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A geographical investigation of Chagas' disease risk in the community of La Brea, Guatemala

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A GEOGRAPHICAL INVESTIGATION OF CHAGAS' DISEASE RISK IN THE COMMUNITY OF LA BREA, GUATEMALA

A Thesis

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DEDICATION

I wish to dedicate this work to my Grandmother Victoria Cristina Godoy, as a way to say thanks for all of your love.

Also, I wish to dedicate this work to my friend Dr. Michael Perich, who was my former employer at the Department of Medical Entomology at Louisiana State University and whose life was cut too short. His dedication to his profession and unending care for others inspired many of the people who had the pleasure to know him and his family.

To Mandy Mayeaux, many thanks for your help, undying support, study time, understanding and love. I could not do it without you.

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ABSTRACT

This thesis will display how the use of a GIS is an important tool in understanding geographic patterns of Chagas' disease vector risk in a rural community in Guatemala. This is an important topic of investigation as Chagas' disease is the leading cause of heart failure in rural Latin America, and yet study has been limited due to a prioritization of national resources to urban diseases. Obviously this can have a severe impact on rural areas, especially if they already lack adequate health care provision. As a response to this deficiency, a collaboration between the Laboratory of Entomology and Applied Parasitology (LENAP) of the University of San Carlos in Guatemala and the World Health Organization Collaboration Center (WHOCC) for Remote Sensing and GIS for Public Health at Louisiana State University has been established. This thesis presents research from that collaboration. This thesis has relied on cartographic and analytical approaches made possible in the GIS environment to display the geographical distribution of Chagas' disease vectors, including infestation and re-infestation in the community. Although triatomines were mostly found inside the houses, they were also found in larger numbers in chicken coops outside the domicile. Four hotspot locations were identified by selecting the house locations that contained the highest 10 percent of the triatomines counts. Then a buffer analysis was incorporated to extract and manipulate epidemiological information at each hotspot. This project also incorporates anthropological risk factors such as the construction materials of choice for house construction, and local attitudes to domesticated animals, in the creation of risk patterns. Although construction materials have an effect on the presence of triatomines, there are other approaches such as the incorporation of community disease surveillance programs

which appears to have an educational legacy effect. Also, clean houses seem to have less to no presence of Chagas' disease vectors in rural environment. Although the results of this thesis have implication for the community under investigation, the larger contribution is in showing how GIS flexibility can be used to gain insight from data not originally collected with spatial analysis as its primary focus.

CHAPTER 1. CHAGAS' DISEASE OVERVIEW

1.1 Introduction

According to the World Health Organization (WHO, 2007a), there is a great need for research with regard to tropical diseases, especially leishmaniasis, schistosomiasis, onchocerciasis, lymphatic filiriasis, Chagas' disease, malaria, leprosy, African trypanosomiasis, Tuberculosis and Dengue. It is notable that with the exception of Schistosomiasis, Leprosy and Tuberculosis, all the remaining diseases are transmitted by an insect vector. With the exception of Chagas' disease which is transmitted by an insect vector from the order hemiptera, the remaining six diseases are transmitted by insects that fall under the same taxonomic classification in the diptera order.

Yadav (2004, 199) suggests that, although there have been several geographical studies on the distribution of diseases or their vectors, the "Application of Geographical Information System (GIS) in health is a relatively new concept." According to Gesler (2003, 492), though modern medical research involving geography began as early as the 1950's, it has gone through an evolutionary process after a series of debates in the mid-1990s which expanded the research agenda to include other subjects related to health, such as: women's health, mental health, and the developing world, instead of just focusing "on disease ecology and health care delivery as topics and spatial analysis as a technique."

Currently, GIS is used not only as a means to analyze and then display disease risk areas, but also as a tool to collect primary field data. Examples of research in the former category include Getis et al. (2003), who describe the spatial pattern of Dengue vectors (mosquitoes) in Iquitos, Peru, with the use of clustering techniques, while Curtis

(1999), employed spatial filtering techniques to identify significant “holes” in disease surveillance surfaces. Other disciplines have also started to implement geographical research techniques to investigate disease patterns. Of relevance to this thesis, Cecere et al.(2004, 2006), and Vazquez- Prokopec et al. (2005), have implemented clustering techniques to identify infestation and re-infestation clusters of several triatomines insect species involved in the transmission of Chagas’ disease in different locations in Argentina. A further benefit of GIS, as mentioned by Yadav (2004), is that simple map outputs can provide invaluable assistance to public health officials. In other words, GIS output can be relevant in helping to solve public health problems in near real time. This last aspect continues to improve as recent technological advances enable on-the-fly medical research data collection and geographical analysis with the use of web-mapping technology.

1.2 Contribution of This Thesis

This thesis will include a descriptive analysis of Chagas’ disease vector presence and re-infestation in a rural community of Guatemala. Apart from providing insight into this particular community, this thesis will also contribute to the literature by showing how GIS flexibility in data manipulation and analysis can extract meaning from spatially incomplete data – a common occurrence in projects not originally designed for GIS analysis.

The first analysis of the thesis focuses on identifying hotspots within the community and the prevalence of Chagas’ disease vectors within these areas. This study aims to identify re-infested locations, as well as locations only infested in 2001, new infestations in 2002, and the locations that where never infested in either year in order to

try to explain the geographic distribution of *Triatoma dimidiata*—the insect vector of Chagas' disease—in the community of La Brea. In addition this study presents prevalence data of *T. dimidiata* reported at the homes as well as in the structures located around them.

The second section of this thesis analyzes the impact of domicile construction materials and the presence of *T. dimidiata*. In particular this study compares the effect of having or not having plaster covering the walls of the houses for two different years—2001, and 2002.

Finally, the last chapter provides an alternative solution to overcome data quality problems for future collaborative research projects. This alternative to standardized data collection is a web based GIS that can be operated by non-GIS trained users to generate maps and associated attribute values in a real-time and interactive exchange with distant research facilities.

In addition this thesis will provide a spatial-relationship focused literature review of control tactics of Chagas' Disease, its transmission cycle, and the factors associated with the prevalence of both the parasite and the insect vectors responsible of the transmission of the disease. This literature review will cover the general distribution of the vectors through out the Americas, and the biology and evolution of the parasite and the vectors. A second section of this study will include a literature review on the current status of Chagas' disease in Guatemala, identifying the endemic zones for the disease, and the cultural factors associated in the maintenance of the disease and its vector in this area.

1.3 Background to Chagas' Disease

Chagas' disease (CD) is an incurable, chronic parasitic disease, which can incapacitate people (Dujardin et al., 2002; Vasquez et al., 2004). CD affects the heart, esophagus, colon and peripheral nervous system, eventually leading to sudden death after a long asymptomatic period caused by organ failure (IDRC, 2006; WHO, 2006). The etiological agent of CD is a flagellate protozoan parasite *Trypanosoma cruzi*, which can be transmitted to humans by Triatomine insect vectors or by direct transfusion of infected blood (WHO, 2006). Other forms of transmission, though less frequent, can include congenital infection, accidental transmission in laboratory exposure or even organ transplant (WHO, 1991). According to Vasquez-Prokopec et al. (2004), in vector infections, *T. cruzi* is present in the feces which are deposited on the skin during the insects' feeding time. The infection of CD occurs passively when *T. cruzi* penetrates the body through the wounds caused by scratching of itchy or irritated skin as a result of the bite. *T. cruzi* can also penetrate the body through mucous membranes and conjunctivae (Lawyer and Perkins, 2000; WHO, 1991).

1.3 Geographical and Historical Reports of Chagas' Disease

Carlos Chagas reported the first case of American Trypanosomiasis in Brazil in 1909 (Figure 1.) (Monroy, 2003; Zeledon, 2004). Carlos Chagas described the symptoms of CD, its etiologic agent and proved the role of the triatomines in the transmission of the disease (Dujardin et al., 2002). This disease would later became known as "Chagas' Disease." According to Zeledon (2004), the second country to report Chagas' Disease in

Latin America was El Salvador in 1913 (Figure 2). El Salvador was considered the focal point of CD in Central America, though it took a further 54 years for all of the countries in the Central American region to report CD, with Belize being the last (Figure 2.).

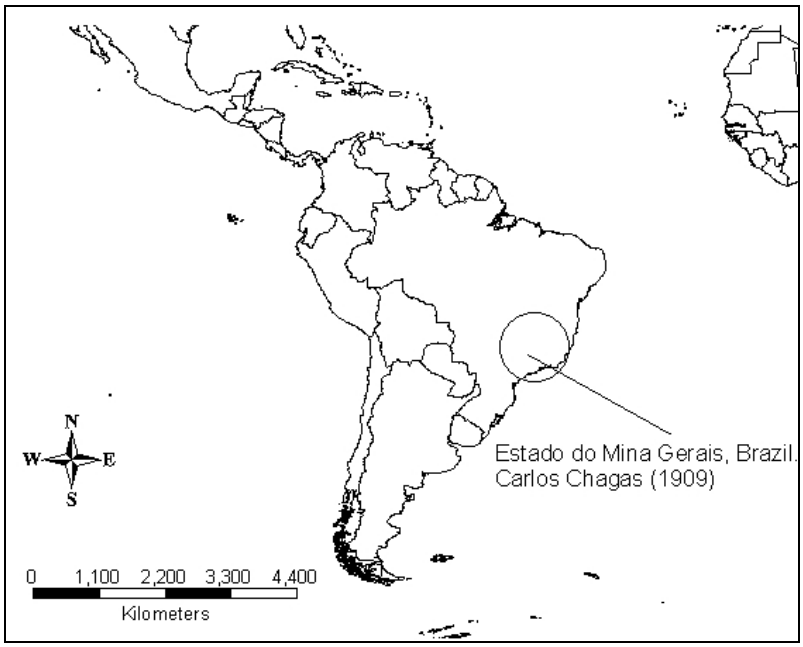


Figure 1. First case report in Latin America. Zeledon R., 2004

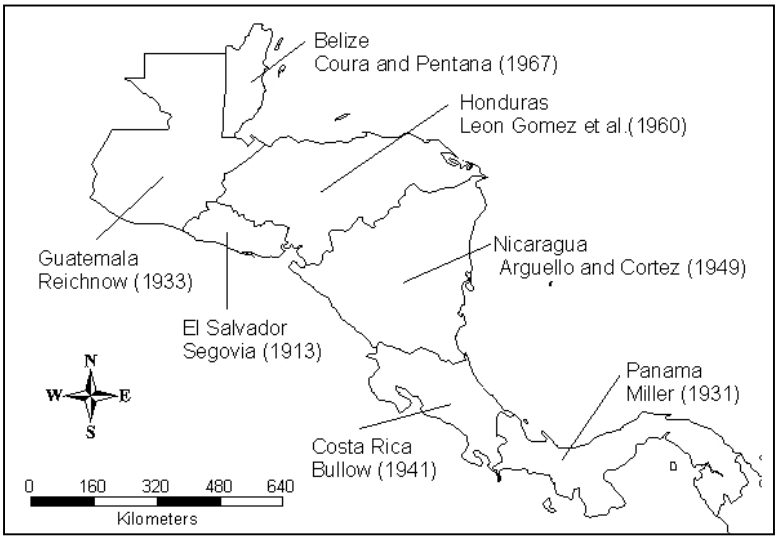


Figure 2.Chagas' Disease in Central America. Information taken from: Zeledon R., 2004

1.5 Phases and Clinical Forms of Chagas' Disease

CD generally undergoes three phases: an acute phase, an intermediate and a chronic phase, with the possibility of mortality occurring during any of the phases (WHO, 1991). From these phases, visual symptoms are only noticeable in the acute phase (Dujardin et al., 2002).

1.5.1 Acute Phase: The detection of the disease is difficult in this phase since it is usually asymptomatic (Lawyer and Perkins, 2000; Dujardin et al., 2002 and WHO, 1991). CD at the acute phase can affect people of any age, but in highly endemic zones, the clinical manifestations of the disease are more evident in children less than two years old (WHO, 1991). This phase lasts one or two months (Dujardin et al., 2002), and is characterized by a local inflammation of the area where the parasite penetrated; this sign is also called Chagoma (WHO, 1991). A common image associated with CD is the Romaña sign which is a form of Chagoma near the eye region, usually caused by the victim rubbing his/her eye allowing the parasite to penetrate (Lawyer and Perkins, 2000; Dujardin et al., 2002 and WHO, 1991). A major complication during this phase is a menignoencephalities—an inflammation of the brain and the central nervous system—where the mortality rate can be 50% (WHO, 1991).

1.5.2 Intermediate Phase: This phase occurs after the acute phase, and its duration is indefinite. The patient presents no visible signs or symptoms, but death can still occur during this phase (Dujardin et al., 2002 and WHO, 1991).

1.5.3 Chronic Phase: The chronic phase has been reported as early as five years and as late as twenty years after infection (Lawyer and Perkins, 2000). WHO (1991, 4)

reported, “An estimated 30% of the people that suffer the undetermined form of the infection will suffer cardiac, digestive and neurological damage 10-20 years after infection, meanwhile the remaining sick [percent of people] will not manifest any organic alteration.”

1.5.4 Social Impact of Chagas’ Disease Phases

According to Gascon et al. (2007), there are many factors that contribute to the social impact of CD in rural communities. Also, the social impact of the disease differs according to the phase of the disease in the patient. For example, Lawyers and Perkings (2000, 285) suggest that children usually present “a daily fever, swelling of the lymph nodes, liver and spleen; rash and heart conditions,” but children usually recover from this condition, although sometimes it can be fatal. On the other hand, with adults “debilitation and death occur most often as a result of complications involving affected heart or digestive tract.” In addition, Gascon et al. (2007) suggest that in many cases, the lack of knowledge of the disease in rural health workers results in the first symptoms being arrhythmia or sudden death. In other words, the disease often goes undiagnosed until its later and most serious manifestation. Thus, CD becomes a greater problem in communities that do not have access to health care. This is especially so in situations where, for example, a pregnant mother transmits CD to her unborn child. Rural locations often have no mechanism for correctly identifying the subsequent cause of death.

1.6 The Vector-Parasite Paradox

According to Schofield (2000), the hematophagic (blood feeding) behavior of CD vectors started approximately less than 5 million years ago, even though recent molecular

studies have demonstrated that *T. cruzi* is a relatively ancient parasite (approx. 65 million years ago). This situation creates the vector-parasite paradox meaning that the parasite is extremely old, yet its corresponding insect vector's hematophagic behavior is relatively recent.

In a recent study, Aufderheide et al. (2004), reported the presence of *T. cruzi* DNA in mummies in northern Chile and southern Peru whose ages ranged from approximately 9000 years before present to the time of the Spanish conquest. This study suggests that these cases were a result of a sylvatic (animal-infected) Chagas' cycle.

1.6.1 Epidemiologic Considerations

Over 100 different animal reservoir species have helped to maintain *T. cruzi* in the Americas (Aufderheide et al., 2004). WHO (1991), reported that approximately 150 species of 24 families of sylvatic, domestic and peridomestic mammals have epidemiological involvement in the survival of *T. cruzi*. Dogs and rodents played a major role in maintaining *T. cruzi* in peridomestic environments; however, Opossums (*Didelphis marsupialis*) may have been the original reservoir and vector of this disease (Schofield, 2000). According to WHO (1991), 20 species of Armadillo (*Dasypus sp.*), and several species of bats and primates have also been implicated as sylvatic reservoirs. In many cases, these reservoir species are comprised of animals that tend to nest (e.g. birds and bats) (Aufderheide et al., 2004).

