Acta Biol. Venez. Vol. 31 (2):33-36
Julio-Diciembre, 2011

Lutzomyia neivai, VECTOR OF LEISHMANIASIS IN NORTHWESTERN ARGENTINA: PRELIMINARY DISTRIBUTION MAP

Lutzomyia neivai, VECTOR DE LA LEISHMANIASIS EN EL NOROESTE DE ARGENTINA: MAPA PRELIMINAR DE DISTRIBUCIÓN

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ABSTRACT

In the last 20 years, it has been evidenced an association between vector-borne re-emerging diseases, such as cutaneous leishmaniasis (CL), and environmental changes mainly due to deforestation, unplanned urban growth and climate / environmental factors. In this study we developed a model to generate a map of potential distribution of vectors in the north-western hyper-endemic CL region of Argentina and to plan spatially focused strategies for surveillance and prevention of CL. Ninety-eight CDC-like light traps to capture sand flies were placed in National Parks and areas of influence of Salta and Jujuy provinces. A total of 12,079 sand flies were captured and subsequently identified as *Lutzomyia neivai* (85.6%), *L. migonei* (11.6%), *L. cortelezzii* (2.6%) and *L. shannoni*, *L. quinquefer* y *Brumptomyia spp* (less than 0.1%). The former two species had epidemiological importance because are the known vectors of *Leishmania braziliensis*. In the analysis, bioclimatic variables and elevation were considered. We used the method of Genetic Algorithm for Rule-set Prediction (GARP) and the Maximum Entropy Modeling System (MaxEnt). As concern the last modelling system, the variables with the highest relative contribution were seasonal rainfall (30.5%), seasonal temperature (21.4%) and elevation (24%). The accuracy was evaluated by the value of the area under the curve (AUC=0.996)). This approach, once validated, would allow us to forecast and assess the impact of environmental changes on CL risk and to design control strategies. Moreover, predictive models based on remote sensing and captures of vectors in sentinel sites would be developed to provide an early warning system for disease outbreaks.

RESUMEN

En los últimos 20 años, se evidenció una asociación entre enfermedades re-emergentes transmitidas por vectores, como la leishmaniasis cutánea (LC), y los cambios ambientales, principalmente debido a la deforestación, el crecimiento urbano no planificado y el clima / factores ambientales. En este estudio se desarrolló un mapa de distribución potencial de los vectores de LC en región endémica en el noroeste de Argentina, a fin de planificar estrategias espaciales enfocadas en la vigilancia y prevención de la LC. Se colocaron 98 trampas tipo CDC para capturar flebótomos en Parques Nacionales y áreas de influencia de las provincias de Salta y Jujuy. Se capturaron un total de 12.079 flebótomos correspondiente a *Lutzomyia neivai* (85,6%), *Lu. migonei* (11,6%), *Lu. cortelezzii* (2,6%) y *Lu. shannoni*, *Lu. quinquefer* y *Brumptomyia spp* (menos de 0,1%). Las dos primeras especies tienen importancia epidemiológica como vectores conocidos de *Leishmania braziliensis*. En el análisis, se consideraron variables bioclimáticas y modelo de elevación. Se utilizó el método de Algoritmo Genético para Predicción de Conjuntos de Reglas (GARP) y el Sistema de Modelado de entropía máxima (MaxEnt). En éste último método, las variables con mayor contribución relativa fueron las precipitaciones estacionales (30,5%), la temperatura estacional (21,4%) y la elevación (24%). La precisión fue evaluada por el valor del área bajo la curva (AUC = 0,996). Esta aproximación, una vez validado, nos permitirá prever y evaluar el impacto de los cambios ambientales sobre el riesgo de transmisión de LC y para diseñar estrategias de control. Por otro lado, debería desarrollarse modelos predictivos basados en información obtenida de sensores remotos y captura de vectores en sitios centinela a fin de proporcionar modelos dinámicos como insumos para un sistema de alerta temprana de brotes de enfermedades.

Keywords: Vector distribution maps and models, Leishmaniasis in Northwest Argentina, remote sensing and vector-borne diseases.

Palabras clave: Mapas y modelos de distribución de vectores. Leishmaniasis en el noroeste argentino, sensores remotos y enfermedades transmitidas por vectores.

INTRODUCTION

Leishmaniasis is a subtropical and tropical disease caused by parasites of the genus *Leishmania* and transmitted by the bite of an insect (Phlebotominae) which in America belongs to the genus *Lutzomyia*. The unplanned urban growth and deforestation have been proposed as the main anthropogenic factors causing the re-emergence of this disease in the world (Mott *et al*., 1990; Walsh *et al*., 1993; Ashford, 2007). In Argentina, the re-emergence of CL occurred through focalized outbreaks, geographically restricted, also associated with deforestation and the subsequent anthropogenic change in deforested areas: safety / housing for workers exposed, colonization and disorderly urbanization (Salomón *et al.*, 2001; Sosa Estani *et al*., 2001; Salomón *et al.*, 2006b). Leishmaniasis in Argentina is endemic in 9 provinces in the north of the country. The country had registered 8126 cases of CL from 1954 to 2006 with 58.2% of the cases reported in the provinces of Salta and Jujuy in the north-western region (Salomón *et al*., 2006a).

