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Spatial risk analysis on occurrences and dispersal of *Biomphalaria straminea* in and endemic area for schistosomiasis

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ABSTRACT

Background & objectives: Schistosomiasis is a rural endemic disease that has been expanding to urban and coastal areas in the state of Pernambuco, Brazil. The aim of this study was to characterize the distribution of breeding sites of the causative vector, *Biomphalaria straminea* in an endemic municipality for schistosomiasis and to present the predictive models for occurrences and dispersal of this vector snail to new areas.

Methods: A malacological survey was conducted during January to December 2015 in the municipality of São Lourenço da Mata, Pernambuco, Brazil to identify the breeding sites of *Biomphalaria*. Faecal contamination was determined by means of the Colitag™ diagnostic kit. Rainfall data were collected, and correlated with snail distribution data. Kernel density estimation, kriging and maximum entropy (MaxEnt) modeling were used for spatial data analysis, by means of the spatial analysis software packages.

Results: Out of the 130 demarcated collection points, 64 were classified as breeding sites for *B. straminea.* A total of 5,250 snails were collected from these sites. Among these 64 sites, four were considered as foci of schistosomiasis transmission and 54 as potential transmission foci. An inverse relationship between rainfall and snail density was observed. Kernel spatial analysis identified three areas at higher risk of snail occurrence, which were also the areas of highest faecal contamination and included two transmission foci. Kriging and MaxEnt modeling simulated the scenarios obtained through the kernel analyses.

Interpretation & conclusion: Use of geostatistical tools (Kriging and MaxEnt) is efficient for identifying areas at risk and for estimating the dispersal of *Biomphalaria* species across the study area. Occurrence of *B. straminea* in the study area is influenced by the rainy season, as it becomes more abundant during the period immediately after the rainy season, increasing the risk of dispersal and the appearance of new transmission foci.

Key words *Biomphalaria straminea;* GIS; kriging; MaxEnt modeling; *Schistosoma mansoni;* spatial risk analysis

INTRODUCTION

Mansonian schistosomiasis is a chronic disease caused by the helminth *Schistosoma mansoni*. It is a hemoparasite with a heteroxenic life cycle, where human act as a definitive host and a freshwater mollusk of the genus *Biomphalaria* as an intermediate host. Schistosomiasis is endemic in the state of Pernambuco and presents higher rates of human infections than the other states in the northeastern region of Brazil. The mean prevalence rates recorded between 2005 and 2010 were ≥ 20%. According to data from the State Health Department, 60.4% of the municipalities in the Zona da Mata ("forest zone") of Pernambuco (n = 26) presented high rate of schistosomiasis infection. These areas have been defined under priority for actions within SANAR—The programme for dealing with neglected diseases in the state of Pernambuco[1]. The municipality of São Lourenço da Mata lies within this zone and has been registering high prevalence rates for this parasitosis for many decades[2]. Though occurrence of two species of *Biomphalaria* (*B. glabrata* and *B. straminea*) have been reported in the state of Pernambuco, only *B. straminea* is reported from the municipality, as an intermediate host for *S. mansoni*. This snail is considered as a weak biological vector because of its low susceptibility to infection by *S. mansoni*[3]. None-the-less, this municipality presents significant prevalence of Manson's schistosomiasis because of its adverse social and sanitation conditions[1].

In an attempt to gain better understanding of the processes related to endemization of schistosomiasis in certain areas, biological factors associated with the intermediate host and the environmental aspects of transmission foci have increasingly been studied. An earlier study found that, influence of biotic and abiotic characteristics, such as climatic, physical and chemical factors, affect the survival and development of snail and *Schistosoma* populations[4]. The study also indicated that temperature and rainfall were the most important determinants of snail population dynamics.

Furthermore, environmental changes caused by disorganised occupation of geographical spaces may be implicated for adaptation among the snails and geographical expansion of schistosomiasis. As an example of this adaptation, the way in which these snails make use of the sediments coming from sewage as a food source, instead of aquatic plants can be cited[5]. This facilitates their establishment in new environments characterized by lack of basic sanitation[6]. A scenario of this nature was analyzed and described in Porto de Galinhas, Pernambuco, Brazil, over the last decade. In this locality, disorganised occupation and anthropic actions on natural environment have favoured the establishment and maintenance of schistosomiasis[7–8].

