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The Spatial Ecology of Larval Mosquitoes in Haiti

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Abstract

The Spatial Ecology of Larval Mosquitoes in Haiti

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Background: Previous research has identified strong associations between land use (deforestation, irrigation, and degenerative land use and farming practices) and vector-borne disease transmission. In Haiti, subsistence farming practices, land tenure, and ineffective irrigation systems have drastically changed the ecological landscape, and have led to land fragmentation, biodiversity reduction, and natural habitat disturbances—all factors that affect vector breeding habitats, behaviors, and human contact rates. Our multi-lateral analysis attempts to determine the effects of these factors on mosquito larvae and any ensuing associations.

Methods: Locations of 5,295 mosquito larval sampling sites in Haiti were mapped and assessed. Individual site data was linked with covariate factors to estimate their effects on mosquito larvae. Thereafter, statistical software was utilized to examine means, distribution variables, intervariable correlation, and pivot tables and the corresponding variables to the land cover. GeoDa and SatScan were used to apply the Local Indicator of Spatial Association (LISA), the Local Join Count (LJC), and Kulldorff's scan statistics to evaluate the site location for significant clustering of mosquito presence and species presence and abundance.

Results: In total, 2,650 sites positive sites were identified. The average density was highest for *Culex* with a density of 86.6 larvae per dip (LPD) followed by *Anopheles* at 73.9 LPD. Density for pupae populations was found to be inconsequential with an average value of 1.0 pupa per dip. Average larval density was highest in the coastal department of Nippes. *Anopheles* average density was found to be 611.9 LPD while *Culex* and pupa levels remained at 613.0 LPD and 609.1 LPD, respectively. LISA and LJC results detected a trend of positive spatial clustering in the southern Sud and Nippes departments for both species. Spatiotemporal analysis revealed three larval presence clusters moving through the country during the rainy season.

Conclusions: Our study found that there are significant high-risk areas of mosquito larvae in urbanized and farmland areas within Haiti. The results suggest that removing likely habitats for larvae and adult mosquitoes can help reduce larvae exposure, adult mosquito bite risk, and general susceptibility for the Haitian people.

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CHAPTER 1

GENERAL BACKGROUND

Global Burden of Vector Borne Disease

Zoonotic diseases account for an estimated 60 – 70% of all new infections globally¹ but nearly 17% of these infections are vector-borne^{1,2}. Vector-borne diseases are caused by parasites, bacteria, or viruses that result in 700,000 deaths annually³ with a significant percentage of these deaths being children under 5. Under the right circumstances, vector-borne diseases can be well-managed or prevented altogether. However, problematic vector-borne diseases such as malaria, dengue, leishmaniasis, and lymphatic filariasis still persist and cause disproportionately high morbidity in humans³. According to the most recent WHO estimates, malaria, a parasitic disease transmitted by *Anopheles* mosquitoes, causes 400,000 annually or nearly 60% of all vector-borne diseases deaths. With 219 million current cases, this disease presents the largest burden of vector borne disease on the global human population^{1,2}. Malaria transmission has been documented in 97 countries worldwide placing 3.4 billion people at risk². As with other vector-borne diseases, historically vulnerable populations such as children under 5, pregnant women and travelers, and those with immunocompromising conditions are most at risk for malaria. Novel therapies and drugs have greatly improved scientific understanding and control, but genetic resistance poses the greatest threat to global elimination. Moreover, opportunistic infections and comorbidities further complicate the burden of malaria and any ensuing treatments. Common comorbidities include bacterial infection, upper respiratory tract infection, and severe diarrhea^{6,13}, but arguably the most severe comorbidity is malarial anemia combined with iron-deficiency anemia. General anemia refers to the lack of healthy red blood cells carrying oxygen to vital body tissues. There are many forms of this disease, but malarial anemia alone causes 24.7% of anemia in West Sub-Saharan Africa⁴.

Lymphatic filariasis is another key neglected tropical vector borne disease that disproportionately affects the populations in low-income countries. This disease is a parasitic infection caused by three

main species of filarial worm nematodes^{1,5} transmitted by *Anopheles*, *Aedes*, *Culex*, and *Mansonia* mosquito genera. Humans are the exclusive host of the most pervasive species, *Wuchereria bancrofti*, causing nearly 90% of all infections^{5,11}. Prolonged infection can cause severe degeneration of the lymphatic system or the organ system responsible for managing bodily waste in tandem with our immune system. System impairment or damage is characterized by dangerous swelling of the limbs and possibly more sensitive areas such as scrotum or genitals. An estimated 120 million people are infected with lymphatic filariasis, with 21% (25 million) of cases displaying genital swelling⁵. Women are particularly impacted as approximately 15 million suffer from lymphoedema symptoms or elephantiasis of the leg and lower abdomen^{1,11}—constituting approximately 13% of all current cases. Advancements in oral, anti-helminthic medicine have interrupted community-level transmission through mass drug administration (MDA) campaigns resulting in over 96 million cases being cured^{1,12}. However, of the total chemotherapy eligible cases, 57% inhabit the secluded and sequestered parts of Southeast Asia while the remaining 3% reside in Africa¹². Furthermore, recent data shows that treating a minimum of 65% of the total population in endemic areas for the next half decade through annual or biannual MDA¹², is the best course of action to attenuate disease transmission. The WHO and similar organizations continue to encourage these campaigns, but a more concerted, global effort is required to fully eliminate this disease.

Dengue fever is another VBD that parallels the alarming epidemiological trends of malaria. In the last half century, dengue fever incidence has increased 30-fold resulting in an average of 100 – 400 million new infections each year^{3,7}. Transmitted by *Aedes* genera mosquitoes, significant burden is seen in tropical and sub-tropical areas, but recent research has revealed that approximately half the global population is now considered at risk for contraction^{3,8}. Many scientific models have indicated that approximately 3.9 billion people are at risk of infection dispersed over 129 countries. Despite this vast range of disease, 70% of the burden lies within Asian and the Asian subcontinent³. Approximately 500,000 of new cases progress into medically severe dengue where patients are hospitalized for plasma leakage, internal hemorrhaging, and organ failure annually³. Given that there

is currently no treatment for dengue, comprehensive prevention efforts must be considered to reduce this burden and the burden placed on healthcare systems worldwide.

Mosquitoes are the primary vectors of the aforementioned diseases, but there are equally fatal VBD transmitted by more inconspicuous vectors. Leishmaniasis, a disease caused by the parasite *leishmania*, is transmitted through the bite of infected female sandflies⁹. After infection, leishmaniasis can clinically manifest into cutaneous or visceral leishmaniasis, with the latter being the most severe form. Improper diagnosis and treatment can result in blistering skin lesions and ulcers, weight loss, and serious organ damage. Current epidemiological studies show a global prevalence approximation of 12 million people with 350 million more people being at risk for infection^{9,10}. In terms of new infections, estimates reveal a global incidence rate between 0.2 – 0.4 million annual cases of visceral leishmaniasis with an even greater rate of 0.7 – 1.2 million annual cases for cutaneous leishmaniasis⁹. 90% of all current visceral leishmaniasis cases are concentrated in the poor, rural areas of Bangladesh, Ethiopia, Brazil, India, Sudan, and South Sudan⁹. This data suggests a strong geographic overlap with current cutaneous leishmaniasis as 75% of cases can be found in the same countries as visceral leishmaniasis in addition to: Costa Rica, Algeria, Iran, Peru, Colombia, and Syria⁹.

Socio-Economic Burden of Vector Borne Disease

Vector-borne diseases also cripple health systems and health systems performance. Nations of various socio-economic statuses expend billions of dollars annually to help combat VBD. This often results in budgetary restrictions being surpassed to account for increases morbidity and mortality. Malaria alone costs over \$12 billion dollars in annual direct costs¹⁴. Economically, this devastating price tag costs countries an additional 1.3% reduction in GDP¹⁴. Depending on the location, malaria can constitute nearly 40% of all public health spending and a staggering 60% of health clinic visits¹⁴. Additionally, the silently growing costs of medication resistant malaria presents future burden for public health practitioners and healthcare providers. Dengue also costs nations substantial amounts of healthcare costs related to prevention and treatment. Public health economists have estimated the

aggregated global cost of dengue illness to be approximately \$9 billion dollar⁸ with 23% (\$2.1 billion) of costs coming from the Americas alone¹⁵.

In SE Asia, dengue was reported to cost \$1.8 billion dollars annually in direct and indirect costs. Even though these figures are significantly less costly than malaria, the proportional, economic deficit directly correlates with disease coverage. Scientists project the figure reported above to be tantamount to the increase of populations in these target areas. Economic productivity loss, stemming from global population growth, also seem to be a significant driver for other common vector borne diseases. Yellow fever, a disease spread by the *Aedes* mosquito, can lead to painful symptoms of muscle pains, fever, and nausea. Like the name suggests, many patients suffer severe fever in conjunction with injuries to or total organ failure of the kidneys or liver¹⁶. Primarily found in South America and certain parts of Africa, scientist estimate that approximately 900 million people live in areas of risk or contraction¹⁶. Moreover, WHO projects future funding needs to eclipse \$330 million dollars in endemic countries alone¹⁶. These projections are expected to exponentially increase in tandem with global population growth and thus, cause more strain on already weak healthcare infrastructure.

Prior to mass drug administration programs (MDA), lymphatic filariasis (LF) was another vector-borne disease-causing significant health and economic burden across the world. The Global Programme to Eliminate Lymphatic Filariasis (GPELF) was an initiative launched in 2000 to help combat LF through morbidity management and mass drug administration^{11,22}. Funded by the WHO, this initiative aimed to eliminate LF as a public health problem by 2030. Efforts in recent years have allowed this initiative to steadily progress towards their goals, but disease burden still remains a strong impediment hindrance to completing their goal—especially in low- and middle-income countries (LMIC's). Across all WHO designated regions. LF has caused more than 5.8 billion dollars annually in total economic burden¹¹. MDA programs have largely reduced these costs, but the WHO estimate that at least \$154 million dollars will be required annually to help completely eliminate LF¹².

Post MDA programs, LF has still resulted in \$10.5 billion dollars in total lost productivity with an additional \$13.8 billion in projected loss in the next 10 years¹².

Studies have shown vector-borne diseases to be influenced by a number of other individual- and country-level socio-economic factors (SES). Age, a common confounder in exposure-disease relationships, has strong influence on vector-disease contraction. Children—especially those under 5—have displayed the highest odds of contraction when compared to other age groups²³. Income has also been found to be another confounder in vector disease borne dynamics. According to Whiteman et al., income was the principal SES driver of vector borne disease contraction for Zika, dengue, and overall aedes occurrence²³ for studies included in their systematic review. Whiteman et al. also found a positive association between virus presence and lower SES status among the studies systematically reviewed, but this finding was clouded by other environmental and cultural practices that ultimately rendered the association weak and inconsistent²³.

Education, namely education level, has also been identified as a possible risk factor for contraction, particularly when comparing individuals with no education to those with primary or secondary level. However, as seen with income and SES, the direction and magnitude of association widely varied by disease and geographic distribution²⁴. A 2018 study by Springer et. al suggested a positive association between Lyme disease (LD) incidence and areas with predominantly educated (Bachelor's degree or greater) persons²⁴. Interestingly, this study also found positive associations between LD incidence in vacant housing areas—areas known to house homeless and other resource poor individuals²⁴. While the comprehensive effects of SES on vector-borne disease remain largely understudied, other SES-related factors that may impact vector borne disease burden include race, unemployment, comorbidities, and systemic health disparities^{23,24}.

Economic Benefits of Vector Borne Disease Alleviation and Control

The known SES costs associated with vector-borne disease have gradually been addressed through many promising prevention and control efforts. Increased insecticide-treated nets have accounted for

approximately 68% of the 663 million clinical cases averted since the year 2000²⁶. Reduction in incidence have saved an estimated \$900 million dollars and post-healthcare costs and case managements on the African continent alone²⁶. Globally, this decline in malaria mortality is projected to save additional 10 million lives and generate more than \$4 trillion dollars of additional economic output. Similarly, for Chagas disease, efforts in the last two decades have resulted in cost effectiveness of vector control figures ranging between \$45 - \$132 dollars per human case averted²⁶. With 8 million cases worldwide, this range yields between \$360 million –\$1.05 billion dollars in potential cost savings. For dengue, economists have calculated the disability adjusted life years (DALY's) averted to range between \$1,992 - \$3,139 dollars. But, vector control management for dengue has been elusive in recent years and so, cost effectiveness ratios are projected to be lower than previously anticipated²⁶.

