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Dengue prevalence in Burkina Faso in 2024

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Abstract

Introduction: Dengue fever, a viral disease caused by arboviruses of the *Flaviviridae* family and transmitted primarily by *Aedes aegypti* mosquitoes, remains a major public health challenge worldwide. In Burkina Faso, dengue has been endemic since 2013, with recurrent outbreaks despite vector control efforts and the establishment of sentinel surveillance in 2017. In 2023 the most severely affected countries by a large-scale dengue outbreak on the African continent. The 2024 study aims to analyze this dynamic to strengthen the national health response.

Methodology: The retrospective study conducted in 2024 at the National Reference Laboratory for Viral Hemorrhagic Fever (LNR-FHV) analyzed 6,048 serum samples collected from suspected or probable dengue cases as part of national surveillance. Samples were transported under cold chain condition, and diagnostic methods varied according to the interval between symptom onset and sample collection. RT-PCR was used cases within 5 days, combined RT-PCR and ELISA for 5 to 7 days and ELISA alone for more than 7 days. RT-PCR positive sample were further serotyped. Sociodemographic data and ELISA/RT-PCR results were analyzed with R 4.4.1 at a 95% confidence interval. Descriptive and statistical analyses, including Chi-square, Welch t-test, Fisher's exact test, and logistic regressions, were performed to identify risk factors and describe monthly trends.

Results: The results revealed a predominance of female patients among suspected cases, but confirmed cases showed a slight male majority. Adults aged 25-64 years were the most affected group, representing 58.77% of confirmed infections. Temporal analysis indicated peaks in suspected cases in October and confirmed cases in November. The overall prevalence among suspected and probable cases was 9.29%. Three serotypes (DENV-1, DENV-2, DENV-3) co-circulated, with DENV-1 being predominant (58.96%).

Conclusions: These findings confirm active dengue virus circulation in Burkina Faso and underscore the urgent need to reinforce, surveillance, and response strategies. Strengthening laboratory capacity, vector control, and public awareness will be essential to mitigate future outbreaks and reduce the burden of this neglected tropical disease.

1. Introduction

Dengue is a viral disease caused by an arbovirus belonging to the *Flaviviridae* family and the Orthoflavivirus genus. It is transmitted to humans through the bite of Aedes mosquitoes, primarily *Aedes aegypti*, and to a lesser extent *Aedes albopictus* [1]. These same vectors can also transmit other viruses such as chikungunya, yellow fever, and Zika [2, 3]. Dengue is one of the most rapidly spreading diseases and remains a major public health concern despite ongoing vector control efforts [4]. It is currently classified as a "re-emerging" disease and is among the most prominent neglected tropical diseases [5]. Four distinct serotypes of the dengue virus (DENV1–4) co-circulate in endemic regions [6]. In addition to these four serotypes, a fifth sylvatic serotype (DENV-5) was isolated for the first time in 2013 from a mosquito [7].

Dengue is often asymptomatic, but some clinical presentations may progress to severe forms, including dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS), which can be fatal [8]. Immunity acquired following infection with one serotype provides lifelong protection against that specific serotype; however, there is no cross-immunity between different serotypes. Secondary infection with a heterologous DENV serotype tends to result in more severe disease than primary infection [9]. To date, there is no specific etiological treatment for dengue [4, 10].

In 2023, the World Health Organization (WHO) estimated approximately 6.5 million dengue cases across more than 80 countries, resulting in nearly 7,300 deaths. In Africa, the true incidence of the disease remains largely underestimated due to frequent misdiagnosis with malaria and the lack of official outbreak reporting to the WHO. Nevertheless, the dengue virus is the most widespread arbovirus on the African continent and accounts for the highest number of arboviral infections [11, 12].

Dengue is endemic in over 100 countries, including 34 in Africa [13]. Serotypes 1 and 2 of the dengue virus were first isolated in West Africa in 1964 in Nigeria [14]. Since then, several African countries have reported sporadic cases or outbreaks associated with the virus [15]. In 2023, dengue outbreaks were reported in 15 of the 47 African countries, including Burkina Faso, Benin, Cape Verde, Côte d'Ivoire, Ethiopia, Ghana, Guinea, Mali, Mauritius, Niger, Nigeria, São Tomé and Príncipe, Senegal, Chad, and Togo [16] .

In Burkina Faso, the first dengue cases were reported in 1925 [15]. Since then, positive cases have been recorded in 1980, 2000, and 2013, indicating intermittent circulation of the virus within the country [15, 16]. Since 2013, dengue has become endemic, marked by recurrent outbreaks that have led to intensified epidemiological surveillance [17]. The first major dengue epidemic was recorded in 2016, prompting the establishment of sentinel surveillance in 2017 [15, 18]. Seven sites were identified as endemic hotspots (sentinel sites) by the Ministry of Health in collaboration with the Centers for Disease Control and Prevention (CDC) Atlanta, for the surveillance of dengue and other arboviruses. These sites serve as reference points for the detection, confirmation, and monitoring of arboviral cases through the National Reference Laboratory for Viral Hemorrhagic Fevers (LNR-FHV) [19]. In addition to these sentinel sites, several other health facilities across the country send samples from suspected or probable dengue cases, other arboviral infections, and suspected hemorrhagic fever cases to the LNR-FHV for confirmation or diagnosis [20].

