
Geoprocessing and Expected Distribution of Diseases (Including Deforestation, Global Warming, and Other Changes)

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Abstract

In epidemiology, in order to estimate risks and plan control measures, it is very important to predict when and where a disease may occur, even in areas not previously studied. It is also relevant for decision making to estimate or predict a priori the impacts resulting from changes in land use, land cover, and climate, among others, on the potential occurrence, distribution, or incidence of a disease. The meteorological and environmental products derived from satellite imagery can be used to monitor some conditions that favor or alternatively preclude the proliferation of vectors or affect the transmission of pathogens. In this chapter, we intend to make an introduction of the use of remote sensing and GIS technology for the study and surveillance of vector populations and for risk assessment of vector-borne diseases. In addition, some of the relations between anthropic and environmental changes and selected vector-borne diseases are revised.

Keywords

Geographic information systems • Remote sensing • Risk mapping • Risk models • Climate change • Biotic homogenization

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In epidemiology, in order to estimate risks and plan control measures, it is very important to predict when and where a disease may occur, even in areas not previously studied. It is also relevant for decision making to estimate or predict a priori the impacts resulting from changes in land use, land cover, and climate, among others, on the potential occurrence, distribution, or incidence of a disease. Zoonosis risk models aim to assess the relative suitability of an environment for the establishment of a disease, that is, to

identify areas where pathogen, vector, and host may coexist spatially and temporally. These models may be developed based on two broad alternative strategies: biology-based models and statistics-based models (Malone et al. 2006). Biology-based models depend on the knowledge (from previous laboratory and/or field studies) of the biological requirements of the species involved: maps are generated for those regions matching a set of conditions previously deemed suitable. Statistics-based models basically correlate data on the spatial (and/or temporal) distribution of a pathogen and/or vector (or a disease) with a set of environmental data (frequently derived from satellite imagery) to determine which variables are more (empirically) relevant to predict distribution and then build maps of areas matching those conditions. They are especially useful when little is known about the biological requirements of the organism of interest. Nevertheless, to avoid producing models that are statistically rather than biologically relevant, predictors should be used that are (potentially) ecologically relevant to the target species, describing the biological and ecological constraints of the species in the spatial range to be modeled (Estrada-Peña et al. 2014). Although either strategy has its limitations, there are several examples of useful applications as well that will be discussed in this chapter.

Among the statistics-based models, the ecological niche models allow approaching the limits of tolerance of the species of interest from the observed data distribution. These models in general relate spatial point data of a species occurrence with geographic information on the environmental characteristics (including climate) of these sites, compared to a random set of point data from the same study area. The aim is to define a set of decision rules that best summarize the factors associated with a species and to produce a hypothesis of the niche dimensions of the species (Peterson and Shaw 2003). This model can then be projected for a region to estimate the potential distribution of the species, based on the identification of zones that either have or lack the niche condition. Models associating climate variables to the current known distribution of a

species are used for projecting the future distribution under different climate change scenarios. These models in general do not take into account interspecific interactions that may affect a species distribution in spite of otherwise adequate environmental conditions.

In any case, both strategies take advantage of the advances in geographic information systems (GIS), Global Positioning System (GPS), and satellite imagery availability. A GIS is a computer-based system designed to capture, store, manipulate, analyze, manage, and display digital geographical data. A GPS is a satellite navigation tool used to determine the position of an object or landscape element on the Earth's surface. Satellite imagery is captured with remote sensors and provides a digital record with excellent spatial and temporal references, covering larger land extensions compared to traditional land survey methods. Data provided by satellite imagery do not (generally) allow the identification of pathogens or vectors per se but may be used to characterize the environment where they develop. Over the last two to three decades, lower costs of electronic and computer equipment and progress in computing and technology of geographic information systems (GIS), Global Positioning Systems (GPS), and remote sensing have favored the development of models for surveillance of pests and vectors, as well as for predicting risk of diseases they transmit. With appropriate field studies they can be used to identify and map with good probability potential habitat of specific vectors and parasites. As historical databases, information on the vector or pathogen distribution in the past can be used to indicate possible future situations, pointing out areas or seasons of higher risk of emergence of problems, and the regions from which new risks could arise.

Currently, sports cameras and other similar economically accessible portable gadgets (such as cell phones) that record GPS-encoded videos can be used to collect fine-scale spatial data that could eventually be used for surveillance and risk mapping (Lee et al. 2016). For an example of these recent developments, see Curtis et al. (2013).

In this chapter, we intend to make an introduction of the use of remote sensing and GIS technology for the study and surveillance of vector

populations and for risk assessment of vector-borne diseases. Also, we revise some of the relations between anthropic and environmental changes and selected vector-borne diseases.

37.1 Remote Sensing and Satellite Imagery

Remote sensors are instruments that can detect the nature of an object without being in direct contact with it. Familiar examples of remote sensors are our eyes and ears. Some instruments measure how surfaces reflect or absorb different bands of electromagnetic radiations, such as visible light, ultraviolet, and infrared rays. Figure 37.1 illustrates a wide spectrum of electromagnetic radiations that may be detected in nature. Each substance reflects or absorbs radiation in a characteristic pattern, resulting in unique “spectral signatures.” Thus, we see plants green

because chlorophyll absorbs most of the visible range radiations and partially reflects green wavelengths (Fig. 37.1). Through the analysis of the interactions between electromagnetic radiation and matter, the presence of a wide variety of phenomena, elements, components, and bodies both in the Earth’s surface and in the oceans and the atmosphere can be detected and even accurately measured. A widely used index is the normalized difference vegetation index (NDVI) that is calculated as the difference between near-infrared and visible reflectance values (most reflected and absorbed, respectively, by plants) normalized over the sum of the two. Still, it should be noted that, although it would be expected that each land cover/Earth’s surface material would have a unique distinctive spectral response pattern that would allow it to be reliably detected by visual or digital means, this is often not the case, due to variations in moisture content, soil type, and phenological state of the vegetation,

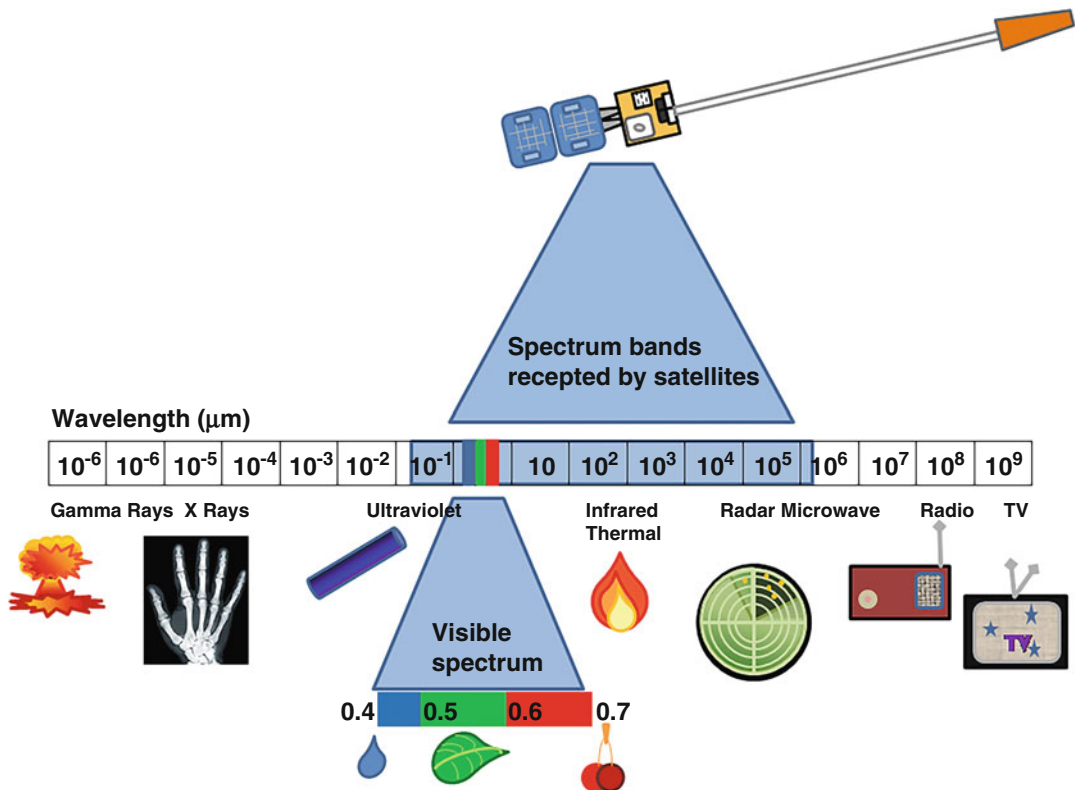


Fig. 37.1 Spectral electromagnetic radiations that can be detected in nature

among others. Rather, the combination of spectral bands and the time of year at which distinctive patterns can be found for each of the information classes of interest must be found.

The sensors on board satellites create the images as a sequence of small rectangular portions of a scene, known as picture elements or “pixels,” arranged in a geometrically regular grid. The data sequence is readily reconstructed to form an image. The intensity of each pixel is represented by numbers, which indicate the different values of reflectance for a particular spectral band, facilitating the handling, processing, and data analysis using digital computers. Although the images are very seductive, actually the numerical data provide more information and allow a better analysis of the phenomena to be studied.

The process of developing interpreted maps from satellite images is known as classification and was traditionally achieved through visual interpretation of terrain features and manual delineation of their boundaries. Currently, human interpretation is added to the computer aided, where various algorithms are applied to assign pixel elements to groups of classes. The classification process can follow one of the two basic approaches, known generically as supervised and unsupervised classification. The *supervised classification* is a decision-making process based on a priori knowledge of the way in which certain ground covers or classes reflect the spectrum bands considered (spectral signatures). First, areas or sites are delimited whose characteristics are known in the field (called ground truth), and then the software generates a statistical description of how the different bands reflect the spectrum in these areas (land cover classes). Next, a statistical procedure is used to assess the likelihood for each pixel of the unknown areas of the image to belong to one of these classes. By contrast, with the *unsupervised classification*, classes are unknown at the beginning, and the process seeks to discover the common occurrence and distinct reflectance patterns in an image, with the assumption that these represent important classes of land cover. The identity of each class is then determined by combining experience and ground truth, namely, by visiting

the area of study and observing the actual types of land cover.

