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Seroprevalence and molecular surveillance for dengue virus infections among febrile patients and mosquito vectors in Ogbomoso, Nigeria

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Abstract

Background: Dengue fever is a leading cause of illness and death in tropical and subtropical regions. The World Health Organization estimates that there are 390 million dengue infections each year, of which 96 million manifest apparently.

Objectives: This study aimed to determine the seroprevalence and molecular surveillance of dengue viral infections among febrile patients and mosquito vectors in Ogbomoso, Nigeria.

Materials and Methods: A cross sectional study was conducted between February and July 2024 in Ogbomoso, Oyo State, Nigeria. Four hundred serum samples from febrile patients of all ages and mosquito vectors were collected. Serum samples were analyzed using DENV RDT kit for IgM and IgG and RT-PCR, while the mosquito samples were subjected to only RT-PCR. Malaria co-infection was detected using an RDT kit confirmed microscopically. Chi-square tool was used to determine the association between socio-demographics, clinical features and risk factors among the febrile patients.

Result: Of the 400 participants, 126(31.5%) were males and 274(68.5%) were females. Dengue IgG was detected in 223/400(55.8%), while DENV IgM was found in 12/400(3.0%), and 165/400(41.3%) had neither IgG nor IgM. Co-infections with malaria were found in 70/400(31.4%) for IgG and 4/400(33.3%) for IgM. All serum samples and mosquitoes were negative for DENV RNA by RT-PCR. The highest infection rates for IgM were in the 11-20 and 21-30 age groups. Environmental and behavioral factors, such as improper water storage and proximity to bushes were not significantly associated with dengue seropositivity.

Conclusion: This study provides evidence that dengue virus is circulating in Ogbomoso, Oyo State, Nigeria. The high rate of coinfection between DENV IgM and malaria, advocates for routine serological screening of febrile patients for both infections, improved diagnostic capacity, and targeted public health interventions to control and prevent dengue outbreaks. Therefore, dengue virus tests should be included in the routine test for aetiology of fever to avoid misdiagnosis

Keywords: Dengue virus; RT-PCR; Serotypes; Co-infections.

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1. Introduction

Dengue fever (DF), one of the neglected tropical diseases (NTDs), accounts for about 390 million dengue infections each year, of which 96 million manifest apparently. It affects large populations, especially in the tropics and subtropics (1). The World Health Organization (WHO) designated it "a disease that may constitute public health emergency of international concern with implication for health security" (2). Unfortunately, it is under-recognized and often misdiagnosed because of similarities in the presenting features with malaria and typhoid fever which are more easily diagnosed (3). In more complicated cases, dengue hemorrhaegic fever (DHF) progresses to Dengue Shock Syndrome (DSS), a condition associated with high mortality following massive plasma leakage. Both DHF and DSS are closely related and are characterized by an increase in vascular permeability, hemorrhagic manifestations, progressive leukopenia, and low platelet count (4). Dengue fever is an infectious disease spread by mosquitoes and is widespread in tropical and subtropical areas. In 2010, it was estimated that 390 million dengue infections occurred worldwide, with 96 million presenting clinically and resulting in 21,000 deaths. Dengue virus (DENV) infection has increased substantially in recent years, with the number of cases almost doubling within a decade from 2.4 million in 2010 to 4.2 million cases in 2019 (5). Explosive outbreaks and regional spread into new locations are factors behind this recent huge increase in the incidence of dengue fever (6). Dengue and malaria infections have similar geographical areas of distribution, and similar factors encourage the spread of both infections. For instance, poor drainage systems and poor environmental sanitation may result in an infestation of day-biting mosquitoes that transmit dengue infection and night-biting mosquitoes that spread malaria, thus an existence of high dengue burden where malaria is endemic may be expected. Therefore, this study set out to assess the seroprevalence and molecular surveillance of dengue viral infections among febrile patients and mosquito vectors in Ogbomoso, Nigeria.

2. Materials and methods

2.1. Study Design and setting

This study was a cross-sectional study designed to assess the seroprevalence and molecular surveillance of dengue viral infections among febrile patients and mosquito vectors in Ogbomoso, Nigeria. The study site was State Hospital, Ogbomoso, Nigeria. Ogbomoso is located on the 8°10 1 North of the equator and 4°10 1 East of the Greenwich meridian.

