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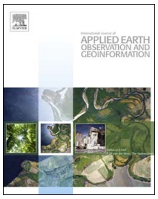

Research Paper

Application of GIS to predict malaria hotspots based on *Anopheles arabiensis* habitat suitability in Southern Africa

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ABSTRACT

Malaria remains a major public health problem and a principal cause of morbidity and mortality in most developing countries. Although malaria still presents health problems, significant successes have been recorded in reducing deaths resulting from the disease. As malaria transmission continues to decline, control interventions will increasingly depend on the ability to define high-risk areas known as malaria hotspots. Therefore, there is urgent need to use geospatial tools such as geographic information system to detect spatial patterns of malaria and delineate disease hot spots for better planning and management. Thus, accurate mapping and prediction of seasonality of malaria hotspots is an important step towards developing strategies for effective malaria control. In this study, we modelled seasonal malaria hotspots as a function of habitat suitability of *Anopheles arabiensis (A. Arabiensis)* as a first step towards predicting likely seasonal malaria hotspots that could provide guidance in targeted malaria control. We used Geographical information system (GIS) and spatial statistic methods to identify seasonal hotspots of malaria cases at the country level. In order to achieve this, we first determined the spatial distribution of seasonal malaria hotspots using the Getis Ord G_i* statistic based on confirmed positive malaria cases recorded at health facilities in Zimbabwe over four years (1996–1999). We then used MAXENT technique to model habitat suitability of *A. arabiensis* from presence data collected from 1990 to 2002 based on bioclimatic variables and altitude. Finally, we used autologistic regression to test the extent to which malaria hotspots can be predicted using *A. arabiensis* habitat suitability. Our results show that *A. arabiensis* habitat suitability consistently and significantly ($p < 0.05$) predicts malaria hotspots from 1996 to 1999. Overall, our results show that malaria hotspots can be predicted using *A. arabiensis* habitat suitability, suggesting the possibility of developing models for malaria early warning based on vector habitat suitability.

1. Introduction

Malaria continues to take a toll in many developing countries where it is endemic through the economic and health burden it imposes on these countries (Alimi et al., 2016). It remains one of the most serious public health problems associated with high morbidity and mortality in the world (Acheson et al., 2015; Dewald et al., 2016). Malaria is a climate-sensitive protozoan disease (Gao et al., 2012; Qayum et al., 2015) caused by parasites of *Plasmodium* genus and transmitted among humans through bites of infected female *Anopheles* mosquitoes (Dambach et al., 2012; Gao et al., 2012; Gwitira et al., 2015; Qayum et al., 2015). An estimated 3.2 billion people remain at risk of malaria world-wide resulting in 438 000 deaths annually (WHO, 2015). Despite significant progress made in reducing malaria morbidity and mortality through intensification of malaria control programs (Carter et al., 2000; Hardy et al., 2015), most developing countries are still at risk of malaria (Hagenlocher and Castro 2015). For instance, an estimated 214 million new cases of malaria were reported in 2015 (WHO, 2015). Therefore, there is urgent need to use geospatial tools such as geographic information system to detect spatial patterns of malaria and delineate disease hot spots for better planning and management (Guerra et al., 2006; Oesterholt et al., 2006; Saxena et al., 2012). Geospatial technology i.e., geographical information system (GIS) combined with spatial statistical tools (Saxena et al., 2012) has been successfully used in modelling malaria risk in different parts of the world (Bautista et al., 2006; Reid et al., 2010). The increasing use of geospatial technologies has been necessitated by the need to locate the foci of infection and predict the potential distribution of diseases (Caprarelli and Fletcher 2014). Thus, it is critical to develop and adopt effective ways to predict malaria occurrence based on geographic information system and spatial statistics, as a preamble to controlling its spread.

The advent of GIS in conjunction with improved spatial statistical

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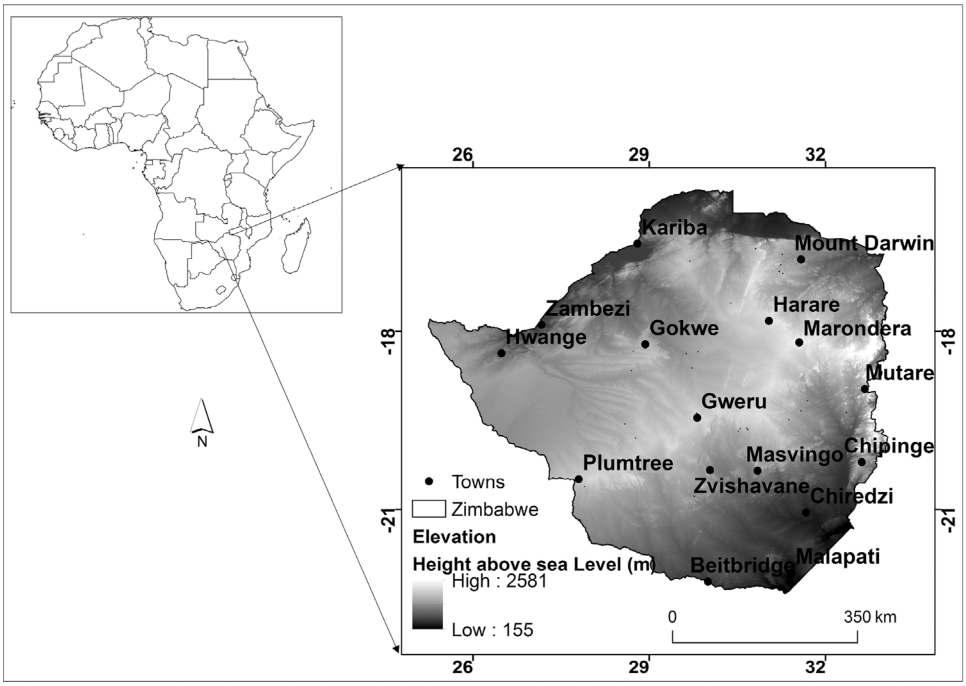

