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## **Environmental risk factors in relation to occurrence of vector borne disease epidemics: Remote sensing and GIS for rapid assessment, picturesque, and monitoring towards sustainable health**

**M Palaniyandi, PH Anand and T Pavendar**

### **Abstract**

Illnesses caused by pathogens and parasites in human populations that are spread by arthropod insects are called vector-borne diseases. The prevalence of vector-borne diseases contribute one-sixth of the illness and disability worldwide, especially, imposes large economic burden and casualty in the world, and has been increasing public health important, especially, challenging problems in more than 100 tropical countries and being affects more than 50% of the population in the world. The both vertical and horizontal structure of the epidemics have become major challenging problems in India. The study of environmental aspects in relation to occurrences of vector borne disease epidemics provides the indicators to stratification of probability of transmission risk. Gaining the preeminent understanding of the spatial aspects of vector borne disease transmission, vector ecology, vector breeding habitats, and the occurrences of vector borne disease epidemics in different part of the country through mapping, monitoring and surveillance of the epidemics; towards the achievements of disease transmission control and management, using remote sensing and geographical information systems (GIS) is the most productively significant scientific methods. The hybrid techniques of remote sensing and GIS are being used to rapid epidemiological mapping of the relevant information to understanding the spatial variation of the vector biodiversity, vector abundance, and the active infection state of vector borne disease transmission, disease surveillance, and perhaps, provides the disease epidemiological information along with geo-coordinates of site specification. The information relevant to the environmental variables in relation to the occurrences of vector borne diseases provides vertical and horizontal structure of the disease transmission risk, and to assess the community at risk of disease infection in different parts of the country, and thus, datum of guidelines to apply suitable prevent measures to control the epidemic transmission early in advance.

**Keywords:** Vector ecology, remote sensing and GIS, environmental risk factors, vector breeding habitats, epidemic transmission

### **1. Introduction**

The seasonal and geographical distribution of vector borne disease epidemic transmission has completely been controlled by the geo-environmental variables (land use / land cover, altitude, mean annual temperature, mean annual rainfall, potential evapotranspiration, readily available soil moisture, soil type's water logging potential, slope of the terrain, and remote sensing of normalized difference vegetation index, etc.) [63, 98]. Remote sensing and GIS has become essential tool for mapping the spatial distribution of malaria, JE, filariasis, dengue, chikungunya and visceral leishmaniasis, and has also been used to analyzing the ecological aspects of epidemic transmission [5-7, 66, 95, 97, 100] and also used to map the vertical and horizontal structure of epidemic vulnerability and the community at risk of infection [12, 14, 40, 70]. Mapping of epidemic transmission are increasingly important now days at global level as well as in the country level [7, 13, 24, 40, 66-70, 83, 97]. The success of the current and future control programme in the country depends on the availability of up-to-date thematic maps of the distribution of the diseases within the country, at a suitable spatial resolution/map scale relevant to control activities. Previous work in this area in the recent past has primarily focused on collating information on the prevalence of disease epidemics as well as endemic situation, and the potential use of availability of health resource allocation, and hence, should be given

priority when and where planning control campaigns, based on the disease transmission risk map [59, 61-64, 66, 76, 89], however, indicates that, rather than focusing on individual districts or states, it may be sensible, if at all possible [82, 83, 88, 97], to carry out the control activities to the whole country all together simultaneously, or at least all districts within discrete, high risk zones [61-64, 73, 74, 76, 89].

The hybrid remote sensing and GIS techniques are used to rapid epidemiological mapping of the relevant information to understanding the spatial variation of the vector biodiversity, vector abundance [7, 10, 12-14, 16-19, 24], and to assess the vector density quickly in the mosquito control districts, and mapping the active infection state of vector borne disease transmission, GIS surveillance for epidemic control, and perhaps, provides the disease epidemiological information along with geo-coordinates of site specification [7, 61-70, 100]. The multispectral satellite data has been used to study the geo-environmental determinant risk variables [27, 29, 31, 38, 62-67], including climate, landscape, and the environments of vector ecology in the urban agglomeration of human settlements as well as vector breeding habitats environment in the country sides [41-43, 45, 47, 49]. A geospatial analysis of socio-economic and environmental risk factors in relation to the occurrences of vector borne diseases, and ecological niche modeling<sup>57</sup> and GIS mapping could be provided the precise guidelines to rapid assessment and priority for both vector and disease control in an efficient manner [1-100].

## 2. Mapping of vector borne disease prevalence

Mapping disease distribution, spatial analysis and spatial modeling of disease epidemic transmission are increasingly important now days at global level as well as in the country level, and the results obtained using remote sensing and GIS has potentially been vital role particularly in the designing and implementation of active disease control programmes, has already been used to demonstrating and implementing the programme for malaria [12-16, 41, 42, 60, 94], tick [19] and *Tsetse* – borne diseases [78, 79] and onchocerciasis<sup>74</sup>. The success of the current and future control programme in country depends on the availability of up-to-date thematic maps of the distribution of the diseases within the country, at a suitable spatial resolution /scale relevant to control activities [45-47, 59, 66, 69, 71, 73, 89, 97]. Previous work in this area in the recent past has primarily focused on collating information on the prevalence of disease epidemics as well as endemic situation, and the potential use of availability of health resource allocation, and hence, should be given priority when and where planning control campaigns, based on the disease transmission risk map [41, 50, 60-64, 73, 76, 89], however, indicates that, rather than focusing on individual districts or states, it may be sensible, if at all possible, to carry out the control activities to the whole country all together simultaneously, or at least all districts

within discrete, high risk zones [59, 62, 82, 89, 97].