2.2. Participants Inclusion and Exclusion Criteria

Febrile patients of all ages receiving care in state Hospital, Ogbomoso, complaining of fever conditions who met the inclusion criteria and gave consent to participate were consecutively recruited for the study between February and July 2024.

2.3. Sample size

The Charan and Biswas formula (2013) (7) was used in estimating the sample size.

A total of 400 participants of all ages presenting with febrile

$$N = \frac{Z^2PQ}{E^2} = \quad N = \frac{(1.96)2 \times 0.172 \times 0.828}{(0.05)}$$

Where: N = Minimum sample size, Z = the standard normal deviate at 5% significance level (1.96), P = Prevalence rate of 17.2% according to study by (Oladipo *et al.,* 2018) was used to calculate sample size for number of subjects required (17.2% = 0.172)

Q = 1-P = (1- 0.172) = 0.828E = level of precision (allowable error) = 5% = (0.05)

2.3.1. Human Sample Collection

A consecutive sampling method was used (8). About 5 ml of whole blood sample was collected by venipuncture into a plain sample bottle from all the participants, centrifuged immedately for 5 minutes at 3000 rpm to obtain the serum which was aliquoted into two parts for serology and molecular testing and then stored frozen at -80^{0}C for further tests.

2.3.2. Collection

Aedes species were collected by trained volunteers using a BG-Sentinel trap. Collected mosquitoes were sorted and identified using colored identification/taxonomic keys (9). The mosquitoes of choice were introduced into a well-labeled Eppendorf tube containing RNA later(shield) and then stored frozen at -80°C.

2.4. Data Collection Instrument and Method

A semi-structured interviewer administered questionnaire was developed for data collection. This was used to obtain relevant history and socio-demographic information from the patients of the subjects.

2.5. Laboratory Analysis

All laboratory analysis were performed at the Center for Human Virology and Genomics, Nigerian Institute of Medical Research (NIMR), Yaba, Lagos, Nigeria.

2.5.1. Malaria diagnosis

Blood samples from participants were tested for malaria using Carestart rapid diagnostic test kits (AccessBio, NJ, USA) following the manufacturer's guidelines. The results were then confirmed under the microscope with thick and thin blood films stained with 10% Giemsa. If no parasites were detected, the sample was marked negative. Each slide was independently reviewed by two trained microscopists, and if their results differed, a third microscopist examined the slide (10).

2.5.2. Determination of IgG and IgM Antibody against Dengue Virus

Denque virus antibody was diagnosed with Dengue IgG/IgM Rapid Kit (Nantong Egens Biotechnology Co., Ltd., China), and the manufacturer's instructions were followed. This immunochromatographic assay is designed to qualitatively detect anti-dengue IgM and IgG antibodies, helping to distinguish between primary and secondary dengue infections. The kit has a relative sensitivity of 95% and a specificity of 96% (11).

2.5.3. . Molecular diagnosis.

RNA Extraction

Female Aedes mosquitoes were manually homogenized with a ceramic Eppendorf pestle in a 1.5 ml microcentrifuge tube containing 200 µl of RNA lysis solution before starting the RNA extraction process. DaAN RNA Extraction kits (Nantong Egens Biotechnology Co., Ltd., China) was used to extract viral RNA from both human sera and homogenized mosquitoes, following the manufacturer's instructions. The extracted RNA were stored at -80°C for further processing.

Real-time PCR

RT-PCR was performed using the Quant Studio5 machine. The PCR mix consisted of 25 µl, including 10 µl of enzyme mix, 0.8 µl each of forward (AAACCGCGTGTCGACTGTGC) and reverse primers (TAGGAAACGAAGGAATGCCACC), 0.4 µl of probes

(FAM-5'CACTTGGAATGCTGCAGGGACGAGGACC), 6 µl of nuclease-free water, and 5 µl of RNA template. A Ct value of less than 38 was considered positive for viral pathogens. Cycling Conditions: Initial denaturation at 94˚C for 5mins, then by 36 cycles of denaturation at 94˚C for 30 seconds, annealing at 55˚C for 30 seconds, and elongation at 72˚C for 45 sec. Followed by a final elongation step at 72˚C for minutes and holding the temperature at 10˚C.

