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Spatial and seasonal dynamics of mosquito species in Harris County, Texas, highlight risk of arbovirus introduction and transmission

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Mosquito-borne diseases pose a significant public health threat, particularly in densely populated urban areas. Climate change, urbanization, and global connectivity have fueled the expansion of mosquitoes and their associated pathogens, increasing the disease burden. Harris County, Texas, is among the most vulnerable regions in the United States for mosquito-borne disease outbreaks, underscoring the critical need for localized insights into mosquito population dynamics to inform vector surveillance and control strategies. This study provides a comprehensive analysis of the population dynamics of mosquito species in Harris County by exploring their species composition, spatial distribution, and seasonal patterns. Our findings reveal the extensive distribution of *Culex quinquefasciatus* and *Aedes albopictus*, with *Aedes aegypti* concentrated in highly urbanized areas. Notably, three of the five most abundant species are primary vectors of human pathogens, highlighting the urgent need for targeted interventions. By leveraging high-resolution surveillance data, this research deepens our understanding of mosquito dynamics and lays the groundwork for future studies investigating the effects of climate change, urbanization, and other environmental drivers on vector populations.

Keywords Mosquito surveillance, Vector ecology, Seasonal dynamics, Urban ecology, Harris County, Public health

Mosquito-borne diseases are a significant global health threat, causing substantial morbidity and over one million deaths annually[1,2]. The risk posed by these diseases is escalating as climate change, urbanization, and global travel and trade accelerate shifts in vector ecology[3–7]. These changes enable the expansion of mosquito species into new geographic regions, resulting in increased disease burden and outbreaks often driven by viral mutations that enhance pathogen transmissibility[8–10]. In light of this increasing threat, developing effective prevention and control strategies is an urgent public health priority.

Tropical and subtropical areas, especially those with high population densities, are particularly vulnerable to the emergence and re-emergence of mosquito-borne pathogens[11]. Along the United States (U.S.) Gulf Coast, several large metropolitan areas face disproportionate risk due to unique geographic and environmental conditions. Harris County, Texas, encompassing the Houston metropolitan area, is a critical area of concern. Its subtropical climate, dense population, high precipitation, and recurrent flooding, combined with the constant movement of goods and people from across the globe, create a conducive environment for the introduction and sustained transmission of mosquito-borne pathogens[12–17]. These pathogens have directly impacted public health in the county, with human cases of West Nile virus reported annually since its introduction in 2002, along with historical outbreaks of Saint Louis encepahlitis[14,18–20]. Additionally, travel-associated cases of chikungunya and dengue, along with reports of Eastern and Western equine encephalitis in nearby counties, raise concerns about the potential introduction and establishment of emerging pathogens. The year-round presence of key vector species further amplifies the threat of outbreaks and pathogen re-emergence.

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Given the absence of effective treatments or preventative vaccines for many mosquito-borne diseases, mosquito abatement and control remain the primary mechanisms for disease prevention. Effective mosquito control depends on robust surveillance programs to provide essential data on mosquito populations, pathogen activity, and environmental factors influencing mosquito dynamics and transmission risk[9,21]. Despite surveillance efforts in many high-risk metropolitan areas, there are specific gaps in knowledge of local mosquito species composition, geographic distribution, and seasonal dynamics. Existing research often focuses on broader geographic regions or particular pathogens, neglecting the local species-specific population dynamics necessary for tailored interventions. This study addresses these gaps by analyzing mosquito species composition, distribution, and seasonality in Harris County, Texas, with an emphasis on medically significant species. By leveraging extensive, high-resolution surveillance data, we provide actionable insights into mosquito dynamics to inform geographically tailored interventions, paving the way for targeted public health campaigns in high-priority areas of Harris County, Texas. Additionally, this study is a foundation for future research on the effects of climate change, urbanization, and other environmental factors on vector population dynamics and understanding mosquito-borne disease risk.

Methods

Study area

Harris County (29° 46′ 58″ N 95° 22′ 20″ W) is located in southeastern Texas, adjacent to the Gulf of Mexico, with Houston as its county seat. As the third most populous U.S. county, Harris County is home to 4.7 million residents within 1706.96 square miles (4428.78 km^2), averaging 2749 people/mi^2 (1061 people/km^2)[22]. The county experiences a humid subtropical climate characterized by hot and humid summers and mild winters, with distinct seasons (spring, summer, fall, and winter). The seasons are generally defined as follows: spring (February–May), summer (June–August), fall (September–November), and winter (December–January). The average monthly temperatures range from 60.7°F (15.9 °C) in January to 80.7°F (27.1 °C), and annual rainfall averages about 52 inches (132 cm), peaking from May through October[23].

Data source

We obtained adult mosquito data from 2018 to 2022 from the Harris County Public Health Mosquito and Vector Control Division (HCMVCD). HCMVCD conducts routine mosquito trapping across the county as part of its surveillance and control program. Mosquito specimens were collected using three trap types: the Biogents Sentinel (BG) trap (Biogents Inc., Regensburg, Germany), the modified Centers for Disease Control and Prevention (CDC) gravid trap (GV; J.W. Hock and Co., Gainesville, FL), and the modified CDC miniature light trap. BG traps utilized a proprietary BG lure to simulate human skin scent (Biogents Inc.) enhanced with carbon dioxide (CO_2) from dry ice to increase collection efficiency[24]. This allows the BG trap to capture a wide range of mosquito species in an urban environment and improves the capability of dengue virus, chikungunya virus, and Zika virus surveillance by collecting *Aedes* spp. mosquitoes[25]. The gravid traps employed a modified Reiter hay infusion medium, ideal for collecting gravid *Culex* spp. mosquitoes and primarily intended to maximize *Cx. quinquefasciatus* collection for WNV and St. Louis Encephalitis (SLE) surveillance[17,26]. The modified CDC miniature light traps, baited with CO_2 from dry ice, were placed in storm drainage systems to surveil mosquitoes in these habitats.

Adult mosquito traps were deployed systematically across the county as part of HCMVCD's routine surveillance program. Trapping was conducted at 494 unique locations, with each location trapped an average of 27 times annually (range 1–89). Traps were placed between 12 and 4 pm and retrieved between 8 and 10 a.m. the following morning, allowing for a collection time of approximately 18 h. The collected mosquitoes were transported to the HCMCVD surveillance laboratory, where they were sorted, sexed, and identified morphologically to the species level by a trained entomologist using taxonomic keys.