Recent Trends in Vector Borne Disease Burden

The dynamics vector borne disease are multifactorial and complex, varying primarily by geographic location, but also sex, age group, and environmental factors. Significant burden is seen in underdeveloped and multi-dimensionally poor countries with particularly strong caseloads on women and children in focal areas of sub-Saharan Africa, Southeast Asia, South and Central America. These historical trends are expected to be further exacerbated by new trends seen in transmission and disease acquisition—the most alarming of which are emerging and re-emerging vectors. Of the major global vector borne diseases, dengue remains the only disease that has categorically increased age standardized DALY rate by over 26%^{15,17}. The seemingly perpetual expansion of dengue has largely been driven by both globalization and urbanization. Such trends have also nearly doubled cases of tickborne diseases over the last decade and accounted for 77% of vector-borne disease reports; with 82% of these reports being cases of Lyme disease¹⁶. Case reports also indicated significant rises in spotted fever rickettsioses, babesiosis, and anaplasmosis¹⁶.

Socio-ecological factors such as urban sprawl, resource depletion, and globalization all significantly influence vector borne disease transmission, but none have been more impactful than climate change. Our planet naturally oscillates through variations in planetary orbit that result in almost imperceptible climate cycles. Climate change, however, refers to the steady change in Earth's climates due to anthropogenic increase of greenhouse gases, deforestation, livestock mismanagement, and fossil fuel consumption. Such change has spurred large, planetary events such as glacial retreat, reduced snow cover, ocean acidification²⁰. Global warming specifically, has resulted in an average temperature rise of 2.12 degrees Fahrenheit since the dawn of the industrial era²⁰. This relatively precipitous increase in temperature directly affects vector borne disease transmission dynamics through the vector itself, pathogen, and ecosystem interactions¹⁷.

Although temperature effects on pathogens will vary by context, most common vectors are ectotherms or organisms with life cycles and activities that increase with rising temperatures¹⁷. As the Earth warms, vector geographic distribution may increase, especially into higher latitudes for mosquitoes and other volant vectors. Using a time-series analysis model in both Colombia and Ethiopia, Siraj et al., found statistically significant evidence a shift in altitudinal malaria distribution in warmer years—a trend that can increase vector borne disease endemicity¹⁸. Additional research has found temperature increases conducive to viral replication, decreased incubation, and accelerated development rates¹⁹. Although the literature remains inconclusive on temperature suitability and climate effects on vector dynamics, there can be no mistake that these dynamics will require prudence in future planning and prevention efforts.

Vector-Borne Disease Alleviation and Prevention Strategies

Vector borne disease alleviation and prevention initiatives have long been key priorities at the forefront of global health. Often galvanized by the WHO, this process has manifested into the areas of health promotion and education, global surveillance, and vaccine development efforts. Currently, the primary method for prevention and alleviation is through integrated vector management (IVM).

Originally proposed in 2004, IVM is a multilateral, decision making system used for optimal utilization of vector control management resources²⁸. Using a holistic health approach, this approach advocates for public health advocacy, capacity building, health sector collaboration, and non-chemical (still-water drainage) and chemical (insecticides nets and spraying) vector control methods²⁸. This approach has been integral in reducing breeding sites and parasite rates along with bolstering positive social outcomes through individual empowerment and community knowledge^{6,29}. However, structural challenges such as resource allocation, environmental change (insecticide resistance), and political instability still prevent many VBD-endemic countries from adopting this strategy^{6,30}. Other vital intervention approaches of IVM include: biological control, genetic control, housing modifications, and personal protective equipment²⁸.

IVM is strongly encouraged by WHO, but other valid prevention strategies have presented themselves in more clinical manifestations with malaria chemoprevention at the forefront. Prophylaxis and preventive measures for malaria have been primarily through antimalarial medicines approved for all ages²⁸. The resulting decline in malaria from these efforts have increased life expectancy in Africa by 1.2 years since 2000³⁰. In addition to malarial chemoprevention, mass treatment options are now also available worldwide for schistosomiasis. Schistosomiasis, caused by trematode flatworms from freshwater snails, can be prevented through repeated treatments of the anthelmintic drug *praziquantel*³⁰. The drug has been successfully administered in several countries and continents, with more than 97.2 million people being treated in 2018³¹. Lymphatic filariasis, another parasitic worm disease, transmission has also been effectively interrupted by global mass treatment efforts. Since being declared eradicable in 1997, 7.7 billion treatments of *albendazole* have been delivered to approximately 910 million people at least once in 68 countries^{32,33}. Although effective treatment requires 5 years of annual administration, current efforts have yielded \$24 billion dollars in cost-savings and \$100.5 billion dollars in economic losses averted³³. Moreover, populations requiring mass treatment has declined by 42% resulting in infection prevalence falling below elimination

thresholds. As of March 2020, 16 countries have officially eliminated lymphatic filariasis as a public health problem, with an additional seven countries currently on the verge of elimination³².

As chemoprevention strategies continue to improve, many promising vaccines are currently under development or already available for some vector borne diseases. People across the globe are now able to receive Japanese encephalitis vaccination. Found mainly in Asia, Japanese encephalitis (JE) is transmitted by the *Culex* species mosquitoes in mostly agricultural or irrigation heavy areas³⁴.

Japanese encephalitis burden is minimal compared to other vector borne diseases, but considerably more fatal with an estimated 5% – 35% case mortality rate. 30 – 50% of case survivors suffer from significant, chronic neurologic debilitation³⁵—a statistic that bolstered research and development into the licensed *IXIARO* vaccine in 2009³⁴. This inactivated two-dose series vaccine has helped avert nearly 310,000 cases over the last 15 years³⁶. Similarly, tick-borne encephalitis, cases have also been curtailed by vaccination efforts. Tick-borne encephalitis is an acute viral disease caused by members of *Flaviviridae* virus family and transmitted by *Ixodes persulcatus* species³⁷.

Endemic in most European countries, tick-borne encephalitis is easily contracted in forested, farmland, and rural travel areas. This form of encephalitis can cause disturbances in 20% – 30% of people infected while one percent die from this disease³⁷. Tick borne encephalitis does not have a licensed vaccine in the United States, but safe and effective vaccines are available in the endemic areas of Europe and Central Asia (Russia)³⁷. Vector-borne disease vaccines have been a colossal tool in the fight against disease resurgence, but the Yellow fever vaccine has arguably been the most impactful vaccine to date. The vaccine is a live, attenuated single-shot vaccine approved for those older than 9 months and provides life-long immunity. In 2018 alone, African countries averted over 10,000 deaths due to mass vaccinations—a value corresponding to a 47% reduction in deaths³⁸. A viable malaria vaccine remains to be seen, but a promising Dengue vaccine is currently in Phase III clinical trials here in the United States. As science continues to improve and we further grasp our understanding of VBD, vaccine development is expected to exponentially grow and substantially contribute to combatting these diseases.

CHAPTER II

VECTOR BORNE DISEASE IN HAITI

Vector Borne Disease Burden

Haiti is plagued by many common vector borne diseases including, but not limited to malaria, dengue, Zika, and lymphatic filariasis (LF). Lying on the Western third of Hispaniola, disease dynamics for the small, island nation are confounded by both population and vector species concentrations. Several disease vectors call Haiti home, but mosquitoes remain the principal vectors sustaining disease transmission. A recent environmental collection assessment found that mosquito density in Haiti was comprised of five genera and ten species. The most abundant species found in Haiti is *Culex quinquefasciatus* followed by *Aedes albopictus*, and *Aedes aegypti*—all of which are prominent vectors for the most pervasive disease of dengue³⁹. According to PAHO, dengue incidence in Haiti has risen by 40% since being officially reported in 1964, with coastal cities carrying the most considerable burden³¹. Dengue's ubiquitous presence has caused nearly 0.17% of all deaths with an age-adjusted death rate of 1.4/100,000. All four serotypes have been isolated in Haiti with both *Ae. Aegypti* and *Ae. Albopictus* vectors found to carry the different strains³¹. While severe dengue remains uncommon, a 2012 study conducted in the Port-au-Prince metropolitan area, revealed a 100% IgG seropositivity rate in all study participants. Various theories have been proposed to account for the rarity of severe dengue, but none have retained scientific traction or validity⁴⁰.

Malaria is another key endemic vector-borne disease that poses substantial burden on Haitians and Haitian communities. According to the CDC, malaria incidence rate has risen to approximately 1,278/100,000 people⁴¹. Transmission is generally low in relative and absolute terms, but there are slight increases during the dual rainy seasons. These sharp increases in incidence and continued prevalence can be explained by the principal malaria vector of Haiti, *Anopheles albimanus*. *Anopheles albimanus* mosquitoes usually bite outdoors which presents deleterious health hazards to not only urban Haitians, but also rural Haitians living in poorly constructed mud homes and shelters. Other

species of *anophelines* documented in Haiti include: *Anopheles argyritarsis*, *Anopheles crucians*, *Anopheles grabhamii*, *Anopheles pseudopunctipennis*, and *Anopheles vestitipennis* but behavioral patterns for these species in Haiti remain scant.

Malaria endemicity in Haiti can be uniquely explained in part by the malaria parasite. Nearly 95% of reported malaria cases are caused by *Plasmodium falciparum*—a sharp contrast to the rest of Central and South America that sees infection from *Plasmodium vivax*. Scientists have hypothesized various human genetic and biological differences to account for this phenomenon, but the data remains inconclusive. Epidemiologic investigations have also revealed local *Plasmodium falciparum* to be particularly susceptible to chloroquine, the principal antimalarial drug used in malaria prophylaxis in travelers to Haiti⁴². Neuberger et. al's recent post-Earthquake study conducted in SW Haiti, found no parasites carrying chloroquine resistance haplotypes in 49 patients diagnosed with falciparum malaria. But, given the study size, external validity must come into question along with the generalizability of chloroquine resistance in Haiti⁴³.

The 2010 Earthquake in addition to other events have spurred urbanization trends that have led to significant increases in suitable habitats for mosquitoes. Research conducted by Samson et. al found all three principal vector species mentioned above in urbanized or newly urbanized areas—an alarming trend seen elsewhere in post-Earthquake rebuilding areas³⁹. Nearly 50% of the Haitian population live in urban areas, with the capital Port-au-Prince housing approximately 2.3 million people (20%) alone. The Haitian government has capitalized on investments and resources to reaffirm its focus on malaria elimination in the months following the earthquake. These efforts have led to full-scale adoption of rapid diagnostic tests, drug resistant monitoring programs, and expedited development of molecular testing for the *P. falciparum* parasite. Furthermore, community based participatory action research methods have also been employed in surveillance efforts to address transmission. Findings from this approach has afforded the Ministry of Health a firm grasp on sources of transmission. As data acquisition and analysis continue to improve, Haiti is well on track

to abate incidence, decrease prevalence, and improve the likelihood of elimination if these approaches can be sustained.

Results from this community-based research has also reinforced the need to address prevalence of lymphatic filariasis. Over 90% of all lymphatic filariasis (LF) cases in the Americas are situated in Haiti, as nearly all genera of mosquitoes found on the island being capable of transmitting LF⁴⁶. Lymphatic filariasis has been hyper-endemic in Haiti as early as the 18th century with many believing the African slave trade being the principal reason for endemicity⁴⁶. Additionally, this disease has been proven to disproportionately affect women and children—both of which being historically vulnerable groups. A study conducted by Oscar et. al found that nearly even with sustained transmission, 8 million people are still considered to be at risk for contraction⁴⁶. Such results indicate that lymphatic filariasis coverage may be more widespread than originally indicated due to, but not limited to, population migration dynamics, rainy season transmission, and expansion of prominent *Culex* species vectors.

Effects of Agricultural Irrigation, Soil Erosion, and Land Use Practices

Like many low-and-middle income countries (LMIC's), Haiti is heavily dependent on farming and subsistence agriculture; the latter of which accounting for nearly 40% of all employment. The most recent census revealed Haiti to have nearly 650,000 farms, but the mountainous terrain limit land availability for cultivation. Of the total 550,000 hectares of land available, it estimated that only 16% of that territory is suitable for agriculture. This steadily decreasing availability of arable land is further exacerbated by soil erosion. Recent studies have estimated soil erosion in Haiti to be approximately 1,319 tons/km²/year. Such rapid soil erosion is in part explained by the mountainous topography that puts the island at a naturally increased risk of erosion, fragmentation, and silt deposits—all factors that can form suitable mosquito breeding sites⁴⁷.