In 2023, Burkina Faso was among the most severely affected countries by a large-scale dengue outbreak on the African continent, resulting in numerous deaths [16]. The prevalence of the disease has significantly increased in recent years, with notable impacts on health, economic, and social levels.

Given this concerning trend, it is essential to have up-to-date data to better understand the scope of the phenomenon. The present study aims to assess the dengue epidemic situation in Burkina Faso in 2024, to provide a detailed overview and better understand the dynamics of the disease in the national context.

2. Methods

2.1. Study Design and Population

The study was conducted at the National Reference Laboratory for Viral Hemorrhagic Fevers (LNR-FHV) in Bobo-Dioulasso, Burkina Faso, using serum and plasma samples collected during dengue surveillance activities across sentinel sites, health districts, and healthcare facilities nationwide.

It was a prospective study covering the period from January 1 to December 31, 2024, and included all suspected or probable dengue cases submitted to the LNR-FHV for confirmation. Only samples accompanied by complete investigation forms were included; those lacking documentation were excluded. The samples transport followed triple packaging procedures via the national postal service, ensuring cold chain compliance.

definition of case [17]:

suspected case: Any person presenting with an acute febrile illness (generally fever > 39°C) lasting 2 to 7 days, associated with at least two of the following clinical criteria: severe headache, retro-orbital pain, myalgia or arthralgia, skin rash, hemorrhagic manifestations, or shock syndrome

Probable Case: A suspected case that additionally meets one of the following criteria: a positive Rapid Diagnostic Test (RDT) for dengue detecting NS1 antigen or IgM/IgG antibodies, or an epidemiological link (close contact or residence in the same locality within the previous 14 days) with a laboratory-confirmed case.

Confirmed Case

A suspected or probable case in which dengue virus infection has been formally validated by a reference laboratory test, including detection of viral genetic material by RT-PCR, detection of NS1 antigen by ELISA, isolation of the virus in cell culture, or a significant increase in antibody titers (seroconversion or a fourfold rise in IgG).

The minimum sample size was calculated using the following formula in Epi Info™ 7 User Guide – StatCalc (Population Survey/Descriptive Study) [18]:

$$n = [DEFF*Np(1-p)] / [(d^2/Z^2_{1-\alpha/2}*(N-1)) + p*(1-p)]$$

Where:

- *n* = minimum sample size required
- *N* = total population of Burkina Faso (used for finite population correction), estimated at 22,752,315
- *p* = expected frequency of the outcome in the population: 50% ± 5%
- *d* = margin of error: 5%
- *DEFF* = design effect (for cluster surveys): 1

- Z = Z-score corresponding to a 95% confidence level

Based on these parameters, the calculated minimum sample size was 384, which was then adjusted by 10%, resulting in a final minimum sample size of 423 suspected or probable chikungunya cases. A total of 6,048 samples were received and analyzed.

2.2. Biological Analyses

Samples from suspected or probable dengue cases received at the LNR-FHV were analyzed using serological (ELISA) and/or molecular (RT-PCR) tests, following the laboratory's diagnostic algorithm (Fig. 1). Samples that tested positive for dengue via molecular testing were further subjected to serotyping.

Figure 1: Algorithm for Dengue Diagnostics at LNR-FHV (Source: LNR-FHV Document, 2024)

Diagnostic algorithm for dengue according to the interval between symptom onset and sample collection. Samples collected within 5 days are tested by RT-PCR; between 5 and 7 days, RT-PCR is complemented by ELISA IgM; after 7 days, ELISA IgM alone is performed. Positive results confirm the case and allow serotyping, while negative results indicate non-confirmation.

2.2.1. Serological Testing (ELISA)

The detection of dengue-specific IgM antibodies was performed using an indirect ELISA technique on a 96-well solid-phase plate, following the CDC protocol for dengue IgM detection over a 48-hour period. The ELISA was performed as described by the CDC [21].

On Day 1, 75 µL of coating solution was dispensed into each well of the plate. The plate was sealed with parafilm and incubated overnight at 4°C. This sensitization step allowed anti-human IgM antibodies to bind to the bottom of the wells.