2.6. Data Analysis

The data were entered into an excel spreadsheet and analyzed using smith's statistical package (version 2.8, California, USA). The chi-square test was used to determine the relationships between the socio-demographic data and the prevalence of dengue virus infection. p-value of ≤ 0.05 was considered statistically significant at a 95% confidence interval.

2.6.1. Ethical Consideration and Consent to Participate

Ethical approval with number: NHREC/OYOSHRIEC/10/11/22 was obtained from the Ethical Review committee of Oyo State Ministry of Health, Secretariat, Ibadan, Oyo State,

3. Results

3.1. Demographic characteristics

Majority of the participants were females 274 (68.5%), while males constituted 126 (31.5%) and the largest group of participants were 21-30 years old (Table 1).

Table 1 Demographic characteristics of study participant's variables.

Variables	Frequency(n=400)	Percent (%)
Age Group (Years)		
0-10	45	11.3
20-Nov	75	18.8
21-30	127	31.8
31-40	57	14.3
41-50	57	14.3
60above	39	9.8
Gender		
Male	126	31.5
Female	274	68.5
Marital Status		
Married	197	49.3
Single	159	39.8
Widow	23	5.8
Divorced	21	5.3
Ethnic group		
Yoruba	313	78.3
Hausa	16	4
Igbo	65	16.3
Fulani	6	1.5

3.2. Sero-molecular Characterization of Human and Mosquitoes Samples (n = 400)

Table 2 Sero-molecular Characterization of Human and Mosquitoes Samples (n = 400)

Variables	Categories	Frequency(n=400)	Percent (%)
Dengue RDT	IgG Positive	223	55.8
	IgM Positive	12	3
	Negative (IgG/IgM)	165	41.3
RT-PCR	Serum (Negative)	400	100
	Mosquitoes (Negative)	400	100

More than half of the samples, 223/400 (55.8%) tested positive for IgG antibodies, 12/400 (3.0%) samples tested positive for IgM antibodies, and 165/400 (41.3%) samples tested negative for both IgG and IgM antibodies. The RT-PCR did not detect Dengue RNA from both human serum and mosquito samples (Table 2).

3.3. Co-infections of Dengue and malaria fever among respondents (n=400)

Out of 400 individuals, 127 (31.8%) were malaria RDT positive, confirmed microscopically. Of the 127 malaria RDT positive, 4 (3.2%) were also Dengue IgM positive and 8 of 273 (68.3%) negative for malaria were Dengue IgM infected (Table 3).

Table 3 Co-infections of Dengue and malaria fever among respondents (n=400)

		Malaria RDT	
Variable	**Categories**	**Positive**	**Negative**
Dengue RDT	IgG Positive	70(31.4%)	153(68.6%)
	IgM Positive	4(33.3%)	8(66.7%)
	Negative (IgG/IgM)	53(32.1%)	112(67.9%)
	Total	127(31.8%)	273(68.3%)

3.4. Association between socio-demographics and Dengue infections among the study participants

There was no significant association between socio-demographic factors and Dengue infections among the study participants, $p>0.05$ (Table 4).

Table 4 Association between socio-demographics and Dengue infections among the study participants