Statistical analysis

Only female mosquitoes were analyzed due to their role in pathogen transmission. Mosquito abundance was standardized as the number of female mosquitoes of each species collected at a unique trap location in one night (trap-night) averaged over weeks to adjust for variations in collection frequency at each trap location. Non-parametric statistical methods were used to analyze data on mosquito abundance due to non-normal distribution. Two-tailed Kruskal–Wallis tests were conducted to assess differences in mosquito abundance during peak season (May–October) across the study years for each trap type. Subsequent pairwise comparisons using Dunn's test with False Discovery Rate (FDR) correction were conducted to determine specific differences in mosquito abundance. Statistical significance was set at $\alpha = 0.05$. These analyses were performed using R version 4.3.1.[27].

We analyzed mosquito population dynamics monthly using relative abundance and distribution. Relative abundance was calculated as the proportion of a specific mosquito species relative to total mosquitoes collected [$R = (n/N) \times 100\%$ where: R = relative abundance, n = number of mosquitoes collected for each species, N = total number of mosquitoes collected]. Species dominance, measured using relative abundance, was categorized according to Heydemann's classification for each month and trap type[21]. Species comprising more than 30% of specimens were classified as eudominant, > 10–30% were dominant, > 5–10% were subdominant, > 1–5% were rare, and ≤ 1% were categorized as subrare.

Species distribution was calculated as the proportion of trap locations where a specific mosquito species was detected [$D = (n/N) \times 100\%$ where: D = distribution, n = the number of trap sites that a mosquito species was found, N = number of all trap sites]. Species were classified as constant if present in more than 80% of trap sites, > 60% to 80% were frequent, > 40% to 60% were moderate, > 20% to 40% were infrequent, and ≤ 20% were sporadic[22,23]. Heatmaps illustrating each species' relative abundance and distribution by month and trap type were generated using the ggplot2 package in R (version 4.4.1)[27,28].

Geospatial analysis

Trap locations were geocoded and mapped using ArcGIS Pro (version 3.3.0; Esri, Redlands, CA). Mosquito abundance per trap-night was calculated by location for the five most abundant species. After confirming spatial autocorrelation using Global Moran's *I*, we applied ordinary kriging to interpolate and visualize mosquito abundance across the county. Ordinary kriging, a commonly used geostatistical method, estimates values at unsampled locations based on the spatial autocorrelation of sample data points[29]. Using the Geostatistical Wizard tool in ArcGIS Pro (Version 3.3.0.; Esri, Redlands, CA), we selected an appropriate semivariogram model through cross-validation (leave-one-out resampling method)[30,31]. The resulting predictive surfaces were classified into ten geometric interval classes for visualization.

Results

Mosquito composition

From January 2018 to December 2022, 3,378,605 adult female mosquitoes were collected across 54,963 trap nights. Forty-three mosquito species from ten genera were identified during the study: *Aedes, Anopheles, Coquillettidia, Culex, Culiseta, Mansonia, Orthopodomyia, Psorophora, Toxorhynchities,* and *Uranotaenia* (Table 1). Nineteen species are known vectors for pathogens reported in North America. Five species made up 97% of total specimens, with *Cx. quinquefasciatus* comprising 88% of the total female mosquitoes collected (over two million mosquitoes). Other notable species included *Ae. albopictus* (4.6%), *Cx. salinarius* (1.8%), *Ae. taeniorhynchus* (1.5%), and *Ae. aegypti* (1.5%). The remaining species had a relative abundance of 0.51% or less.

Gravid traps yielded the highest abundance, capturing 1,702,057 mosquitoes (50% of the total) and 39 species (91% of all observed species), with *Cx. quinquefasciatus* comprising 97% of mosquitoes collected by gravid traps. BG traps captured 636,759 mosquitoes (19% of the total) and 40 species (93% of all observed species). *Culex quinquefasciatus* was the most prevalent species (47% of mosquitoes collected by BG traps), followed by *Ae. albopictus* (22%), *Ae. taeniorhynchus* (8%), *Ae. aegypti* (7%), and *Cx. salinarius* (6%). CDC light traps collected 1,039,789 mosquitoes (31% of the total) and 28 species (65% of all observed species), predominantly *Cx. quinquefasciatus* (97% of mosquitoes collected by CDC light traps) (Table 1).

Mosquito abundance change over the study period

Seasonal and yearly variations in mosquito abundance varied by trap type (Fig. 1). Standardized mosquito abundance by week was visualized to highlight variations in abundance throughout the study period. Mosquito abundance in the BG trap had a unimodal peak in mid to late summer (June–September) each year (Fig. 1A). The average mosquito abundance did not differ between years in the BG trap (Kruskal–Wallis, $H(4) = 1.90$, $p = 0.755$) (Fig. 1B). The gravid traps generally exhibited a unimodal peak in early summer (Fig. 1C), with average abundance steadily rising and peaking in 2020 and 2021 before declining to baseline in 2022 (Kruskal–Wallis, $H(4) = 18.7$, $p < 0.001$) (Fig. 1D). Conversely, CDC light traps demonstrated a bimodal peak in the early and late summer (April and October) (Fig. 1E), with abundance decreasing after 2018, followed by a statistically significant increase in 2022 (Kruskal–Wallis, $H(4) = 1.90$, $p < 0.001$) (Fig. 1F). Posthoc Dunn's tests with FDR-adjusted p-values are illustrated in panels (d) and (e), with p-values in Supplementary Table S1.

