

Ecological Dominance, Biting Behavior, and Molecular Detection of *Brugia malayi* in *Culex quinquefasciatus* from Filariasis Endemic Wetlands of South Sumatra, Indonesia

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Abstract

Lymphatic filariasis (LF) remains endemic in Indonesian wetland ecosystems despite long-term mass drug administration (MDA). Environmental modification may alter mosquito community structure and promote the emergence of alternative vector species. A longitudinal entomological survey was conducted in two endemic villages in Banyuasin Regency, South Sumatra. Adult mosquitoes were collected using indoor and outdoor human landing collections and resting collections. Ecological indices, including abundance, dominance, man-hour density (MHD), and man-biting rate (MBR), were calculated. Molecular detection of *Brugia malayi* was performed using PCR targeting the yACA gene, followed by sequencing confirmation. A total of 1,342 female *Culex* mosquitoes representing eight species were collected. *Culex quinquefasciatus* was overwhelmingly dominant (92.4%), particularly in Muara Sugih Village, and exhibited marked endophagic and endophilic behavior. Biting density and MBR were substantially higher in Muara Sugih than in Sedang Village. PCR and sequencing confirmed the presence of *B. malayi* DNA in *Cx. quinquefasciatus*. The ecological dominance, indoor feeding behavior, and molecular evidence of *B. malayi* infection in *Cx. quinquefasciatus* suggest its potential role as a supplementary vector in modified wetland ecosystems. Integration of ecological surveillance and molecular xenomonitoring is essential to detect residual transmission and support LF elimination in post-MDA settings.

Keywords: *lymphatic filariasis; Culex quinquefasciatus; vector ecology; biting behavior; molecular xenomonitoring*

1. INTRODUCTION

Lymphatic filariasis (LF) is a mosquito-borne neglected tropical disease caused by filarial nematodes, primarily *Wuchereria bancrofti*, *Brugia malayi*, and *Brugia timori*, leading to chronic lymphatic dysfunction, lymphedema,

elephantiasis, and hydrocele. These clinical manifestations result in long-term disability, social stigma, and economic burden, particularly among rural and peri-urban populations in endemic countries.¹ Consequently, LF remains a major public

health concern and a disease closely linked to poverty and environmental vulnerability.

Since the implementation of the Global Programme to Eliminate Lymphatic Filariasis (GPELF), annual mass drug administration (MDA) has substantially reduced microfilaremia prevalence and transmission in many endemic areas. However, complete interruption of transmission remains challenging in ecologically favorable settings such as wetlands, floodplains, and irrigated agricultural landscapes, where mosquito breeding and survival are sustained throughout the year.² In these environments, residual transmission may persist despite repeated MDA cycles, necessitating enhanced vector surveillance.

Indonesia remains endemic for all three filarial species, with *Brugia malayi* contributing substantially to LF burden in swampy and agricultural regions. Historically, transmission of *Brugia malayi* has been strongly associated with *Mansonia* mosquitoes, whose larvae attach to aquatic plants for respiration, making vegetated wetlands optimal habitats for their development.^{4,5} Consequently, vector surveillance and control programs have traditionally focused on *Mansonia spp.* as the principal targets of brugian filariasis transmission.

However, rapid land-use change, expansion of irrigation networks, drainage modification, and accumulation of peri-domestic wastewater have transformed many natural wetlands into anthropogenically modified ecosystems. These environmental changes tend to favor ecologically tolerant species such as *Culex quinquefasciatus*, which breeds in organically polluted water and frequently exhibits indoor feeding and resting behavior.⁷ Such ecological shifts may alter

traditional transmission dynamics by increasing the relative importance of non-classical vectors in maintaining residual transmission.

Recent molecular xenomonitoring studies have demonstrated that filarial DNA can be detected in multiple mosquito species within the same ecological setting, indicating that LF transmission systems may involve more than one vector species, particularly in post-MDA contexts where parasite prevalence in humans is low^{3,8,9}. This multi-vector potential highlights the need for integrated ecological and molecular approaches to accurately assess ongoing transmission risk.

Banyuasin Regency, South Sumatra, represents a wetland–agricultural mosaic characterized by tidal swamps, irrigated rice fields, drainage canals, rivers, and plantation areas. Despite repeated MDA rounds, sporadic clinical cases and positive entomological findings have been reported, suggesting that LF transmission may not have been fully interrupted. However, comprehensive studies integrating mosquito ecology, biting behavior, and molecular detection of filarial infection in this area remain limited.

Therefore, this study aimed to analyze mosquito species composition, ecological dominance, biting and resting behavior, and molecular evidence of *Brugia malayi* infection in *Culex mosquitoes* from two filariasis-endemic villages in Banyuasin Regency. By integrating classical entomological indices with PCR and sequencing, this study evaluates the potential role of *Culex quinquefasciatus* as a supplementary vector in modified wetland ecosystems and provides evidence to refine vector surveillance strategies in post-MDA elimination settings.

2. METHODS

Study Area

A longitudinal entomological survey was conducted from April to May 2018 in two lymphatic filariasis–endemic villages in Banyuasin Regency, South Sumatra, Indonesia: Sedang Village (Suak Tapeh Sub-district) and Muara Sugih Village (Tanjung Lago Sub-district). Both villages are located in lowland wetland ecosystems characterized by tidal swamps, irrigated rice fields, drainage canals, rivers, and surrounding plantation areas. These environments provide heterogeneous aquatic habitats suitable for mosquito breeding throughout the year.

