environment due to cultivation of wild land. Expansions in the human population have prompted the infringement of people into creatures' territories previously empty by people. These conditions add to people interacting with creatures with which they wouldn't normally connect, jeopardizing them from being exposed to zoonotic infections that are tracked down in the neighborhood by natural life populations. The transmission of zoonotic infections to people can happen straightforwardly or by implication. For instance, most infected individuals during a 276-occurrence Nipah outbreak in Malaysia and Singapore in 1998-1999 had contact with exterminated pigs that were raised as animals for commercial purposes before being killed for meat. The neighboring bats were thought to have been the source of the pigs' Nipah illness, dispersing it either through their faeces or by dropping partially consumed natural materials into the pigs' stomachs (9). Human contamination with Nipah infection causes encephalitis, fever, migraines, and decreased awareness. During this outburst, a bit less than half of the affected people perished. Bats are not symptomatically infected by the Nipah virus. The Nipah illness has been spread directly from bats to people in Bangladesh, as opposed to the indirect mechanism seen in the 1998–1999 event in Malaysia and Singapore. Date palm sap tainted with infected bat spit is the primary method of transmission. Human -to-human transmission of the Nipah infection happened likewise after the infection entered the human populace. Climate and environmental change also play a part in the rise of novel viral illnesses. These can be momentary and provincial changes in weather conditions or longer-term environmental change patterns. For instance, expansions in precipitation in specific regions lead to the development of the vegetation that upholds rat populations. The same thing happened in Sin nombre disease with severe respiratory condition, a hantavirus infection in southwest United States. This caused 42 people to become infected with Sin nombre infection, a previously undetected hantavirus spread by deer mice whose population swelled because of excessive rain. 62 percent of patients who had the Sin nombre infection had hantavirus pneumonic disease. The ability of stagnant pools and puddles to serve as additional favorable habitats for the bugs is another way that increases in precipitation have an impact on mosquito populations. Precipitation essentially affects how widespread the mosquito-borne diseases dengue infection (DENV) and rift valley fever are. Similarly, West Nile Virus is a sporadic scourge in the US, appearing in the late spring and fall, when precipitation supports mosquito larval habitats. These include, among other things, mean temperature, wind speed, dew point, soil moisture content, and rainfall collection. Because of the alteration in the environment, the viral infection may return after an extended period of rising global temperatures. Higher average daily temperatures in a place also increase the habitat for particular mosquito populations, expanding the populations that can become infected by the diseases they spread. The return of zoonotic illnesses into places where the ecosystems didn't previously support these mosquito species will coincide with the expansion of normal temperatures in those states. Environmental changes also affect how ticks spread and how birds and other animals migrate, which alters which regions are exposed to the zoonotic diseases they transmit. This includes flu infections and WNV because of birds, among other things (10).

Viral factors

Although human ways of behaving and natural/biological elements are all the more normally connected with flare-ups, microbe attributes are additionally associated with the progress of emanant/reemergent irresistible infections. For infections, the atomic cosmetics of the viral genome frequently decide if the infection will effectively integrate into the new populace. For the most part, this happens through reassortment, recombination, or change. Many arising infections can't secure themselves on the grounds that they have the capability as "impasse" diseases that don't support one individual to another in spreading. The major antigenic change, antigenic shift results from shift of animal subtypes of flu to humans. The characteristics of the infection determine whether or not the antigenic shift can spread from person to person and cause a pandemic. H5N1 and H7N9 infections have only been transmitted to people through close contact with birds, unlike the 1918 H1N1 epidemic, which had the potential to spread over the whole human population (11). The co-infection of a susceptible host with both avian and human flu infections, however, could result in the reassortment of hereditary portions of the two illnesses and the creation of a unique human flu infection subtype since flu infections are portioned. To stop the spread of H5N2, which has a high mortality rate in poultry and later in humans, a significant number of chickens, turkeys, and ducks were isolated in the Midwest of the United States in 2015. Recombination occurs in "Infection Replication" when the RNA or DNA polymerase that is copying the viral genome switches to the format of a different type of infection, creating a cross-bred genome from two different forms of infection. Recombination has the potential to produce results that are neutral or detrimental to development. Compared to DNA infections, RNA infections have a higher rate of change, making them the most frequently acknowledged cause of human sickness. The RNA-subordinate RNA polymerases (counting reverse transcriptase) do not have editing capability, unlike the DNA-subordinate DNA polymerases of living things and DNA infections. This prompts a diminishing in chemical loyalty, embedding an erroneous nucleotide every 105 bases. RNA infections have probably the most elevated transformation rates of every single organic substance. This ensures a range of genetic variation that keeps pace with destructiveness and raises the possibility of transfer. One of the challenges in avoiding episodes is that the need for crisis reactions elsewhere overshadows the need for alleviation reactions as the number of cases, apprehension, and public interest decline. Furthermore, it is known that on the off chance that a microbe isn't disposed of, it might become endemic. Low socioeconomic level, a degraded environment, a lack of availability, and moderateness all increase the risk of bouts of irresistible infection. a weak framework for monitoring and a lack of knowledge of the numerous epidemiological components needed for the development, management, and prevention of these flare-ups. Many of the reported flare-ups occurred in the country's west. Subclinical and irregular contaminations, as well as those not recognized by the wellbeing office, are many times missed by the observation frameworks. The extent of detailed episodes is straightforwardly connected with the general wellbeing foundation and observation organization, with flare-up alarms beginning most effectively from those states with a well-working general wellbeing framework and illness reconnaissance framework. Customary observing and assessment would be basic to the general outcome of the National Vector Borne Disease Control Program (NVBDCP). The number of cases of dengue and chikungunya have increased in recent years (12). The mass gathering can occur in various religious events like *Kumbh Mela* in Uttar Pradesh, *Maha Pushkaram* festival in Andhra Pradesh, pilgrimage to Sabarimala in Kerala, Catholic pilgrimage to Velankanni in India and several religious festivals, sporting and political events attended by smaller groups in India (12). Such opportunities create situations of human proximity over very short distances, create more public health worries because of transmission of respiratory and gastrointestinal diseases and the challenges they pose for maintaining sanitation. Many of these gatherings saw outbreaks of infectious diseases, most illustrated by the cholera epidemic at the Kumbh Mela celebration in 1817, which resulted in the Asian cholera pandemic (1817-1824) when afflicted pilgrims returned. These gatherings might create problems in new recurrent infections and for the exchange of genomic materials in different viruses. Many Muslim adherents return each year from the Hajj and Umrah pilgrimages who might face problem in transport of MERS-CoV to India, However, no cases of MERS-CoV infection have been identified in the country so far, although reports indicate the spread of the flu via returning infected pilgrims (13). The treatment of persons in institutions with reduced immunity like elderly diabetic patients, pregnant women, premature infants, patients on anticancer chemotherapy and hematopoietic stem cell transplantation can acquire viral infections. The blood borne infections like hepatitis B, human immunodeficiency virus and hepatitis C infections can be transmitted through sharing of injection needles, religious practices like tattoos, ear and nose piercing and acupuncture. Significant dangers also occur in places like dental offices, hemodialysis centres, etc., when patient care devices' sterilization and disinfection procedures are not carefully followed. The medical personnel are also at risk of contracting several viral infections like HIV, HBS, HCV and infections like viral hemorrhagic fever and Nipah. Transmission of hospital-related infections was a notable discovery during the Nipah infection outbreaks in West Bengal (13) and Kerala, with several health care workers becoming victims of the infection. Human metapneumovirus also has caused severe infection (14).