The use of remotely sensed data has been used to correlative spatial analysis [98], the distribution of scrub typhus in southeast Asia and breeding sites of *Aedes sollicitans* near New Orleans, LA, on the basis of associated vegetative types, describing the landscape characteristics of the sites in Philippines where the prevalence of schistosomiasis was very high [16], and inferring ecological parameters associated with Rift Valley Fever in Kenya [48]. The classic example of studies carried out to use remotely sensed data to predict both the spatial and temporal dynamics of vector populations and assess the risk of disease transmission [58, 98]. The megabyte quantities of multispectral raster data have been integrated with geographical information systems (GIS) to study the landscape environments of surrounding villages of known vector abundance for malaria transmission, consequently, mapping of the villages at high, moderate, and low risk of malaria transmission was completed successfully with greatest accuracy [7]. GIS platform has facilitate to capture and integrate remotely sensed data with ground truth data for mapping and the risk assessment of Lyme disease transmission, and thus, preparing disease transmission risk map becomes datum of base line for control programme at the national level [60-64, 79, 80].

## 3. Change in epidemic situation

The change in endemic situation in the country has been directly or indirectly caused by the water resource irrigation projects, land use / land cover changes [63, 64, 66], regional climate changes [9, 27, 28, 44, 54], increase of sea change population [27, 63, 64, 66], urban agglomeration, industrial development and the past development of towns [63, 64, 66, 71], and thus, the disease epidemics have been steadily increased too, and, besides, it has been found ubiquitous across the country, such diseases known as, filariasis, malaria, JE, dengue, chikungunya, and visceral leishmaniasis / otherwise known as Kala azar in India [63, 64, 66], as a result, the increase of both mosquito nuisances and disease transmissions has receive public health importance and is challenging problems in India [63, 64, 66]. The burden of vector borne diseases are increasing day by day in India; and therefore, the urgent need for both intervention measures of vector control and transmission control through the appropriate, most efficient, speedy and scientific way. The implementation of conventional method of vector control in the field has significant effect, however, the problem is not manageable and it has been increased steadily [63, 64, 66]. Therefore, the present study is made to a systematic review on remote sensing and GIS to mapping the vector breeding habitats, vector borne disease epidemics, and the environments of vector ecology (Fig.1, 2) [41, 50, 60-64, 73, 76, 89].



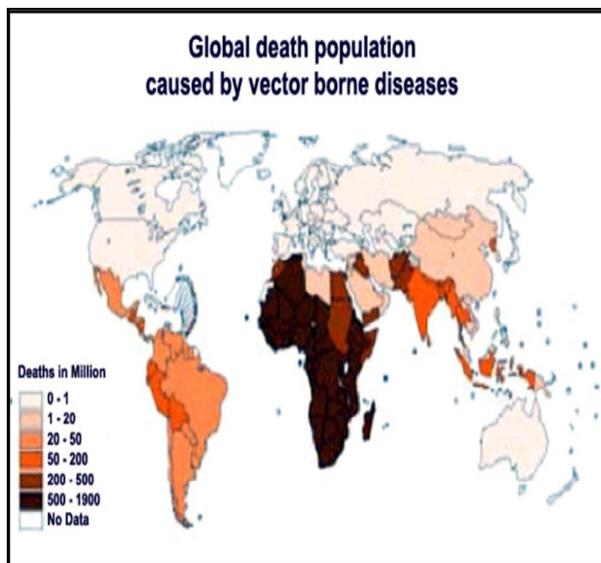
**Fig 1:** Vector breeding habitats of *Culex quinquefasciatus* and *mansonia* (Filriasis vector), *Anopheles* genus mosquitoes (malaria vector), and *Aedes* genus mosquitoes (dengue and chikungunya vector) in the human settlement areas



**Fig 2:** Field pictures of vector mosquitoes breeding sources, pictures (a) and (b) JE vector (*Culexvishnui* groups), and malaria vector *Anopheles* genus mosquitoes breeding habitats, pictures (c) and (d) dengue and chikungunya vector (*Aedes* genus) breeding sources, pictures (e) and (f) malaria vector (*Anopheles* genus) breeding grounds and pictures (g) and (h) filariasis vectors (*Culex quinquefasciatus*) breeding habitat sources

**4. Global distribution of vector borne diseases**

The prevalence of geographical distribution of vector borne diseases has been increasing public health important and challenging problems in more than 100 tropical countries and it has been affecting more than 50% of the population in the world, especially, it is very big problem in the tropical and subtropical countries [54, 99] (Fig.3). The occurrences of diseases are influenced by several parameters including demography [27, 63, 64], climate [1, 9, 15, 54], landscape [3, 4], environments [21, 26, 56], socio-economic variables [50, 52] and other factors related to vector ecology [38] and host parasites [61-70]. With the availability of high tech remote sensing and GIS is used for the present study, it is possible to make reliable estimates about the areas that are vulnerable to risk of disease transmission, and hence, assist to design to specific control strategy and to take rational decision in time to prevent the possible outbreaks of diseases in advance.



**Fig 3:** Global death population caused by vector borne diseases as on 2012, source WHO/TDR, 2012

#### 4.1 The Environmental Determinants of vector borne diseases Transmission

There are complex of phenomenon functioning and determining on the prevalence of epidemic transmission, however, the natural risk factors [28, 31, 43] particularly, the geo-climatic and environmental variables are most important determinant key factors [27, 44, 61-64] and has complete control over the vector survival, parasite development, and disease transmission (Fig 4a). The prevalence of vector borne diseases (filariasis, malaria, JE, dengue, chikungunya, and visceral leishmaniasis) caused by the vector mosquitoes namely *Culex*

*quinquefasciatus* and *mansonia*, *Anopheles* genus mosquitoes, *Culex* genus mosquitoes and *Aedes* genus mosquitoes respectively. (Fig.4b), and which has been spread over most of the regions in the tropical and sub tropical climate countries. The spatial epidemiology of disease occurrences and disease transmission in the world are directly controlled by climate, landscape and the environments, and consequently, the epidemiology of disease prevalence [1-100] are spatially associated with the vegetation indices, and which are determining the profusion of mosquitoes vectors [10, 13, 16-49].