1.7 The Parasite

T. cruzi is an asexual parasite and a flagellated protozoan that belongs to Order Kinetoplastid, Suborder Trypanosomatina and Family Trypanosomatidae (WHO 1991;

Lawyer and Perkins, 2000). According to Tulane (2006), "Members of this group parasitize virtually all animal groups as well as plants and insects. There are also free-living kinetoplastids which feed on bacteria in aquatic, marine and terrestrial environments." *T. cruzi* falls under the Order Kinetoplastid because it possesses a kinetoplast, which is an organelle in the mitochondria of the cell (WHO, 1991). *T. cruzi* alternates between humans and their insect vector (Figure 3.) (Lawyer and Perkins, 2000). This means that *T. cruzi* infects and reproduces in both vertebrate and invertebrate hosts, with the only difference being it will not kill the insect vector.

Although the parasites of both American Trypanosomiasis (Chagas' Disease), and African Trypanosomiasis (African Sleeping Sickness) belong to the same taxonomic genus, and they both alternate between human and insect hosts, they differ from each other in the mode of transmission. In the transmission of CD, the infection will not occur at the moment of bite, as opposed to African Trypanosomiasis (Lawyer and Perkins, 2000).

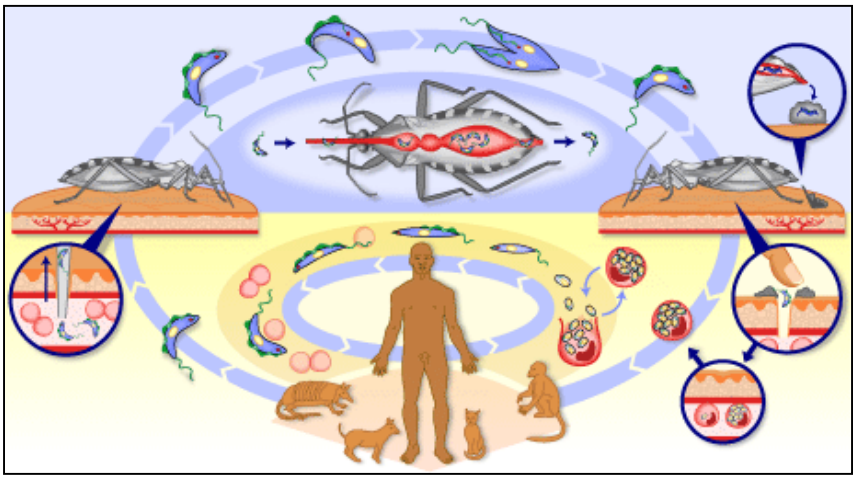
1.7.1 Vertebrate Host Cycle

According to Lawyer and Perkins (2000, 288), "*Trypanosoma cruzi* infections occur by the entry of compacted blood or liquid bug feces containing metacyclics into feeding lesions caused by the bite of the bug (Figure 3)." *Trypanosoma cruzi* "is also capable of penetrating mucous membranes and hair follicles" (Tulane, 2006). Once the parasite is in the blood stream of the vertebrate host, it goes through a series of developmental stages after it has penetrated different types of tissue, most commonly the spleen, liver, lymph nodes, and muscle (Lawyer and Perkins, 2000; Tulane, 2006). After the parasites differentiate into amastigotes, the amastigotes will form a structure that

looks like a peudocyst in the cells of the affected tissue for its reproduction (Lawyer and Perkins, 2000). Here, the amastigotes will mature inside the peudocyst and rupture it to differentiate into epimastigotes, which eventually will differentiate into infective trypomastigotes (Tulane, 2006).

1.7.2 Invertebrate Host Cycle

After the insect has taken a blood meal from an infected reservoir, the parasite migrates to the midgut of the insect, where it will differentiate into an epimastigote—non-infective stage of the parasite (Tulane, 2006). One to two weeks later, metacyclic trypomastigotes appear in the hind gut, becoming the only stage in the life cycle that is capable of infecting vertebrates through the insect's feces (Figure 3) (Lawyer and Perkins, 2000).



Source: http: Life cycle of *Trypanosoma cruzi* //www.who.int/tdr/diseases/chagas/lifecycle.htm

Figure 3. Chagas' Disease Life Cycle

1.8 The Vectors

Chagas' disease is endemic to 21 countries (WHO, 2006), and it is present in two ecological zones: in Central America, Triatomines live both inside and outside the

domiciles, while in South America, they only live inside human houses (WHO/TDR, 2004). *T. cruzi*, as well as the majority of its insect vectors, "occurs primarily in the Americas (except for the aberrant genus *Linshcosteus*, and the tropicopolitan *Triatoma rubrofasciata* and its asian relatives)" (Schofield, 2000, 535). This is due to the geographic distribution of the domestic and sylvatic reservoir hosts which overlap with the latitudes where triatomines (Figure 4) are usually found (Latitude 43ºN from USA to Latitude 46ºS to the Patagonia in Argentina) (WHO, 1991). It is within these latitudes that at least 25% of the population of Latin America resides, and therefore are at risk (Moncayo, 1999 and WHO, 2006).

It is important to note that triatomines can also survive outside of the previously described latitudes. In fact, seropositive triatomines—*Triatoma sanguisuga*, the most important Chagas' disease vector reported in the United States were reported attacking humans in Louisiana (Dorn et al., 2007). In previous studies, other triatomine species—*T. gerstaekeri* and *T. rubida*—have been reported in the United States, but mainly attacking dogs (Beard et al., 2003). Dorn et al. (2007), suggest that the presence of *T. sanguisuga* might be a result of an increase of the armadillo population nine months after Hurricane Katrina hit New Orleans.

1.8.1 Origin and Distribution of the Main Vectors

At present, CD vectors constitute 128 recognized species grouped in 17 genera in 5 tribes (Schofield et al., 1999), however only the genera *Triatoma, Rhodnius* and *Pastrongylus* have key vectors: *T. infestans, T. dimidiata, T. brasielsis, R. prolixus* and *P. megistus* (Monroy, 2003). The role of these vectors varies geographically as humans manage to alter natural environments (WHO, 1991). According to WHO (1991),

R. prolixus and *T. dimidiata* are the main vectors of CD in the Central American and northern region of south America, while *T. infestans* is the main vector in South America.

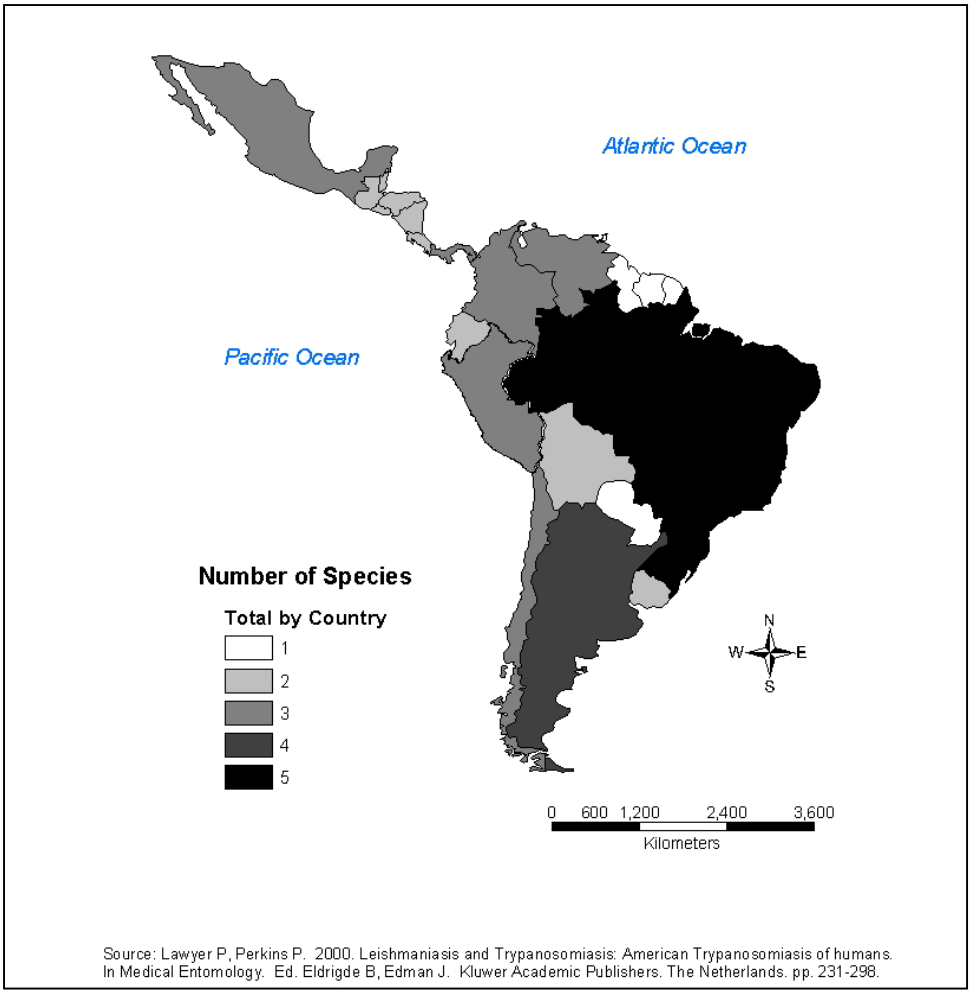


Figure 4. Vector Diversity in the Americas

1.8.2 General Biology of the Insect Vectors

1.8.2.1 *Triatoma dimidiata*

In the Yucatan peninsula, Mexico is the presumed origin of *T. dimidiata* which has spread through Mexico, Central America, Colombia and Ecuador (Figure 5.) (Lehmann et al. 2005). Dumontiel et al. (2002), suggests that the seasonal abundance and flying behavior of this species plays a bigger role in the transmission of CD than just the

domicile transmission. According to Monroy (2003), *T. dimidiata* is the vector with the most versatile habitat adaptation. Contrary to the versatile behavior of *T. dimidiata* in Central America, *T. dimidiata* has only been documented as entirely domestic in Ecuador (Abad-Franch et al., 2001). Archeological evidence by Meggers & Evans (1963), suggests that *T. dimidiata* might have been transported through the pre-Columbian maritime routes (Dias et al., 2002). *T. dimidiata* mainly feeds on the blood of humans, dogs, rodents, opossums, chickens and cats, with the primary blood meal varying with geography (WHO, 1991).

1.8.2.2 *Rhodnius prolixus*

R. prolixus is the main CD vector in Central America even though it is not native to the area (Figure 5.) (Schofield and Dujardin, 1997). It is suspected that imported *R. prolixus* from France escaped from research facilities in El Salvador (Zeledon, 2004). *R. prolixus* is a species native to the northern part of South America, where it has been associated with sylvatic nesting mammals and birds. In Central America, *R. prolixus* is found only as a domestic vector (WHO, 1991). According to Zeledon (2004), *R. prolixus* is an integral part of the dispersion of CD in Central America since CD cases were reported shortly after the escape of the infected bugs in El Salvador. Although its control and eradication seems feasible in Central America (Zeledon, 2004), *R. prolixus* has shown pesticide resistance against dieldrin in Venezuela (WHO, 1991).

1.8.2.3 *Triatoma infestans*

T. infestans is the main vector for Chagas' disease in South America, and it is the primary control target of the Southern Cone Initiative, an international CD control

strategy (Dias et al., 2002). *T. infestans* is the oldest domiciliary triatomine species, but has also been reported in silvatic habitats (WHO, 1991). According to Dujardin et al. (1998), Bolivia is believed to be the origin of *T. infestans*, the most widespread domestic vector of CD which is distributed in the southern countries of South America (Figure 5.). *T. infestans* mainly feeds on the blood of humans, dogs, chickens and cats, but, like *T. dimidiata*, the blood source of choice varies geographically (WHO, 1991).

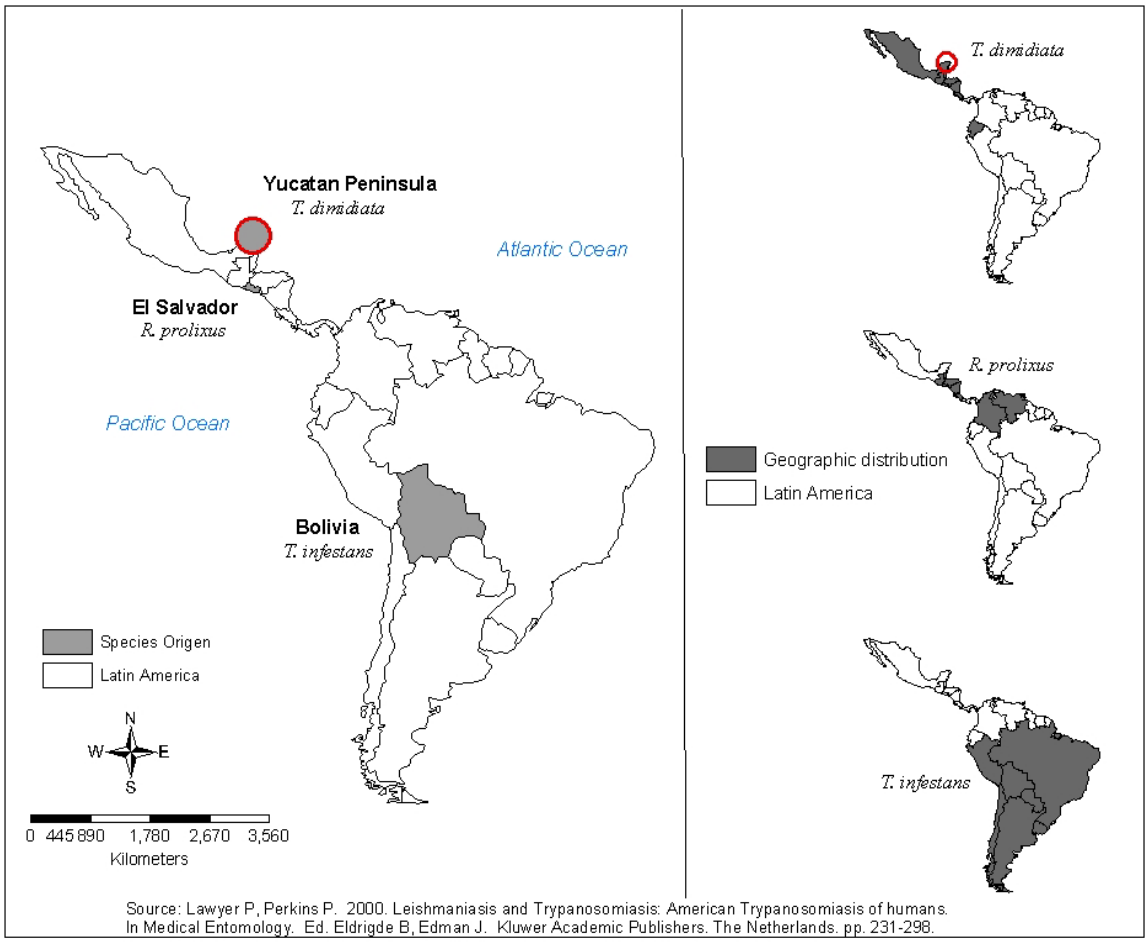


Figure 5. Origin and distribution of CD Vectors in Latin America

1.9 Vector Control

The goal of vector control is to interrupt the transmission of CD, but this can only be achieved through spraying of residual insecticide, house improvements, and health

education (WHO/TDR, 2004). These control strategies started in Brazil in 1940 and expanded to the rest of America through 1970 (Dias et al., 2002). However, vector control needs to be adapted to the unique entomological conditions of the countries involved (WHO/TDR, 2004). As a result of the vector control efforts during the 1960's and 1970's (WHO, 2006), the Pan American Health Organization (PAHO) launched and coordinated two international control initiatives: the "Southern Cone Initiative" in 1991, and a strategy for the Andean region and Central America in 1997 (Dias et al., 2002). According to Dias et al. (2002), blood screening of infected blood donors in Latin America started in 1980 after the emergence of AIDS. In 1993, the countries with the highest risk probability of transfusion-transmitted infection per 10,000 individuals were Bolivia (219.28) and Peru (49.56) from South America, and El Salvador (17.75) and Guatemala (7.35) in Central America (Schmunis et al., 1998). Guatemala is far from eliminating *T. cruzi* through blood transfusion since serology testing for *T. cruzi* started (in limited scope) in Guatemala in 2003, performed mainly by universities and was not available in all of the blood banks (Monroy, 2003). According to Dias et al. (2002), contiguous control in endemic countries can lead to elimination of the most highly domestic vectors, significantly reducing the transmission of CD by widely spread triatomines species in rural communities. Currently, the integrated control strategies have helped decrease the annual incidence of new cases in Latin America, reducing it from 700,000 - 800,000 in 1980 to approximately 200,000 in 2006 (WHO, 2006). With this promising decrease, PAHO's CD control initiative goal is to cease the transmission of CD by 2010 (Monroy, 2003).