Even considering that all electromagnetic radiation, one way or another, acts on the matter, there are restrictions on the type of radiation that can potentially be used to know remotely the Earth’s surface materials, as the atmospheric gases absorb certain wave lengths. The electromagnetic registry tracks that can be used are known as “atmospheric windows.” Additionally, only wavelengths in the microwave band pass through the clouds and other particles suspended in the atmosphere.

Since the 1960s several satellites bearing remote sensors were launched. Geostationary satellites orbit at about 41,000 km of altitude, and their movement is synchronized with the Earth at such a speed that they always face the same hemisphere. As they transmit very frequent images, they are particularly useful for climate observations, although their spatial resolution is low. Other satellites, known as polar orbiting or simply polar, cover an orbit that passes near the poles and progressively scans the surface of the Earth, sending images of the entire planet. They are in lower heights (between 600 and 950 km) and provide images of higher spatial resolution, but with lower temporal resolution. These satellites run synchronized orbits with the sun, that is, their orbits remain fixed relative to the sun, so that they routinely see the same point in the same local time.

Most of these sensors are optically passive because they only measure the energy reflected from the sun, or reemission of solar (or volcanic) radiation stored as heat in the Earth’s surface, not allowing information of the Earth’s surface through cloud cover. This can be a major problem in some regions or periods of the year, in which the most coverage coincides with the satellite passing time. An alternative is taking photographs from aircraft which may carry the same type of sensors as satellites. While the problem of clouds can be avoided, its use is limited to small areas, for practical problems and cost. Other options are the active sensors, such as synthetic aperture radar, which can provide high-resolution data uninterrupted by cloud cover. Table 37.1 summarizes the main characteristics of some satellites available to the public.

Table 37.1 Summary of the main characteristics of some satellites available to the public. Temporal resolution refers to the image acquisition rate for a particular site

Satellite ^a	Source	Orbit height (km)	Temporal resolution	Bands or channels ^b	Spatial resolution	Width imaging swath (km)	More information
<i>Sun synchronous orbit</i>							
SAR-Lupe (series)	Germany	500	<24 h	X (3.1 cm 9,65 GHz)	0.5 m; 1 m	5.5; 8	http://www.lspace.com/
TerraSAR	Germany	514	1–3 days	X (31 mm, frequency 9.6 GHz)	1 m	10–100	http://lhrs.gsfc.nasa.gov/
IKONOS	USA (commercial)	681	3 days	Vis, NIV, Pan (5)	1 m, 4 m	11–14	http://www.digitalglobe.com
OrbView	USA (commercial)	470	<3 days	Vis, NIV, Pan (5)	1 m, 4 m	8	http://www.digitalglobe.com
QuickBird	USA (commercial)	450	1–3 days	Vis, NIV, Pan (5)	55 cm, 2.16 m	14.9	http://www.digitalglobe.com/
IRS (series)	India	817	5 and 24 days	Vis, NIR, MIR (4)	24 m; 2.5–360 m	70–7400	http://dos.gov.in/satellites.aspx
SPOT (series)	France	830	26 days			2250	https://earth.esa.int/
HRV-IR				Vis, NIR, MIR, Pan	5 m, 10 m, 20 m		
Vegetation	France (+other EU)		Daily	Vis, NIR, MIR, (4)	1000 m		http://www.vgt.vito.be/
Radarsat	Canada	798	24 days	Microwaves, C (5.3 GHz)	8–100 m	50–500	http://gs.mdacorporation.com/
	(+industry, NASA)						
Landsat	USA	705	16 days				http://www.nasa.gov/
				VNIR, SWIR, LWIR, pan (8)	15–100 m	170	
EOS/Terra	USA and multinational (Canada, Japan)	705	16 days				
Terra ASTER				Vis, NIR, SWIR, TIR (14)	15–90 m	2330	http://terra.nasa.gov/
Terra-Água MODIS				Vis a SWIR (36)	250–1000 m		
CBERS (series)	Brazil-China	778					http://www.cbbers.inpe.br/
WFI			5 days	Vis, IR	260 m	890	
CCD			3–26 days	Vis, NIR (4)	20 m	120	
IRMSS			26 days	pan + IR, TIR (4)	80 m	120	
EUMETSAT	Mainly Europe (intergovernmental organization)						http://www.eumetsat.int/
METOP/AVHRR		817	12 h	Vis/IR, TIR (6)	1000 m	1464	
HIRS				Vis (1), IR (19)	10,000 m	2160	
AMSU-A		837		Microwave (15sch; (23–90 GHz)	48 km	2074	

(continued)

Table 37.2 (continued)

Satellite ^a	Source	Orbit height (km)	Temporal resolution	Bands or channels ^b	Spatial resolution	Width imaging swath (km)	More information
NOAA	USA	870	12 h				http://www.ncdc.noaa.gov/ http://noaasis.noaa.gov/
AVHRR				Vis/NIR, TIR (6)	1100 m	2700	
<i>Geostationary orbit</i>							
GOES (series)	USA	35,800	≤26 min	Vis, IR, TIR, other atmospheric	1000–8000 m	Hemisphere	http://www.nsof.class.noaa.gov/ http://www.goes.noaa.gov/ http://www.eumetsat.int/
EUMETSAT Meteosat (series)	(Intergovernmental organization)	36,000	15 min	Vis, IR (12)	1000–3000 m	Hemisphere	

Sun synchronous orbit = polar orbiting

Vis visible, IR infrared, LWIR long-wave infrared, MWIR/MWV near infrared, SWIR short-wave infrared, TIR thermal infrared, WV water vapor

^aOnly some sensors aboard the satellites are included on the Table

^bThe number in brackets indicates the approximate number of detected spectrum bands

Depending on the sensor characteristics, the satellite images may have different resolutions: spectral or radiometric, spatial or geometric, and temporal. The spectral resolution refers to the spectrum of the electromagnetic field represented in each band and is the basis for the development of spectral signatures identifying the various elements of landscape or Earth's surface features. The spatial resolution is the smallest area of land which can be individualized. For example, in an image with a spatial resolution of 1 km, each pixel represents the average reflectance spectrum within a 1×1 km parcel of land, and so elements measuring few meters in diameter cannot be discriminated. However, if they represent values sufficiently contrasting against their surrounding area, their presence may eventually be inferred by the effect they have on the average pixel reflectance. The temporal resolution indicates the time interval between two successive passes of the satellite over the same spot on the earth (see Table 37.1).

From the data collected by remote sensors, different products can be derived, including meteorological products, vegetation indices, digital elevation models (DEM), and groundcover. The meteorological products (precipitation, temperature, humidity), as exemplified in the following sections, can be used to monitor the conditions that favor or alternatively preclude the proliferation of vectors or affect the transmission of pathogens. Vegetation indices and land cover maps are used to identify or define suitable habitats for vectors or reservoirs, as well as suitable conditions (e.g., deforestation exposure). In turn, the vegetation can be an indicator of humidity and availability of larval habitats (Linthicum et al. 1991; Gleiser et al. 1997; Gleiser and Zalazar 2009). The DEM can be used to detect low and flood prone areas where larval habitats are more frequent or to analyze the distribution of the species, since the elevation/height can limit the distribution of vectors and their associated pathogens (McCann et al. 2014).

During the late 1990s, a series of very resourceful large-scale studies was developed to map the habitats of tsetse flies, based on the analysis of climate data and vegetation provided by

remote sensors (Rogers et al. 1996). Their findings of correlations between NDVI, standard meteorological variables, and estimated mortality rate of *Glossina* allowed to predict regions where the flies could not occur. Further studies that integrated more information and more complex analyses improved the accuracy of the maps and showed habitat differences between subspecies, besides producing risk maps of disease transmission (Hendrickx et al. 1999).

NDVI may also be used as a surrogate ("proxy") to other variables that affect the problem populations. Thus, the abundance of *Culicoides imicola* (Diptera: Ceratopogonidae), vector of African horse sickness (AHS), is affected by soil moisture level, which in turn affects vegetation characteristics. Studies in Morocco showed a positive correlation between the average annual abundance of this gnat and the minimum annual average value of the vegetation index (Baylis et al. 1998). Similarly, the distribution and abundance of the tick *Rhipicephalus appendiculatus*, vector of *Theileria parva* group piroplasmas, are affected by the minimum deficit and the saturation temperature variables which were related to NDVI. Larval abundance is related positively with the NDVI values, due to the effect that the above climatic conditions have on variations in vegetation, detected by satellite. In South Texas, within the context of an eradication program of the Southern cattle tick, *Rhipicephalus (Boophilus) microplus* (Canestrini) (Ixodida: Ixodidae), sampling sites of the invasive tick were selected by first locating favorable white-tailed deer (tick host) habitat using NDVI and another vegetation index (modified soil-adjusted vegetation index) (Phillips et al. 2014).

Studies conducted in Kenya were pioneers in demonstrating that it is possible to combine passive and active remote sensing in surveillance and warning programs of animal diseases, because they provide ecological parameters associated with the earliest indicators of viral activity (Linthicum et al. 1991). Based on 3-week composed NDVI images from NOAA satellite (15 km resolution), a potential viral activity factor was developed that allowed prediction of time and areas of higher risk of mos-

quito-borne Rift Valley fever (RVF) epidemics. Outbreaks are associated with the amount and duration of rainfall flooding the mosquito habitats (“dambos”). By comparing dry and wet season data obtained from satellite with higher resolution, such as Landsat TM sensors, larval habitats of a size similar to that of the satellite resolution (50 m) can be identified. This is possible because the vegetation and the soil of dambos are characterized by higher moisture content than the surrounding areas, keeping the vegetation greener during the dry season, with less seasonal variation in the reflectance of vegetation. The NDVI values of SPOT allow not only to locate the potential larval habitat but also to differentiate those that are flooded and appear with higher values than adjacent areas.

