

Environmental changes, disease ecology and geographic information system-based tools for risk assessment

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Summary

In recent years, several vector-borne, parasitic or zoonotic diseases have emerged or re-emerged in different parts of the world, with major public health, socio-economic and political consequences. Emergence of these diseases is linked to climatic change, human-induced landscape changes and human activities that have affected disease ecology. The authors illustrate geographic information system-based approaches to understand epidemiological processes and predict disease patterns. Continent-wide approaches are used to explore vector and host distributions and identify areas where substantial changes in vector and vector-borne disease distributions have occurred. Time series of high-resolution satellite data and locally collected data reveal the spatial relationships between factors impacting disease dynamics. Using Rift Valley fever as a case study, a conceptual approach is proposed to integrate all of these data and to identify key parameters for disease modelling. Some of the challenges posed by different spatial and temporal scales of the biological processes and associated indicators are highlighted.

Keywords

Early warning, EDEN, Emerging disease, Environment, Model, Rift Valley fever, Satellite.

Mutamenti ambientali, ecologia delle malattie e strumenti basati sui sistemi d'informazione geografica per la determinazione del rischio

Riassunto

Negli ultimi anni sono emerse o riemerse in diverse parti del mondo molte malattie trasmesse da vettori, parassitarie o zoonotiche con conseguenze di primaria importanza socio-economiche, politiche e di salute pubblica. L'insorgenza di tali malattie è legata al mutamento del clima, alle modificazioni ambientali dovute all'azione dell'uomo e alle sue attività, che hanno influito sull'ecologia delle malattie. Gli autori illustrano approcci basati sui sistemi d'informazione geografica, GIS, per comprendere i processi epidemiologici e predire il quadro delle malattie. Vengono utilizzati degli approcci olistici per analizzare la distribuzione dei vettori e degli ospiti e identificare le aree in cui si sono verificati mutamenti sostanziali nei vettori e nella diffusione di malattie da loro trasmesse.

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Successioni temporali di dati, sia forniti da satellite ad alta risoluzione sia raccolti localmente, rivelano le relazioni spaziali esistenti tra i fattori che hanno un impatto sulla dinamica delle malattie. Utilizzando la febbre della Valle del Rift, viene proposto un approccio concettuale per integrare tutti questi dati e identificare parametri chiave per la costruzione di modelli di malattia. Viene dato rilievo ad alcune tra le sfide rappresentate da differenti componenti spaziali e temporali di processi biologici ed associati indicatori.

Parole chiave

Allarme precoce, Ambiente, Febbre della Valle del Rift, Malattie emergenti, Modelli, Satelliti.

Introduction

In recent years, several veterinary and zoonotic diseases have emerged or re-emerged in different parts of the world, with major impacts on public and veterinary health, trade and economic activities. In some cases, there have been substantial social, societal and political consequences in affected countries. Introduction of pathogens into new areas may be the consequence of the increased movement of people, animals and goods. There have also been increased opportunities for vectors to spread from their historical distribution areas, via passive transportation (28). Once introduced, some pathogens and/or vectors are able to survive and to persist in naive ecosystems, leading to new diseases outbreaks (2, 26). The ecology of many vector-borne diseases is largely dependent on biotic and abiotic parameters; for example, local climatic conditions can have an impact on the distribution of arthropod vectors, their biology and vectorial capacity, or the synchrony with host availability (19). Habitat fragmentation, linked to human settlement and activities, may increase contacts with vectors or alter the distribution and the behaviour of wild or domestic animals and their interaction with humans. In addition, newly introduced pathogens may find suitable vectors, as has been demonstrated for bluetongue virus in Europe (17). In such cases, the natural history of the disease has to be reviewed.

The impact of environmental change, including climatic change, on diseases has been widely discussed in the media. Unfortunately, a partial understanding of the epidemiological processes may lead to 'convenient' shortcuts where emblematic parameters of global change are linked to suspected or predicted changes in disease incidence or distribution. As an example, the spatial scales at which climatic variability is quantified often is not consistent with the scales at which land-use changes or the biology of arthropod populations (in particular, vector populations) are studied (25). In addition, characterisation of the impact of climate-driven forces on risk factors is further masked or confused by sanitary interventions (hygiene improvement, vaccination campaigns, development of health centres, changes in regulations or collapse of existing healthcare systems), evolving farming systems (for example, agricultural intensification) and social transformations (migration patterns, international travel, poverty, recreational activities) (12, 27).