On Day 2, the plate layout sheet was completed prior to any manipulation. The sensitized plate was washed four times with wash buffer and gently blotted on absorbent paper. Then, 200 µL of blocking solution was added to each well, the plate was sealed and incubated for 1 hour at 37°C to block residual binding sites. After incubation, the plate was washed again four times. Subsequently, 75 µL of diluted samples and controls were added to the wells according to the plate layout, followed by incubation for 1 hour at 37°C. After washing, 75 µL of diluted antigen was added and incubated for 1 hour at 37°C. The plate was washed again, and 75 µL of diluted conjugate (a monoclonal antibody linked to an enzyme) was added and incubated for 1 hour at 37°C. After incubation, the plate was washed to remove unbound conjugate. Then, 100 µL of tetramethylbenzidine (TMB) substrate was added to each well, the plate was covered with aluminum foil and incubated for 10 minutes in the dark. A stop solution (100 µL) was added to each well after incubation, and optical densities were read using a spectrophotometer at 450 nm and 620 nm.

For the assay to be considered valid, the ratio between the mean optical density of the positive control at the specific antigen (P) and the mean optical density of the negative control at the same antigen (N) must be ≥ 2, i.e., P/N ≥ 2. A sample was classified as positive if the following two conditions were met. First, the ratio between the mean optical density of the sample at the specific antigen (P_1) and the mean optical density of the negative control at the specific antigen (N) was ≥ 2 ($P_1/N \geq 2$). Second, the mean optical density of the sample at the specific antigen (P_1) was greater than or equal to twice the mean optical density of the same sample at the normal antigen (N_1), i.e., $P_1 \geq 2\ N_1$. Samples fulfilling both criteria were considered positive.

2.2.2. Molecular testing (RT-PCR)

RNA extraction

Viral RNA was extracted from 140 µL of human serum samples or plasma using the QIAmp®viral RNA minit kits 250 (Qiagen, Hilden, Germany) according to the manufacturer's instructions and stored at -80 ◦C until further processing.

Real-time RT-PCR

The molecular test was performed using the BIO-RAD ZDC RT-PCR Assay multiplex kit, Catalog #12003818, Bio-Rad Laboratories, Hercules, CA, USA, which allows simultaneous detection of the RNA of three arboviruses (chikungunya, dengue, and Zika). Briefly, the RT-PCR reaction was performed in a final volume of 25 µL. The mixture contained PCR-grade water 4.9 µL, 12.5 µL of Taq Polymerase master mix (corresponding to a final concentration of 1×), 2 µL of ZDC Mix (final concentration according to manufacturer’s instructions), 0.6 µL of iScript Reverse Transcriptase (final concentration as recommended), and 5 µL of RNA extract. The amplification was done with the Magnetic Induction Cycler (MIC) PCR Bio Molecular Systems (bms, Unit 5/3 Northward Street, Springfield, Queensland, Australia). The cycling conditions consisted of a reverse transcription step at 50°C for 15 min, denaturation at 94°C for 2 min, followed by 45 cycles of 94°C for 15 s, 55°C for 40 s and 68°C for 30 s. The assay was considered valid when the negative control showed no amplification and the positive control displayed a cycle threshold (Ct) value was equal/ or less than 37 cycles with an exponential amplification curve. Samples were classified as positive if their Ct values were ≤ 37 with an exponential amplification curve.

Samples that tested positive for dengue using the BIO-RAD ZDC RT-PCR Assay multiplex kit, were subsequently subjected to serotyping using either the Mic or QuantStudio 5 (Thermo fisher, applied Biosystems, A28139) thermocycler. For this purpose, a reaction mix was prepared using the CDC DENV-1-4 Real-Time RT-PCR Assay kit (Catalog No. KK0128, 1324 Canada Street, San Juan, PR 00920), and amplification was carried out using the RNA extracts from dengue-positive samples according to the manufacturer’s instruction.

2.3. Statistical Analysis

Sociodemographic data were extracted from notification forms, while ELISA and real-time RT-PCR test results were retrieved from the Microsoft Excel 2016. Statistical analysis was performed using R version 4.4.1 software. Dengue prevalence was estimated by dividing the number of confirmed cases by the total number of suspected or probable cases tested, with 95% confidence intervals calculated. Descriptive analyses were conducted to characterize the study population based on variables such as age, sex, diagnostic results, monthly trends, and risk factors using Pearson's Chi-square test, were compared with a significance threshold of 0.05. A univariate logistic regression was used to identify potential risk factors, followed by a multivariate analysis including variables with a p-value ≤ 0.20. Pearson's Chi-squared test was applied for categorical variables, Welch Two Sample t-test was used to compare means between two independent groups, and Fisher's exact test was employed when sample sizes were small. Monthly case trends were also analyzed to identify periods of high incidence, and results were presented in the form of tables, graphs, and trend curves.

