

Spatial relationship between *Aedes egypti* (Linnaeus, 1762) and dengue disease in Guatemala

Relación espacial entre *Aedes aegypti* (Linnaeus, 1762) y la enfermedad del dengue en Guatemala

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Abstract: *Aedes aegypti* mosquito, main transmitter of dengue disease in the Americas, has been responsible for more than 50,000 dengue cases in Guatemala between 2010 and 2017. Two generalized linear models were developed in order to establish the potential distribution area of *A. aegypti* in Guatemala based on climate data, to define the spatial relationship of dengue cases with probability of vector presence and to focus on potential transmission locations of dengue in the country. Vector distribution model was fed with data from the Global GBIF network. The relationship model between the vector and the case incidence was also fed with data from the Health Management System (SIGSA, *by its acronym in Spanish*). Climate variables from WorldClim- Global Climate Data (1050-2000) were used for both models. Logarithms were calculated and evaluated in the statistical platform R and plotted in the Quantum Geographic Information System. The results show a high probability (.75-1.00) of vector occurrences in any region in 21 departments out of 22, excluding Totonicapán. Precipitation and humidity are the main variables related to vector presence. Moreover, It is shown that in the northern region of the country, the case incidence is not related to the potential distribution of *A. aegypti*, which indicates possible evidence of presence of *Aedes albopictus* as possible responsible for the transmission of this arbovirosis. Finally, five high-risk central regions of dengue transmission was

obtained, which can be used as backup for the selection of sentinel sites used for vector surveillance.

Keywords: Dengue, *Aedes aegypti*, distribution, incidence, Guatemala.

Resumen: El mosquito *Aedes aegypti*, principal transmisor de la enfermedad de dengue en América, ha sido el responsable de más de 50 000 casos en Guatemala entre los años 2010-2017. Con el fin de establecer el área de distribución potencial de *A. aegypti* en Guatemala con base en datos climáticos, definir la relación espacial de casos de dengue con la probabilidad de presencia del vector y enfocar los puntos de transmisión potencial de dengue en Guatemala se llevaron a cabo dos modelos lineales generalizados. El modelo de distribución del vector fue alimentado con datos de la red Global Biodiversity Information Facility (GBIF), y el modelo de la relación entre el vector y la incidencia de casos, fue alimentado además, con datos del Sistema de Información Gerencial de Salud (SIGSA). Para ambos modelos se utilizó variables climáticas de WorldClim-Global Climate (1950-2000). Los logaritmos fueron calculados y evaluados en la plataforma estadística R y graficados en Quantum Geographic Information System. Los resultados muestran una alta probabilidad (.75-1.00) de presentar ocurrencias del vector en alguna región en 21 de los 22 departamentos con excepción de Totonicapán. Las principales variables que se encuentran relacionadas con la presencia del vector son la precipitación y la humedad. Se muestra además que en la región norte del país la incidencia de casos no se encuentra relacionada con la distribución potencial de *A. aegypti* lo que indica posible evidencia de la presencia de *Aedes albopictus*, como responsable de la transmisión de esta arbovirosis. Por último, se obtuvieron cinco regiones focales de mayor riesgo de transmisión de dengue las cuales pueden ser utilizadas como respaldo para la elección de sitios centinela para el control de este vector.

Palabras clave: Dengue, *Aedes aegypti*, distribución, incidencia, Guatemala.

Introduction

Aedes aegypti has been the main vector of arbovirus in the Americas, such as yellow fever (Jentes et al., 2011), chikungunya (Leparc-Goffart, Nougairede, Cassadou, Prat, & Lamballerie, 2014) and dengue (Simons, Farrar, Chau, & Wills, 2012). Despite mosquito eradication programs around the most part of the Americas in 1970, (Gubler, 2014; Organización Panamericana de la Salud & Organización Mundial de la Salud, 1959), vector presence is reported nowadays in 21 regions, out of 22 departments in Guatemala (Lepe et al., 2016). However, the awareness of such distribution is limited, approached by means of entomological surveys carried out by the Ministry of Public Health and Social

Assistance (MSPAS, by its acronym in Spanish). Also, the factors that rule such distribution in the region of Guatemala is scarce (Lepe et al., 2016).

These mosquitos, probably originated in Africa and transported into the Americas by the ships during the first European explorations and colonizations back in the 15th century, are found in sites with isotherms between 10° C [50° F] and 45° C [113° F] (Nelson, 1986). Temperatures, below the aforementioned, produce difficulties in mosquito development, in population density and in female fertilization (Patz, Martens, Focks, & Jetten, 1998). Reason why they are generally found in regions under 1 000 masl (Nelson, 1986). This variable restricts the geographical limits of *A. aegypti* current distribution in Guatemala.