A multi-criteria analysis (considering coverage variables, distance to rice paddies, human density, temperature, elevation, etc.) permitted the development of malaria risk maps for different geographical areas of Madagascar (Rakotomanana et al. 2007). Environmental variables were estimated from Landsat 7 ETM+ images (resolution 30 m), SPOT 4 (resolution 10 m), Synthetic Aperture Radar Precision Images (SAR PRI) of ERS-2, and Advanced Synthetic Aperture Radar Image Mode Precision images (ASAR_IMP_1P) from Envisat. In Kenya’s western plains, larval *Anopheles gambiae* s.l. habitats are generally small and murky water, and therefore it is difficult or impossible to detect them even in high-resolution images (ca. 1 m) as IKONOS. However, this type of image was useful for finding larval habitats indirectly, from the associations between the presence of habitats and specific types of land cover, which can be distinguished through image classifications (Mutuku et al. 2009). Landsat TM (30 m) and IKONOS (4 m) images were used to map coverage and changes in land use in Kenya and evaluate their relation with suitable habitats for *Cx. quinquefasciatus*. The images were classified into three classes: built, rice fields, and fallow. Most preponderance of positive aquatic habitats for *Cx. quinquefasciatus* was associated with areas in which temporal modifications were observed, mainly paddy to fallow and vice versa (Jacob et al. 2006).

In South Korea, Landsat 7 ETM+ and a QuickBird images were used to identify by supervised classification classes of land use that were considered of interest to estimate malaria vector mosquito habitats. Significant correlations were found between land use classes and positive habitats for larvae and adult *Anopheles sinensis* abundance. The larvae were concentrated mainly in rice paddies, while adults were more common in bare soil and forest, although these relationships varied geographically. For this species and *An. pullus*, *An. sineroides*, and *An. lesteri*, negative correlations between the distribution of larvae and adults were detected, suggesting that adults leave the rice fields to search for human blood meals.

On the other hand, not always are images, even with high resolution, effective to locate larval habitats. In Belize, SPOT (10 and 20 m resolution) and IKONOS (1 and 4 m resolution) images were assessed to locate positive habitats for *An. darlingi*. In this region, the species is associated with bamboos and fallen trees constituents in watercourses. Although different habitat evaluation criteria (supervised and unsupervised classification) were explored, no image or test strategy was efficient to sort efficiently sets of bamboo, as these could be mixed with other plant species. Nor were significant correlations found between positive mosquito sites and land cover categories (Achee et al. 2006).

Another study in Connecticut (USA) on West Nile virus vectors also failed to identify predictors of abundance of *Cx. restuans* from Landsat TM, ETM +, MSS, and ETM, possibly because this species uses a large variety of larval habitats. However, significant correlations were found for *Ae. vexans*, *Cx. pipiens*, *Cx. salinarius*, and *Cs. melanura* and NDVI-derived parameters (Diuk-Wasser et al. 2006).

The examples described above generally classify images in land cover or land use categories or extract the reflectance values themselves. Images can also serve only as a reference to digitize (or locate) sites and landscape elements analyzed in the field, as shown in a study on the spatiotemporal pattern of reinfestation by *Triatoma guasayana* in northwest Argentina (Vazquez-Prokopec et al. 2005). In this paper, IKONOS images of

1 and 4 m resolution were used to digitize the sites visited in the field, vegetation, and other landscape elements such as houses, which soon served as reference to digitize premises and constructions visited on the field, but not visible in the images.

The epidemiological risk models developed for a particular region may serve as a reference or starting point for application in other areas or other similar diseases. However, direct extrapolation from one area to another is not recommended without validation studies in the field, as there may be subtle differences in the natural environment and/or the human activities that affect markedly the validity of the proposed model. For example, in Thailand the seropositivity risk factors for dengue differ between urban and rural sites. In rural areas, people living in the center of towns and further away from natural or agricultural coverage would have increased risk of seropositivity, while in periurban areas, risk factors would be linked to other factors, such as knowledge of the disease, use of preventive measures, and quality of homes, rather than the land cover features per se.

37.2 Changes in Land Use, Anthropogenic Effects, and Arthropod-Borne Diseases

Human activities such as agriculture, farming, and urbanization, among others, cause significant changes in the environment and generate mosaics of different types of coverage with similar patterns in different parts of the world. One of the most severe land uses is urbanization, an expanding process due to a change from rural to urban populations. There is great concern about the transformation and loss of natural environments on a large scale that is occurring as a result of human activities, which lead on one side to biodiversity loss and increased risk of species extinction, and secondly, an increase in the problems associated with pests and pathogens vectors.

Land use changes linked to human activity can influence the distribution and incidence of

arthropod vector-borne diseases. For example, by modifying the availability and distribution of water collections, either intentionally (creating water reservoirs, prevention of flooding, wetland drainage) or unintentionally (changes in relief, accumulation of waste and artificial containers, etc.), the new conditions can benefit the production of diverse mosquitoes. In the Amazon basin, the reemergence of malaria has associated with deforestation, which has encouraged the proliferation of the predominant vector, *Anopheles darlingi*. This mosquito develops in sunny pools generated with the removal of forest cover, but not in intact shaded forests. In turn, the human advance on the forest facilitates contact with other species of mosquito vectors and pathogen reservoirs.

Cities are highly disturbed and fragmented complex systems characterized by the presence of patches of different types, sizes, and shapes, generally smaller in relation to natural environments, with extreme environmental conditions, particular microclimates, and high (or, alternatively, low) nutrient availability for different species. Strong impacts of urbanization on the environment include, among others, fragmentation and degradation of habitats, deposition of heavy metals and other pollutants, changes in flow and nutrient cycling, creation of heterogeneous microhabitats, and a change in temperature due to the presence of various greenhouse gases, forming new environments where the thermal variation is reduced, so that various species of animals and plants can establish and persist throughout the year in the same sites. These conditions have diverse impacts on the structure, function, and dynamics of ecosystems, affecting biodiversity, biogeochemical cycles, and climatic conditions. In turn, the complex nature of urban habitats can have different effects on biotic communities, fostering a strong dominance of those species best adapted to humans and their activities. Elevated levels of disturbance often favor small species that can quickly take advantage of unpredictable resources, while larger species and predators are often disadvantaged, but this pattern (Martinson and Raupp 2013) is not always verified. Studies in birds, mammals, and insects

indicate that increasing the degree of urbanization increases the abundance of nonnative or cosmopolitan species, so it is possible to find increasing and decreasing gradients of species throughout the landscape. While some studies show that urbanization can promote increased levels of biodiversity due to the addition of exotic species that replace the native faster than these are lost, globally urbanization can produce a decrease in species diversity, since, in general, many exotic species manage to exploit these new heterogeneous habitats, replacing native species and producing a biological homogenization of these environments.

Biotic homogenization is a process by which native communities are gradually replaced by range-expanding, cosmopolitan, exotic communities. Among the many human activities, urbanization is the main promoter of biotic homogenization, one reason being that cities are physically very similar throughout the world. Synanthropic species are considered “global homogenizers” because they may be found in cities worldwide, reducing biodiversity at a global level and resulting in biotas from distant cities resembling more each other than their own native ecosystems. The mosquitoes *Ae. aegypti*, *Ae. albopictus*, and *Culex pipiens/quinqüefasciatus*, the housefly *Musca domestica*, and the cockroaches *Periplaneta americana* and *Blattella germanica* are but a few examples of arthropods of medical relevance that can be found in many cities worldwide.

It is still unclear whether urbanization influences in the same way on the arthropod fauna in different parts of the world. While some groups of species respond consistently in different cities, others vary depending on local conditions (Martinson and Raupp 2013). For example, *Muscina stabulans*, a cosmopolitan fly of medical interest as a mechanical vector of pathogens, has shown a higher degree of synanthropism in temperate Buenos Aires, Argentina, compared to studies in more tropical areas in Brazil (Patitucci et al. 2010).

Very diverse communities of potential hosts have been associated with a lower risk of infection to various arthropod-borne diseases, proba-

bly reducing human exposure to pathogens by a “dilution effect.” As a result, biodiversity losses associated with deterioration of natural ecosystems could have a negative effect on the risk of human infection. Keesing et al. (2006) discuss several mechanisms underlying the effects of species diversity on disease transmission. Among vector-borne diseases, some of them include encounter reduction between susceptible host and vector by redistributing vector meals, regulating the abundance of susceptible host species (by interspecific competition, predation etc.), and vector regulation. A connection between species diversity and transmission of vector-borne diseases of humans is the base for zooprophylaxis, which is the use of nonhuman animals to protect human health by diverting vectors searching for a meal away from humans. This approach has been proposed to reduce malaria transmission. It has also been suggested that under certain conditions, increased diversity could actually increase the risk of transmission, when the provision of additional meal sources increases vector numbers or activity, or when added species function as alternative sources of infection, especially when an added species in a species-poor community is actually the most competent reservoir, resulting in an amplification of disease risk.

Human activities can contribute to the expansion of the range of a species to regions where it had not occurred, a phenomenon known generally as biological invasion, by deliberate or accidental introduction. The introduction of vectors and/or pathogens can have direct impacts on human and domestic animals’ health and on native fauna. It has been hypothesized that the spatial expansion of *Anopheles arabiensis* and *An. gambiae* s.l., mosquito vectors of malaria, could be linked to the development of agriculture in Africa, south of the Sahara, through the significant production of new larval habitats and availability of blood sources, both from humans and domestic animals. *Anopheles arabiensis* and *An. gambiae* s.s. are usually sympatric species in several African regions, although *An. arabiensis*, more adapted to arid areas, has a wider distribution. Actually, based on genetic-based studies, it seems the later species is expanding from the savannas to drought prone

areas, where it could substitute *An. gambiae* s.s. as a main vector (Matthews et al. 2007).

Habitats modified as a result of urbanization are more susceptible to invasion or colonization by alien species than those undisturbed. One hypothesis to explain the success of invasive species is that they exploit “empty niches” not used by native species. Human activities generate empty niches or “niche opportunities” by providing resources, reducing or removing the threat of natural enemies or competing species, and/or altering the physical environment (e.g., temperature, creation of new habitats) improving habitability for the invader. For instance, *Aedes aegypti* (Diptera: Culicidae), the principal vector of dengue in the world, native to Africa, is a mosquito markedly adapted to anthropogenic environments that uses artificial water containers as larval habitats and females preferentially ingest human blood. Among the factors that favor their proliferation are rapid urban area growth with little planning, water storage containers in areas where the supply is low or unpredictable, and high production of disposable containers that are adequate larval habitats. Consistently, surveys of larval habitats used by *Ae. aegypti* in general concentrate in artificial containers (Vezzani and Carbajo 2008 and references therein). Although this mosquito may use natural cavities such as tree holes (as in its native range) that could allow it to disperse to natural environments, their presence is usually restricted to the urban environment (Mangudo et al. 2015).

