

Satellite Imaging and Surveillance of Infectious Diseases

Rajeev Singh¹, Koushlesh Ranjan² and Harshit Verma¹

¹Department of Veterinary Microbiology, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, India

²Department of Veterinary Physiology & Biochemistry, College of Veterinary & Animal Sciences, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut-250 110, India

Abstract

The Geographical Information Systems (GIS) and satellite image data can provide useful information for detection and management of both human and animal diseases outbreaks. The satellite surveillance can be used for monitoring of several environmental variables such as temperature, precipitation, humidity, wind speed and direction etc that influences the activity of pathogens, vectors and their interactions with human and animal hosts. By statistical analysis of satellite surveillance data the models based on geographic and vegetation of a particular landscape providing conducive environment to pathogens, spatial and temporal factors determining the distribution of disease can be framed. The GIS data analysis may help in several aspects during outbreak such as identification and spread of diseases over time, population groups at risk, patterns of disease outbreaks, facility available to healthcare and program intervention planning and assessment in disease outbreak. The satellite surveillance have been used in study of several water and vector borne diseases such as diarrhoea, cholera, typhoid, leptospirosis, Rift Valley Fever, Foot and mouth disease, bluetongue, West Nile Virus disease, Japanese encephalitis etc. The remote sensing and GIS data analysis is proved as powerful tools for disease surveillance, predicting its outbreaks, and monitoring control programs.

Keywords: Remote sensing; Geographical information systems; vector; Satellite surveillance

Introduction

The sufficient amount of knowledge has accumulated over the past decades on relationship of the environment and disease, but present time demands the identification of the most robust environmental correlates of animal disease and accurately linking it with remote sensing technology in order to develop early and effective disease warning system. Recently, scientists have made efforts in using remote sensing technology in predicting the few vector- and waterborne diseases of humans and animals and it is expected that the role of remote sensing technology in developing emergency programs for disease surveillance, treatment and control will increase in near future. A brief review on the applications of satellite imaging in disease transmission, control and prevention is presented as under.

Infectious Diseases

The first effort of linking the satellite based environmental data with the disease was made in an eradication campaign of dracunculiasis at the Republic of Benin. Later on, the satellite imaging was used to develop risk maps and control of few water and vector borne diseases.

Waterborne diseases

Water and climate are very closely linked. The excessive precipitation results in flooding which is a major cause of water-borne diseases viz. cholera, diarrhoea, typhoid, leptospirosis, hepatitis and even tetanus. The remote sensing technology can help the officials to determine the time and cause of contamination of water bodies used as source of drinking water and allows them to institute the rigorous prophylaxis and control measures in advance before the actual outbreak occurs. However, there are some requirements that must be met before predicting the effect of environmental changes on waterborne diseases viz., detailed knowledge of the disease incidence and transmission cycle, factors determining the contamination and survival of pathogen in water, specific and detectable indicators of microbial contamination of water and better health surveillance data and this information can be better used as determinants of waterborne disease outbreaks in

remote sensing technologies. The prediction of a few of these water-borne diseases has been made using satellite imaging and is discussed as under.

Cholera: The cholera is a bacterial disease of small intestine. It can be fatal to humans. The disease is caused by *Vibrio cholera*, a gram negative, non-spore forming and toxin producing curved organism. The infection may result in extreme diarrhoea, vomiting, loss of ions and dehydration. The victims can die within a day or so unless ions and water are replenished quickly. The transmission occurs through faecal contamination of food and water from an infected person. The spread of disease can be checked through consumption of chemically disinfected or boiled water. The seventh cholera pandemic began in 1961, but, still has its effects in six continents. An estimated 3-5 million cases and over 10,000 deaths occur globally every year. The *Vibrio cholera* survives on the phytoplankton and zooplankton in inter epidemic period. The inorganic and organic content of water, pH, salinity, surface temperature and exposure to ultraviolet rays in sunlight affect the distribution of organism. The satellite is providing the new insight from space to track the blooms of tiny floating planktons that carry cholera bacteria, ocean temperatures, sea height and other related variables to predict outbreaks of cholera. In a study of this kind, the Advanced Very High Resolution Radiometer (AVHRR) sensed National Oceanographic and Atmospheric Administration (NOAA) satellite data was used to infer the presence and to monitor the temporal spread of cholera in order to develop the early warning system of cholera outbreaks in Bangladesh [1]. In the study, the public domain remote sensing data of

***Corresponding author:** Rajeev Singh, Department of Veterinary Microbiology, Sardar Vallabhbhai Patel University of Agriculture and technology, Meerut, India, Tel: 91 9419255261; E-mail: rajeev201126@yahoo.in

Received November 10, 2015; **Accepted** November 23, 2015; **Published** November 30, 2015