Relative abundance of mosquito species

Figure 2 presents heat maps illustrating the relative abundance of mosquito species by month and trap type, highlighting seasonal variations in species composition. We categorized species as eudominant (comprising > 30% of specimens), dominant (> 10–30%), subdominant (> 5–10%), rare (> 1–5%), and subrare (≤ 1%). Aggregating the entire study period, *Cx. quinquefasciatus* comprised over 30% of the total female mosquitoes collected across all trap types. BG traps had one dominant species (*Ae. albopictus*), three subdominant species (*Ae. aegypti, Ae. taeniorhynchus,* and *Cx. salinarius*), three rare species (*Ae. vexans, Ps. columbiae, and Ps. ferox*), and 32 subrare species (Fig. 2A). Gravid traps exhibited no dominant, subdominant, or rare species, and 38 subrare species (Fig. 2B). CDC light traps had no dominant or subdominant species, one rare species (*Cx. salinarius*), and 27 subrare species (Fig. 2C) (Supplementary Table S2). When assessing the species' dominance structure by month and trap type, two distinct patterns were observed. Some mosquito species showed higher relative abundance during hotter summer months, while others were less prevalent or nearly absent during the hotter summer months. Seasonal patterns showed that *Ae. albopictus* peaked in mid-summer, while *Cx. quinquefasciatus* was abundant throughout the year. This visualization helps identify seasonal trends in mosquito species composition, which is crucial for optimizing targeted mosquito control interventions.

Distribution of mosquito species

Figure 3 presents heat maps illustrating the distribution of mosquito species across months and trap types, showing seasonal variations in the proportion of traps in which species were captured. BG traps consistently captured seven species in > 80% of traps during at least one month during the study period (Fig. 3A). These species include *Ae. albopictus, Ae. aegypti, Ae. taeniorhynchus, Ae. vexans, Cx. quinquefasciatus, Cx. salinarius,* and *Ps. columbiae*. In gravid traps, three species were captured in > 80% of traps during at least one month: *Ae. albopictus*, *Cx. quinquefasciatus*, and *Cx. salinarius*. A majority of the remaining species were present in < 20% of traps (classified as "sporadic") (Fig. 3B). CDC light traps had three species captured in > 80% of traps for at least one month: *Cx. quinquefasciatus*, *Cx. restuans*, and *Cx. salinarius*. *Culex quinquefasciatus* was consistently captured in > 80% of traps nearly every month in the gravid and CDC light traps (Fig. 3A–C). Seasonal variations were evident, with some species more widespread during summer. *Ae. albopictus* was regularly found in more than 80% of traps from April to November, while *Ae. aegypti* exhibited a broader distribution during late summer.

Genus	Species	BG-sentinel (n = 13,396)	Gravid (n = 22,658)	CDC light (n = 18,909)	Total (n = 54,962)* indicates < 0.1%
Aedes	*Ae. aegypti*	44,832	3,385	1,515	49,732 (1.5%)
	Ae. albopictus	137,316	14,505	2,763	154,584 (4.6%)
	Ae. atlanticus	422	36	0	458*
	Ae. canadensis	0	2	0	2*
	Ae. epactius	55	0	1	56*
	Ae. fulvus pallens	311	1	0	312*
	Ae. hendersoni	10	2	0	12*
	Ae. infirmatus	638	46	8	692*
	Ae. sollicitans	2,770	97	16	2,883 (0.1%)
	Ae. sticticus	4	0	0	4*
	Ae. taeniorhynchus	50,416	555	480	51,451 (1.5%)
	Ae. triseriatus	173	102	8	283*
	Ae. trivittatus	13	4	0	17*
	Ae. vexans	14,887	132	288	15,307 (0.5%)
Anopheles	*An. crucians*	846	129	74	1,049*
	An. psuedopunctipennis	1	2	0	3*
	An. punctipennis	87	18	65	170*
	An. quadrimaculatus	2,640	564	296	3,500 (0.1%)
Coquillettidia	*Cq. perturbans*	134	19	1	154*
Culex	*Cx. abominator*	0	25	0	25*
	Cx. coronator	2,678	1,179	926	4,783 (0.1%)
	Cx. erraticus	1,312	1,095	1,056	3,463 (0.1%)
	Cx. interrogator	5	0	0	5*
	Cx. nigripalpus	5,489	3,543	4,318	13,350 (0.4%)
	Cx. quinquefasciatus	300,811	1,651,896	1,009,519	2,962,226 (87.7%)
	Cx. restuans	854	14,215	2,044	17,113 (0.5%)
	Cx. salinarius	35,174	9,088	16,104	60,366 (1.8%)
	Cx. tarsalis	34	4	2	40*
	Cx. territans	6	10	0	16*
Culiseta	*Cs. inornata*	1,176	530	61	1,767 (0.1%)
Mansonia	*Ma. titillans*	1,287	124	5	1416*
Orthopodomyia	*Or. signifera*	16	81	14	111*
Psorophora	*Ps. ciliata*	759	10	0	769*
	Ps. columbiae	14,686	378	82	15,146 (0.4%)
	Ps. cyanescens	1,181	27	6	1,214*
	Ps. ferox	14,912	105	25	15,042 (0.4%)
	Ps. horrida	10	0	0	10*
	Ps. howardii	383	19	3	405*
	Ps. longipalpus	66	1	0	67*
	Ps. mathesoni	1	1	0	2*
Toxorhynchities	*Tx. rutilus*	360	94	0	454*
Uranotaenia	*Ur. lowii*	4	29	99	132*
	Ur. sapphirina	0	4	10	14*
Grand total		636,759	1,702,057	1,039,789	3,378,605

Table 1. Mosquito species collected in Harris County, Texas from January 2018 to December 2022. Total number of mosquitoes collected by species and trap type for all study years are provided.