Analysis on all of these conditioning factors that relate to reproduction of this vector provides valuable data in the transmission knowledge of schistosomiasis. However, these data need to be analyzed together using tools that can integrate the dataset from the perspective of constructing health indicators and epidemiological landscapes that characterize the real situation of schistosomiasis in such locations. This is important in relation to São Lourenço da Mata, given that many environmental changes occurred in this region due to urban growth, increased real estate development and construction of the soccer stadium that hosted the FIFA world cup in 2014. Construction of this stadium was also responsible for increase in transit of people in the municipality on match days.

In this context, spatial data analysis has been used on a large-scale within epidemiology studies. Among several spatial data analysis methods, kernel density estimation has been one of the most widely used methods[9]. This technique makes it possible to construct risk maps, which are fundamental of planning actions of controlling environmental harm.

Drawing up risk maps and analysis on the findings have been used to construct predictive models for schistosomiasis around the world[10]. These predictive models aim to provide analyses on the situation and forecasting the epidemiological and spatial dimensions of a given disease, through diagnosing the risk factors implicated. Several methods can be used to spatialize and predict occurrences of schistosomiasis, such as kernel analysis[11], regression with spatial weighting[12], kriging[13–14] and maximum entropy modeling (MaxEnt), *i.e.* species distribution modeling[15].

It is evident that the current methods used by healthcare services for diagnosing and controlling areas at risk of schistosomiasis transmission are ineffective, given that this parasitic disease has been expanding geographically. Therefore, the aim of this study was to present predictive models for occurrences and dispersal of the vector snails to new areas of the São Lourenço da Mata municipality. Within this perspective, the present study made use of several spatial data analysis tools to represent and analyze the current epidemiological situation of schistosomiasis in the municipality.

MATERIAL & METHODS

Study area

This study was conducted in the municipality of São Lourenço da Mata, Pernambuco, which is located at latitude 08°00' 08"S and longitude 35°01'06"W (Fig. 1). The municipality has an area of 262,106 km^2 and is located within the Atlantic Forest biome[16]. The Capibaribe river runs through the municipality and its manancials serve as natural breeding site for *Biomphalaria* snails, which, through their contamination by human waste, become transmission foci of schistosomiasis. All the water resources identified in Fig. 1 (drainage) are affluents or effluents of this river.

The study area was surveyed in December 2014. A Garmin GPS receiver (eTrex Vista Cx) was used to georeference all the data collection points, *i.e.* water bodies with or without presence of snails (ditches, streams, rainwater drainage channels and sewage channels). All water bodies that contained snails of the genus *Biomphalaria* were considered "breeding sites". Those that contained

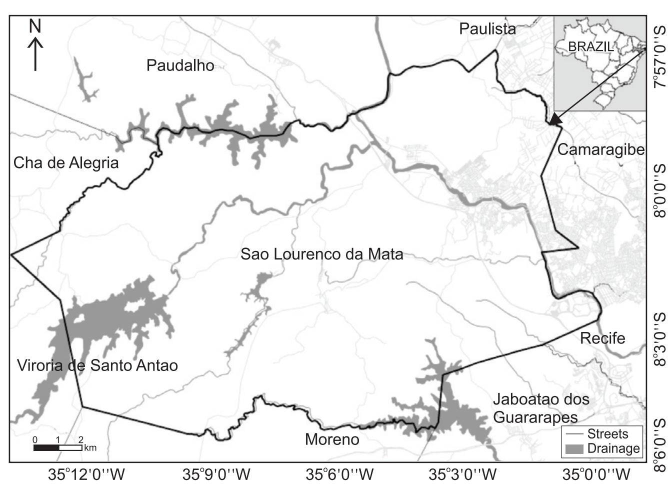

Fig. 1: Map of the study área, São Lourenço da Mata, Pernambuco, Brazil.

snails infected with *S. mansoni* were considered "foci". The foci were classified as potential foci when *S. mansoni* DNA was detected in the snails that were collected, using molecular biology techniques, or as active transmission foci when the collected snails released cercariae of *S. mansoni,* identified through the technique of exposure to light.