Influenza

Influenza virus member of Orthomyxoviridae family can undergo antigenic variation because of segmented RNA and is responsible for various epidemics and pandemics like swine flu which occurred in 1918, Asian flu in 1957, Hong Kong flu in 1968 and influenza A H1N1 IN 2009(14). Antigenic surface glycoproteins are subject to two main types of antigenic variation. The three mechanisms of development of pandemic influenza strains are reassortment of genetic material, direct avian/mammalian-human transmission, and virus recycling. The minor antigenic variation antigenic drift in influenza peplomers can cause frequent outbreaks (15). Influenza pandemic which occurred in 1918 killed thousands of young adults, nearly 3% of world population with a normal immunity. In comparison to other diseases, viruses, and RNA viruses, are better able to quickly adapt to new hosts and changing environments. The virulence of foot and mouth disease and polio virus was maintained by mutation. The main mechanism of adaptation in RNA viruses is mutation caused by RNA polymerase which could be lethal or beneficial to growth of the virus which helps those viruses to adapt to new host or environment. The first vector borne infection reported was yellow fever by Walter Reed in 1901. Rearrangement and recombination are additional pathways for adaptation. The influenza virus has changed over time by rearrangement of its genes. Recombination could result in the emergence of new virus strains. If two identical viruses infect the same cell and swap genetic material, a new virus can emerge. This recombination mechanism primarily occurs in enteroviruses that persistently infect the gastrointestinal system. In addition to genetic mechanisms, the following factors also play a role in the emergence and reemergence of infectious diseases: Treatment resistance (from animal to human). The developing RNA viruses that infect people and may lead to fatal diseases are the main topic of this review. The illnesses that are the focus of our attention include ZIKA, Dengue, West Nile (WNV), Ebola, influenza, SARS-CoV, MERS-CoV, Nipah Virus, and enteroviruses. Another new virus that affects a variety of animals and is a member of the Orthomyxoviridae family is the influenza virus. The influenza virus is an enclosed pathogen with an 8-segment negative-stranded RNA genome. The two viruses with segmented RNA infecting the same cells can result in reassortment. The possibility of pandemics increases due to the reassortment of viruses, which enables virus adaption to a new host. Between 250,000 and 500,000 people are killed by seasonal influenza viruses every year, with the elderly making up most of these fatalities. Wild waterfowl serve as the primary influenza viral reservoir. As a result, they are the primary catalyst for the spread and reemergence of influenza viruses. Due to its high pathogenic potential and ongoing global emergence and reemergence, avian influenza has been responsible for numerous epidemics and pandemics. The avian influenza virus was known as ‘the plague of the birds’ for more than 130 years. Pigs, chickens, and ducks all serve as influenza virus reservoirs and as a breeding ground for newly undiscovered influenza virus strains. The influenza pandemic which started in 1918 killed millions of young adults with normal immunity which was the worst disaster in human life (16).