Mosquito Collection

Adult mosquitoes were collected monthly using standardized indoor and outdoor human landing collections (HLC) and resting collections. HLC was performed continuously for 24 hours (18:00–18:00) by trained collectors using exposed lower limbs. Indoor and outdoor collections were conducted simultaneously, and collectors rotated hourly to minimize individual bias. Resting mosquitoes were captured using manual aspirators inside houses and in peri-domestic structures. All collectors followed safety protocols and provided informed consent.

Mosquito Identification and Ecological Indices

Female mosquitoes were morphologically identified to species level using regional taxonomic keys based on proboscis characteristics, wing venation, leg banding, and abdominal scaling. Ecological parameters assessed included abundance, frequency, dominance index, man-hour density (MHD), and man-biting

rate (MBR). Species diversity was calculated using the Shannon–Wiener diversity index (H'). These indices were used to describe mosquito community structure and evaluate potential transmission risk. Such parameters are formulated as follow:

$$H' = -\sum(p_i \ln p_i) \text{ where } p_i = n_i/N$$

$$MBR = \frac{\sum \text{mosquitoes biting per species}}{\sum \text{collectors} \times \text{collection hours}}$$

$$MHD = \frac{\sum \text{mosquitoes captured per species}}{\sum \text{collectors} \times \text{collection hours} \times \text{number of collection days}}$$

$$\text{Abundance} = \frac{\sum \text{mosquitoes captured per species by certain methods}}{\sum \text{all mosquitoes caught with certain methods}} \times 100\%$$

$$\text{Frequency} = \frac{\sum \text{arrested containing certain species}}{\sum \text{all certain arrests in the same way}}$$

$$\text{Dominance Rate} = \text{Frequency} \times \text{Abundance}$$

$$\text{Resting Rate} = \frac{\sum \text{resting mosquitoes of certain caught species}}{\sum \text{all caught resting mosquitoes}} \times 100\%$$

Molecular Detection of *Brugia malayi*

For molecular analysis, the head–thorax segments of individual mosquitoes were subjected to DNA extraction. Polymerase chain reaction (PCR) was performed using *Brugia*-specific primers targeting the *yACA* gene. PCR products were visualized by agarose gel electrophoresis. Positive amplicons were sequenced, and sequence identity was confirmed using BLAST analysis against reference sequences in GenBank.

Environmental Data Collection

Environmental characteristics recorded at each site included types of water bodies, dominant aquatic vegetation, land use patterns, temperature, and relative humidity. These parameters supported ecological interpretation of mosquito dominance and behavioral patterns.

Ethical Approval

Ethical clearance was obtained from the Ethics Committee of the Faculty of Medicine, Universitas Sriwijaya (No. 522/kepkrsmhfkunsri/2016). All mosquito collectors provided written informed consent prior to participation.

3. RESULTS

Environmental Characteristics of Study Sites

Both study villages were situated at low elevation, with Sedang Village located at approximately 10 m above sea level and Muara Sugih Village at 12 m above sea level. Sedang Village was characterized by tidal swamps dominated by floating vegetation, particularly *Pistia stratiotes*, indicating eutrophic and low-flow aquatic conditions. In contrast, Muara Sugih Village consisted mainly of irrigated rice fields and river channels, reflecting intensive agricultural land use with periodic flooding and irrigation cycles.

Mean temperature and relative humidity were 27.14 ± 1.96 °C and $91.18 \pm 5.35\%$ in Sedang Village, and 25.64 ± 1.46 °C and $86.92 \pm 11.89\%$ in Muara Sugih Village. These microclimatic conditions were within optimal ranges for mosquito survival, flight activity, and gonotrophic cycle completion, supporting persistent vector populations in both locations (Table 1).

Table 1. Environmental characteristics of Sedang and Muara Sugih Villages Banyuasin Regency, South Sumatra, Indonesia (13).

Variable	Sedang Village	Muara Sugih Village
Location	2049.395'S and 1040 25.381"E longitude	2047.048'S and 1040 45.371"E longitude
Altitude	10 meters above sea level	12 meters above sea level
Water bodies	Tidal swamps	Rivers, rice fields
Temperature	27,14+1,960 C	25,64+1,460C
Humidity	91,18+5,35%	86,92+11,897 %
Aquatic plant dominant	<i>Pistia stratiotes</i>	<i>Oryza sativa</i>
Land Use	Rubber and oil palm plantation	Rice fields

Species Composition and Ecological Dominance

A total of 1,342 female *Culex* mosquitoes representing eight species were collected from both villages. Overall species diversity was low ($H' = 0.37$), indicating strong dominance by a single species. *Culex quinquefasciatus* accounted for 92.4% of all specimens and was particularly dominant in Muara Sugih Village, where diversity was extremely low ($H' = 0.18$). Sedang Village showed moderate diversity ($H' = 1.19$), reflecting a more heterogeneous mosquito community structure (Tables 2–4).

Table 2. Species diversity and abundance of *Culex spp* in Sedang and Muara Sugih Villages, Banyuasin Regency, South Sumatra, Indonesia.