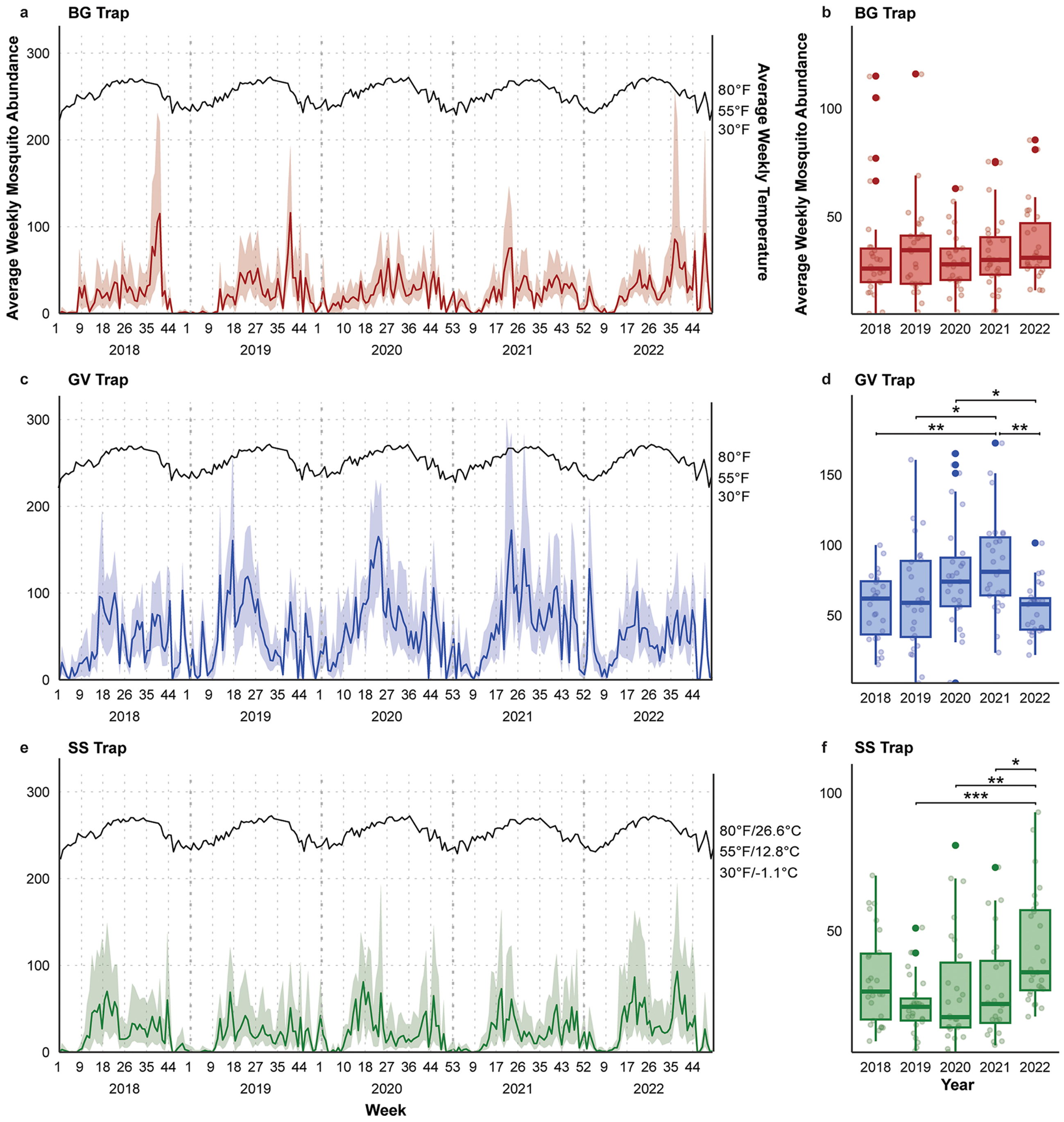
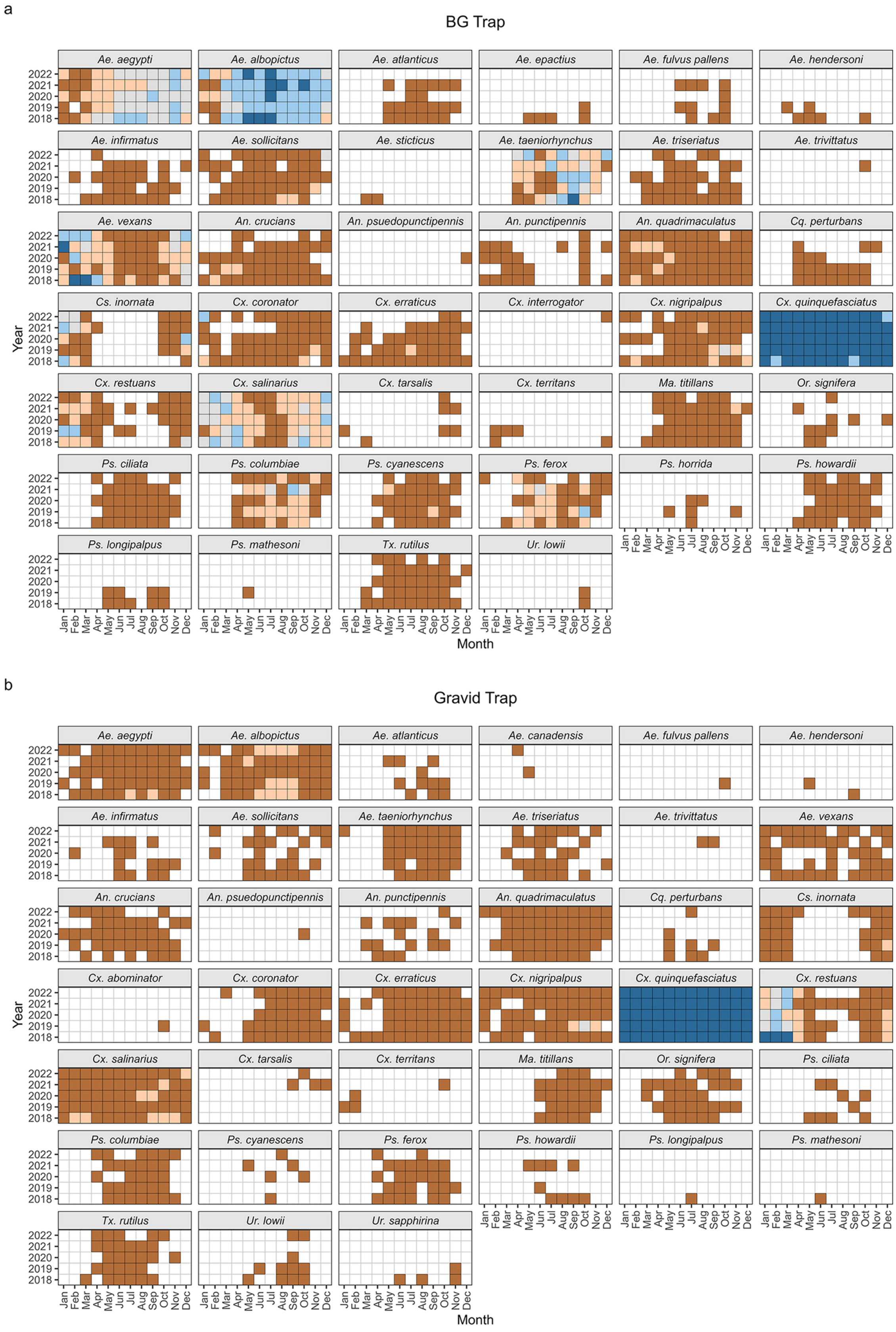