H1N1 flu

The morbidity and mortality were high in humans in case of the H1N1.The H1N1 influenza virus triggered a pandemic in 1918. Segmental reassortment has been crucial in the development of the H1N1 virus. H1N1 was the cause of the 1918–19 influenza pandemic that killed half a million people in the United States during the First World War. Pigs were thought to have served as the pandemic's mixing bowls. Because the influenza pandemic had not previously been publicized, soldiers and civilians were unaware and unable to take precautions. The United States established the quarantine to stop the virus' spread since many individuals were passing away and bodies were piling up. H1N1 experienced intra-sub typic reassortment in 1947. The then-current immunization did not protect against this new subtype, leading to more severe disease. Based on antigenic diversity, the virus was given the moniker "A-prime" and kept spreading throughout the world. The NA region was retained while the HA segment was altered in this variant. In 1957, the H1N1 strain vanished from human populations, and a new one, H2N2, emerged. This novel strain consists of five segments from the H1N1 1918 strain lineage and three segments from an avian source. In 1977, a brand-new subtype of H1N1 appeared. In 1977, influenza A (H1N1) reemerged, especially affecting children and young people in Northeastern China, the Soviet Union, and Hong Kong. New strains with the potential to cause a global pandemic are created because of reassortment between various influenza strains obtained from various host species, for example reassortment between human and bird influenza strain which is responsible for 1957 and 1968 influenza pandemics. The novel strain of influenza virus has been created in H3N2 recently by genetic reassortment (17). In 1997, a particularly dangerous avian virus in 1998, a brand-new H3N2 strain appeared in North America and spread among swine there. In addition, a novel strain of influenza A (H1N1) with swine origins was discovered in 2009 and infected humans. Influenza A was created through the reassortment of human H3N2, classical swine H1N1, and North American avian influenza strain genes (S-OIV). Between 2005 and 2009, 642 confirmed cases in humans were found in the United States. Additionally, the mixing and co-circulation of H3N2 led to the production of H1N1 and H1N2, which led to sporadic human infection.H1N1 reached Italy in 1976 when pigs were imported from the United States. Other pigs are quickly exposed to this strain. A novel influenza A virus with an avian origin was discovered in European swine. A new H1N1 virus which originated from pigs came into sight in Mexico in 2009. Using the human-to-human transmission method, this virus spread quickly to 30 nations, prompting WHO to issue a level 5 of 6 pandemic alert (18). The WHO states that level 5 pandemic alert is defined as virus transmission from human to human in at least two nations within a single WHO region, while level 6 is defined as community-level outbreaks across multiple WHO regions in addition to phase 5 level criteria. The possibility of an influenza pandemic in the twenty-first century is thought to exist with this new strain of influenza virus. The influenza is characterized by fever, headache, running nose, body ache and sore throat. Influenza symptoms vary from person to person depending on immune system, age, and underlying medical conditions. The laboratory methods used for diagnosis of influenza are cultivation of virus, rapid antigen tests, serological tests RT-PCR and immunofluorescence. Because the influenza virus changes so quickly, influenza vaccinations, often known as influenza injections, are created twice a year. According to WHO and CDC recommendations, nearly everyone over the age of six should get the influenza vaccine. The immunization's effectiveness varies from year to year and ranges from providing only fair to excellent protection against influenza.

Between May and August 2017, Hong Kong experienced a recent outbreak of the unusual summer influenza, which had a high mortality and morbidity rate. This flu is uncommon in several ways, including the fact that death was higher, and the number of cases and length of sickness were very different from the previous season. This outbreak may be related to the fact that the flu vaccine from last year is beginning to expire and may not be as effective at providing the recipients with a protective immunity. It could also be because fewer people developed natural immunity due to the flu's weak peak the previous year (19). The H3N2 flu strain's mutation of a dominant antigenic epitope may also be to blame for this outbreak, rendering the previous two years' flu vaccine useless. The severe acute respiratory syndrome (SARS), a coronavirus that is currently in circulation and is thought to pose a threat to human health. SARS-CoV is passed from one person to another through coughing, sneezing, or direct contact with droplets that are infectious. In the digestive system and lungs, the SARS virus reproduces. SARS cannot be treated with a vaccine or antiviral medications. The cause of SARS is the coronavirus. In China's Foshan city, SARS was first noted in November 2002. Acute respiratory syndrome epidemic in 2002 was reported to WHO by the Chinese Ministry of Health. The signs resembled those of atypical pneumonia. A 64-year-old physician who contracted SARS while treating SARS patients has died. While visiting Hong Kong, this doctor stayed at the metropole hotel, where 16 additional guests contracted SARS. These individuals transported the virus to Hanoi, Toronto, and Singapore. The doctor became seriously ill the next day and passed away in a hospital on March 4. The WHO issued a global alert on SARS, a newly emergent respiratory disease, on March 15. Within the following six months, SARS expanded to 36 nations in Asia, Europe, and North America. The Guangdong province in southern China is thought to be the SARS outbreak's primary genesis. There were 8096 documented cases in total, with 774 people dying because of infection. Infected individuals displayed symptoms similar to the flu, including headaches, fevers, myalgia, respiratory failure, and death. Four people were impacted by the 2003–2004 resurgence of SARS. These four people have been located. It was believed that raccoon dogs and Himalayan palm civets had a virus that is strikingly like SARS (20). After 2004, there were no more SARS cases recorded, but Middle East respiratory sickness (MERS) cases continued to emerge. The Corona virus was the cause of MERS. In June 2012, Saudi Arabia reported its first MERS case. Even MERS cases were reported from Oman, Qatar, and UAE. Up until January 2015, travelers' rapid spread of MERS to other countries in Asia, Europe, and Africa resulted in a total of 1626 illnesses with 36% mortality (21).