Species	Abundance in number (N)		Abundance in percentage (%)			
	Sedang Village	Muara Sugih Village	Totally	Sedang Village	Muara Sugih Village	Totally
<i>Culex quinquefasciatus</i>	92	1148	1240	6,85	85,54	92,39
<i>Culex gelidus</i>	30	12	42	2,2	0,9	3,1
<i>Culex vishnui</i>	22	14	36	1,64	1,04	2,68
<i>Culex lophoceraomyia</i>	0	2	2	0	0,15	0,15
<i>Culex tritaeniorhynchus</i>	7	8	15	0,52	0,6	1,12
<i>Culex nigropunctatus</i>	0	1	1	0	0,08	0,08
<i>Culex fuscocephala</i>	5	0	5	0,4	0	0,4
<i>Culex sitiens</i>	1	0	1	0,08	0	0,08
Totally	157	1185	1342	11,69	88,31	100

Table 3. Shannon–Wiener Diversity Index (H') of *Culex spp* in Sedang and Muara Sugih Villages, Banyuasin Regency, South Sumatra, Indonesia.

Species	Sedang Village			Muara sugih Village		
	Abundance (n_i)	p_i	$p_i \ln p_i$	Abundance (n_i)	p_i	$p_i \ln p_i$
<i>Culex quinquefasciatus</i>	92	0.586	-0.313	1148	0.969	-0.030
<i>Culex gelidus</i>	30	0.191	-0.316	12	0.010	-0.046
<i>Culex vishnui</i>	22	0.140	-0.275	14	0.012	-0.053
<i>Culex lophoceraomyia</i>	0	0	0	2	0.002	-0.013
<i>Culex tritaeniorhynchus</i>	7	0.045	-0.139	8	0.007	-0.035
<i>Culex nigropunctatus</i>	0	0	0	1	0.001	-0.006
<i>Culex fuscocephala</i>	5	0.032	-0.110	0	0	0
<i>Culex sitiens</i>	1	0.006	-0.032	0	0	0
Totally (N)	157	1.000		1185	0	0
Shannon–Wiener Index (H')			1,19			0,18

The marked dominance of *Culex quinquefasciatus* in Muara Sugih Village highlights the strong influence of land use patterns and water management practices on mosquito community composition.

Rice field ecosystems with high organic content and stable standing water appear to favor proliferation of pollution tolerant *Culex* species more strongly than tidal swamp environments.

Table 4. Combined Data Shannon–Wiener Diversity Index (H') of *Culex spp*

Species	Combanined Sedang dan Muara Sugih villages		
	Abundance (n_i)	p_i	$p_i \ln p_i$
<i>Culex quinquefasciatus</i>	1240	0.924	-0.073
<i>Culex gelidus</i>	42	0.031	-0.108
<i>Culex vishnui</i>	36	0.027	-0.097
<i>Culex lophoceraomyia</i>	2	0,001	-0,010
<i>Culex tritaeniorhynchus</i>	15	0.011	-0.051
<i>Culex nigropunctatus</i>	1	0,001	-0,006
<i>Culex fuscocephala</i>	5	0.004	-0.020
<i>Culex sitiens</i>	1	0.001	-0.006
Totally (N)	1342	1.000	
Shannon–Wiener Index (H')			0,37

The combined dominance and frequency indices confirmed that *Cx. quinquefasciatus* was consistently present across sampling periods and locations, whereas other *Culex* species occurred sporadically and at much lower densities. This ecological pattern suggests habitat homogenization favoring pollution-tolerant mosquitoes, particularly in rice field-dominated landscapes.

These findings underscore the importance of integrated vector management (IVM) approaches that incorporate environmental modification, improved irrigation practices, and vegetation management to reduce suitable larval habitats. Furthermore, the presence of multiple *Culex* species, even at low densities, suggests potential risks for multi-pathogen transmission, particularly in wetland ecosystems undergoing rapid land-use changes.

Biting Behavior and Transmission Indices

Analysis of biting behavior revealed predominantly nocturnal activity with marked endophagic and endophilic tendencies. In Sedang Village, overall biting activity of *Culex* mosquitoes was relatively low, with 81 individuals collected and a total MBR of 0.56. Biting occurred almost equally outdoors and

indoors, indicating mixed feeding behavior. *Culex quinquefasciatus* was the dominant biting species and demonstrated flexible feeding behavior, indicating its potential role as the primary vector in this village despite lower transmission pressure. Secondary species such as *Culex gelidus* and *Culex vishnui* contributed modestly to biting rates, whereas other species were present at very low densities and were epidemiologically negligible (Table 5, Figure 1).

These graphical representations highlight the importance of species-specific behavioral heterogeneity in shaping local transmission dynamics and informing targeted vector control strategies. The observed biting behavior patterns indicate that vector control strategies in Sedang Village should not rely solely on outdoor-based interventions. Indoor-focused measures, such as long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS), are highly relevant given the significant indoor biting activity. Concurrently, the presence of exophagic species necessitates integrated vector management, including environmental management and reduction of breeding habitats in peridomestic areas.