1.9.1 Social Health Problems in Vector Control

Even though there has been success controlling or decreasing the incidence of new cases of CD, it is important to remember that the vulnerable populations are located in poor rural communities. In some cases, these populations are politically prioritized, especially when it is perceived that populations in urban areas are at risk from other disease outbreaks. For example, in Brazil, mosquito control campaigns made the CD campaign subordinate to re-emerging mosquito-borne diseases, even though many of these diseases transmitted by the Yellow Fever Mosquito *Aedes aegypti* are treatable and non life-threatening (Dias et al., 2002). Treatable and non life-threatening infections in urban areas and ignorance of CD threats become larger problems in rural communities where CD vectors are native to the area due to residual foci remaining in silvatic habitats (Schofield and Dujardin, 1997). The role geography plays in CD foci and re-infection will be discussed later.

1.10 Socio-economic and Cultural Risk Factors of Chagas' Disease

According to Cecere et al. (2004), Chagas' disease is often associated with rural poverty, with communities that have poor housing conditions being especially vulnerable. Unfortunately, in these poor rural areas, CD usually goes undetected, and the houses, which are usually constructed of thatched roofs and adobe or mud over wood walls and dirt floors, continue to provide suitable habitat for the bug (Lawyer and Perkins, 2000). Even though transmission of CD can be interrupted by physically removing the vector (Dujardin et al., 2002), if these building materials remain, reinfestation is likely to occur (Lawyer and Perkins, 2000).

1.10.1 Domestic Factors

Much of the literature indicates that the presence of *T. dimidiata* or other CD vectors—*T. infestans, T. guasayana, T. nitida, T. pallidipenis*—is linked to multiple cultural factors such as the type of building materials used for the house, and structures around a house (Table 1.). Most of the time, CD vectors are reported to be present in houses that are built with adobe walls and thatched roofs (Table 1.). Enger et al. (2004), suggests that data collection should not just be limited to recording house construction materials, though these remain the most commonly reported. In their research, Enger et al. (2004, 760), concluded that apart from the type of house construction materials, other variables, such as "agricultural products, junk piles and number of rabbits" are also associated to the domiciliary presence of CD vectors. In addition, Greer et al. (1999), reported in a *T. cruzi* surveillance study that individuals that had dogs living inside of the houses had a higher seropositivity compared to people without dogs.

Enger et al. (2004) emphasize that accurate information is critical to develop a successful vector control program. In other words, it cannot be assumed that what worked in one area is going to work in another area. The same analogy can be applied to the CD vector species in the sense that different species differ in biology, ecology and behavior.

1.10.2 Peridomestic Factors

Researchers have reported (Table 2.) several peridomiciliary structures in different countries, and it is notable that some of these structures are related to agriculture. In addition to these, the tabulated reports display a geographic overlap between the countries in terms of Peridomiciliary Risk Factors despite the geographic difference of the locations: Mexico from North America, Costa Rica and Guatemala from

Central America, and finally Argentina in south America. In general, most of the countries (Table 2.) reported presence of CD vectors in locations where chickens were also present. Other structures such as corrals were mentioned, though mostly in Argentina. Another noteworthy fact is that CD vectors were reported in areas related to the storage of human food, for example in Argentina (Vazquez-Prokopec et al., 2005; and Cecere et. al . 2004, and 2006), just as they were for the Mayans (Monroy et al., 2003b).

It is important to note that different species have different behavior and habitat requirements. Despite these biological differences, studies have reported similarity in the geography between the two main ecological zones—Central and South America. For example, Chagas' disease vectors have been reported in environments that range from semiarid to rain forest throughout the Americas (Vazquez-Prokopec et al., 2005; and Cecere et. al. 2004, and 2006; Zeledon, 2001). Also, forested areas that suffer an increase in human activity pose a greater risk for infestation of Chagas' disease vectors (Monroy et al., 2003; Cecere et al., 2006). Zeledon (2001) also suggests that sylvatic Chagas' disease vectors are attracted to lights at nights.

From the previously mentioned studies (Table 2), few studies report actual infestation and re-infestation distances of Chagas' disease vectors in rural communities (Table 3). Distances that are reported range from 100-150m in one cluster and from 400-1000m in a second cluster of infestation for *T. guasayana* (Vazquez-Procopek et al., 2005). For the same species, re-infestation clusters were reported at distances of 1000m away from the source. Other studies (Cecere et al. 2004) report a reduction of the cluster distances in subsequent years for *T. infestans*. In another study, *T. infestans* showed the opposite behavior, increasing re-infestation clustering distance in a subsequent year from

50 m, to clusters reported to be significant at distances from 100-250m (Cecere et, al., 2006). In other words, there appears to be no consistent geography, at least from the limited number of studies reported (Vazquez-Prokopec et al., 2005; and Cecere et al. 2004, and 2006). Hotspot distances, and the geographic extent of re-infestation are likely to vary from species to species, and from location to location (Table 3).

Table 1. Reports of structural characteristics of houses where CD have been present by Country

		Publication									
		Catala et al., 2004	Enger et al., 2004	Nakagawa et al., 2003	Rizzo et al., 2003	Greer et al., 1999	Tabaru et al.,1999	Monroy et al., 1998	Monroy et al., 1999	Goldsmith et al., 1992	Vazquez-Prokopec et al., 2005
Description of wall construction materials	Adobe (unfired mud bricks)		M	G	G	G	G				A
	Bajareque (plastered unfired mud bricks)			G	G	G	G				
	Brick walls	A	M								
	Cane				G						
	Cement				G						
	Corrugated Metal				G						
	Mud Walls							G	G		
	Mudstick walls--Unplastered--		M								
	Wood				G						
	Wood poles									M	

A= Argentina, G=Guatemala, M= México

Table 2. Reports of Peridomiciliary structures where CD vectors have been present by Country

		Publication					
		Cecere et al 2004	Monroy et al.2003	Zeledon et al. 2001	Vazquez-Prokopec et al., 2005	Cecere et al., 2006	Enger et al., 2004
Peridomiciliary Risk Factors	**Animal Related**						
	Chicken coops			CR	A		
	Chicken coops (Experimental)		G				
	Chicken House or Nest	A					
	Chultunes (Ancient holes built by Mayans)		G				
	Corral	A					
	Corral (Cow or Horse)	A					
	Corral (Goat)	A				A	
	Corrals				A		
	Tree with Chicken	A					
	Tree with out Chicken	A					
	Other Peridomiciliary Structures						
	Fire wood	A		CR			
	Kitchen or Store Room	A					
	Latrine	A					
	Light traps			CR			
	Mud Oven	A					
	Orchard Fence	A					
	Small Granary					A	
	Store rooms				A	A	
	Junk Piles						M
	Agricultural products in yard						M

A=Argentina, CR=Costa Rica, G= Guatemala, M=México

Table 3. GIS, clustering distances and spatial approaches by species

Author	Specie	GIS/ Spatial Analysis	Type of infestation	Time period	Distance Reported
Cecere et al. 2004	*T. infestans*	Local Spatial Statistics Gi [d]	Re-infestation	1995	400 m
		Local Spatial Statistics Gi [d]	Re-infestation	1996	25-175 m
Vazquez-Procopek et al. 2005	*T. guasayana*	Local Spatial Statistic Gi*[d]	Infestation, (Northern Cluster) Infestation, (Southern Cluster)	N/A	400 - 1000m 100 - 150m
		Local Spatial Statistics Gi [d]	Re-infestation (Northern Cluster) Re-infestation (Southern Cluster)	1996-1998	400-1000m No Clusters
Cecere et al. 2006	*T. infestans*	Local Spatial Statistics Gi [d]	Re-infestation	1995	50 m
			Re-infestation	1996	100-250 m

CHAPTER 2. GEOGRAPHICAL DISTRIBUTION OF CHAGAS' DISEASE (CD) VECTORS IN GUATEMALA

2.1 Chagas' Disease in Guatemala

According to Nakagawa (2002), "Chagas' disease is one of the most serious vector-born diseases in Guatemala. It is estimated that in Guatemala 4,000,000 people are at risk for Chagas' disease; 730,000 people are currently infected; and 30,000 people are infected annually." The parasites *T. cruzi* and *T. rangeli* were first reported in Guatemala in humans in 1932 and 1934 (Reichnow, 1933; Blanco, 1943). Only three triatomine vectors were suspected of transmitting CD between 1932 and 1934 (Monroy, 2003a). In addition to the insect vector transmission, *T. cruzi* has also been reported in the Guatemalan blood banks (WHO, 1991), and congenital transmission has also been documented (Matta, 1992).

2.2 Vector Competence and Biological Diversity in Guatemala

Monroy (2003), reported four different vector species distributed in Guatemala: *R. prolixus*, *T. nitida*, *T. dimidiata*, and *T. ryckmani*. From these, *T. dimidiata* and *R. prolixus* are of the highest epidemiological importance and concern. The vector populations of Guatemala are 64.4%, 30.7% and 4.7% of *T. dimidiata*, *R. prolixus*, and *T. nitida* respectively (Tabaru et al., 1999). Even though *T. nitida* has also been reported as a competent vector of CD, it is considered of low importance since it is only present in low numbers and is not widely distributed (Monroy et al., 2003a). Of the two highly important vectors, *R. prolixus* is not native to Central America and can be eliminated with insecticidal control (Hashimoto et al., 2005). Conversely, *T. dimidiata* is endemic to the area, occupying a variety of habitats including sylvatic, domestic and peridomestic

environments in 21 of 22 Guatemalan departments (Calderon et al., 2005; Monroy, 2003; Monroy et al., 2003a). It is important to note that even though there is an overall geographical distribution overlap among species (Figure 6), each species is specifically predominant in different departments when analyzed individually. For example, according to Hashimoto et al. (2005), of all departments, Santa Rosa had the highest numbers of *T. dimidiata* though Jutiapa had the highest *T. dimidiata* house infestation rate (18%).

2.3 Geographical Distribution and Physical Implications of CD Vectors

Chagas' disease has been frequently reported in humans in the Guatemalan departments of Chiquimulilla, Jalapa, El Progreso, Santa Rosa, and Zacapa (WHO, 1991). Rizzo et al. (2003), believes that these areas constitute the principal CD endemic areas in Guatemala. Previous studies (Tabaru et al., 1999) have reported that the vector distribution occurs mainly in the east and southeastern parts of the country, specifically in the departments neighboring the countries of Honduras and El Salvador. Tabaru et al. (1999), and Monroy et al. (2003a), have reported *T. dimidiata* as the vector with the widest geographic distribution in the country, although other CD vectors are widely distributed in 16 of 22 departments (Figure 6). Altitude may play a role in the presence of triatomine vectors since Tabaru et al. (1999), reported that 85% of triatomines collected in his geographical study were in communities between 800-1400 meters above sea level. Also, Greer et al. (1999), performed a serological study in three villages in Chiquimula and reported that human seropositivity was related to altitude. In many cases, *T. nitida* is usually not found in altitudes below 950 meters above sea level, and as reported, *T. nitida* was consistently found in conjunction with *T. dimidiata* and *R. prolixus* (Monroy et al., 2003b). In

addition, Rizzo et al. (2003) reported *T. cruzi* infection among school–age children in communities less than 2000 meters above sea level.

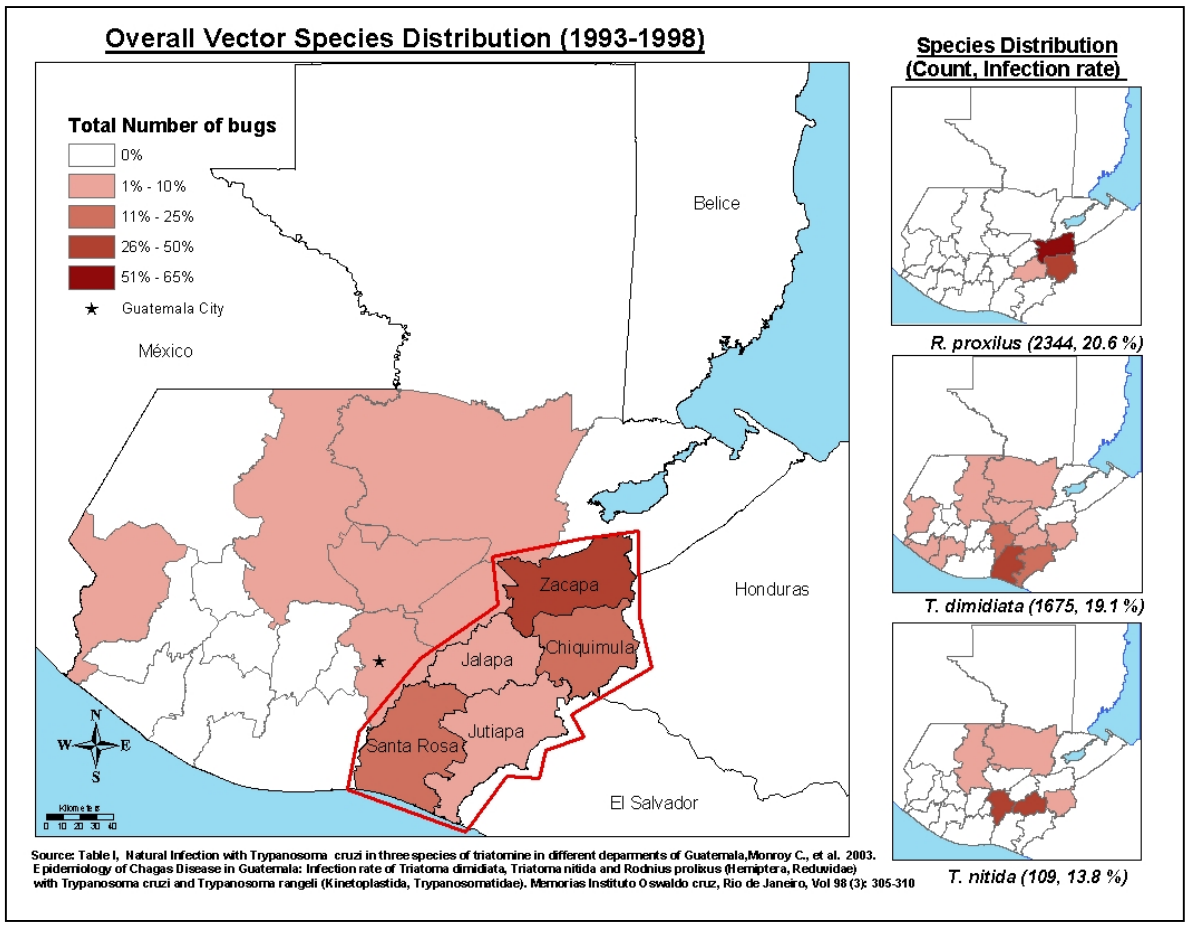


Figure 6. Chagas' Disease Endemic area and distribution of CD Vectors in Guatemala