Zika

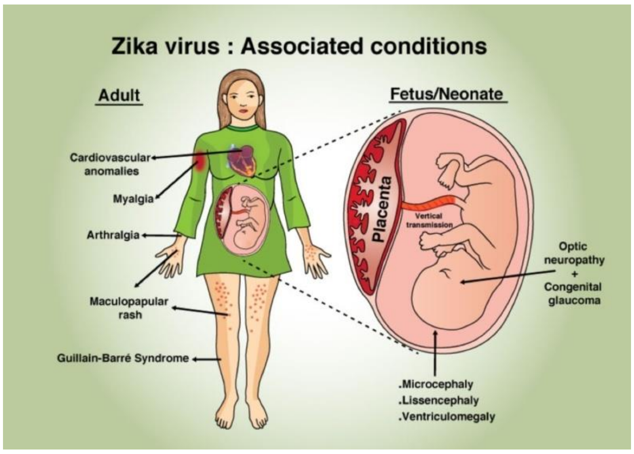

Fig.1: Symptoms and complications of Zika virus infection

The Zika virus which created panic all over the world was first detected in Uganda in 1947.The Zika virus is transmitted through bite of mosquito and sexual contact. The confirmed cases of Zika virus were reported by the Ministry of Health and Family Welfare in May 2017 at Bapunagar, Ahmedabad. In 2007, the WHO's Western Pacific region reported the island of Yap as the site of the first Zika virus disease outbreak. Zika virus is one among four public health emergencies of international concern which relates to congenital anomalies. Monkeys and humans are the hosts for the Zika virus a single stranded enveloped RNA virus which belongs to the flavi group. There is consensus among scientists that the Zika virus can cause congenital brain malformations such as Guillain-Barré syndrome (GBS), microcephaly, and others (Fig.1). Although it is rarely severe in adults, it can affect fetal development and cause serious neurodevelopmental problems (22). The mosquito borne viruses like yellow fever, dengue and west Nile are connected to mosquito borne ZIKV. According to some, the recent emergence of ZIKV and its spread to 48 different countries worldwide signify an emerging global public health problem. Currently, there isn't an effective ZIKV vaccine on the market. It was established that ZIKV is spread by mosquito bites when it was first discovered in *Aedes aegypti* mosquitoes in Malaysia in 1966. When a mosquito feeds on blood, the ZIKV, which is present in its salivary glands, gets introduced into the victim's body through the bite of the mosquito. It has been proved that ZIKV is transmitted sexually because the virus has been found in sperm and urine even after two months of contamination. ZIKV contamination in Asia turned up in Indonesia, wherein seven people had been struck by fever, bellyache, dizziness, and anorexia. The widespread infection due to ZIKV occurred in Yap Island in Micronesia in 2007.Reverse-transcription polymerase chain reaction (RTPCR) and serological analysis revealed that a total of 59 individuals had been infected with ZIKV. It was discovered that up to 73% of Yap Island residents had contracted ZIKV, and *Aede shensilli* was thought to be a key vector for ZIKV transmission. In 2013, French Polynesia saw the epidemic of ZIKV with the classic symptoms associated with Guillain-Barre syndrome. The majority of ZIKV exposure is asymptomatic, and the precise incubation period isn't usually known. The incidents often happen three to thirteen days after a mosquito bite, though. Clinical manifestations of ZIKV infection include headaches, migraines, conjunctivitis, skin rashes, joint and muscle pains, and mild fever. Anorexia, lightheadedness, diarrhea, constipation, retro-orbital pain, edema, and stomach pain are further medical symptoms. A ZIKA vaccine that consists of a DNA vaccine, a neutralizing antibody vaccine, a subunit vaccine, as well as other components, is currently being developed. RT-PCR, ELISA, IgM antibodies, and plaque discount neutralization tests can all be used to identify ZIKV contamination in inflamed individuals (PRNT). In response to certain flaviviruses, IgM response. The Centers for Disease Control and Prevention advice utilizing both RT-PCR and serological testing to determine ZIKV infection (23).

DENGUE

Dengue caused by a member of the flavi group is not an uncommon viral illness, inflicting 50 million instances each year in more than a hundred nations in tropical and subtropical areas. Dengue is taken into consideration as the 2nd biggest mosquito-borne sickness after malaria. Most dengue virus infections are asymptomatic, but in a rare number of instances, circulatory failure-causing dengue hemorrhagic fever (DHF), also known as dengue surprise syndrome (DSS), develops. Additionally linked to dengue virus infection in humans are neurological symptoms (24). Dengue virus has four antigenically distinct serotypes known as DENV 1-four. The mode of transmission of dengue virus to humans is through the bite of a mosquito, *Aedes aegypti*. Most dengue virus contamination symptoms are non-existent. As a result, the first human exposure to dengue is exceedingly unlikely. Although the origin of the dengue virus is difficult to pinpoint, some research indicates that it may have started in Africa, where numerous mosquito-borne diseases occur, and primates are frequently affected. (25).