The objective of this paper is to propose a conceptual approach and to evaluate some tools for exploring interactions between ecological change and disease occurrence. Such an approach may facilitate linkages between environmental change and public health within an interdisciplinary research framework (15). Factors related to disease emergence at various scales in time and space and their potential use for quantitative risk assessment are illustrated using African vector-borne diseases as an example.

Predicting disease distribution

During the past 15 years, remotely-sensed data have been widely used on regional and continental scales to predict vectors and disease distribution. Early models developed for the Food and Agriculture Organization (FAO) Program Against African Trypanosomosis – Information Systems (PAAT-IS) (6) correlated low resolution satellite-derived measures of atmospheric characteristics and land-surface data from Meteosat and National

Oceanic and Atmospheric Administration-Advanced Very High Resolution Radiometer (NOAA-AVHRR) with the presence of tsetse flies, the African vector of human and animal trypanosomosis. Much of the focus was on innovative approaches, including multi-temporal analysis of annual, bi-annual and triannual component variations quantified by Fourier analysis and intermediary outputs on the predicted distribution of ecotypes, agricultural and breeding systems (21, 22, 30). These maps are still widely used by decision-makers for the identification of priority areas for tsetse control (9) and development programmes for poverty alleviation in Africa (26). Last but not least, these new approaches have in turn generated new methods for processing and predicting disease distribution, which have been applied to other diseases (8).

Indicators of environmental change

Environmental change over time can be assessed using temporal series from which trends or anomalies (amplitude or timing) are correlated with particular changes in disease distribution or seasonality as a measure of disease incidence. A highly illustrative example is the focal distribution of tick-borne encephalitis virus in Europe, which is related to the geographically variable degree of synchrony in seasonal activity of larval and nymphal *Ixodes ricinus* ticks. As persistent cycles of tick-borne encephalitis (TBE) virus depend on non-systemic viral infections transmitted from infected nymphs to large numbers of infectible larvae co-feeding on the same individual rodent (19), synchronous seasonal activity of larval and nymphal ticks is essential. This has been shown to be correlated with a rapid fall in ground-level temperatures during the autumn, although the biological processes underlying this correlation have not yet been fully revealed. A satellite-derived index of land surface temperature was successfully used to characterise seasonal temperature profiles of locations at risk (19). On the local scale, land-use changes can also be detected by diachronic analysis of classifications of high-resolution images, emphasising changes in vector habitats or host availability. For tsetse flies, such a study was

conducted in Burkina Faso on riverine tsetse flies (flies living in the forest gallery along the rivers). This study suggested that the increase in agriculture surfaces could result in the disappearance of some tsetse species, as their habitat is destroyed by neighbouring crop fields, rainfall runoff and erosion of banks. Nevertheless, tsetse populations were maintained or even increased when the expansion of crops was limited by unsuitable soils to about 150 m from the river (4). In this example, the main parameter for tsetse prediction was not the density of agriculture, but the location of plots in the valley. This highlights the concept of indicators, which:

- are translating factors affecting diseases processes
- are (easily) measurable
- can be monitored.

These indicators can either be crudely measured (for example, extracted from field surveys or remotely-sensed) or synthesised (that is, created from a combination of crudely measured variables). Their identification supposes both a holistic and detailed knowledge of the ecology of the disease under study within the ecosystems. The potential and limits of specific-scale methods and indicators for African animal trypanosomosis assessment and control have been reviewed in detail (9).