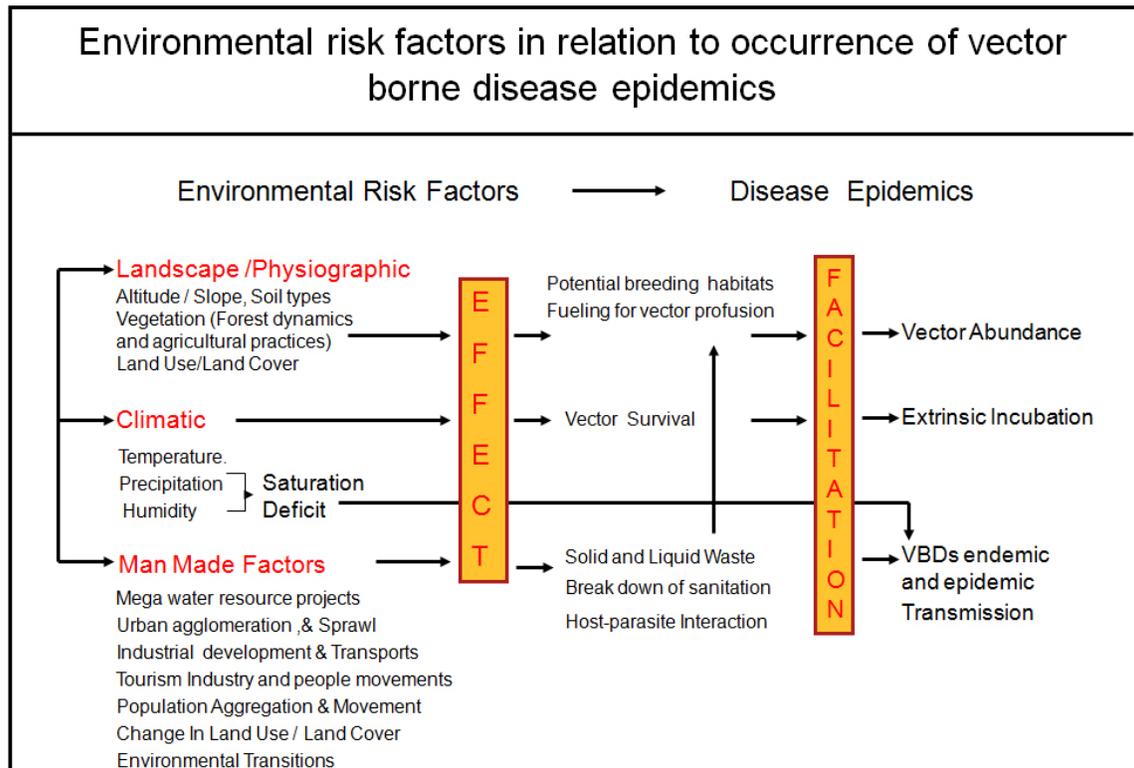


Fig 4a: The determinants of environmental variables and vector borne disease transmission model

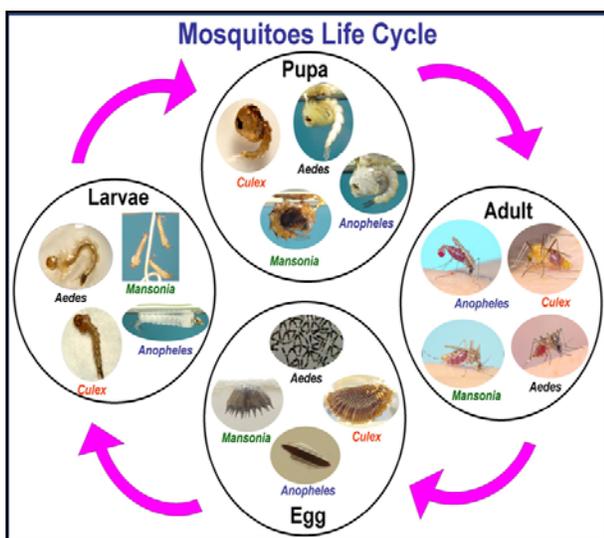


Fig 4b: The vector mosquitoes of vector borne disease transmission in the world

Vector-borne diseases are directly linked to the environment by the ecology of the vectors and of their hosts, including humans. Vector-borne diseases still constitute a serious threat to human health (including malaria, trypanosomiasis, chagas disease, leishmaniasis, lymphatic filariasis, onchocerciasis, dengue and Japanese encephalitis), among these diseases, one third of the death is caused by mosquito-borne diseases [13, 99]. Vector borne diseases surveillance most often includes monitoring (1) the vertical and horizontal distribution of disease prevalence in human populations, (2) Geographical distribution and spatial patterns of susceptible population in various age and sex, socio-economic groups, (3) pattern of drug resistance in parasites, and (4) intensity of epidemic transmission by vector populations in different time point with reference to space. In vector borne disease control programs where vector control constitutes an important component in the overall strategy, a surveillance system to accurately estimate vector abundance is essential. A basic understanding of the ecology of vector breeding habitats is also extremely significant to launch appropriate strategy to epidemic control and management. The vector of malaria and