EBOLA virus (EBOV)

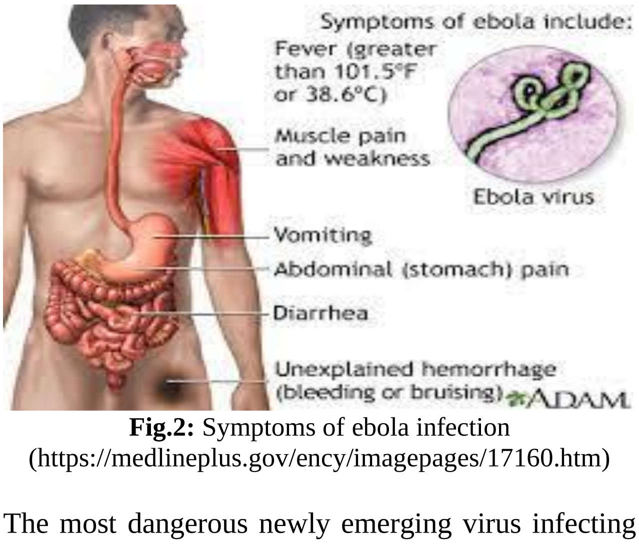

Fig.2: Symptoms of ebola infection (https://medlineplus.gov/ency/imagepages/17160.htm)

The most dangerous newly emerging virus infecting both humans and nonhuman primates is an enveloped single stranded RNA virus. Humans contract hemorrhagic fever from this filovirus. The EBOV virus genome encodes for seven genes, ensuing nine proteins. EBOVs, collectively with Marburg viruses, represent the Filoviridae's own circle of relatives. The FDA has not approved any medication or vaccine to treat human Ebola virus infection. The easiest way to control the illness is to isolate the patients, protect the health care professionals, and maintain tabs on individuals who interact with the patients (24).

Bats serve as a reservoir for EBOV transmission throughout Africa. Humans who encounter inflamed tissues, blood, bats, patients, or inadvertent hosts become infected with EBOV (apes). When several animal employees and staff at Marburg, Germany, were administered inflamed, EBOV was first identified there. These individuals had been assembling kidney cells from imported Ugandan monkey samples to test the poliomyelitis vaccine. The first major Ebola outbreak, which resulted in 318 cases of fatalities in Northern Zaire and southern Sudan, was identified in 1976. (284 instances). Among these subtypes, the Ebola virus from Zaire became more dangerous and resulted in 90% of case fatalities, whereas the variant from Sudan caused 50% of case fatalities. Throughout 1979, EBOV flared up once more, infecting 34 people in Africa and resulting in 12 fatalities. The following EBOV infections have been shown to have three more species. Reston EBOV was found to be contaminating Cynomolgus Macaques brought in from the Philippines in 1989.Until 1994, only a few cases of symptomatic EBOV contamination in humans had been discovered in the 1980s and 1990s. In the Gabonese Minooka district in 1994, EBOV infection resulted in the deaths of 31 persons. After thereafter, outbreaks of EBOV occurred in Sudan, Congo, Sudan, and Gabon every four years. In 2007, Uganda experienced a significant EBOV outbreak with 149 patients and a 25% death rate. Another EBOV outbreak occurred in Guinea in December 2013, and it soon spread to many neighboring countries, including Sierra Leone and Liberia. It was taken into consideration as the most important outbreak in records. The EBOV strain from Zaire that caused this outbreak was given the name Makona, after the river that forms the borders of all three nations (26). As the EBOLA virus persisted in surfacing, the epidemic spread to further African countries. As a result, up to 2013, a total of 2347 occurrences in West Africa had been recorded. An unrelated ZEBOV epidemic occurred in the Democratic Republic of the Congo in August 2014, resulting in 66 cases with a mortality rate of 74%. In 10 countries, a total of 28,646 cases of EBOV disease and 11,323 fatalities were reported as of March 2016. (Liberia, Guinea, Sierra Leone, Italy, Mali, Senegal, Spain, Nigeria, and the United States). The EBOV virus has an incubation period of 2 to 21 days. Fever, chills, nausea, vomiting, anorexia, stomach aches, and diarrhea are symptoms of the illness (Fig.2).

Failure of a few organs leads to death. Humans become infected with EBOV by mucous membrane access, wounds and abrasions to the skin and pores, or through parental transfer. Through a different mechanism for each mobile variety, EBOV can enter almost all the cells of the frame. Usually, lipid rafts, endocytosis, and macropinocytosis are the routes through which EBOV penetrates cells. Early in the outbreak, it can be exceedingly challenging to distinguish EBOV infection from other illnesses including typhoid fever and malaria. The blood is the first place where EBOV is found once an infection has started (27).