Table 5. Biting Behaviour, MHD and MBR in Sedang Village, Banyuasin Regency, South Sumatra, Indonesia

Species	Biting Behaviour in number				Totally	MBR
	Outdoor	MHD	Indoor	MHD		
<i>Culex quinquefasciatus</i>	21	0,145	25	0,173	46	0,319
<i>Culex gelidus</i>	9	0,062	6	0,041	15	0,104
<i>Culex vishnui</i>	5	0,034	9	0,062	14	0,791
<i>Culex lophoceraomyia</i>	0	0	0	0	0	0
<i>Culex tritaeniorhynchus</i>	4	0,027	0	0	4	0,027
<i>Culex nigropunctatus</i>	0	0	0	0	0	0
<i>Culex fuscocephala</i>	2	0,013	0	0	2	0,013
<i>Culex sitiens</i>	0	0	0	0	0	0
Totally	41	0,28	40	0,277	81	0,562

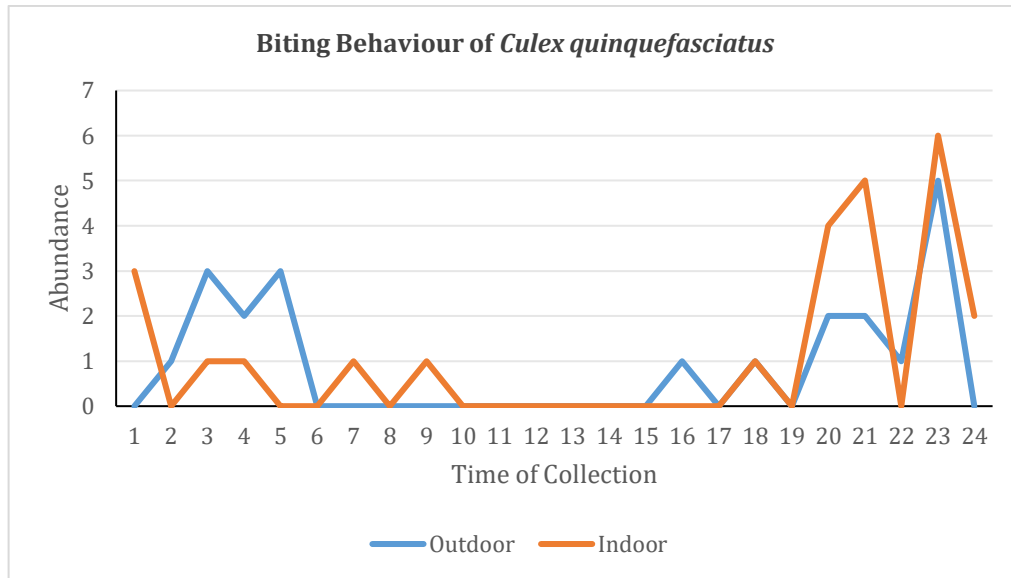


Figure 1. Biting Behaviour of *Culex quinquefasciatus* in Sedang Village, Banyuasin Regency, South Sumatra, Indonesia.

In contrast, Muara Sugih Village exhibited substantially higher biting density, with an overall MBR of 4.3. Both indoor (MHD = 2.02) and outdoor (MHD = 2.30) biting densities were elevated, indicating continuous human–vector contact throughout the night. *Culex quinquefasciatus* overwhelmingly dominated biting activity, accounting for nearly all indoor and outdoor bites (Table 6, Figure 2). High MHD values both indoors and outdoors indicate intense and continuous human–vector contact, suggesting a markedly higher

transmission risk in Muara Sugih Village compared with Sedang Village.

Comparison between villages revealed that MBR in Muara Sugih was nearly eight times higher than in Sedang Village, indicating substantially greater transmission potential. This difference corresponds with environmental conditions that favor vector proliferation, particularly irrigated rice fields and peri-domestic water accumulation.

Table 6. Biting Behaviour, MHD and MBR in Muara Sugih Village, Banyuasin Regency, South Sumatra, Indonesia

Species	Biting Behaviour in number				Totally	MBR
	Outdoor	MHD	Indoor	MHD		
<i>Culex quinquefasciatus</i>	326	2,2	283	1,96	609	4,2
<i>Culex gelidus</i>	2	0,013	1	0,006	3	0,02
<i>Culex vishnui</i>	2	0,013	2	0,013	4	0,03
<i>Culex lophoceraomyia</i>	1	0,006	1	0,006	2	0,01
<i>Culex tritaeniorhynchus</i>	2	0,013	2	0,013	4	0,03
<i>Culex nigropunctatus</i>	0	0	1	0	1	0,006
<i>Culex fuscocephala</i>	0	0,	0	0	0	0
<i>Culex sitiens</i>	0	0	0	0	0	0
Totally	333	2,3	291	2,02	623	4,3

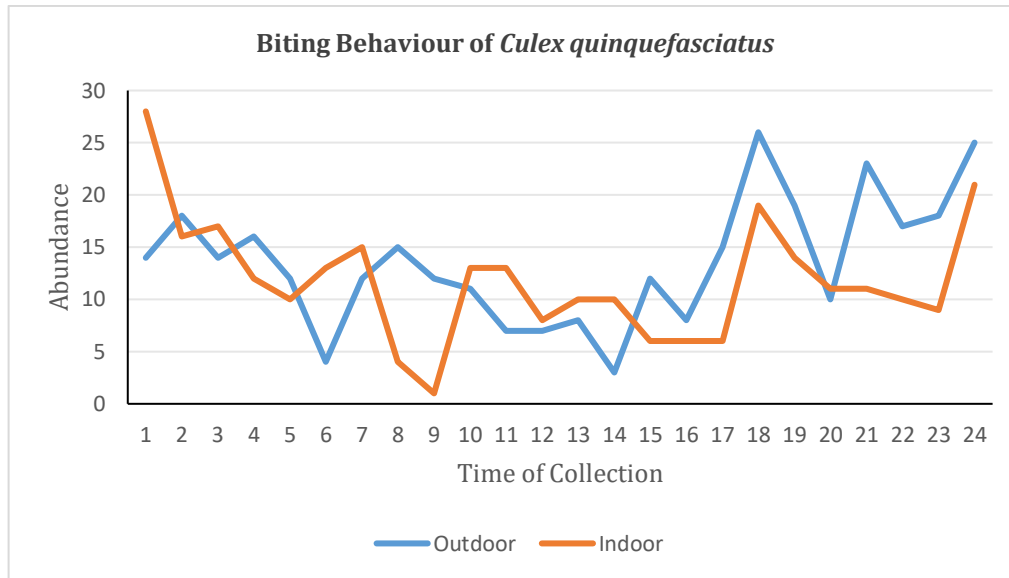


Figure 2. Biting Behaviour of *Culex quinquefasciatus* in Muara Sugih Village, Banyuasin Regency, South Sumatra, Indonesia.

