Original Article

MOSQUITO (DIPTERA: CULICIDAE) DISTRIBUTION, DIVERSITY, AND ZIKA VIRUS RNA DETECTION IN MULTIPLE SPECIES IN KOTA KINABALU, SABAH, MALAYSIA

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ABSTRACT

Malaysia, particularly the state of Sabah, has experienced autochthonous transmission of the Zika virus (ZIKV), highlighting an ongoing public health concern. The objective of this study was to determine the distribution and diversity of potential mosquito vectors in Kota Kinabalu, Sabah, and to detect the presence of ZIKV RNA in field-caught specimens. A total of 1,288 mosquito specimens, comprising adult and larval stages, were collected using six sampling methods: handheld mosquito aspirator, human landing catch, Centres for Disease Control and Prevention light trap, sticky ovitrap, larval surveillance, and conventional ovitrap. A total of 14 species belonging to seven genera were identified, among which *Aedes albopictus* was the predominant species (77.02%), followed by *Tripteroides* sp. (10.01%). Zika virus RNA was detected exclusively in adult mosquitoes collected using the sticky ovitrap, with positive detections in *Ae. albopictus*, *Ae. paullusi*, *Niveus* group, *Cx. quinquefasciatus*, *Cx. sitiens*, and *Tripteroides* sp. via real-time reverse transcription polymerase chain reaction. The data obtained in this study provide pivotal information on other mosquito species that may play a significant role in Zika virus transmission.

KEYWORDS: Zika, arbovirus, mosquito surveillance, *Aedes, Culex*

INTRODUCTION

Discovery and global epidemiology

Zika virus (ZIKV) is a mosquito-borne *Flavivirus* that was first isolated in 1947 from the blood of a monkey in the Zika Forest of Uganda, East Africa, followed shortly thereafter by isolation from *Aedes africanus* mosquitoes collected in the same forest (1). The first human case of Zika fever was reported in Nigeria in 1954, and since then, outbreaks have occurred across tropical Africa, Southeast Asia, and the Pacific Islands (2). Before 2007, at least 14 human cases had been documented, though many earlier cases are believed to have been underreported (3). Between 2007 and the 2015–2016 epidemic in the Americas, ZIKV emerged as a global public health threat.

Clinical significance and public health challenges

ZIKV infection is transmitted to humans primarily through the bite of an infected *Aedes* species mosquito resulting in Zika fever, a condition that ranges from asymptomatic infection to a self-limiting febrile illness with low fever, headache, arthralgia, maculopapular rash, and conjunctivitis (4). Importantly, ZIKV poses serious public health challenges due to its association with severe neurological complications, including Guillain-Barré syndrome in adults, and microcephaly in newborns (5,6).

Currently, no vaccines or antiviral drugs are specifically approved for the prevention or treatment of ZIKV infection. Consequently, public health efforts focus on preventive measures: reducing mosquito populations through environmental management and insecticides, minimising mosquito-human contact using repellents, long sleeves, and mosquito nets, and raising community awareness to eliminate standing water breeding sites (7). These challenges are particularly acute in rural areas with limited healthcare infrastructure and poor vector control, where uncovered water containers and natural water bodies facilitate the proliferation of *Aedes aegypti* and *Aedes albopictus* (8).

ZIKV in Malaysia and Sabah: historical and recent evidence

a) Early evidence in Malaysia

In 1969, Marchette et al. (9) reported the first isolation of ZIKV in Malaysia from *Ae. aegypti* mosquitoes collected around shophouses in Bentong, Pahang. During the 1960s, serological evidence of ZIKV infection was also detected among indigenous (aborigine) populations in the country (10). These early findings suggest that ZIKV may have been circulating in Malaysia for decades, possibly involving other mosquito vectors beyond *Ae. aegypti*.

b) Confirmed human cases and recent detections

In 2014, a confirmed case of Zika fever with clinical evidence was reported in a German tourist returning from a visit to Sabah, Malaysian Borneo (11). Subsequently, between September 2016 and November 2019, the Malaysian Ministry of Health confirmed nine locally acquired ZIKV cases. Among these, research by Dony et al. (12) identified two autochthonous (locally transmitted) cases in Kota Kinabalu, Sabah. Notably, that study detected no ZIKV in *Ae. albopictus* or *Culex* species collected around the residences of those cases.