Nipah virus

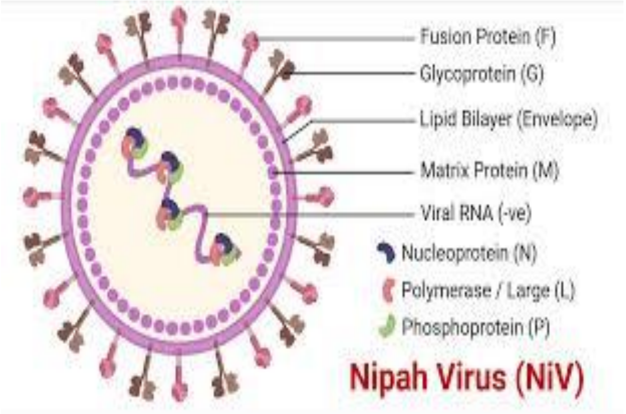

Fig.3: Morphology of Nipah virus (https://microbenotes.com/nipah-virus-niv)

The latest outbreak of a Nipah virus was reported in Kozhikode in Kerala on 17th July 2018. India has sent panic ripples throughout the sector. A total of nineteen instances were visible, with 17 of them dying. The causative agent is Nipah virus (own circle of relatives, Paramyxoviridae) and the hosts are pigs and bats. When the Nipah virus first broke out in Malaysia in 1998, it resulted in several fatalities and the collapse of the pig farming industry. A similar outbreak appeared in Siliguri. India and Bangladesh through reservoir pteropods bats in 2001. It is necessary to suspect Nipah virus infection in travelers suffering from acute encephalitis who had contact with pigs or bats. The location of the animals must be immediately quarantined if a virus is suspected. Nipah virus is included in class C bioterrorism which can be easily produced and spread to kill large numbers of populations. A non-segmented RNA virus that has recently been identified, the Nipah virus is a member of the paramyxovirus family (Fig.3). It is an exceptionally pathogenic virus and laboratory paintings call for bio-protection level-four containment. With a fatality rate of 40-75%, the Nipah virus infects the central nervous system (CNS) and causes encephalitis in infected individuals. The Nipah virus's precise entry point into the CNS is unknown, nevertheless. However, testing has shown that it can penetrate through the nasal turbinates' olfactory epithelium (28). The six genes (N-P-M-F-G-L) in the NiV genome are flanked by a five-'trailer and a three-'chief region. The pteropus fruit bat is the primary source of NiV. Numerous mammals, including cats, horses, pups, and pigs, are susceptible to The NiV infection. As a virus concerns human fitness in Southeast Asia, NiV has been considered. The NiV is regarded as a particularly mutagenic virus because of its non-segmented RNA genome. In NiV, there are more reservoir hosts and a higher rate of death. In 1998, when it caused an outbreak of viral encephalitis in Malaysia, this virus was initially identified. This outbreak inflamed three hundred people with a 35% mortality rate. The management of the outbreak required the culling of one million pigs because of NiV transmission from pigs to humans. At first, it was believed that the outbreak was brought on by the RNA virus known as Japanese encephalitis (JE), which is spread by mosquitoes, and that the JE vaccine was ineffective in protecting against the disease. NiV reemerged in Bangladesh in 2001, 2003, 2004, 2005, 2007, and 2008 after initial outbreaks, causing foetal human encephalitis. Additionally, NiV made a comeback in India in 2001 and 2007. Still, it results in fatal human encephalitis. NiV contamination can also be found by antibody detection (IgG and IgM). With the correct nursing approaches and universal exercise, nosocomial NiV contamination can be prevented. Although the medicine ribavirin is effective *in vitro*, its potential medicinal applications are still unknown (29).

Kyasanur forest disease (KFD) -monkey fever

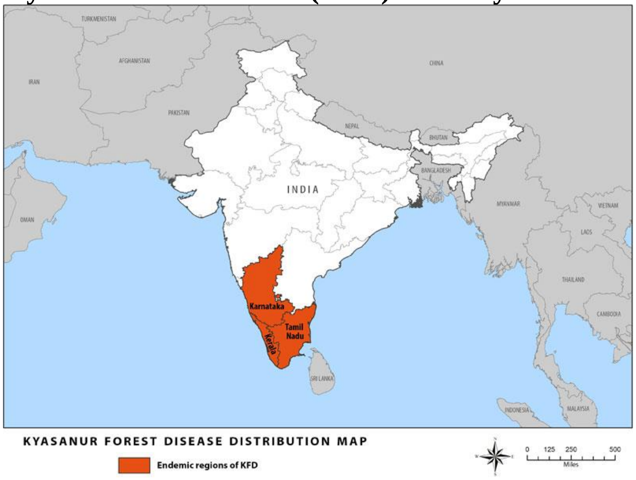

Fig. 4: Distribution of Kyasanur Forest Disease in India. https://www.cdc.gov/vhf/kyasanur/outbreaks/distribution-map.html

In Sindhudurg, Maharashtra, India, KFD was proposed in 2016, and out of 488 suspected cases, 130 were confirmed, resulting in three fatalities. In the Kyasanur woodland area of India's Shimoga district, it was initially discovered in 1957. (Fig.4). KFD is a public fitness track that runs beside India's Western Ghats. Deforestation reduces the quantity of shrubs that provide birds and rodents with a healthy environment. (30). The interaction between hosts, vectors and reservoirs is enhanced by these rodents in which nymphs and larvae develop. To manage the tick populace, wooded areas are treated with gamma hexachlorocyclohexane. Ticks can be destroyed by using dimethyl phthalate. The antigenic resemblance between KFD and Russian spring summer encephalitis virus has been used by Indian Council of Medical Research (ICMR) for preparation of vaccines. Karnataka country authorities are following KFD vaccination coverage in endemic areas. The vaccine is a formalin-inactivated tissue vaccine. It is advised for a group of people aged 55 to 75, with a dose of 1 milliliter for those over the age of 6 and 0.5 milliliter for those under 6. Three planned dosages are given at 0, 1, and 6 months (31,32).