Mathematical models

Many factors must be considered in risk assessment. These factors differ in terms of origin, thematic field, and spatial and temporal scale. A method of integrating such factors is mathematical modelling. The most commonly used method for vector-borne disease is the basic disease reproduction rate (R_0), which describes the number of new cases that arise from one case introduced into a population of susceptible hosts (11, 21). If R_0 is lower than 1, the disease will probably not establish itself; when R_0 is above 1 the disease might spread. For vector-borne diseases, R_0 is expressed as:

$$R_0 = \frac{mbca^2 e^{-\mu t}}{\mu r}$$

where:

m = the ratio of vector numbers to host numbers

- b = the transmission coefficient from vertebrate to vector
- c = the transmission coefficient from vector to vertebrate
- a = the biting rate of the vector
- μ = the mortality rate of the vectors
- T = the extrinsic incubation period of the infection in the vectors
- r = the recovery rate of the host from infection.

A major challenge in vector-borne disease modelling is to estimate the above parameters in a geographical grid so that an R_0 map can be produced. To achieve this objective, the selected parameters must be representative of a wide range of environmental conditions and be readily measurable over large areas. However, mathematical model parameters are often difficult to measure directly; they vary with changing local conditions and seasonally over time and may be affected by other factors that impact changes over a longer time-frame. It is therefore necessary to identify the most suitable indicators for each of the mathematical model parameters.

Design of system and conceptual models

Factors that have an impact on the transmission and ecology of pathogens may be classified into three thematic fields or 'boxes' (Table I), as follows:

- the host-vector-pathogen box includes epidemiological factors that affect the relationships between hosts, vectors and pathogens
- the habitat box includes factors affecting biotic and abiotic parameters of the landscape
- the human activities box includes factors that affect the epidemiology of diseases through individual behaviour patterns or institutional policies.

A final box including biodiversity parameters, such as the abundance of other living organisms potentially impacting on the system (for example, as reservoir species), may also be included.

Such a conceptual framework can be used to study diseases by taking into account all links

between the host-pathogen system and the environment (biotope, communities, human); it is also designed to facilitate interdisciplinary research, particularly communication between epidemiologists and researchers from others fields, such as ecology, geography and sociology.

The conceptual model should help us identify and characterise the main factors involved in the epidemiologic process. Then, the interactions within and between each 'box' should be described. Finally, it is necessary to describe the temporal dynamics of the different factors and their relationships in this system.

Table I
Classification of the factors that have an impact disease on transmission into three thematic boxes

Box	Factors
Host-vector-pathogen	Hosts: diversity of susceptible species, receptivity, immunity Vectors: diversity of species, biology, ecology. Pathogens: diversity between strains, virulence
Habitat	Climate, landscape, ecozone
Human activities	Individual behaviour, institutional policies

Towards quantifying R_0

The conceptual model is used to describe the links between the above factors. It indicates the potential repercussions of any change in one factor on linked factors. It may also be used to highlight from which part of the conceptual model R_0 variables may be extracted. As an example, for mosquito-borne diseases of livestock in Sahelian areas of Africa (such as Rift Valley fever), climate is one of the key factors that affects the presence and abundance of vectors in and around seasonal wetlands and the distribution of hosts. The host-vector ratio (m) may be estimated from a compilation of vector and host distribution spatio-temporal maps derived from remotely-sensed data as an indicator. The following section describes a pilot study on Rift Valley fever in sub-Saharan West Africa to extract some of the factors that

impact m . It highlights some critical issues regarding scale and the limits of extrapolation.

Example of application: study of Rift Valley fever in Sahelian Africa

Rift Valley fever is an arthropod-borne, viral disease of ruminants, camels and humans. It is an important zoonosis, with symptoms varying from an uncomplicated influenza-like illness to a haemorrhagic disease with severe liver damage and ocular or neurological lesions. In ruminants, the disease may be unapparent in non-pregnant adults, but outbreaks are characterised by abortions and high neonatal mortality. Transmission to humans may occur through the bites of infected mosquitoes or as a result of close contact with contaminated animal material (for example, during slaughter). In livestock populations, Rift Valley fever virus (Phlebovirus) is transmitted by various arthropods, including six mosquito genera (*Aedes*, *Culex*, *Mansonia*, *Anopheles*, *Coquillettidia* and *Eretmapodites*). It has been isolated from more than 30 species of mosquitoes, of which some have been confirmed as vectors that are able to transmit the virus (13). Most of these vectors acquire infection by biting infected vertebrates. In addition, transovarial transmission occurs in some *Aedes* species (3). Infected pools of eggs survive desiccation for months or years, so that transmission of the virus to livestock and humans can occur shortly after a flooding event. Vertical infection (from imago to eggs to adults) in 'primary' vector species may explain how the virus can persist between outbreaks. Other 'secondary' vectors (such as *Culex* spp.) then become involved in transmission and amplify the circulation of the virus (3, 10).