		Dengue RDT					
Variables	**Categories**	**IgG Positive**	**IgM Positive**	**Negative (IgG/IgM)**	**Total**	**Statistics**	**OR (95% CI)**
Age group	0-10	23(5.8%)	1(0.3%)	21(5.3%)	45(11.3%)	χ^2=5.175 p=0.879	0.895 (0.865-0.925)
	20-Nov	42(10.5%)	4(1.0%)	29(7.3%)	75(18.8%)		
	21-30	72(18.0%)	4(1.0%)	51(12.8%)	127(31.8%)		
	31-40	28(7.0%)	2(0.5%)	27(6.8%)	57(14.3%)		
	41-50	34(8.5%)	1(0.3%)	22(5.5%)	57(14.3%)		
	60above	24(6.0%)	0(0.0%)	15(3.8%)	39(9.8%)		
Gender	Male	72(18.0%)	3(0.8%)	51(12.8%)	126(31.5%)	χ^2=0.326 p=0.85	0.845 (0.810-0.880)
	Female	151(37.8%)	9(2.3%)	114(28.5%)	274(68.5%)		
Marital status	Married	109(27.3%)	5(1.3%)	83(20.8%)	197(49.3%)	χ^2=3.847 p=0.697	0.698 (0.652-0.743)
	Single	94(23.5%)	5(1.3%)	60(15.0%)	159(39.8%)		
	Widow	9(2.3%)	1(0.3%)	13(3.3%)	23(5.8%)		
	Divorced	11(2.8%)	1(0.3%)	9(2.3%)	21(5.3%)		
Ethnic group	Yoruba	167(41.8%)	11(2.8%)	135(33.8%)	313(78.3%)	χ^2=5.392 p=0.495	0.495 (0.446-0.544)
	Hausa	12(3.0%)	0(0.0%)	4(1.0%)	16(4.0%)		
	Igbo	41(10.3%)	1(0.3%)	23(5.8%)	65(16.3%)		
	Fulani	3(.8%)	0(0.0%)	3(.8%)	6(1.5%)		
	Not educated	18(4.5%)	0(0.0%)	15(3.8%)	33(8.3%)		0.885 (0.854-0.916)

Education	Primary	42(10.5%)	3(0.8%)	31(7.8%)	76(19.0%)	χ^2=2.403 p=0.879	
	secondary	100(25.0%)	7(1.8%)	74(18.5%)	181(45.3%)		
	Tertiary	63(15.8%)	2(0.5%)	45(11.3%)	110(27.5%)		
Occupation	Student	79(19.8%)	6(1.5%)	66(16.5%)	151(37.8%)	χ^2=7.203 p=0.927	0.95 (0.929-0.971)
	Civil servant	23(5.8%)	2(0.5%)	22(5.5%)	47(11.8%)		
	Business	44(11.0%)	2(0.5%)	25(6.3%)	71(17.8%)		
	Entrepreneur	25(6.3%)	0(0.0%)	14(3.5%)	39(9.8%)		
	Retired	9(2.3%)	0(0.0%)	8(2.0%)	17(4.3%)		
	Farmer	16(4.0%)	1(0.3%)	14(3.5%)	31(7.8%)		
	Artisans	21(5.3%)	1(0.3%)	11(2.8%)	33(8.3%)		
	Unemployed	6(1.5%)	0(0.0%)	5(1.3%)	11(2.8%)		

3.5. Prevalence of symptoms among individuals tested for malaria and Dengue fever (n = 400).

There was no association between the clinical features and Dengue. Headache was a common symptom among participants who tested positive for Dengue IgM 8 (2.7%). Vomiting was present in 6 (5.5%) of IgM-positive cases. Nausea was reported by 8 (3.0%) of IgM-positive participants, other symptoms did not show a significant association with Dengue infection. Joint pain was found in 8 (3.7%) of IgM-positive cases. Body ache was another common symptom among IgM-positive cases, 6 (2.3%). Abdominal pain was reported by 3 (2.3%) of IgM-positive cases (Table 5).

Table 5 Prevalence of symptoms among individuals tested for malaria and Dengue fever (n = 400).