These graphical patterns emphasize the importance of species-specific behavioral assessments in understanding local transmission dynamics. The high indoor and outdoor biting rates observed in Muara Sugih Village indicate that single-focus interventions are unlikely to be sufficient. An integrated vector management approach is required, combining indoor residual spraying (IRS), long-lasting insecticidal nets (LLINs), and environmental management to reduce breeding sites in surrounding wetlands and peridomestic areas.

In both villages, *Culex quinquefasciatus* was the dominant species; however, its dominance was extreme in Muara Sugih Village, where it accounted for almost all biting activity and contributed the vast majority of MBR. This pattern suggests that local environmental conditions in Muara Sugih strongly favor the proliferation and feeding success of this species. The findings indicate a substantially higher risk of vector-borne disease transmission in Muara Sugih Village, driven by the abundance and aggressive biting behavior

of *Culex quinquefasciatus*. These results highlight the need for intensive, integrated vector control strategies in Muara Sugih, particularly targeting indoor transmission and wetland breeding habitats, while lower-intensity surveillance and environmental management may be sufficient in Sedang Village.

Abundance, Frequency, and Dominance of Biting Mosquitoes

Indices of abundance, frequency, and dominance further confirmed the epidemiological importance of *Culex quinquefasciatus*. In Sedang Village, this species showed the highest abundance and frequency among biting mosquitoes, indicating consistent occurrence across sampling periods. In Muara Sugih Village, *Culex quinquefasciatus* exhibited extreme dominance, being present in all sampling events and accounting for almost all human–mosquito contact (Tables 7 and 8).

These findings suggest that local transmission dynamics in both villages, particularly in Muara Sugih, are driven almost exclusively by *Culex quinquefasciatus*, reinforcing its primary

epidemiological relevance in modified wetland settings.

Table 7. The abundance, frequency, and dominance of biting mosquitoes in Sedang Village, Banyuasin Regency, South Sumatra, Indonesia

Species	Mosquitos' collection		
	Abundance (%)	Frequency	Dominance
<i>Culex quinquefasciatus</i>	60,5	0,41	24,8
<i>Culex gelidus</i>	19,7	0,16	3,15
<i>Culex vishnui</i>	1,05	0,16	0,17
<i>Culex lophoceraomyia</i>	0	0	0
<i>Culex tritaeniorhynchus</i>	3,94	0,08	0,32
<i>Culex nigropunctatus</i>	0	0	0
<i>Culex fuscocephala</i>	3,94	0,08	0,32
<i>Culex sitiens</i>	1,31	0,04	0,05

Table 8. The abundance, frequency, and dominance of biting mosquitoes in Muara Sugih Village, Banyuasin Regency, South Sumatra, Indonesia

Species	Mosquitos' collection		
	Abundance (%)	Frequency	Dominance
<i>Culex quinquefasciatus</i>	95,9	1	95,9
<i>Culex gelidus</i>	1,6	0,13	0,21
<i>Culex vishnui</i>	1,8	0,13	0,23
<i>Culex lophoceraomyia</i>	0	0	0
<i>Culex tritaeniorhynchus</i>	0,71	0,04	0,03
<i>Culex nigropunctatus</i>	0	0	0
<i>Culex fuscocephala</i>	0	0	0
<i>Culex fuscocephala</i>	0	0	0

Other species such as *Culex gelidus* and *Culex vishnui* were present at moderate abundance but exhibited much lower dominance values, suggesting limited epidemiological importance, while remaining species contributed minimally to biting activity.

Resting Behavior

Resting collections revealed marked differences between villages. In Sedang Village, *Culex quinquefasciatus* dominated both indoor and outdoor resting sites but shared resting habitats with several other species, indicating more heterogeneous resting patterns. In contrast, Muara Sugih Village showed near-total dominance of *Culex quinquefasciatus* in both indoor and outdoor resting collections, reflecting strong environmental selection favoring this species and reinforcing its role in maintaining close contact with human dwellings (Table 9, Figures 3 and Figures 4).

Resting collections showed a strong preference for indoor and peri-domestic resting sites by *Culex quinquefasciatus* in both villages. In Muara Sugih Village, this species constituted more than 95% of resting mosquitoes indoors and outdoors, indicating near-monospecific resting behavior. Other *Culex* species were rarely encountered and contributed minimally to resting collections. These findings further support the ecological dominance and behavioral adaptability of *Culex quinquefasciatus*. The high proportion of indoor-resting mosquitoes in Muara Sugih suggests increased mosquito survival and prolonged vector longevity, factors that are critical for successful parasite development and sustained transmission.