The conceptual model for Rift Valley fever in Sahelian West Africa

Figure 1 details the conceptual model for Rift Valley fever in a savannah area of sub-Saharan West Africa, where the disease is transmitted to domestic livestock during the rainy season when temporary water points are flooded and

pastoral herds are present (1). The main elements to be included in the three boxes are described below. The links between these elements, including those from which the parameters for R_0 can be extracted, are shown in Figure 1.

- The **host-vector-pathogen box** includes diversity of susceptible hosts (cattle, sheep, goats), the herd immunity in relation to the age of the animals in the herd and the susceptibility of individuals depending on their genotype and on factors (such as nutrition and other diseases) impacting on their resistance to the disease. Factors related to vectors include the different potential species of mosquitoes (primary and secondary species) involved in transmission, seasonal variations in their populations, feeding behaviour, vectorial capacity and other considerations, such as vertical transmission of the virus. Factors related to the virus include the diversity and virulence of different strains.
- The **habitat box** includes habitat factors influencing biotic and abiotic conditions. Climatic factors, such as mean, extreme values, amplitude and temporal variations of rainfall, humidity and temperature must be considered, as well as unusual events (floods, droughts). Elements of ecotype and landscape include topographic features, vegetation, soils, hydrologic elements, land-cover mosaic and grazing areas, and human settlements.
- The **human activities box** includes the individual behaviour of livestock owners to protect animals or people from infection (related to education and public/animal health facilities and supplies), as well as considerations related to traditional breeding practices, religious and social identity. In this part of Africa, for instance, traditional rules for access to strategic points (grazing areas and watering points) and increasing competition between ethnic groups are a key element in the understanding of host distribution patterns. In addition, local and government policies and infrastructure (serological surveys, vaccination campaigns, information and education) may mitigate the