2.4 Cultural Factors Associated with the Presence of CD in Rural Guatemala

2.4.1 Structural Materials of Houses and CD

In Guatemala, rural houses are usually only 40-50 m^2 (Monroy, 1998). According to Tabaru et al. (1999, 20), the inside of houses in the village of Santa Rosa Ixhuatan consist of "one room including a kitchenette with a fire stove, 2-3 humble beds and a few baskets for storing clothes and food items."Aside from the inner amenities, another important factor related to CD is the construction materials used to build houses. For example, Ferrer et al. (2003) reported in the Paraguayan Gran Chaco region that

individuals who lived in houses made of dried mud had a higher seropositivity compared to those that used manufactured materials. During his research, Greer et al. (1999), found that people from houses in three rural villages in the department of Chiquimula, Guatemala, made out of mud-brick, mud-stick, bamboo strip, and straw or banana leaf walls were also seropositive to *T. cruzi* (Figure 7). Although Greer et al. (1999) also analyzed the effect of roof type and animal presence; he determined that wall type was a more determining factor for the presence of *T. cruzi*. Based on this fact, it is likely that construction materials dictate the presence of *T. cruzi* and therefore should dictate the control strategy to utilize for vector control. For example, Monroy et al. (1998), suggest insecticide application to mud-walls to target *T. dimidiata* and directed to the roof in houses that had palm-thatched roofs to target *R. prolixus.*

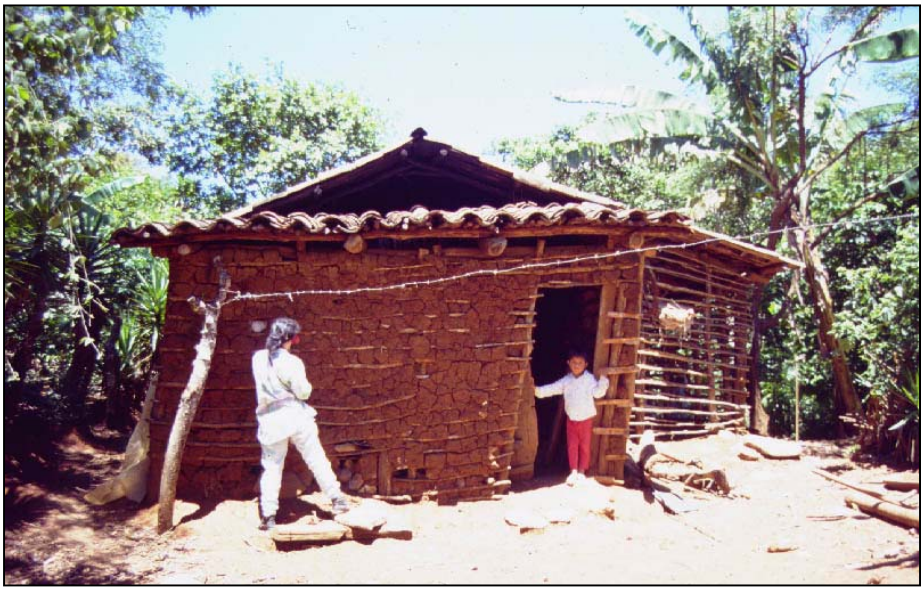


Figure 7. Typical infected house made of mud
Source: Patricia Dorn 2006. www.loyno.edu/~dorn/Images/house.jpg

2.4.2 The Role of Local Health Education in Vector Identification and Control of CD

In an entomological study in Guatemala from 1995-1996, Tabaru et al. (1999) reported that local people in rural villages lacked knowledge of CD or its vectors. For

example, in some instances, villagers had misidentified CD vectors as “cockroaches” (Tabaru et al., 1999; Hashimoto et al., 2005). This misidentification of CD vectors appears to be a common mistake in different parts of Latin America though the extent varies by country. For example, Salazar-Schettino (1983), reported in the state of Nayarit, Mexico that the locals believed that the triatomine *Triatoma phyllosoma picturata* had aphrodisiac properties instead of being harmful; in the state of Oaxaca, the villagers rubbed the triatomine feces on warts believing that the feces had medicinal properties. Also, an important result of a cross sectional study in Guatemala performed on school-aged children of 58 municipios by Rizzo et al. (2003) showed that only 5.35% of the children had heard of CD. Examples like these indicate that more education programs should be implemented in endemic areas.

Previous educational strategies have shown positive results in increasing CD awareness. According to Hashimoto et al. (2005), between August of 2000 and October of 2001, a School-based Information Education and Communication program was launched in the state of Jutiapa to train primary school teachers on how to teach health education to primary school kids. This program was a joint effort between the Japan International Cooperation Agency (JICA), the Japan Overseas Cooperation Volunteers (JOCVs) and the Ministry of health of Guatemala. The program showed an increase in local awareness of CD, which provided local vector control teams with new information of vector presence in approximately 52% of the communities they surveyed (Hashimoto et al., 2005).

CHAPTER 3. GEOGRAPHICAL DISTRIBUTION OF CHAGAS' DISEASE VECTORS IN THE COMMUNITY OF LA BREA

3.1 Introduction

The purpose of this study is to use and analyze existing geographical databases that contain CD vector prevalence to determine risk areas in the community of La Brea, Guatemala, with the use of a Geographical Information System (GIS). This project was possible due to a research collaboration between the Laboratory of Applied Entomology and Parasitology (LENAP) from the University of San Carlos in Guatemala and the World Health Collaboration Center (WHOCC) for Remote Sensing and GIS for Public Health at Louisiana State University. This study aims to provide a geographical description that will explain the distribution of CD vectors in the community of La Brea.

The community of La Brea is located in the municipio of Quezada, northwest of the department of Jutiapa, Guatemala (Figure 8). Jutiapa is located in south Guatemala and shares a border with El Salvador; west of Jutiapa is the department of Santa Rosa, which is the department that has the highest presence of *T. dimidiata* in Guatemala (Monroy et al., 2003). However, Jutiapa is the department with the highest *T. dimidiata* house infestation rate (Hashimoto, 2005).

La Brea is located at Latitude 14° 20' 9N and Longitude 90° 4' 32W at an altitude of 1310 meters (Falling Rain Genomics, 2004). The houses are situated in both agricultural and forested areas (Figure 9). The majority of the houses have walls made of adobe (mud), dust floors, and tiled roofs. Many domiciles have a variety of domestic animals which include dogs, chicken, cats, pigs, donkeys, ducks and horses. Silvatic host species of *T. cruzi* such as opossums, rat, and mice are also present in the La Brea area (LENAP, 2001).

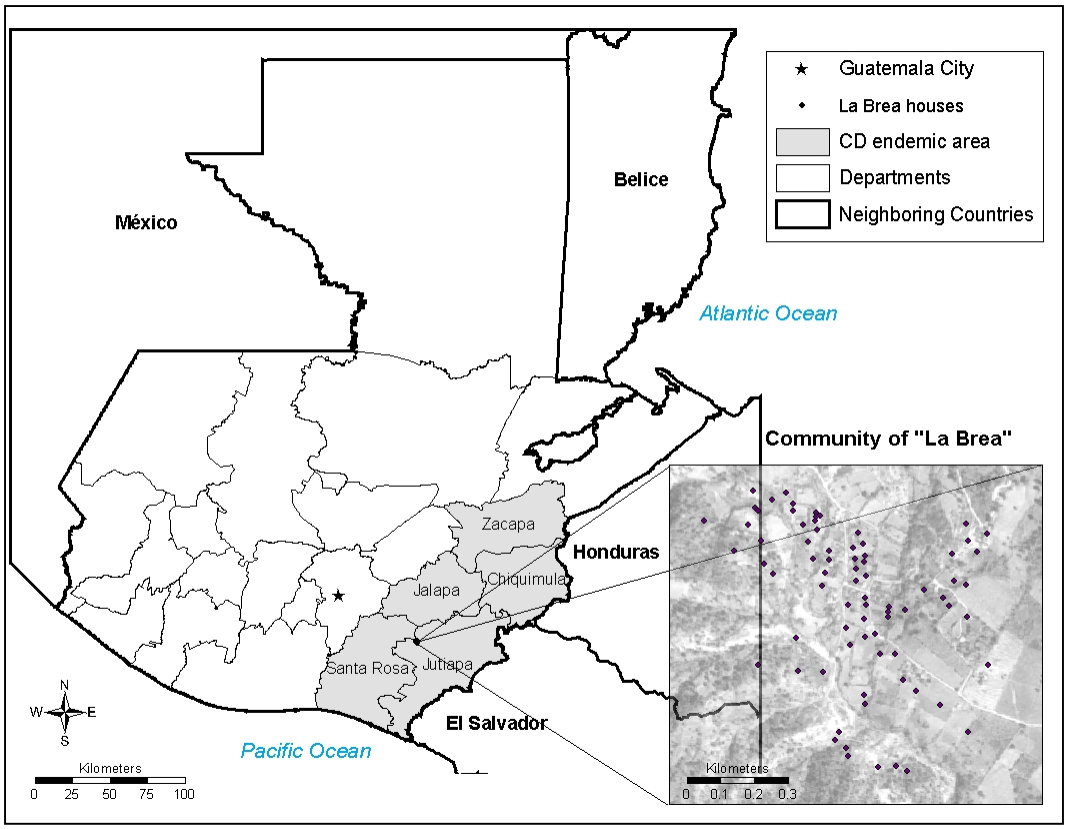


Figure 8. Site location

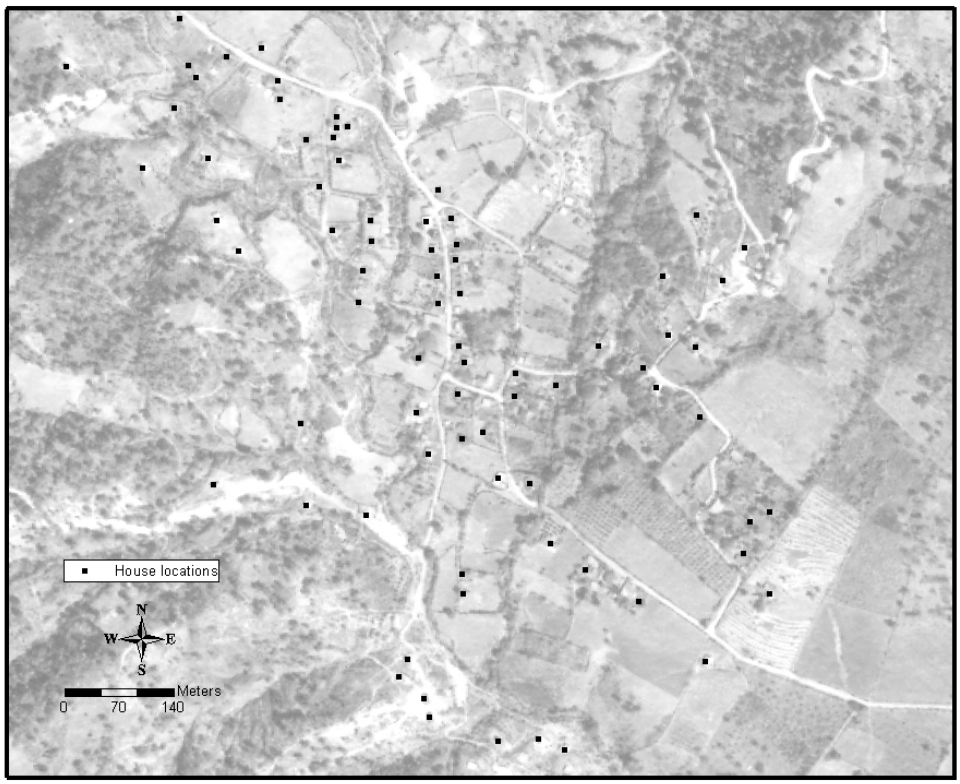


Figure 9. House distribution in the community of La Brea

3.2 Materials and Methods

3.2.1 Data Collection

Entomological surveys (Table 4.) and the house location coordinates were collected from 77 houses in the community of La Brea for the years 2001 and 2002 by the GIS personnel of the Laboratory of Applied Entomology and Parasitology (LENAP) of the University of San Carlos in Guatemala. Aerial photos and entomological information related to the houses of the community of La Brea were also supplied by LENAP.

3.2.2 Entomological Survey

The research team from LENAP performed an entomological survey utilizing the man-hour method in which groups of two people search the houses for triatomines with the help of a flashlight (Monroy et al., 1998). In order to achieve this method, the researchers need to spend a certain amount of time in the house. This time is dependent on the number of people that go inside the house so that man hours are standardized. For example, if two people go inside a house, they each spend 30 minutes; in the case of three people searching, they should only spend 20 minutes searching for triatomines. This survey intended to collect information relating to *T. dimidiata* in rural areas. While performing the search for the insect vectors, the team from LENAP also recorded data of the houses' structural materials (walls, roof and floor), the presence of domestic and sylvatic animals, plus the exact collection site of the triatomine—wall, chicken coop, under a bed and so on.

These entomological surveys consist of an initial base line survey administered before the application of -insecticide, and a second survey to identify re-infestation. Each

survey was performed in a days' worth of work. The houses where treated with a Deltamethrine insecticide (5%) by the Guatemalan Health Ministry Vector Control Division—Sección de Entomología del Ministerio de Salud Pública y Asistencia Social (MSPAS). For the insecticide application, MSPAS used backpack sprayers from the Hudson X-pert brand.

Table 4. Entomologic survey data

Data	**Attributes**		
Survey date	2001 and 2002		
Name of house owner			
Location ID	Assigned geographic Id number		
House coordinates	Geographic coordinates		
Residence time	In years		
Wall materials	Adobe	Brick	
Floor Materials	Dirt	No dirt	Cement
Ceiling Materials	Tile	Metal	
Plaster information	Yes	No	
Location of different structures	Kitchen	Woodpiles	
Presence of animals	Sylvatic	Domestic	
Vector information	Sex	Stage	Counts
Place of collection	Wall	Bed	Chicken coop
Location infestation	Domicile	Peridomicile	

3.2.3 Data Problems and Limitations

Although the entomologic (vector counts) data were well recorded, there were inconsistencies in other aspects of the survey that failed to provide information that would have allowed for a more robust analysis. In some cases, the collectors failed to fill the survey forms correctly, forcing the person that entered the data to report several data attributes for the houses of the community of La Brea as "non-determined" (Figure 10). These situations forced the data analysis to be performed only on locations that contained complete attributes.