Citation: Singh R, Ranjan K, Verma H (2015) Satellite Imaging and Surveillance of Infectious Diseases. J Trop Dis: S1-004. doi:10.4172/2329891X.S1-004

Copyright: © 2015 Singh R, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

1992-1995, for Bay of Bengal were compared with the cholera cases in Bangladesh. The remote sensing data of sea surface temperature and sea surface height at the coastal region of Bangladesh were included in the study. The sea surface temperature was related to phytoplankton and zooplankton concentration and sea surface height was related to human plankton contact, as Bangladesh is only slightly above of sea level with tidal intrusion of plankton into inland water of Dhaka, where, water is consumed from river system without treatment. The superimposition of the data revealed a statistically significant correlation of the sea surface temperature, sea surface height and the annual cycle of cholera outbreaks. The extensive studies conducted during the previous decades, confirming the autochthonous existence of *V. cholerae* in the aquatic environment as commensal of zooplankton, i.e., copepods and present satellite data provides strong evidence of climate dependency of cholera outbreaks. This Bangladesh model of cholera prediction can be extended to the global scale as an early warning system for effective prevention of cholera outbreaks in cholera-endemic regions.

Colibacillosis: The colibacillosis is a bacterial disease of human and livestock caused by *E. coli*. The *E. coli* is normal inhabitant of intestine, but the *E. coli* that harbour virulence gene coding for colonization factors or toxins, produce disease. The diarrhoea, colic, vomition, septicaemia, dehydration, urinary tract infection and renal failure are major clinical manifestations. The coliform bacteria generally feed on decaying animal and plant tissue, whereas, *E. coli* feed on faecal matter. The faecal contamination of water is one of the main ways of disease transmission and the presence of *E. coli* in water is a strong indication of recent sewage or animal waste contamination. The satellite imaging may be helpful in monitoring of water quality and controlling future outbreaks in human population.

The LANDSAT-TM algorithms was developed for mapping the surface freshwater contents of cyanobacteria, total coliform bacteria and faecal coliform *E. coli*, the three main bacterial contaminants of drinking water sources [2]. The algorithm for cyanobacteria was developed based on the two pigments, chlorophyll *a* and phycocyanin, of which phycocyanin was targeted especially as it is the pigment found only in cyanobacteria. The phycocyanin content was measured in targeted surface water samples and algorithm was developed for mapping of bacteria in streams with widths ≥ 90 m and drinking water reservoirs ≥ 5 hectares in area, for water depths of ≥ 2 m. The same methodology was used to develop algorithms for total coliform bacterial (TC) and faecal *E. coli* (EC) contents in Lake and river water of ≥ 2 m depth. The results revealed that the LANDSAT-TM algorithm has a potential to play unique role in monitoring the water quality of small drinking reservoirs in cities, towns and villages throughout the world.

Later on, Low-Earth-Orbit Satellites was used in data communication networking between portable hydro-meteorological measuring stations that allowed automated event sampling and short time monitoring on increments of *E. coli* in the alpine Karstic spring water, the important drinking water resource for humans [3]. The activities of the event-sampling were monitored on Linux-Server based internet platform. The results of samples collected conventionally by hand and with the auto-sampling procedure were analysed and were found in agreement with ISO 9308-1 reference method. The two large summer events of 2005 & 2006 were monitored for comprehensive hydrological characterizations and detailed analysis of *E. coli* dynamics ($n = 271$) in spring water. The *E. coli* concentrations were corrected individually for event specific die-off rates ($0.10-0.14 \text{ day}^{-1}$) of *E. coli* to compensate the losses in the water samples stored at spring temperature in auto sampler. The high resolution temporal analysis of faecal contamination of drinking water

revealed a sudden increase in the *E. coli* concentrations (approx. $2 \log_{10}$ units) in the spring water with a specific time lapse after the beginning of the event. The statistical analysis revealed that the spectral absorbent coefficient measured at 254nm may act as an early warning indicator for monitoring the time of faecal input in the drinking water.

Recently, a five year research project has been submitted, entitled Globolakes to monitor the water health of over 1000 lakes around the globe and to develop the first satellite-based early warning system [4]. This project was intended to study the effect of impact of climate change and associated factors on the algal blooms that can deplete the oxygen concentrations and produce the toxins harmful to human health in lakes and water reservoirs frequently used to supply the human drinking water. The Globolakes programme was builds on the satellites, Sentinel 2 and 3 of the European Space Agency's program, Global Monitoring for Environment and Security that will provide the images of the lakes.