Lutzomyia neivai and *L. migonei* are the vectors of *Leishmania braziliensis*, a parasite responsible for the outbreaks of CL in this region (Córdoba-Lanús *et al*., 2006). The study of the modulation mechanisms involved in the correlation between environmental changes and vector-borne diseases incidence could have a strong impact on the development of control strategies (Walsh *et al*., 1993; Beck *et al*., 2000; Heymann *et al.*, 2001). This approach is particularly important in diseases such as CL where the distribution and abundance of the vectors is the best indicator in time and space of the transmission rate. On the other hand, the analysis based on human case records usually introduces errors due to missing data on asymptomatic case incidence and the ambiguity of time-space data obtained by anamnesis (incubation period, microfocal accidental transmission). For this reason, it is not possible to obtain useful conclusions on the scale of operational control (Peterson, 2006).

In the last decade, algorithms to model vector ecological niches was used for several applications including eco-epidemiology. These models are applied to explore possible relationships between the values of biotics (type of vegetation) and abiotic factors (temperature, precipitation, etc) and data on presence, presence-absence and / or abundance of the vector species.

The aim of this study was to develop a map of the potential distribution of vectors in the northwestern hyper-endemic CL region of Argentina, based on biotic and abiotic variables that could explain the abundance and distribution of vectors in the different environments. This map would contribute to design spatially focused strategies for surveillance and prevention of leishmaniasis.

MATERIALS Y METHODS

The study area covered two phytogeographical provinces: the Yungas forest, with an average annual temperature of 21.5ºC and annual rainfall between 1000 and 2000 mm, and the Dry Chaco with temperatures between 18º-26ºC and an average annual rainfall about 500 mm. Samples of Phlebotominae were obtained during November 2006 using CDC-type light minitraps that were placed overnight within National Parks (Baritú, Calilegua, El Rey), General Pizarro National Reserve and the city of Orán, as well as in their zones of influence or mitigation (Figure 1). The 98 points were placed according to altitudinal and latitudinal gradients, watersheds, environmental changes and history of human CL cases. The collected specimens were carried to the laboratory for subsequent processing and identification at the species level following a taxonomic key.

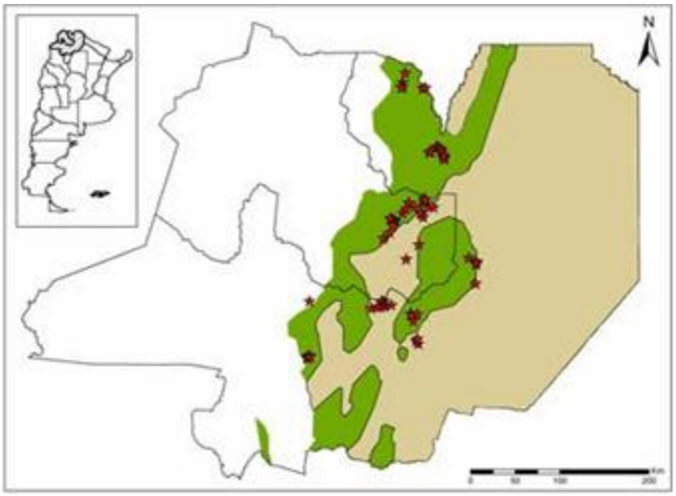

Figure 1. Study area. Capture sites of adult Phlebotominae. Green: Yungas Forest. Ligth brown: Dry Chaco.

The points of vector occurrence were combined with six bioclimatic variables obtained from Worldclim (Hijmans *et al*., 2005): annual precipitation, seasonality of precipitation, maximum, minimum, annual and seasonal temperature and a topographic layer of elevation (http://glcfapp.umiacs.umd.edu:8080/esdi/index.jsp).

We used the method of Genetic Algorithm for Rule-set Prediction (GARP) (Stockwell *et al*., 1992; http://www.nhm.ku.edu/desktopgarp/Download.html) and the Maximum Entropy Modeling System Version 3.1.0 (MaxEnt) (Phillips *et al*., 2006). Here are presented the results obtained using MaxEnt for the main species incriminated as a vector in the area, *Lutzomyia neivai*. To run MaxEnt, the maximum number of iterations introduced was 500, setting the limit of convergence in 0.00001. These values are adequate to ensure the convergence of the algorithm (Phillips *et al*., 2006).