SEOW	NUMPERS	LIVINGTIME	WALLMAT	FLOOR	CEILINGMA	PLASTED	KITCHEN	FIREWOOI	FWOODPLC	ANIMINSIDE	ANIMOUTSI	SILVANIM	BU
o de	4	nd	adobe	cement	tile	yes	ne	nd	nd	no	chicken	no	no
ela	3	30	adobe	cement	metal she	yes	inside	nd	nd	nd	chicken	nd	Td
cupie	0	nd	adobe	dust	tile	yes	nd	nd	nd	nd	nd	nd	no
rmin	0	nd	adobe	dust	tile	partial	outside	outside	nd	nd	nd	nd	no
cupie	0	nd	adobe	dust	metal she	nd	nd	nd	nd	nd	nd	nd	no
io M	7	20	block,ado	cement	tile	yes	outside	outside	nd	nd	chicken	nd	no
o Ro	10	15	adobe	nd	nd	no	nd	nd	nd	nd	nd	nd	fec
io R	7	nd	adobe	cement	tile	yes	outside	nd	nd	nd	chicken	nd	Td
acio	4	30	adobe	cement	tile	yes	outside	outside	nd	no	nd	nd	Td
el de	10	nd	adobe	dust	tile	no	outside	nd	nd	nd	chicken	nd	Td
an R	2	50	adobe	dust	tile	no	outside	nd	nd	nd	chicken	nd	Td
Ber	9	22	nd	cement	tile	no	nd	outside	nd	nd	nd	nd	Td
o Ra	8	8	adobe	dust	tile	no	outside	outside	kitchen,y	nd	dog,chick	rat	Td
a	3	30	adobe	dust	tile	yes	outside	outside	nd	nd	cat,dog,c	rat	no
del	6	40	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	Td
Ram	1	0.5	adobe	dust	tile	yes	nd	nd	nd	no	no	nd	no
es Pe	10	14	adobe	cement	tile	no	outside	outside	nd	nd	nd	nd	Td
a Fl	9	nd	adobe	dust	tile	partial	outside	outside	nd	nd	nd	nd	fec

Figure 10. Displays a snapshot of some locations with missing information

3.2.4 Entomologic and Geographic Data Manipulation

LENAP provided the entomological data tabulated in Microsoft Excel. The files included survey information for the years of 2001 and 2002. These data were joined with the house number ID from the entomological survey to a house point data shapefile that contained the coordinates of the houses of the community of La Brea. These coordinates were provided by LENAP from a previous study in the area and were obtained with the use of a GPS. These coordinates were joined to the entomologic database to generate a GIS shapefile.

3.2.5 Aerial Photos

For this project, LENAP provided a series of aerial photos, topographic sheets for the country of Guatemala (Scale 1:50,000) and satellite images of the community. Aerial photos were preferred due to the lack of spatial resolution (a 30 meter pixel size) in the satellite images which resulted in each pixel having an area greater than the houses in the community. The aerial photos were geo-referenced at the “World Health Organization Collaboration Center for Remote Sensing and GIS for Public Health” (WHOCC) at Louisiana State University using the Geo-referencing tool bar from the menu in ArcGIS

9.0. For this purpose, Guatemalan topographic sheets (scale 1:50,000) were used as reference to geo-reference the aerial photos. The geo-referenced images were stored at WHOCC Lab at LSU.

3.3 Geographical Analysis

The goal of the study was to analyze existing geospatial databases of prevalence data of disease vectors, in this case CD. For this, a GIS was constructed to respond to questions such as: where are the vector hotspots in the community, and what factors might cause vector presence or absence?

3.3.1 Descriptive Re-infestation Data Analysis

On an initial observation of the data tables, it appeared that many of the locations in the community of La Brea had either houses or structures outside of the houses that were re-infested by *T. dimidiata* after a pesticide application after the initial survey in 2001. A location was defined as a geographic unit that included aggregated entomologic information of the domicile and peridomicile for each house. To analyze reinfestation, four locations were identified as hotspots in 2001 (Figure 11). The goal of this study is to describe the characteristics of the houses around the following hotspots at multiple distances- 50m, 100m, 150 m, and 200m.

3.4 Hotspots Identification

For this study, the “hot spots” were identified by querying out the locations in the top 10% of locations with the highest number of bug totals. This method was chosen over other traditional techniques, such as the Gi*and Gi (Vazquez-Prokopec et al., 2005; and Cecere et. al. 2004, and 2006) due to a small sample size and the heavily skewed

distribution of CD vectors concentrated on few locations. For example, locations 17 and 18, had 30 and 107 *T. dimidiata* while the rest of the locations reported an average of 3 *T. dimidiata.* These 130 *T. dimidiata* constituted at least one-third of the total sample. A hotspot was defined as the top ten percent of locations (by bug totals) and an area of 50 meters surrounding it. Locations with the ID number 3 and 153 were not included as hotspots, even though their bug totals placed them in the top 10%, because they where isolated from the rest of the locations. The remaining hotspot locations were used to perform a buffer analysis at each individual hotspot location to determine the amount of infested houses in 2001 and to determine which houses were re-infested in 2002. These buffers around were made in ARCGIS 9.0 at four different radii-50 m, 100 m, 150 m and 200 m. Greater distances would cover at least half of the community and produce greater overlap between hotspots, making the analysis more difficult and less specific.

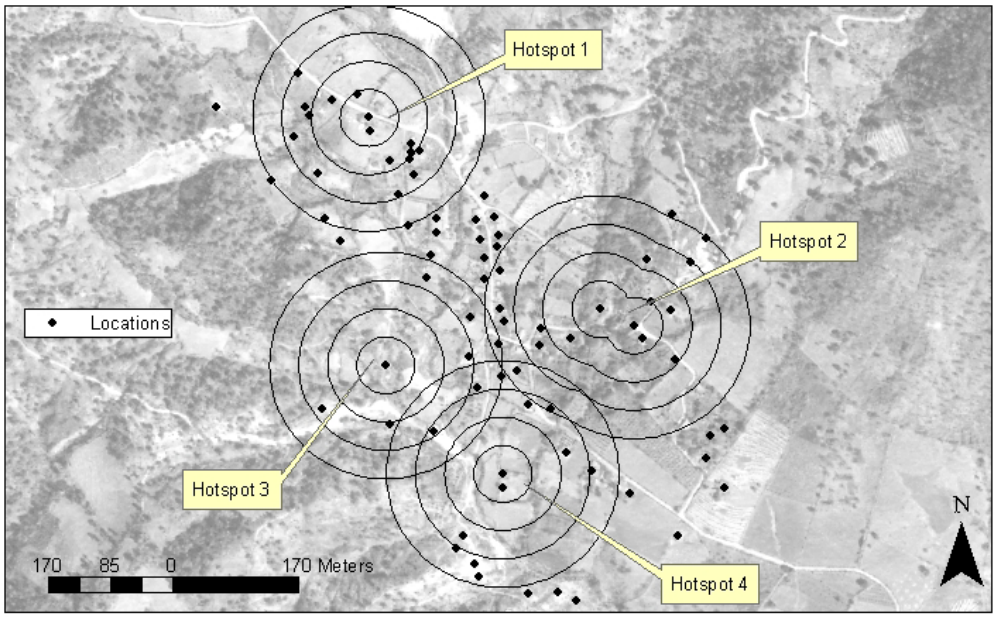


Figure11. Hotspots locations and buffer zones

3.4.1 Numbers of Vectors Present by Hotspot

A spatial intersection analysis was performed in ArcGIS 9.0 to determine the absolute total number of vectors present at each hotspot. The spatial intersection query was performed using the buffer zones created in ArcGIS 9.0. The location information was overlaid over a buffer zone to identify which locations shared the same surface with the specified buffer zone at each hotspot. These analyses were performed 16 times, one run per individual buffer zone. The results of the queries were tabulated to count the number of vectors present at each hotspot, at all distances, and for both years.

3.4.2 Presence/Absence of *T. dimidiata*

The goal of this objective was to identify which locations were reinfested in 2002 (+/+), which locations presented *T. dimidiata* infestations in 2001 only (+/-), newly infested locations in 2002 (-/+) and locations that were never infested either year (-/-). The analysis used multiple spatial intersection queries in ARCGIS 9.0 to acquire the infestation information (e.g. +/+, +/-) for each year at each hotspot. This information was tabulated to determine the Chagas' disease vectors prevalence at each hotspot. Another table was created from the same dataset to specify the re-infestation data according to the place of collection—domicile or peridomicile— for 2002. This determined if the place of collection changed from year to year for the re-infested locations. Also, a general map with four subsets –one for each hotspot- was created to display and complement the infestation information and the presence of *T. dimidiata* at each hotspot in the community of La Brea.

3.4.3 Infestation Description

A table containing the total number of *T. dimidiata* collected at each hotspot was created to report the numbers of *T. dimidiata* according to the type of infestation -domicile or peridomicile- in 2001 and 2002. This table did not include *T. dimidata* counts where the exact place of collection was unknown. Also, a summary table that included all *T. dimidiata* counts was created for discussion.

3.4.4 Environmental Description

A location description was completed for the houses' structural materials (domiciliary infestation) and for the surrounding structures (peridomiciliary). A further location description was completed separately according to where the vectors were collected. Also, the total numbers of vectors present inside the 200 meter radius were calculated by the location description of the place of capture –domicile or peridomicile. For this objective, the houses that did not have a complete description of the house materials were excluded from the analysis. If a house is excluded from the analysis, an "nd" (not determined) classification appears under the associated material descriptions columns.

3.5 Results

3.5.1 Entomological Survey

The community of La Brea is comprised of 79 houses, from which a total of 337 *T. dimidiata* were collected during the years of 2001 and 2002 (Table 5). From this survey, the majority of the *T. dimidiata* reported in both years were collected in peridomiciliary structures—chicken coops— but these *T. dimidiata* were concentrated in

only a few locations (Table 5). In contrast, the domiciliary—inside of the house—collections had fewer numbers, but *T. dimidiata* was distributed over a greater number of locations inside the community (Table 5). Also, the numbers of infested houses in 2001 were slightly greater than the number of infested houses in 2002. Yet, in 2002, peridomiciliary infestations were reported in one more house than 2001, but the total numbers of peridomicile infestations were twice as many in 2001 than in 2002.

Table 5. Number of houses infested with T. dimidiata by infested site location

	Domicile		**Peridomicile**		
Year	**Infested locations**	***T. dimidiata* counts**	**Infested locations**	***T. dimidiata* counts**	**Total *T. dimidiata***
2001	21	55	8	162	**217**
2002	14	40	9	80	**120**
		95		**242**	**337**

It is also important to point out that even though the data reported that there was a decrease in the number of *T. dimidiata* in 2002, the number of infested locations was fairly consistent from year to year. On the other hand, the number of infested domiciles was lower in 2002, though the decrease in actual numbers of *T. dimidiata* was not as drastic as that observed in the peridomiciliary infestations.

3.5.2 Numbers of Vectors Present by Hotspot

The hotspots with the highest numbers of vectors (Table 6) present in 2001 and 2002 were hotspot 2 and hotspot 1, respectively. Hotspot 4 reported the lowest number of vectors in both years. In 2001, hotspot 2 had the highest number of vectors followed by hotspots 1, 4 and 3, respectively (Table 6). Finally, in 2002, hotspots 2 and 1 had the highest presence of *T. dimidiate* particularly at a radius of 150 and 200 m (Table 6).

However, the majority of CD vectors (137) in hotspot 2 were collected in peridomiciliary structures—chicken coops located outside of the houses.

Certainly, the only hotspots that showed a consistent decrease in the numbers of CD vectors present in the community were hotspots 2 and 4 (Table 6). In general, a decrease in numbers at each hotspot was to be expected after the pesticide application following the initial survey in 2001. Nevertheless, hotspot 1 reported 22 *T. dimidiata* in 2002 while only reporting 14 *T. dimidiata* in 2001 (Table 6). From the 22 *T. dimidiata* collected in hotspot 1, 16 were reported in both peridomicile and domicile structures.

Table 6. Vector abundance by hotspot and each buffer radius

	Total number of vectors by hotspot							
	Hotspot 1		**Hotspot 2**		**Hotspot 3**		**Hotspot 4**	
Radius	**2001**	**2002**	**2001**	**2002**	**2001**	**2002**	**2001**	**2002**
50	11	4	139	11	4	0	9	0
100	13	6	141	21	4	7	9	0
150	14	22	145	23	9	2	10	5
200	14	22	153	27	11	12	12	6

3.6 Presence/Absence of *T. dimidiata*

Only hotspot 2 had more than a single house (one other location being present) within the 50m buffer, while the remaining 3 locations only contained one infestation location, that of the hotspot center. The number of locations that were contained in each hotspot varied with buffer distance (Figure 12.). At a distance of 200m, hotspot 2 had the highest location count from all the hotspots, followed by hotspots 1, 3 and 4, respectively (Figure 12). Sometimes these house counts can be misleading because hotspots 3 and 2 had two houses that fell in a buffer of both hotspots. The same situation occurred with hotspots 3 and 4. Also, three of the four hotspots—hotspots 2, 3 and 4—had locations

that overlapped at a distance greater than 150m (Figure 13. A), but not all of those overlapped locations had presence of *T. dimidiata*.

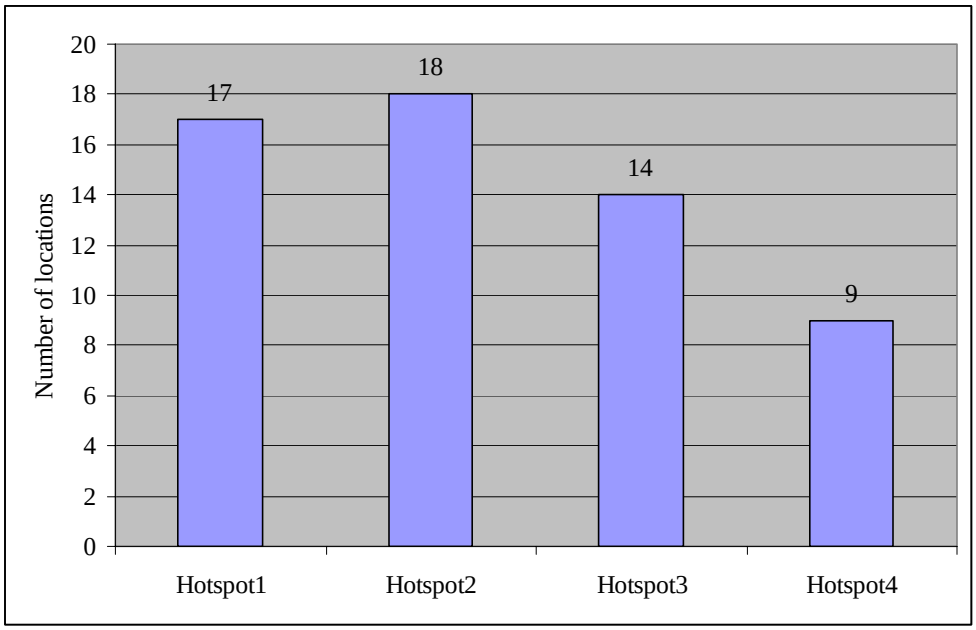


Figure 12. House counts per hotspot

3.6.1 Re-infested Locations (+, +)

Hotspot 4 was the only hotspot that did not report any re-infestation at all and, hotspot 2 had the highest re-infestation (Table 7). In hotspots 2 and 3, half of the re-infested locations had a presence of *T. dimidiata* in both peridomicile and domicile structures (Table 6). However, Hotspot 1 was the only hotspot that reported migration of *T. dimidiata* from the peridomicile to domicile structures (Table 8). The only exception was location ID 104a which reported infestation in the domicile in 2001, and re-infestation in both domicile and peridomicile structures for 2002.