Arthropod vector borne diseases

The vectors are the insect carriers' viz. mosquitoes, ticks, lice, fleas and flies etc that spread the germs to the humans or animals. These vectors transmit a number of deadly diseases viz. malaria, dengue fever, yellow fever, equine encephalitis, Japanese encephalitis, west Nile fever, rift valley fever, louping ill, three day sickness, blue tongue, Q fever, ehrlichiosis, endemic thypus, bubonic plague, anaplasmosis, babesiosis, theleriosis, trypanosomiosis, leishmaniosis, tularemia, vesicular stomatitis, lyme disease etc. The environmental conditions such as rainfall and temperature, influence the vector biology along with the host biology as well as host-vector interaction and therefore to a greater extent the spread of vector borne diseases. The satellite measurements and other remote sensing techniques directly cannot identify the vector themselves, therefore, the satellite derived environmental variables viz. temperature, humidity, precipitation, land cover type, health of vegetation that are conducive for breeding of vector are used to identify and characterized the habitat in which vector thrives and these help in anticipating the outbreak of vector borne diseases.

Mosquitoes borne diseases: The mosquitoes play an important role in existence, persistence, multiplication, development and transmission of a number of infectious agents that cause diseases and death in human and animals. A number of mosquitoes including *Aedes*, *Culex*, *Anopheles*, *Psorophora*, *Mansonia* spp are major parasites as well as vectors of infections in domestic animals. These vectors prefer still water for breeding. They lay their eggs in stagnant water of dams, ponds, shallow pits near the roadside, paddy fields, water bodies, standing water in channels of cultivated land, fountain water, tree holes, wet underside surface of vegetation, leaf axils, open drainage channels, water spilled near wells, man-made water containers such as domestic water storage containers, metal drums, automobile tyres, recycling containers, cooler water, swamps, marshy area and foot pits of animals. Most eggs hatch out in larvae in 48 hrs. The larvae feed in water and changes into pupa. The pupa develops into adult mosquitoes. The factors like temperature, rainfall, humidity, wind, direction, duration and speed influence the hatching and life cycle of mosquitoes. The seasonal density of mosquitoes in space and time, microbial adaptability in mosquito's biological life, abundance of infected mosquitoes, biting rates, inoculums per bite, proximity to breeding grounds and interaction with definitive host determine the ecology, demography, incidence and spread of mosquito-borne diseases. There is a long history of developing effective models for prediction and assessment of mosquitoes borne diseases based on environmental indicators and few are given as under.

Rift valley fever: The Rift Valley fever (RVF) is a viral disease that

affects humans and animals. Amongst animals, cattle, sheep and goats are principle victim. Besides, the disease also occurs in wild ruminants and buffaloes. In humans, the disease is characterized by flu like fever, muscle pain, joint pain, headache, photosensitivity, vomiting and death in severely affected patients. In animals, infection results in fever, diarrhoea, abortion in pregnant animals and high mortality rate of new borns. The disease was first time reported in Kenya and there after remains confined in Africa. In 2001, the disease was reported for the first time outside Africa in Arabian Peninsula and increases the fear of expansion of area especially in direction of the Asia and Europe. The virus is primarily transmitted by mosquitoes of different species. In endemic areas, virus regularly circulates between ruminants and haematophagous mosquitoes. Certain *Aedes* species act as reservoir of virus during inter epidemic period and may transmit virus to their eggs. Increased precipitation in dry areas leads to an explosive hatching of mosquito eggs, many of which harbour RVF virus. Satellite imaging has been used to confirm the historic importance of precipitation in RVF outbreaks and in forecasting high risk areas in future.

The ground rainfall and moisture pattern data recorded from 1981 to 1988 through National Oceanic and Atmospheric Administration (NOAA) satellite 7 and 9 was used in measuring the green leafy vegetation dynamics as indicator of mosquito breeding habitat in Kenya and correlated it with the Rift Fever Virus ecology and used it as alarm for start of mosquitoes control programme much earlier to actual commencement of RVF outbreaks [5]. The efforts were made in modelling the mosquitoes breeding habitat in East Africa. The mosquito breeding habitats in East Africa are locally known as “dambos”. The rain water gets accumulated in “dambos”. The still water in “dambos” builds-up the vector mosquito population. The high density of mosquitoes increases the RVF outbreaks in susceptible hosts. In the model testing the satellite derived normalized difference vegetation index (NDVI) was correlated with the cause input of variations in rainfall and effect output of fluctuation in RVF incidence. Further, the global precipitation impact of El Nino Southern Oscillation and concurrent elevations in sea surface temperature (SST) in the Pacific and Indian oceans when incorporated as associated variables along with increased rainfall in Eastern Africa, improve the prediction of RVF up to 5 months in advance [6, 7].