3. Results

3.1. Sociodemographic characteristics according to dengue status infection

A total of 6,048 samples from suspected and probable dengue patients were analyzed, with a female predominance, representing 54.27% of the cases. Among these samples, 562 were confirmed positive, with 95.37% confirmed by real-time RT-PCR and 4.63% by ELISA, showing a statistically significance between male and female patients (p = 0.021). Among the positive cases, males were slightly more represented at 50.35% compared to females.

The average age in the study was 29.8 ± 19.3 years, with extremes ranging from 0 to 114 years. The median age was 28 years, meaning that half of the patients were younger than 28 years. Quantile analysis showed that 10% of patients were ≤ 5 years, 23% were ≤ 14 years, and 58% were ≤ 32 years. The age group 25–64 years was the most represented in our study, accounting for 50.93% of participants. This group also constituted the population most affected by dengue, with 58.77% of all confirmed dengue cases. It was followed by the 15–24-year age group, which represented 26.87% of confirmed cases. Additionally, 1.22% of patients (74 cases) had an unknown age; among them, 8 tested positive for dengue, representing 1.49% of positive cases. Statistical analysis showed no significant difference between groups (p = 0.5) (Table 1).

Table 1
Distribution of dengue cases by age and sex

characteristics	Number of Suspected or probable dengue Cases N = 6048	Frequency of Suspected or probable dengue Cases (%)	Number of Confirmed dengue Cases N = 562	Frequency of Confirmed dengue Cases (%)	positivity rate	p-value
Age Range						
[0–14[	1427	23.59	55	9.79	3.85	
[15–24[	1111	18.37	144	25.62	12.96	
[25–64[	3080	50.93	315	56.05	10.23	0.5
≥ 65	356	5.89	14	2.49	3.93	
Unk	74	1,22	8	1,41	10.81	
SEX	Suspected or probable cases N = 6048	Negative cases N = 5486	Positive cases N = 562		Positivity rate	
F	3282 (54.27%)	3003 (54.74%)	279 (49.65%)		8.50	0.021
M	2766 (45.73%)	2483 (45.26%)	283 (50.35%)		10.23	

Table 1. Distribution of suspected/probable and confirmed dengue cases by age and sex. Absolute and relative frequencies are presented for each category, along with positivity rates and p-values associated with statistical comparisons. Distribution of dengue cases by age groups according to Statistics Canada classification [22]: Children [0–14[, Adolescents [15–24[, Adults [25–64[, and Elderly ≥ 65

N = Number of samples;

Unk= Unknown;

F= Female;

M= Male.

3.2. Distribution of Dengue Cases by Region

In 2024, the spatial distribution of dengue cases in Burkina Faso showed a high rate of suspected cases in the regions of Guiriko and Kadiogo, with respective frequencies of 23.99% and 15.76%. Conversely,

regions such as Liptako, Soum, Tapoa, and Sourou did not submit any samples to the National Reference Laboratory for Viral Hemorrhagic Fevers (NRL-VHF). Confirmed cases were predominantly reported from Guiriko (17.97%), followed by Nando (15.84%). These findings are summarized in Table 2.

Table 2
Distribution of Dengue Cases by Region

Region of Burkina Faso	Health Facility	Suspected and Probable Cases	Frequency of Suspected and Probable Dengue Cases (%)	Confirmed Cases	Frequency of Confirmed Dengue Cases (%)	Pvalue
Bankui	Dédougou	354	5.85	40	7.12	0.001
Djoro	Gaoua, Batié, Kampti, Dano	174	2.88	68	12.10	0.001
Goulmou	Fada, Manni	4	0.07	1	0.18	0.001
Guiriko	Dandé, Do, Chuss, Houndé, Lena, Dafra, Dispensaire Muraz, Mangodara, Orodara, N'dorola	1451	23.99	101	17.97	0.001
Kadiogo	Bogodogo, Marcoussi, Tengandogo, Kossodo, nongre-massom, CH-YO	953	15.76	45	8.01	0.001
Kuilsé	Kaya	120	1.98	0	0.00	-
Liptako	Dori	0	0.00	0	0.00	-
Nando	Koudougou	486	8.04	89	15.84	0.001
Nakambé	Tenkodogo, Pouytenga	771	12.75	39	6.94	0.001
Nazinon	Manga, Kombissiri	15	0.25	7	1.24	0.001
Oubri	Ziniaré, Boussé, Zorgho	838	13.86	31	5.52	0.001
Sirba	Bogandé	5	0.08	0	0.00	0.001
Soum	Djibo	0	0.00	0	0.00	0.001
Tannounyan	Banfora, sindou	788	13.03	84	14.95	0.001

Region of Burkina Faso	Health Facility	Suspected and Probable Cases	Frequency of Suspected and Probable Dengue Cases (%)	Confirmed Cases	Frequency of Confirmed Dengue Cases (%)	Pvalue
Tapoa	Diapaga	0	0.00	0	0.00	-
Sourou	Tougan	0	0.00	0	0.00	-
Yaadga	Ouahigouya	89	1.47	31	5.52	0.001

Table 2. Distribution of suspected/probable and confirmed dengue cases by health regions and health facilities in Burkina Faso. Absolute and relative frequencies are presented for each region, together with positivity rates and p-values from statistical comparisons.