Soil erosion is also spurred by the poor agricultural practices in rural Haiti. Techniques such as rapid land reuse, slash burning, and most notably, flood irrigation have all contributed to the depletion of

arable land. Flood irrigation specifically is an archaic irrigation method that “floods” the farming plot with copious amounts of water to grow crops. Primarily used on commercial farms, this irrigation method is not only ineffective, but also results in still-water overflow, crop damage, and most importantly, potential breeding grounds for various mosquito vector species. Haiti’s bimodal rainfall pattern also contributes to growing patterns of soil erosion and land use. This natural, seasonal pattern results in extreme climatic conditions that induce soil erosion by both moisture surplus during rainy seasons along with winds during the intermittent dry seasons. While the effects of rainfall volume on mosquito dynamics vary, rainfall has been proven to increase breeding activity and form breeding sites. Moreover, several studies have found a significant, bidirectional relationship between egg hatch rates and relative humidity increases in temperate climates such as Haiti^{48,50}. Coupled with the ubiquity of natural disasters and inclement weather in Haiti, these findings will only magnify the risk of vector-borne disease contraction⁴⁸.

In addition to the biophysical factors mentioned above, vector-borne diseases have been accelerated by various human activities. Specifically, constant demand for fuel wood and charcoal have galvanized the process and uptick of deforestation across the island. Recent landcover data from have approximated a 3% forest cover rate in rural areas placing Haiti among the most deforested countries worldwide. Five monumental mountain ranges cover 75% of Haiti’s land surface, but according to Hedges et. al, 42 of the 50 largest mountains have lost all primary forest cover⁵¹. This widespread reduction in tree and forest cover have forced many poor, rural families resort to poor subsistence strategies for survival resulting in trends that increase landscape fragmentation and create potentially suitable mosquito habitats. Furthermore, another epidemiologic study conducted by Macdonald et. al found a positive, bidirectional correlation between deforestation and malaria incidence in temperate climates putting countries such as Haiti at significant risk if deforestation efforts remain unaddressed⁵². Approximately 85% of the total population use fuel wood for household energy, cooking, and warmth during rainy seasons through deforestation, with over 137,000 farms engaging in active wood pyrolysis. The early 2000’s saw average plot sizes on Haitian

farms increased by 50% to compensate for continual low crop yield and loss largely by deforestation and tree removal^{50,51}. These efforts may provide temporary respite from the health insecurities, but the larger effects of deforestation cause soils to be exposed to wind and rainfall—both of which catalyze mosquito activity patterns and disease transmission.

Mosquito Borne Disease Prevention and Control Efforts

Indoor Residual and Space Spraying

Indoor Residual Spraying (IRS) refers to the application of residual insecticide to potential vector resting surfaces such as walls, eaves, and other relevant structures. Prior research has established a strong, positive association between IRS and a decrease in vector-borne disease rates, even when adjusting for various common comorbidities. IRS has been thought to significantly reduce vector-borne disease with the greatest reduction seen in the early 1960's. Specifically from 1962 to 1963, IRS helped reduce malaria slide positivity rate, or the number of laboratory confirmed cases per 100 suspected cases, by 77% countrywide. Coupled with DDT, active surveillance, and chloroquine distribution, slide positivity rates were reduced to nearly 0.1% by 1965. However, these gains were not sustained as both abnormal rain patterns and natural disasters propelled sharp increases in positivity rates through much of the 70's and 80's⁵². Retrospective studies by the Service National des Endemies Majeures found widespread DDT resistance across the country that also contributed to the rise in malaria and vector borne disease risk.

In addition to IRS, space spraying has been proven to be effective in combatting vector-borne disease. Space spraying refers to the outdoor release of fog or mist insecticide from ground or aerial applications through three forms: thermal fogging, low volume spray, and outdoor residual spray. In Haiti, space spraying is primarily conducted through thermal fogging, or diluted insecticide spray mixture applied through a heated vaporizer over large areas. A 1973 systematic review study conducted by Krogstad et. al found that thermal fogging reduced malaria incidence burden by 71% in sprayed areas. Poor resource allocation, dwindling funds, and mortality of other animal species has

led to discontinued use of thermal spray. Socio-political, ecological, and environmental factors since then have also contributed to the precipitous rise in malaria endemicity in Haiti⁵³.

Bed Nets

Years of past research has proven insecticide-treated or fortified bed nets (ITN) to be a mainstay of mosquito borne disease management. Robust studies in primarily sub-Saharan Africa found bed nets to significantly contribute to the prevention these diseases by repelling or killing nearby mosquitoes upon contact. While research continues to bolster ITN, data on use in Haiti remain largely scant. A literature search for prior use of ITNs to examine the relationship between usage and disease prevention yielded only one study. According to Steinhardt et. al, the vast majority of available data on ITN has come as a byproduct of the renewed interest in post-Earthquake public health infrastructure improvements⁵³. This renewed interest has strengthened mosquito-borne disease control and elimination through increased funding, health access, health education, and most importantly, resource distribution. In 2012, a nationwide Global Fund sponsored health campaign was administered to distribute 1 ITN per household in rural areas and 2 per household in the Port-au-Prince metropolitan area. However, for various reasons, many Haitians reported low-adherence and usage rates resulting in negligible protection against mosquito borne disease⁵³.

Larvae Source Management

Larvae source management (LSM) is the targeted management of mosquito larval habitats to suppress and control larval abundance. While specific documentation on larvae habitats remain variable in Haiti, known habitats include rice-fields, ditches, tire nests, ground pools, and hoof/footprints. LSM, therefore, is used to manipulate these habitats through environmental management, larvicide, larvivoracious fish, or various combinations of these control methods. More recent innovations to larval management have included the use of bacterium *Bacillus thuringiensis israelensis* (*Bti*) in conjunction to larvicide to reinforce disease prevention efforts, but these approaches have not been evaluated for impact or effectiveness⁵⁴. However, organized LSM and other vector

control approaches can be dated back to the early U.S. occupation of Haiti. Between 1919 and 1936, the United States introduced and utilized traditional drainage and oiling methods to protect U.S. soldiers and Haitian citizens.

These vector control projects continued through the rest of the occupation, but their greatest success came from a large-scale drainage that resulted in a 200% decrease malaria in Petit Goâve from 1970 – 1972⁵⁴. Other recent studies have advocated for community-led and informed LSM as supplements to LSM in future integration and use—all factors that will be considered in the following study, but the research remains largely scant on additional environmental and land cover factors affecting larvae development and proliferation. Therefore, for the following study, we hypothesize that areas with suitable breeding sites for mosquitoes experience a greater increase in larvae presence and potentially, increased exposure to these deadly vector borne diseases. We will use a nationally representative data from the Centers of Disease Control and Prevention (CDC) Division of Parasitic Diseases and Malaria and Haiti’s malarial control program to test this hypothesis using a geospatial distribution approach and arrive at results that will have public health and policy implications.

CHAPTER III

MATERIALS AND METHODS

Methods

Mosquito Larval Dataset

We utilized a 5,295 cross-sectional point dataset from the Centers of Disease Control and Prevention (CDC) Division of Parasitic Diseases and Malaria. Access to the data was granted by the division with specific, additional approval provided by principal investigator of the study, Dr. Daniel Impoinvil. Given the nature of the non-human subjects data, the study protocol was deemed exempt and did not require additional Emory University eIRB approval. Funding for the data collection was advised and provided by the Global Fund—a disease burden alleviation organization aimed at reducing vector-borne disease burden through larval site management and control. Data were collected by Haiti’s National Malaria Program from January 2016 to December 2016. Collectors were mosquito control brigades consisting of 12 teams of 5 members located in each of the 10 departments of Haiti. With the high population density (3,093,698 people) and second largest department by land area (4,595 km²), the Ouest department warranted 2 additional teams to provide supplemental support for data collection.

Teams were dispatched to various regions of their assigned department where there was perceived burden of malaria but varied in capability of collecting data. Standard dipping techniques were used to sample mosquitoes, with any ensuing data plotted by Garmin GPSMAP 64st units. The resulting dataset included the variables of population, sunlight exposure, vegetation concentration, water use, and larvae density count of *Anopheles* and *Culex* mosquito species. Variables were then cross-referenced with elevation and land cover raster data from the European Space Agency: Center for Climate Initiative. Geographic variables in this dataset included latitude/longitude coordinates, department, commune, and sub-communal geopolitical boundaries.

Land Cover Types in Haiti

After larval habitat survey completion, we estimated land cover types using raster data and satellite imagery across all of Haiti. The 300-meter, multispectral ground resolution satellite image was provided courtesy of European Space Agency: Climate Change Initiative (ESACCI). Land cover types were broadly classified into seven categories: broadleaf or needleleaf trees, mosaic or natural cropland, mosaic and natural vegetation, grassland, flooded shrub, flooded tree cover, and waterbodies. Tree cover was characterized by the presence of either evergreen or deciduous tree covering >15% surface area (m²). Cropland was characterized by the presence of any agricultural crop or any area prepared for rainfed, farming activities. Mosaic or natural vegetation land cover was an area with >50% herbaceous and <50% cropland area.

Grassland were pastures used for animal grazing, while shrubland referred to any area containing presence of plants with wood stems. Flooded shrubs were shrubland areas surrounded by saline or brackish water. Similarly, flooded tree cover were tree cover areas as defined above, but with the presence of saline, brackish, or freshwater. Lastly, waterbodies were areas characterized by permanent bodies of water such as lakes, rivers, or large ponds. Each land cover type was digitized using geographic information system software QGIS (Version 3.18 – “Zurich”). Using this approach, land cover types were first estimated by projecting the raster file into Universal Transverse Mercator (UTM) Zone 18N and then visualized by easily recognizable color categories (**Figure 13**).

Spatial and Landcover Analysis

Spatial analysis was conducted via geographic information system software QGIS (Version 3.18 – “Zurich”) and Kulldorff spatial scan statistic on both positive (presence) and negative (absence) larval sites. Data points were first uploaded into QGIS via delimited text and then transformed to a vector shapefile to plot both presence and absence visualizations (**Figure 4**). Thereafter, general descriptive maps were constructed first with QGIS for all species and pupa larvae found in the data, but specific geostatistical tests were only conducted for *Anopheles* and *Culex* species data.

Kulldorff spatial scan statistic SatScan (Version 9.7) refers to the study of spatial arrangements of points across a geographic space and time using point, counts, rates, or other aggregate data.

Kulldorff's Bernoulli spatial scan specifically, was used to spatially analyze the clustering point counts given the presence of controls. Clustering via Kulldorff SatScan (Bernoulli) was calculated by measuring the concentration of events or points found within an infinite number of distance circles with each radii being set at certain threshold level. Each circle was cross-referenced via chi-square methods and then compared with other circles to form likelihood functions.

Log likelihood ratios (LR) were then geospatially inferenced by generating random replicas of the data under the set null-hypothesis and compared again across most likely clusters in real and random datasets to create statistically significant clusters and estimate relative risk (RR). Kulldorff spatial scan statistic was calculated with a case, control, and coordinate file of larvae positive, larvae negative, and both positive and negative sites file, respectively. Purely spatial and space-time retrospective spatial scan statistic analyses were conducted for all point locations. Purely spatial scan statistics were calculated using circle window shapes, with maximum threshold of 50% of the population at risk. 999 Monte Carlo simulations, non-overlapping windows, and 1-year time aggregation unit were applied. Space time special scans were conducted with circular window shapes, with a maximum threshold of 25% of the population at risk. 999 Monte Carlo simulations, non-overlapping windows, and a month time aggregation unit were also applied in accordance with the previous spatial scan.

Kernel density estimation techniques (KDE) were used to calculate heatmaps and positive-larval site species densities. Kernel density estimation is a mathematical process that aims to estimate probability density function of a variable. In spatial analysis, KDE calculates the density of point features around each output raster cell, where layers are then smoothed to a new heatmap layer with the variable(s) of interest. Raster analysis tools were used to calculate density of *Anopheles* and *Culex* mosquito species. Supplemental geostatistical analysis to these relationships were done through univariate local indicator of spatial association (LISA) and local join count tests in GeoDa. LISA

provides autocorrelation information on location of clusters by allotting a statistic for each location with a significance value.