3.6.2 Locations Infested Only in 2001 (+, -)

In 2001, hotspots 1, 3 and 4 had locations infested at distances less than 100 m away from their respective hotspot (Table 7). For hotspots 2, 3 and 4, the number of

locations infested in 2001 increased with distance (in terms of buffer bands) away from the central location. Only hotspot 1 did not experience an increase of infested locations with distance. It should be noted that the increased number of infected locations occurred at distances of 150m and greater.

3.6.3 Newly Infested Locations in 2002 (-, +)

Hotspots 2, 3 and 4 reported newly infested locations in 2002 (Table 7). However, hotspot 2 reported new locations infested at a shorter distance away from the hotspot compared to hotspots 3 and 4 (Table7). Hotspots 3 and 4 reported newly infested locations at distances greater than 150 meters respectively. Although hotspot 4 overlapped with hotspots 2 and 3, hotspot 4 only had overlapping newly infested locations with hotspot 2 (Figure 13.C, E).

3.6.4 Non Infested Locations (-, -)

Although hotspots 1 and 3 reported non infested locations (-,-) at all distances, hotspot 2 and 4 reported non-infested locations at a distance greater than 100m and 150m away respectively from the hotspot. Compared to all hotspots, hotspot 1 reported the highest number of non-infested locations followed by hotspot 2, 3 and hotspot 4 respectively (Table 7).

3.7 Infestation Description

Overall, the total number of houses that reported the peridomiciliary infestation was less than the number of houses in the domiciliary infestation (Table 9), however the highest numbers of *T. dimidiata* were reported in the peridomiciliary structures—chicken coops. A total of 263 CD vectors were present in the four hotspots (Table 9). Of the four

hotspots, hotspot 2 reported the highest peridomiciliary number of *T. dimidiata* infestation from both years (Table 9), hotspot 4 reported the highest number of *T. dimidiata* present in domiciliary structures (Table 9).

Three hotspots 1, 2, and 3 presented peridomiciliary and domiciliary infested locations (Table 10), but only hotspots 1 (2002) and 3 (2001) reported locations where *T. dimidiata* was present in both environments at the same time though not specifying the number of insects collected at each site. For this reason, this count was not included in Table 9 since there was a lack of information on the specific place of collection. From all of the hotspots, hotspot 2 was the only one to report two locations with an unusual abundance of *T. dimidiata* in 2001, in close proximity to one another (less than 50 m apart). (Figure 13.C).

3.7.1 Domiciliary Infestation

The hotspot with the highest domiciliary infestation in both 2001 and 2002 was hotspot 2 (Table 10), and there actually was an increase in the number of *T. dimidiata* for 2002. This was unlike hotspots 3 and 4, which reported a decrease in the numbers of *T. dimidiata* present at each hotspot from the previous year.

3.7.2 Peridomiciliary Infestation

In 2001, hotspot 2 reported the highest peridomicile infestation, with 139 *T. dimidiata* as compared to 8, 2 and 0 in hotspots 1, 3, 4, respectively (Table 10). In 2002, only hotspot 3 reported an increase in peridomiciliary infestations. Hotspot 1 was excluded from this analysis because of lack of specific information of the collection environment- both for domicile and peridomicile- of the 16 *T. dimidiata* found in location

ID 104a. It should be noted that for all of the results presented, only actual counts and not rates (per location) are recorded. In addition, for hotspots with small numbers, absolute changes in counts should be interpreted with caution.

3.8 Discussion

Most publications studying the distribution of Chagas' disease in Guatemala usually report disease prevalence aggregated to a municipal level (Greer et al., 1999 and Rizzo et al., 2003). For many studies that report disease prevalence at a larger scale (Monroy et al., 2003) focus extends to the dispersion and invasion of sylvatic *T. dimidiata* instead of domiciliary type infestations in a community. In addition, the goal of these sylvatic infestations of *T. dimidiata* studies is not the spatial distribution and risk factors associated with the presence of *T. dimidiata* in a community.

In contrast to the lack of geographical studies of Chagas' disease in Guatemala, some researchers in Argentina have accomplished macro geographical analyses of other CD vector species (Vazquez- Prokopec, et al., 2005; Cecere et al., 2006 and Cecere et al., 2004). In general, the data sets from these studies are comprised of entomological surveillance reports which have been performed over multiple years in the same area, with community participation in the surveillance. The resulting data is of a high enough spatial quality to allow for GIS facilitated spatial analysis.

The La Brea community displays how GIS can be utilized to gain insight into the geographic pattern of CD where the nature of the data does not allow the use of advanced spatial statistics. By determining the spatial hotspots of the infested locations, the project studied the distribution of *T. dimidiata* at different distances away from a hotspot. In addition, it also enabled comparison between the types of infestation at multiple distances

for each hotspot. Another benefit of buffer analysis for each hotspot was the integration of a temporal component to each hotspot analysis based on bug presence/absence for the years 2001 and 2002.

Hotspot 2 also had the highest number of locations reporting bugs, and the highest number of bug totals. Although, *ceteris paribus*, this is what one would expect; hotspot 2 exceeds hotspot 1 by only one location, but has 144 cumulative *T. dimidiata* more in both years than hotspot 1. By overlaying the house locations, infestation information and buffers, it is noticeable that hotspot 2 had a more diverse environment compared to the rest of the hotspots. Visual interpretation of aerial photography identified that hotspot 2 had a higher forest density that the rest of the hotspots.

During communication with the LENAP research team in Guatemala, a group consensus was reached that the small creek which ran by hotspot 2 could have placed a geographic limit on bug dispersal. It is therefore possible that the combination of forest density and water boundary might have played a large role in the distribution of *T. dimidiata*, in combination with traditional explanations of sylvatic and domestic food sources in the community.

3.9 Conclusions

Despite the volume of data collected from both entomological surveys in 2001 and 2002, for several locations entries in the survey were incomplete. In some cases, the data were not collected appropriately, leaving many of the attributes as not determined. For this reason, there is not enough data to perform rigorous spatial analyses. However, datasets of this type are more common than perfect records of CD infestation through time. As long as the majority of these data are complete and defensible, and given that no

systematic bias exists within the omissions, data manipulation within a GIS environment can still reveal interesting patterns worthy of further investigation.

For example, our results displayed that geographically there is not a continuum between infestations –many non-infested houses were proximate to infested locations.

In other words, vector dispersal is facilitated and halted by anthropogenic factors.

Based on our results, it is imperative that more research should be done to identify crucial house structural elements that help elucidate why *T. dimidiata* was not present in houses that had apparently the same characteristics of the infested houses. Data collection must extend beyond just house construction materials to include other variables such as the degree of house neatness (especially the resting place), the availability of restraining structures to keep animals outside of a house, and type of domestic animals—including dogs, chicken cows.

Since the entomologic surveys were performed in the community in such a small period of time—one or two days—one of two things need to happen: either the surveys need to be performed multiple times or there is a need of starting a community participatory surveillance system in this community. In previous studies, Monroy et al. (2003a), suggests that community-based surveillance can help detect new infestations, organize chemical treatment and effect subsequent reduction of new acute CD cases. The obvious benefit of such a system, beyond improving data quality, is improving community involvement and understanding about the risks involved with CD.

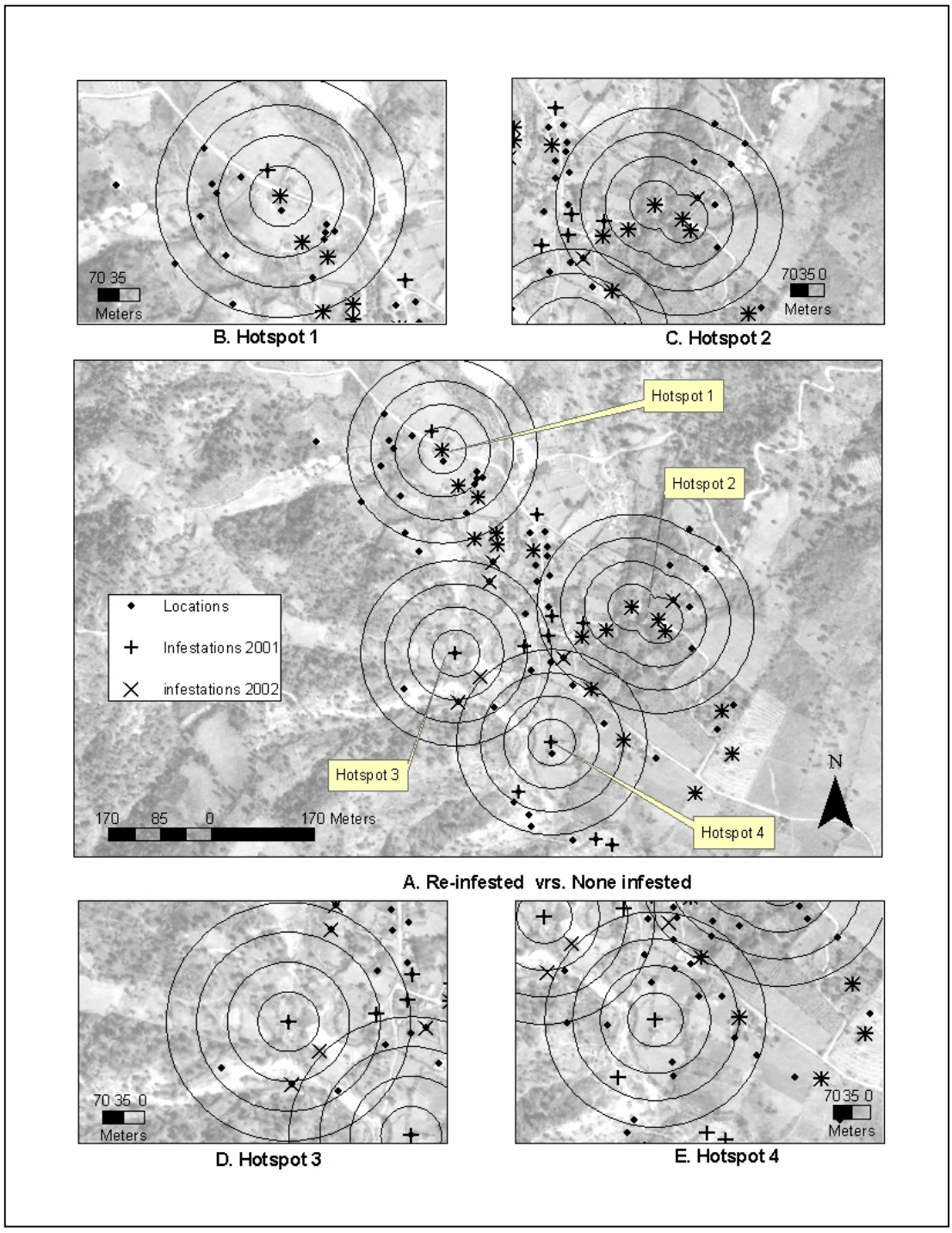


Figure 13. Infested Locations by hotspot

Table 7. Presence of T. dimidiata at multiple distances away from the Hotspots

Hotspot 1					
Number of locations with presence of *T. dimidiata* (2001, 2002)					
Buffer Distance (m)	**(+,+)**	**(+,-)**	**(-,+)**	**(-,-)**	**Number of Locations**
50	1	1	0	1	3
100	2	1	0	4	7
150	3	1	0	12	16
200	3	1	0	13	17
Hotspot 2					
50	3	0	0	0	3
100	4	0	1	2	7
150	5	1	1	4	11
200	6	3	2	7	18
Hotspot 3					
50	0	1	0	1	2
100	0	1	0	1	2
150	1	2	2	2	7
200	2	3	3	6	14
Hotspot 4					
50	0	1	0	0	1
100	0	1	0	0	1
150	0	2	1	2	7
200	0	3	2	4	9

Table 8. T. dimidiata re-infestation site reports

Hotspot 1						
	Peridomicile		Domicile		Both	
(House ID)	2001	2002	2001	2002	2001	2002
*98	X			X		
105			X	X		
**104a			X			X
Hotspot2						
9	X	X				
17	X	X				
18	X	X				
20			X	X		
22			X	X		
24			X	X		
Hotspot 3						
24			X	X		
150	X	X				

* Locations where *T. dimidiata* presence shifted

** Locations where *T. dimidiata* shifted and reported in both the domicile and the peridomicile

.

Table 9. Number of houses and abundance of *T. dimidiata* by infestation type

		Domicile		Peridomicile		
Year	**Hotspot**	**Number of houses**	**Number of *T. dimidiata***	**Number of houses**	**Number of *T. dimidiata***	**Total of *T.dimidiata***
2001	1	4	6	1	8	14
2002	*1	2	6	0	0	6
2001	2	6	11	3	139	150
2002	2	3	16	3	11	27
2001	**3	2	5	1	2	7
2002	3	2	4	1	8	12
2001	4	3	12	0	0	12
2002	4	2	16	0	0	16
	Total 2001	15	37	5	149	186
	Total 2002	9	44	4	19	63
	Overall Total	24	81	9	168	249

*16 *T. dimidiata* reported in houses present in both domicile and peridomicile at the same time were excluded.
** 4 *T. dimidiata* reported in houses present in both domicile and peridomicile at the same time were excluded

Table 10. Total number of *T. dimidiata* present by infestation type

	Hotspot 1			Hotspot 2			Hotspot 3			Hotspot 4		
	*Peri	**Dom	Both	Peri	Dom	Both	Peri	Dom	Both	Peri	Dom	Both
2001	8	6	0	139	11	0	2	5	4	0	6	0
2002	0	6	16	11	16	0	8	4	0	0	0	0
Total	8	12	16	150	27	0	10	9	4	0	6	0

*Peri = Peridomicile, ** Dom= Domicile

CHAPTER 4. GEOGRAPHIC DISTRIBUTION OF THE WALL PLASTER STATUS OF THE LOCATIONS INFESTED WITH *T. DIMIDIATA* IN THE COMMUNITY OF LA BREA

4.1 Introduction

Monroy et al. (1998), found that the use of different wall plastering materials and paints reduced the presence of CD vectors in three villages in the department of Guatemala, Guatemala. In their study, the authors compared the number of *T. dimidiata* found in houses with no wall plastering treatment, against two wall treatments—walls covered with cement and lime, and walls painted with just lime. Unlike the wall types and plasterings found in the studies of Greer et al. (1999) and Monroy et al. (1998), the wall treatments of La Brea are less diverse. The houses of the community of La Brea were reported to have a wall plaster that was made out of a mud-like material called "revoque" or "revoco"— made primarily out of mud mixed with sugar or salt, sand, and lime. The "revoque" can have an average durability of 1-2 years. The "revoque" or "revoco" can also be mixed with cement to increase durability.

4.2Materials and Methods

4.2.1 Geographical Analysis of the Anthropogenic Factors Associated with the Presence/Absence of *T. dimidiata* in the Community of La Brea

Although total counts of *T. dimidiata* per house were collected, an odds ratio analysis was performed to determine if there was an association between the wall plaster status of the houses and the presence or absence of *T. dimidiata*. Other parametric and none parametric statistics, and spatial statistics were considered, but these were discarded because of data problems, including that the distribution was severely skewed and violated the assumption of normality.

The houses that had partial plaster on the wall were reclassified with a plaster status of “yes” for each year. Also, the houses that had reports of plaster status as “non-determined” were excluded from the analysis. The locations that had infested peridomiciliary building structures—structures located outside of the houses—were not considered for this analysis because there were no existing data on the plaster status of these locations, although they represented the locations that contained the majority of the *T. dimidiata* infestation.