		Malaria RDT				Dengue RDT			
Variables	**Categories**	**Positive**	**Negative**	**Statistics (Malaria)**	**OR (95% CI)**	**IgM Positive**	**Negative (IgG/IgM)**	**Statistics (Dengue)**	**OR (95% CI)**
Headache	Yes	125(43.0%)	166(57.0%)	χ^2 =61.877 p=<0.001	40.286(9.758-166.323)	8(2.7%)	117(40.2%)	χ^2 =0.827 p=0.661	0.668(0.621-0.714)
	No	2(1.8%)	107(98.2%)			4(3.7%)	48(44.0%)		
Vomiting	Yes	57(51.8%)	53(48.2%)	χ^2 =28.198 p=< 0.001	3.380(2.132-2.132)	6(5.5%)	46(41.8%)	χ^2 =3.308 p=0.191	0.180(0.142-0.218)
	No	70(24.1%)	220(75.9%)			6(2.1%)	119(41.0%)		
Nausea	Yes	78(29.7%)	185(70.3%)	χ^2 =1.551 p=0.213	0.757(0.489-1.174)	8(3.0%)	114(43.3%)	χ^2 =1.452 p=0.484	0.513(0.464-0.561)
	No	49(35.8%)	88(64.2%)			4(2.9%)	51(37.2%)		
Joint pain	Yes	71(32.4%)	148(67.6%)	χ^2 =0.100 p=0.751	1.071(0.701-1.63)	8(3.7%)	89(40.6%)	χ^2 =0.732 p=0.694	0.725(0.681-0.769)
	No	56(30.9%)	125(69.1%)			4(2.2%)	76(42.0%)		
Body ache	Yes	103(39.2%)	160(60.8%)	χ^2 =19.476 p=< 0.001	3.031(1.829-5.024)	6(2.3%)	112(42.6%)	χ^2 =1.706 p=0.426	0.435(0.386-0.484)
	No	24(17.5%)	113(82.5%)			6(4.4%)	53(38.7%)		
Abdominal pain	Yes	55(42.6%)	74(57.4%)	χ^2 =10.412 p=< 0.001	2.054(1.322-1.322)	3(2.3%)	51(39.5%)	χ^2 =0.619 p=0.734	0.753(0.71-0.795)
	No	72(26.6%)	199(73.4%)			9(3.3%)	114(42.1%)		

hi-squared values, degree of freedom and p-values for the statistical tests, indicating the significance of the associations.

3.6. Risk factors associated with Dengue infections

Open gutter, houses near bushes and storing water in an open containers can be a risk factors, although the statistical significance was low. Other preventive measures were not statistically significant risk factors too. This findings suggest that while certain preventive measures may play a role in Dengue infection, they are not definitive predictors of infection (Table 6).

Table 6 Risk factors associated with Dengue infections

		Dengue RDT			
Variables	**Categories**	**IgG Positive**	**IgM Positive**	**Negative (IgG/IgM)**	**Statistics**
Mean of preventing malaria	Insecticide spray	136	6	99	(χ^2)=4.511 p=0.608
	Mosquito repellant cream	32	3	18	
	Insecticide treated net	24	1	26	
	Local mosquito insecticides	31	2	22	
Where is domestic water stored	Inside open container	105	4	65	**(χ^2)**=8.147 p=0.228
	Overhead tanks	104	8	80	
	Kegs with cover	14	0	19	
	Others	0	0	1	
House near bush	Yes	76	5	59	**(χ^2)**=0.359 p=0.836
	No	147	7	106	
Open gutter	Yes	85	3	46	**(χ^2)**=4.863 p=0.088
	No	138	9	119	
Open water container	Yes	96	5	64	**(χ^2)**=0.712 p=0.701
	No	127	7	101	
Water around House	Yes	82	3	60	**(χ^2)**=0.684 p=0.710
	No	141	9	105	
Spray surrounding daily	Yes	19	1	16	**(χ^2)**=0.167 p=0.920
	No	204	11	149	
Clean surrounding regularly	Yes	180	11	141	**(χ^2)**=2.167 p=0.338
	No	43	1	24	
Travelled out of Ogbomoso	Yes	147	5	108	**(χ^2)**=2.97 p=0.227
	No	76	7	57	
House window nets	Yes	160	7	113	**(χ^2)**=1.283 p=0.527
	No	63	5	52	
Waste around the House	Yes	58	2	30	**(χ^2)**=3.573 p=0.168
	No	165	10	135	
Regular disposal of waste	Yes	176	10	140	**(χ^2)**=2.235 p=0.327
	No	47	2	25	

4. Discussion

Dengue is a major public health concern in tropical and subtropical regions, including Nigeria. The virus is primarily transmitted by Aedes mosquitoes, and its incidence has been increasing globally, posing significant challenges to healthcare systems.