JE requires an aquatic environment frequently described in terms of vegetation and water. Unfortunately, current techniques for locating larval habitats and monitoring mosquito populations are labour-intensive, time-consuming, and impractical over large areas. When assessing the risk of emergence of vector-borne diseases, it is crucial to be able to characterize the arthropod vector's spatial distribution. Satellite data have been used successfully for monitoring environmental conditions that influence the patterns of such arthropod vector-borne diseases<sup>43</sup>. The accelerating trend of vector borne disease epidemic worldwide has led many agencies and institutions, including the World Health Organization (WHO), to call for the development of new scientific and innovative approaches to vector borne disease surveillance, control and management [66, 70, 77, 95, 97, 98]. An essential element in this development is the recognition of the variability of environmental and epidemiological parameters that influence the patterns of malaria, JE, and dengue vector population density and epidemic risk [61-64].

Several mosquito habitat models have been developed to predict the location of mosquito habitats [31-36, 64, 84], data source on the aquatic environment to represent surface water availability, curvature, and distance to streams, vegetation cover and wetness index. Wetness index indicates soil moisture level in relation to water flow patterns, which is calculated based on the local upslope contributing area and slope [3, 4]. The vectors *A. fluviatilis*, *A. annularis* and *A. culicifacies* breed in all types of habitats. Streams were most productive for the main vector, *A. fluviatilis* and breeding was intense during winter and early summer. In the rainy season, breeding occurred in terraced paddy fields [64, 98]. The freshwater breeding habit of *An. culicifacies* is well established, and the result shows that the major two *An. species* were identified as *An. culicifacies s.l.* and as *An. subpictus s.l.* *Anopheles culicifacies s.l.*, the major vector of malaria in the Indian subcontinent, is generally regarded to be intolerant of salinity preferring to breed in newly-dug freshwater pits, domestic wells and pits used for plantation of coconuts and casurina in India. However *An. culicifacies* larvae have reportedly been collected from concrete reservoir tanks containing brackish water<sup>61</sup>. The delineation of wet irrigation rice cultivation land use from a range of distances from the villages and determined which distance resulted in the highest correlation with mosquito abundance [52, 64, 98].

*An. culicifacies* are produced in large numbers in rivers in summer and in paddy fields in rainy and cold seasons [20, 64, 98]. The effect of rice cultivation patterns on malaria vector abundance in rice-growing villages, mosquito abundance is highly variable across villages and seasons, the result provides the area of young rice explained 86% of the inter-village variability in *An. gambiae* abundance in August before the peak in malaria transmission [20]. The surface areas of larval habitats of *Anopheles* vectors of human malaria were associated with certain land cover types, of largely agricultural origin, and close to streams. Water sources especially irrigation networks are affecting the magnitude and distribution of malaria and schistosomiasis, significant correlations found between the diseases and the environmental variables, proximity to snail breeding sites and irrigation networks and the highly agricultural areas are identified as the most common factors that define the high prevalence areas for schistosomiasis confirming the fact that

conditions that support the snail populations, and hence, the presence of the disease [43]. The results of the initial models, based on rice-field canopy development and proximity to blood meal sources, and land cover mixture within buffers provide the basis for a more sophisticated malaria vector population dynamics model [77]. In addition to these aquatic environmental factors, the spatial and temporal patterns of *Anopheline* vector populations are strongly influenced by elevation [3], temperature, precipitation and humidity [1, 9, 15, 27, 28, 31, 44, 54].

#### 4.2 Global burden of Filariasis

Globally, lymphatic filariasis is endemic in 81 tropical and sub-tropical countries, 1,410 million people live in the 73 countries where the disease filariasis is known to be endemic in Africa and South-East Asia regions, Of the endemic population, 879 million (62%) live in the South-East Asia region (9 endemic countries) and 460 million (33%) live in the African region (34 countries). The Region of the Americas, Eastern Mediterranean region and Western Pacific region with 44 and 22 endemic countries, respectively [61, 62, 82, 99].

#### 4.3 Global burden of Malaria

Malaria has been found in the vast areas in different regions of the world. Particularly many people in the tropical and subtropical regions suffer from the dangerous and deadly malaria disease. 40 percent of the earth's population lives in zones where malaria is endemic. Malaria remains one of the greatest killers of young children in the developing world [99]. Currently, more than two billion people live at risk of contracting malaria, and WHO estimated that global annual incidence of clinically confirmed malaria is greater than 110 million cases, about 300 million estimated malaria cases worldwide and more than one million people die every year from the direct causes of malaria, with children less than five years of age living in sub-Saharan Africa at highest risk, and approximately 90% of this burden is fueled by geo-environmental factors [31-36]. Malaria is transmitted by *Anopheline* mosquitoes, which breed in surface water pools where environmental conditions are suitable for both vector survival and parasite development [1, 7, 26, 38, 43, 47, 52, 64, 81, 87, 94-98]. It also imposes a considerable economic burden resulting from high morbidity levels within the adult population. Although statistics on the scale of the disease vary considerably, it is inevitably the poorer sections of the poorest nations that suffer most [64, 98].