Table 9. Resting Rate in Sedang and Muara Sugih Villages, Banyuasin Regency, South Sumatra, Indonesia

Species	Sedang Village				Muara Sugih Village			
	Outdoor		Indoor		Outdoor		Indoor	
	N	%	N	%	N	%	N	%
<i>Culex quinquefasciatus</i>	19	57,5	27	62,8	205	93,6	334	97,4
<i>Culex gelidus</i>	6	18,2	9	20,9	8	3,7	1	0,3
<i>Culex vishnui</i>	6	18,2	2	4,7	4	1,8	6	1,7
<i>Culex lophoceraomyia</i>	0	0	0	0	0	0	0	0
<i>Culex tritaeniorhynchus</i>	0	0	3	6,96	2	0,9	2	0,6
<i>Culex nigropunctatus</i>	0	0	0	0	0	0	0	0
<i>Culex fuscocephala</i>	2	6,1	1	2,32	0	0	0	0
<i>Culex sitiens</i>	0	0	1	2,32	0	0	0	0
Totally	33	100	43	100	219	100	343	100

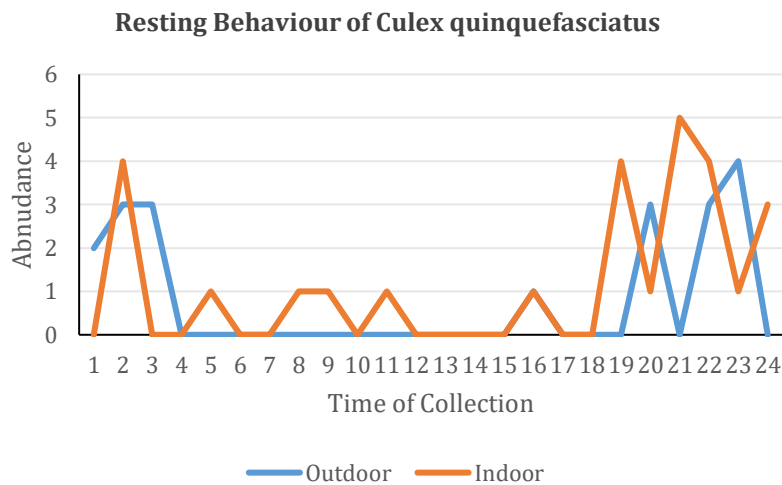


Figure 3. Resting Behaviour of *Culex quinquefasciatus* in Sedang Village, Banyuasin Regency, South Sumatra, Indonesia

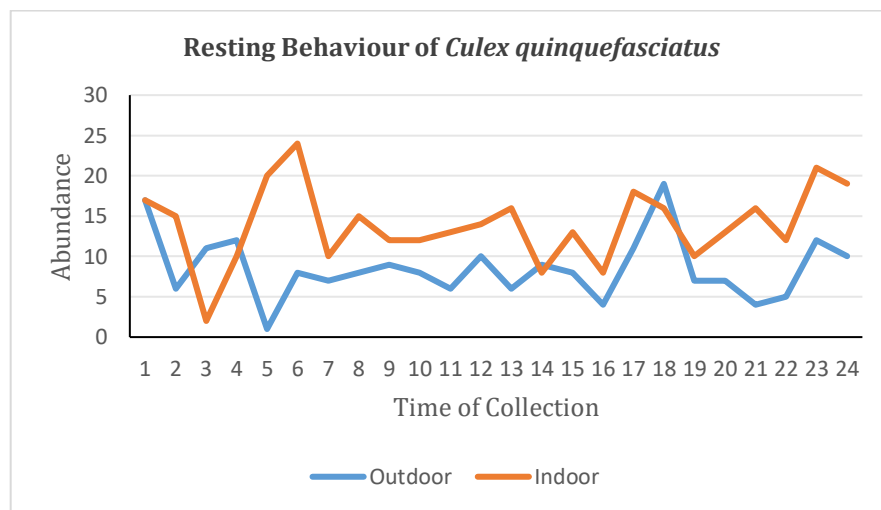


Figure 4. Resting Behaviour of *Culex quinquefasciatus* in Muara Sugih Village, Banyuasin Regency, South Sumatra, Indonesia.

In Sedang Village, *Culex quinquefasciatus* dominated both outdoor and indoor-resting collections, indicating flexible resting behavior and adaptation to multiple habitat types, while other species were present at much lower and inconsistent proportions, suggesting limited ecological roles. In contrast, Muara Sugih Village exhibited near-total dominance of *Culex quinquefasciatus* in both resting environments, with very few individuals from other species detected. This highly homogeneous resting pattern reflects strong environmental selection favoring *Culex quinquefasciatus* and supports its primary role in local transmission dynamics across both domestic and peridomestic settings.

Molecular Detection of *Brugia malayi*

PCR analysis detected *Brugia malayi* DNA in *Culex quinquefasciatus* collected from Sedang Village. Sequencing confirmed high similarity (93–95%) with reference *B. malayi* sequences in GenBank (Accession MG030487.1). This finding provides molecular evidence of parasite–vector contact under natural field conditions (Figures 5 and 6).

Although detection of parasite DNA does not confirm development of infective-stage larvae, it indicates ongoing exposure of mosquitoes to infected hosts and supports the potential role of *Culex quinquefasciatus* in maintaining residual transmission.