4.2.2 Odds Ratio

An odds ratio analysis was performed utilizing the Statistical Analysis Software (SAS, v 9.1.3). For the analysis, SAS constructs 2x2 contingency tables with the Proc Freq procedure. Also, Fisher’s exact test was utilized due to small sample size. The analysis was performed on all of the houses for each year—2001 and 2002. It is important to note that all of the peridomiciliary counts were collected from chicken coops that were built as a separate structure from the house, so these locations were excluded from the analysis. Therefore, only infested domiciles were included. The condition of the plaster of the house was tabulated according to plaster status (yes/no) and the presence or absence of *T. dimidiata*. In other words, the odds ratio is going to compare the odds of the plaster condition—yes, no—to the presence/absence of *T. dimidiata* of the houses of the community of “La Brea”.

4.3 Geographical Analysis

In addition to the odds ratio analysis, the number of *T. dimidiata* present by locations was sorted from highest to lowest to perform a hotspot analysis. Consequently, the locations that contained the highest 10% of the total counts of *T. dimidiata* were

identified as the hotspots, and multiple buffers of distance 50, 100, 150 and 200 meters drawn, just as described in the previous chapter. The goal of this study was to compare the number of houses counted by construction materials and the number of *T. dimidiata* present in each hotspot. In addition, two maps displaying the disease status and the wall plastering status for all of the houses were created, one map for each year. A complete construction materials description were available for 51 houses in 2001 and 56 houses in 2002, and these houses reported 39 and 38 *T. dimidiata* respectively.

4.3.1 Domiciliary Environment Description

These data were obtained and manipulated as described previously according to each hotspot. From this, an overall table was created to summarize the different wall and roof construction materials present in the community of La Brea. This table also included the number of *T. dimidiata* collected per construction material —wall and roof. Each domicile description profile only considered the materials from which each house was made; it did not include any type of information about the source of the materials, its colors. Although the profiles were determined for both years, changes in profiles were not specified from year to year at each house since the objective was only to determine the numbers of *T. dimidiata* present at each location. In addition, a second table was created reporting the number of *T. dimidiata* collected according to each house material profile classification given at each hotspot This table also contains cumulative counts of the number of houses and *T. dimidiata* collections per year and per profile. Finally, a map displaying each location's wall construction materials and the presence/absence of *T. dimidiata* was created.

4.3.2 Peri-domiciliary Environment Description

The data set contained the information of the location of the kitchen as well as for the location of wood piles; however, it did not report any other structures around the houses unless LENAP had collected triatomines from them. For example, there are peridomiciliary reports of chicken coops, but these were only reported if the chicken coop had a triatomine. This presented a problem for analysis because the presence of chicken was a common factor across almost all of the houses. It was therefore hard to draw any general conclusions about the risk associated with chicken coops.

4.4 Results

4.4.1 Wall Plaster Status and Vector Presence/Absence

The raw data showed that the total number of houses infested (Table 11) with *T. dimidiata* in the community of La Brea was lower in houses that had plastered walls than those houses that had non-plastered walls (Table 11). As the mudplaster covering walls in houses can break apart from one year to the next, the number of houses that had non-plastered walls had increased from 16 to 32 in 2002 (Table 11). Although the non-plastered houses increased, there was also a decrease in the amount of houses that had presence of *T. dimidiata*.

Houses that had non-plastered walls were almost 14 times more likely to have presence of *T. dimidiata* in 2001 and 3 times more likely in 2002 respectively, than those houses that had mud plastered walls (Table 12).

In 2001, in the best scenario for *T. dimidiata* to infest a house, houses that had non-plastered wall status are at least 4 times more likely to have the presence of *T. dimidiata* than houses with plastered walls (Table12). Conversely, in 2002, the effect of

the plastered cover walls has no effect on protecting the house from the presence of *T. dimidiata* in an ideal situation. This might be a result of the poor quality condition of the plaster when applied to the wall, as cracks in the plaster would serve as a perfect niche for *T. dimidiata.*

Table 11. Number of houses infested with T. dimidiata by Wall plaster status of the house

	2001			2002		
	Wall Plaster Status		2001	Wall Plaster Status		2002
Vector	Yes	No	Total	Yes	No	Total
Absent	41	4	**45**	27	22	**49**
Present	9	12	**21**	4	10	**14**
	50	**16**	**66**	**31**	**32**	**63**

Table 12. Total number of houses infested by year

	Wall Plaster status			
Year	Yes	No	Odds Ratio	95% Confidence Interval
2001	21	45	13.7	3.60 - 52.30
2002	14	49	3.1	0.84 - 11.13

In 2001, there were only three houses in La Brea that had no plaster on the walls and no CD vectors for both years, yet the rest of the houses with no plaster reported infestation in one or both years (Figures 14 and 15). Figure 14 also shows that in 2001 there were many houses with plaster, these being predominantly in hotspot one. However, in 2002 hotspot 1 had the highest number of houses that changed its wall plaster status from plastered to non-plastered. Hotspots 2 and 4 also had some houses that had changed in wall plastered status but not as many as in hotspot 1. Contrary to the changes seen in hotspots 1, 2 and 4, hotspot 3 was the only hotspot where no houses changed in wall plaster status.

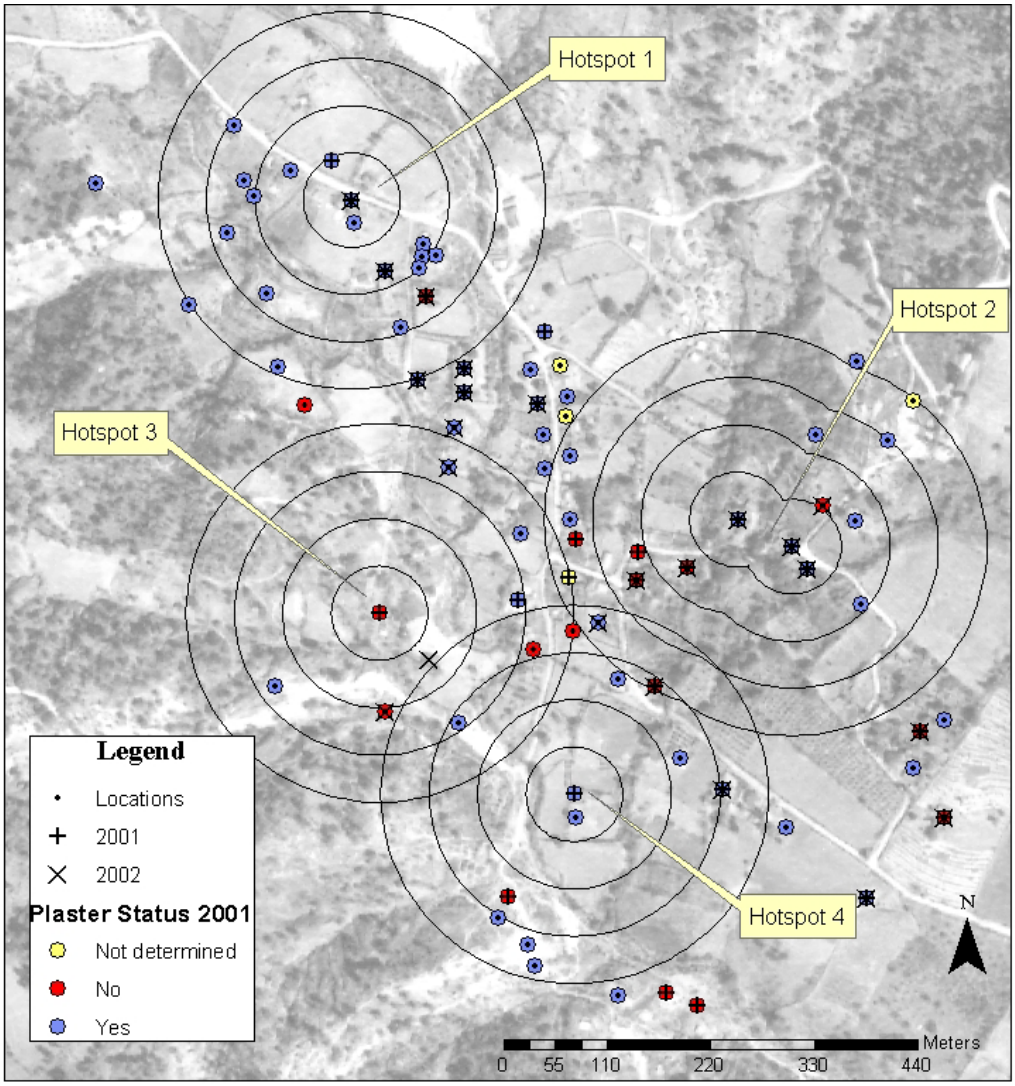


Figure 14. Distribution of the wall plastering status in the community of La Brea in 2001

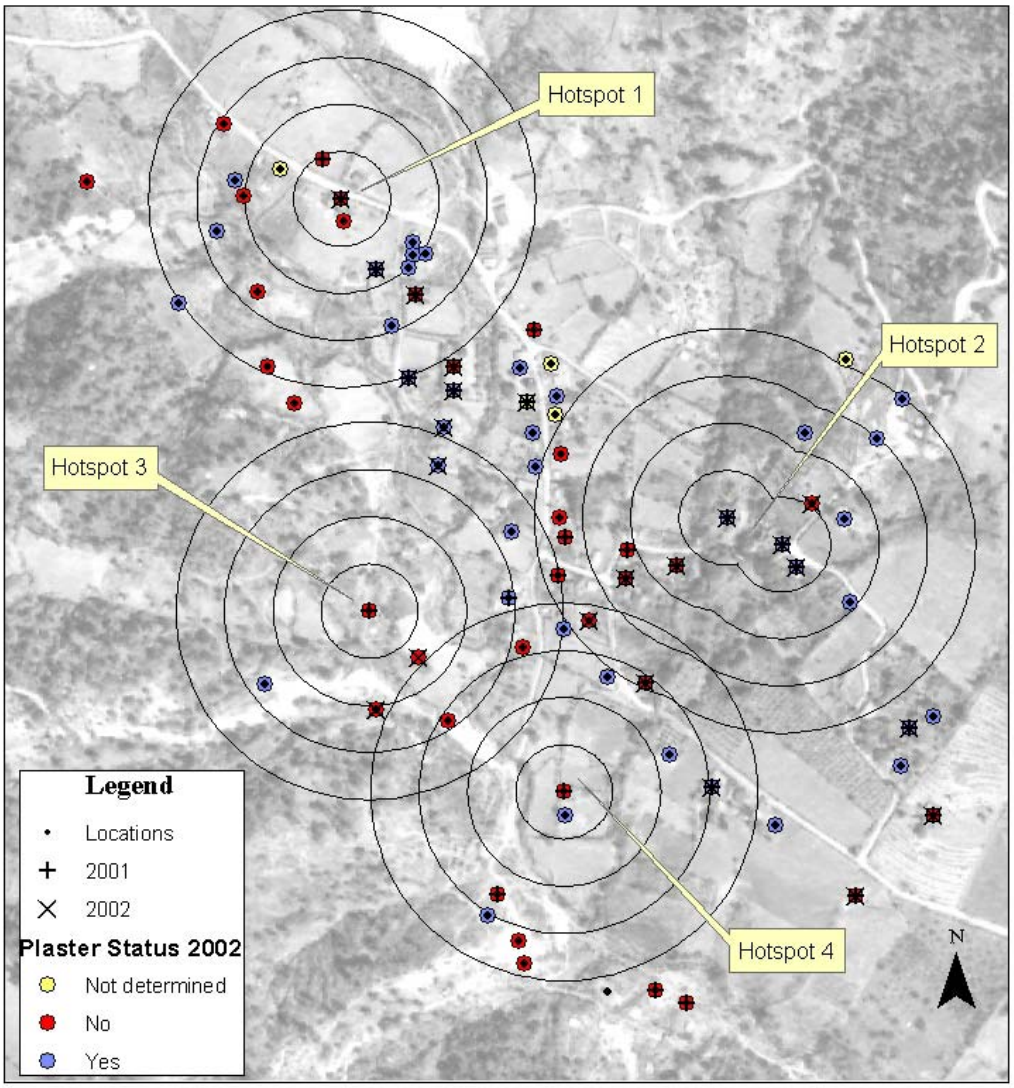


Figure 15. Distribution of the wall plastering status in the community of La Brea in 2002

4.4.2 Geographical Analysis of the Anthropogenic Factors Associated with the Presence/Absence of *T. dimidiata* in the Community of La Brea

From the aerial photo it can be seen that the houses in hotspot 2 were located in an area that was more forested than the rest of the hotspots (Figures 14 and 15). Hotspots 1 and 4 showed land patterns that are more similar to agricultural land forms (Figures 14 and 15).

4.4.2.1 Domicile Description

The majority (80%) of houses present within the hotspots areas (200 meters) were made of adobe walls and tiled roofs (Table 13). No other combination of house materials presented as many *T. dimidiata* (Table 13) as adobe*tile combination in both years. Other combinations of construction materials included houses made of adobe walls with mixed roofs (tile and metal) and houses made of block walls with tile only or mixed roofs.

Table 13. Overall house construction materials and *T. dimidiata* presence by year

	2001		2002	
Walls*Roof materials	**Number of houses**	***T. dimidiata* counts**	**Number of houses**	***T. dimidiata* counts**
adobe*tile	39	34	38	26
adobe*metal	7	1	9	1
adobe*tile, metal	-	-	2	0
block*metal	0	0	1	0
block, adobe*tile	1	0	-	-
block*tile, metal	-	-	1	0
Grand Total	47	35	51	27

Figure 16. Geographic distribution of houses by type of wall material

The houses made of adobe walls and tile roofs from hotspot 2 (Figure 16) had the highest cumulative counts of *T. dimidiata* (Table 14), followed by hotspots 3 and 4. Hotspot 1 had the lowest counts of *T. dimidiata*; this number was almost 3 times smaller than that for hotspot 2.

4.4.2.2 Peridomicile Description

The only peridomicile structures reported consistently were kitchens and woodpiles. Despite this, no records indicated presence of *T. dimidiata* in any of these structures. Data on other structures such as stables, chicken coops or confined areas for animals were only recorded when *T. dimidiata* was present inside the structure. For

example, chicken coops were only reported when they had presence of triatomines inside; otherwise, no data was recorded if they were absent. The database also reported presence of other animals (dogs, horses, etc.), but no data was reported about their resting places. From all the potential peridomiciliary structures present and recorded in La Brea, only a few locations reported the presence of *T. dimidiata* in one particular peridomicile structure—the chicken coop.

In other words, kitchens and woodpiles were reported systematically inside or outside of the houses, but they did not report presence of CD vectors in both years. On the other hand, the few peridomicile structures that reported presence of CD vectors were all chicken coops.

4.5 Discussion

In 2001, results suggest that houses with plastered walls were less likely to have presence of *T. dimidiata*. Although the results from 2002 also indicate that houses with plastered walls are less likely to have the presence of CD vectors, the confidence intervals from the odds ratio indicate that wall plastering using “revoco” might also be beneficial for CD vectors, possibly because the plaster tends to crack and fall off the walls, creating crevices which are ideal environments for *T. dimidiata*.

In agreement with Ferrer et al. (2003), and Monroy et. al. (1998), wall plastering had a protective effect against the presence of T. *dimidiata* in the community of La Brea. Ferrer et al (2003), detected greater presence of antibodies to *T. cruzi* in Indians (43.5%) than in non-Indian (2.8) residents from the Paraguayan region of Gran Chaco. In their research Ferrer et. al (2003), attribute the difference in presence of *T.* cruzi antibodies between Indians and non-Indians to the differences in quality of the homes between both

groups. For example, he reported that the houses of most non-Indians had plastered walls and screened doors. Despite the geographic difference between the location of the community of La Brea, Guatemala and the Gran Chaco region from Paraguay, both sets of domiciles had either plastered or non-plastered walls of homes. Another similarity is that, like Gran Chaco, the La Brea community also lets animals roam freely in the houses.

