Applied Geography 48 (2014) 1–7

Contents lists available at ScienceDirect

Applied Geography

journal homepage: www.elsevier.com/locate/apgeog

Participatory risk mapping of malaria vector exposure in northern South America using environmental and population data

D.O. Fuller [a,*], A. Troyo [b], T.O. Alimi [c], J.C. Beier [d]

[a] Department of Geography and Regional Studies, University of Miami, 1000 Memorial Drive, Coral Gables, FL 33124-2221, USA
[b] Centro de Investigación en Enfermedades Tropicales, Facultad de Microbiología, Universidad de Costa Rica, San José, Costa Rica
[c] Abess Center for Ecosystem Science and Policy, University of Miami, Coral Gables, FL, USA
[d] Department of Public Health Sciences, Miller School of Medicine, University of Miami, Miami, FL, USA

Keywords:
Participatory GIS
Malaria
Risk mapping
Multi-criteria decision analysis
Anopheles species

ABSTRACT

Malaria elimination remains a major public health challenge in many tropical regions, including large areas of northern South America. In this study, we present a new high spatial resolution (90 × 90 m) risk map for Colombia and surrounding areas based on environmental and human population data. The map was created through a participatory multi-criteria decision analysis in which expert opinion was solicited to determine key environmental and population risk factors, different fuzzy functions to standardize risk factor inputs, and variable factor weights to combine risk factors in a geographic information system. The new risk map was compared to a map of malaria cases in which cases were aggregated to the municipio (municipality) level. The relationship between mean municipio risk scores and total cases by muncipio showed a weak correlation. However, the relationship between pixel-level risk scores and vector occurrence points for two dominant vector species, *Anopheles albimanus* and *Anopheles darlingi*, was significantly different ($p < 0.05$) from a random point distribution, as was a pooled point distribution for these two vector species and *Anopheles nuneztovari*. Thus, we conclude that the new risk map based on expert opinion provides an accurate spatial representation of risk of potential vector exposure rather than malaria transmission as shown by the pattern of malaria cases, and therefore it may be used to inform public health authorities as to where vector control measures should be prioritized to limit human-vector contact in future malaria outbreaks.

Introduction

Malaria represents a major global health threat that resulted in some 219 million cases and 660,000 deaths in 2010 (WHO, 2012). While most mortality and morbidity associated with the disease occur in Sub-Saharan Africa, parts of the Neotropics experience significant case burdens, particularly in the Amazon Basin and western Colombia (Herrera et al., 2012; Oliveira-Ferreira, Lacerda, Brasil, Tauil, & Daniel-Ribeiro, 2010). Unlike Africa, where the principal malaria parasite is *Plasmodium falciparum*, most cases in Latin America and the Caribbean involve infection by *Plasmodium vivax*, which may produce relapsing infections in some patients. All *Plasmodium* parasites are transmitted to humans through the bite of several species of mosquitoes in the genus *Anopheles* and some dominant species are highly effective in transmitting malaria parasites (Sinka et al., 2010). While application of control measures aimed at limiting exposure to vectors such as use of insecticide treated nets (ITNs), indoor residual spraying (IRS), and early detection, diagnosis, and treatment have reduced malaria incidence in the region over the past decade, elimination of malaria remains elusive as uneven application of control measures may limit their effectiveness in reducing transmission (Ulrich, Naranjo, Alimi, Mueller, & Beier, 2013). Further, anopheline vectors may develop insecticide resistance or behaviors that lead them to avoid control measures, thus making elimination in some areas extremely challenging (Govella, Chacki, & Killeen, 2013).

In large parts of northern South America, transmission of malaria is considered low and unstable, thus malaria is generally hypoendemic and *Plasmodium* infection rates of anophelines are typically low relative to parts of Africa where vectors such as *Anopheles gambiae* are involved in transmission (Arévalo-Herrera et al., 2012). In addition, vectors and human populations vary in space and time, so that outbreaks may occur, especially in frontier agricultural areas or where extractive activities such as mining and logging take place (Caldas de Castro, Monte-Mór, Sawyer, & Singer, 2006; da Silva-Nunes et al., 2012). Nevertheless, some areas are

---

* Corresponding author. Tel.: +1 305 284 6695.
E-mail address: dofuller@miami.edu (D.O. Fuller).

0143-6228/$ – see front matter © 2014 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.apgeog.2014.01.002

prone to malaria endemicity because they possess a confluence of socioeconomic and environmental factors such as slow-flowing water bodies, wetlands, frontier settlements, resource-extractive activities, and warm-humid climates that favor mosquito breeding and contact between vectors and humans. Over the past decade, data on such environmentally based risk factors have become publically available for most parts of the globe, such that they may be incorporated into decision-support algorithms within geographic information systems (GIS) and combined in various ways to depict composite risk of diseases such as malaria that have strong environmental components. However, many different methods exist for modeling and mapping disease risk, including probabilistic models, deterministic models, and knowledge-based approaches that rely on a combination of expert opinion (EO) and statistics. The choice of approach is generally determined by the availability of georeferenced disease data (Stevens & Pfeiffer, 2011), which is often limited in developing countries either to small localities where intensive field studies have taken place or to national-level data, which are often aggregated to variably-sized political units like states and counties. Spatial representation of risk using limited disease data may result in maps that are highly generalized, contain artifacts relating to human-defined boundaries (i.e., political units), and broad risk categories (e.g., high risk, moderate risk, low risk, etc.). For example, the Pan American Health Organization (PAHO) produced a malaria risk map for South America that embodies all these characteristics, including highly generalized polygons that follow international borders along with broad risk categorization (da Silva-Nunes et al., 2012). Thus, given the public availability of high-resolution environmental data, there is great potential and need to produce more highly detailed maps that depict spatial patterns of malaria risk consistent with landscape features that may influence vector ecology and human activities.