Gap in knowledge: unknown vector status of other mosquito species

Although laboratory infection studies have established the vector competence of several mosquito species for ZIKV, including *Culex quinquefasciatus, Ae. albopictus,* and *Ae. hensilli* (13-15), and field studies have detected ZIKV RNA in wild-caught mosquitoes (16-18), little is known about the vector capacity of other mosquito species under natural conditions in Malaysia. Furthermore, the competence of local *Ae. aegypti* for ZIKV transmission has been confirmed under laboratory conditions (19), but evidence regarding other potential vectors remains limited.

Given that ecological factors, such as changes in geographic range, population density, climate shifts, and land use can alter vector behaviour and distribution over time (20), it is critical to re-examine the potential vector landscape in regions with recent human cases. Screening for ZIKV in field-caught mosquitoes is pivotal for outbreak preparedness and control, as virus infection rates in mosquitoes help predict human transmission activity levels (21).

Rationale and objectives of the current study

Following the report of two confirmed human ZIKV cases in Kota Kinabalu, Sabah, ZIKV vector surveillance was conducted in the vicinity of these confirmed cases. Because different mosquito sampling methods yield considerable disparities in capture efficiency (22,23), our study employed a comprehensive range of catching techniques to ensure thorough monitoring. Given that the maximum mosquito flight range is approximately 200 m (22), this study also aimed to document the distribution of mosquito species across the respective study sites. The primary aim was to identify any potential ZIKV vectors other than *Ae. aegypti* in Kota Kinabalu, Sabah. Additionally, the data acquired from this study can inform targeted control measures, particularly during future Zika outbreaks in Malaysia.

MATERIALS AND METHODS

Study area and study period

The study was conducted in the Kota Kinabalu district, Sabah, Malaysian Borneo. Two sites were selected based on confirmed cases of Zika infection reported in Likas (N 5°58'52.1148", E 116°6'19.508"), and Luyang (N 5°58'14.196", E 116°5'30.3504") (Figure 1). Both Likas and Luyang were approximately 4 km from Kota Kinabalu's city centre, and 2 km apart. Likas was categorised as a residential area in the city's suburbs, consisting of low-cost high-rise buildings, whereas Luyang was identified as a housing area comprising terrace and semi-detached houses. Following the reported human Zika cases in September and November 2016, mosquito surveillance was conducted in November of the same year.