The study found that 223/400 (55.8%) of the patients tested positive for IgG antibodies, indicating a history of exposure to the dengue virus, while only 12/400 (3.0%) tested positive for IgM antibodies, which are typically indicative of a recent infection. These findings suggest that dengue has been circulating in the population for a considerable time, leading to a significant proportion of individuals developing long-term immunity. The prevalence rates of IgG and IgM antibodies observed in this study are consistent with findings from other regions in Nigeria and across sub-Saharan Africa (12). Similarly, research from Cameroon reported IgG prevalence rates ranging from 50% to 70% among febrile individuals, further supporting the notion of widespread exposure to the virus in endemic areas (13). The high prevalence of IgG antibodies observed in this study may have an important implication for the herd immunity to dengue virus infection in Ogbomoso. "To develop herd immunity against a highly contagious disease, about 70% to 90% of a population needs to be immune. This is believed to be the threshold for herd immunity. However, depending on the severity of infection, the herd immunity threshold can be as low as 40%.''. The presence of a substantial proportion of IgG-positive individuals suggests that a significant segment of the population has developed immunity to dengue, which could potentially reduce the risk of large-scale outbreaks.

In this study, the prevalence of co-infections of dengue virus (DENV) and malaria parasites showed 4 (33.3%). These findings are consistent with study conducted elsewhere in sub-Saharan Africa, where high rates of co-morbidity have been reported, and dengue and malaria are co-occurring in these areas (14).

The study found no statistically significant associations between socio-demographic variables and dengue infection. These findings are similar to a study in Vietnam (15). Similarly, studies from Kenya also found no significant association between socio-demographic factors and dengue disease (16). The gender and age distribution of dengue cases in this study revealed that females in the 21-30 age group were more frequently affected by dengue, though these findings were not statistically significant. The higher incidence among females could be attributed to social and behavioral factors that increased their exposure to mosquito bites, such as household duties that involves spending more time outdoors or near potential mosquito breeding sites. The age distribution observed in this study, is consistent with patterns reported in other endemic regions (17;18). Though socio-economic factors were not significantly associated with dengue infection in this study, some other studies have shown that urbanization and inadequate infrastructure are significant risk factors for dengue, as they create environments conducive to mosquito proliferation (19). In this context, public health interventions aimed at improving living conditions, increasing mosquito control education, and increasing access to health services may be effective in reducing dengue fever.

In this study, the clinical features observed in people with dengue are common symptoms such as headache, vomiting, nausea, joint pain, body aches, and pain. The study found that headache 8 (2.7%), nausea 8 (3.0%)and Joint pain 8 (3.7%) were the most common symptoms among the people who tested positive for dengue, though there was no significant association between clinical symptoms and the presence of dengue in this study, other studies have found a significant association (20;18). The overlap in symptoms between dengue and malaria presents a significant challenge for healthcare providers, particularly in regions where both diseases are endemic like Ogbomoso. In this study, symptoms such as headache, nausea, and joint pain were common in both dengue and malaria patients, making it difficult to distinguish between the two diseases based on clinical presentation alone. This overlap may be problematic because misdiagnosis or delayed diagnosis can lead to inappropriate treatment, which may exacerbate the patient's condition or result in severe complications. This finding is consistent with a study conducted in Tanzania (19).

Proximity to bushes and open rivers were not associated with higher rates of dengue infection in this study. Although many participants reported the use of insecticides, the lack of a significant association with the reduction in dengue infection indicates that these measures alone may not be sufficient. This finding aligns with research from other endemic regions, which has shown that while insecticide use can reduce mosquito populations they are not definitive predictors of infection (21). Regular waste disposal and the elimination of stagnant water, which are key components of environmental management, were found to be associated with a lower risk of dengue infection. These practices help reduce mosquito breeding sites, thereby lowering the risk of mosquito-human contact. However, the study also highlighted the need for community-wide adherence to these practices, as individual efforts may not be effective if the broader environment remains conducive to mosquito breeding. The broader implications of these findings suggest that while individual preventive measures are important, they must be part of a comprehensive strategy that includes community engagement, public education, and government-led initiatives to improve environmental conditions and

reduce mosquito habitats. The findings of this study emphasized the need for a multifaceted approach to dengue prevention that integrates environmental management, social education, and vector control measures. Effective prevention of dengue fever requires a comprehensive strategy that addresses the complex interrelationships among factors that influence the disease. Environmental management is a cornerstone of dengue prevention, involving the removal of mosquito breeding sites through improved sanitation, proper waste disposal, and the management of water storage. These efforts must be supported by community education campaigns that raises awareness about the importance of these practices and encourage widespread participation. Vector control measures, such as the use of insecticides, larvicides, and insecticide-treated nets, are also critical components of a comprehensive prevention strategy. However, these measures must be implemented consistently and in combination with other interventions to be effective.