The main vector of dengue virus is the mosquito, the most extended arbovirus on the planet presenting cases worldwide (Simons, et al., 1012). It is estimated that around 390 million of dengue cases happen in a year, out of which only 96 million are identified through surveillance in health care centers in every country (Bhatt et al., 2013). This disease is found throughout the tropics, and the variation regarding the risk of infection, is greatly due to precipitation, temperature and urbanization (Simons, et al., 2012). In 2016, dengue virus was transmitted to over 2 million people in the American continent. Around 50 000 cases were reported from 2010 to April 2017 in Guatemala (Sistema de Información Gerencial de Salud [SIGSA] 2017).

There are different required conditions for virus transmission, it is necessary to gather a series of vector conditions, such as temperature, relative humidity, solar radiation or insect survival. Also, a combination of essential factors from the virus like virus genetic characteristics, and essential factors to the virus such as the intrinsic incubation period, which depends on the mosquito external temperature (Hardy, Houk, Kramer, & Reeves, 1983; Samuel, Adelman, & Myles, 2016). There are contradictions in regard to the ideal temperature for the virus to replicate, as well as for its dissemination inside the imago digestive tract. Fairly wide fluctuations in temperature decrease virus transmission in the case of *A. aegypti*, whereas the ideal temperature for the transmission is 30°C (Lambrechts et al., 2011; Watts, Burke, Harrison, Whitmire, & Nisalak, 1987).

The mosquito *Aedes albopictus* Skkuse 1895 (Díptera: Culicidae) was found in the caribbean region of the country in 1995 (Ogata & Samayoa, 1996; Tabaru et al., 1998). Currently, its presence is known to be in some locations of at least 11 departments all over northern Guatemala (Lepe et al., 2016). Thus, this mosquito could be playing an important role in arbovirosis transmission dynamic in

regions of the country where *A. aegypti* is not present. It has been reported as a competent vector of multiple viral diseases such as dengue (Simmons et al., 2012; Villatoro, 2006), chikungunya (Thiberville et al., 2013), y zika (Grard et al., 2014). It is believed that it has some Asian origin (southeast Asian). Today, it is found all over around the world, surrounding human communities and serving as the main transmitter of diseases like dengue in rural areas, where *A. aegypti* is not present (Gratz, 2004). The vector presents advantages over other vectors due to the capacity that it demonstrates to survive within environments with limited resources and high combined densities (Juliano, 1998).

Two generalized linear models were created from the methodology proposed by Barbosa (2015), in order to 1) establish the potential area of distribution of *A. aegypti* in Guatemala based on the climate data by WorldClim- Global Climate Data (Hijmans, Cameron, Parra, Jones, & Jarvis, 2005), 2) to define the potential area of dengue cases based on the existence of *A. aegypti*, data by Global Biodiversity Information Facility (GBIF) between 1990 and 2016. Finally, 3) to determine high risk locations of potential dengue transmission in Guatemala. The amplitude of this study is limited in the following points: resolution scale of the database obtained from WorldClim- Global Climate Data (Hijmans et al., 2005) 2.5 km, mosquito occurrence data extending to a greater geographical area to the reported in the database from GBIF (GBIF, 2017), lack of data in the country of study, as well as scarce anthropogenic information like population density, urbanization, access to water or drainage systems. This study will provide an approach on the vector current distribution around the region, define its potential distribution so that prioritized regions can then be indicated for vector surveillance in Guatemala, and define regions that should be prioritized due to the emergence risk of dengue outbreaks.

Materials and methods

Study area

On account of the lack of data in Guatemala, the first model was carried out with occurrence data of *A. aegypti* in Mexico, Belize, Honduras, Nicaragua, Costa Rica, El Salvador and Panama, geo-referenced on the database from Global Biodiversity Information Facility (GBIF, 2017). Intergovernmental initiative formed by 97 participants, including countries and international organizations, which cooperate to promote free and open access to biodiversity data. Occurrence geographical coordinates were downloaded with *rgbif* package by

using filters as “*Aedes aegypti*” for Scientific Name, search countries “Mexico, Guatemala, Belize, El Salvador, Honduras, Nicaragua, Costa Rica and Panama” (Real, Barbosa, & Vargas, 2006), off the statistical software R console (R Core team, 2017).