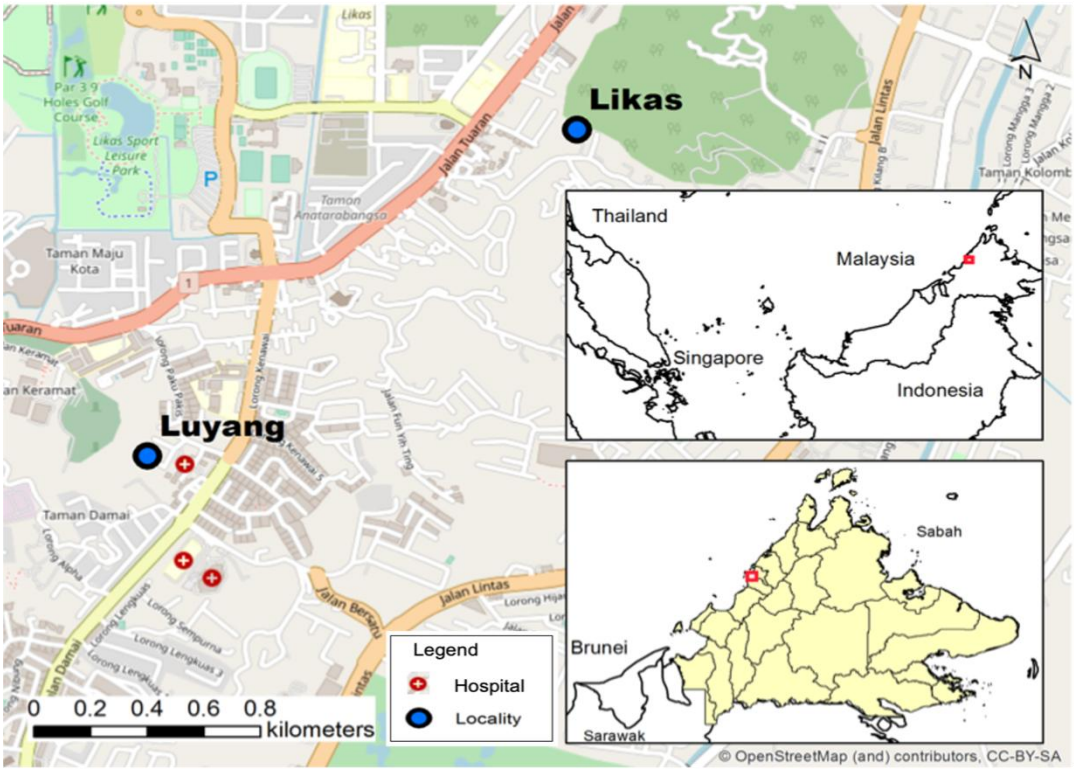


Figure 1. Study localities: Luyang and Likas, Kota Kinabalu, Sabah

a) Mosquito sampling methods

Six mosquito collection methods were used during the study: conventional ovitrap, sticky ovitrap, Centres for Disease Control and Prevention (CDC) light trap, human landing catch (HLC), handheld mosquito aspirator, and larval surveillance.

- Conventional ovitrap & sticky ovitrap: Conventional ovitrap is a black plastic container with a capacity of 300 mL, measuring approximately 8.0 cm in diameter at the opening, and 9.0 cm in height. It contained water to a depth of 5.5 cm, with a wooden paddle measuring 10 cm × 2.5 cm × 0.3 cm, used as an oviposition substrate for female mosquitoes. For the modified sticky ovitrap, the study followed the method described by Ali et al. (13). A total of 100 modified sticky ovitraps and 30 conventional ovitraps were placed in households, indoors and

outdoors, within a 200-meter radius of each case house, respectively. In this study, "indoor" refers to any parts of the premises that are directly under the roof, meanwhile "outdoor" refers to the areas beyond the roofed structure but within the immediate vicinity of the premises. Both types of ovitraps were deployed in the field for 4–5 days before being collected and returned to the laboratory for specimen processing.

- CDC light trap: A total of eight CDC light traps (CDC-LT) were placed near the infected case house and operated for 14 hours, which included the peak biting hours of *Culex* sp. from 5:00 p.m. to 7:00 a.m. The peak biting hours of *Culex* sp. (dusk to dawn, 6:00 p.m. to 6:00 a.m.) were chosen as a reference because *Culex quinquefasciatus* is predominantly nocturnal and highly abundant in urban environments like Kota Kinabalu. Furthermore, this time period captures the crepuscular activity of *Aedes* species, maximising the probability of capturing diverse mosquito fauna with different activity patterns. The traps were placed in dark areas to avoid any preference by mosquitoes for other sources of light.
- Human landing catch: The human landing catch (HLC) technique was performed by catchers who sat on low chairs with a flashlight and trapped adult mosquitoes that were resting on the leg using a collection glass tube. The activity was conducted during the peak biting hours of mosquitoes, especially for *Aedes* spp., from 6:00 a.m. to 8:00 a.m., and 6:00 p.m. until 8:00 p.m. The activity was performed by 6–7 catchers during each session, and informed consent was obtained from all participants prior to their involvement.
- Handheld aspirators: Adult mosquito collection was also conducted by handheld aspirators at the study sites. The collectors inspected potential resting sites, such as bushes, trees, potted plants, walls, and captured resting mosquitoes using an electrically operated aspirator. Specimens were transferred into clean paper cups and transported to the laboratory for subsequent processing.
- Larval surveillance: Larval collection was carried out within a 200-metre radius of the case house. All potential indoor and outdoor mosquito breeding sites were inspected. Larvae and pupae were collected using pipettes and placed in separate labelled containers. Important information, such as the type of habitat (natural or artificial), the number of samples, and stages of the life cycle, was recorded on prescribed forms.

b) Specimen identification and transportation

Adult mosquitoes collected were identified morphologically in the field using standard taxonomic keys (24). This on-site identification process ensured accurate and timely classification of the specimens. The mosquitoes were then sorted and pooled into groups by species, sex, location, and collection method, with approximately 25 mosquitoes per pool. Caught adult mosquitoes were anaesthetised on dry ice for sorting and pooling. All specimens were kept in cold boxes at the sites and during transport before PCR-based virus detection. All immature stages of conventional ovitrap and larval surveillance specimens were transferred to the laboratory for additional processing. The remaining ovitrap water was transferred to a clean container and monitored daily for 6–7 days for larval emergence. Larvae were reared to the third instar for identification.