The RT-PCR analysis performed on serum samples from humans and mosquitoes were negative for infection with active dengue virus (DENV). These findings showed the absence of detectable viral RNA in the sample population during the time of testing, indicating that dengue virus transmission was not active during the study period The absence of active infections in this study contrasts with findings from study in Southeast Asia and Latin America (22). For surveillance programs in Ogbomoso and similar settings, these results suggested the importance of regular monitoring, particularly during the peak transmission seasons, to ensure the timely detection of outbreaks. However, negative RT-PCR results does not rule out the possibility of future outbreaks, especially in areas known to have dengue. Therefore, it is important to maintain a robust surveillance system that can detect early signs of increased transmission, such as an increase in dengue-like symptoms or an increase in cases of seropositive, even without severe disease. In addition, the introduction of vector surveillance, especially the monitoring of Aedes mosquito populations for the presence of dengue, can strengthen early warning systems and guide official interventions against the vector. Such a multifaceted approach is critical to reducing the impact of dengue and preventing major outbreaks.

5. Conclusion

Dengue fever remains a significant public health challenge, particularly in tropical and subtropical regions where it is endemic. This study highlights the importance of sero-molecular surveillance in understanding the epidemiology of Dengue infections among febrile patients and mosquito vectors in Ogbomoso, Nigeria. The findings indicated a notable prevalence of IgG antibodies, suggesting past exposure to the virus, while active infections were not detected through RT-PCR. The co-infection rates with malaria emphasized the necessity for integrated diagnostic approaches in managing febrile illnesses. Continued research and public health initiatives are essential to mitigate the impact of Dengue and enhance disease recognition and response strategies.

Compliance with ethical standards

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Disclosure of conflict of interest

The authors declared that no competing interests exist.

Statement of ethical approval

Ethical approval with number: NHREC/OYOSHRIEC/10/11/22 was obtained from the Ethical Review committee of Oyo State Ministry of Health, Secretariat, Ibadan, Oyo State, as part of the prerequisite before research of this nature is carried out on Human respondents. Informed consent was obtained from study participants.

Statement of informed consent

Written informed consent was obtained from the parents or guardian while assent was obtained from participants 10 years and above.

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References

[1] Bhatt, S., Gething, P. W. and Brady, O. J. (2013). The global distribution and burden of dengue. Nature. **496 (7446):** 504-507.

[2] World Health Organization, (2005). International Health Regulations. Second. WHO Report. Geneva: WHO Press; **2005:**43.

[3] Amarasinghe, A., Kuritsky, J. N., William Letson, G., and Margolis, H. S. (2011). Dengue virus infection in Africa. Emerging Infectious Diseases. **17(8):**1349– 1354.

[4] Lee, K. S., Thein, T. L., Tan, L. K., Gan, V. C., Yung, C. F., Wong, J. G. X., Lye, D. C., Ng, L. C. and Leo, Y. S. (2015). Dengue serotype-specific differences in clinical manifestation, laboratory parameters and risk of severe disease in adults, Singapore. *American Journal of Tropical Medical Hygene.***92(5):** 999-1005.

[5] Ng, V., Rees, E. E., Lindsay, L. R., Drebot, M. A., Brownstone, T., Sadeghieh, T. and Khan, S. U. (2019). Climate change and infectious diseases: the challenges: Could exotic mosquito-borne diseases emerge in Canada with climate change. *Canada Communicable Disease Report*. **45(4):** 98.

[6] Kazaura, M. (2020). Knowledge, attitude and practices about dengue fever among adults living in Pwani Region, Tanzania in 2019. *African Health Sciences*. **20(4):** 1601.