Landset data was used in determining the green leaf area index (LAI) of rice fields and relating it with the build-up of *Aedes* mosquito density [8]. They compared LAI with number of *Aedes freeborni* larval present at the outskirts of the rice fields and the minimum distance between the centre of each field and the nearest animal pastures serving as source of blood meal. The results revealed that rice fields with high LAI and near to animal pastures produced more numbers of mosquitoes, compared to fields with low LAI and far from the pastures. The discriminate analysis used the spectral measurements obtained from the satellite and minimum distance to animal pastures to accurately identify the high mosquito producing areas.

West Nile virus: West Nile is mosquito borne viral disease that causes encephalitis and fatal neurological disorders in human and animals. The disease has been reported from Africa, Asia, Europe and United States. The virus is maintained in nature in a cycle involving transmission between wild birds and mosquitoes. Wild birds act as amplifying host. Humans, horses and other mammals can be infected through bite of infected mosquitoes and act as dead end host. The virulent strain also causes encephalitis and paralysis in crows. The *Culex* mosquitoes are generally considered the principle vector and in low rate virus is maintained in mosquito's population through vertical transmission.

The migratory birds introduce the virus in new areas.

Climate variability is one of the most important factors influencing the virus multiplication and circulation; vector abundance, biology, physiology and vector contact to susceptible avian communities and may help in forecasting the future WNV disease risk areas. The everyday reporting of dead birds, active virus surveillance of birds, reports of infection in humans and horses, virus detection in mosquito's vector along with satellite derived virus spread sensitive climatic variables may help in control or exclusion of disease in risk identified areas [9].

The multiple environmental predictors viz. land surface temperature (LST), normalized difference vegetation index (NDVI) and actual evapotranspiration (ETa) data derived from moderate resolution imaging spectroradiometer (MODIS) was used to develop predictive model of West Nile virus transmission risk in humans of northern great plains of United State, which is considered as hotspot of human disease and found that environmental monitoring using remote sensed data have a good space in surveillance of West Nile virus risk prediction in space and time [10].

Japanese encephalitis: The Japanese encephalitis (JE) is another mosquito-borne viral disease. The disease is caused by Japanese encephalitis (JEV) virus of genus *Flavivirus*. The wild birds (especially herons) and domestic pigs act as reservoirs for JEV and transmission to human host may lead to severe symptoms. It is endemic in several parts of the world including India and Republic of Korea. The disease is caused by Japanese encephalitis (JEV) virus of genus *Flavivirus*. The mosquito *Culex tritaeniorhynchus* transmit the disease to humans. The experts note an increase in the density of *Culex tritaeniorhynchus* with the cultivation of rice in field. The rice fields provide site for breeding and shelter required for vector *Culex tritaeniorhynchus*. The rice field satellite surveillance showed a linear relationship between area of rice field cover and mosquito trapped in that area [11]. The Verma and Gupta (2013) successfully used the LANDSAT ETM remote sensing data of rice field as potent ground for mosquito vector breeding place and related them with the JE outbreaks in Gorakhpur district of Uttar Pradesh state [12]. The other closely related mosquito-borne Murray Valley encephalitis virus is enzootic in northern Australia and Papua New Guinea. The disease is directly related to tropical rain fall in these areas. The Schuster et al. (2011) used the remote sensing (RS) data of Tropical Rainfall Measurement Mission (TRMM) in developing the logistic regression models based on Multi-satellite Precipitation Analysis (TMPA) and recorded a direct relation between tropical rain fall and MVEV outbreak in these areas [13].

Venezuelan equine encephalitis: The Venezuelan equine encephalitis is a mosquito transmitted viral disease of donkeys, horses and zebras. Occasionally it may infect humans. The disease is caused by *Alphavirus*. The Barrera et al., (2001) used the Landsat 5 Thematic Mapper satellite imagery and remote sensing data in detecting the reflectance pattern of VEE endemic foci in lowland tropical forests of western Venezuela and predicting the VEE in other locations having similar reflectance patterns [14]. The Brault et al., (2004) used the remote sensing and satellite data in detecting the change in vector preference by virus [15]. The intensive satellite surveillance in Mexican region showed the absence of previously identified vector, *C. taeniopus* of VEEV due to habitat destruction. However, this vector was later on replaced by an abundant mosquito, *O. Taeniorhynchus* which has enhanced ability to spread the virus.