From there, it then establishes a proportional relationship between the sum of the local statistics and the corresponding global statistic for the specified area or region. After LISA, the data were reviewed for errors and then re-coded by binary code for all applicable sections in preparation for a univariate local join test. For binary variables, local join count tests are used to measure spatial autocorrelation by counting the joins that correspond to occurrences of value pairs at neighboring locations. These values are then identified through a matching system of 1:1, 0:0, 1:0, and 0:1, with the former two being indicators of positive spatial autocorrelation. All spatial analyses were performed on the entire regional boundaries of mainland and territorial Haiti.

CHAPTER IV

RESULTS

Species Composition and Distribution

In total, 196, 283 larvae were found among the 2,650 positive sites sampled. Of the total larvae positive sites found, 129,345 (65.9%) were found to be *Culex* species larvae while 40,617 (20.7%) belonged to the *Anopheles* species. The remaining organisms found within the sample sites were found to be nymph or pupa of various species totaling 26,321 (13.4%). The Ouest department was found to have the highest total sum larvae (196,283) of both *Anopheles* and *Culex* species larvae with values of 15,003 (7.7%) and 59,045 (30.0%) respectively. Pupa were also predominantly concentrated in the Ouest department with a value of 12,465 (6.3%) (**Figure 1**). Outside of the Ouest department, the Nord and Artibonite departments supported the next highest segments of larvae distribution across all species and organisms. *Anopheles* species in the Nord department amounted to 8,387 (20.6%) while *Culex* species were 22,817 (17.6%). 5,569 (21.1%) pupa were also found in this department.

Similarly, in Artibonite, the largest department by land area and also in Northern Haiti, *Anopheles* and *Culex* species were found at 4,123 (10.1%) and 14,628 (11.3%), respectively. However, the pupa counts in this department did not follow previous trends. Instead of Artibonite, the third highest pupal count was found in the Sud department at 1,881 (7.1%). Total average density was highest for *Culex* species larvae with a value of 86.6 (mg/L) followed closely by *Anopheles* /L at 73.9 (mg). Density for pupae populations were found to be inconsequential with an average value of 1.0 (mg/L). Similar to total concentration distributions seen above, average larval density was strongest in the coastal, maritime department of Nippes. *Anopheles* average density was found to be 611.9 (mg/L) while *Culex* and pupa levels remained at 613.0 (mg/L) and 609.1 (mg/L) respectively (**Figure 2**).

Spatial distribution of total *Anopheles* only positive sites varied across the country. *Anopheles* concentration was strongest in the Limbé, Dessalines, and Aquin arrondissements. Strongest commune concentrations were found in Acul du Nord, Baradères, and Abricot. Interpolation concentration was strongest in arrondissements found in the Nippes department (**Figure 5**). *Culex* species distribution followed a similar pattern to *Anopheles* distribution. *Culex* concentration was strongest in the Saint-Louis du Nord and Las Cahobas arrondissements. Strongest commune concentrations were found in the Sau-D'eau, Mirebalais, Acul du Nord, Marigot, Maniche, and Les Irois. Interpolation concentration was strongest in arrondissements found in the Nippes department (**Figure 6**). Pupa concentrations were more sparsely located with no identifiable trends in distribution. Pupa concentration was strongest in the Borgne, Baradères, and Bainets arrondissements. Strongest commune concentrations were found in Mole Saint Nicolas, Gros Morne, and Mirebalais. Interpolation concentration was strongest in arrondissements found in the Nippes department, with smaller, uniform density found throughout the rest of Haiti (**Figure 7**). Both Kulldorff spatial scan statistics resulted in variable clustering throughout the country. Our purely spatial analysis revealed 6 distinct clusters for mosquito vector species exposure, but only clusters 2 through 6 were found to be a significant GINI cluster. Cluster 1 (LR=242.9, RR=1.73),

Cluster 2 (LR=108.9, RR=1.76), Cluster 3 (LR=89.3, RR=1.69), Cluster 4 (LR=33.3, RR=1.84), and Cluster 5 (LR=29.4, RR=1.62) were all found to be statistically significant at the $< 1\%$ ($p < 1.0 \times 10^{-17}$) level. Cluster 6 (blue) (LR=13.6, RR=1.44) was the weaker statistically significant hotspot at the $< 5\%$ ($p = 0.032$) level (**Figure 12**). Space-time scan statistics resulted in distribution of point data stratified by months of the calendar year, with Clusters A, B, and C all found to be significant at the $< 1\%$ ($p < 1.0 \times 10^{-17}$) level. Cluster A points (orange) (LR=146.7, RR=1.65) aggregated between January 2016 – April 2016 primarily in West and Southwest Haiti while Cluster B points (red) (LR=210.8, RR=1.74) aggregated between February 2016 – June 2016 primarily in the Northern regions of the country. The last significant cluster, Cluster C (blue) (LR=84.9, RR=1.54), was found to have aggregated between April 2016 – June 2016 in the South-Central and Southeastern regions (**Figure 11**).

Both our kernel density and LISA estimates also supported the general trend of positive spatial clustering, with significant ($p < 0.05$) high-high (red) concentrations found in the Southern Sud and Nippes departments of Haiti for both species (**Figures 8 and 9**). Low-low (blue) positive spatial clustering was scattered throughout the country, but significant clusters were found in the Grande Anse, Nord, Artibonite, and Ouest departments—a trend also consistent with our species composition and land cover results. Negative spatial clusters were found sporadically through the country with no discernible clusters or notable hotspots found anywhere. Local join count data supported the positive hotspots found above, but with emphasis in the Ouest (Port-au-Prince) and Nord (Cap-Haitien) departments—departments that combined, constitute nearly 50% of Haiti's total population (**Figure 10**).

Relationships with Landscape Cover and Topography

Grasslands, mosaic, and natural cropland were major land cover types found across all of Haiti. Consistent with the species composition results, the Ouest, Nord, and Grande Anse departments constituted the bulk of positive site composition. Within the Ouest department, urban areas were the

primary habitat of all positive larval sites across all three species and organisms of interest with a value of 11.8% for *Anopheles*, 20.46% for *Culex*, and 21% for pupa. However, in the Nord department, flooded shrub cover was the primary habitat for all species with values of 8.5%, 4.7%, and 5.4% for *Anopheles*, *Culex*, and pupa species respectively. The Grande Anse department showed more variation in distribution of positive larval sites by landscape cover. *Anopheles* species larvae were most prominent in all tree cover areas, while *Culex* species were primarily found in urban areas. The remaining pupa were predominantly concentrated in broadleaf trees. Waterbodies, which are common habitats for mosquito species, constituted a negligible amount of positive-larval sites across all departments. Significant percentages for waterbodies were found in the three largest departments above, but also at negligible values (**Figure 3**).

CHAPTER V

DISCUSSION

Our results were found to be consistent with the trends seen and documented in the literature, namely the work conducted by Samson et. al.⁴⁴ Similar to Samson et. al's work, our spatial analysis framework found significant abundance of mosquito larvae in between urban and coastal environments supplemented by conducive land covers. As seen in **Figures 14 and 15**, urban areas are hotspots for both species and pupa, with the greatest concentration being found in the Port-au-Prince metropolitan area. Other notable hotspots were found in departmental capital cities of: Cap-Haitien (Nord Department), Gonaives (Artibonite), Jacmel (Sud-Est), Miragoâne (Nippes), and Les Cayes (Sud). These findings suggest that infection and transmission are not only limited to the rural, poorer areas of the country. Moreover, Haiti's sanitation and waste management system remains largely underdeveloped in both rural and urban areas. So, those who remain in the heart of these cities are also at risk not only by industrial habitat disturbances, but also by the lack of improved management systems.

As these cities continue to urbanize, open air sewers, free latrines, and floating plastics can serve as breeding grounds for these vectors due to the resulting suitable water and habitat conditions suitable for both species. Port-au-Prince inhabitants in particular are at excess risk as it is one of the only cities in the world without an established sewer system. This not only endangers residents through mosquito vector-borne diseases, but other common water, sanitation, and hygiene-associated and diarrheal diseases. Moreover, species abundance seemed to be concentrated in the coastal, flooded areas of the country, with specific focus in the southern part of the country. Our Geoda LISA and Local Join Count tests found statistically significant positive clustering in flooded tree and shrub cover areas of Grande Anse, Artibonite, Nord, and Sud departments—all coastal departments ripe with suitable breeding locations.

This alarming trend of increased disease vector concentration is in part due to habitat disturbances³⁹. Three out of the five significant hotspots mentioned above show notable bare areas, or dry areas with low levels of vegetation, and cropland in close proximity. These areas are now being furnished with houses, apartments, and other settlements in order to decongest the departmental capital cities. Such trends in themselves are relatively inconsequential, but based on our results, mosquito vectors have a strong presence in all forms of cropland surrounding these areas. As discussed in Hedges et. al, this increased human activity can likely contribute to landscape fragmentation that creates suitable mosquito habitats⁵⁰. Therefore, those who settle in these areas, but still access the wet cropland as a subsistence strategy may be at risk of disease. Farmers, irrigators, sugarcane mill operators, and other agriculturists in particular may be in danger of these vector-borne infections as this field constitutes nearly two-fifths of all employment in the country. As seen in Macdonald et. al, deforestation and malaria incidence have a positive, bidirectional correlation in tropical areas⁵¹. So, along with those mentioned above, arborists and others who actively engage in similar, outdoor activities can significantly increase the likelihood of disease transmission within and near these high-risk areas. Our Kulldorff Bernoulli scan statistics also found strong clustering along the coasts near and within large cities. Space-time clustering was found to be consistent with the timeframe of the country's

bimodal rainfall pattern (March – May and August – October), with strongly significant clusters being found in the first arm of this rainfall pattern (March – May). Generally, mosquito vector breeding activity generally increases during the wet, rainy season and decreases during dry seasons in Haiti. Our results were also consistent with this trend as very few statistically significant points were found within inland areas—areas known to have sparse vegetation, low tree cover, and reduction in average rainfall (**Figure 13**). Findings are also compounded by the lack of tree cover and dense vegetation found within the central plateau. As noted in **Figure 13**, Haiti's central plateau primary landcover are dry, grasslands. These areas are not conducive to mosquito breeding patterns due to temperature, lack of viable breeding sites, and increased sunlight exposure, which further reinforces our hypothesis of increased mosquito activity with increase in suitable breeding sites.

Limitations

Limitations for our study were primarily found in the sampling and confounders of the collected data. While sampling was extensive and widespread, the points were aggregated across the whole nation which may have introduced various forms of bias. First, the sampling teams collected samples from different parts of the country where there was perceived burden of malaria. Transmission in these areas were not necessarily occurring nor verified to be occurring. Therefore, the data likely holds distribution bias since a random sampling was not utilized. Moreover, different teams had varied capability in collecting and documenting data. Some teams were experienced in this type of data collection while others were relatively inexperienced which may have caused rifts in the data. This was specifically seen when recording values for larval-negative sites, where the corresponding “dips” with each negative site were imprecisely recorded as “0”. These inconsistencies in collection and recording likely led to discrepancies and thus, data misclassification.

These issues in data acquisition and sampling highlights the need for advanced training and tools to accurately gather data. Secondly, our study only controlled for pre-determined confounders. Other confounders associated with the landscape and vector breeding patterns were not examined and

could impact both direction and magnitude of our results. This was the case specifically with land temperature and weather data analysis, as the dataset did not measure or incorporate information on land temperature for each point. Aside from land cover data, our analysis only analyzed and controlled for variables included in the dataset, and therefore cannot be deemed as unbiased. Future data collection should attempt to collect data during rainy seasons or during both dry and rainy seasons as applicable to diversify the data and better assess the impacts of these variables on larvae distribution. Lastly, more accurate dipping methods are needed not only to increase data validity, but statistical confidence in any observed relationship found. Nonetheless, our study elucidates the potential for future mosquito larval management work in Haiti and abroad. Using this as a baseline, we are confident that future work can continue to identify effective strategies to breeding site mitigation and hopefully, reductions in vector-borne disease as a whole.

