

Review

Vector-borne parasitic diseases: new trends in data collection and risk assessment

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Abstract

Climates and topography effectively restrict vector-borne infections to certain geographical areas, a clear illustration of how strongly the spatial distributions of these diseases rely on environmental factors. This is hardly a new revelation, but just a few years back, without the support of computer-assisted collection and handling of data, we were far less able to grasp the full picture. Fortunately climate data collection by Remote Sensing (RS) by earth-observing satellites, a technology particularly well suited to pinpointing constraining endemic factors, has not only become affordable but also reached a high degree of sophistication. Meanwhile, geographical information systems (GIS) and global positioning systems (GPS) permit spatial information of great accuracy as well as digitalization of collected data on the spot enabling visualization of the data in relation to physical maps and facilitating comparisons of the results of longitudinal investigations. Adoption of these technologies at the national level promotes intersectoral collaboration and promises improved planning and management in the control of endemic diseases. Applications in areas such as malaria, onchocerciasis, lymphatic filariasis, trypanosomiasis and schistosomiasis are briefly reviewed. Reports in the fields of the former two diseases dominate the literature, while information is lagging with regard to the others. The need for a broadening of the GIS approach is emphasized with the aim of rejuvenating the dynamic aspect of epidemiological studies. © 2001 Elsevier Science B.V. All rights reserved.

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1. Introduction

Humans depend on guiding representations of the land they inhabit, and physical maps probably

go as far back in history as the first settlements. Map-making has come a long way since then, and the modern equivalents no longer exist only for simple orientation needs but serve a multitude of specific economic, sociological, and military purposes. The distribution of various diseases is now generally well described, and accurate illustrations

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of endemic areas are readily available in textbooks. Thanks to the foresight and effort at WHO by the late Dr K.E. Mott, the emphasis, previously focused at the departmental and national level, was broadened in the early 1980s. After many years of work, his idea of consolidating all available information on schistosomiasis transmission resulted in the publication of the Atlas of the Global Distribution of Schistosomiasis in 1987 (Doumenge et al., 1987). The Atlas is still useful, but it has never been updated or reprinted, as it appeared at the turning point between traditional distribution of printed maps and the rapidly growing field of computer-assisted mapping. Control programmes must always have access to the latest data, and their task of epidemiological mapping has been facilitated since updated material became immediately available to anybody with a computer and Internet connection. Meanwhile, remote sensing (RS) by earth-observing satellites has become increasingly important for the analysis and integration of various data. The heterogeneity of climates and landscapes determines the distribution of vector-borne diseases, and the new technologies, through their propensity for powerful data collection and data handling, are particularly well suited to pinpointing constraining factors. Meanwhile, geographical information systems (GIS) and global positioning systems (GPS) have strengthened data collection in the field and the gauging of spatial distribution of infected people. As a consequence, the epidemiology of vector-borne infections is undergoing a rapid change with GIS, GPS and RS providing the major impetus. The possibility of displaying almost limitless numbers and values of the vectors and tensors that make up the full picture of transmission patterns, incorporating spatial as well as temporal aspects of the epidemiological situation, provides a new freedom. For example, topography, temperatures of water bodies and land, rainfall, and other environmental parameters can be presented in a multi-layered fashion or the data sets merged into probability maps of vector distribution that directly depict the risk for human infection.

GIS has proved extremely useful for gauging the extent of various infections in the world. For

example, WHO and United Nations Children's Fund (UNICEF) have introduced "HealthMapper" (1999), a simplified GIS-supported database management tool that facilitates the collection, storage, retrieval and analysis of data for Public Health purposes, and Kitron (2000) has suggested establishing "risk maps", i.e. outcomes of transmission models in which environmental information has been merged with data from the fields of epidemiology and vector biology. The falling costs of electronic equipment coinciding with its rising performance make this a realistic goal. For example, the Rapid Epidemiological Mapping of Onchocerciasis (REMO), promoted by TDR as a platform for the African Programme for Onchocerciasis Control (APOC), has proved invaluable for practical control efforts. This is only the first practical application of GIS in a major control programme, and successful examples already exist for a number of endemic diseases, some of which are outlined below.