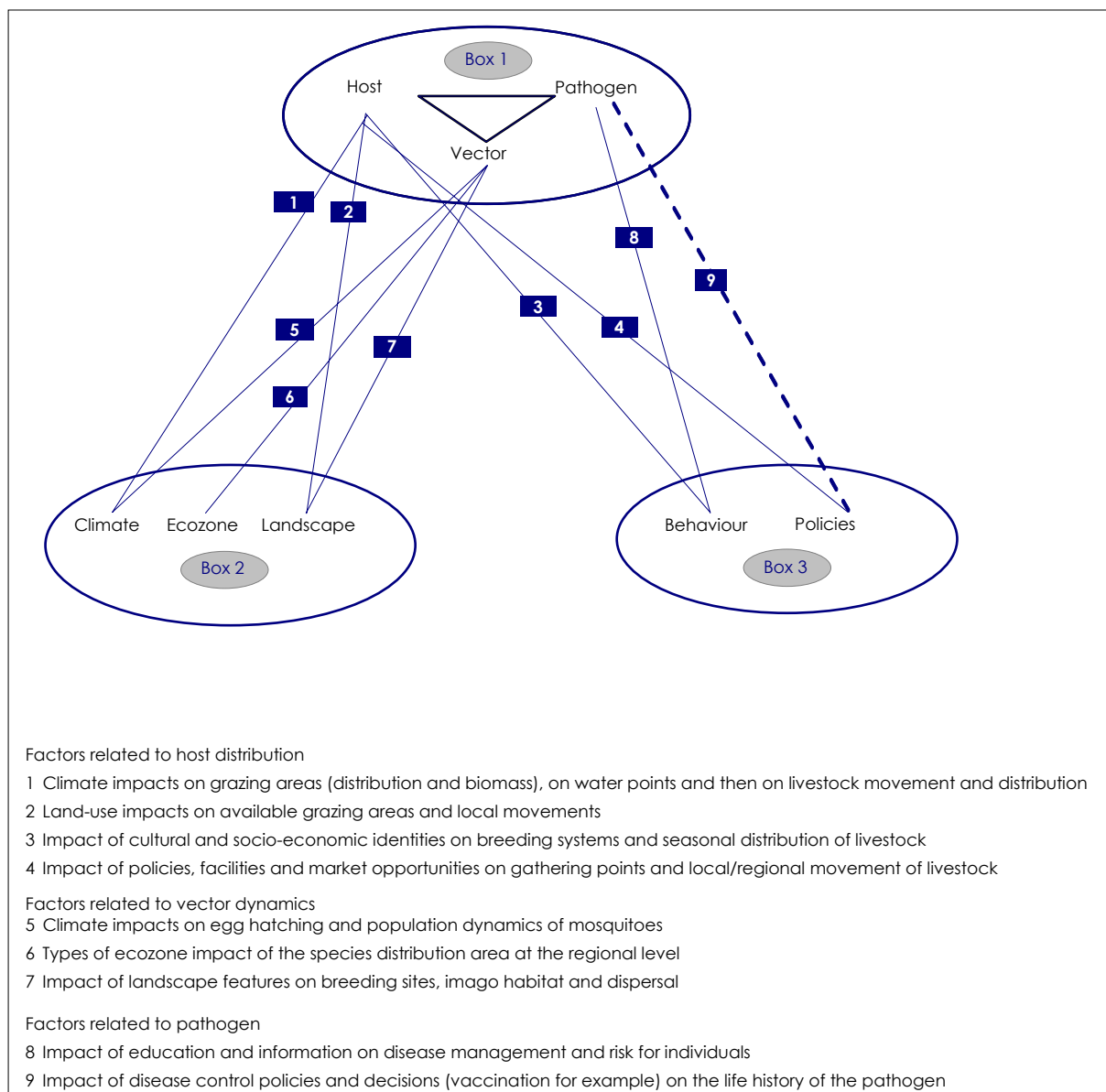


Figure 1
A conceptual model of Rift Valley fever in a Sahelian area of West Africa and the links from which R_0 parameters may be extracted

disease process. Livestock trade opportunities also have an impact the potential spread of the virus.

Exploration of one of the R_0 parameters

A method for extracting some of the indicators of the vector-host ratio (m) is described and used to illustrate some key problems related to scale. We explore the relationships between the habitat box (especially climatic factors) and the host-vector-pathogen box, with special

emphasis on the numerator and the denominator of the vector-host ratio (m).

The data are extracted from a study conducted in a pastoral area of north Senegal, subject to a typical Sahelian climate (isohyete 100-500 mm), where entomological, serological and virological surveys confirmed the circulation of Rift Valley fever virus (1). The Ferlo area is a valley of approximately 6 000 km² where ponds are filled by rainfall during the rainy season. For 4-5 months each year, transhumant herds concentrate around these ponds, benefiting from the grassland in the

neighbouring savannah. Most of the herds leave the area as ponds progressively dry up. The remaining animals are kept around permanent boreholes to supply the family needs of the breeders. These ponds are the principal breeding sites for Rift Valley fever vectors, mainly species of *Aedes*, *Culex* and *Anopheles* genera. Recently, intensive studies on the epidemiology of Rift Valley fever in villages close to some of these ponds have been conducted; these include serological and virological surveys, entomological surveys, description of seasonal livestock distribution and land cover description from low-resolution satellite images.

Hosts distribution: mainly in space

On the landscape scale, the relationship between seasonal livestock distribution and resources has been explored in depth (16). A land cover map was produced through supervised classification of a Landsat 7 image. Monthly time-series of normalized difference vegetation index (NDVI) values from Spot vegetation were correlated with grazing resources. Data from field censuses of livestock at different times of the year and results of the typology of the various breeding systems were used to predict the distribution of livestock based on land cover and landscape units. Using 1-km resolution grids of the NDVI series, livestock distribution during the rainy season was predicted with an accuracy of 70%. As a result, one map is available for the entire season, with a low temporal resolution (4 months) but a relatively high spatial resolution (1 km).