c) Zika virus detection in mosquito pool

Pooled mosquitoes or larvae (a maximum of 25 per pool) were homogenised with 300 µL of Minimum Essential Media Eagle (MEM) solution using a sterile pestle on ice. A total of 200 µL homogenate was used for RNA extraction using QIAamp RNA Viral Kit (Qiagen, Heiden, Germany), following the manufacturer's protocol. The final RNA pellet was dissolved in 60 µL of the provided Buffer AVE and stored at -80 °C before virus screening. ZIKV RNA detection was performed using a real-time reverse

transcription PCR (RT-PCR) assay. RNA was amplified using iTaq™ Universal Probes One-Step Kit and BioRad CFX96 Touch Real Time PCR in a 20 µL reaction volume containing 5 µL of extracted RNA, 0.5 µL iScript advanced reverse transcriptase, 10 µM of each primer, 25 µM of fluorogenic probe, and addition of nuclease-free water. Zika virus (ATCC® VR-84™) was utilised as a positive control, while nuclease-free water was employed as a negative control. The primers and probe were followed as described by Lanciotti et al. (2).

d) Data analysis

The data were analysed using descriptive statistics, and the Mann-Whitney U test was used to compare the number of mosquitoes collected between the two locations. The minimum infection rates (MIRs) were calculated by dividing the number of positive pools by the total number of mosquitoes tested and then multiplying by 1,000. The locations of the ZIKV-positive mosquito samples were plotted using spatial mapping data and coordinates from the Department of Survey and Mapping Malaysia (JUPEM).

e) Ethical approval

This study was funded by the Ministry of Health (MOH) Malaysia, and the collection of mosquito samples was approved by the Medical Research and Ethics Committee (MREC), Ministry of Health (MOH) Malaysia, with ethical clearance number NMRR-17-44-33896.

RESULTS

Mosquitoes collection

A total of 1,288 mosquitoes, comprising 14 species from seven genera, were collected from both study localities (Table 1). The most commonly captured species was *Aedes albopictus* (*n* = 992, 77.02%), which comprised 289 adults (22.44%) and 703 larvae (54.58%). *Ae. albopictus* was collected at both life stages from both localities using all sampling methods employed in this study. Mann-Whitney U test revealed no significant difference ($p>0.05$) in the number of mosquitoes of all species collected between Likas and Luyang. Regarding the sampling method, the HLC technique captured the highest number of species (10 species), followed by the sticky ovitrap (8 species).

Table 1: Composition of mosquitoes collected and collection methods

Species	Location	Total Collected (%)	Aspirator	HLC	CDC-LT	Sticky Ovitrap	Conventional Ovitrap	Larval Survey
Aedes albopictus	Likas	199 (71.84%)	8	1	1	16	54	119
	Luyang	793 (78.44%)	16	17	1	53	147	559
Aedes butleri	Likas	3 (1.08%)	0	1	0	2	0	0
	Luyang	6 (0.59%)	0	3	0	3	0	0
Aedes paullusi	Likas	24 (8.66%)	4	0	0	20	0	0
	Luyang	11 (1.09%)	3	0	0	8	0	0
Aedes sp.	Likas	5 (1.81%)	0	0	0	0	0	5
	Luyang	0	0	0	0	0	0	0
Aedes vexans	Likas	1 (0.36%)	1	0	0	0	0	0
	Luyang	2 (0.20%)	1	1	0	0	0	0
Anopheles pujutensis	Likas	0	0	0	0	0	0	0
	Luyang	1 (0.10%)	0	1	0	0	0	0
Armigeres subalbatus	Likas	0	0	0	0	0	0	0
	Luyang	3 (0.30%)	0	3	0	0	0	0
Coquillettidia crassipes	Likas	2 (0.72%)	0	1	0	1	0	0
	Luyang	16 (1.58%)	0	13	0	3	0	0
Culex alienus	Likas	0	0	0	0	0	0	0
	Luyang	1 (0.10%)	0	1	0	0	0	0
Culex quinquefasciatus	Likas	19 (6.86%)	0	6	0	9	0	4
	Luyang	45 (4.45%)	0	13	0	29	0	3
Culex sitiens	Likas	1 (0.36%)	0	0	0	1	0	0
	Luyang	17 (1.68%)	0	1	0	16	0	0
Culex sp.	Likas	1 (0.36%)	0	0	0	1	0	0
	Luyang	1 (0.10%)	0	0	0	1	0	0
Culex tritaeniorhynchus	Likas	0	0	0	0	0	0	0
	Luyang	4 (0.40%)	3	0	1	0	0	0