Fig. 1. Seasonal and annual variations in mosquito abundance by trap type in Harris County, Texas (2018–2022). Panels (**a**), (**c**), and (**e**) display median weekly mosquito abundance, with shaded regions representing the interquartile range for (**a**) BG traps, (**c**) gravid traps, and (**e**) CDC light traps placed in storm sewers. The secondary axis shows mean weekly temperature. Panels (**b**), (**d**), and (**f**) present boxplots summarizing mosquito abundance from May to October for (**b**) BG traps, (**d**) gravid traps, and (**f**) CDC light traps placed in storm sewers. In the boxplots, lower and upper fences correspond to the 25th and 75th percentiles, with bars extending to 1.5 times the interquartile range. Statistically significant FDR-adjusted p-values are displayed with asterisks [$p < 0.05$ (*), $p < 0.01$ (**), $p < 0.001$ (***)]. Kruskal–Wallis tests indicated significant differences in mosquito abundance across years in the gravid and CDC light traps. Post hoc Dunn's tests, corrected for multiple comparisons using the false discovery rate, were performed for pairwise comparisons with significant differences summarized in Supplementary Table S1.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BG Trap
Ae. aegypti
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Ae. fulvus pallens
Ae. hendersoni
Ae. infirmatus
Ae. sollicitans
Ae. sticticus
Ae. taeniorhynchus
Ae. triseriatus
Ae. trivittatus
Ae. vexans
An. crucians
An. psuedopunctipennis
An. punctipennis
An. quadrimaculatus
Cq. perturbans
Cs. inornata
Cx. coronator
Cx. erraticus
Cx. interrogator
Cx. nigripalpus
Cx. quinquefasciatus
Cx. restuans
Cx. salinarius
Cx. tarsalis
Cx. territans
Ma. titillans
Or. signifera
Ps. ciliata
Ps. columbiae
Ps. cyanescens
Ps. ferox
Ps. horrida
Ps. howardii
Ps. longipalpus
Ps. mathesoni
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◀**Fig. 2**. Heatmap illustrating the relative abundance of mosquito species by trap type, month, and year in Harris County, Texas (2018–2022). Relative abundance was calculated as the proportion of each mosquito species captured per month within each trap type in the (**a**) BG trap, (**b**) GV trap, and (**c**) CDC light trap placed in storm sewers. Each tile corresponds to a species, with months on the x-axis and study years on the y-axis. The color gradient indicates relative abundance, categorizing species as eudominant (comprising > 30% of specimens), dominant (> 10–30%), subdominant (> 5–10%), rare (> 1–5%), and subrare (≤ 1%). White indicates that the species was not identified in collections. The color graduation allows for quickly identifying seasonal variations in the relative abundance of mosquito species across different trap types.

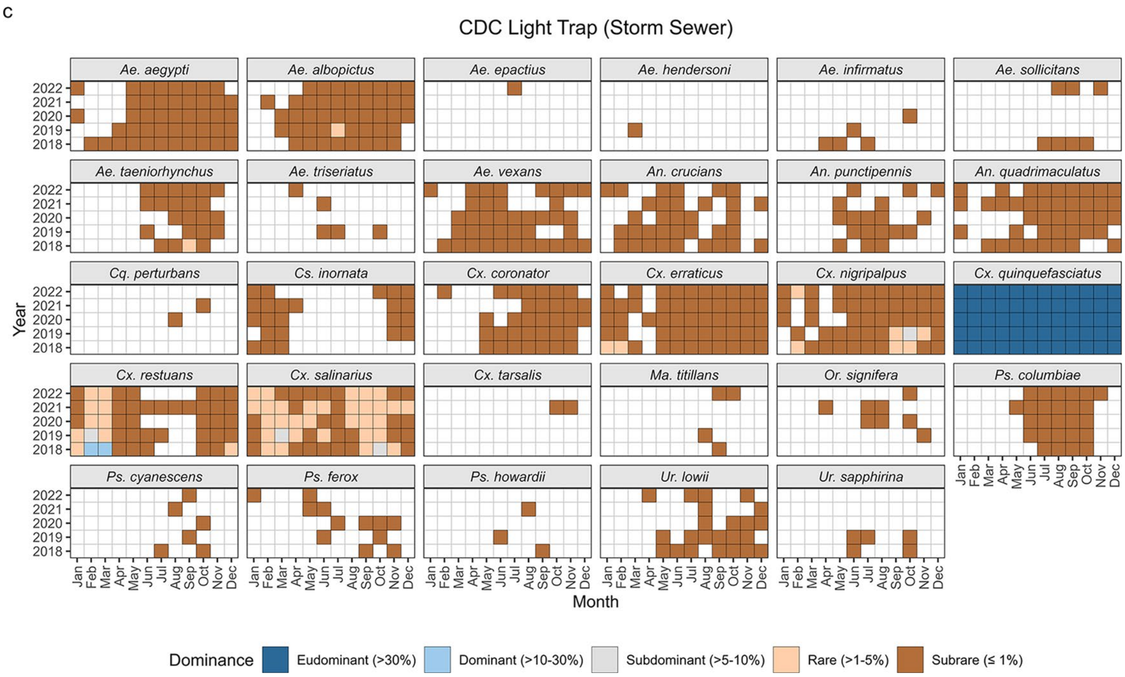


Figure 2. (continued)