Vector dynamics: mainly in time

Different species of mosquitoes may act as vectors for Rift Valley fever. At the beginning of the rainy season, *Aedes vexans* is thought to play a major role in the persistence of the virus during dry years: virus has been isolated from local populations (7) and vertical transmission is suspected (29). The seasonal dynamics of *Ae. vexans*, following the first rainfall, has recently been described in detail (14). In a two-year follow-up study which included daily mosquito catches and rainfall records, Mondet *et al.* (14) demonstrated that *Ae. vexans*

populations are abundant at the very beginning of the rainy season when the majority of quiescent eggs are flooded. In addition, hatched females lay eggs on the wet soil. These eggs undergo dormancy as the water level falls. Seven days of dormancy without flooding are necessary for embryogenesis and then these eggs hatch after subsequent rainfall, as illustrated by the presence of high proportions of nulliparous females. Thus, several generations of adults can simultaneously occur during the same rainy season.

Quantitative estimates of rainfall over sub-Saharan Africa can be derived from Meteosat data capturing the cloud top temperature (cold cloud duration or 'CCD'). These data are provided by the FAO Artemis system (Africa Real-Time Environmental Monitoring System) (5) on a decadal temporal base and an approximate 8 km pixel. The potential of such maps to capture local rainfall patterns and the subsequent development of *Ae. vexans* populations has been explored (Fig. 2) (S. de la Rocque, unpublished data). Most of the emergence of both nulliparous and parous females can be related to successive dry and rainy CCD events. The succession of dry and wet CCD events is the key element that explains the emergence of mosquitoes; the capture of a decadal summary of CCD is an efficient way of monitoring the potential emergence of *Aedes* and subsequently the presence of Rift Valley fever virus, at least during the initial weeks of the rainy season. As noted earlier, other species of mosquitoes (whose eggs need permanent water to develop) are also involved in the transmission of Rift Valley fever later in the season. As a result, times-series of low spatial resolution (7.6×7.6 km²) but quite high time-resolution (10 days) maps need to be monitored.

Discussion and conclusion

This example illustrates the major problem of scales in time and space, using one of the most important parameters in the disease risk assessment. The challenge for the epidemiologist is to quantify the interface