The data on the sampled area map was subsequently superimposed with maps package (Becker & Wilks 2018) in order to exclude the wrong data, regarding the lack of information in the geographic coordinates. The data that wasn’t within the interest area was considered as erroneous. Such values were directly eliminated from the R console. Search helped to obtain 13,840 points of geo-referenced occurrence.

The study area was chosen based on the report of constant culicoides infestation, besides the access to this data. The climate data correspond to 19 variables (Table 1) extracted from WorldClim- Global Climate Data (Hijmans et al., 2005).

Table 1.

Evaluated climate variables for model development

Evaluated variables	Model 1	Model 2
Mean annual temperature	Mean diurnal range	Seasonal temperature
Mean diurnal range	Mean temperature of the coldest quartile	Mean temperature of the wettest quartile
Isothermal	Precipitation of the wettest month	Precipitation of seasonality
Maximum temperature of the warmest month		
Minimum temperature of the coldest month		
Annual temperature range		
Mean temperature of the wettest quartile		
Mean temperature of the warmest quartile		
Mean temperature of the driest quartile		
Mean temperature of the coldest quartile		
Annual precipitation		
Precipitation of the wettest month		

Precipitation of the coldest month		
Precipitation of seasonality		
Precipitation of the coldest quartile		
Precipitation of the warmest quartile		
Precipitation of the wettest quartile		
Precipitation of the driest quartile		

WorldClim- Global Climate Data (Hijmans et al., 2005).

Selection of logarithmic modeling

Potential vector distribution can be addressed based on ecological niche models (Escobar et al., 2016; Peterson et al., 2011). They allow the characterization of favorable climate conditions for a species presence in one territory without any immigration required (Peterson et al., 2011). Models of potential distribution have been done, showing that the area, to which they are restricted to *A. aegypti* in the Americas, goes from the north of the United States (Hahn et al., 2016) down to the north of Argentina. General maps are available, leaving the interest of making maps with the autochthonous distribution of *A. aegypti* in every country (Kraemer et al., 2015).

In Guatemala, it has been addressed only by Lepe y colaboradores (2016). In the case of dengue, there are maps at a global level to delimit the areas with dengue incidence. Its results reveal evidence of cases showing connection with climate variables and vector presence. (Brady et al., 2012; Van, Bambrick, & Hales, 2017; Lover et al., 2014).

In order to predict the occurrence/absence of a species based on multiple variables in a particular site, the model generation can be carried out by means of multiple algorithms (Van et al., 2017). For instance, the flexible model to plot the potential distribution of species (DOMAIN) (Elith et al., 2006), Maximum entropy (Carpenter, Gillison, & Winter, 1993), Modeling System of genetic algorithm for rule-set production (GARP) (Stockwell & Peters, 1999) or machine-learning models (BRT) (Van et al., 2017).

The comparison between regions, through the presence and absence of species individuals, generally shows several intrinsic errors to the methodology used. Among them, it can be mentioned that climate or spatial proximity is not taken

into account between occurrence sites, which increases false absences resulting in two similar and nearby sites to be totally different, the same as two sites in opposite geographic areas (Barbosa & Real, 2012).

Databases present unavoidable errors, false absences, errors when introducing data or false positives (Rocchini et al., 2011). Because of this, Rocchini y colaboradores (2011) and Barbosa (2015) recommend the use of species distribution as “fuzzy”, areas with a degree of uncertainty of presence or absence rather than purative presences or absences. Owing to this, the method proposed by Barbosa (2015) was used, included in the package fuzzySim within R statistical method (Barbosa 2014). This allows the conversion of presences/absences of species data into continuous and fuzzy surfaces based on a generalized linear model, in addition to converting probability to favorable values (favorability), prevalence-independent, which have proven to be of appropriate use within a fuzzy logic framework. (Barbosa 2015; Stockwell & Peters, 1999).

However, there are model limitations in regards of the information obtained from databases. Among some of them: heterogeneous reports all around the origin country, information gaps, geographic coordinate incongruences, lack of information on strict absences, duplicate records, errors in nomenclature, different coordinate systems, and others. Despite that, these limitations are resolved through extrapolation of the conditions where there is record, by means of models.