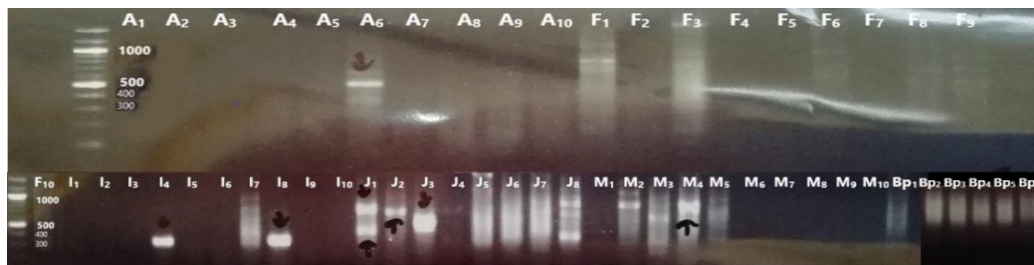


Figure 5. Band Positif of *Brugia malayi* in *Culex quinquefasciatus* sample

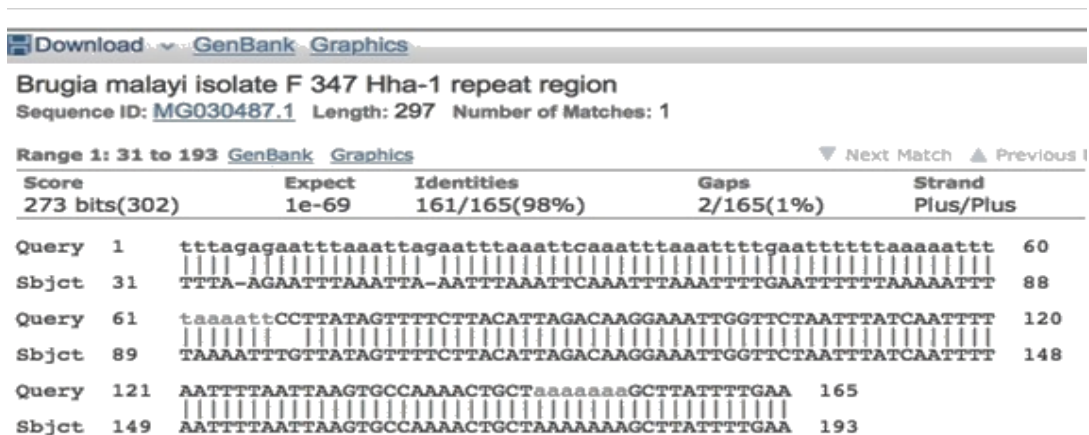


Figure 6. Result of sequencing blast of I8

4. DISCUSSION

This study provides strong evidence that lymphatic filariasis transmission in modified wetland ecosystems of South Sumatra is driven by complex ecological interactions involving environmental change, mosquito behavioral plasticity, and the potential participation of multiple vector species. The overwhelming dominance of *Culex quinquefasciatus* in both villages, particularly in Muara Sugih, where it accounted for more than 97% of biting activity, likely reflects habitat homogenization resulting from agricultural intensification and accumulation of peri-domestic wastewater. Such environmental conditions favor ecologically tolerant generalist species capable of exploiting polluted and stagnant water, while simultaneously reducing suitable habitats for specialist vectors such as *Mansonia spp.* that depend on aquatic vegetation for larval respiration.

These findings are consistent with recent studies reporting that agricultural intensification and land-use change in Southeast Asia shift mosquito community composition toward *Culex* dominance, especially in irrigated and peri-urban settings with high organic loads in water bodies.^{7,10} In Indonesia, post-MDA endemic areas have also reported declining *Mansonia* populations and increasing abundance of *Culex quinquefasciatus*, suggesting that environmental transformation may progressively alter traditional transmission patterns of brugian filariasis.⁴ Therefore, vector ecology in endemic wetlands should be considered dynamic and strongly shaped by socio-environmental processes.

Biting behavior analysis further highlights the epidemiological importance of *Culex quinquefasciatus*. In Muara Sugih Village, both indoor and outdoor MHD and MBR values were markedly high, indicating intense and continuous human–vector contact. In contrast, Sedang Village showed lower overall biting density, although *Culex quinquefasciatus* remained the dominant biting species. The strong endophagic and endophilic tendencies observed, particularly in Muara Sugih, are critical because indoor feeding increases exposure during sleeping hours, while indoor resting enhances mosquito survival by reducing environmental stress and predation, thereby increasing vectorial capacity.

Similar indoor-oriented behavior of *Culex quinquefasciatus* has been reported in urban and peri-urban filariasis settings, where this species contributes substantially to sustained transmission despite vector control interventions [6,13]. Behavioral flexibility enables *Culex* populations to persist under diverse ecological conditions and may explain why transmission can continue even after repeated MDA cycles, particularly in areas with persistent breeding habitats.

Molecular detection of *Brugia malayi* DNA in *Culex quinquefasciatus* provides further evidence that this species may function as a supplementary or bridge vector in post-MDA settings. Although PCR positivity does not confirm development of infective third-stage larvae or full vector competence, it indicates epidemiologically relevant contact between mosquitoes and infected hosts. Molecular xenomonitoring has been increasingly recognized as a sensitive surveillance tool capable of detecting ongoing transmission when human infection prevalence becomes very low following MDA.^{3,8,9}

Traditionally, transmission of *Brugia malayi* in Indonesia has been associated with *Mansonia spp.* in swamp ecosystems.^{4,5} However, recent molecular studies have detected filarial DNA in multiple mosquito genera, suggesting that transmission systems may involve more than one vector species, particularly in ecologically altered environments.^{8,9} The detection of *Brugia malayi* DNA in *Culex quinquefasciatus* in the present study supports the hypothesis that environmental modification may facilitate shifts in vector participation, allowing ecologically tolerant species to contribute to residual transmission.