Sample collection and snail analysis

During January–December 2015, a malacological survey was conducted in the region. All the collection points were visited quarterly to collect snails. The snails were collected using scoops and tweezers over a 15 min period at the demarcated collection points. They were then packed into moistened ventilated plastic containers and labeled for transportation to the Schistosomiasis Referral Service and Laboratory at the Aggeu Magalhães Institute, Fiocruz. From each batch, a random sample of 5% of the snails was removed for dissection and taxonomic confirmation of the species[17].

To diagnose the infection and identify the transmission foci, the snails were exposed to artificial illumination for the initiation of cercarial emergence[18]. Snails that were found to be negative were re-examined using the same technique 15 days after the first examination and those that continued to be negative were subsequently tested for the presence of *S. mansoni* DNA using the polymerase chain reaction (PCR), a sensitive and specific technique for diagnosing infections with a low parasite load[19–20].

Environmental and GIS analysis

Data relating to faecal contamination of the environment of these water bodies were gathered through visual observation of the sewage discharged directly into the water body, and through the presence of faecal Coliforms detected using the Colitag™ diagnostic kit (Neogen, US). The latter technique detects total Coliforms and *Escherichia coli* using a chromogenic substrate that is incubated at 35°C in plate wells (iMPNplate™ 1600).

The information of the geolocation of the breeding sites and foci of transmission of the disease that was collected through GPS and the results from the malacological, biological and environmental examinations were stored in a geographic database named BD-SLM. The result was then imported to a geographical information system (GIS) in the Geoprocessing Laboratory of the Evandro Chagas Institute (LabGeo/IEC/SVS/MS). A distribution map of the collection points was produced by superimposing the snail data obtained from the field, on a database containing the limits of the municipality, roads and drainage that was obtained from the Brazilian Institute for Geography and Statistics (IBGE), Brazil.

Kernel density estimation, a non-parametric statistical interpolation technique[21], was applied to evaluate spatial patterns, *i.e.* the existence of an agglomerated pattern (the mean distance between points is small) and random and regular patterns (the distance between points is large). Kriging was applied with the aim of spatializing and estimating information on species once it is a statistical inference technique that enables estimation of values and uncertainties that are associated with the attribute, during a spatialization process on a sampled property[22–23]. MaxEnt 3.3.3 (maximum entropy method) was applied to model ecological behaviour based on the environmental characteristics of the locality (temperature, rainfall, humidity, topography, *etc*)[24].

These analyses were performed in the GIS using the following software: ArcGis 10.3 (*http://www.esri.com/*); Spring 5.3 (*http://www.dpi.inpe.br/spring/*); and TerraView 4.2.2 (*http://www.dpi.inpe.br/br/terralib5/wiki/doku.php*). Environmental variables obtained from World Clim Global Climate Data (*http://www.worldclim.org/*) and from the United States Geological Survey Hydro-1K Data (*https://gcmd.nasa.gov/records/GCMD_HYDRO1k.html*) were used to the predictive models for the occurrence of new breeding sites and foci of transmission.

RESULTS

A total of 130 collection points were demarcated of which 64 were classified as breeding sites for *B. straminea.* In total 5,250 snails were collected from these sites over the course of the study. Out of the 64 breeding sites identified, 4 (6.25%) were considered to be foci for schistosomiasis transmission; 54 (84.4%) were considered to be potential transmission foci; and only 6 (9.4%) did not present any indication of infection of the snails by *S. mansoni*.

The lowest snail density was identified in the first trimester (January to March 2015), which was the dry season, when 1,091 snails were collected. The highest density was recorded in the third trimester (July to September), which was the period immediately after the rainy season, when 1,528 snails were collected. In the 2nd and 4th trimesters, the densities recorded were 1,210 snails (April to June) and 1,421 snails (October to December). Figure 2 shows this variability over the period studied and correlates this with the fluctuation of the rainfall curve recorded in the Zona da Mata region of Pernambuco.