Malaria: Malaria is an acute febrile illness caused by four different species of a protozoan parasite Plasmodium viz. *P. falciparum*, *P. vivax*,

P. malariae and *P. ovale*. The *P. falciparum* causes most severe form of malaria and is characterized by fever, chills, headache, muscle ache, weakness and vomiting. The disease is fatal if treatment is delayed. The parasite is transmitted to human through bite of female Anopheles mosquitoes. There are about 3500 species of mosquitoes and 430 species of Anopheles. Approximately 40 Anopheles species transmit malaria. The mosquitoes breed in standing water bodies that can present for more than two weeks to support the aquatic phase of life cycle. The too little rains create fewer breeding habitats. The heavy rains destroy and wash away the larvae and eggs. The extremes of temperature also affect the life cycle. The mosquitoes develop at optimum temperature of 27 °C. The development of the plasmodium parasites within the mosquito vectors also depends upon the temperature. The *Plasmodium falciparum* sporozoites complete its development in gut and to reach to the salivary glands of mosquitoes in about 10 days. It can be more or less depending upon the decrease or increase in temperature. A variation in extrinsic incubation period in parasite in mosquito's vector have been recorded with fluctuation of air temperature from optimum. The disease is seasonal and incidence of malaria correlates well with temperature, rainfall and humidity patterns. However, irrigated paddy fields, marshes and wetlands are very favourable for the breeding of mosquito species.

The environmental variables that determine the habitat climatology and subsequent build-up of mosquito population density along with infectious bite and quantum of parasite in inoculums have been used to model the malaria. Ford (2012) used the amount and location of stagnant water supporting the mosquitoes breeding in forecasting the malaria outbreak through satellite imaging [16]. The Rogers et al (2002) discussed in detail the use of satellite images in describing the distribution of important species of *Anopheles gambiae* complex and the number of infectious bites per person per year (entomological inoculation rate/EIR) to predict the risk of malaria in Africa in a discriminate analytical model [17]. The Charoenpanyanet and Chen (2008) used Landsat 5 TM data of land cover and related it with the densities of Anopheles mosquitoes vector to develop predictive model of malaria in western Thailand [18]. Rahman (2011) developed a predictive model for malaria vector distribution in Bangladesh from meteorological data collected from remote sensing [19].

Culicoides borne diseases

Bluetongue: The bluetongue (BT) is a vector borne (*Culicoides*) disease caused by 27 different serotype of bluetongue virus (BTV). The BTV outbreaks can be forecasted by prediction of *Culicoides* migration in a geographical area. The BT forecasting model based on presence of *C. imicola* vector across Europe and north Africa was validated which predicted the presence and high abundance of BT epizootics, in several regions including Sardinia, Balearics, Sicily, Corsica, areas of mainland Italy, large areas of western Turkey, Greece and northern Algeria and Tunisia [20]. The Guis et al., (2007) used the high resolution satellite imagery to identify the environmental variables assisting in BT outbreak in several area of Europe including Corsica, a French Mediterranean island [21]. The Hartemink et al., (2009) used the basic reproduction number (R_0) of BTV to estimate the risk of BT outbreak in an area after its introduction [22]. In Netherlands, integrating the satellite imagery data with vector abundance and biologically mechanistic modelling, BTV outbreak was predicted.

Flies borne diseases

Trypanosomiasis: Trypanosomiasis is a group of several diseases in vertebrates caused by flagellated protozoan parasite of genus

Trypanosoma. Human infection results in sleeping sickness and chagas. The animal infection results in nagana, surra and chagas. The developmental stages like promastigote, epimastigote and amastigote generally occurs in blood sucking arthropods vectors. The mechanical transmission without development in biting flies such as *Stomoxys* and *Tabanus* as syringe passage may be possible if flies feed the healthy one in short period after feeding on sick one. The *Trypanosoma equiperdum*, the causative agent of dourine in equine is transmitted mechanically by coitus. The tsetse flies, biting flies, bugs transmit the protozoan parasite. There are 30 species or subspecies of tsetse flies that transmit the *Trypanosoma brucei gambiense* and *Trypanosoma brucei rhodesiense*, the causative agents of chronic and more acute sleeping sickness of humans, respectively. The riverine tsetse flies like *Glossina palpalis*, *G. tachinoides* transmit the *Trypanosoma brucei gambiense* at western coast of Africa and savannah flies like *G. morsitans*, *G. pallidipes* transmit the *Trypanosoma brucei rhodesiense* in East Africa. The life cycle of tsetse flies is highly dependent upon microclimatic conditions suitable for their survival. The models of disease transmission based on the climatic variables determining the biology of the insect vectors are robust. The air temperature and vapour pressure deficit records of climatology have been used to model the birth, death and density rates of tsetse flies in Africa. These climatic factors can easily be recorded as normalized difference vegetation index (NDVI), land surface temperature (LST), and cold cloud top temperature duration (CCD) in meteorological satellites and with the help of statistical techniques such as Fourier analysis and discriminate analysis etc the distribution of tsetse can be predicted with accuracies of more than eighty per cent. The NDVI ranks first and is closely followed by CCD and land surface temperature amongst the input variables used for monitoring the tsetse flies distribution in the model. Roger and William (1993) reviewed the different methods used in modelling arthropod vectors from satellite data [23].