Data analysis:

The data in this study consists of two variable of binomial response: presence/absence of *A. aegypti*, presence/absence of dengue cases (GBIF, 2017) and a series of continuous climate variables accessible to the public WorldClim-Global Climate Data (Hijmans et al., 2005). (Table 1). Dengue cases were requested to Health Management Information System (SIGSA) in Guatemala, information corresponding from January 2010 to April 2017. These cases were geo-referenced with Quantum Gis version 2.18, in the Geographic Information System (QGIS Development Team, 2017). A binomial generalized linear model (Barbosa 2014; Barbosa, 2017) was used in order to determine the vector distribution based on temperature and precipitation variables.

The results by the grid probabilities, obtained from the R model, were imported to Quantum Gis. They were then converted into a raster format and plotted with the design complement, particular of the geographic information system. Model

1, which included México, Guatemala, Belize, Honduras, Nicaragua, El Salvador, Costa Rica and Panama (Figure 1), was reduced within Guatemala limits and replotted (Figure 2). The values of grid probabilities of this country were imported to R for Model 2 development.

Subsequently, a generalized linear model was made to determine the current distribution of dengue cases in relation to potential vector distribution and climate variables. In order to create the following models, 19 variables were used, a priori, evaluated and filtered afterwards (Table 1), which represent the database by WorldClim- Global Climate Data (Hijmans et al., 2005):

Model 1: *A. aegypti* ~ Intercept + climate variables

Model 2: Dengue ~ Intercept + Probability of *A. aegypti* presence/absence + 3 climate variables

The generalized linear models matched by using MultGLM function off fuzzySim package (Barbosa, 2014) in R, through the script developed by Barbosa (2017). Both models were evaluated by modEvA package (Barbosa, Brown, Jiménez-Valverde, & Real, 2016). The discrimination and classification capacity was determined (Table 2) threshold-independent, meaning that a cut-off threshold is not used to classify presence/absence values. Instead, directly upon map continuous values (Legendre & Legendre, 2012) through the area under the Receptive Operative Characteristic (ROC) curve, with “AUC” option off modEVA package, true skill statistic (TTS) (Allouche, Tsoar, & Kadmon, 2006) and the correct classification rate (CCR) with optiTresh function off modEVA package in R. The goodness-of-fit, or the calibration of both models, was carried out through the Miller calibration straight line (Pliscoff & Fuentes-Castillo, 2011), with MillerCalib function off modEVA package.

Both models (model 1 &2) used 15% of data as validation data. The variables that represented false negatives were deleted by using False Discovery Rate (Benjamini & Hochberg, 1995), with FDR function, collinearity with multicoll function, and correlation between variables over .75 (Marquardt, 1970), with cor function off fuzzySim package. The variables selection process was step-by-step, choosing them from a saturated model in both directions.

Results

Predictive models

Aedes aegypti

In figure 1, you can see that Mexico, Guatemala, Belize, Honduras, Nicaragua and Costa Rica, represent high probability of *A. aegypti* presence in some region, excluding Panama. This high probability (between .75 to 1.00) is represented along the Pacific Ocean coasts, starting from the west area of Sierra Madre Occidental in Mexico, passing through Balsas Depression, moving forward the area located between the volcanic chain of Guatemala and the Pacific Coast, El Salvador, the lowlands of Nicaragua (depression of Nicaraguan lakes) and lowlands of Costa Rica. On the other hand, there is a high probability in the Sierra Madre Oriental in Mexico and Yucatán, northeast-wise (.5 - .75), followed by the Atlantic Ocean coasts (.25 - .75). The areas with low probability (0 - .25) are located in highlands, such as Sierra Madre Oriental and Occidental in México, the volcanic chain, altiplano, Cuchumatanes mountain range, Sierra de las Minas in Guatemala, and the highlands of Belize (Sierra Maya): the Atlantic coast of Central America and the territory of Panama.

Figure 1.

Probability map of *A. aegypti* presence in Mexico and Central America: map generated in Quantum GIS. Date: June 2017. The map depicts the favorable conditions for mosquito occurrence, from 0 (blue) to 1 (red), in a 10 km x 10 km resolution.

Map generated in Quantum GIS. Date: June 2017.

In Guatemala (Figure 2), a high probability of presence can be observed (.75 – 1) in all southern lowlands of the country up to the volcanic range. In the east of the country, a probability of vector presence can be observed between .5 and .7 including the department territories of Guatemala, El Progreso, Jalapa, Jutiapa, Zacapa y Chiquimula. Meanwhile, a .75 probability is observed in the northeast region of the department of Huehuetenango, western Guatemala. In the department of Petén, northern Guatemala, there are probabilities of finding a vector from .75, in the north area, up until zero probability in the southeast area. Escuintla, Santa Rosa, Suchitepéquez, Retalhuleu, San Marcos, Quetzaltenango and Jutiapa are high-probability department territories of *A. aegypti* presence (> .75).