3.3. Monthly and Seasonal Distribution of Dengue Cases

Figure 2 present the monthly and seasonal dynamics of dengue cases recorded during the study period. A progressive increase in the number of suspected cases was observed starting in August, peaking sharply in October. In contrast, the number of confirmed cases reached its maximum in November, indicating a lag between clinical suspected cases and confirmed cases.

Figure 2: Monthly and Seasonal Distribution of Dengue Cases in Burkina Faso in 2024.

Monthly trends of suspected and confirmed dengue cases in Burkina Faso, 2024. The blue line represents suspected/probable cases, while the orange line shows confirmed cases. A sharp increase is observed from July, with suspected cases peaking in October and confirmed cases peaking in November, followed by a decline in December.

3.4. Dengue Prevalence

In this study, a total of 6,048 suspected and probable cases were analyzed. In total, 96.25% of samples were tested by real-time RT-PCR, of which 536 were positive. The remaining 3.75% were examined using the ELISA, identifying 26 positive cases. In total, 562 dengue cases were confirmed, corresponding to an overall prevalence among suspected and probable cases of 9.29% (Table 3).

Table 3
Dengue Prevalence among suspected and probable cases

Results	RT-PCR	ELISA	Overall
	N = 5821 (96.25%)	N = 227 (3.75%)	N = 6048
Negative	5285 (96.34%)	201 (3.66%)	5486
Positive	536 (95.37%)	26 (4.63%)	562
Prevalence	9.21	11.45	9.29

Table 3. Results of dengue diagnostic testing by RT-PCR and ELISA. Absolute and relative frequencies of negative and positive cases are presented, together with prevalence estimates for each method and the overall prevalence.

3.5. Serotyping

Among the samples received at the LNR-FHV in 2024, three serotypes were found to co-circulate: DENV-1, DENV-2, and DENV-3, with serotype 1 (DENV-1) predominating at 58.96%. Furthermore, cases of co-infection between serotypes were observed, although rare. Two combinations were identified: DENV-1 + DENV-2 and DENV-1 + DENV-3, each accounting for 0.56% of cases, as shown in Table 4.

Table 4
Serotyping of Dengue-positive samples

Dengue Type	Positive Cases	Frequency (%)
DENV1	316	58.96
DENV2	123	22.95
DENV3	84	15.67
DENV1 + DENV2	3	0.56
DENV1 + DENV3	3	0.56
Unk	7	1.30

Table 4. Distribution of confirmed dengue cases by viral serotypes (DENV-1, DENV-2, DENV-3), including co-infections and untyped cases. Absolute and relative frequencies are presented for each serotypes.

4. Discussion

During the study, a total of 6,048 samples were analyzed. Of these, 5,821 samples were tested by real-time RT-PCR, with 536 positives for dengue viral RNA, corresponding to a prevalence of 9.21%. Regarding ELISA results, 227 samples were tested, of which 26 were positive for dengue IgM, corresponding to a prevalence of 11.45%. The detection of IgM indicates a recent infection, likely explained by the timely testing of patients. These findings highlight the effectiveness of the diagnostic algorithm used at the

LNR-FHV, ensuring that positive cases are not missed, particularly those that real-time RT-PCR might fail to detect. Detection of viral RNA reflects an early infection during the viremic phase. These positive results confirm the circulation of the dengue virus in the study population. According to Muller et al. (2017), RT-PCR confirmation is generally associated with a recent infection within the first seven days after symptom onset. The findings of this study suggest that most confirmed cases were in the early phase, indicating that patients sought care promptly after symptom onset. This trend may be linked to greater public awareness or fear of complications associated with delayed treatment. It also reflects the efficiency of the diagnostic algorithm implemented at the LNR-FHV to identify suspected dengue cases. However, our results remain lower than those reported by Lim et al. (2019), who observed a positivity rate of 72% by RT-PCR [13].

However, the samples from suspected and probable dengue patients were analyzed at the LNR-FHV, showing a female predominance of 54.27% and a male-to-female sex ratio of 0.84. This result may be explained by the higher proportion of females in the population of Burkina Faso (51.61%), according to the National Institute of Statistics and Demography (2022) [23]. In addition, women tend to visit healthcare facilities more frequently than men, who generally seek care only in cases of emergency. Although our results indicate a female predominance, they remain lower than those reported by Mberkadji Dingamwal Emmanuel (2022), who recorded 69.1% females in his study on dengue in community settings in Bamako, focusing on epidemiological, clinical, diagnostic, and evolutionary aspects [9]. Conversely, studies conducted by Boubacar Sidiki Traoré and Sondo et al. revealed a male predominance of 55.8% and 57.5%, respectively [24, 25].