Changes in the composition and structure of natural ecosystems by invasive species can alter pathogen transmission cycles by favoring (or alternatively reducing) the development conditions of the vectors and changing the contact of the vectors with reservoir and accidental hosts. For example, in an endemic area of Lyme disease in the United States, in areas dominated by exotic shrubs, the number of larvae and nymphs/ticks searching hosts was twice that in regions dominated by native species. In this region, feeding habits of white-tailed deer (tick hosts) favor the dominance of invader shrubs. Therefore, the invasion of exotic plants favored by deer grazing increases the risk of exposure to the vector of

Lyme disease (Elias et al. 2006). The expansion of *Juniperus virginiana* tree from the Eastern United States into former grassland areas in the west may influence mosquito populations by positively or negatively altering host availability as a consequence of changes in the landscape. Moreover, populations of the invasive mosquito *Ae. albopictus* may benefit from high-quality *J. virginiana* litter components’ input into container habitats. In experimental conditions, this plant material could support positive population growth rates as a function of initial larval density where the native leaf could not (Reiskind and Zarrabi 2011). *Lonicera maackii* is an Asian shrub that was introduced to the United States as an ornamental plant in the late nineteenth century. In the Eastern United States, the forest invasion by *L. maackii* alters forest understory structure and the oviposition behavior of container mosquito *Ochlerotatus triseriatus* (Say) (= *Aedes triseriatus*), the primary vector of La Crosse virus (LACV) in the United States and potential vector of other arboviruses (yellow fever, eastern equine encephalitis, and dengue). Greater oviposition rate is associated with plots surrounded by larger proportions of grassland or cropland in uninvaded forest, while in invaded forest, oviposition rates are not linked to the availability of open habitat. Since the presence and density of *L. maackii* may be difficult to assess or be undetectable in the most commonly used satellite images, invasion by this invasive plant may negatively affect the accuracy of remote sensor-based risk models (Conley et al. 2011).

The introduction of an alien species can, moreover, alter the abundance of other and even cause local extinction of native species, thus contributing to loss of biodiversity and landscape homogenization. It has been shown, for example, that an increase in larval competition between *Ae. aegypti* and *Ae. albopictus* mosquitoes increases the proportion of the second species that transmits dengue virus. The presence of *Ae. albopictus* decreases *Oc. triseriatus* larval survival, but in turn, from surviving larvae emerge larger adult females that are more likely to develop disseminated virus infections, thereby affecting the risk of pathogen transmission. The *Chrysomya albi-*

ceps fly along with two others of the same genus was introduced to the New World about 35 years ago and since then has spread throughout America as far south as Argentina. Since its introduction, it is showing a strong impact on the structure of local communities, replacing (removing?) native species such as *Cochliomyia macellaria* and *Lucilia sericata*. During the larval stage, *Chrysomya* exhibits aggressive behavior based on a combination of competition and predation, including killing and eating prey that uses the same resource (intraguild predator).

Other human activity factors besides land cover change that have been cited as main contributors to the reemergence of vector-borne diseases such as dengue and other flavivirus include human population density, poverty and associated poor sanitation conditions, inadequate vector (mosquito) control, and migrations and international travel. International commerce of used tires started and/or aided a rapid global dispersal of species such as *Ae. aegypti* and *Ae. albopictus*, by dispersal of their drought-resistant eggs. The latter species is native from Asia and has medical relevance as an aggressive and efficient vector of diverse flavivirus (including dengue, chikungunya, yellow fever, West Nile fever), alphavirus, and bunyaviruses. Risk maps of global *Ae. albopictus* dispersal based on ecological niche modeling combined with risk analysis due to tire importation and proximity to infested countries indicated that all South American countries had adequate areas for the establishment of the vector, though Suriname, Ecuador, and Chile are still free from this vector (and in Argentina the species has only been reported from a small area, northeast of the country). If the restrictions and controls on used tire commerce are maintained, Chile would be in an advantageous situation because the areas that are adequate for the mosquito are geographically isolated from the neighboring infested countries.

The patterns of daily activities and housing characteristics in a community may increase or decrease vulnerability. For example, air conditioning and TV reduce time outdoors and contact with mosquito vectors (Reiter et al. 2003). The current tendency to a decreased immune compe-

tence of human populations, as a consequence, for example, of HIV infections, chemotherapies, an increase in the elderly population in developed countries, etc. could enhance the risk of vector-borne diseases. On the other hand, the application of vector control measures, chemotherapy, and vaccination may be significant for reducing risk. These factors should be taken in account together with meteorological (or climatic, in climate change scenarios) and landscape variables when estimating risk of vector-borne diseases.

37.3 Climate and Arthropod-Borne Diseases

Over the last century, an increase in global temperatures has been recorded, more pronounced in elevated latitudes of the northern hemisphere. Consistent with this pattern, a decrease of the snow and mountain glacier cover has been recorded in both hemispheres, together with an expansion of the surface undergoing seasonal freezing. Since arthropods are small ectothermic organisms, that is, they control their body temperature through means that are external to their bodies, they are particularly sensitive to fluctuations of temperature and humidity levels. Consequently, their distribution and habitat use are frequently linked to climate. Temperature and soil moisture may affect arthropods' distribution directly through their physiological tolerance, but also indirectly, through their impact on the availability of adequate habitat and hosts (in the case of parasites).

Considering that climate limits species distribution, it is expected that climate change will lead to changes in several species, especially expansions or shifts to higher latitudes and altitudes. Climate change could particularly affect pathogens, since they spend an important part of their cycles in invertebrate hosts, whose temperature is maintained close to environmental conditions. In fact, successive reports from Intergovernmental Panel on Climate Change (IPCC) predict an expansion of the distribution of vector-borne diseases from tropical to temperate regions, an increase in the incidence of patholo-

gies, and the emergence (or reemergence) of new diseases.

Temperature changes in a region may impact disease transmission by vectors through varying effects on the host, vector, and/or pathogen communities. Numerical responses include amplification and emergence of vector populations associated with changes in their development rates and survival and alterations in the seasonal disease transmission. Functional responses include biotic expansions of the hosts (and vectors) with potential to colonize new geographic regions, changes in habitat use, changes of ecotones and contact zones, local extinctions, changes in feeding behavior, and host exposure, modifying the susceptibility of the vector to the pathogens. Microevolutionary responses include ephemeral patterns of local adaptation, directed changes in the frequency of genes through mutation, and selection of vectors or pathogens associated with the emergence.

At a regional or ocean basin scale, other climatic changes have been observed besides warming. In parts of North and South America, north of Europe, and Central-North Asia, rainfall will increase, while on the Sahel and south of Africa, Mediterranean, and South Asia, they are expected to decrease. Also, it is likely that the frequency of heavy rainfall increases. In general, it is assumed that increases in rainfall could enhance vector-borne disease transmission by diverse mechanisms. Higher rainfall could boost vegetation and allow the expansion of vertebrate host populations. Flooding may force more close contact between vertebrate hosts and humans or alternatively can eliminate both vector and their hosts' habitats. In the case of mosquitoes, the amount of rainfall affects the availability, persistence and dimensions of larval habitats, as well as the formation of new larval sites. On the other hand, rainfall could have a detrimental effect on larval survival, by flushing them out of their larval sites and killing them, mainly in early developmental stages. It has been observed that pupae developing in containers tend to spend more time away from the water surface than those dwelling in open water bodies. This kind of behavior would contribute to avoiding flushing from an overflow-

ing container and also help the pupae survive from potential mechanic shocks from raindrops. During a rain episode, water currents can exhaust the larvae if they actively dip away from the surface to avoid being hit by raindrops or being swept away by the currents.

Not only volume of rainfall but also their frequency, that is, how isolated are rain events in time, may affect vector production. For example, explosive population peaks of the floodwater mosquito *Oc. albifasciatus* (vector of west equine encephalitis) are associated with fluctuations of the flood level of the larval habitats, depending not only on rainfall amount but also on rain frequency (Gleiser et al. 1997, 2000) (very frequent rains do not allow for the ground pool to shrink and expose enough mud/soil surfaces for egg laying). Wetland mosquito outbreaks following drought years could also be explained by the elimination of mosquito predators and competitors when (semi)permanent wetlands dry (Chase and Knight 2003). On the other hand, droughts reduce waterways flow, creating small stagnant pools where a number mosquito species can develop and where vectors and hosts congregate enhancing the potential for arbovirus transmission (Shaman et al. 2002).

Several studies show the convenience of considering only (or mostly) the effects of diverse meteorological variables or their estimators to predict changes in the vector population. Malaria research in Eritrea validates a combination of degree-days¹ with a relation between rainfall and evapotranspiration rate as a biologically relevant measure of the habitat moisture conditions and temperature allowing the development of pathogens and vectors (Malone et al. 2006). Dynamic hydrologic models have been used to represent the availability of *An. walkeri* larval habitats. However, one should not forget that, even though temperature and humidity are important factors for the transmission of pathogens by

¹Degree-days are temperature units above a threshold, accumulated over 24-h periods, that are used to measure or represent the physiological time (or age) of a poikilotherm organism, i.e., the amount of heat the organism requires to develop from one stage to the next.

arthropods, the relations between disease incidence and biophysical environment are not simple, and thus only using meteorological variables is usually not sufficient to explain development times, behavior and geographic distribution of the vectors, and the pathogens they transmit. Moreover, even conditions experienced during larval development may impact interactions between the emerging adult hosts and parasites. In the following sections, some examples are presented on relations between anthropic and environmental changes and some vector-borne diseases. These diseases (and other related) were selected from the IPCC (McCarthy et al. 2006) as those most sensitive to climatic changes.