Notably, this study provides field-based molecular evidence of *Brugia malayi* DNA in *Culex quinquefasciatus* combined with quantitative ecological dominance and indoor biting behavior data within modified wetland ecosystems of South Sumatra. This integrated ecological-behavioral-molecular approach has rarely been applied in brugian filariasis settings in Indonesia and reveals a potential shift in vector contribution driven by environmental transformation, representing an important refinement of current vector surveillance paradigms in post-MDA contexts.

The integration of ecological indices, behavioral analysis, and molecular detection represents a major strength of this study, enabling a multidimensional assessment of transmission risk. Nevertheless, several limitations should be acknowledged. First, the relatively small number of PCR-positive samples limits conclusions regarding infection prevalence in mosquito populations. Second, the absence of parity analysis and larval development assessment prevents confirmation of full vector competence. Third, sampling was conducted over a

limited temporal window and may not capture seasonal variation in species composition and infection rates. Longitudinal studies incorporating age-grading techniques, larval habitat productivity assessment, and experimental infection models would be valuable to clarify the true transmission potential of *Culex quinquefasciatus* in wetland ecosystems. From a public health perspective, these findings indicate that vector surveillance in brugian filariasis-endemic wetlands should not be restricted to *Mansonia spp.* alone. Integrated vector management strategies should address indoor transmission through long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS), while also targeting larval habitats associated with irrigation systems, rice fields, and peri-domestic wastewater. In addition, routine incorporation of molecular xenomonitoring into surveillance systems may improve early detection of residual transmission and guide evidence-based decisions during the final stages of LF elimination programs.

5. CONCLUSION

Culex quinquefasciatus is ecologically dominant and behaviorally adapted to indoor environments in modified wetland ecosystems of Banyuasin Regency and harbors *Brugia malayi* DNA under natural field conditions. The integration of ecological indices, biting behavior analysis, and molecular xenomonitoring represents a novel and comprehensive framework for assessing residual transmission risk in post-MDA settings. These findings suggest a potential shift in vector contribution from classical swamp-associated vectors toward ecologically tolerant species in anthropogenically

altered wetlands, highlighting the need to update vector surveillance and control strategies in brugian filariasis elimination programs.

AUTHOR CONTRIBUTIONS

RP conceived and designed the study and drafted the manuscript. PK conducted field collections and ecological data recording. FY performed molecular laboratory analysis and sequence interpretation. DL revised and critically reviewed the manuscript. All authors approved the final version.

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REFERENCES

1. Nutman TB. Insights into the pathogenesis of lymphatic filariasis. *N Engl J Med*. 2022;386(24):2331–2343. doi:10.1056/NEJMra2110404
2. World Health Organization. Global programme to eliminate lymphatic filariasis: progress report 2022. *Wkly Epidemiol Rec*. 2023;98(41):513–536.
3. Weil GJ, Curtis KC, Fischer PU, et al. A multilayered approach to assessing lymphatic filariasis transmission using molecular xenomonitoring. *Clin Microbiol Rev*. 2017;30(1):1–23. doi:10.1128/CMR.00095-16
4. Santoso, Yahya, Suryaningtyas NH, et al. Detection of *Brugia malayi* DNA in mosquitoes using PCR in endemic areas of Indonesia. *Parasit Vectors*. 2021;14:79. doi:10.1186/s13071-021-04589-3
5. Apiwathnasorn C, Samung Y, Prummongkol S, et al. Vector competence of mosquitoes for *Brugia malayi* in wetland areas. *J Med Entomol*. 2006;43:122–130.
6. Simonsen PE, Mwakitalu ME. Urban lymphatic filariasis: ecological and entomological perspectives. *Parasit Vectors*. 2013;6:218. doi:10.1186/1756-3305-6-218
7. Xavier A, et al. Environmental and socioeconomic predictors of *Culex quinquefasciatus* abundance in filariasis-endemic areas. *Pathogens*. 2024;13(11):985. doi:10.3390/pathogens13110985
8. Phukaijam C, et al. Molecular xenomonitoring of filarial parasites in mosquitoes from Thailand. *Parasit Vectors*. 2019;12:123. doi:10.1186/s13071-019-3387-6
9. Farid HA, et al. Xenomonitoring for detection of filarial parasites in mosquito vectors. *Trop Med Infect Dis*. 2018;3(1):8. doi:10.3390/tropicalmed3010008
10. Tuno N, et al. Habitat modification and mosquito species dominance in agricultural ecosystems. *Med Vet Entomol*. 2017;31(2):147–156. doi:10.1111/mve.12220
11. Kanyi H, et al. Molecular xenomonitoring after triple-drug therapy in coastal Kenya. *PLoS Glob Public Health*. 2025;5:e0004877. doi:10.1371/journal.pgph.0004877
12. Irvine MA, et al. Surveillance strategies in post-MDA filariasis settings. *Parasit Vectors*. 2018;11:1–12. doi:10.1186/s13071-018-3046-4
13. Rini Pratiwi, Chairil Anwar, Salni, Hermansyah, Novrikasari, Ahmad Ghiffari, Raden Putra, Adri Huda. Species diversity and community composition of mosquitoes in a filariasis endemic area in Banyuasin

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