CHAPTER VI

PUBLIC HEALTH IMPLICATIONS

Vector-borne diseases continue to be a crippling public health issue globally, with significant burden being placed on many low-and-middle income countries (LMIC's). The island nation of Haiti has faced the brunt of these afflictions in recent years with high rates of endemicity and seropositivity for malaria, Dengue, and a plethora of other diseases. While progress has been made to decrease vector-borne disease prevalence in Haiti, much work remains to be done, with the principal challenge being public health systems surveillance and strengthening. The evidence presented in this study suggest that removing likely habitats for larvae and adult mosquitoes can help reduce susceptibility, bite risk, and bite rate for the Haitian people. To achieve this goal, we must first strengthen our surveillance and prevention efforts within the country. Aside from the few national programs, there is very little evidence of a collective, synchronized surveillance system. Systems, advocates, and organizations simply do not adequately communicate with each other which causes lapses in data and work to be in vain.

These shortcomings have been compounded by the physical and sociopolitical terrain of Haiti. Haiti is plagued by of torrential rainfall, hurricanes, and earthquakes, with the 2010 Earthquake being the most notable. This Earthquake literally shook the foundations of the country that not only further debilitated progress in health systems strengthening, but also spurred mosquito vector disease dynamics that have put significant Haitians at risk as discussed above. Coupled with the recurring political instability and upheaval within the country, rural and urban laymen become increasingly marginalized and disadvantaged to help combat these diseases. Therefore, from a public health perspective, all efforts on all fronts to combat these issues in unified way—starting first with improved surveillance. From there, public health practitioners can segue into prevention through education with an emphasis on meeting at risk individuals where they are at rather than where they need to be at all levels.

Vector disease education and management must go beyond didactic lecture and learning. Novel community based participatory methods must be incorporated into these efforts to truly provide outreach and support for urban and rural communities alike. Moreover, these approaches must be grounded in a durable, long-term model to provide consistency to these communities. Far too often are these efforts short-lived or disingenuous because they are rooted in a savior's complex rather than a public health framework. Especially as Haiti continually relies on external support for multifaceted aid, both the intention and impact must be well-placed and sustainable for true public health change to take hold. While there are socio-political and economic reasons why this may be challenging, the need to address these systemic issues still remains and as such, our will and desire to change must also remain. This study only examined a small glimpse of the complex issue that is public health in Haiti. It is not intended to suggest concrete interventions, but rather serve as a baseline for mosquito larval research and any ensuing management efforts. Using the geospatial distribution results, the next step is to integrate and incorporate these findings established organizations to help alleviate the public health burden of vector-borne disease.

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TABLES AND GRAPHS

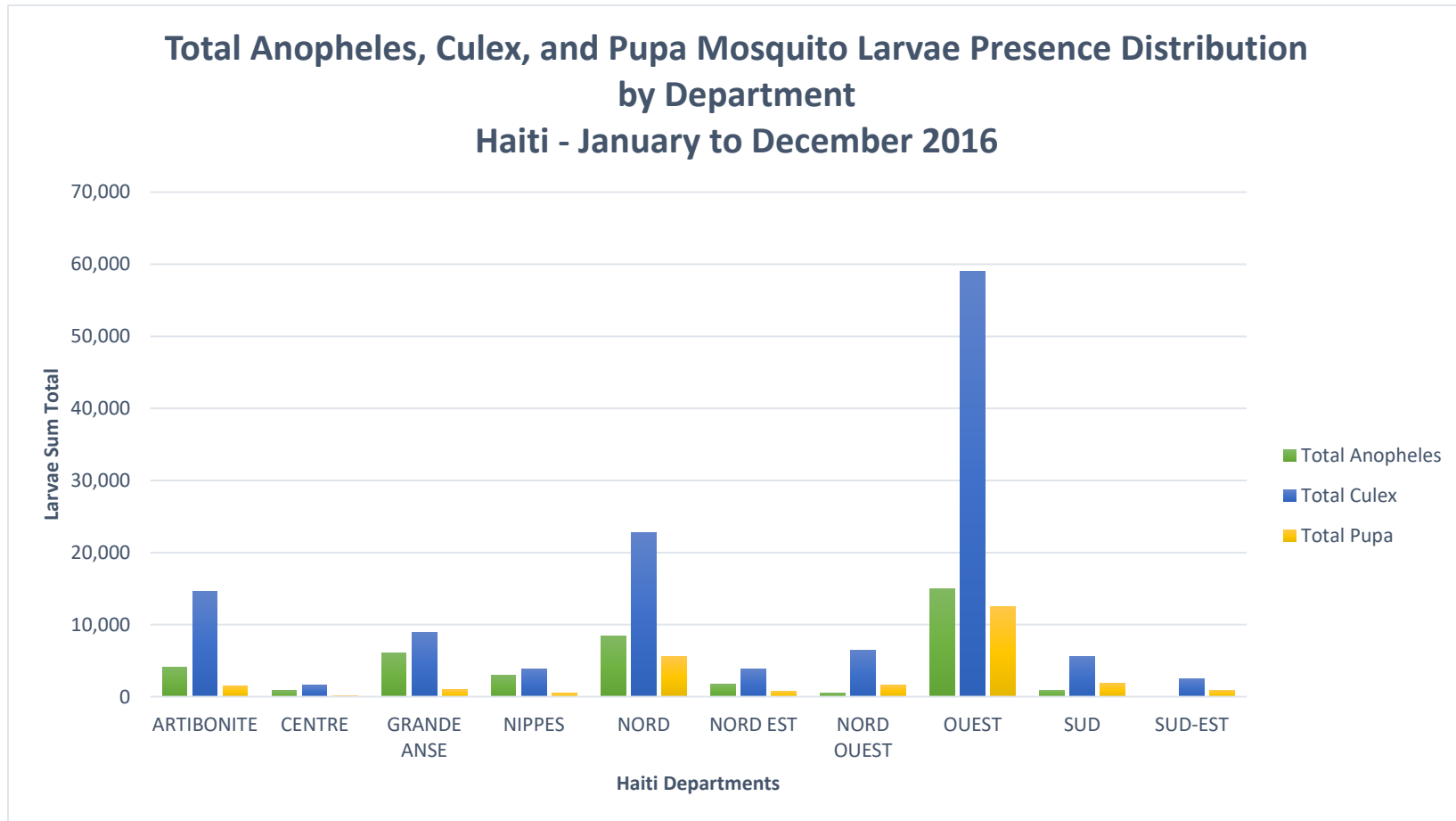


Figure 1: Total positive mosquito larvae distribution across Haiti departments. Largest concentration was found in the Ouest department followed by the Nord department for both species and pupa. *Anopheles* and *Culex* species in the Ouest department were found with values of 15,003 (7.7%) and 59,045 (30.0%) respectively. Pupa were also predominantly concentrated in the Ouest department with a value of 12,465 (6.3%).

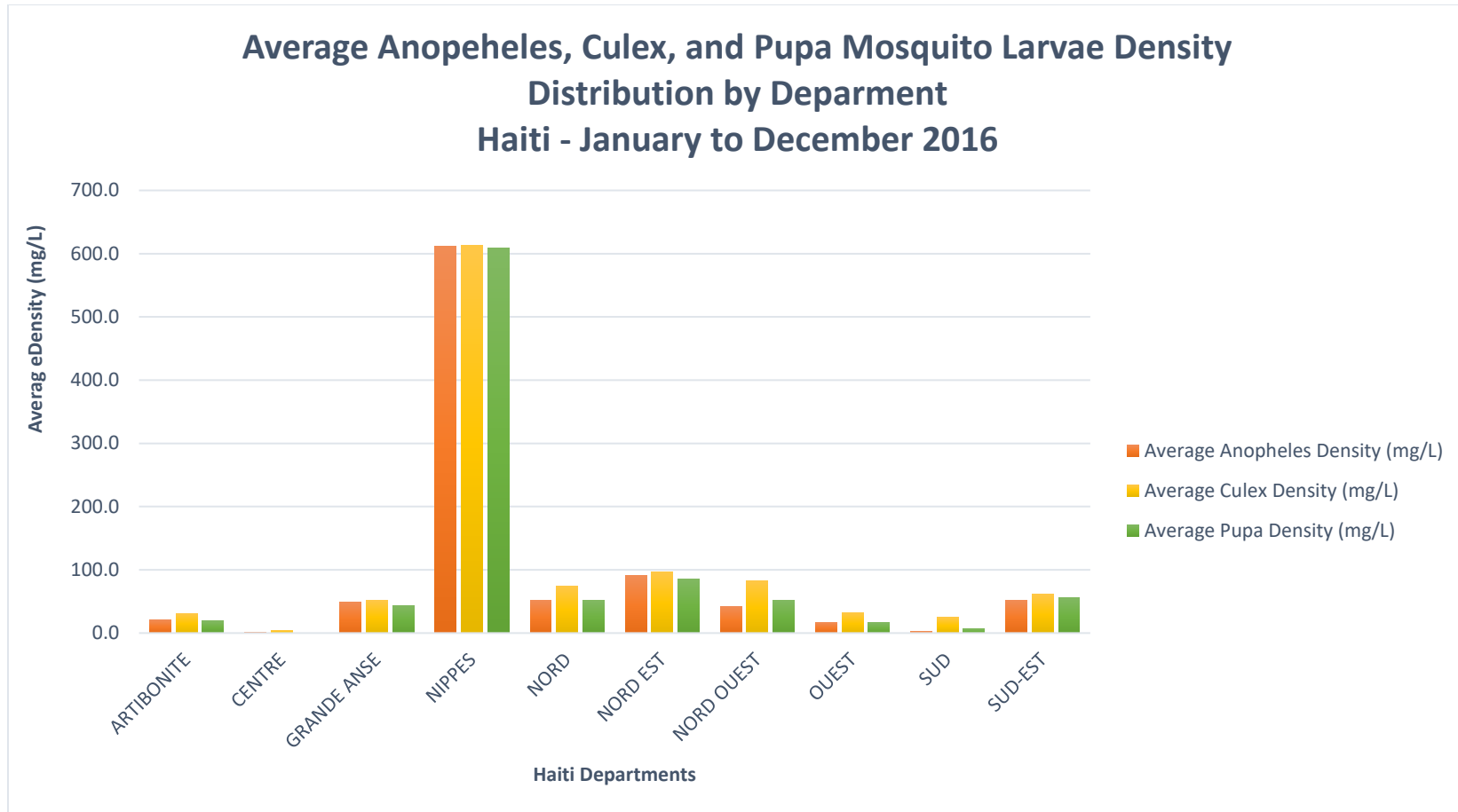


Figure 2: Positive mosquito larvae density distribution across Haiti departments. Largest concentration was found in the Nippes department followed by the Nord-Est department for both species and pupa. Average *Anopheles* density was found to be 611.9 (mg/L) while *Culex* and pupa levels remained at 613.0 (mg/L) and 609.1 (mg/L) respectively.