Ticks: The metrological data from environmental satellite are of great value in selecting the input indicators for modeling the effect of climate on the life cycle and epidemiology of tick borne diseases. The climate changes can explain about fifty five per cent of tick-borne encephalitis. A positive association between preceding people's visit to forests and succeeding increase in the number of cases of tick-borne encephalitis was recorded. In this way the satellite monitoring of climate change and human population movement can help in predicting and preventing the outbreaks of this vector-borne disease.

Crimean-Congo haemorrhagic fever: The Crimean-Congo haemorrhagic fever (CCHF) is a widespread disease caused by a tick-borne Nairovirus of Bunyaviridae family. It is endemic in several parts of the world including Africa, Middle East and Asia. The satellite based surveillance of ground vegetation, agro climatic condition and tick prevalence in area can be correlated with disease outbreak. In Turkey, a predictive model using Landsat images system of satellite surveillance was developed to map the habitat suitability for tick vector. The area having higher report of CCHF were directly correlated ($p < 0.05$) with area of higher climatic suitability for tick vector [24]. The medium-resolution MODIS satellite imagery showed the potential spread and mixing of *H. marginatum* tick populations from eastern Europe viz. Turkey, Russia, and Balkans to western Europe viz., Italy, Spain and northern Africa [25]. This type changes might be possible due to climatic changes which replicates the virus speared in newer areas.

Rodent vector/rat fleas borne diseases

Bubonic plague: The bubonic plague is a fatal disease of human caused by the bacteria *Yersinia pestis*. The organism is found in the rodent

population of various continents. The rat fleas serve as vector for spreading the infection in rat and human. In several plague infected areas the disease exhibited seasonal pattern. The climate variables such as precipitation and temperature directly influence the population density and disease transmission efficiency of fleas and may be used as important indicator in modelling the human plague outbreaks.

Debien et al., in a satellite based study established the relationship between the precipitation and greenness and observed a positive correlation between the precipitation and one or two months lagging higher normalized difference vegetation index (NDVI) [26]. Finally they found the positive association in the cases of plague and climatic variables.

Hanta virus infection: Hanta virus pulmonary syndrome is a serious illness of humans. The symptoms are flu like and include fever, chill, headache, nausea, vomiting, muscle ache, diarrhea, abdominal pain, coughing and shortness of breath. The mice and rats spread the disease. They excrete the virus in the urine, droppings and saliva which form the tiny air droplets of virus. The breathing the infected air or contact of infected rodents or their urine or droppings transmits the disease in the people. There is no specific chemotherapy. The vaccine is also not available. The control of rodents in and around of house is best way to prevent the infection.

Studies have been conducted to predict the rare but deadly Hantavirus outbreaks in months ahead of time using satellite images through monitoring surges in vegetation that boosts mouse population. The numerous satellite images were used to understand the variations in the amount of green vegetations covering the Earth's surface and to track mice, the carrier of Hanta virus. It was observed that rise in vegetation create more food for the mice with increase in mice population, contact rate of mice and human that leads to more outbreaks of Hanta virus in humans. In 2006, Glass et al. developed a logistic regression model based on Landsat Thematic Mapping (LTM) imagery of 1992-2005 for estimating risk of Hanta virus Pulmonary Syndrome (HPS) in 2006 and reported that increased precipitation succeeding the prior drought years in northern New Mexico and southern Colorado increased the risk for HPS [27]. Later on, in 2011 Cao et al., combined the satellite imagery along with total number of captured mice, proportion of infected mice with the disease outbreaks and found that both climbed after peaks in greenery [28].

Bat vector borne diseases

Rabies: Rabies is a highly fatal viral disease of serious concern in different parts of world including Asia and America. The satellite telemetry surveillance and GIS data were used for study the disease at coarse scale. The bat (*Tadarida brasiliensis*) borne rabies in Chile during 2002-2012 was studied using ecological niche model (ENM) to find the association of rabies occurrence and environmental factors. The rabies virus variant AgV4 in bat was related with the Normalized Difference Vegetation Index obtained from Moderate Resolution Imaging Spectroradiometer satellite. The scenario build for rabies in bats and reliable anticipation of human rabies revealed the usefulness of ENM for rabies and other zoonotic pathogens [29]. The Satellite surveillance was also helpful in dispensing of vaccine products to its target wild animals. The Bait vaccines against rabies were distributed aerially in a region having large number of wild foxes (*Vulpes vulpes*) using a satellite navigated automatic bait drop system in Italy [30].