With the advent of high-resolution environmental data sets originating from orbital platforms, such as the Shuttle Radar Topography Mission (SRTM) global elevation data, highly detailed environmental information now exists for discerning landscape-level spatial patterns that influence disease risk. However, at national-to-regional scales, detailed georeferenced data on location of transmission in northern South America is generally unavailable in part because patients can only speculate as to where they were bitten by infected anophelines, geocoding of patient addresses is limited by low availability of street-level GIS data, and ethics policies may restrict data to ensure patient confidentiality. And, even if available, data on patient addresses may not represent the location of transmission (Wesolowski et al., 2012). Although georeferenced malaria data for Colombia and surrounding countries are generally restricted or unavailable, environmental data are relatively abundant, thus we elected to use a knowledge-based approach with EO known as multi-criteria decision analysis (MCDA). MCDA provides a way to combine different environmental covariates (e.g., elevation, hydrography, population density, etc.) to evaluate disease risk. Further, EO is becoming a more widely used input to disease modeling as a way to incorporate insights of epidemiologists, vector biologists, and other public health specialists in the decision-making process (Hay et al., 2013; Sinka et al., 2010). MCDA is a preferred method for participatory problem solving as it provides a means for expert interaction, it is computationally fast and easy to understand, and involves a mix of statistical methods and human intuition (Stevens & Pfeiffer, 2011). For example, MCDA methods have been used to predict suitable areas for Rift Valley Fever in Africa (Clements, Pfeiffer, & Martin, 2006) and for prioritizing areas for malaria vector control in Madagascar (Rakotomanana et al., 2007). Moreover, because MCDA methods produce data on a continuous scale, small differences in risk can be mapped and parametric statistics may be used to validate MCDA outputs if suitable disease or vector data are available (Stevens & Pfeiffer, 2011). Cell- or pixel based methods such as these also can elucidate gradients and hotspots independent of political boundaries and therefore may provide improved guidance for *post-hoc* analysis that seeks to identify causation associated with model outliers. Thus, the over-arching objective of this research effort was the production of a new high-resolution malaria risk map for Colombia and surrounding areas of Ecuador, Venezuela, Panama, Brazil, and Peru based on EO guidance and participatory decision-support methods implemented with GIS raster-based software.

Materials and methods

Twenty-seven malaria scientists from seven countries (Colombia, Honduras, Guatemala, Panama, Costa Rica, the United States of America, and Peru) participated in a three-day risk mapping workshop in Cali, Colombia, in January 2013. The workshop was designed primarily to incorporate EO on environmental risk factors affecting malaria transmission and vector ecology in the region. Malaria remains problematic in Colombia and therefore we centered our investigation there (Fig. 1). According to the Colombian National Health Service (INS in Spanish), 85% of Colombia's rural land area is below 1600 m elevation, which the INS uses as a rough threshold to assess areas suitable for malaria transmission; i.e., where transmission may potentially occur (INS, 2014). Further, the average annual number of malaria cases reported for 2003–2007 was close to 120,000 with a predominance of *P. vivax* cases (80%) (Arévalo-Herrera et al., 2012). As part of the MCDA mapping exercise, workshop participants were asked about the types of environmental risk factors to include in the analysis, how they should be scaled, and their relative importance. Six risk factors were utilized, including layers depicting possible vector breeding sites (rivers, streams and wetlands), sources of human blood meals (urban areas, population density, and major roads) and thermal gradients and limits controlled by elevation that affect vector distributions (Table 1). To avoid loss of spatial detail from vector GIS data, all coverages were gridded to 90 m spatial resolution and projected to Universal Transverse Mercator projection zone 18 north. We resampled the population data, originally provided at 1000 m resolution, to 90 m using a nearest neighbor algorithm, which was done to maintain consistency with other layers for subsequent analysis. Downscaling gridded data in this way may introduce spatial artifacts in the final map in the form of a coarse-grid square pattern, especially if large weights are assigned to the downscaled layer. Details on the specific data sources and layers are provided in Table 1.

Fuzzy membership functions (FMF) were employed to scale spatial data layers in terms of degree of risk membership along an 8-bit number range (0–255), with the shape of the FMF determined by control points guided by EO. Different fuzzy functions were used, which assume that the degree of risk membership ranges from 0 (no risk) to 255 (full membership). The shape and direction (i.e., increasing or decreasing) of the functions was selected experimentally with control points informed through EO and through previous experience using fuzzy set methodology in different risk mapping applications (Fuller, Meijaard, Christy, & Jessup, 2010; Fuller, Williamson, Jeffe, & James, 2003). Thus, for example, linear decreasing functions were used to scale risk from potential breeding sites such as wetlands and streams by assuming maximum risk proximate to such features and zero risk more than 3000 m from the feature. The elevation layer from SRTM was used as a constraint (or mask) to eliminate areas where risk of transmission is assumed to be vanishingly small in high-elevation areas (>1800 m). As the underlying method relies on fuzzy logic, each cell