Fig. 1. Location of Zimbabwe. (Coordinates are in geographic based on the WGS84 spheroid).

methods has enhanced our capability to spatially model diseases based on vector habitat suitability as well as based on incidences. For example, niche modelling (Peterson 2006; Moffett et al., 2007; Elith and Leathwick 2009; Phillips et al., 2009), generalised linear mixed models (Bousema et al., 2013), non-linear equations (Lindsay et al., 1998), Ordinary least squares regression (Kulkarni et al., 2010) and Bayesian analytical framework (Mabaso et al., 2005) are among other techniques that have been used to model vector suitability across various spatial scales. Most of the above methods require both presence and absence data which are not always easy to obtain (Stevens and Pfeiffer 2011). Recently MAXENT algorithm has been found to consistently provide reliable species distribution modelling results and retains its effectiveness even with limited species distribution data (Hernandez et al., 2008; Kulkarni et al., 2010). The algorithm has also been successfully and extensively used in the fields of ecology and conservation for modelling species distribution and habitat suitability (Stevens and Pfeiffer 2011). Most of the spatial models on disease modelling have recently been conducted in a GIS environment (Rogers et al., 2002b, 2002a; Levine et al., 2004; Peterson 2006; Zeilhofer et al., 2007; Kulkarni et al., 2010; Alimi et al., 2015; Yoep et al., 2015) although a few have been developed based on vector habitat suitability.

Although considerable GIS-based disease modelling has been conducted based on vector suitability (Laporta et al., 2011; Dhimal et al., 2014), rarely have these studies gone further to relate seasonal malaria hotspots to vector suitability in addition to spatially predicting seasonal malaria hotspots based on vector habitat suitability. The use of vector habitat suitability to explain seasonal malaria hotspots is crucial considering the fact that malaria is a seasonal disease and cases tend to occur in transmission clusters referred to as malaria hotspots (Oesterholt et al., 2006; Mosha et al., 2013). Understanding the seasonality of malaria transmission is not only important in malaria risk mapping but also for timely and spatially targeted malaria control interventions such as indoor residual spraying (Mabaso et al., 2005). A malaria hotspot can therefore be defined as a geographic region in which malaria cases are significantly higher than the average malaria cases in the surrounding areas (Kangoye et al., 2016). Thus, hotspots are likely to fuel transmission to surrounding areas if they remain undetected (Bousema et al., 2012). In this regard, understanding seasonal malaria hotspot dynamics is important given the reliance of malaria prevention and control interventions on knowledge of high-risk areas.

Furthermore, the few studies on detecting malaria hotspots have mainly focused on factors such as land cover, altitude, housing design and roofing material in explaining malaria hotspots (Paaijmans et al., 2009; Dhimal et al., 2014; Hardy et al., 2015). Most of these factors are basically static and thus, may fail to consistently explain seasonal malaria hotspots which are dynamic in nature as they respond to variation in vector habitat suitability. It is therefore reasonable to suggest that by utilising vector habitat suitability developed using dynamic bioclimatic variables derived from climate data, we may obtain reliable prediction of seasonal malaria hotspots over time. In this regard, we assert that the development of methods that allow spatially explicit prediction of seasonal malaria hotspots based on vector habitat suitability may provide a means for targeted malaria control.

In this study, we tested whether and to what extent we can use GIS-based spatial models to predict seasonal malaria hotspots derived from modelled mosquito, specifically *A. arabiensis* habitat suitability in Zimbabwe. In order to accomplish this we first used bioclimatic variables and altitude to predict *A. arabiensis* habitat suitability using a presence-only species distribution model before mapping the suitability surfaces in a GIS. Secondly, we determined the seasonal malaria hotspots based on confirmed positive malaria cases recorded at health facilities in Zimbabwe using geospatial methods. Finally, we used autologistic regression to relate seasonal malaria hotspots to *A. arabiensis* habitat suitability while considering spatial autocorrelation based on data from 1996 to 1999. These years were selected as they have comprehensive and validated data on malaria cases, essential for the development of meaningful spatial malaria hotspot models.

2. Materials and methods

2.1. Study area

The study was conducted in Zimbabwe (Fig. 1). Zimbabwe's altitude varies between 300 m to 2500 m above mean sea level. Mean monthly temperatures vary from 15 °C in July to 24 °C in November while annual rainfall ranges between 400 mm to 1000 mm (http://www.weather.co.zw/). Thus, the climate of Zimbabwe is largely subtropical with distinct seasons moderated by altitude resulting in relatively