#### 4.4 Global Burden of Japanese Encephalitis (JE)

The prevalence of JE epidemics have been occurred in the countries of east, south east and south Asia, such as Japan, Korea, China, Eastern Siberia, Vietnam, Thailand, Sri Lanka, Nepal, Indonesia, Malaysia, Myanmar, Taiwan, Bangladesh and India (Table.1) [50, 52, 61, 90, 99]. Approximately 50,000 sporadic and epidemic cases of JE are estimated to occur annually in China, the Republic of Korea, and Japan, South and Southeast Asia and some parts of Oceania. Patterns of JE transmission vary within individual countries and from year to year [50, 52, 90]. In endemic areas, annual incidence ranges from 1 to 10 per 10,000 populations. In recent years, the epidemiological patterns and especially the distribution of JE have changed. There has been a steady decline in the

incidence of disease in Japan, China and Republic of Korea. However, it is increasing and spreading to new areas where wet irrigation rice cultivation has been practiced in different parts of India [63, 64]. Thailand, Myanmar and Nepal. Sporadic incidences were also reported from Malaysia, Singapore, Sri Lanka, Indonesia and Philippines [50, 52].

**Table 1:** The geographical distribution of *Culex* genus vector mosquitoes and its role in JE transmission in different part of the countries

S. No.	Species	Country
1	<i>Cx. tritaeniorhynchus</i>	Japan, Vietnam, Thailand, Taiwan, India
2	<i>Cx. gelidus</i>	Vietnam, Thailand
3	<i>Cx. fuscocephala</i>	Thailand, Taiwan, Malaysia
4	<i>Cx. vishnui (annulus)</i>	Taiwan, India
5	<i>Cx. pseudo vishnui</i>	India

Source: WHO 2014

#### 4.5 Global Burden of Dengue

The incidence of dengue has grown dramatically around the world in recent decades. Over 2.5 billion people – over 40% of the world's population – are now at risk of dengue. There have been 50 –100 million people affected worldwide by dengue annually [2, 8, 25, 69]. Before 1970, only nine countries had experienced severe dengue epidemics [24, 99]. The disease is now endemic in more than 100 countries in Africa, the Americas, the Eastern Mediterranean, South-east Asia and the Western Pacific. The American, South-east Asia and the Western Pacific regions are the most seriously affected. Cases across the Americas, South-east Asia and Western Pacific have exceeded 1.2 million cases in 2008 and over 2.3 million in 2010 [8, 99]. Recently the number of reported cases has continued to increase. Not only the report of cases is increasing, but explosive outbreaks are occurring as the disease spreads to new areas. The threat of a possible outbreak of dengue fever now exists in Europe and local transmission of dengue was reported for the first time in France and Croatia in 2010 and imported cases were detected in three other European countries. A recent outbreak of dengue on Madeira Islands of Portugal has resulted in over 1800 cases and imported cases were detected in five other countries in Europe apart from mainland Portugal during 2012. The estimated 500 000 people with severe dengue fever require hospitalization each year, a large proportion of whom are children, and about 2.5% of those affected lead to death [99].

#### 4.6 Global distribution of chikungunya

In recent years, it has been reported from the country of Mayotte in southern Africa, Mauritius and Seychelles. European countries like France, Germany, Italy, Norway and Switzerland have reported importing cases, courtesy people returning from these islands [67, 99]. The experience of epidemics has been reported regularly in the countries of Africa, the Americas, the Eastern Mediterranean, South-east Asia and the Western Pacific [99]. The American, South-east Asia and the Western Pacific regions including the southern part of India are the most seriously affected, during 2006 and report of epidemic is occurred every year since then [53, 67, 99].

#### 4.7 Global distribution of Visceral Leishmaniasis

Visceral Leishmaniasis is a chronic disease, caused by *Leishmania a donovani* parasite is transmitted by female phlebotomine sandfly, *Phlebotomous argentipes* [6, 10, 21-23, 55, 68, 92, 99]. It has been a serious threat to the public, is endemic in Brazil, Bangladesh, Nepal, Sudan and India. In India, it is endemic in the states of Bihar, Uttar Pradesh and West Bengal, and it has been reported that Bihar state alone account to 40 to 50% of the total case in India [56, 68]. India alone contributes 90 % of the total cases of world reports, and hence, it is a very serious challenging problem to India. The vector abundance and the disease transmission are directly or indirectly controlled by the climate, landscape environment variables and which are fueling to the occurrences of epidemic cases. It has been claimed heavy death toll of human lives in South-east Asia [99], especially in India, where it is one of the major causes of morbidity and mortality, creating a significant impediment to human life. The distribution of Visceral Leishmaniasis (VL) extends from the Asian shores of the Pacific Ocean to the straits of Gibraltar [21-23].

#### 5. The Geographical distribution of vector borne diseases in India

India have been steadily increased to progress economic development, but on the other hand, the change of epidemic transmission into the endemic situation in the country in the recent years [9, 11, 61-70, 96], besides, it has been found ubiquitous, such diseases known as, malaria, filariasis, JE, dengue and chikungunya, consequently, the increase of both mosquito nuisances and disease transmissions has become public health importance and big challenging problems in India [9, 61-71, 82-85, 89, 90]. The vector borne disease burden of India has become challenging problem and has been increasing day by day; therefore, the both intervention measures vector control and treatment measures for controlling the diseases through the most efficient way of controlling disease transmission by vector control method. The implementation of conventional method of vector control in the field has a significant effect, however, the problem is not manageable and it has been increased steadily. Therefore, the present study is designed for mapping the geographical distribution and geo-spatial analysis of vector borne diseases, and to study the both vector and disease ecology and probability of disease transmission risk in India [61-72, 90, 96].