Chandipura virus

In June 2003, the Chandipura virus outbreak got going. Encephalitis affected 329 children in Andhra Pradesh, ranging in age from nine months to fourteen years, and it resulted in 183 fatalities. The young people in need complained of nausea, stomachaches, and other symptoms like the Japanese encephalitis virus. The first Chandipura virus infection was discovered in 1965 in a village in Maharashtra, India. It belongs to the Rhabdoviridae family of related viruses and is spread via mosquitoes, ticks, and sand flies, among other vectors. There is no special treatment to be obtained, therefore only symptomatic treatments are used (33).

Japanese encephalitis

The Japanese encephalitis virus, which is a member of the flavi group of Arboviruses, is the main cause of viral encephalitis in Asia. The first case of Japanese B encephalitis was recorded in Japan in 1871. JE transmission will intensify as the number of vectors rises during the wet season. In about 1 in 250 situations, a serious medical condition develops. There are effective and secure JE vaccinations available to protect you from this illness (32).

Coronavirus disease (COVID-19)

Wuhan was where the most recent corona pandemic initially surfaced in China in December 2019. In India, the second wave also started in 2021. Continued hospital isolation of cases, touch tracing, and domestic contact quarantine (34).

Tomato Fever

Tomato fever is caused by coxsackie a 16 virus. Primarily infecting infants, tomato flu has inflamed almost one hundred youngsters under the age of five in Kerala. The health officials could identify the cases early. The name of the disease was derived from crimson blisters which were found over the entire body of the affected person. Due to enough awareness, children are being dealt with nicely inside the time frame. Researchers have no longer been capable of discovering the principal motive at the back of the tomato flu. Neighboring states, inclusive of Tamil Nadu and Karnataka, are also on alert for viable infections (35).

Fig.5: Skin infections in tomato fever (https://apnlive.com/web-stories/tips-to-prevent-tomato-flu)

Symptoms

According to the professional, some of the most common and not unusual symptoms include rashes, skin inflammation, and dehydration (Fig. 5). ‘The flu has additionally brought on nausea, belly cramps, vomiting, diarrhea, coughing, frame ache, sneezing, runny nose, tiredness, and aches in joints,’ in keeping with a few reviews (35).

Prevention

Prevent youngsters from scratching the blisters resulting from the flu, as it could make them worse.
Doctors have additionally suggested proper relaxation and hygiene. Fluid consumption ought to additionally be accelerated to counter dehydration. Parents must at once seek advice from a physician in the event of any of the signs like different sorts of flu,

tomato fever is likewise contagious. So, if a person is inflamed, they want to be kept in isolation (35).

West Nile fever

West Nile fever case was reported in Kerala in 2019 when a six-year-old child died of the disease. Even as the sector battles with the coronavirus pandemic and the sister editions of Omicron, a few areas around the world are seeing clean outbreaks of the latest illnesses, which have placed fitness professionals on alert. While those infections are incredibly plentiful in terms of scale, the already-battered fitness infrastructure may be strained in case the scenario worsens. In India, Kerala is reporting new sorts of illnesses, one in all that's endemic to the country. In the United States and Canada, scientific networks are involved in the clean outbreak of Hepatitis A instances in recent months. Here’s all we recognize of approximately those illnesses so far: The fever has claimed one existence in the Thrissur district of Kerala. The contacts were identified by local fitness management. Officials say that they're additionally exploring the opportunity of the sufferer contracting the fever from everywhere outside the country. It turned out in 2006 that Alappuzha had a severe case of West Nile Fever. The main vector of West Nile fever is mosquitoes of culex species. However, one must recognize that West Nile Fever isn't always air-borne like coronavirus and cannot be transmitted through close contact with the inflamed individual. Severe fever is the most common symptom of this sickness, as most of the instances stay asymptomatic (36).

Humans are reporting Hepatitis A infections from Dakota, California, outside the United States, to Canada. The main problem is the long incubation period before the person exhibits symptoms. US health officials have identified the link between strawberries and Hepatitis A epidemic and in lots of instances, an affected person might also stay asymptomatic. Loss of appetite, yellow eyes, and aches in joints are several of the primary signs of Hepatitis A contamination.

Monkey pox

The first case of monkeypox in India was reported from Ghaziabad district in Uttar Pradesh in a five-year-old boy with rashes all over the body. At the same time, it was reported from Thiruvananthapuram, Kerala in a 35-year-old man who arrived from middle east. The samples were sent to ICMR, NIV Pune for confirmation. Till date ten monkeypox cases have been reported from India. Currently the United States is free from monkeypox.