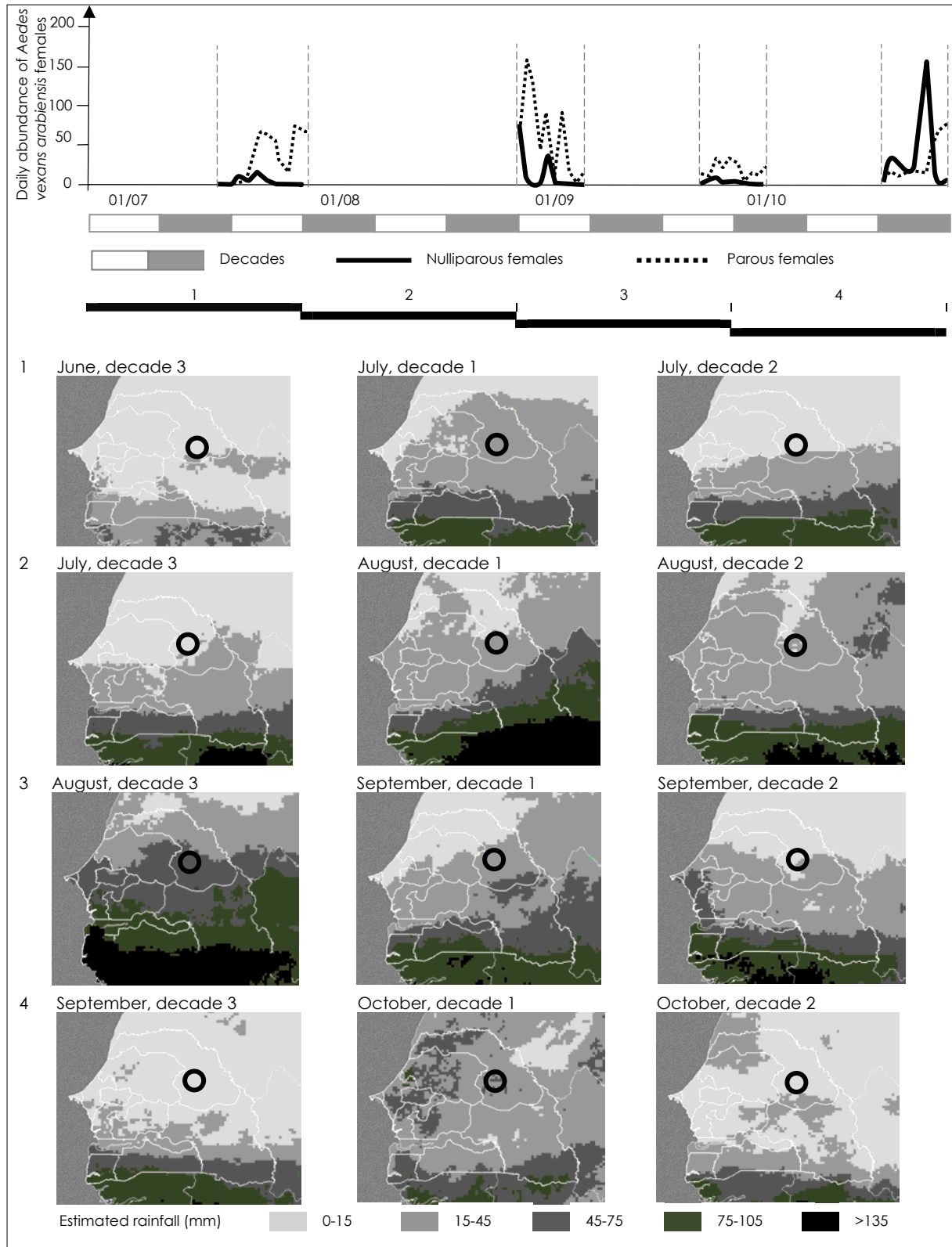


Figure 2
 Daily abundance of *Aedes vexans* females (nulliparous and parous) in Barkedji, Ferlo region, Senegal during the 2002 rainy season and estimated rainfall (in mm) per 10 days (decades)
 Hatching of *Aedes vexans* females follows significant rainfall, but a minimum period of dryness is required for embryogenesis in the eggs
 The succession of flooding and drying of the breeding sites is the key parameter for the emergence of new potentially infected generations (nulliparous females)
 Entomological data from Mondet *et al.* (15); estimated rainfall from Artemis, FAO (5)

between mosquitoes dispersing a few hundred metres around typical habitats and hosts moving hundreds of kilometres each year. The *rendez vous* in key areas and during key seasons has to be captured and one method (at least for the spatial scale issue) is the projection in a grid of patterns at the lower pixel size. However, the temporal scales remain unresolved, as one image per season is provided for the host whilst mosquito dynamics should be followed at a decadal time resolution. Different methods of time-series analysis are currently being explored.

From the conceptual model, it appears that many other interactions between thematic boxes and parameters have to be explored, based on a fine description of the ecological processes involved in any specific ecosystem. At a latter stage, the conceptual model should be joined with a multi-agent model where any change in any of the boxes could be simulated.

Such an approach, based on the identification of indicators, is critical for disease monitoring and predicting the impact of environmental changes. Results could be of great benefit to users, such as those international organisations responsible for public and veterinary health, wishing to develop disease information, management and early warning systems. This type of research is part of the current EDEN (emerging diseases in a changing European environment) Integrated Project (www.eden-fp6project.net) which aims to identify, evaluate and catalogue European ecosystems and environmental conditions linked to global change that can influence the spatial and temporal distribution and dynamics of human

pathogenic agents. EDEN uses geographic information system (GIS) analysis to detect environmental changes through multi-temporal image processing, spatial and mathematical modelling and risk mapping for the development of generic methods, tools and skills, such as predictive emergence and spread models, early warning, surveillance and monitoring tools and scenarios.

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