#### 5.1 Malaria Prevalence in India

The malaria endemic problem is a major concern in the 14 states and the highland areas of north eastern states and the eight other states of India have highly public health importance Though a significant result was obtained by the national malaria programs, the urban malaria is a challenging problem in India [64, 71, 83-85]. The annual prevalence of malaria is estimated 75 million and the death rate is 8 lakhs during the year 1953, and it is gradually reduced to 1.04 million cases and a death rate is 678 in the year 2010. The Indian subcontinent has malaria endemic problems especially in the North-eastern states (Assam, Arunachal Pradesh, Manipur, Meghalaya, Nagaland), Orissa, Chhattisgarh, West Bengal, Rajasthan, Gujarat, Jharkhand, Karnataka, Madhya Pradesh, Uttar Pradesh, Haryana, Maharashtra, Tamil Nadu and Andhra Pradesh. All the four malaria parasites are risk of malaria transmission in India, however, the malaria parasites

transmission of malaria parasites (*P. vivax* and *P. falciparum*) are major prevalent in India and are transmitted by about 12 *Anopheline* species. The entire population in the rural and highland areas in the country is at the risk of infection [64, 71, 83, 84].

### 5.2 The prevalence of lymphatic filariasis in India

The prevalence of lymphatic filariasis is endemic in 18 States and 6 Union Territories In India, there have been types of filariasis namely, the *Wuchereria bancrofti* parasite of Bancrofti filariasis transmitted by *Culex quinquefasciatus*, the *Brugia malayi* parasite of Brugian filariasis transmitted by *Mansonia annulifera* and *Mansonia uniformis* and, the prevalent of sub periodic filariasis in Andaman and Nicobar Islands has been transmitted by *Ae. niveus* mosquitoes [62, 66, 82]. As on 2010, the 33 million people are positive for microfilaraemia (mF), 23 million people affected with symptomatic filariasis, The 473 million people potentially at the risk of filarial infection [62, 66, 82, 99]. National Filariasis Control Programme through vector control and selective chemotherapy protects about 40 million people, effectively and most importantly in the urban areas in the country [62, 66, 82].

### 5.3 Japanese Encephalitis (JE) epidemics in India

The mapping of spatial extends of district level JE epidemics in different parts of the country was updated for the past 58 years. Totally, 152 districts of 20 states in the country were experienced and affected with JE epidemics [63] from 1955 to 2012. The environmental changes of land use / land cover are most probably causing the conducting environments for survival of JE vector mosquitoes i.e. Culline mosquitoes mainly *Culex vishnui* group (*Culex tritaeniorhynchus*, *Cx. vishnui*, *Cx. pseudovishnui*, *Cx. whitmorei*, *Cx. epidemus*, *Cx. fuscocephala*, *Cx. gelidus*, and *Cx. bitaeniorhynchus*) and which are directly influencing the changing nature of epidemiology [50] of the disease in the country [63, 90]. The report of major epidemics of JE death were recorded between 1500 to 4000 cases were occurred [63] mainly in the states of Assam, Andhra Pradesh, Tamil Nadu, Karnataka, Kerala, West Bengal, Goa, Uttar Pradesh, Manipur, Haryana, and Bihar during the period of 2007 to 2012.

### 5.4 Dengue epidemics in India

The dengue and chikungunya epidemics have major challenging problems and become essentially public health important in India for the recent years, and it has been transmitted by the *Aedes* genus (*Aedes aegypti* or *Aedes albopictus*) vector mosquitoes [2, 8, 27, 53, 67]. The both disease epidemic situation in the country brings high attention for the past 12 years. The causes must be revealed for the profusion of dengue vectors for the recent years. The 1000 of dengue cases clinically confirmed from different part of the country, during 2012-2016 and the epidemics in the country has become daily news now days [67]. The dengue epidemics were reported from 24 states / union territories of India and it was steadily increased to become very serious threat to the public (NVBDCP, reports 2012-2016). The both dengue and chikungunya have been transmitted by the *Aedes* genus (*Aedes aegypti* or *Aedes albopictus*) mosquito vectors [2, 8, 27, 53]. The environmental determinants have been creating conducting environment and manmade factors are fueling and

responsible for the occurrences of disease epidemics across the country [53, 67].

### 5.5 Chikungunya epidemics in India

The occurring of chikungunya epidemics was reported in India during the year 2006, especially, in South India, thirty-two years after its last outbreak in India, during 1974 National Vector Borne Disease Control Programme (NVBDCP). The chikungunya epidemic was reported in 213 districts especially in South India during 2006 with lakhs of suspected fever cases were reported, 15,504 cases were screened for blood samples and 1985 cases were clinically confirmed chikungunya fever in the country [67]. A mixed outbreak of chikungunya along with symptoms of dengue fever was reported from Andhra Pradesh between December 2005 and February 2006. It was reported more than a 100,000 people in the states of Andhra Pradesh (AP), Karnataka and Maharashtra of south India during 2006, and it was accounted to 30,000 cases in Andhra Pradesh (Chittoor is the worst affected district); over 70,000 in Karnataka (17,000 cases in Gulbarga district alone); and, the disease has been affected in Maharashtra too. India has suitable climate, landscape, and the environment for survival, longevity and profusion of vector as well as chikungunya virus [65-67]. As the result, the report of epidemic cases occurring during 2006 and it has been gained national public health importance in India, since then [67].

### 5.6 Visceral Leishmaniasis in India

The Indian sub-continent is prone to the occurrences of chronic Visceral Leishmaniasis (VL) or Kala-azar, and geographical distribution of disease is endemic in the states of Bihar, West Bengal, Uttar Pradesh, Jharkhand, Delhi, Gujarat, Madhya Pradesh and Kerala in India [72, 89]. The world distribution of Kala-azar chronic cases occurring in the countries, such as, Brazil, India, Nepal, Bangladesh and Sudan, and the 90 % of the disease has been mainly affected the children of below 9 - 15 years old [6, 10, 21-23, 55, 58, 72, 89], and it has been causing 50% of the cases turn to become deaths incidents occurred annually in India [68, 72, 89]. The north-eastern regions of India, southern region of Nepal and eastern and central division of Bangladesh in South-East Asia are prone to endemic regions of Visceral Leishmaniasis transmission. The reports of Kala-azar cases occurring in Bihar state in India, which is 40% to 50 %, of the world cases, and is severely affected states, and account to 90% of the total recorded cases in India. Visceral Leishmaniasis not only guides to fabulous human sufferings since unprocessed cases result in death, but also has an insightful bang on the livelihood of affected households [68].