Reviews state that the suspected toddler exhibits symptoms of the monkeypox virus. The woman reported rashes and itching on her body. However, trying out components is only a precautionary measure. Lesions had been on the frame of the kid who came here for ear remedy. It appeared to be of the pox variety. They are not positive if it's miles of monkeypox. The officers similarly introduced that the kid has been relocated and the fitness branch is carefully tracking the case (37). As cases of monkeypox reach 6000, the WHO may declare a global health emergency**.**

Fig.6: Skin lesions in Monkeypox
(WHO. int)

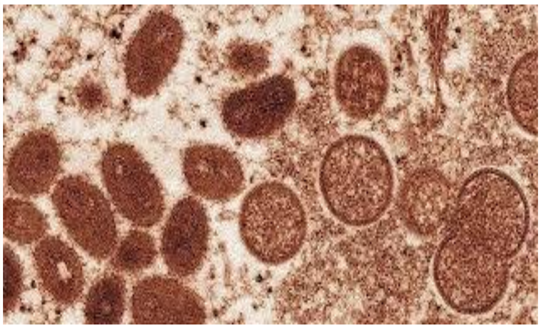

Fig.7: Monkeypox virus
(PC-CDC/ Cynthia S. Goldsmith)

Monkeypox virus

Monkeypox is a remarkable virus illness that has been linked to, but is much less severe than, smallpox. The disease is characterized by rash all over the body, fever, chills, and acute dehydration (Fig. 6). Monkeypox virus belongs to the pox group of viruses (Fig.7). The virus isn't always new, but to date, it has turned into the most dominant outside the areas of Southern and Central Africa.

Recently, the authorities of India launched hints to live blankets towards the lethal monkeypox virus that's spreading unexpectedly throughout the globe. The suggestions suggest that a laboratory case of the monkeypox virus can be established by detecting viral DNA sequences using PCR or sequencing.

In western African countries including Gabon, Central African Republic, Democratic Republic of the Congo, and Cameron, the monkeypox has been designated a pandemic (38).

CONCLUSION

In the age of globalization, viral infections' resurgence and appearance are seen as a constant threat to human existence. Among the emerging and reemerging viruses, the RNA viruses are the main culprit. The RNA polymerase of RNA viruses is error prone. As the genetic material of RNA viruses mutate over time, a new strain of virus with distinct immunogenic and antigenic properties emerges (39). This new virus strain possesses the potential to cause a pandemic. Environmental elements like climate change and tropical deforestation, in addition to genetic variation, are significant contributors to the formation of viral diseases (40). The formation of a new disease and the resurgence of established viral infections are also caused by a variety of other factors. 12. Viruses, in particular RNA viruses, have the natural ability to alter their genetic makeup in response to shifting environmental factors. Emerging RNA viruses can infect different host species since they cannot be conserved in their ecological niche. Viral illnesses are more likely to spread over the world due to factors including population expansion that is accelerating, poverty, and international travel by workers, immigrants, refugees, and tourists. Our capacity to comprehend the process of illness formation has expanded because of recent developments in whole genome and transcriptome sequencing, as well as in the invention of structure-based vaccines and medications. An infectious disease's past can reveal information about the bacterium that caused it. Sequencing the genome of an emerging virus at different stages of its emergence can reveal the evolution of a particular virus at the nucleotide and protein levels. Viruses have the innate ability to change their nucleotides through mutation, recombination, genome segment reassortment, and combinations of these molecular processes to form a new progeny that is typically more diverse than the parental virus. The structural and nonstructural proteins of viruses can mutate, leading to the extension of the viral host range and human infection. Many ecological, sociocultural, and changing contexts contribute to the creation of novel viruses, which are zoonotic in origin and cause the majority of developing viral illnesses. The use of various preventive measures, such as using mosquito nets, decanting rainwater that has been collected so that mosquitoes cannot spawn, and applying mosquito disinfectant, has helped to contain the several emergent pandemics brought on by the dengue virus and WNV. The elements that govern the transmission, reassortment, and emergence of new viruses remain unknown. It's possible that the causes of previous pandemics will play a key role in the development of fresh pandemics in the future. Real-time analysis of virus evolution may give us vital knowledge on the pathogenicity, emergence, and reemergence of viruses. Emerging viral illness prevention: To understand the mechanism and elements that contribute to the genesis of a viral disease or other infectious disease, experts from a variety of fields, including biologists, chemists, physicians, environmental scientists, and ecologists, must work together. Early warning of the new pathogens can be provided by monitoring an emerging disease.

It should be investigated to produce novel, effective drugs, vaccines, including DNA vaccines and subunit immunizations, and other approaches to manage the expanding viral and other infectious diseases. In collaboration with the World Organization for Animal Health and the Food and Agriculture Organization, WHO has been successful in creating a global early warning system (GLEWS). The goal of GLEWS is to offer zoonotic and newly developing infectious disease early warning and risk assessment. The geographical distribution of newly emerging and reemerging viruses is another topic covered by GLEWS. We can create effective tactics to stop the progression of diseases by comprehending the causes of disease onset and reemergence. Due to its tremendous geoclimatic diversity, India is constantly at risk from newly emerging and reemerging viral illnesses that are significant for public health. A stronger focus on epidemiology and disease burden is required for disease surveillance in the nation. It is also crucially necessary to have a thorough grasp of disease biomes, including vector biology and environmental factors that affect the diseases. Additionally, it is essential to increase emergency preparedness for these diseases and responses by focusing on a ‘one health’ strategy.

CONFLICT OF INTEREST

Authors declare no conflict of interest.

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