Among the 130 collection points, total coliforms were present in 71 points. Among the breeding sites (n = 64), total coliforms were identified in 51 (79.7%) and *E.*

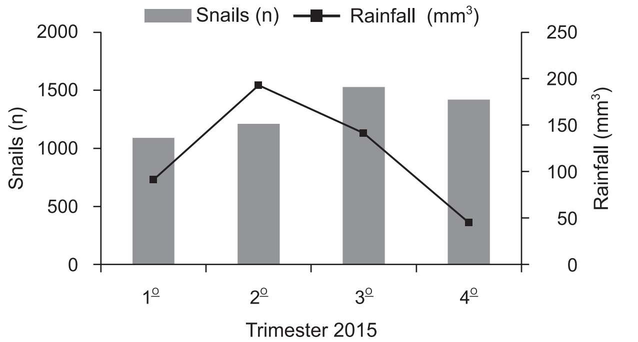

Fig. 2: Snail density correlated with the variability of mean quarterly rainfall in São Lourenço da Mata, Pernambuco, Brazil.

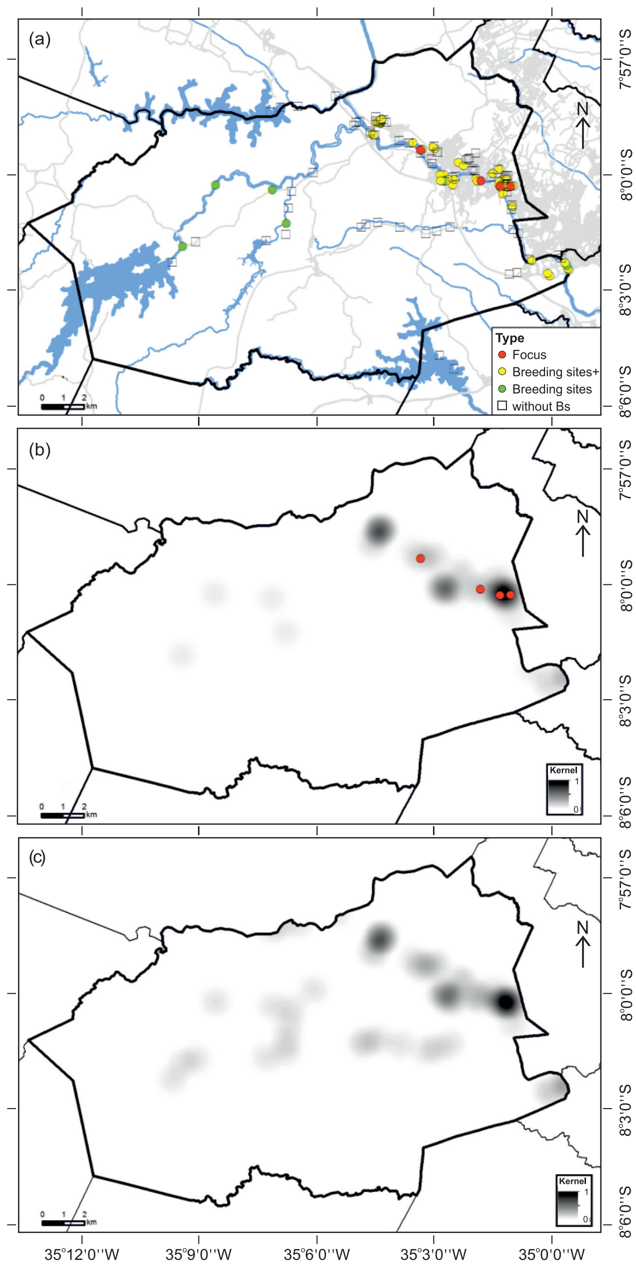

Fig. 3: (a) Spatial distribution of collection points; (b) Kernel applied to *B. straminea* data/density of snail per breeding site; and (c) Kernel applied to the data of the presence of total coliforms and *E. coli* per collection points.

coli was present in 49 (76.5%) sites. Figure 3a shows the spatial distribution map for the collection points in the municipality. Kernel density estimation with a radius of 1 km applied to the study area showed the presence of three agglomerates of greater intensity. These were located in the northeastern part of the municipality (urban area), along with other agglomerates of lower intensity, as observed in Fig. 3b (*B. straminea*) and Fig. 3c (total coliforms and *E. coli*). The two kernel images also show another agg lomerate of lower intensity in the southeastern part of the municipality (the boundary with the municipality of Recife). Figure 3c also shows other agglomerates of lower intensity located in the central part of the municipality.