## 6. Vector borne disease transmission and the environment, using remote sensing and GIS

### 6.1 Climate, landscape and the environment of vector borne diseases

The survival and longevity of infected mosquitoes and the prevalence of the disease are spatially determined by the geo-climatic variables [1-7, 9-23, 26-73, 76, 77, 81-98]. The logistic regression model shows the results of 0.76 sensitivity and specificity of 0.78 of larval index within a buffer around the trap location of rice fields which suitable for vector breeding of malaria and JE [63, 95]. Considering the maximum flight

range of adult mosquito vectors demonstrate that the community is exposure to malaria transmission in the buffer zone of villages where the distances is less than 2.5 km from mosquito breeding sites [36, 48, 49, 51, 55, 58, 61, 64, 92], Soil moisture with vegetation cover information of the remote sensing and GIS based model could be predicted the malaria transmission in advance [63, 95]. The *Anopheles gambiae s.l.* are seen to breed more prolifically in temporary and turbid water bodies, which are ones formed by rain, while in permanent bodies predation becomes important. By contrast, *An. funestus* the principal vectors, which cause malaria. The *An. culicifacies* – a rural vector, *An. stephensi* – an urban vector and *An. fluviatilis* a resident of hilly-forested areas are causing malaria in most parts of India except at elevations >1800m and in some coastal areas [9, 11, 83-86]. The climate model fitted with the temperature range of between 20 °C to 30 °C for the survival and longevity of infected mosquitoes of the *Anopheles genus* malaria vector species [14, 26, 38, 45, 47, 49, 61], but, the survival of *P. vivax* and *P. falciparum* in the minimum temperature of 15 °C and 19 °C respectively. It has been observed that the *P. vivax* vector requires 15 to 25 days to complete its cycle if the temperature remains within 15°C to 20 °C, and its life cycle may get completed even within 6 to 10 days, if the temperature range remains within 25°C to 30 °C. In both the cases, the relative humidity (RH) remains within 55 to 80%, when the temperature fluctuations are increased or decreased to 2 °C to 4 °C with respect to the current climate in India [9, 61, 66].

The environmental changes of land use / land cover are most probably causing the conducting environments for survival of JE vector mosquitoes [63, 64, 66]. The introduction irrigation water resource projects for extending the wet cultivation rice fields have been providing the conducting environment for habitats, vector survival, and fueling for propagation of JE vector mosquitoes and the adult vector abundance [50, 63, 64, 90]. The intensive irrigation rice cultivation areas are potential for mosquitoes breeding sites. The Spearman correlation was found the spatial relationship between land use / land cover changes (dry land to wet land cultivation) and JE epidemics in the country. The recent years has been witnessed by increasing the JE epidemics in different parts of our country, and more frequently in the districts where the water resource / irrigation projects brought out, and fueled for mosquito abundance in and around the buffer zone of 2.5 Km radius of the water resource projects (Irrigation canals, lake, perennial or semi-perennial River / stream, water pools), irrigation wet cultivation areas. The ecological aspects of spatial dependence of vectors were well established [63, 64]. The multivariate analysis proved that collective effect of geo-environmental and a climate variable has statically significant with filariasis prevalent in different parts of India, and the NDVI of remote sensing of IRS WiFS data has a significant association with filariasis endemic areas in India [62, 66].

The dengue and chikungunya epidemics were caused by the *Aedes* mosquitoes species (*Aedes aegypti* or *Aedes albopictus*) were highly associated with the large amount of dengue vectors breeding habitats sources [65]. The epidemics of dengue situation are highly associated with climate variables (temperature, rainfall, and relative humidity). A linear discriminant analysis could be providing the abundance of dengue vectors (*Aedes aegypti* or *Aedes albopictus*) are highly associated with a range of temperature and relative humidity

and the amount of rainfall in the number of days [65, 67]. The monsoon mean temperature is ranging from 17°C to 27°C and the relative humidity is ranging from 60 % to 80 % in the semi-Arid, sub humid and humid climate zones in India supporting for mosquitoes vector breeding [65, 67].

Many aspects of the VL burden of disease are complex in nature, and are not clear. However, one of the major opportunities now-a-days for the elimination initiatives of this disease is the advent of geo-spatial tool and technology which might help us understand the total gamut of the peril and to realize the measures of control through environmental modeling while precisely identifying the VL risk areas [6, 10, 21-23, 55, 68]. Earlier researchers/scientists have developed and employed alterations or vegetation indices based on band amalgamations in an assortment of ways to appraise vegetation parameters. The vegetation indices (NDVI) have been provided the distinctiveness of high sensitivity to vegetation insensitivity to soil background alters and be only somewhat exaggerated by atmospheric path radiance [6, 10, 21-23]. The vegetation indices are used to explore risk evaluation and possibility modeling for kala-azar epidemic and endemic. Since, sand fly (the vector of VL) populations diverge with temperature and moisture conditions on the surrounding environment, vegetation indices along with seasonal climate are influential predictors of sandfly distribution patterns and level of transmission of leishmania parasites by these sand flies [6, 10, 21-23, 55].