37.3.1 Malaria

Even though it is usually assumed that malaria is a tropical disease, up to the mid-nineteenth century, this ailment affected latitudes as high as Sweden. This is because, even though climate limits where transmission may occur, other environmental, economical, political, and social factors may positively or negatively affect the risk of transmission. The deterioration of health and vector control programs, the emergence of drug resistance, changes in land use, construction of dams, and irrigation networks (which provide larval breeding) may affect the transmission. At the same time, this may only take place in spatial and temporal adequate zones in climatic terms.

The basic reproductive number (R_0) is generally defined as the expected number of new hosts who would be infected after one generation of the parasite by a single infectious person (host) introduced into an otherwise nonimmune population. Thus, the number of people infected by the plasmodium increases when R_0 is larger than one, while it declines if R_0 is less than one. The principal component of the reproductive rate is the vectorial capacity, which is determined by complex interactions between the host, vector, parasite, and environmental factors (see Chap. 2). Climate has a big influence on vector capacity, since variables such as mosquito population density and survival, blood meal frequency, and the mosquito

intrinsic incubation period depend on temperature. In laboratory studies, it was observed that temperatures under which optimal survival levels were detected for *An. gambiae* were lower than those where development was faster, suggesting a critical relation between temperature and the insect's life cycle. Longevity of larval stages affects the survival rate of adults and, thus, the intensity of disease transmission. Rainfall may also have an effect on vector populations, for example, from their relation with larval habitat formation. Both in South America and in Asia, malaria prevalence generally varies in relation to El Niño events.² This relation is partly explained by increases in temperatures and partly by precipitation, increasing water collections, and consequently the availability of larval habitats for the mosquitoes. By contrast, in Peru a significantly lower *An. darlingi* human bite rate was detected during the rainy season, which may be due to flushing effects of larvae from the larval habitats and low temperatures that may decrease larval survival (Vittor et al. 2006).

In general, models produced to predict the impacts of global climate change on malaria risk distribution vary regarding the potential number of persons in risk, but they estimate few changes in the potential spatial distribution of the disease. These models agree that malaria incidence will increase in endemic tropical African areas and also in current areas of low endemicity. On the other hand, in some of the regions that are climatically adequate for disease transmission, such as the north of Australia, malaria has been eradicated. Simulations considering different climate change scenarios that also include non-climate components (e.g., a worldwide economy/energy model, a land use change model, a carbon-cycle model, etc.) predict a risk of reintroduction of the disease in developed countries such as the United States, Australia, and the south of Europe. However, the reestablishment of endemism would be more difficult because of the economy of these regions that allow the implementation of

²More information on the influence of climate on diseases, on R_0 and on vector capacity may be found in Chap. 2 (Epidemiology) (CBM).

control measures and access to better health services.

Because 90% of malaria cases occur in Africa, it is in this continent where most studies are developed relating effects of climate and climate change with the prevalence and outbreaks of malaria. Climate changes recorded by remote sensors have shown to be particularly useful when there is little ground cover (Ceccato et al. 2007). Among the most interesting results, from different climate change scenarios, it was estimated that the increase in the number of people infected each month in 2100 will be 16–28%, related to increases in the length of the transmission season. Changes will be more evident in terms of altitude than latitude. On the other hand, several countries of the west and south of Africa expect a decrease of the number of persons exposed monthly due to drier conditions. Regions where rainfall are a main limiting factor will be especially vulnerable to epidemics, as occurred in Ethiopia in 1958, in association to rainfall on higher quantities than the average for a long period.

Although climate has the leading impact on malaria changes, population growth, urbanization, and land use change impacts, among other factors, can also be significant on the local scale to determine the presence and distribution of vectors and risk of exposure to malaria vectors. For example, the house construction characteristics, such as the height above ground and ventilation openings, may affect exposure to *An. gambiae*, and plant cover may favor survival and affect fecundity rate of adult vectors such as *An. funestus* and *An. gambiae* s.s. (Zhou et al. 2007). In high areas of Kenya, it was reported that adult *An. arabiensis* (a species adapted to arid environments) increased in deforested areas, while *An. gambiae* s.s. (better adapted to humid environments) showed an inverse pattern. These studies showed that changes in land use might lead to the establishment of new vectors and thus increase the risk of malaria in previously non-endemic regions.

In the Brazilian Amazonia, *An. darlingi* is found mainly on sites that have been modified by human activity, such as hydroelectric dams and roads, but not in unaltered sites, suggesting that

certain types of human activities increase the risk for malaria transmission. A similar pattern was reported from Peruvian Amazonia, where higher human bite rates were recorded in deforested areas. This could be explained by *An. darlingi* preferring larval habitats in pastures or crops with secondary growth and shrubs, leading to an increase of the adult mosquito population in these zones. Since the entomological inoculation rate (EIR) is proportional to *An. darlingi* biting rate, it is very likely that a higher bite rate by *An. darlingi* results in a higher malaria transmission when compared to forested areas. Time elapsed from deforestation to the occurrence of malaria epidemics in a region is variable, depending on the geographic region. For example, in Rondonia (Brazil), new towns had a higher case incidence than older communities, while in Amazonian regions of Peru, there was a malaria outbreak over a decade after intense deforestation periods.

Between 1930 and 1940, a serious malaria epidemic occurred in the northeast of Brazil, after the introduction and expansion of *An. gambiae* s.l. from Africa; the vector was removed by an eradication campaign in 1940. Models based on climate data from their native range in Africa indicated that *An. arabiensis* (one of the species of the *gambiae* complex) had an extremely limited potential distribution in Brazil, while the environment would be adequate for *An. gambiae* s.s., not only in its introduction site but also in a wider area of continental America and the Caribbean. Recent studies of DNA extracted from museum specimens collected in various localities during the 1930 decade confirmed that the invasive species was *An. arabiensis* (Parmakelis et al. 2008). Since this species is adapted to arid environments, it is probable that its expansion at the time was restricted by the rainforests surrounding the invaded area. The increasing destruction of tropical rainforest in South America, together with a transformation from forest to savanna of the oriental Amazonia as a consequence of global climate and land cover change, would provide the ideal conditions for the establishment and expansion of this vector and its sister species *An. gambiae* s.s. In the north of Argentina, the anti-malaria campaign (“anti-

palúdica”) began during the 1930s and continued for 70 years, resulting in a pronounced reduction of the affected area. Particularly in tropical areas, the campaigns have had partial results due to impaired access, caused by climate and terrain, favoring discontinuity of control actions. During the 1990s, the endemic area suffered a small expansion. Malaria was considered endemic in the northwest of the country, where it persisted in sub-Andean valleys, and epidemic in the northeast. However, it should be noted that no autochthonous cases have been reported since 2010. Besides, there are sites with predominance of imported cases near the international frontier, associated with migrations. The overlay of maps of historical and recent positive localities with maps of the vector distribution may explain this endemic pattern in the northwest and epidemic pattern in the northeast. On the northwest, the vector associated with the disease is *An. pseudo-punctipennis*, which in South America is distributed along the Andes mountain range (40 °N to 32 °S) and whose larval habitats are freshwater running mountain rivers with green algae year round. The stable presence of the species makes the natural continuity of transmission and the endemic condition of the disease possible in the northwest. On the northeast and center of the country, the epidemic character of the disease is linked to the sporadic presence of *An. darlingi*, the primary vector. This species is anthropophilic and domiciliary; however, the female, once blood fed, returns outdoors. In areas where the presence of *An. darlingi* has not been recorded, epidemics may be attributed to *An. albitarsis*, even though its vectorial capacity has not been well studied. In the center and south of the country, besides, transmission is interrupted by winter temperatures.

Environmental factors can be fundamental to predict malaria prevalence at large spatial scales (regional, continental), but at local scale individual level factors may be more relevant. A study of the spatial pattern and risk factors of *Plasmodium falciparum* prevalence at low spatial scale, in schoolchildren in Ivory Coast, detected relevant risk factors such as age, socioeconomic level, sleeping without mosquito nets, distance to pri-

mary health centers, and environmental variables (e.g., plant cover based on NVDI, rainfall, and distance to rivers representing larval habitats). These observations in principle are consistent with descriptions for other geographic regions. Besides these, children from schools located close to rivers (<500 m) have a lower risk than those from school at intermediate distances (500–1000 m), probably because the use of mosquito nets was more frequent in the former group to avoid mosquito nuisance. However, when spatial correlation between variables was considered, only age continued to be significant among the different associations found and the vegetation index only marginally so (Silue et al. 2008). A more detailed understanding of the spatial distribution of malaria to a local scale is paramount to focus control efforts.

In some countries, a reduction of malaria incidence was recorded, attributed in part to intense prevention and control programs at a national level, besides influence of climatic fluctuations, such as rainfall occurrence anomalies (Ceccato et al. 2007). Indoor residual spraying and impregnated mosquito nets have significantly contributed to reducing cases; larval control efficiency is usually only significant in non-endemic areas. A higher urbanization and human population density may influence on the vectors' life cycle and vector capacity, contributing to the observed transmission reduction. In Peru, since the eradication campaigns of the 1960s, prevalence of *P. falciparum* was very low. However, since the beginning of the 1990s, the number of cases increased in the Amazon region parallel to population growth, mainly in Andean regions, and with the economic and land use changes in the region. In 1993, Brazil, in collaboration with PAHO, established a new strategy to control malaria in the country, based on the concentration of control efforts in high-risk municipalities, which required a strengthening of surveillance and evaluation of activity, in order to direct more precisely control efforts. The program is based on the selective application of indoor residual spraying, environmental management, and anti-malaria treatment of suspect cases.

37.3.2 Arboviruses

Arboviruses are zoonosis whose natural maintenance and amplification involve susceptible vertebrate hosts and hematophagous arthropod vectors. Mosquitoes are the main vectors of arbovirus. Even though arboviruses have a worldwide distribution, climate has a strong influence on their transmission and on risk of disease outbreaks. Temperature and relative humidity influence the development rate, survival, and activity of the vectors. In turn, temperature markedly affects replication, maturation, and infectivity period of arbovirus. Laboratory studies indicate that the extrinsic incubation periods (or viral development rates) are linearly reduced with increasing temperatures, increasing the proportion of arthropods that become infective during a given period. The role of temperature on arbovirus transmission is corroborated by studies showing correlations between the detection of flavivirus or their transmission rates and cumulative temperatures above a degree-day threshold that depend on specific vector/pathogen complexes. Rainfall may affect larval habitat availability, and for mosquitoes, an increase in surface moisture associated with rainfall stimulates their flight activity and search for blood meal hosts.