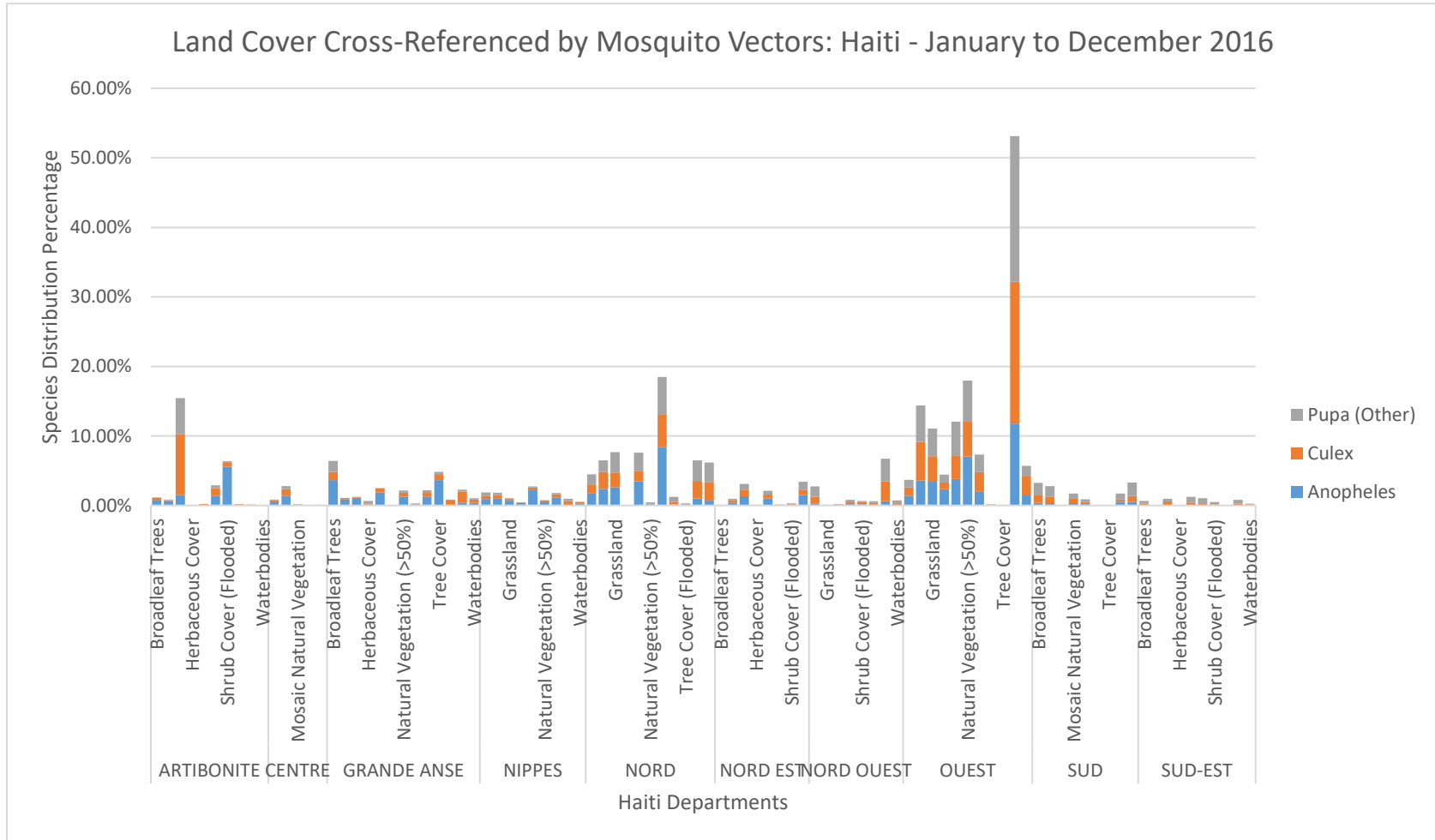


Figure 3: Land cover distribution cross referenced by species concentration. Strong concentrations were found in the Ouest, Nord, and Artibonite departments. Within the Ouest department urban areas were the primary habitat of all positive larval sites across all three species and organisms of interest with a value of 11.8% for *Anopheles*, 20.46% for *Culex*, and 21% for pupa. However, in the Nord department, flooded shrub cover was the primary habitat for all species with values of 8.5%, 4.7%, and 5.4% for *Anopheles*, *Culex*, and pupa species respectively.

Presence and Absence of Mosquito Vectors in Haiti: Jan. - Dec. 2016

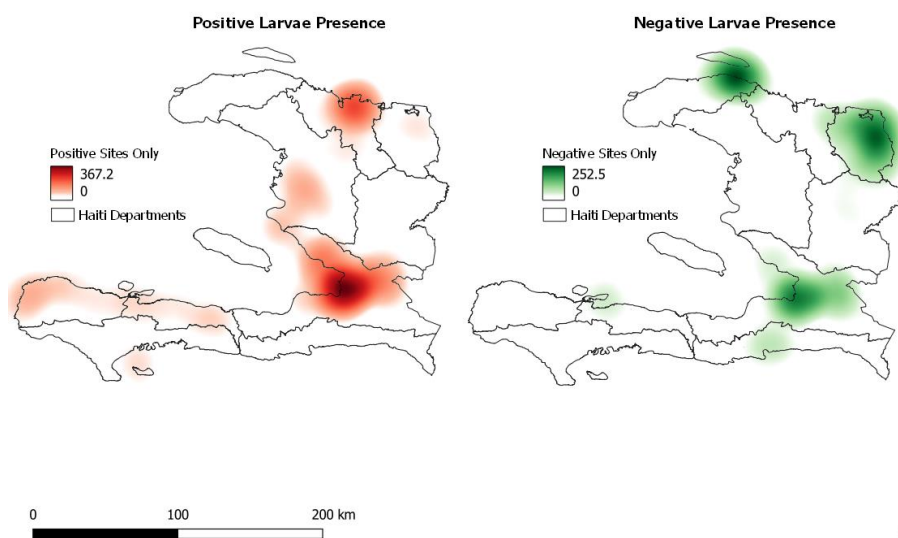


Figure 4: Kernel density interpolation of mosquito disease vector presence (larvae positive) and absence (larvae negative) by departments surveyed between January 2016 and December 2016. Larvae positive sites (hotspots) were strongest in the Nord, Artibonite, Ouest, and Grande Anse departments. Larvae negative sites (cold spots) were strongest in the Nord-Ouest, Nord-Est, and Ouest departments.

Anopheles Mosquito Larvae Distribution Across Haiti: Jan. - Dec. 2016

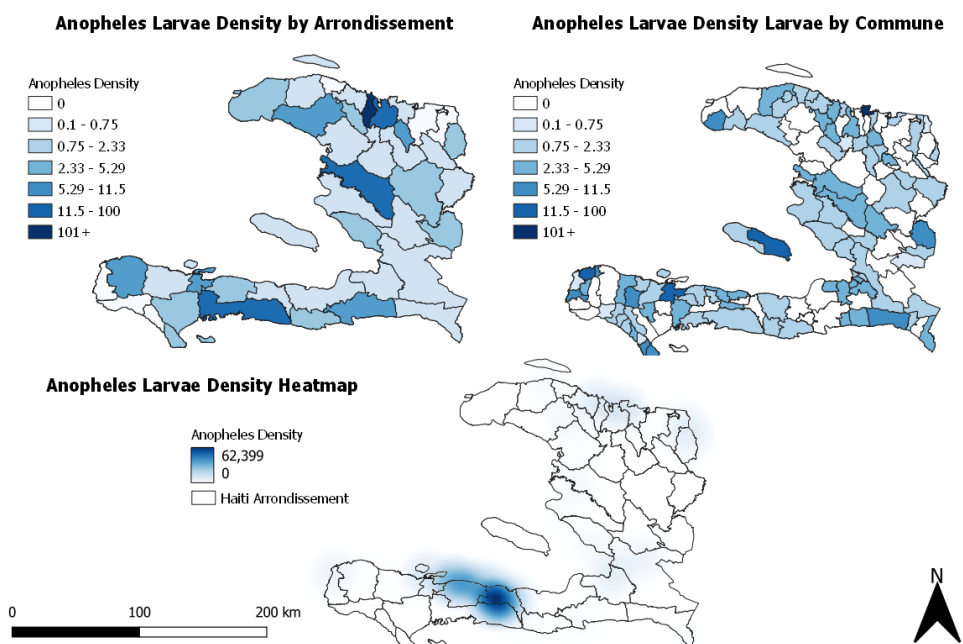


Figure 5: Spatial distribution of total Anopheles only positive sites across arrondissement, commune, and Anopheles interpolation by average density. Anopheles concentration was strongest in the Acul du Nord, Dessalines, and Aquin arrondissements. Strongest commune concentrations were found in Anse à Galets, Baradères, and Cap-Haitien. Interpolation concentration was strongest in arrondissements found in the Nippes department.

Culex Mosquito Larvae Distribution Across Haiti: Jan. - Dec. 2016

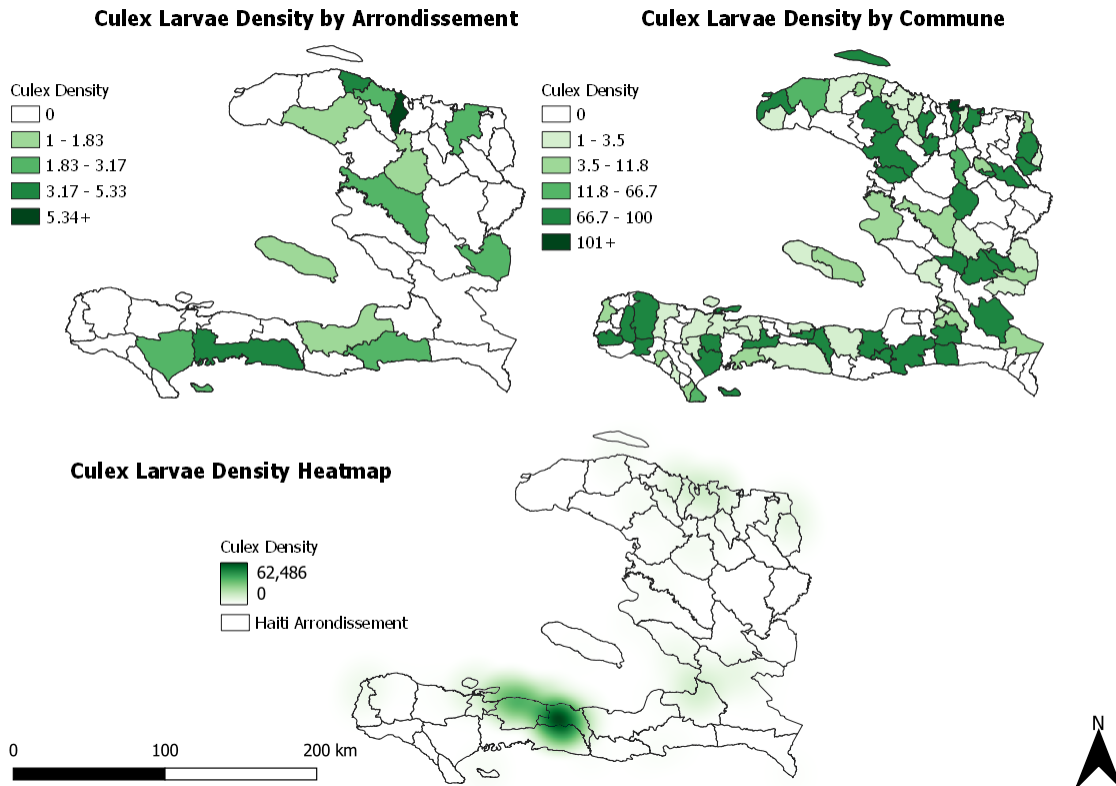


Figure 6: Spatial distribution of total culex only positive sites only across arrondissement, commune, and *Culex* interpolation by average density. *Culex* concentration was strongest in the Saint-Louis du Nord, Acul du Nord, Aquin arrondissements. Strongest commune concentrations were found in the Sau-D'eau, Mirebalais, Marigot, Maniche, Cap-Haitien, and Les Irois. Interpolation concentration was strongest in arrondissements found in the Nippes department.

Mosquito Pupa Larvae Distribution Across Haiti: Jan. - Dec. 2016

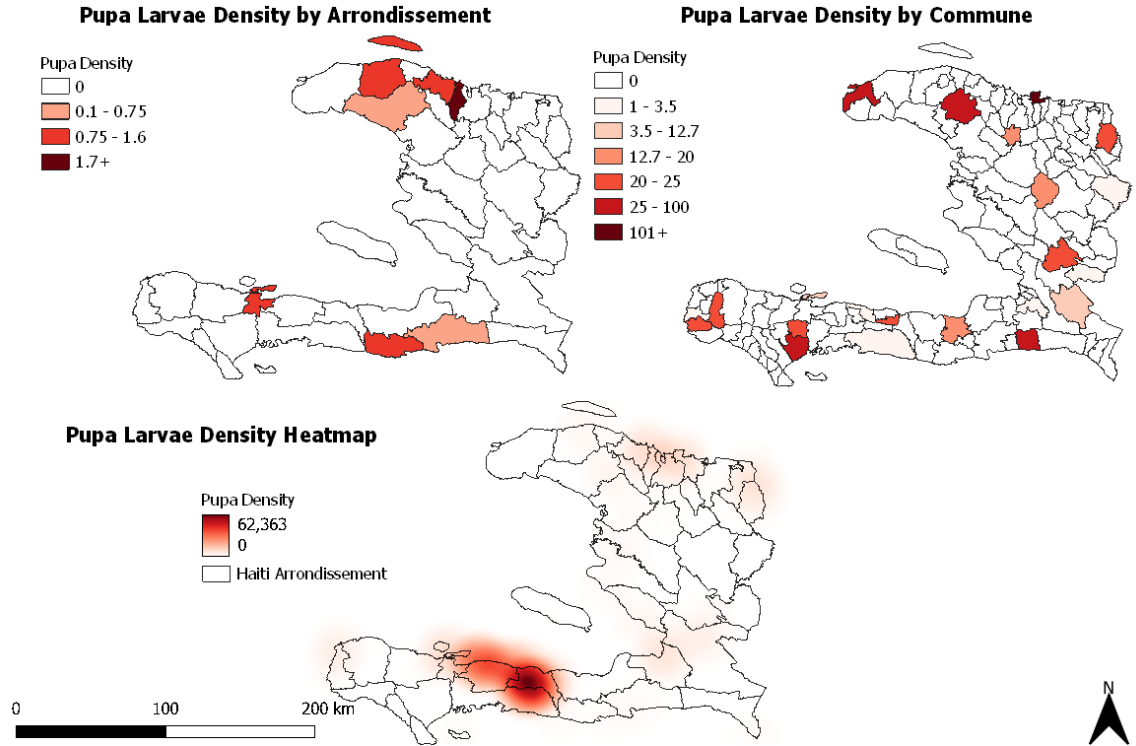


Figure 7: Spatial distribution of total pupa only positive sites only across arrondissement, commune, and pupa interpolation by average density. Pupa concentration was strongest in the Borgne, Baradères, Acul du Nord and Bainets arrondissements. Strongest commune concentrations were found in Mole Saint Nicolas, Gros Morne, and Mirebalais. Interpolation concentration was strongest in arrondissements found in the Nippes department, with uniform density throughout Haiti.