Geographical distribution and abundance of species

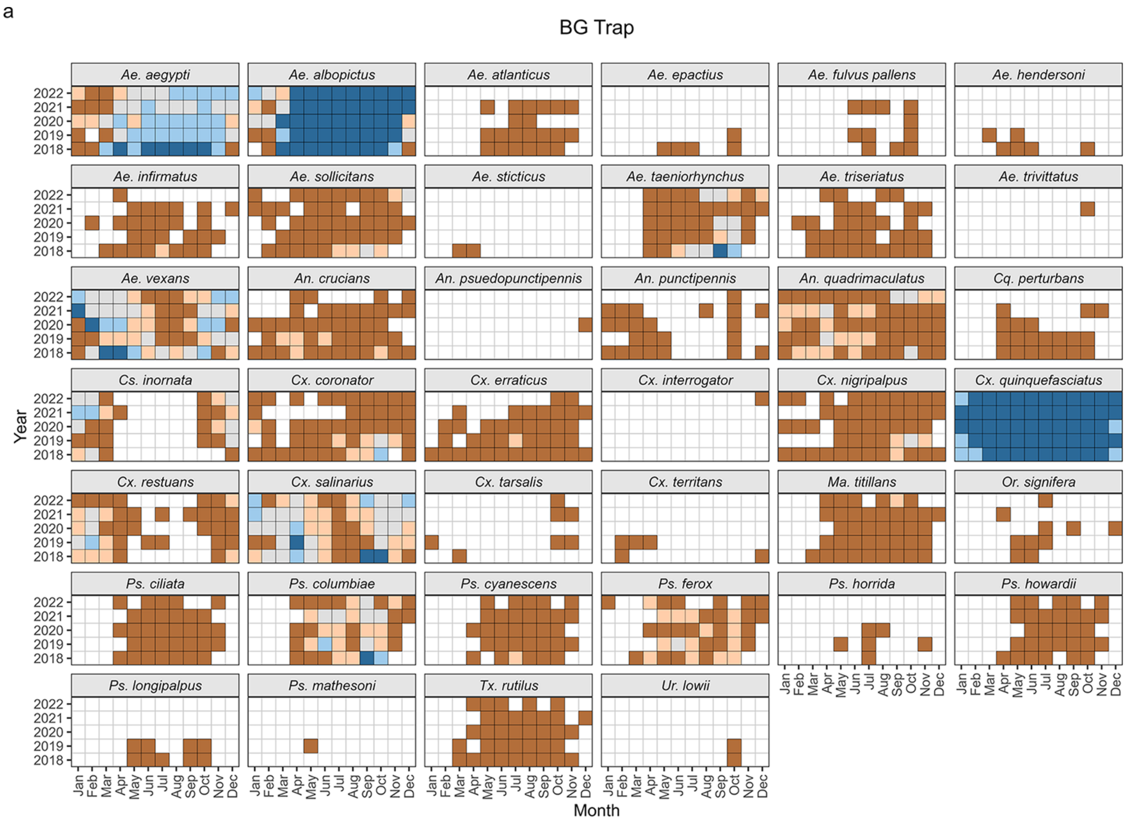
Positive Global Moran's *I* statistics were significant for all five mosquito species, indicating that there is non-random distribution of mosquito abundance (Supplementary Table S3). Ordinary kriging was performed to estimate and visualize the adult female mosquito abundance for the five most abundant species across the study period (2018–2022). The best-fit semivariogram model for each mosquito species was K-Bessel for each instance. We used a smoothed circular neighborhood. The cross-validation and error analysis results are provided in Supplementary Table S3. The cross-validation results indicated that abundance estimates could be refined by including explanatory factors in future models.

Mosquito species exhibited notable variability in their distributions. Figure 4A provides an overview of Harris County with the City of Houston limits shown for reference. *Aedes albopictus* was consistently captured in low numbers across the county, indicating its adaptation to urban and suburban environments in Harris County (Fig. 4B). In contrast, *Ae. aegypti* was more concentrated in the densely urbanized central areas (Fig. 4C). Coastal regions, especially near the Houston Ship Channel, showed higher abundances of *Ae. taeniorhynchus* (Fig. 4D) and *Cx. salinarius* (Fig. 4E). In contrast, *Cx. quinquefasciatus* was widespread but more abundant in developed areas within Houston city limits (Fig. 4F).

Discussion

Based on the data presented in this study, we believe that Harris County is one of the most vulnerable counties in the U.S. for mosquito-borne disease outbreaks, emphasizing the need to understand local mosquito population dynamics for effective vector surveillance and control. Our study identified 43 mosquito species across three trap types, representing a subset of the 56 species previously documented in the county[32]. BG and gravid traps captured more species than CDC light traps, possibly due to the limited diversity of mosquitoes in storm sewers rather than the trap limitations, as these traps use a general CO_2 lure. These findings emphasize the importance of using varied trap types for comprehensive mosquito surveillance[32,33].