1.1. Onchocerciasis and lymphatic filariasis

The REMO approach was first field tested in the early 1990s in forest and savannah areas of Cameroon carrying a high risk of onchocerciasis (Ngoumou et al., 1994). The method proved so effective in mapping the prevalence and distribution of onchocerciasis in all areas studied that it was adapted as a model in the design of national onchocerciasis control programmes. Later, the authors participated in a larger study group using REMO as the basis for the repartition of onchocerciasis after analysing estimates of the prevalence of infection in local communities in Cameroon provided by (REA) interventions. A map, based on previous epidemiological data, clinico-parasitological surveys and results of Rapid Epidemiological Assessment (REA), was produced. As predicted in the earlier paper, the approach allowed the main onchocerciasis foci in the country to be accurately delineated. In addition, several new foci were discovered. The total population at risk was estimated by combining the epidemiological results with demographical data available from an administrative census by Mace et al. (1997)

In Nigeria, REA teams selected sample villages based on ordinary topographical maps and carried out a survey in which subjects were randomly picked and examined for the presence of palpable skin nodules (Gemade et al., 1998). The results, presented as percentage prevalences using GIS, were cross-validated before being used by APOC to prioritize proposals in a rational and effective manner. Abanobi (1999) validated the usefulness of REMO in Anambra state, Nigeria, while Katarbarwa et al. (2000) investigated its suitability for mapping of onchocerciasis in foci in rural Uganda where *S. neavei* sl is the primary vector. It was concluded that the REMO approach is not only useful for the identification of communities requiring mass treatment with ivermectin but vital to the goals and activities of APOC.

When the World Health Assembly agreed to target lymphatic filariasis for global eradication in 1997, it was apparent that detailed information on its geographical distribution would first need to be produced. Lindsay and Thomas (2000) had estimated populations in Africa at risk for the disease and found that sites with microfilaraemic patients could be predicted with a good degree of accuracy by consulting recorded climate variables. Using a GIS-based approach to map the risk for lymphatic filariasis infection across Africa, the authors were able to report results that compared favourably with expert opinion. Further validation showed that the model correctly predicted 88% of infection foci, and, by adding results obtained by a similar procedure carried out in Egypt, they concluded that around 420 million people were exposed to *Filaria* infection in Africa in the year 2000. The model provided a valuable risk map but did not predict the actual distribution of the disease in sufficient detail to allow planning of mass treatment programmes. In order to assist the WHO move towards eradication, TDR embarked on an initiative aiming to producing a tool suitable for large-scale applications by control programmes. A method for the Rapid Geographic Assessment of Bancroftian Filariasis (RAGFIL) was developed and successfully field tested in Ghana, India, Myanmar and Tanzania (Gyapong and Remme, submitted for publication). Based on these results, a rapid mapping

procedure was designed that is currently being applied to map the distribution of lymphatic filariasis throughout Africa. In terms of organization and manpower employed, this is probably the largest mapping exercise of a vector-borne disease to date.

Operational guidelines for rapid mapping of both onchocerciasis and Bancroftian lymphatic filariasis are available from WHO in the form of a series of pamphlets (WHO, 1993, 1998, 1998a, 1999, 2000).

1.2. Malaria and dengue

Before the advent of modern approaches, the true extent of malaria endemic areas was only vaguely known, and available distribution maps could not be compared in a straightforward manner. Clearly, GIS improves the representation of epidemiological data, and much progress has been made. For example, the South African Medical Research Council (SAMRC) and the Wellcome Trust have with support from the International Development Research Centre (IDRC), established a GIS-based approach to Mapping Malaria Risk in Africa (MARA, 1998). This project is an excellent example of an approach that should be useful also for other vector-borne infections. The MARA project includes statistical modelling, climatological charts and field work to produce a state-of-the-art map of malaria risk in Africa. The information is regularly updated and made available via a non-restricted web site.

Craig et al. (1999) has proposed to define the distribution of malaria transmission numerically based on biological constraints of climate on parasite and vector development. The model compares well with field data and historical maps and provides a basis for predicting the impact of climate changes. Further work along these lines, adding population, morbidity and mortality data, is leading to the creation of a powerful tool for malaria control. Hay et al. (2000) reviewed the progress and current status of RS and GIS with reference to *Plasmodium falciparum* malaria in sub-Saharan Africa. Struck by the paucity of accurate and recent information on the nature and extent of the disease, they focused on the ecology

of *P. falciparum* and its major anopheline vectors to provide a background for the study of transmission processes and their environmental correlates. The evidence presented confirms that the outcomes of clinical infection are strongly determined by the intensity of parasite exposure. In Kenya, Omumbo et al. (1998) noted the limited use of epidemiological maps in malaria control, which they felt was due to the lack of spatially defined data and a clear understanding of how epidemiological variables relate to disease outcome. To show the way forward, the authors abstracted parasitological data from available cross-sectional surveys and defined them spatially. Based on GIS and a combination of parasitological, geographical, demographic and climatic data, the risk of *P. falciparum* infection in Kenyan children was estimated as low for 2.9 million, stable but low for another 1.3 million, moderate for 3.0 million and high for 0.8 million.