Wild birds borne diseases

Avian Influenza: Satellite surveillance of waterfowl on tracks of

migratory birds may help in understanding the transmission cycle of highly pathogenic avian influenza. For this purpose the satellite-derived movement of eight species of ducks captured in water bodies at Hong Kong, Bangladesh and Turkey were analysed [31]. Satellite based surveillance of migratory birds and Avian influenza specially in South east Asia was done by several researcher [32, 33]. Satellite telemetry based surveillance was used for Brown-headed gulls (*Larus brunnicephalus*) in winter season in Thailand during 2008-2011 for investigating their roles in spread of highly pathogenic avian influenza H5N1 virus. However, the surveillance did not show any bird infected with H5N1 virus during the study period and no H5N1 outbreaks were reported in Brown-headed gulls during the test period [34].

Conclusions

The gradual change in climate due to global warming are bound to alter the ecology, habits and habitats of hosts, agent and vectors and so drastically that incidences of vector and waterborne diseases such as malaria, dengue, diarrhea are bound to increase in endemic areas. Further, these diseases may expand the geographical range and new epidemic and pandemic of these diseases may occur in areas previously free of disease. So there is need of (1) construction of potential risk areas maps based on conditions favorable to vector proliferation of exotic diseases before their entry in new country, (2) development of early warning system before harmful exposures, (3) improved prevention initiative targeting ingress of risk, (4) reduction of environmental-related diseases, and (5) improvement in bio-terrorism event information management. The use of satellite in prediction and monitoring of diseases is a very recent & exciting approach, though in infancy and needs more refinement yet has potential of worth due to high speed in time series.

Acknowledgement

Authors are thankful to College of veterinary and animal sciences, SVP University of Agriculture and Technology, Meerut to provide infrastructure facility to prepare the manuscript.

References

1. Lobitz B, Beck L, Huq A, Wood B, Fuchs G, et al. (2000) Climate and infectious disease: use of remote sensing for detection of Vibrio cholerae by indirect measurement. Proc Natl Acad Sci U S A 97: 1438-1443.
2. Vincet RK, Michael R, Mamoon MK, Al-Rshaidt MD, Czajkowski K, et al (2005) Mapping the bacterial content of surface waters with LANDSAT-TM data: importance for monitoring global surface sources of potable water. Pecora 16 "Global Priorities in Land Remote Sensing" October 23-27, 2005 Sioux Falls, South Dakota.
3. Stadler H, Skritek P, Sommer R, Mach RL, Zerbin W, et al. (2008) Microbiological monitoring and automated event sampling at karst springs using LEO-satellites. Water Sci Technol 58: 899-909.
4. Tyler A, Hunter P, Maberly S, Carvalho L, Elliot A, et al. (2012) Globolakes, Global Observatory of Lake Responses to Environmental Change.
5. Linthicum KJ, Bailey CL, Tucker CJ, Mitchell KD, Logan TM, et al. (1990) Application of polar orbiting, meteorological satellite data to detect flooding of Rift Valley Fever virus vector mosquitoes habitat in Kenya. Med Vet Entomol 4: 433-438.
6. Anyamba A, Linthicum KJ, Mohoney R, Tucker CJ, Kelley PW (2002) Mapping potential risk of rift valley fever in African Savannas using vegetation index time series data. Photogrammetric Engineering & Remote Sensing 68: 137-145.
7. Anyamba A, Chretien JP, Small J, Tucker CJ, Formenty PB, et al. (2009) Prediction of a Rift Valley fever outbreak. Proc Natl Acad Sci U S A 106: 955-959.
8. Wood BL, Beck LR, Washino RK, Palchick SM, Sebesta D (1991) Spectral and spatial characterization of rice field mosquito habitat. Inter J Remote Sensing 12: 621-626.