Niveus group	Likas	1 (0.36%)	0	0	0	1	0	0
	Luyang	0	0	0	0	0	0	0
Toxorhynchites sp.	Likas	2 (0.72%)	0	0	0	0	2	0
	Luyang	0	0	0	0	0	0	0
Tripteroides sp.	Likas	19 (6.86%)	0	0	0	0	19	0
	Luyang	110 (10.88%)	0	3	0	4	103	0
Unknown	Likas	0	0	0	0	0	0	0
	Luyang	1 (0.10%)	0	0	0	1	0	0
TOTAL		1,288 (100%)	36	65	3	169	325	690

Taxonomic notes: group = mosquitoes identified to group level; sp. = unidentified species due to missing morphological features; unknown = identification to genus level not possible due to specimen damage. Abbreviations: HLC = human landing catch; CDC-LT = Centres for Disease Control light trap.

Detection of Zika virus RNA in mosquitoes

We tested 250 mosquito pools, comprising a total of 1,288 specimens, for the presence of ZIKV RNA. Of these, 108 were from Likas and 142 from Luyang, with 194 pools comprising adults and 56 comprising larvae.

The findings indicated that ZIKV RNA was identified in six mosquito species, namely *Ae. albopictus*, *Ae. paullusi*, *Niveus* group, *Cx. quinquefasciatus*, *Cx. sitiens,* and *Tripteroides* sp. ZIKV RNA was present in *Ae. albopictus*, *Ae. paullusi*, and *Cx. quinquefasciatus* specimens collected from both study regions. Conversely, ZIKV RNA was detected in the *Niveus* group and *Cx. sitiens* mosquitoes collected in Likas but not in Luyang. Additionally, *Tripteroides* sp. tested positive for ZIKV RNA in Luyang but not in Likas. Furthermore, the study revealed that ZIKV-infected mosquito samples were obtained exclusively using sticky ovitraps. It is also noteworthy that ZIKV RNA detection was limited to adult mosquito specimens.

The MIRs of ZIKV were calculated for mosquito pooled samples by location and species (Table 2). The highest MIRs were observed in the *Niveus* group and *Cx. sitiens* from Likas, and *Tripteroides* sp. from Luyang. However, due to small sample sizes, differences in infection rates could not be reliably assessed, and these estimates should be interpreted with caution.

Figure 2 depicts the distribution of the presence of ZIKV RNA in different mosquito species from both locations. The maps showed that specimens of *Ae. albopictus* that tested positive for ZIKV RNA were widely spread across the research areas.

Table 2. Zika virus RNA detection was used to calculate minimum infection rate (MIR) estimates by location and species.