Srivastava et al. (1999) studied villages with unstable malaria in India using topographical and satellite-generated maps and ArcInfo software. By sequentially integrating environmental parameters such as hydro-geomorphology, water-table levels, water quality, soil type, relief and irrigation channels, a composite map featuring 13 stratification classes appeared. Twelve of these fell in non-irrigated tracts exhibiting 95% matching of areas of high receptivity, while the 13th turned out to be an irrigated area with poor matching, but the ground verification established a low receptivity. The study established that the incidence of malaria is mainly related to the water table, soil type, irrigation and water quality. Hu et al. (1998) attempted to apply GIS and a multiple regression analysis for the determination of the nature and extent of factors influencing malaria transmission in Yunnan Province, China. When county-based data covering the period 1990–1996 were collected and analysed, it was found that the combined effects of the physical environment, the presence of compatible vectors and the degree of population mobility influence the malaria situation most. Indaratna et al. (1998) applied GIS to analyse disease and economic resources with reference to dengue fever and malaria in Thailand examining per capita gross provincial product and health-care resources

in relation to geographic distribution. The authors argue that useful inferences can be drawn for overall planning at both national and multi-country levels but admit that the collection of socio-economic and disease data by different means and in different time frames limits the dynamic interpolation of the two data sets.

1.3. African trypanosomiasis

In spite of the fact that this disease lends itself well to environmental analysis, comparatively few applications exist (notwithstanding early observations by Rogers and Williams (1993) that the spatial distribution of the disease is best studied by focusing on vector requirements using data from the National Oceanic Atmospheric Administration (NOAA) series of meteorological satellites). These authors monitored insect characteristics in various African settings. In Zimbabwe, their conclusion was that a single climatic variable, the maximum of the mean monthly temperature, predicts the pre-rinderpest distribution of tsetse flies with a high probability and that additional variables do not improve this figure much. In Kenya and Tanzania, however, they found that the maximum of the mean monthly Normalised Difference Vegetation Index (NDVI), is the single most important variable. This type of analysis constitutes an excellent guide towards reliable interpretations of the distributional limits of vectors. Like the model created by Craig et al. (1999) referred to above, it can also be used for the prediction of the impact of global warming. According to their model, mean temperature increases as small as 1°C would make large currently non-endemic areas climatically suitable for transmission of trypanosomiasis. Mott et al. (1995) realized the potential of this approach, emphasized the need to understand the environmental factors, and predicted that geographical representation and spatial analysis using databases from different sectors would provide vastly improved control of tropical diseases. They stated that the focal nature of the transmission of vector-borne diseases, recognition of the importance of animal reservoirs, and increasing use of GIS would open a new perspective.

1.4. Leishmaniasis

Recent epidemics of visceral leishmaniasis in various parts of the world, particularly in Sudan, underline the need to identify the limiting factors. Elnaiem et al. (1998) investigated the environmental determinants of the distribution of *Phlebotomus orientalis*, the dominant vector in the wooded areas of the central savannah belt of Sudan. They collected sandflies at a number of sites and compared the findings with the local ecology, adding data such as rainfall, minimum and maximum temperatures, soil class, vegetation and land-surface-temperature indices, available from the NOAA satellites series. Analysing this information, sites positive for *P. orientalis* were found to have significantly higher annual mean maximum and minimum daily temperatures than the negative sites. The annual mean maximum NDVI value was also found to be significantly higher in these sites than in other locations where no *P. orientalis* were found. Continuing this work to identify variables associated with the vector, Thomson et al. (1999) estimated the probability of the presence of the vector at collecting sites. The logistic regression model used indicated the mean annual maximum daily temperature and soil type as the two single most important determinants of *P. orientalis* distribution.

Cross et al. (1996) was interested in the distribution of *Leishmania* in the Middle East from the military point of view since leishmaniasis was a common infection there during World War II. *P. papatasi*, the common vector in the Persian Gulf, requires specific temperatures and relative humidity, so the NDVI levels were determined at all weather stations using Advanced Very High Resolution Radiometer (AVHRR) satellites. By the probability of occurrence based on the results of the frequency of NDVI levels, a map of the probable distribution of *P. papatasi* was generated. This map made it possible to expand the analysis to areas where there were no weather stations, and from where no information had been reported.