A total of 562 samples tested positive by real-time RT-PCR and IgM ELISA, representing 95.37% and 4.63%, respectively. The study showed a slight similarity in RNA-positive cases between males (50.35%) and females (49.65%), with a slight increase in IgM-positive cases among females compared to males (51.52% vs. 48.48%). Statistical analysis revealed a p-value of 0.021, indicating that the observed difference between sex and disease occurrence was statistically significant. Real-time RT-PCR results indicate early infection, distributed almost equally between sexes. However, the slight female predominance in IgM cases may suggest that women seek care at a slightly later stage, when the immune response has already begun.

The mean age of the study population was 29.7 ± 19.13 years, with the 25–64 age group being the most represented, corresponding to adults according to Statistics Canada. This can be explained by the generally active and mobile lifestyle of adults, which increases their exposure to daytime mosquito vectors, particularly due to frequent movement to areas with high vector density and professional activities. In comparison, Ouattara et al., in their study reported a slightly lower mean age of 26.82 ± 17.81 years [26]. In contrast, Ilboudo et al., in their study reported a mean age of 30.57 ± 12.54 years [27]. The most affected age group was 25–64 years, corresponding to adults, with a p-value of 0.5. This age group is often the most involved in economic, agricultural, or commercial activities, sometimes in areas with high vector density or low coverage of preventive measures (e.g., bed nets, spraying). Their exposure may also be increased by less attention to personal protection compared to children or the

elderly, who often benefit from closer family supervision. Adults may also be more likely to seek care quickly when symptoms appear, particularly to maintain their ability to work, which explains their apparent overrepresentation in the data. Unlike children and the elderly, adults are less confined to the home and less supervised in applying protective measures (bed nets, repellents, protective clothing). This could explain their more frequent exposure, even if it is not statistically significant in this study. Our findings are consistent with those of Ouattara et al., who reported in their study that the 16–30 age group was the most affected, with a p-value of 0.351.

As Burkina Faso is an endemic country for dengue, the samples came from various regions and healthcare facilities across the country for confirmation, with a predominance in the Guiriko region (23.99%), which includes several healthcare facilities, followed by the Kadiogo region (15.76%). In contrast, no samples were sent from regions such as Liptako, Soum, Tapoa, and Sourou for confirmation. According to Africa CDC data (2024), Burkina Faso recorded a total of 176,481 suspected dengue cases nationwide, with the Kadiogo region alone accounting for 51% of these cases, indicating a strong predominance of dengue. This high number of cases in Kadiogo and Guiriko can be explained by the fact that these regions were the main epicenters of the 2023 dengue outbreak, leading to enhanced surveillance in these areas. Furthermore, these two regions are characterized by high population density, which favors hygiene issues such as the presence of breeding sites conducive to the proliferation of dengue vector mosquitoes. Finally, the absence of samples from some healthcare facilities in Liptako, Soum, Tapoa, and Sourou may be due to persistent security constraints in these areas since 2017, hindering effective national epidemiological surveillance. The distribution of confirmed results by region showed more positive cases in the Guiriko and Nando regions, with respective frequencies of 17.97% and 15.84%. However, all healthcare facilities that sent samples recorded at least one positive case, either RNA or IgM, except in the Sirba region (low sample submission rate). Our results suggest high dengue cases in certain healthcare facilities, particularly in the Guiriko, Nando, and Djoro regions. Indeed, Burkina Faso has been endemic for dengue virus since 2013, which explains the positivity rates in different regions [31].

Regarding the monthly distribution of suspected dengue cases, September and October were the most represented months. The high proportion of samples observed during these periods may be explained by an increase in suspected dengue cases, likely linked to the climatic conditions of September and October. These months, corresponding to the rainy season and its end in Burkina Faso, create an environment favorable to the proliferation of dengue vectors and other disease vectors such as malaria [28]. Humidity, stagnant water, and increased exposure to mosquito bites promote vector proliferation, resulting in high vector density [29]. Moreover, the similarity of symptoms between dengue and other diseases such as malaria makes clinical diagnosis difficult, which may lead to an increase in the number of suspected and probable cases reported [30]. Our findings are consistent with those of Seogo et al., who reported a peak during October and November in their study [15]. A peak in confirmed dengue cases was observed in November (32.09%), followed by October (26.12%). Such a trend was described in studies by Runge Ranzinger et al. (2014) on dengue surveillance [32]. Our results can be explained by the fact that these months correspond to the rainy season and its end in Burkina Faso, where climatic

conditions such as humidity and stagnant water, combined with increased exposure to mosquito bites during these periods, favor the breeding of Aedes aegypti and Aedes albopictus, the main dengue vectors.