In a seroprevalance study in Guatemala, Greer et al. (1999) reported more individuals with antibodies to *T. cruzi* in houses where dogs had access to sleeping areas. Tabaru et al. (1999) also reported animals kept inside houses in the village of Santa Maria Ixhuatan, Santa Rosa state. Here the houses were also made of the same materials used in the community of La Brea. Tabaru et al.(1999, 20) noticed that these houses were "very dark inside because of a lack of any windows and proper ventilation even in daytime." According to Ramsey and Schofield (2002), domestic environments that are not kept tidy and have animals present would provide blood sources and shelter for CD vectors. In Argentina, Catala et al. (2004), identified houses with higher *T. cruzi* transmission risk in houses where the owners allowed dogs and chickens to access sleeping areas. Results from the same study also indicated that homes that are tidy and did not allow animals inside sleeping areas had lower *T. cruzi* transmission risk.

Apparently as insecticides made little difference in the community of La Brea, possibly due to its adaptability to different environments and seasonal feeding habits (Monroy, 2003), it might be more beneficial to redirect control strategies into encouraging homeowners to keep their homes tidy instead of relying on the use of insecticides. Such a simple strategy might also allow resources that were destined to

house modifications to be re-distributed to perform supplemental research studies such as serologic tests in other CD risk areas.

In 2004, LENAP started a community participatory surveillance program in La Brea. This program is a result of the Chagas'-Canada project which intends to evaluate multiple parameters inside that house and determine the relationships between cleanliness and CD vectors. A secondary benefit of the project is that it creates community involvement and at the same time provides education. Recently, Hashimoto et al. (2005) reported in the state of Jutiapa that only a small number of individuals per every 10-15 houses knew that the CD vectors were harmful. Also, as Rizzo et al. (2003) stated in their research, educational programs increase community awareness. According to Monroy et al. (2003a), community-based surveillance can help detect new infestations, organize chemical treatment, and reduce new acute CD cases.

4.6 Conclusions

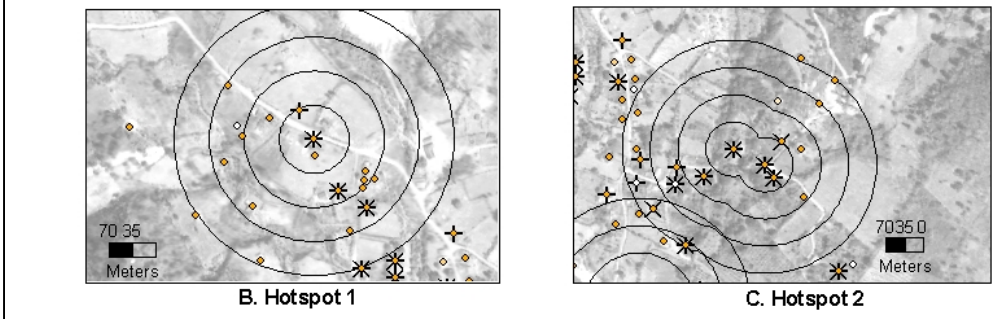
More research needs to be conducted on vector control strategies and the role that wall plaster plays in the reduction of the infestation rates of CD vectors. Simple changes like restraining animals from roaming in sleeping spaces and the use of screens for windows and doors might significantly reduce the presence of CD vectors in houses. Another strategy change that could be effective is home maintenance. By keeping homes neat and organized, it will be easier to reduce CD vectors habitats and to spot CD vectors. Keeping a house clean and organized could even make pesticide applications more efficient and effective.

It is obvious that the environment also plays a major role in the behavior and biology of CD vectors. Many times CD vectors, like *T. dimidiata*, are also a result of

anthropogenic changes to the environment. For example, if the habitants of a community remove refuse piles, there will be a reduction of hiding places for CD vectors. Consequently, cleanliness and maintenance also need to be applied to the peridomiciliary structures. Cleaning and maintaining chicken coops, corrals and other peridomicile structures might have an impact not only in the presence of Chagas' disease but with other diseases as well.

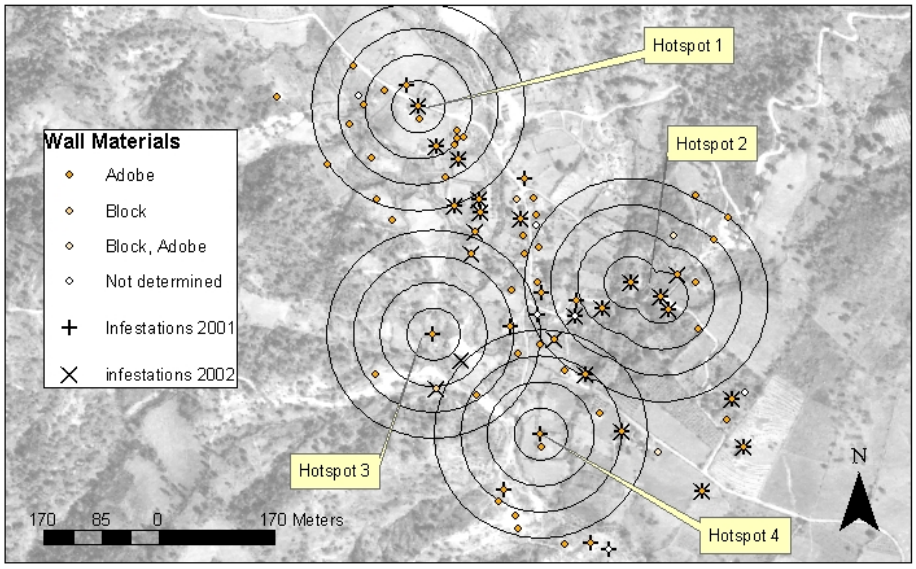
Also, in order to control disease vectors, it is necessary that both health officials and the general public do not rely entirely on a single insecticide treatment. Previous research has shown that unless such an application is widespread and effectively deployed, vector hotspots will be missed and re-infestation will occur. In order to prepare against this possibly, there should be continuous surveillance by the population for CD or other disease vectors.

In situations like the one in La Brea, where surveying all of the village takes a couple of days, the population should be encouraged to continue with a community surveillance program in order to have a better appreciation of the CD vector prevalence and incidence in the area. Short period surveys do not supply enough entomologic and spatial information to determine spatial vector clusters.

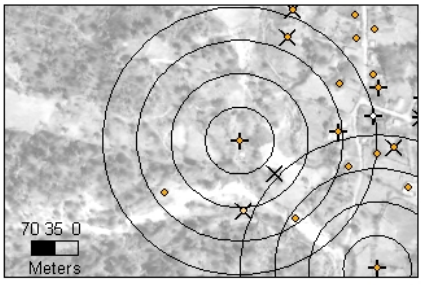


B. Hotspot 1

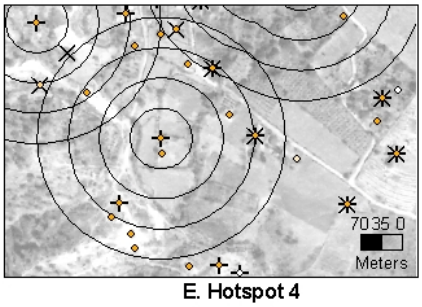
C. Hotspot 2



A. Re-infested vrs. None infested



D. Hotspot 3



E. Hotspot 4

Table 14. House construction materials and *T. dimidiata* presence by hotspot

		2001		2002		
Hotspot	**Profile**	**Number of houses**	***T. dimidiata* counts**	**Number of houses**	***T. dimidiata* counts**	**Cumulative count of *T. dimidiata***
1	adobe*tile	14	3	11	6	9
	adobe*metal	1	1	3	0	1
	adobe*mixed	-	-	1	0	0
2	adobe*tile	10	10	13	15	25
	adobe*metal	-	-	3	1	1
	block,ado*tile	1	0	-	-	0
3	adobe*tile	10	11	9	4	15
	adobe*metal	4	0	2	0	0
	block*metal	0	0	1	0	0
4	adobe*tile	5	10	5	1	11
	adobe*metal	2	0	1	0	0
	adobe*mixed	0	0	1	0	0
	block*mixed	0	0	1	0	0
	Total	47	35	51	27	62

CHAPTER 5: THE CONTRIBUTION OF THIS THESIS AND COMMENTS ON DATA

This thesis has shown how the use of a GIS can extract spatial insight into a disease system even if the original data collection was not initially designed for this purpose. This is an important contribution to the field of epidemiology in developing world areas where there is still a general deficiency in spatial analytical investigations of diseases. Most disease systems display geographic patterns, and by identifying these patterns both prevention (vector control) and health care delivery can be prioritized. However, in many developing world locations, the goals of public health research are not geographical. Nonetheless, these studies sometimes provide enough geographical information in addition to their primarily epidemiological focus. When this is the case, these datasets can be analyzed to gain knowledge of the geographical implications of the occurrence of a disease or its vector. For example, this thesis focused on the risk factors associated with the presence of Chagas' disease vectors in the community of La Brea, using an entomological dataset provided by the Laboratory of Entomology and Applied Parasitology (LENAP). This dataset contained entomological and anthropological information that allowed for the creation of multiple maps displaying prevalence and distribution of Chagas' disease vectors in the community. It is important to note that in some situations, the database did not provide enough geographical information to be analyzed. This does not mean that it was bad research; it is important to clarify that no criticism should be leveled at data collection when geographical investigation is not a primary goal of the project. Indeed, two outcomes of this thesis are, a: areas of further investigation have been identified within La Brea, and b: more effort needs to be exerted

from the developing world to standardize data collection so that more sophisticated, and therefore more revealing, spatial analyses can be employed.

5.1 What Can Be Done?

High quality datasets are essential for analysis; therefore it is crucial for future research to use standardized databases. Standardized databases will also help reduce data manipulation time needed for analysis. In response to these obvious data needs the World Health Collaboration Center for Remote Sensing and GIS (WHOCC) at Louisiana State University (LSU) has developed a web based Chagas' disease surveillance project to demonstrate the benefit of this technology (Figure 16). This technology allows GIS and non-GIS users to enter standardized data into a server and generate real-time maps, with the database being updated as soon as new information is entered.

5.2 How Can We Achieve Good Quality Datasets From a Web Based GIS?

By using a web-based database you automatically standardize the dataset because the database programmer writes specific commands that control information input and storage requirements. In this way, the database will store the information in a specific format, reducing individual error and variation. Each cell has a specific command that tells it if the data are numerical or alphanumerical characters. The database can also be programmed to make sure that the person in charge of data entry is forced to input specific information in all of the fields, otherwise it will alert the person during the data entry and reduce the chances of producing incomplete databases.

5.3 What Does This Mean for Public Health?

Web based GIS applications for disease surveillance can provide a great service to public health officials because it can display almost real-time surveillance information which can be crucial to a community and the reduction or eradication of disease vectors. The generated map can be used, for example, to identify houses with positive bugs, houses located within a set distance to these positive bugs, or known locations of hotspots (such as woodpiles). Using this map, medical doctors can prioritize both their educational strategies designed to control the vector, and where blood samples should initially be drawn. This interactive mechanism will also lead to better community and public health participation as residents and health care workers will be able to see how their collected data is being analyzed and returned to the community. This involvement, or participation in the process, will not only maintain a high profile of the disease within the community, but help improve the quality and quantity of data allowing for more sophisticated and insightful geographical analyses.

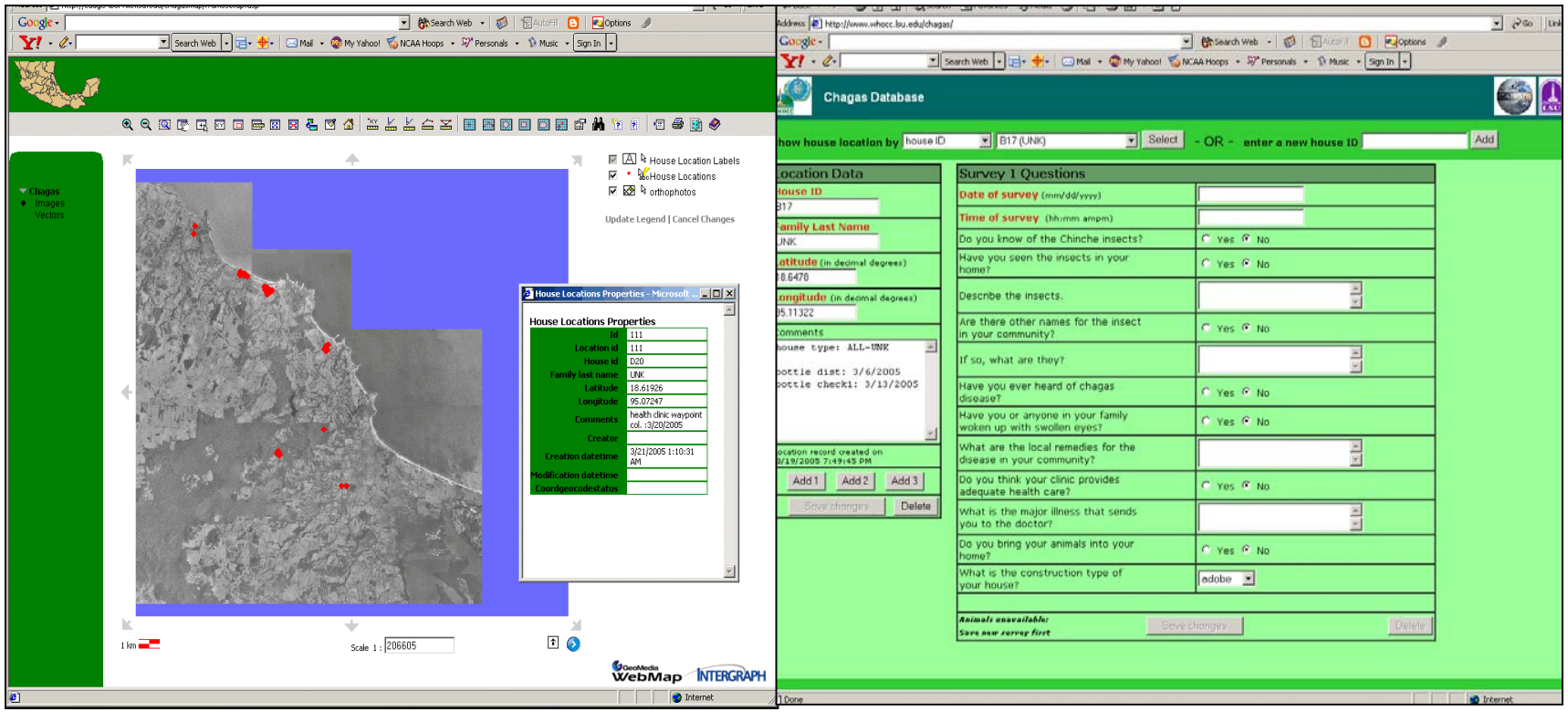


Figure 17. Webmapper: Data entry and display

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Gerardo was accepted into Graduate school in the summer of 2005. During his studies in a master of science program, he volunteered, contacted and collaborated with many researchers of a diversity of disciplines. He succeeded in integrating his studies into other disciplines and even published some of his work in a Middle Eastern Political Science Book in 2007.