Figure 2

Probability map of *A. aegypti* presence in Guatemala: map generated in Quantum GIS. Date: June 2017. The map depicts favorable conditions for mosquito occurrence from 0 (blue) to 1 (red), in a 10 km x 10 km resolution.

Map generated in Quantum GIS. Date: June 2017.

Dengue

As shown in figure 3, the coastal area, bordering the Pacific Ocean, presents a high probability (.75 – 1) as opposed to the coasts in contact with the Atlantic Ocean, which present a low probability (0 - .25). The locations with the highest probability of incidence presence of dengue cases are in the northwest area of Huehuetenango, the area including Ciudad Tecún Umán and the Pacific coast of San Marcos, the communities surrounding Atitlán Lake in Sololá, the northeast area of Escuintla and the mountain area between Pueblo Nuevo Viñas, Tecuamburro volcano, Cruz Quemada volcano and Moyuta volcano in Santa Rosa. The highest probability for dengue cases incidence in Guatemala is found in 19 departments out of 22.

In mountain systems, the areas with the highest probability of case presence is located between the Mountain System of Sierra Madre. San Juan mountains, Sierra de Chuacus and Sierra de las Minas have the highest probability (.75 – 1). Another high-probability area is found in western Huehuetenango, in the low area of Cuchumatanes mountain range (.75 – 1). It should be noticed that the lowlands southern Guatemala have areas with the highest probability of case incidence, whereas the lowlands of Petén do not present probability of case incidence.

Figure 3

Probability map of dengue incidence in Guatemala: map generated in Quantum GIS. Date: June 2017. The map depicts favorable conditions for dengue case occurrence from 0 (blue) to 1 (red), in a 10 km x 10 km resolution.

Map generated in Quantum GIS. Date: June 2017.

According to figure 4, dengue case incidence corresponds, for the most part, to the data obtained through the model and the prediction performed. In figures 4 and 5, it can be observed that the departments coincidently with low probability of case dengue have a low percentage of cases. Petén present only 3.7 % of reported cases, Izabal reports only 1.42 % of cases and Alta Verapaz with 6.41 %, resulting into 11.53 % of total cases. Case incidence conditions are concentrated in departments like Guatemala (27.45 % of cases), Quetzaltenango (8.76 % of cases), Santa Rosa (8.61 % of cases) and Escuintla (7.4 % of cases), all departments resulting into the 52.2 % of cases. Chimaltenango (0.32 %),

Totonicapán (0.02 %) and Jalapa (1.11 %) are departments with high probability, but a low percentage of reported cases.

It should be mentioned that the number of cases that arise in dry season (November-April) is higher than the number of sites that present cases in rainy season (May-October). When observing cases by season (Figure 4), departments like Petén, Izabal, Huehuetenango, Retalhuleu, Totonicapán and Zacapa, are appeared to present dengue cases only in dry season, as opposed to the other 16 departments presenting dengue cases in both seasons.

Figure 4

Sites presenting dengue cases in both rainy and dry season, shown on the probability map of dengue incidence in Guatemala. Dry season: May, June, July, August, September, and October. Rainy season: November, December, January, February, March and April. Map generated in Quantum GIS. Date: June 2017. The map depicts favorable conditions for dengue case occurrence, from 0 (blue) to 1 (red), in a 10 km x 10 km resolution.

Map generated in Quantum GIS. Date: June 2017.

Figure 5

Dengue case percentage by departments, from 2010-2017 to the epistemological week 16 (April 22, 2017). Source: Dissemination of Health Statistics Unit, Health Management Information System (SIGSA), Public Health Ministry and Social Assistance. Date: June 2017

Dissemination of Health Statistics Unit, Health Management Information System (SIGSA), Public Health Ministry and Social Assistance. Date: June 2017

Miller calibration straight line revealed that the generated models met the data with intercept values close to 0 and slopes close to 1. Based on the area below the curve, the discriminative and classification capacity present values above 0.7 (Table 2). In order to transform the results obtained into a presence/absence map, values of the correct classification rate of model 1 and 2, plus the true skill statistics of both are shown on the same table.

Table 2.