The dengue overall prevalence among suspected or probable cases observed in our study was 9.29%. According to Africa CDC, dengue prevalence in 2023 was 46.53%, and in 2024 it was 17.18%. Our results confirm the circulation of dengue in Burkina Faso in 2024. These findings suggest that control measures were implemented during the 2023 outbreak, which explains the decline in prevalence in 2024.

Three serotypes co-circulated (DENV-1, DENV-2, and DENV-3) during the study period, with a predominance of serotype 1, and co-infections of serotypes 1–3 and 1–2. Since the establishment of the dengue sentinel surveillance system in Burkina Faso in 2017, three serotypes have co-circulated, with one serotype predominating.

5. Study Limitations

The main challenge of this study was the incomplete filling of investigation forms (e.g., age, disease onset date, sample collection date), which led to a significant loss of key information. These gaps prevented the selection of appropriate diagnostic techniques for certain samples according to the laboratory's algorithm. The lack of data also limited the inclusion of certain variables in statistical analyses, thereby restricting the precise characterization of patient profiles.

6. Conclusion

The study on dengue prevalence in 2024 conducted at the LNR-FHV falls within the framework of surveillance activities in Burkina Faso. A total of 6,048 samples were analyzed using real-time RT-PCR and/or ELISA techniques. The results showed a male predominance among confirmed cases (50.35%). The average age was 29.7 years, with most cases occurring in the 25–64 age group. The Guiriko region recorded the highest number of confirmed dengue cases. Three serotypes co-circulated during the study period. The distribution of confirmed cases by sex and age, as well as the infection peak observed in October, highlight recurrent epidemiological trends. The overall dengue prevalence was 9.29%.

These findings confirm the active and persistent circulation of the dengue virus and should be considered in response strategies. The sharp increase in prevalence in 2024 underscores the limitations of current measures and the urgent need to strengthen detection, prevention, and rapid response capacities.

Given the growing endemicity of dengue and the threat posed by other emerging arboviruses, it is imperative to consolidate multisectoral efforts, intensify community awareness, and improve vector management to sustainably contain the spread of the disease.

Abbreviations

CDC
Centers for Disease Control and Prevention
CERBA
Centre de Recherche Biomoléculaire Pietro Annigoni
DEN
Dengue
DENV
Dengue viirus
DHF
Dengue Hemorrhagic Fever
DPSP
Direction de la Protection de la Santé de la Population
DSS
Dengue Shock Syndrome
Ct
Cycle threshold
ELISA
Enzyme-Linked Immunosorbent Assay
GIZ
Deutsche Gesellschaft für Internationale Zusammenarbeit
IgG
Immunoglobulin G
IgM
Immunoglobulin M
IMB
Institut für Mikrobiologie der Bundeswerh
IRSS
Institut de Recherche en Sciences de la Santé
LNR-FHV
Laboratoire National de Référence des Fièvres Hémorragiques Virales
NS1
Nonstructural protein 1
MIC
Magnetic Induction Cycler
PAHO
Pan American Health Organization
PCR
Polymerase Chain Reaction
RDT
Rapid Diagnostic Test

RNA
Ribonucleic Acid
RT-PCR
Reverse Transcription Polymerase Chain Reaction
TMB
Tetramethylbenzidine
WAHO
West African Health Organization
WHO
World Health Organization
ZDC
Zika Dengue Chikungunya

Declarations

Ethical approval and consent to participate

This study utilized routine, de-identified public health surveillance data collected under the SIMR guidelines, the need for individual informed consent was waived by the ethical committees of the Health Science Research, Burkina Faso No 2024-042/MSHP/MESRI/CERS. All patient data were fully anonymized prior to analysis, and strict confidentiality was maintained throughout the study to ensure the protection of personal information.

Consent for publication

Not applicable

Availability Data and materials

The data are included in the manuscript, and the database can be provided upon request.

Competing interest

The authors declare that there is no conflict of interest**.**

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Clinical trial number

Not applicable

Declaration regarding the use of Artificial Intelligence (AI)

Artificial Intelligence tools (Copilot AI) were employed during the preparation of this manuscript to assist in reducing word count and reformulating certain sentences. The authors confirm that all scientific content, interpretations, and conclusions remain their own responsibility**.**