Geographical information systems (GIS) and remote sensing has been used to identify important geographical risk factors and stratify a region into different areas of transmission risk, thereby providing a potentially valuable tool to help guide visceral leishmaniasis control. In India, visceral leishmaniasis is thought to be caused predominantly by *Leishmania donovani*, transmitted anthropologically by the sandfly *Phlebotomus argentipes*. Even within endemic foci, there was tremendous heterogeneity in infection levels. Numerous factors act to determine such heterogeneities. At large spatial scales, these include environmental factors, such as temperature, rainfall, and relative humidity, vegetation and others environmental factors including soil types, soil moistures, soil texture, soils water holding capacity and chemical properties of the soils, which has been directly influenced the vector distribution and abundance [6, 10, 21-23, 55, 92], and thus, disease transmission have persistent in India [66, 68].

## 6.2 The cumulative effect of geo-environmental variables of vector borne diseases

The coefficient model of rainfall and temperature with the mosquito abundance are highly correlated with the normalized difference vegetation index (NDVI), and it is useful in the estimation of mosquito larval abundance and used to predict adult abundance 7 days in advance [7, 12-14, 18, 40, 49, 64] and also estimating *Anopheline* malaria vector mosquito abundance in the mosquito habitats of rice fields: [12, 29-38, 43, 49, 52, 64, 100]. The results of logistic regression model provides the spatial agreement between the observed and predicted values of larval index within a buffer around the trap location of rice fields which suitable for breeding of malaria and JE vector mosquitoes [63, 95]. Discriminant analysis could able to correctly distinguish between villages with high and low vector abundance, with an overall accuracy of 90%.

Regression results found both transitional swamp and unmanaged pasture proportions to be predictive of vector abundance during the wet season [7, 63]. The image classification of the spectral signature of the satellite data imported in to the GIS platform to create the buffer zones of the average adult mosquito flight range of 2.5 km radius around the breeding habitats for mapping the breeding habitats and describing the areas at risk of disease transmission [43, 49, 52, 64]. The remote sensing data was also used for landscape determinants of *anopheline* mosquito larval habitats in the highlands [56]. The range of monsoon temperature and the relative humidity has the good agreement with the profusion of mosquito's vector breeding. [31-36, 41-43, 49, 64].

### 6.3 Rapid assessment of vector borne diseases, using remote sensing and GIS

The integrated remote sensing and GIS has been significantly used for ecological modeling with special emphasis on vector ecology and vector borne disease transmission [61, 63, 67, 75, 81]. The data pertaining to the prevalence of vector borne diseases, layers of thematic map information of geo-climatic variables have been integrated with satellite data pertaining to land use / land cover information and the vegetation cover information over laid with vector borne disease prevalence data for stratification of problematic areas and risk of epidemics [63, 64, 66, 76-84]. To beyond the mapping aspects, the remote sensing and GIS has been provided the key risk factors index value according to its statistical significance, and stratification of areas vulnerable to risk of infection, and at the final stage programming to choosing the appropriate vector control and a strategy to apply prevention measures in the endemic and epidemic transmission risk zones [39, 70], using the hybrid environmental remote sensing and GIS [5-7, 14, 17, 19, 40, 46, 61]. Mapping disease distribution, spatial analysis and spatial modeling of disease epidemic transmission are increasingly important now days at global level as well as in the country level, and the results obtained using remote sensing and GIS has potentially been vital role particularly in the designing and implementation of active disease control programmes [74]. The success of the current and future control programme in country depends on the availability of up-to-date thematic maps of the distribution of the diseases within the country, at a suitable map scale relevant to control activities. Previous work in this area in the recent past has primarily focused on collating information on the prevalence of disease epidemics as well as endemic situation, and the potential use of availability of health resource allocation, and hence, priority should be given, based on the level of epidemic risk [20, 26, 30, 39, 63], to epidemic control and management [70].

### 7. Conclusion

The present review is included the global distribution of vector borne diseases, disease burden and with special emphasis on the geographical distribution of vector born disease (filariasis, malaria, Japanese encephalitis, dengue and chikungunya) transmission and environment in India. The systematic review of previous classical studies on climate, landscape, spatial analysis and spatial modeling and the environment of vector borne disease transmission risk are highly commented. The detailed information are highlighted and the contribution summarized on the geo-climate,

landscape, and the environmental aspects of malaria prevalence and transmission risk, land use land cover changes and JE epidemics, the study of environmental aspects of dengue and chikungunya epidemics, the environments of Visceral Leishmaniasis transmission, using remote sensing and GIS. The geo-climatic variables are the most important determining key factors that enable to control the vector survival, longevity and disease transmission. Climate, landscape, and the environments have been completely controlled the spatial occurrences of horizontal and vertical structure of both vector and disease epidemiology. The results of the recent previous research studies of classical and advanced remote sensing and GIS applications provides result clear visualization of the geographic distributions of vector borne disease prevalence, and has been spatially controlled by geo-environmental determinants including climate, vegetation cover, vegetation types and soils, and the result is statistically significant and spatially auto correlation. It is concluded that remote sensing and GIS has vital role in environmental epidemiology and entomology studies, and besides, it could be applied to vector borne disease epidemic transmission control and management. Finally, it includes the role of remote sensing and GIS to mapping of disease prevalence, and geographical analysis of vector presents, sifting of epidemics, spatial analysis of geographical variation in disease transmission and horizontal diffusion, moreover, a geo-environmental aspects of vector borne diseases, and spatial modeling for spatial prediction of vector borne disease transmission risk in India. Perhaps, provides the useful guidelines and recommendation for both vector mosquitoes and vector borne disease transmission control in the country.

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