9. Brown H, Wasser MD, Andreadis T, Fish D (2008) Remotely sensed vegetation indices identify mosquito clusters of west Nile virus vectors in an urban landscape in the Northeastern United States. *Vector Borne Zoonotic Dis* 8: 197-206.
10. Chuang TW, Wimberly MC (2012) Remote sensing of climatic anomalies and West Nile virus incidence in the northern Great Plains of the United States. *PLoS One* 7: e46882.
11. Richards EE, Masuoka P, Brett-Major D, Smith M, Klein TA, et al. (2010) The relationship between mosquito abundance and rice field density in the Republic of Korea. *Int J Health Geogr* 9: 32.
12. Verma S, Gupta RD (2013) Utilising satellite data for identifying the risk of Japanese Encephalitis. *Geospatial World*.
13. Schuster G, Ebert EE, Stevenson MA, Corner RJ, Johansen CA (2011) Application of satellite precipitation data to analyse and model arbovirus activity in the tropics. *Int J Health Geogr* 10: 8.
14. Barrera R, Torres N, Freier JE, Navarro JC, García CZ, et al. (2001) Characterization of enzootic foci of Venezuelan equine encephalitis virus in western Venezuela. *Vector Borne Zoonotic Dis* 1: 219-230.
15. Brault AC, Powers AM, Ortiz D, Estrada-Franco JG, Navarro-Lopez R, et al. (2004) Venezuelan equine encephalitis emergence: enhanced vector infection from a single amino acid substitution in the envelope glycoprotein. *Proc Natl Acad Sci USA* 101: 11344-11349.
16. Ford TE, Colewell RR, Rose JB, Morse SS, Rogers DJ, et al. (2012) Using satellite images of environmental changes to predict infectious disease outbreaks. *Emerg Infect Dis* 15: 1341-1346.
17. Rogers DJ, Randolph SE, Snow RW, Hay SI (2002) Satellite imagery in the study and forecast of malaria. *Nature* 415: 710-715.
18. Charoenpanyanet A, Chen X (2008) Satellite based modelling of Anopheles mosquito densities on heterogenous land cover in western Thailand. *The International Archives of the Photogrammetry, Remote sensing and spatial information Sciences XXXVII B8*:159-164.
19. Rahman A, Kogan F, Roytman L, Goldberg M, Guo W (2011) Modeling and prediction of malaria vector distribution in Bangladesh from remote sensing data. *Int J Remote Sensing* 32: 1233-1251.
20. Tatem AJ, Baylis M, Mellor PS, Purse BV, Capela R, et al. (2003) Prediction of bluetongue vector distribution in Europe and north Africa using satellite imagery. *Vet Microbiol* 97: 13-29.
21. Guis H, Tran A, de La Rocque S, Baldet T, Gerbier G, et al. (2007) Use of high spatial resolution satellite imagery to characterize landscapes at risk for bluetongue. *Vet Res* 38: 669-683.
22. Hartemink NA, Purse BV, Meiswinkel R, Brown HE, de Koeijer A, et al. (2009) Mapping the basic reproduction number (R_0) for vector-borne diseases: a case study on bluetongue virus. *Epidemics* 1: 153-161.
23. Rogers DJ, Williams BG (1993) Monitoring trypanosomiasis in space and time. *Parasitology* 106 Suppl: S77-92.
24. Estrada-Peña A, Zatansever Z, Gargili A, Aktas M, Uzun R, et al. (2007) Modeling the spatial distribution of crimean-congo hemorrhagic fever outbreaks in Turkey. *Vector Borne Zoonotic Dis* 7: 667-678.
25. Estrada-Peña A, Sánchez N, Estrada-Sánchez A (2012) An assessment of the distribution and spread of the tick *Hyalomma marginatum* in the western Palearctic under different climate scenarios. *Vector Borne Zoonotic Dis* 12: 758-768.
26. Debien A, Neerinckx S, Kimaro D, Gulincx H (2010) Influence of satellite-derived rainfall patterns on plague occurrence in northeast Tanzania. *Int J Health Geogr* 9: 60.
27. Glass GE, Shields TM, Parmenter RR, Goade D, Mills JN, et al. (2006) Predicted hantavirus risk in 2006 for the southwestern U.S. *Occasional Papers of the Museum of Texas Tech University* 255:1-16.
28. Cao L, Cova TJ, Dennison PE, Dearing MD (2011) Using MODIS satellite imagery to predict Hanta virus risk. *Global ecology Biogeography* 20: 620-629.
29. Escobar LE, Peterson AT, Papes M, Favi M, Yung V, et al. (2015) Ecological approaches in veterinary epidemiology: mapping the risk of bat-borne rabies using vegetation indices and night-time light satellite imagery. *Vet Res* 46: 92.
30. Mulatti P, Ferrè N, Patregnani T, Bonfanti L, Marangon S (2011) Geographical information systems in the management of the 2009-2010 emergency oral anti-rabies vaccination of foxes in north-eastern Italy. *Geospat Health* 5: 217-226.
31. Bridge ES, Kelly JF, Xiao X, Takekawa JY, Hill NJ, et al. (2014) Bird Migration and Avian Influenza: A Comparison of Hydrogen Stable Isotopes and Satellite Tracking Methods. *Ecol Indic* 45: 266-273.
32. Gilbert M, Xiao X, Pfeiffer DU, Epprecht M, Boles S, et al. (2008) Mapping H5N1 highly pathogenic avian influenza risk in Southeast Asia. *Proc Natl Acad Sci U S A* 105: 4769-4774.
33. Martin V, Pfeiffer DU, Zhou X, Xiao X, Prosser DJ, et al. (2011) Spatial distribution and risk factors of highly pathogenic avian influenza (HPAI) H5N1 in China. *PLoS Pathog* 7: e1001308.
34. Ratanakorn P, Wiratsudakul A, Wiriyarat W, Eiamampai K, Farmer AH, et al. (2012) Satellite tracking on the flyways of brown-headed gulls and their potential role in the spread of highly pathogenic avian influenza H5N1 virus. *PLoS One* 7: e49939.