In the Americas, the number of virus isolated from mosquitoes is increasing, while most of their transmission cycles and epidemiology remain little known. In the Amazonian region of Brazil, a fever caused by Oropouche virus manifests itself in cycles associated to the beginning of the rainy season (Githeko et al. 2000). Rocio virus circulates in birds and involves *Oc. scapularis* and *Psorophora ferox* as vectors. *Ochlerotatus scapularis* was also found infected with other arboviruses, such as Cache Valley, Ilhéus, Mayaro, SLE, VEE, and Minaçu. Since this species develops in transient aquatic environments, it is likely that rainfall has an effect on the epidemiology of these arboviruses, although these relations have not been explored yet.

In general, mosquito-borne viral encephalitides are very sensitive to climate. However, IPCC experts agree that predicting the influence of cli-

mate change on their distribution and incidence is difficult, due to the complexity of their transmission cycles. In the meantime, an increase of the global prevalence of diseases such as those from Zika and Chikungunya virus, previously restricted to tropical regions, justifies paying more attention to studies of the ecology and epidemiology of these pathogens and their vectors. Next are provided details on some of the best-known arboviruses.

37.3.3 Dengue and Yellow Fever

Dengue is the arthropod-borne disease of major world impact in terms of morbidity and mortality. An estimated burden of dengue in 2010 was 96 (67.1–135.6) million apparent infections globally and 13.3 (9.5–18.5) million in the Americas. This virus, original from tropical Asia, is transmitted between humans by *Aedes aegypti* in urban environments. Transmission is currently mostly restricted to the tropical and subtropical regions, because freezing temperatures kill the eggs and the mosquito larvae; however, outbreaks may occur at higher latitudes during the summer. The dispersal of *Aedes albopictus*, another potential vector, may contribute to changing this situation, because this species presents diapause. Considering the favorable or restrictive temperature limits for the survival of *Ae. aegypti* and a model that calculates the capacity of the virus to complete an extrinsic incubation period in a mosquito, as a function of air temperature, dengue risk maps were produced for Argentina (Carbajo et al. 2001) that could be applied to other countries. These maps showed a maximum transmission risk year round in the north and northeast of the country and on the summer time in the central region.

Using general circulation models (GCM) of climate change, it was found that the epidemic potential of dengue increased with relatively small temperature increases, indicating that fewer mosquitoes would be needed to maintain or transmit the disease in a vulnerable population (Patz et al. 1998). In turn, it has been observed that climate change could lead to longer periods

of intensive transmission. This increase in transmission strength would result in greater seroprevalence and therefore a higher number of individuals at risk for an additional exposure to dengue virus, augmenting the risk of hemorrhagic dengue. The reduction of the age at which people are exposed to the virus for the first time increases the chance of a second exposure. This is particularly relevant for the preteen age group, which is the largest group with higher risk of having the hemorrhagic form of the disease. It is projected that the warming of 2 °C expected for 2100 will increase in latitude and altitude the potential risk areas and increase the length of the transmission season in the temperate regions. The rainfall regime may also influence the seasonal variations in the abundance of the vector, resulting in some regions in a “dengue season,” limited to certain periods of the year. For example, in Trinidad a positive correlation was found between the incidence of dengue and rainfall, concentrated between June and November.

Another simulation study done for an area of annual dengue transmission in Far North Queensland, Australia, utilizing a field-validated mechanistic mosquito population model and climate projections, showed inconsistent patterns in dengue risk between climate change scenarios (Williams et al. 2014). Under one scenario (B1, lower carbon dioxide emissions, global temperature increases from 1.1–2.9 °C), *Ae. aegypti* abundance is predicted to increase, while it is predicted to decrease under a higher carbon emission scenario (A2 scenario, global temperature increases from 2.0 to 5.4 °C by the end of the twenty-first century), probably in relation to changes in rainfall patterns. A reduction in body size was predicted for both climate change scenarios compared to present climate, with the B1 scenario causing the largest decrease. However, these body size reductions were not linked to a reduction in oviposition rates, which were predicted to increase for both B1 and A2 scenarios. Shorter extrinsic incubation periods were projected, potentially increasing transmission.

Although climatic factors are relevant to the distribution and transmission of dengue, as with

other vector-borne diseases, studies to date indicate that they are not sufficient by themselves to predict the occurrence of cases or the risk of disease in a region. For example, an analysis of the association between the incidence of hemorrhagic dengue and satellite estimates of land surface temperature (estimated by NOAA thermal infrared sensor, which combine land surface temperature and atmospheric vapor concentration) found positive correlations in only 21% of the analyzed provinces, and correlations, in turn, were significant during the non-epidemic months, not on epidemic months (Nitapattana et al. 2007). These results could be explained by the importance of non-climatic factors to the risk of incidence. In highly endemic tropical areas, the transmission of dengue virus could saturate the population, and thus the migration of human populations likely would have greater weight than climatic factors. The public health infrastructure contribution may reduce the risk of transmission, especially in developed countries. Considering that *Ae. aegypti* finds suitable larval habitat in water vessels of various kinds, both domestic and outdoors, water storage practices of a community may be more important in its impact on the mosquito population density than the rainfall regime itself (Patz et al. 1998).

Yellow fever originated in Africa and was initially dispersed together with its vector (*Ae. aegypti*), with the slave trade in the sixteenth and seventeenth centuries. This arbovirus is maintained in South America in wild cycles involving primates and forest species of mosquitoes. In urban environments, it can cause outbreaks, with *Ae. aegypti* as a vector, and, as dengue, is also likely susceptible to climate change. The invasion of urban centers by the African mosquito and the advancement of urbanization on the rain forests could increase the risk of epidemic outbreaks of this disease in tropical America.

Rogers et al. (2006) carried out an extensive review of point data records of yellow fever and dengue outbreaks worldwide, gleaned from archived reports and literature surveys. They used high-spatial-resolution environmental information derived from satellites (from the Advanced Very

High-Resolution Radiometer (AVHRR) on board the National Oceanographic and Atmospheric Administration (NOAA) satellites) to create risk maps of environmental suitability for both diseases. A digital elevation model (DEM) was also considered besides the satellite-derived environmental data (including land surface temperatures (LST) and NDVI). The maps resulting from the most suitable models predicted high-risk areas localized within the broad boundaries of the 2003 World Health Organization maps for these diseases and predicted areas of high risk outside these boundaries. These discrepancies could be due mostly to under-reporting of outbreaks but also to limitations of the models that did not include human population variables. Nevertheless, the results highlighted some interesting contrasts in environmental suitability for each pathology: yellow fever distribution seems particularly sensitive to the greenness or humidity of the environment and especially to variability of these factors. On the other hand, in the case of dengue, the variability of environmental temperature rather than of moisture appears to be very important to its distribution.

37.3.4 Arboviral Encephalitis

The Saint Louis encephalitis virus (SLE) has been detected from Canada to Argentina. In South America, this virus is widely distributed, with antibody prevalence in humans ranging from 3 to 50 %, and the occurrence of outbreaks is sporadic. Little is known about its ecology, and a marked association with weather conditions has not been determined yet. In contrast, in the northern hemisphere, this disease has been better studied. It is usually restricted to regions south of the isotherm of 20 °C in June, although it can extend further north in particularly warm years. The outbreaks of encephalitis by SLE tend to occur in the second half of the summer and early fall, after warm periods, when the temperature exceeds 30 °C for 7 consecutive days (Hunter 2003).

Both abundant rains and droughts have been associated with SLE epidemics, observing a significant association between years with unusually

dry autumns and the activity of this virus. As an explanation, it was proposed that during drought periods, pregnant female vectors, particularly *Culex nigripalpus*, may not find suitable sites for oviposition or simply rest waiting for the right conditions. This resting period allows the virus incubation period to be completed in the infected females. When rains restart, soon after oviposition there would be a concentration of infected mosquitoes in search of new hosts. Moreover, precipitation stimulate the ingestion of blood in *Cx. nigripalpus* females, and therefore the abundant autumn rains could stimulate females to perform long flights seeking blood meals and reach hosts in locations that were harsh during the dry periods of the year. This could even be a cause of the change from bird to mammals' blood intake observed in the fall. A negative association was also detected between the abundance of adult *Cx. pipiens* (vector of SLE and West Nile virus) and surface moisture in the previous 10 days, modeled from a dynamic hydrological model based on topographic maps. This negative association is consistent with the preference of *Cx. pipiens* for contaminated water collections, as in times of drought, water collections reduce their dimensions and become eutrophic.

In 1999, West Nile virus (WNV) was first detected in North America and quickly dispersed, being found as far south as Argentina in 2005. This virus normally circulates in the bird population, mainly transmitted by mosquitoes, and can occasionally infect incidental hosts such as horses and humans. In subtropical and moderately temperate zones, significant correlations have been observed between the number of human cases of WNV and monthly temperature, while the correlations with rainfall are low. Mosquito catches increase with increases in monthly temperatures. In turn, human cases are correlated with positive *Cx. quinquefasciatus* and *Ae. albopictus* mosquitoes and infected birds (reservoirs of the virus).

There is an interesting example of interaction between vector species and climate in *Culex* populations from the north hemisphere. The populations of *Cx. restuans* increase from spring until they become the predominant population in the

middle of summer, replaced by fall by *Cx. pipiens*. The seasonal change in *Cx. restuans* dominance for *Cx. pipiens* suggests that the first species begins the enzootic cycle of WNV, while *Cx. pipiens* amplifies the number of infected bird host. The time when both species are represented in similar proportions is called “crossover.” Correlations between historical records, dates of crossovers, and parameters derived from temperature records (such as maximum and minimum temperatures, degree-days, etc.) suggest that high temperatures can accelerate the crossover and therefore lead to longer periods of transmission, encouraging the involvement of accidental hosts.