The kriging technique applied to the spatial distribution data on *B. straminea* and to the sites where no snails were found can be seen in Fig. 4. It should be noted that the areas estimated as presenting *B. straminea* (Fig. 4a) are the same as those presenting high-intensity agglomerates, like the agglomerate close to Recife.

Figure 4b shows the application of MaxEnt to the estimated ecological model for the spatial distribution of *B. straminea*. It is evident from MaxEnt estimation that, the eastern region has a higher likelihood of *B. straminea*

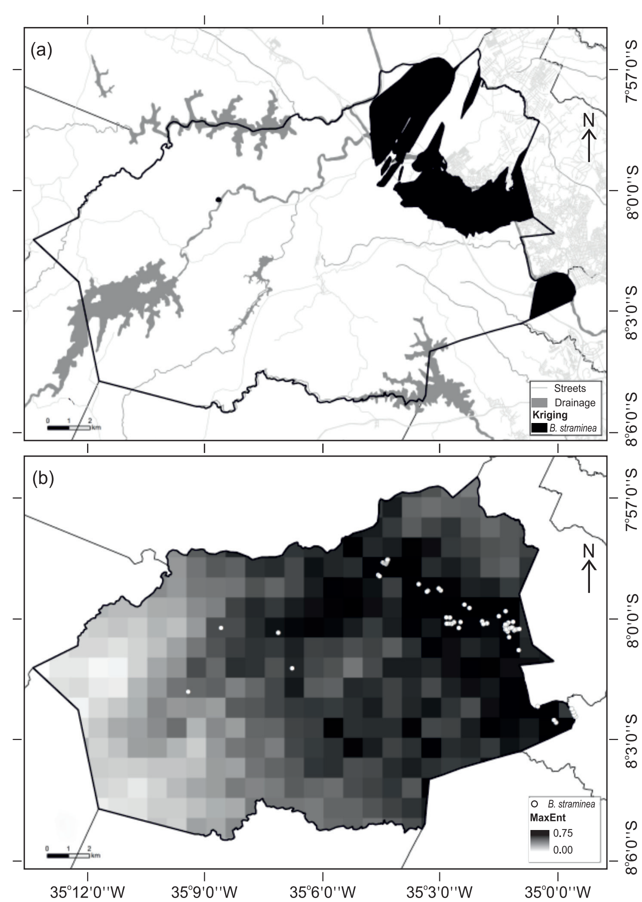

Fig. 4: (a) Kriging; and (b) MaxEnt modeling applied to the spatial distribution data on *B. straminea.*

occurrence, similar to the kriging (Fig. 4a) and kernel estimation (Fig. 3b).

DISCUSSION

Occurrence of the species *B. straminea* alone in the municipality of São Lourenço da Mata was expected, given that this species presented wide distribution in the Zona da Mata of Pernambuco[2, 25]. The analysis of infection in these snails with *S. mansoni* identified four foci of schistosomiasis transmission. Although, these represent a small percentage in relation to the total number of breeding sites identified (64), these findings could be of great epidemiological importance, given the natural resistance of *B. straminea* to infection by *S. mansoni* and the release of cercariae through the technique of exposure to light[3].