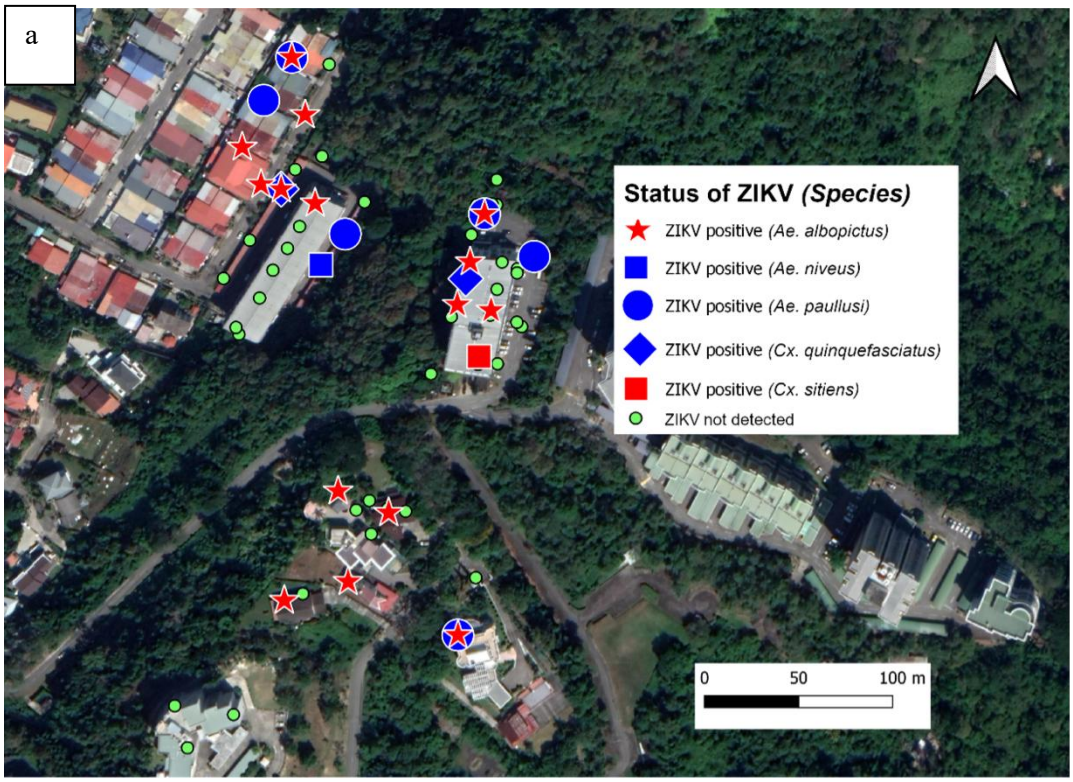
Study areas	Species	No. of individuals tested[#]	No. of pools tested	No. of positive pools	MIR[*]
Likas	*Aedes albopictus*	54	24	1	19
	Niveus group	1	1	1	1000[†]
	Aedes paullusi	20	17	1	50
	Culex quinquefasciatus	9	9	1	111
	Culex sitiens	1	1	1	1000[†]
Luyang	*Aedes albopictus*	58	56	4	69
	Aedes paullusi	20	2	1	50
	Culex quinquefasciatus	29	19	2	69
	Tripteroides sp.	4	3	2	500[‡]

#Number of individuals tested refers to the total number of mosquitoes of a specific species tested.

*MIR = minimum infection rate per 1,000 mosquitoes, calculated as (no. of positive pools/no. of individuals tested) × 1,000, rounded to the nearest whole number.

†An MIR of 1,000 indicates that all mosquitoes tested were positive. This estimate is based on a single specimen and should be interpreted with extreme caution due to the very small sample size.

‡The MIR of 500 is based on only four specimens (two positive pools). This estimate is unstable, given the small sample size, and should be interpreted with caution.