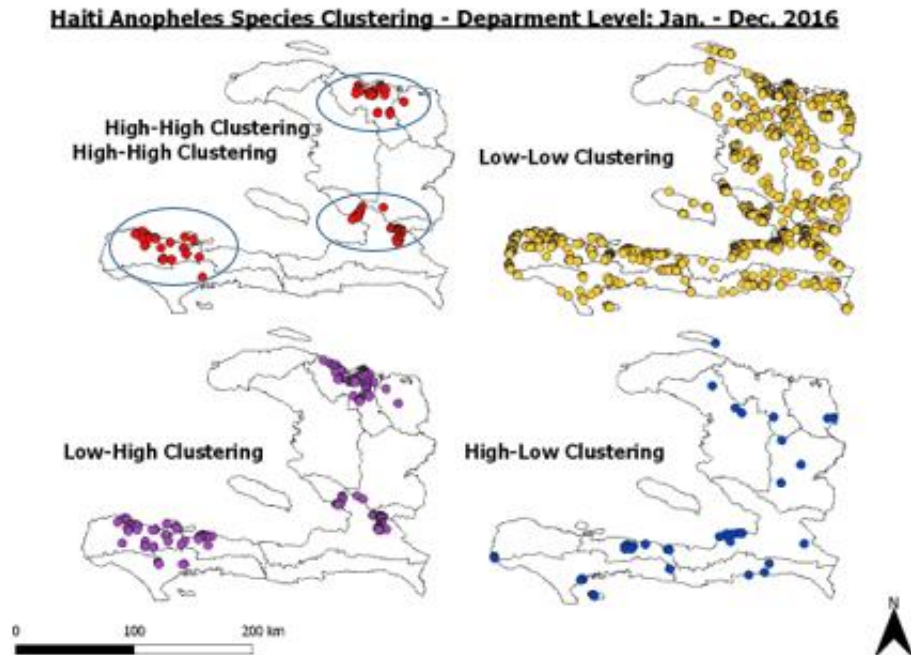


Figure 8: Statistically significant clustering ($p < 0.05$) (5%) clustering of *Anopheles* species mosquito larvae across department for positively correlated clusters (high-high and low-low). 3 distinct, significant high-high clusters were found in the Nord, Ouest, and Grande Anse departments while low-low correlated points were scattered throughout all departments of Haiti.

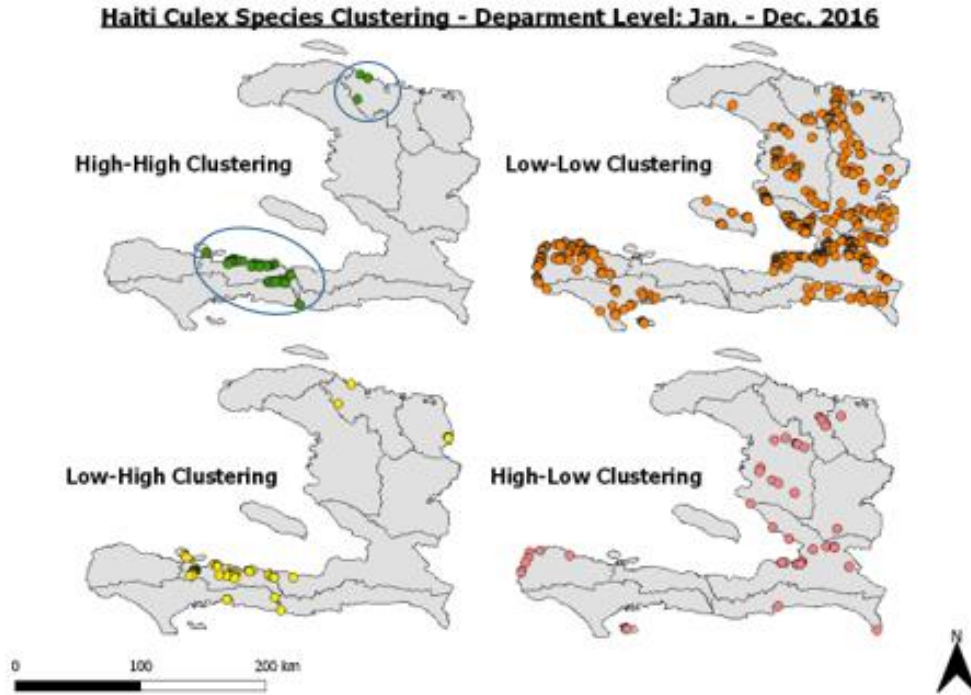


Figure 9: Statistically significant clustering ($p < 0.05$) (5%) clustering of *Culex* species mosquito larvae across department for positively correlated clusters (high-high and low-low). 2 distinct, significant high-high clustering was strongest in the Nord and Nippes departments while low-low correlated points were scattered throughout all departments of Haiti, with strong clustering in Ouest, Nord, and Grande Anse departments.

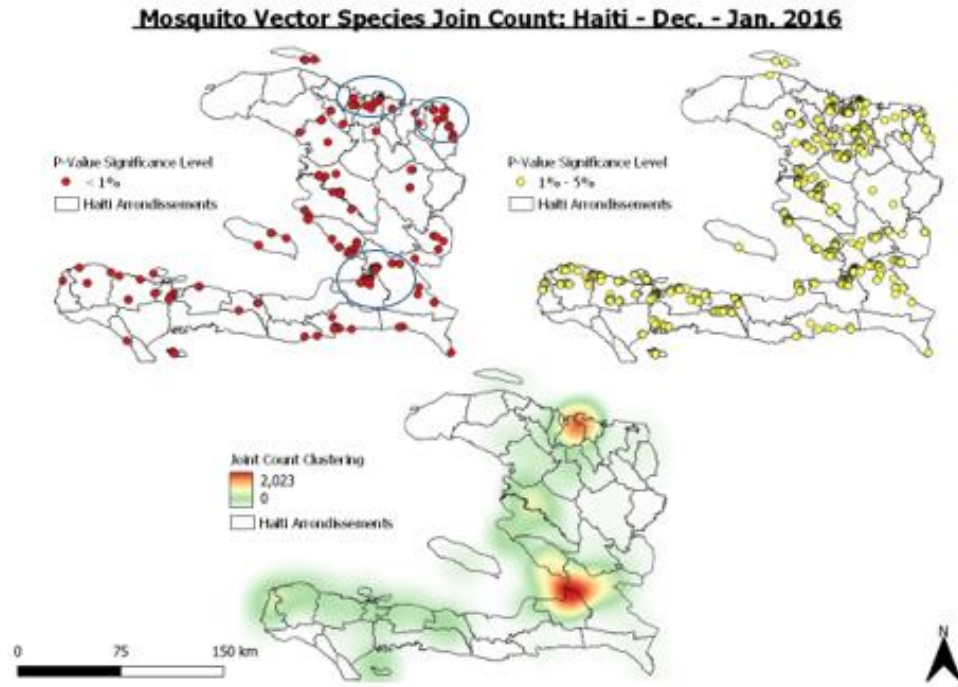


Figure 10: Statistically significant mosquito vector point distribution cross-referenced with kernel density interpolation across arrondissements. Results indicate sporadic distribution of all vectors at the ($p < 0.01$) (1%) significance threshold, throughout the country with small clusters in the Cap-Haitien, Port-au-Prince, Fort-Liberté, and Ouanaminthe arrondissements. Interpolation results indicate significant hotspots in Limbé, Cap-Haitien, Port-au-Prince, and Croix-de-Bouquet areas.

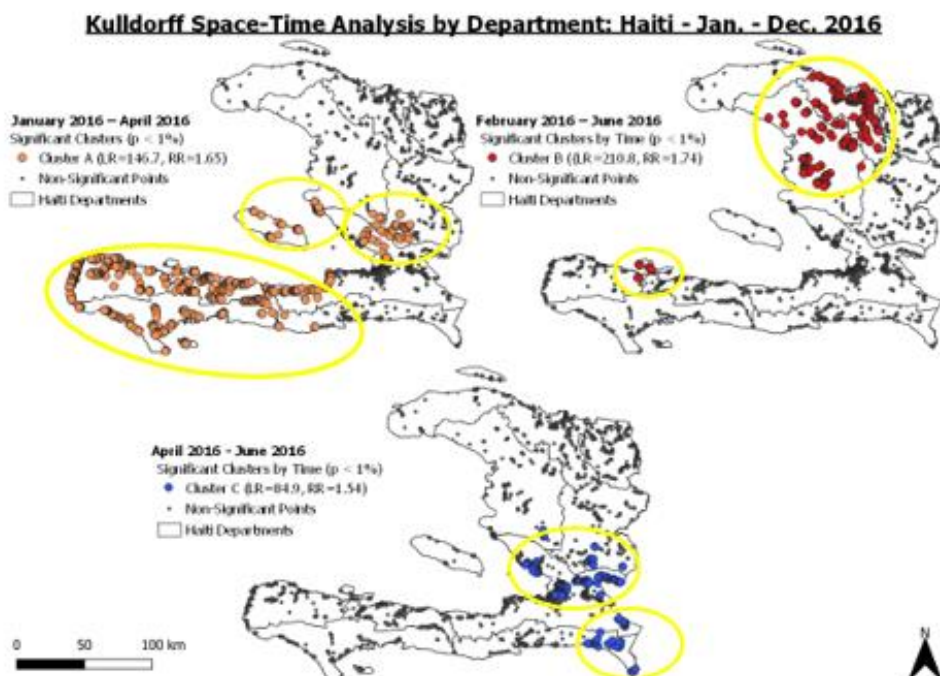


Figure 11: Kulldorff spatiotemporal distribution of *Anopheles* and *Culex* mosquito vector species by department across Haiti from January 2016 – December 2016. Circles denote significant clusters within that geographic region. From January 2015 – April 2016, clustering aggregated in the Southern departments of Grande Anse, Sud, Nippes, along with smaller clusters in the Sud-Est, Ouest, and the southern portion of the centrally located Centre department. From February 2016 – June 2016, clusters shifted to aggregate in the North of Haiti within the Artibonite and Nord departments, with an isolated clusters straddled between Nippes and Grande Anse. April 2016 – June 2016 saw clusters shift back to the Central-Southeast region of Haiti in the Sud-Est and Ouest departments.