The high incidence of potential transmission foci of the disease (84.4%) that has been identified earlier using the technique of molecular biology can also be highlighted[19–20]. Snails infected with the parasite were found at these foci implying that those environments presented the three essential components for schistosomiasis transmission: an environment contaminated through direct and/or indirect discharge of human waste into aquatic environments; infected vectors (snails) living in their natural habitat (freshwater); and humans who are susceptible to infection (definitive hosts)[26]. Thus, under ideal conditions, these snails may release cercariae and transform these environments into places with high risk of disease transmission. It should be emphasized that >75% of the breeding sites were found to be contaminated with faeces, as proven through detection of faecal coliforms and *E. coli* in the water, implicating that the epidemiological scenario in this locality is favourable for disease transmission.

The variation in snail population density over the course of the year corroborates the findings of other studies[27–28]. These authors also correlated higher snail density with the period immediately after the rainy season, as observed in this study (Fig. 2). During this period, the breeding sites are full of water, but no longer subject to the influence of currents due to water runoff during rainfall, which sweep through the breeding sites and dislodge the snails. After the rainy season, these water bodies become ideal environments for these mollusks to become established.

The map of the collection point distribution (Fig. 3a) demonstrates that most of the breeding sites are located within the urban sprawl of the municipality along the Capibaribe River. This provides a greater chance of contact between the intermediate host and humans, thus favouring transmission of schistosomiasis. This contact may occur actively, giving rise to the classical means of disease transmission, in which humans come directly into contact with foci of disease transmission while working, undertaking domestic or leisure activities[29], or passively, when flooding occurs during the rainy season and river water invades streets, backyards and homes, exposing the population to the risk of becoming accidentally infected[8].

The kernel risk map based on snail population density per breeding site (Fig. 3b) identified three areas with a greater concentration of risk where the chance of contact between the intermediate host and humans were higher. This risk is epidemiologically important given that two of the four foci of active disease transmission were located within the agglomeration of greater intensity (higher risk), which was also the area with greatest faecal contamination among the breeding sites investigated (Fig. 3c). Other researchers have also used kernel analysis to identify areas at risk of schistosomiasis transmission, thus demonstrating that this data analysis tool is of great importance for studies on the epidemiology of schistosomiasis transmission[11, 30–31].

The modeling (kriging and MaxEnt) that was applied to the data collected in order to identify new areas potentially at risk for occurrence of the species *B. straminea* (Figs. 4 a and b), reinforces the results highlighted in Fig. 3b, in which the urban areas surrounding the Capibaribe River and its tributaries were at greatest risk. In the state of Minas Gerais, some studies have shown the potential of using kriging to estimate areas of occurrence of *Biomphalaria*[13–14]. It should be emphasized that the estimate of occurrence of this species on the boundary with the municipality of Recife (Fig. 4a) may represent an area of influence in this municipality, which is not an endemic area for this disease, indicating a risk for expansion of schistosomiasis transmission to new areas. Further studies and more detailed analyses of the municipality surroundings are necessary to better understand the risk condition. This would also help towards better calibration of the models used, as in kriging, the quantity and spatial distribution of the input data for the modeling influence the results of the analysis[14].

CONCLUSION

Geostatistical tools used in this study, seemed to be efficient for: (i) identifying areas of occurrence of *B. straminea* snails; (ii) showing the potential risk of schistosomiasis transmission in the population of São Lourenço da Mata; and (iii) estimating the dispersion of this species across the municipality, based on ecological modeling.

Occurrences of this species of *Biomphalaria* in this municipality are influenced by the rainy season, as the species become more abundant during the period immediately after the rainy season. The foci of active disease transmission present a direct relationship with contamination of the environment with human waste, and this is an important parameter for classifying the risk presented by transmission foci. It was also observed that the highest risk of occurrences of this species was found in the urban regions adjacent to the Capibaribe River. These are priority areas for healthcare interventions.

The results obtained from this study is expected to help in improving health care services in diagnosis, planning, implementing and evaluating schistosomiasis control measures in São Lourenço da Mata, to reduce the risk of transmission and protect the health of residents and tourists. More comprehensive studies are needed in the municipalities that border São Lourenço da Mata, so that the geospatial modeling can provide even more accurate estimates of the risk of occurrences of breeding sites of *Biomphalaria* or foci of schistosomiasis transmission.

Conflict of interest

The authors declare that they do not have any conflict of interest.

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