Five species—*Cx. quinquefasciatus, Ae. aegypti, Ae. albopictus, Cx. salinarius,* and *Ae. taeniorhynchus*—dominated mosquito populations. Among these, *Cx. quinquefasciatus, Ae. aegypti, and Ae. albopictus* are significant arbovirus vectors, while *Cx. salinarius* has only demonstrated wild infection with various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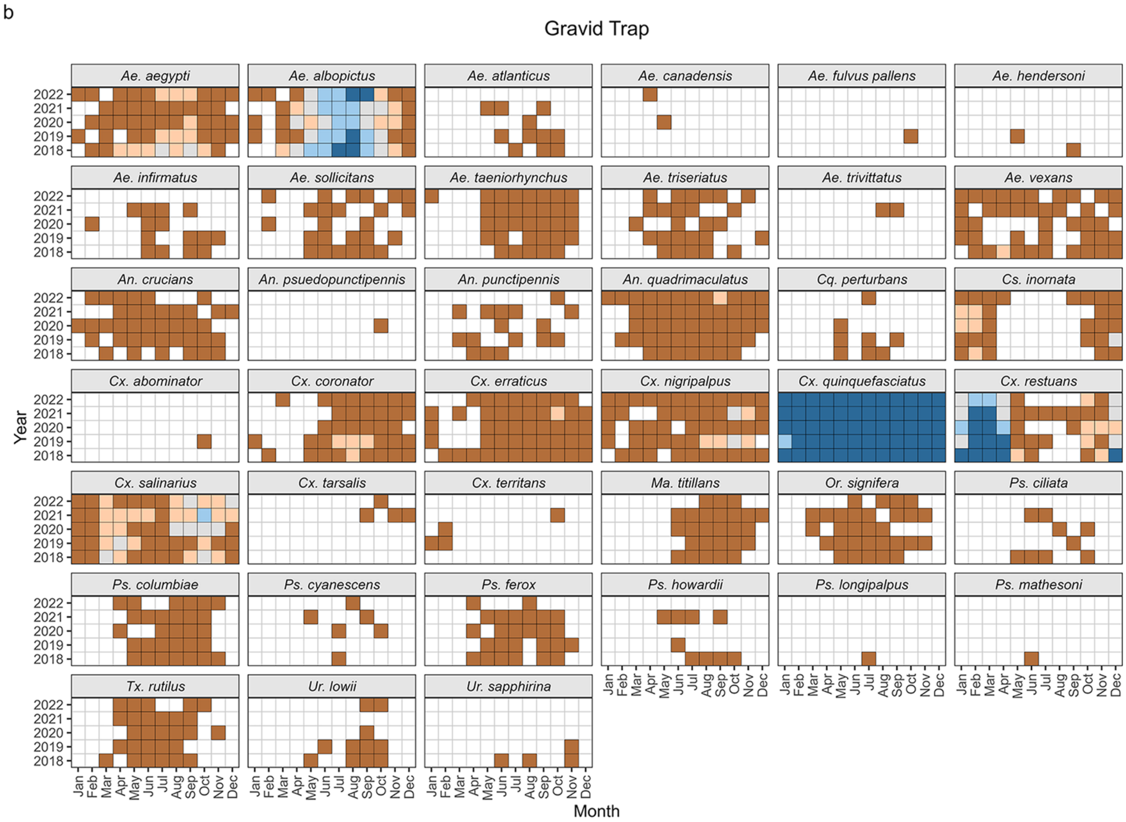
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◀**Fig. 3**. Heatmap illustrating the distribution of mosquito species by trap type, month, and year in Harris County, Texas (2018–2022). Distribution was calculated as the number of trap sites where a mosquito species was captured per month and trap type in the (**a**) BG trap, (**b**) GV trap, and (**c**) CDC light trap placed in storm sewers. Each tile corresponds to a species, with months on the x-axis and study years on the y-axis. The color gradient indicates the distribution of mosquito species, with the darker blue shade indicating a broader distribution. White indicates that the species was not identified in collections. The color graduation allows for quick identification of spatial and temporal variations of mosquito species in different trap types across Harris County.

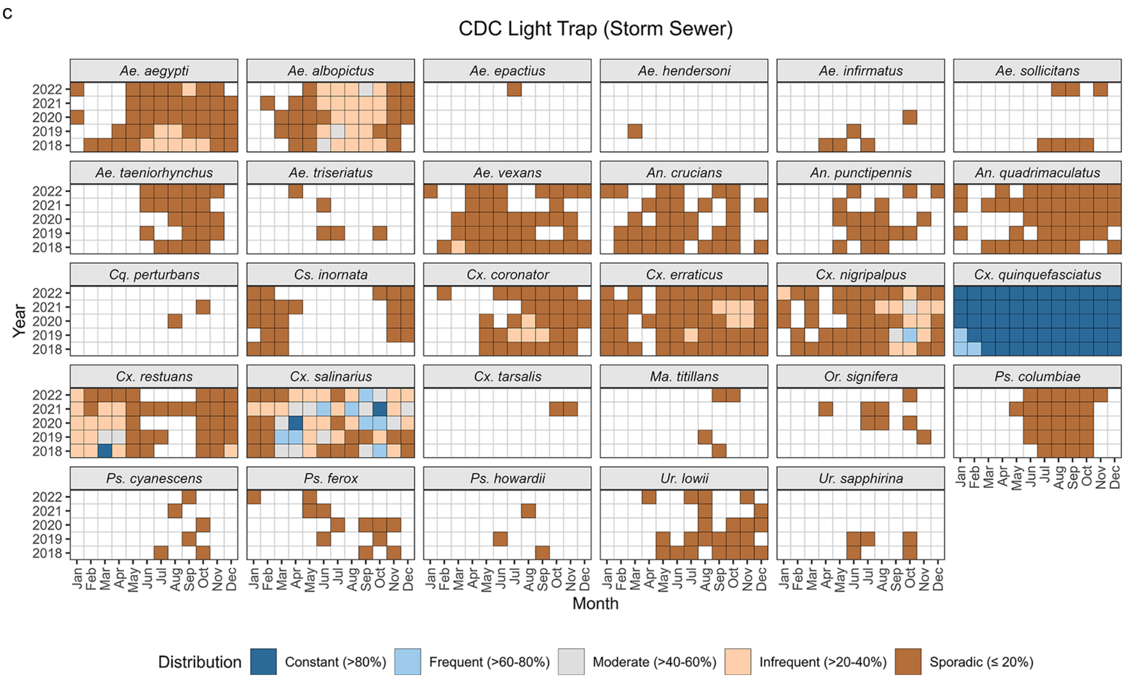

Figure 3. (continued)

pathogens[32–36]. *Culex quinquefasciatus*, the primary vector for West Nile virus and St. Louis Encephalitis virus, was the most abundant species collected in routine surveillance[38–41]. This species was distributed at nearly every trap site, including storm drains, indicating its ability to thrive in diverse environmental conditions in Harris County. Its high abundance throughout the year underscores its adaptability and potential for sustained pathogen transmission. In contrast to a study in Miami-Dade County, another coastal metropolitan area, we found that *Ae. aegypti* varied by urbanization level, with higher concentrations in Harris County's urban center[34]. This underscores the need for targeted vector control in densely populated areas to prevent pathogen transmission[39]. *Ae. albopictus* was consistently observed in over 80% of traps, demonstrating its invasive nature and adaptability to urban and suburban environments. Urbanization has historically led to decreased diversity of mosquito species, favoring *Ae. aegypti* and *Ae. albopictus* that thrive in anthropogenic environments[35–40]. Both species have a marked preference for feeding on humans, making them a critical focus for mosquito control efforts in Harris County[41–43]. As known vectors for pathogens, including dengue, Eastern Equine Encephalitis, yellow fever, and Zika viruses, their concentration in densely populated urban areas of Harris County suggests a higher risk for *Aedes*-borne pathogen outbreaks[45]. These findings align with the perspective of Wilke et al., who highlighted Miami-Dade as a potential gateway for the introduction and spread of arboviruses into the U.S., and we believe that Harris County may serve as a similar gateway[34].