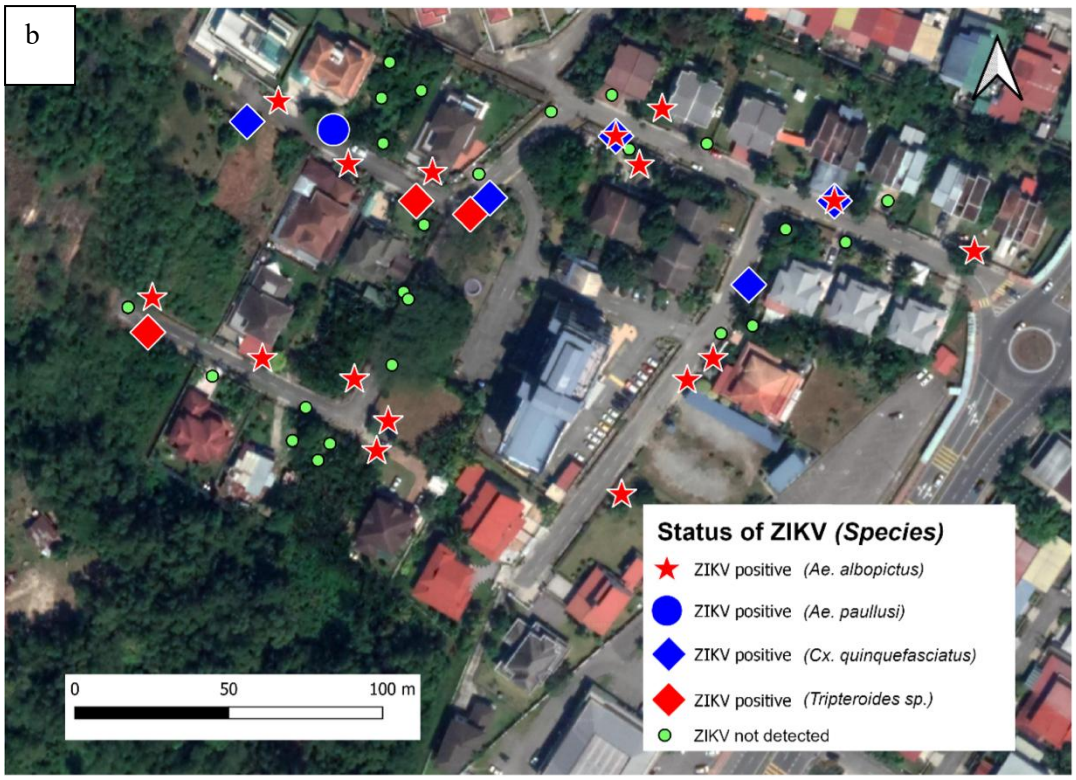


Figure 2: Location of (a) Likas, and (b) Luyang indicating ZIKV RNA detected from mosquito samples

DISCUSSION

The foundational data on mosquito diversity and ZIKV RNA prevalence captured during the documented local outbreak in this study remain highly relevant for current arbovirus monitoring. As the Zika virus continues to pose a risk of re-emergence in Southeast Asia, these findings offer a critical baseline for predicting and managing future outbreaks.

This investigation aimed to identify potential ZIKV vectors other than *Ae. aegypti*. Although studies by Ali et al. (16) and Johari et al. (17) identified additional potential vector species beyond *Ae. aegypti*, further investigation is warranted due to differences in geography and study scopes. Johari's study focused on sites in Peninsular Malaysia and screened only two mosquito species, examining only the immature stages (larvae). In contrast, both Ali's and this study targeted areas with documented human infections in Sabah, allowing the exploration of vector populations in regions directly impacted by ZIKV transmission. Furthermore, our study screened a wider range of potential vector species and included both adult and immature stages, providing a more comprehensive picture of the vector landscape.

Although *Ae. aegypti* has been recognised as a key vector in ZIKV transmission, our findings revealed that *Ae. aegypti* was absent from all catching techniques and traps used in both localities. Even though the ovitrap was touted as the best method for collecting *Aedes* spp. (25), no *Ae. aegypti* was found in traps placed both indoors and outdoors. Furthermore, a previous study showed that *Ae. aegypti* is distributed in the same geographical area as *Ae. albopictus* (26). The absence of *Ae. aegypti* in this study's collections may be due to trapping methodology and environmental factors, both of which can influence capture rates. *Ae. aegypti* is highly anthropophilic and tends to rest within or near human structures, making it more challenging to capture using standard traps. Staunton et al. (27) reported

that trap deployment position and surrounding landscapes can affect catch rates, a finding with important implications for mosquito surveillance efforts.

In contrast to the absence of *Ae. aegypti*, *Ae. albopictus* was collected at both sites where human ZIKV cases were confirmed. A previous study in Kota Kinabalu, Sabah, reported autochthonous Zika infections in humans and subsequent mosquito surveillance identified *Ae. albopictus* as the most prevalent *Aedes* species in the area (12). The current investigation similarly found *Ae. albopictus* to be the most frequently collected mosquito at both study sites, consistent with the entomological data from Murphy et al. (26), which demonstrated *Ae. albopictus* outnumbering *Ae. aegypti* in Sabah. *Ae. albopictus* is often considered as an invasive species widely distributed across tropical and temperate regions. Furthermore, it is opportunistic in its feeding behaviour, readily biting both animals and humans (28). ZIKV RNA was detected in *Ae. albopictus* in this study, aligning with this study's prior finding of ZIKV-positive *Ae. albopictus* in Miri, Sarawak (16). Although virus viability was not assessed in both studies, local *Ae. albopictus* should be considered susceptible, as laboratory studies have demonstrated its capacity to transmit ZIKV (14, 29). Taken together, the abundance of *Ae. albopictus*, the detection of ZIKV RNA, and its demonstrated vector competence in laboratory studies suggest that this species could be a key vector for ZIKV transmission in Kota Kinabalu.

ZIKV RNA was also detected in several other mosquito species from Kota Kinabalu. These findings suggest that, in addition to *Ae. albopictus*, other mosquito species including *Ae. paullusi*, *Cx. quinquefasciatus*, and *Tripteroides* sp. may play a role in ZIKV transmission. This discovery is consistent with previous studies that have detected ZIKV in various field-caught mosquito species, including *Cx. quinquefasciatus* and *Ar. subalbatus* (30-32).