A. aegypti and dengue models calibration

A. aegypti model	Dengue incidence model
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	Validation	Model 1	validation	Model 2
Model calibration				
Miller calibration straight line				
Intercept	0.42	0	0.19	0
Slopes	1.15	1	1.09	1
Predictive statistics				
ROC/AUC	0.743	0.709	0.799	0.791
Maximized Correct Classification Rate (CCR)	0.962	0.960	0.788	0.775
Maximized True Skill Statistics (TTS)	0.697	0.663	0.74	0.761

Discussion

The results show a high probability of conditions for *A. aegypti* presence in 21 of 22 departments in Guatemala, in one region minimum (probability between .5 and 1). The results reported by Lepe y colaboradores (2016), which obtain the same distribution in regards of departments, find support in the results in this article. Very cold climates are limitations for ectotherms organism development that require an external heat source as opposed to their own heat production. Thus, the department of Totonicapán hasn't reported neither dengue presence nor Chagas (Tabaru et al., 1998), in comparison to departments with warmer climates like Escuintla and Santa Rosa.

Map presentation and production, which could provide alarm information of febrile case outbreaks, are greatly complexified by geo-referenced data absence, obtained from the Vector-borne Diseases Programme.

According to model 2 (Figure 2 and 3), the vector potential distribution does not correspond to the disease potential distribution in the north region of the country, which brings up the suspicion of a second agent in virus transmission. Distribution of *A. albopictus* (Lepe et al., 2016), competing vector for the two same resources used by the first *A. aegypti*, could be the reason of incidence high probabilities in these regions. In fact, an *A. aegypti* displacement has been

discovered in rural ambiances by *A. albopictus*, due to the high survivorship capacity that the second one has under unfavorable conditions to other vectors. Conditions such as overcrowding, temperatures under 20° C [68° F] or breeding grounds with more jungle-like characteristics present in anthropogenic communities located in rural areas (Black, Rai, Turco, & Arroyo, 1989).

Another factor that could explain the most extensive incidence distribution of cases in relation with vector distribution, observed all over the country, is the existence of underreporting. This is caused by patients failing to attend health care centers or staff of public institutions not having the appropriate tools to distinguish between dengue cases from other arboviruses with similar symptomatology to chikungunya fever or Zika.

In order to properly address this disease, it is necessary to rely on professional staff, besides the staff willing to perform essential vector surveillance interventions to avoid virus dissemination. In Guatemala, the most common used measure to determine the risk of dengue outbreaks is monitoring mosquito breeding grounds through larval and pupal house index in every community (MSPAS, OPS, & Organización Mundial de la Salud [OMS], 2015). The methodology demands can't be met due to the shortage of staff in the Health Ministry, which is in charge of surveillance. Therefore, the same sites are sampled (MSPAS, OPS & OMS, 2015). Because of this, vector surveillance should be addressed through different methods, such as sentinel sites or ovitrap use, in locations like: a) La Unión, Nentón, Huehuetenango, b) Ciudad Tecún Umán San Marcos and c) Palín, Escuintla. Sentinel sites, defined as high-recurrent sites of dengue cases and vector populations, should be selected based on different information sources.

In Guatemala, sentinel sites can be selected by using the information presented in this study, concerning high-risk areas of possible dengue transmission, which are: 1) the northwest region of Huehuetenango, 2) the region located between Ciudad Tecún Umán and the Pacific coast of San Marcos, 3) the communities surrounding Atitlán Lake in Sololá, 4) the northeast region of Escuintla and 5) the mountain area between Pueblo Nuevo Viñas, Tecuamburro volcano, Cruz Quemada volcano and Moyuta volcano in Santa Rosa (Figure 3). It is advisable to perform necessary field researches to establish the effectiveness in studied regions, since the current study shows highly wide-scale ecological data. Therefore, it is necessary to do research regarding the implicated elements at a microclimate scale (Jansen & Beebe, 2010) to understand the cultural aspects of

human population in regions related to the disease (Bastos & Camus, 2004) and entomological indices.

As a conclusion, dengue case incidence in the territory of Guatemala seems to be highly influenced by *A. aegypti* vector presence. However, dengue cases do not present any causal relation with spatial vector distribution. Thus, it is recommended 1. To deeply research the relationship between *A. albopictus* vector and its role in dengue transmission in northern Guatemala, 2. To establish sentinel sites for vector surveillance, which could possibly be a) the northwest region of Huehuetenango, b) the region located between Ciudad Tecún Umán and the Pacific coast of San Marcos and c) the northeast region of Escuintla. Finally, 3. To evaluate the vector surveillance process used by authorities and the impact on the population health.

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