Associations have been found between urban characteristics and the prevalence of WNV, noting lower prevalence in suburbs with higher vegetation cover and diversity and higher prevalence in suburban areas dominated by houses over 40 years with moderate vegetation cover. This relationship could be explained by the conditions of the rainwater drainage system, which allows the accumulation of water (most relevant in times of drought) combined with organic matter, creating an enabling environment for the *Culex* species (Ruiz et al. 2007). On the other hand, as discussed in earlier sections of this chapter, low biodiversity areas could favor the set of birds and mosquito species necessary to keep transmission, since the mosquitoes can use containers and bodies of water (drainage, ditches) generated by humans.

37.3.5 Filariasis

The filarial worms are parasitic nematodes transmitted by several species of mosquitoes, which vary geographically. In each region, there is a close association between the frequency of filariasis and blood intake by mosquitoes. *Wuchereria bancrofti* predominates in urban and suburban areas of South and Central America, where *Cx. quinquefasciatus* is their main vector, though infective larvae have been isolated from *An. darlingi* and other species of mosquitoes as well. Human filariases are in general distributed in tropical and subtropical regions of the world.

This could be due to climatic conditions and soil characteristics, influencing the availability and activity of vectors, as above, but also to its effect on the infectivity of the parasites. At least in laboratory tests, the amount of *Brugia pahangi* filarial larvae that penetrate a mammal host, bitten by the vector *Ae. aegypti*, is greater in high relative humidity conditions. But both the number of larvae leaving the female mosquitoes during feeding and the female’s predisposition to feed are independent of relative humidity. When the filarial larva emerges from the proboscis of the mosquito, it is covered by a fluid, composed of the mosquito hemolymph. It has been proposed that evaporation of this protective hemolymph cover is the main factor regulating the penetration of filarial larvae in the host. The areas where this filariasis is endemic are limited to the tropics, where the evaporation rate is high. However, in these regions the mosquitoes feed predominantly at night and up to the sunrise, when temperatures are lower, the humidity increases and evaporation decreases. Local factors such as plant cover, the presence of large water surfaces, or other characteristics such as architecture, among others, that create or maintain the higher humidity conditions could increase the potential for transmission.

The larval habitats of *Cx. pipiens*, one of the principal filariasis vectors, can be identified by the analysis of the daily changes of land surface temperature, recorded by remote sensors, such as AVHRR NOAA (Malone et al. 2006), and soil moisture indicators derived from higher-spatial-resolution Landsat images. This is due to the buffering effect of water, which causes wetlands and other flooded land to have lower daily variations relative to neighboring non-flooded fields.

Dirofilaria immitis is widely distributed in tropical regions. In the Americas, potential vectors are species of *Culex*, *Anopheles*, *Mansonia*, and *Ochlerotatus*. Landscape features may affect the transmission of the disease, such as a negative relation reported between the degree of urbanization and the prevalence in dogs. Heartworm risk maps for Argentina were generated that considered the lower temperature thresholds for the development of the *D. immitis* in the mosquito (about 14-°C), the number of potential mosquito

vector species, and a heat measurement (about 130-°C-days), necessary for the microfilariae to reach the infectious stage. These models indicated that the risk increases from the southwest to northeast, which is consistent with the highest values of prevalence of the disease in the north. The maps also stressed that the transmission in the Southern Cone of the subcontinent is markedly seasonal, even in the warmest regions (Vezzani and Carbajo 2006). This type of approach, complemented with more specific information on population parameters and habitat requirements of the vectors involved in various geographical regions, could serve as a starting point for evaluating the different climate change scenarios on the distribution of this disease.

37.3.6 Leishmaniasis

Leishmaniasis are among the main reemerging diseases of the Americas in two main types of clinical manifestations: cutaneous and visceral (see Chap. 16). These diseases are caused by intracellular parasites of the genus *Leishmania*, transmitted between mammals by several species of *Lutzomyia* (Diptera: Psychodidae) with reservoirs varying according to the species of the parasite and the region. The dynamics of the disease are strongly associated with the presence of reservoirs, which act as sources of infection, and humans are generally regarded as accidental hosts. In Brazil, the main vector of zoonotic visceral leishmaniasis is *Lutzomyia longipalpis*, a species of endophilic and exophilic habitats, which bites humans during dusk and night rest (Ximenes et al. 2006). Mass migration of people from rural areas to the outskirts of cities, as a result of drought, malnutrition, and lack of land for agriculture, favors the formation of slums. In these settlements of predominantly young families, health and infrastructure conditions are poor. The combination of nonimmune hosts in malnutrition conditions with the habit of keeping domestic animals (dogs, chickens, horses) in or near households allows the proliferation of sand flies and increases the risk of infection by *L. chagasi* and eventually developing visceral leishmaniasis.

Weather conditions, besides affecting the migrations of hosts, have a more direct effect on development and proliferation of the vectors. The increases in visceral leishmaniasis are preceded by increases in population densities of *Lu. longipalpis*, which in turn are negatively correlated with relative humidity and wind speed and positively with average temperature in the previous months (Ximenes et al. 2006). In Rio Grande do Norte (Brazil), the insects have a peak incidence in May, when rain predominates and the temperatures are lower, and a second peak in November, when the rains are light and temperatures are higher, while the females only show a peak in May. The population peaks depend on the combination of appropriate temperature and humidity conditions for the development of the immature forms; high temperatures can accelerate the development of the larvae, but reducing the relative humidity can stop its development.

Time series analysis of the incidence of cutaneous leishmaniasis in Costa Rica showed that this disease has cycles of about 3 years, consistent with the temperature indexes and the El Niño-Southern Oscillation. Linear models were developed based on temperature estimates and El Niño-Southern Oscillation rates that could predict with accuracy greater than 70% the incidence of cutaneous leishmaniasis, up to 12 months in advance (Chaves and Pascual 2006). In Brazil, visceral leishmaniasis has peaks approximately every 10 years, which probably reflect not only the vector responses to environmental change but also their interaction with human hosts and susceptible dogs.

As the vector species (sand flies) generally prefer forest and moist environments, data derived from remote sensors included in geographic information systems are suitable tools to generate vector distribution and leishmaniasis risk maps. For example, in East Africa distribution maps of the main vectors of visceral leishmaniasis, *Phlebotomus martini* and *Ph. orientalis*, were created using NVDI derived from AVHRR NOAA, maximum temperature analysis, agroclimatic data from FAO/CPSZ (Food and Agriculture Organization of the United Nations/Crop Production System Zone), and FAO 1998

soil maps (Gebre-Michael et al. 2004). In the Brazilian state of São Paulo, the distribution of the five dominant species (*Pintomyia fischeri*, *Nyssomyia intermedia*, *Migonemyia migonei*, *Pi. pessoai*, and *Ny. whitmani*) was estimated from municipal data of occurrence of the species and ecological niche modeling approach using genetic algorithm to adjust the decision rule (GARP). This model considered aspects of topography (elevation, slope, tendency to accumulate surface water), climate (temperature parameters, precipitation, and relative air humidity), land use, and ground cover (estimated from AVHRR NOAA satellites). The resulting models allowed the production of general distribution maps of the species, covering areas not sampled or sparsely sampled (Peterson et al. 2004). On the other hand, in the state of Mato Grosso, *Ny. whitmani* s.l., originally associated with forest ecosystems, occurs in anthropogenic habitats and therefore may occur in different environmental profiles, sylvan or periurban. A supervised classification of NVDI MODIS images in four classes of vegetation/land cover showed that the spatial distribution of “species” is positively correlated with the rate of deforestation and negatively correlated with socioeconomic development indicators. Their adaptation to anthropogenic environments could explain why deforestation does not result in widespread loss of sand fly habitat in this state (Zeilhofer et al. 2008).

Whether driven by natural or human forcing, climate change together with changes in the ecosystems driven by human activities is expected to be reflected in the spatial distribution and dynamics of transmission of leishmaniasis, among other diseases. Potential geographical distribution of leishmaniasis vectors in South America based on ecological niche models indicates, for different climate change scenarios, the improvement of conditions for *Ny. whitmani* in the southeastern Brazil, influencing the transmission of cutaneous leishmaniasis (Peterson and Shaw 2003). The southern range of cutaneous and visceral leishmaniasis could be extended from northern Argentina to more austral latitudes. In addition, the improvement in conditions for *Ny. whitmani* on the eastern slopes of the Peruvian Andes could

allow the expansion of cutaneous leishmaniasis in this region (Peterson and Shaw 2003). The reduction of natural habitats could favor the urbanization of the vectors and diseases, since, although the sand flies are more abundant with taller, dense vegetation and with high moisture content, some species may invade the home and surrounding dwellings, developing in the vegetation near the houses, and even in outdoor environments (latrines, pens). In the northeastern Brazil, a region subject to periodic droughts, a resurgence of visceral leishmaniasis has been noted in urban areas, and major epidemics coincided with more pronounced droughts caused by El Niño.

Salomón et al. (2012) argued that an increase in temperature or humidity due to climate change would change the transmission risk of leishmaniasis in Argentina (its southern range), by increasing duration of night activity of the females and human exposure from changes of the habits of humans. The increased vulnerability would be discriminated by socioeconomic variables, since, for example, families spending more time in the courtyard during very hot and humid nights would be more exposed than families spending this period indoors with air conditioning (a similar situation to dengue in Texas, see above). At a regional scale, an increase in precipitation and humidity by global trends and/or water reservoir-irrigation development projects could change the vector community and increase the area of dispersion of species such as *Lu. longipalpis*.

37.3.7 Chagas Disease

Chagas disease is widely distributed in Latin America, from Argentina to Mexico, and recently human cases were reported in the Southern United States. It is estimated to affect 15 million people and the population at risk of becoming infected is 28 million. Due to its slow development, it is considered the parasitic disease with the greatest economic importance in Latin America. As the parasite can also be transmitted by other means, such as blood transfusion and organ transplantation, even via contaminated

food ingestion, including in countries where there is no vectorial transmission (e.g., Spain), Chagas disease shows up as a major public health problem due to the migration of infected people.

Considering only the regions where transmission is vectorial, this parasitosis is a complex zoonosis, involving several vertebrate reservoirs and various species of triatomines, which makes eradication complex or even impossible in most of its range. The number of triatomine species increases significantly from the poles to the equator and from the west to east, with a maximum of species between 5 and 10°S. The Amazon region has the greatest diversity of wild species, adapted to very humid microclimates of rainforest, and a variety of patterns and complexity of transmission cycles has been found. In this region, the home infestations are restricted to drier subregions of the Amazon, that is, those heavily modified by deforestation.