However, the detection of ZIKV RNA does not indicate the presence of infectious Zika virus; it merely indicates the presence of the viral genome. This genome detection could result from incidental blood feeding on a viraemic host, for example, a *Cx. quinquefasciatus* adult feeding on a Zika patient or infected animal. During and after blood digestion, remnants of the viral genome may persist in the mosquito and be detected via PCR. Therefore, the detection of ZIKV RNA in adult *Cx. quinquefasciatus* alone does not constitute evidence of vector competence. Although this study evaluated only a small number of *Cx. quinquefasciatus* individuals, multiple studies suggest that *Culex* mosquitoes may play a secondary role in ZIKV spread (33-35). Nevertheless, further research including laboratory-based vector competence assays and larger-scale field surveillance is needed to conclusively determine whether *Culex* species serve as ZIKV vectors, as their status remains unknown.

The disproportionately high MIRs observed in the *Niveus* group and *Cx. sitiens* from Likas, and *Tripteroides* sp. from Luyang, are likely overestimated due to the very small sample sizes. Therefore, comparisons of infection rates between species would be more reliable with larger and more balanced sample sizes. It is also worth noting that ZIKV RNA was detected only in adult mosquitoes collected with sticky ovitraps. This may be explained by the behaviour of female mosquitoes seeking resting or oviposition sites on the water surface after taking an infectious blood meal, making them more likely to be captured by this trap type. ZIKV RNA was not detected in any of the larval specimens, suggesting that vertical transmission, if present, was below the detection levels in this study.

A limitation of this study is its exclusive reliance on the MIR to calculate ZIKV prevalence. The MIR estimates are based on the assumption of only one infected mosquito per positive pool, which is often invalid when infection rates are high and pool sizes vary. Both conditions apply to this investigation: surveillance was carried out during an active ZIKV outbreak in Kota Kinabalu, and pool sizes ranged

from 1 to 25 mosquitoes per pool. Under such circumstances, the MIR can significantly underestimate the actual infection rates (36). Consequently, the MIR values presented herein should be regarded as conservative lower bounds, with the true ZIKV infection rates in the local mosquito populations likely being higher. Future surveillance initiatives should preserve raw pool-level data to facilitate maximum likelihood estimation with confidence intervals.

CONCLUSION

In conclusion, this study confirms the presence of ZIKV RNA in multiple field-caught mosquito species in Kota Kinabalu, Sabah, including *Ae. albopictus*, *Ae. paullusi*, *Cx. quinquefasciatus*, *Cx. sitiens*, the *Niveus* group, and *Tripteroides* sp. The abundance of *Ae. albopictus* in the study areas, combined with the detection of ZIKV RNA in this species, highlights its likely role as a primary vector in the region. Furthermore, its exophagic and endophilic behaviour facilitates virus transmission to both outdoor and indoor human populations, making it a challenging species to control. The spatial distribution of ZIKV-infected *Ae. albopictus* documented here provides a foundation for mitigating future outbreaks, while ZIKV RNA detections in other species underscore the need for further vector competence studies. Collectively, these findings offer critical baseline data for outbreak preparedness and emphasise the importance of targeted, integrated vector management strategies including source reduction, targeted larviciding, and community-based education, to control potential future Zika virus transmission in Malaysia.

Supplementary Materials: Not applicable.

Data Availability: The data that support the findings of this study are available from the corresponding author upon reasonable request.

Author Contributions: A.R., N.W.A., L.H.L. (Study conceptualisation; study design), A.R., A.R.A., A.S.M.F., N.M.T., A.H.A., M.K.A. (Data acquisition); A.R. (Formal analysis; interpretation of results; preparation of the original manuscript draft); A.R.A., A.S.M.F., N.M.T., A.H.A., M.K.A. (Performed the investigation), C.Y.L., O.T. (Data curation and visualisation); A.R., R.R., W.K.L. (Proofreading; manuscript correction), N.W.A., O.T. (Resources). All authors have read and agreed to the published version of the manuscript.

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Institutional Review Board Statement: This study was registered under the National Medical Research Registry (NMRR-17-44-3389) and received approval from the Medical Research and Ethics Committee (MREC), Ministry of Health (MOH), Malaysia, under ethical clearance number NMRR-17-44-3389.

Informed Consent Statement: Written informed consent was obtained from all personnel who participated in the human landing catch activity.

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CITATION

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