RESULTS AND DISCUSSION

A total of 12.079 sand flies were captured and identified as *L. neivai* (85.6%), *L. migonei* (11.6%), *L. cortelezzii* (2.6%) and *L. shannoni*, *L. quinquefer* and *Brumptomyia spp* (less than 0.1%). The former two species had epidemiological importance because are the known vectors of *Leishmania braziliensis*. The algorithms obtained by in GARP and MaxEnt of the species *L. neivai*, depicted on the maps, can be seen in Figure 2 A and B. The environmental variables that had a higher percentage of contribution were the seasonal temperature (30.5%), seasonal precipitation (21.4%) and elevation (24%). Using the Jacknife test it was shown that the variable seasonal rainfall represent the factor giving the maximum contribution followed by the seasonal temperature and finally by elevation. The former two variables allowed an acceptable adjustment. The accuracy was evaluated by the value of the area under the curve (AUC=0.996).

The areas marked with the most intense green colour in the MaxEnt map correspond to the areas showing epidemic potential or actual risk. They are found mostly in the Yungas Forest, along the basins of San Francisco-Bermejo rivers. It has been identified two types of landscapes: the areas recently anthropized of the Yungas Forest and the adjacent sites where the man has settled and with steady sources of food for insects (humans and pets). The potential distribution of *L. neivai*, predicted by the model and based on bioclimatic variables, is coincidental, as expected, with previous data on vector captures and recorded CL human cases (Salomon *et al*., 2001; Salomon *et al*., 2004; Salomon *et al*., 2006b). These data confirm the association in the medium-term between deforestation and the outbreaks of leishmaniasis, due to the adaptation of a competent vector to peridomestic habitats and the increase of its abundance due to steady food-sources of blood. Therefore, any extensive environmental change in the defined risk area, especially if it is close to sites with current cases of CL, can generate an epidemic transmission of CL.

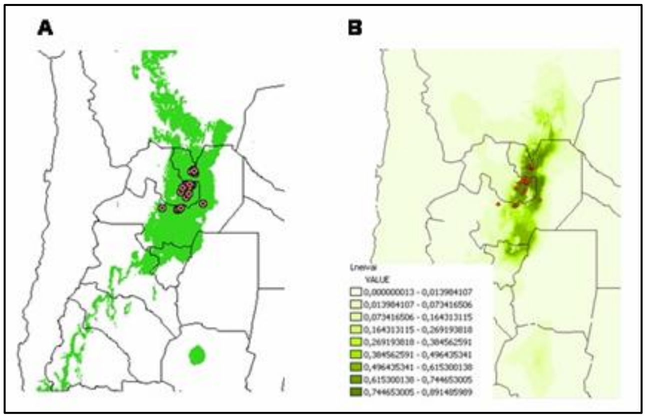

Figure 2. Distribution of *L. neivai* in northwestern Argentina (red circles). The potential distribution of the species is shown in green in A) GARP, and with wide green B) MaxEnt. The darker shades indicate a higher probability of occurrence.

The use of predictive models of species distribution is of great value to extrapolate the known data to other unsampled areas where environmental conditions are suitable for the species. The modelling allows forecasting the distribution of the entity studied, as a disease vector and its related risk, with a high degree of accuracy. It is important to emphasize that in this study, the same sample was used to train and to evaluate the model. We are still at the initial stage and further validation is necessary. In order to improve the model we are raising more points of sampling and re-analyzing the data using a set to train and a different one to evaluate the models. In this way it would be possible to calculate those cases correctly classified and those wrongly classified to calculate different rates of assessment from a matrix of confusion. Even so, this preliminary modelling with the algorithm MaxEnt provides a new potential tool and an optimal resource to design appropriate operational strategies and prevention measures based on evidence.

CONCLUSIONS

Based on the preliminary results here described on the spatial distribution of *L. neivai* as a risk surrogate to establish the CL risk, some preventive recommendations for the north-western region can be suggested: i) on sites with high density of *L. neivai* and clustering of cases of CL it should be settled an active case surveillance and vector control and ii) to extend the recommendation of the National Program of Leishmaniasis from "vectorial monitoring before any environmental changes on the outskirts of towns in the endemic area" to "vectorial monitoring before any environmental changes extend throughout the area of the Bermejo River-San Francisco". On the other hand, in the Chaco region the transmission of this disease is sporadic, related with at risk behaviour associated with environmental management and deforestation.

ACKNOWLEDGMENTS

We want to thank for their contribution to this study: Administración de Parques Nacionales (APN); Wichi community, Pizarro; Ministerio de Salud de la Nación; ANLIS-CeNDIE; Dr Zaidenberg from CNCV Salta, Güemes Delegation; Dr. Ripoll from Ministerio de Salud de Jujuy; Dr Gentile from Ministerio de Salud de Salta; Los Toldos and San Pedro Hospitals and Ingenio Ledesma: Eng. Ullivarri, Eng. Entrocassi. The sampling was made in the framework of the agreement APN-ANLIS/CeNDIE, the project PICTR 275 ANPCyT and with the permission of the local health authorities.

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