Outside the Amazon region, most of the transmission of Chagas disease depends on the household and outdoor premises' populations of vectors. The poor condition of houses, associated with poverty in both rural and "poverty belts" of big cities, facilitates the establishment of the vectors adapted to indoors and peridomestic environments. Domestic animals closely associated with the inhabitants, even living inside human homes, are a source of abundant blood and easy to access, allowing the insects to reach high densities.

Anthropogenic changes in land use can lead gradually to synanthropy of the triatomines. The pattern of invasion by *Rhodnius* in Amazon rainforests illustrates this. Selective removal of the forest, which only keeps palm trees in the peridomestic environment, is a common factor that reduces the populations of wild vertebrates. Although during the first stage of land use change the populations of wild triatomines (especially *Rhodnius*) suffer great reductions, individuals who persist adopt the palm trees as suitable refuges, where they coexist with marsupials and opportunistic rodents, which proliferate in environments modified by humans. Once the triatomine population saturates the palm trees' habitats, in search of new dwellings, they can invade nearby human homes and thus increase the risk of Chagas transmission. In the Alto Beni region,

Bolivia, intensive deforestation and creation of new urban settlements have gone on for the last 20 years. The materials used to build houses, mainly palm leaves, may have facilitated the introduction of *Rhodnius stahli*, a normally wild species, to the home, where adults, nymphs, and eggs have been collected. *Triatoma dimidiata* is a widely distributed species in Mexico, Central America, Colombia, and Ecuador, both in wild habitats as inside and outside the house. They may colonize artificial environments in the Amazon, since their natural populations are present in very diverse ecoregions, including wet or dry forest environments.

Triatoma infestans is the main Chagas vector in the Southern Cone of South America, where it is closely associated with household and outdoor structures. The microenvironmental conditions of human habitation are better buffers of the largest outdoor temperature variations, compared to peridomestic sites such as pens of goats and chicken. The latter are open structures, exposed to sunlight, rain, and wind; thus, the differences in relation to external conditions are small. Therefore, temperature variations will affect more outdoor than indoor insect populations. Both empirical field data and ecogeographic models (Ceccarelli et al. 2015) suggest that *T. infestans* has a limited capacity to thrive in hot and humid climatic conditions of most forest regions of the Amazon. In fact, on a regional scale, the analysis suggests that the distribution of *T. infestans* is affected by environmental characteristics, mainly linked to annual cycles of air temperature and soil moisture, not necessarily linked to the availability of human habitation. In turn, temperature contributes to *T. infestans* dispersal, since it influences the proportion of specimens flying and also the distance they travel.

In Brazil, it is assumed that the characteristics of the indigenous settlements, added to their nomadic habits, prevent the establishment of *T. infestans* in the homes and thus reduce the likelihood of infection by *Trypanosoma cruzi* (at least by this vector). In fact, it was proposed that the beginning of protozoan infections was associated with domiciliation of *T. infestans*, due to the building of mud shacks from the European colonization. However, the detection of *T. cruzi*

infection in 4500–7000 years human mummies shows that human infections, at least in Brazil, occurred in populations of hunter-gatherers, before *T. infestans* adopted indoor environments.

Not only the land use changes may affect the *T. cruzi* transmission cycles but also climate change could modify the risk of infection (McCarthy et al. 2001; Medone et al. 2015). Temperature affects the major components of the vectorial capacity: at higher temperatures, insects can accelerate development and achieve higher densities, and the development of *T. cruzi* is also accelerated. However, the relationship between the temperature and the infection rate is not necessarily linear, as when the densities of these insects are very high, competition density-dependent processes affect the amount of ingested blood, which reacts on the elapsed time between blood intake and the first defecation (lower ingestion → higher delay to excrete) and therefore on the infection risk.

It has been observed that large-scale climate disturbances, such as hurricanes, can increase the risk of transmission of Chagas disease, although the causes are still unclear. Among the possible explanations, it is speculated that the reduction of sources of wild hosts, due to the death of animals, could encourage the spread of vectors searching for a blood meal, favoring the invasion of houses and human contact. Alternatively, populations of some reservoirs, such as armadillos in Louisiana, can grow markedly after the hurricanes and encourage population growth of insects. Upon returning these reservoirs to their levels before the hurricane, the triatomine bugs seek alternative blood sources.

37.3.8 Tick-Borne Diseases

Tick-borne diseases, such as Lyme disease, ehrlichioses, encephalitis, and spotted fever, are common in temperate regions, mainly in the northern hemisphere. In general, species that transmit these diseases have complex cycles involving different hosts depending on the stage of development of the ticks. The distribution of these diseases is affected both by climate, which limits the distribution of vectors, their develop-

ment, and their survival rates, as well as the habitat characteristics, which may condition the contact between the ticks and the reservoir hosts of different pathogens. For example, *Amblyomma americanum* (vector of *Ehrlichia chaffeensis*, the causative agent of human monocytotropic ehrlichiosis) and *Ixodes scapularis* (vector of *Borrelia burgdorferi*, which causes Lyme disease, and *Anaplasma phagocytophilum*, causing human granulocytic anaplasmosis) prefer higher temperatures and humidity. However, these relations are variable in space. Detailed analysis of plant cover (30-m resolution) pointed out that in the drier regions of the ticks' distribution, coverage by forests and fragmentation are important to predict the presence of *E. chaffeensis* and *A. phagocytophilum*. This would be because the tree cover would maintain adequate moisture conditions for the survival of the vector ticks. In turn, the presence of forest and agricultural land or urban areas fragments can affect the density of deer and small mammals (pathogen reservoirs) which are hosts of the various development stages of ticks (Wimberly et al. 2008).

Over the last two decades, increases in the abundance of ticks and incidence of diseases caused by them have been registered, which has been attributed to climate, land use change, and also greater awareness of these diseases. Models of the effects of weather on ticks in the temperate regions suggest that as the temperature rises, the larvae feed and are active earlier in the year, and a higher proportion of the nymphs feeds during autumn of the same year they fed as larvae. This growing overlap in the activity of larvae and nymphs could increase the pathogen transmission cycles that are transmitted efficiently between reservoirs and ticks only for short periods of the year, such as *A. phagocytophilum* (Ogden et al. 2006). An analysis of the distribution of ticks in different climate change scenarios (GCM) was consistent in presenting an expansion to lower latitudes of favorable climatic conditions for the establishment of *I. scapularis* populations and eventually the pathogen they transmit (Ogden et al. 2006). However, a study in the United Kingdom showed no correlation between cases of Lyme disease and average summer temperature (Hunter 2003). On the other hand, in Sweden, between 1980 and

1994, an expansion of the northern distribution limit and an increase in *I. ricinus* tick density were recorded, concomitant with milder winters. Another approach to elucidate the impact of climate change on the distribution and phenology of *I. ricinus* considered a stage structured Leslie matrix of a Western Palearctic region tick population and temperature, saturation deficit, and hours of light of the previous 2 weeks as independent variables. An advantage of this model is that the sensitivity of each stage to changes in climate as well as their impact on the whole life cycle of the tick can be assessed. Geographic variations were detected in the relative importance (elasticity) of the development processes, such as development and mortality rates, to the final population performance. For example, in most of the northern distribution range, the mortality rates associated with the molting processes had higher elasticity than development rates, while at southern latitudes, the duration and mortality of questing periods for adults were the greatest contributors to the final performance of the life cycle. Consistently, different sensitivity of the complete life cycle of the tick to proportional changes in temperature and saturation deficit was evidenced according to the performance of the tick in the geographic range (Estrada-Peña and Estrada-Sánchez 2014).

High-spatial-resolution remote sensing, such as Landsat™, can distinguish fine-scale features of the landscape composition that can be used to assess the risk of exposure to Lyme disease. The abundance of *I. scapularis* ticks can be associated with ground cover, distance to forests borders, elevation and soil type, environmental characteristics that can be estimated from satellite images, and/or modeled in geographic information systems (Bunnell et al. 2003). In urban and suburban environments, if reservoirs are present, the urbanization characteristics may influence the risk for diseases such as Lyme. Estimates from satellite images of structure, humidity, and “greenness” of vegetation showed a higher relative risk of exposure to the disease in the greener and most humid premises, containing a higher proportion of trees with broad leaves, while premises with lower risk had higher proportion of areas without vegetation or open grass cover (Dister et al. 1997).

The biological interactions involved in disease incidence are complex and include environmental components that are extrinsic to transmission cycles. Thus, for example, Lyme disease outbreaks can be predicted based on the productivity of oak seeds. The *Borrelia burgdorferi* spirochete complex causing this disease normally circulates in populations of a rodent (*Peromyscus leucopus*) and white-tailed deer, which also disperse the ticks. These acari can accidentally bite humans and transmit them the pathogen. Every 1 or 5 year’s oaks produce large amounts of acorns (phenomena known as mast-ing). The plenty availability of acorns leads to rodent population growth and attracts deer, with the consequent proliferation of ticks and facilitating contact with the infected rodents (Randolph 1998).

AVHRR satellite images, estimating vegetation and surface temperature, in combination with standard geostatistical methods can be used to analyze dynamically in time the suitability of habitat for *Boophilus microplus*. This type of study in central and south of North America indicated that the most suitable areas for the tick have relatively stable temperatures year round (20–25 °C) and have intermediate plant coverage. Gradual heating of the region would decrease the quality of habitats in areas where the tick is established and favor their establishment in other regions currently too cold to support their populations (Estrada-Peña 2001).

Considering the strong association between the ecology of the vectors, access to reservoirs, climate, and land cover, it is expected that climate and land cover changes have important repercussions on vector-borne diseases worldwide. Even though vaccines and other means of chemoprophylaxis are being developed for the more common/widespread diseases, the emergence or reemergence of novel vector-borne diseases is a widespread phenomenon. Thus, it is of paramount importance that more detailed studies on the biology and ecology of the vectors and the transmission cycles of these pathogens be encouraged. Deeper understanding of the processes and mechanisms involved should allow for more efficient application of vector control and disease prevention.

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