1.5. Schistosomiasis and intestinal helminth infections

Intestinal helminths are the most common of all human parasites, and schistosomiasis is second only to malaria in the public health impact of vector-borne tropical diseases. Reported estimates of mortality are low for helminth infections, but schistosomiasis is probably responsible for hundreds of thousands of deaths annually. Although these numbers are comparatively low, the latter disease produces chronic debilitating symptoms in large numbers of people. The magnitude of the problem is evident from the figures available from WHO:

More than 600 million people in 74 countries at risk

More than 200 millions infected

About 20 million severely ill and 120 million with symptoms.

The large areas that are endemic for schistosomiasis, and their continuous change, is one strong reason for applying the new tools without delay. On the one hand, the development of water resources and population displacements have spread the disease to previously non-endemic areas and risk spreading it to others. On the other hand, many countries have succeeded in reducing morbidity and, in some cases, even eradicated transmission in parts of their territories. More than 85% of all schistosomiasis occurs in Sub-Saharan Africa, while Brazil, Venezuela and many Caribbean islands in Latin America, Egypt, Morocco and Tunisia in North Africa, and China and the Philippines in the Far East have been very successful in controlling the disease. In this connection, it should not be forgotten that the vectors continue to play a central epidemiological role, even if there is no transmission. Uninfected snails may remain in the area of interrupted transmission (Tanaka and Tsuji, 1997), they may disappear (Giboda et al., 1997) or compatible vectors may migrate from neighbouring water bodies. The situation can also change rapidly if non-local schistosome strains compatible with local snails are imported (Attwood et al., 1997).

Studies using satellites for schistosomiasis were initiated in the early 1990s. Malone et al. (1994) reported on applying data from polar orbiting environmental satellites to the study of schistosomiasis distribution of in Egypt. They used an AVHRR instrument to produce temperature maximum, temperature minimum, and diurnal temperature difference maps of the lower Nile River valley at a spatial resolution of 1.1 km. They interpreted AVHRR thermal difference maps, obtained as a reflection of regional hydrologic conditions, and found that these can be used to predict the environmental risk for schistosomiasis. Kloos et al. (1998) studied geographical patterns of schistosomiasis and water-contact behaviour examining the results of spatial water contact/schistosomiasis studies in an Egyptian, Kenyan and Brazilian community. They applied traditional cartographic and statistical methods, and GIS in one. They observed advantages of the used GIS approach and recommended further spatial studies on the transmission and control of schistosomiasis.

Brooker and Michael (2000) reviewed the early applications of GIS for helminth infections and concluded that such tools can serve as effective tools for data collection and handling. They also emphasized their use for modelling spatial distribution of infection in relation to environmental variables and their potential as tools for parasite control. In a communication with a similar focus Brooker et al. (2000) points out the value and limitations of empirical mapping suggesting that progress is needed and describing their approach to mapping helminth infections in sub-Saharan Africa. Lwambo et al. (1999) discuss patterns of hookworm infection and schistosomiasis in schoolchildren in a district near Lake Victoria in Tanzania. Employing GIS made it clear that *S. mansoni* infection was highly prevalent only along the shore of Lake Victoria, whilst *S. haematobium* was homogeneously prevalent everywhere else except at the lakeshore. Hookworm and *S. mansoni* occurred more frequently as multiple infections with other helminths than as single-species infections. The prevalences of *S. haematobium* and hookworm

tended to be normally distributed, while the distribution of *S. mansoni* was markedly skewed such that only 17% of schools had a prevalence greater than 20%. An inverse association between *S. mansoni* and *S. haematobium* was observed. The results imply that joint treatment for hookworm infection and schistosomiasis would be beneficial throughout the district.

2. Conclusions

GIS and RS are increasingly used for the study of spatial and temporal patterns of vector-borne diseases. While WHO has provided the lead in introducing GIS in areas such as onchocerciasis and lymphatic filariasis, other potential applications lag. Despite the recognition that a stronger emphasis on these tools would have profound effects on parasite population dynamics and almost surely contribute to improve control programmes, a broadening of studies relying on GIS/RS has only recently started. The value of a geographical/environmental perspective is obvious if one considers the advantages of easy access to detailed maps, which can be instantly updated over the Internet. With the possible exception of onchocerciasis, globally covering details of the spatial distribution are missing for all parasitic infections, and recommendations for the routine use of GIS-based health or risk maps in national control programs are lacking. To that end, a concerted effort involving a realistic plan of promoting application of the new technology, research collaboration and data sharing must be urgently developed. The new multi-layered cartographic approaches can play a major role in focusing research and helping to guide control activities in the right direction. In the field of schistosomiasis, particularly, the development of GIS/RS models for predicting health impacts of climate variations and water-development projects, such as mega-dams and irrigation schemes, could contribute to better documentation, facilitating decisions that could pre-empt increased transmission and potential epidemics in previously non-endemic areas.

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