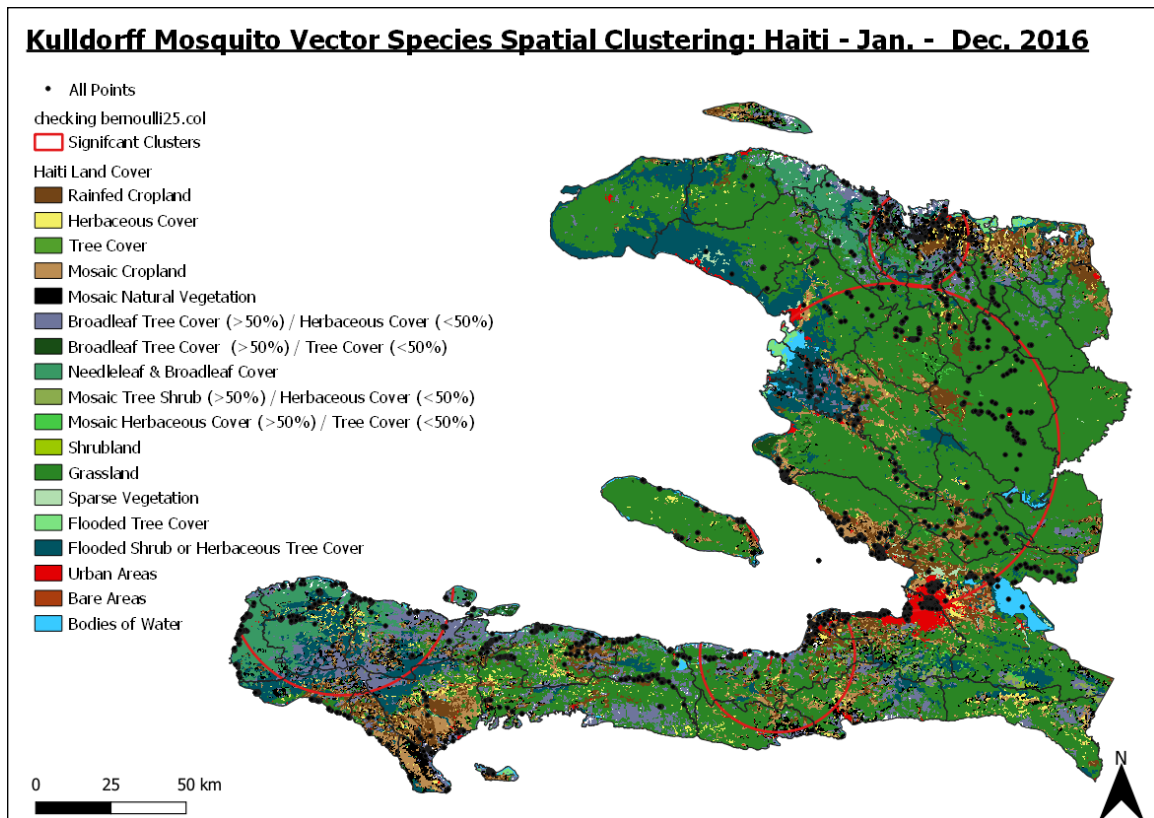


Figure 12: Kulldorff purely spatial scan of presence of either *Anopheles* or *Culex* mosquito vector species by department across Haiti. Colors denote varying cluster aggregation between January 2016 – December 2016. Smallest points (black) denote non-significant points extracted from the original dataset.

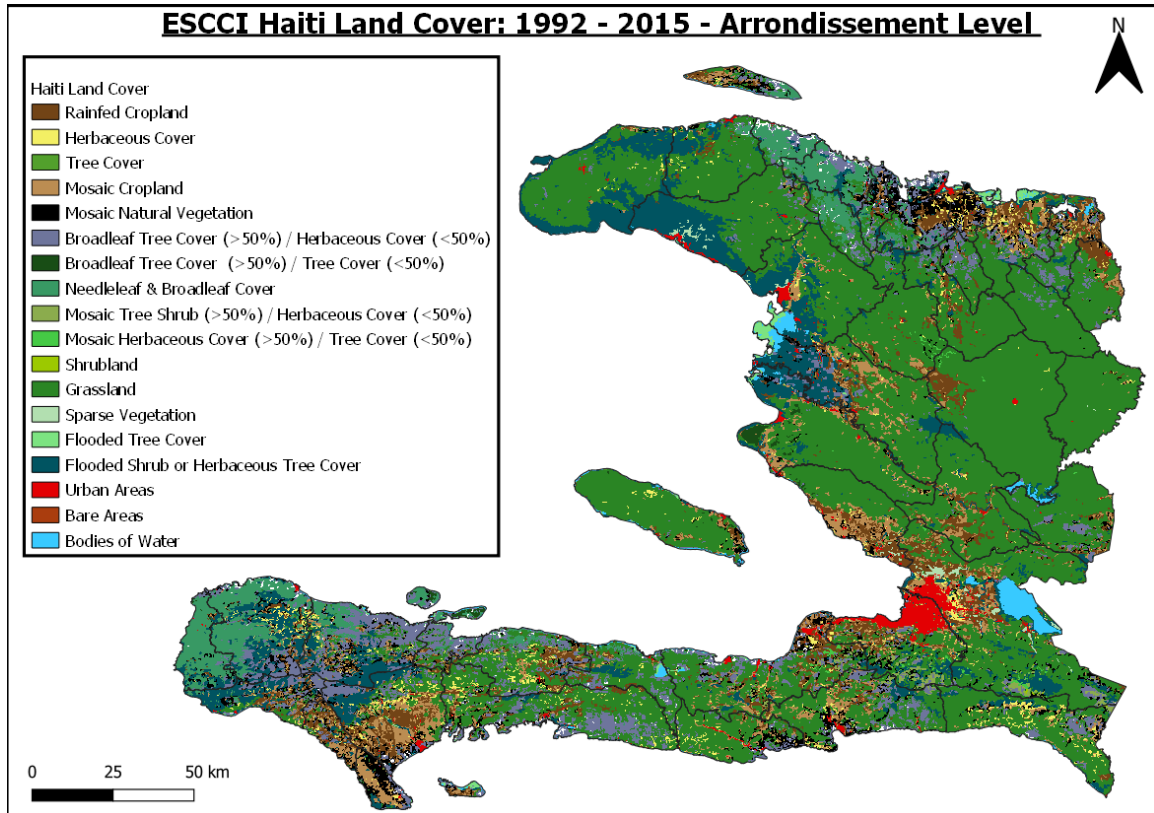


Figure 13: General landcover across Haiti by arrondissement. Color patterns denote specific forms of land cover or topography, with urban areas (red), cropland (black and brown), and flooded areas (blue-green) being areas of significant coverage.

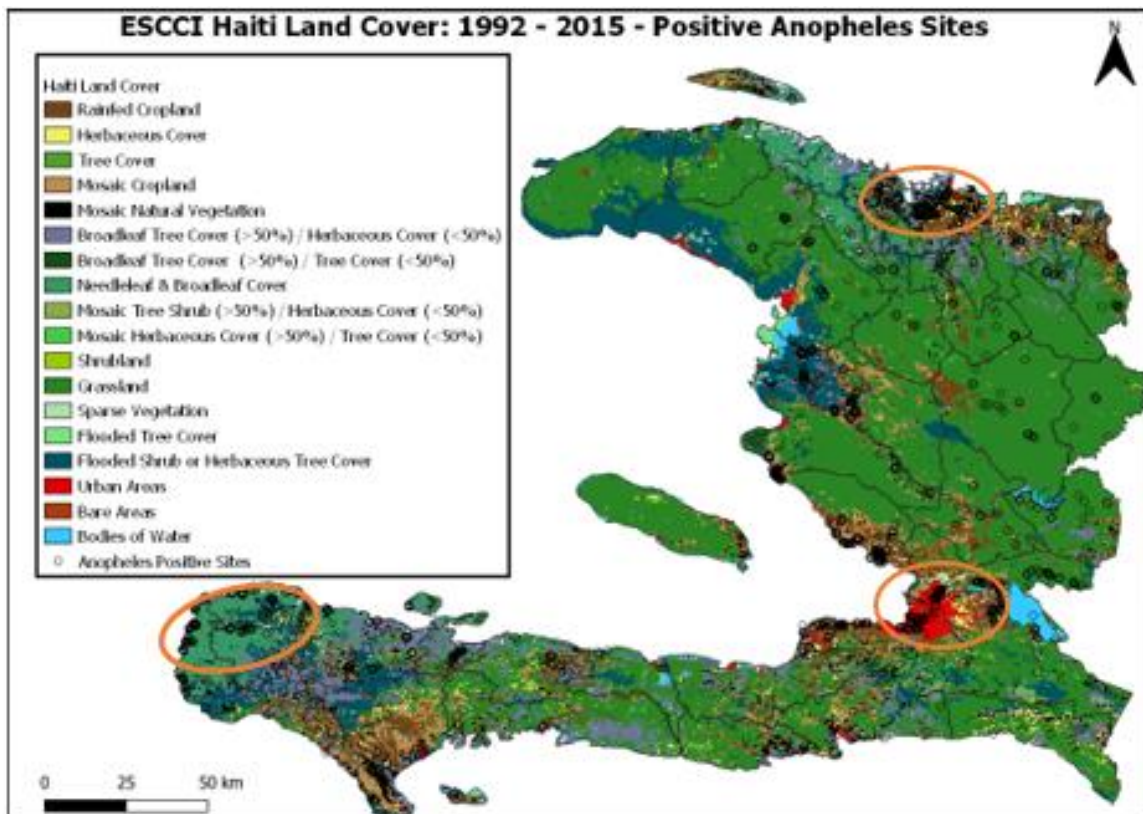


Figure 14: *Anopheles* larvae positive sites only across arrondissement cross-referenced by land cover distribution. Strong clustering was found in urban areas (red), flood shrub cover (navy blue), needleleaf tree cover (mint green), and all forms of cropland (brown and black) across all regions of the country.

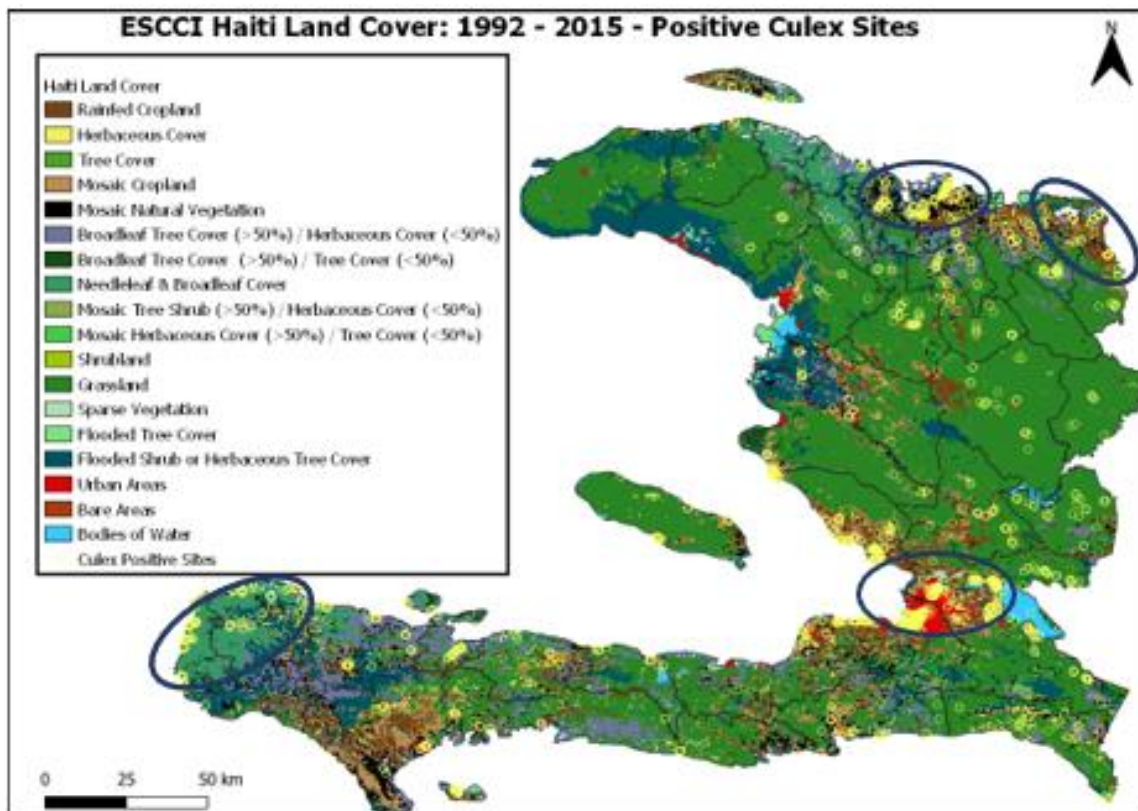


Figure 15: *Culex* larvae positive sites only across arrondissement cross-referenced by land cover distribution. Strong clustering was found in urban areas (red), flood shrub cover (navy blue), needleleaf tree cover (mint green), and all forms of cropland (brown and black) across all regions of the country.