While we identified trends in mosquito abundance and species composition, we did not directly measure disease transmission risk or public health implications. Additionally, historic mosquito surveillance data has inherent limitations regarding trap placement and sampling frequency. For instance, the BG and gravid traps must be placed on residential private property, potentially affecting the representativeness of the data. The study's strengths include comprehensive surveillance data and detailed population assessments. Leveraging data from the Harris County Public Health Mosquito and Vector Control Division, this study used systematic trapping methods across a network of operational areas with various trap types. This systematic trapping enabled the

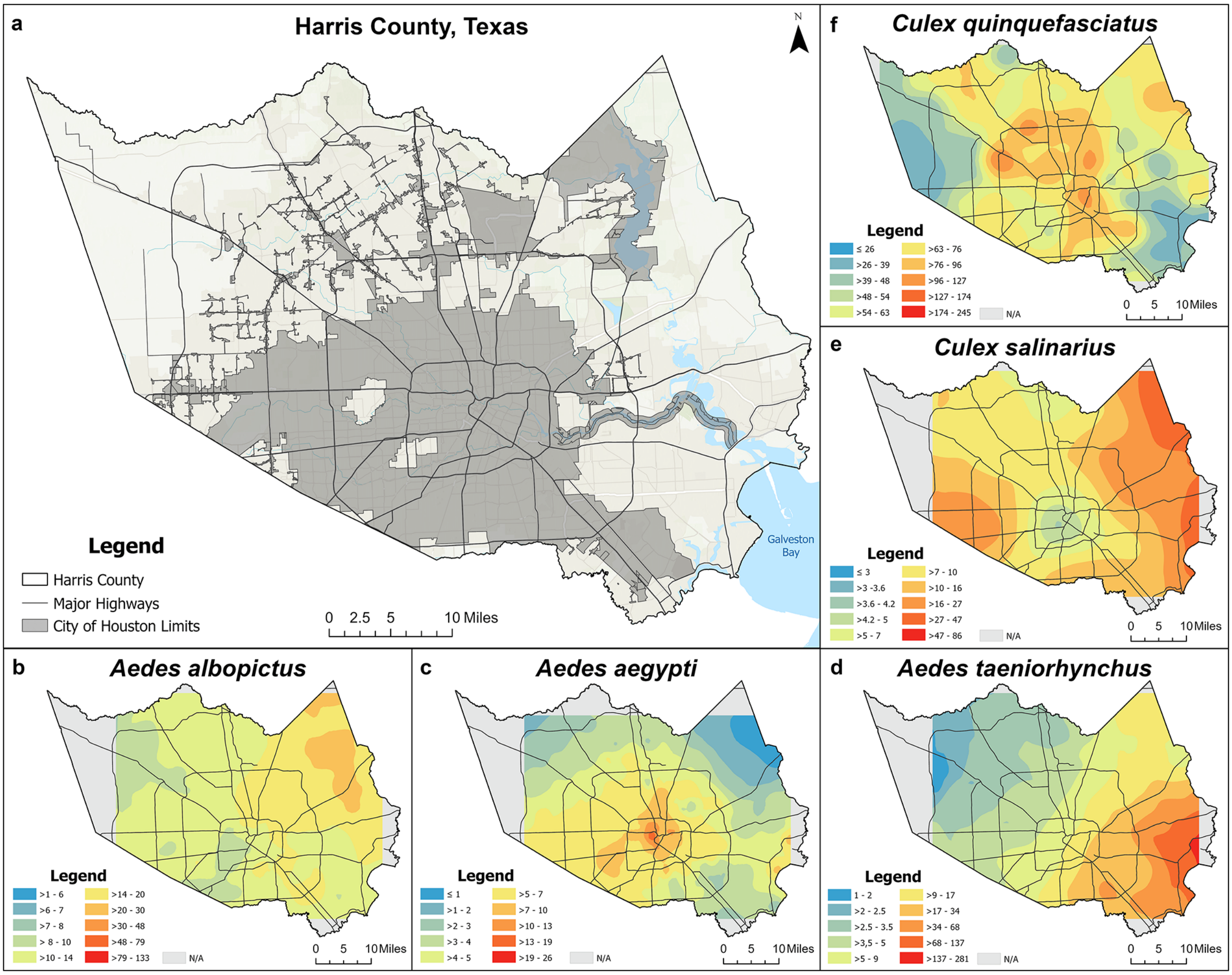

Fig. 4. Geographic distribution of adult female mosquito abundance standardized by trap-nights in Harris County, Texas (2018–2022) for (**b**) *Ae. albopictus,* (**c**) *Aedes aegypti*, (**d**) *Aedes taeniorhynchus,* (**e**) *Cu. salinarius,* and (**f**) *Cx. quinquefasciatus*. Panel (**a**) provides a reference map showing Houston city limits and Galveston Bay. Smoothed abundance surfaces were generated using ordinary kriging, with classification based on ten geometric intervals shown in each legend. The Harris County boundary and major highways are overlayed. Analysis and mapping were conducted using ArcGIS Pro 3.3.0 (Esri, Redlands, CA).

identification of trap-specific variations in mosquito populations and highlighted the importance of considering trap characteristics.

Future research should leverage geospatial analysis to assess microscale variations in mosquito abundance and distribution across Harris County. This approach could pinpoint higher-risk areas and refine our understanding of vector dynamics. Longitudinal studies are also essential to examine longer-term trends, including responses to environmental changes, such as land use and climate shifts. By monitoring mosquito distribution and abundance over time, we can enhance our ability to predict and respond to changes in vector dynamics. Continued surveillance will remain crucial to identify potential transmission and emergence risks, inform targeted interventions, and ultimately reduce the burden of mosquito-borne diseases and protect the health of Harris County, Texas residents.

Data availability

Data analyzed in this study are not publicly available due to privacy reasons and are available from the corresponding author on reasonable request.

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Author contributions

M.J. and S.M.G. conceptualized and developed the methodology of the study. M.V. oversaw the data collection. M.J. analyzed the data, prepared the original figures, and wrote the original draft of the paper. A.N. and A.L.C. assisted with investigation. E.L.B. and S.M.G. were responsible for project administration, resources, and supervision of this study. S.M.G. was responsible for the validation and funding acquisition of the study. All authors contributed to reviewing and editing the manuscript.

Competing interests

The authors declare no competing interests.

Additional information

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