[7] Charan, J., and Biswas, T. (2013). How to Calculate Sample Size for Different Study Designs in Medical Research? *Indian Journal of Psychological Medicine*, **35(2):** 121-126.

[8] Fleetwood, D. (2018). Consecutive Sampling- Definition, Example, and Advantages. *Question Pro*. https://www.questionpro.com/blog/consecutive-sampling.

[9] Rueda, Leopoldo (2004). Pictorial keys for the identification of mosquitoes (Diptera: Culicidae) associated with dengue virus transmission. Zootaxa. **589:**1–60.

[10] Noedl, H., Wernsdorfer, W. H., Miller, R. S., and Wongsrichanalai, C. (2002). Histidine-rich protein II: a novel approach to malaria drug sensitivity testing. *Antimicrobial agents and chemotherapy*, **46(6):** 1658-1664.

[11] Innis, B. L., Nisalak, A., Nimmannitya, S., Kusalerdchariya, S., Chongswasdi, V., Suntayakorn, S., Puttisri, P. and Hoke, C. H. (1989). An enzyme-linked immunosorbent assay to characterize dengue infections where dengue and Japanese encephalitis co-circulate. *Am J Trop. Med. Hyg.***40(4):** 418-27.

[12] Fagbami, A. H., Onoja, A. B., Omilabu, S. A., Odaibo, G. N. and Olaleye, D. O. (2020). Dengue virus seroprevalence among febrile patients in Lagos, Nigeria. *Acta Tropica*, ***206*:** 105454**.**

[13] Simmons, C. P., Farrar, J. J. and Nguyen, V. C. (2019). Current concepts: Dengue. *New England Journal of Medicine*, **366(15):** 1423-1432.

[14] Chipwaza, B., Mugasa, J. P., Mayumana, I., Amuri, M., Makungu, C. and Gwakisa, P. S. (2014). Dengue and malaria co-infections among febrile patients seeking healthcare in Tanzania: A cross-sectional study. *BMC Infectious Diseases*, **14(1):** 1-8.

[15] Huy, N. T., Thao, N. T. T. and Watanabe, K. (2019). Epidemiology and clinical features of dengue infection in the Greater Mekong Subregion. *Tropical Medicine and Infectious Disease*, **4(3):** 110.

[16] Agha, S. B., Tchouassi, D. P., Turell, M. J., Bastos, A. D. and Sang, R. (2019). Entomological assessment of dengue virus transmission risk in three urban areas of Kenya. *PLoS neglected tropical diseases*, **13(8):** e0007686.

[17] Shepard, D. S., Undurraga, E. A., Halasa, Y. A. and Stanaway, J. D. (2018). The global economic burden of dengue: A systematic analysis. *The Lancet Infectious Diseases*. **16(8):** 935-941.

[18] Teixeira, M. G., Costa, M. D. C. N. and Barreto, M. L. (2019). Dengue: Twenty-five years since re-emergence in Brazil. *Journal of Health, Population, and Nutrition*, **37(1):** 11.

[19] Lai, S., Huang, Z., Zhou, H., Anders, K. L., Perkins, T. A., Yin, W. and Hay, S. I. (2018). The changing epidemiology of dengue in China, 1990–2014: A descriptive analysis of 25 years of nationwide surveillance data. *BMC Medicine*. **16(1):** 1-11.

[20] Yap, G., Li, C. and Muñoz-Jordán, J. L. (2018). Dengue virus pathogenesis: Implications for vaccine design. *Current Opinion in Immunology*, **53:** 19-25.

[21] Achee, N. L., Gould, F., Perkins, T. A., Reiner, R. C., Morrison, A. C., Ritchie, S. A. and Vasilakis, N. (2019). A critical assessment of vector control for dengue prevention. *PLoS Neglected Tropical Diseases*, **13(5):** e0007383.

[22] Katzelnick, L. C., Coello Escoto, A., Huang, A. T., Garcia-Carreras, B., Chowdhury, N., Maljkovic Berry, I. and Cummings, D. A. (2021). Antigenic evolution of dengue viruses over 20 years. *Science*. **374(6570):** 999-1004 .