References

1. Lwande OW, Obanda V, Lindström A, Ahlm C, Evander M, Näslund J, Bucht G. Globe-Trotting *Aedes aegypti* and *Aedes albopictus* : Risk Factors for Arbovirus Pandemics. Vector-Borne Zoonotic Dis. 2020; doi:10.1089/vbz.2019.2486.
2. Adam A, Jassoy C. Epidemiology and Laboratory Diagnostics of Dengue, Yellow Fever, Zika, and Chikungunya Virus Infections in Africa. Pathogens. 2021; doi:10.3390/pathogens10101324.
3. Sow A. Emergences virales en Afrique de l'ouest, dynamique et modélisation, l ' exemple des arboviroses émergentes et ré-émergentes dans l ' écosystème de Kédougou , Sénégal.Thèse de doctorat à l'université de Bordeaux. https://tel.archives-ouvertes.fr/tel-01782408/document.
4. World Health Organization : Dengue and severe dengue – Fact sheet. https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue (2024). Consulted on January 13, 2026.
5. Aubry P, Gaüzère B-A. Maladies tropicales négligées. Médecine Trop des pays l'océan Indien. 2015;2012:1–4.
6. Prommool T, Sethanant P, Phaenthaisong N, Tangthawornchaikul N, Songjaeng A, Avirutnan P, Mairiang D, Luangaram P, Scrisawat C, Kasinrerk W, Vasanawathana S, Sriruksa K, Limpitikul W, Malasit P, Puttikhunt C. High performance dengue virus antigen-based serotyping-NS1-ELISA (plus): A simple alternative approach to identify dengue virus serotypes in acute dengue specimens. Forshey BM, editor. PLoS Negl Trop Dis. 2021; doi:10.1371/journal.pntd.0009065.
7. Mustafa MS, Rasotgi V, Jain S, Gupta V. Discovery of fifth serotype of dengue virus (denv-5): A new public health dilemma in dengue control. Med J Armed Forces India. 2015; doi.org/10.1016/j.mjafi.2014.09.011.

8. Liang G, Gao X, Gould EA. Factors responsible for the emergence of arboviruses; strategies, challenges and limitations for their control. Emerg Microbes Infect. 2015; doi:10.1038/emi.2015.18.
9. Emmanuel. La dengue en milieu communautaire de Bamako: aspects épidémio-cliniques, diagnostiques et évolutifs. Thèse de doctorat à universite des Sciences, des Techniques et des Technologies de Bamako; 2022.
10. Brézillon-Dubus L, Dupuis B, Failloux AB. Traitements et vaccins contre la dengue. médecine/sciences. 2025; doi:10.1051/medsci/2025025.
11. Brathwaite Dick O, San Martín JL, Montoya RH, Del Diego J, Zambrano B, Dayan GH. The History of Dengue Outbreaks in the Americas. Am Soc Trop Med Hyg. 2012; doi:10.4269/ajtmh.2012.11-0770.
12. San Martín JL, Brathwaite O, Zambrano B, Solórzano JO, Bouckenooghe A, Dayan GH, Guzman MG. The Epidemiology of Dengue in the Americas Over the Last Three Decades: A Worrisome Reality. Am Soc Trop Med Hyg. 2010; doi:10.4269/ajtmh.2010.09-0346.
13. Lim JK, Seydou Y, Carabali M, Barro A, Dahourou DL, Lee KS, Nikiema T, Namkung S, Lee J-S, Shin MY, Bonnet E, Kagone T, Losseni K, Edwards T, Somé P-A, Yang JS, Alexander N, Yoon I-K. Clinical and epidemiologic characteristics associated with dengue during and outside the 2016 outbreak identified in health facility-based surveillance in Ouagadougou, Burkina Faso. PLoS Negl Trop Dis. 2019; doi.org/10.1371/journal.pntd.0007882.
14. Onoja BA, Maiga M, Adesola RO, Adamu AM, Adegboye OA. Changing Ecotypes of Dengue Virus 2 Serotype in Nigeria and the Emergence of Cosmopolitan and Asian I Lineages, 1966–2019. Vaccines. 2023; doi:10.3390/vaccines11030547.
15. Seogo PH, Bicaba BW, Yameogo I, Moussa G, Charlemangne KJ, Ouadraogo S, Sawadogo B, Yelbeogo D, Svadogo Yacouba, Sow H, Ouedraogo T, Nitiema A, Koussoubé D, Bationo T, Sawadogo M, Medah I, Saka B, Tarnagda Z. Magnitude of dengue fever in the city of Ouagadougou, Burkina-Faso, 2016. J Interv Epidemiol Public Health. 2021; doi:10.37432/jieph.supp.2021.4.3.03.1.
16. World Health Organization : Epidemic Bulletin, Dengue — Global Situation. https://www.who.int/fr/emergencies/disease-outbreak-news/item/2023 (2023). Consulted on January 18, 2026.
17. Tinto B, Kania D, Kagone TS, Dicko A, Traore I, de Rekeneire N, Bicaba BW, Hien H, Perre BW, Simonin Y, Salinas S. Dengue virus circulation in West Africa: An emerging public health. médecine/sciences. 2022; doi:10.1051/medsci/2022007.
18. Tinto B, Kaboré DPA, Kania D, Kagoné TS, Kiba-Koumaré A, Pinceloup L, Thaurignac G, Perre PV, Dabire RK, Baldet T, Guitierrez S, Gil Patricia, Ayouba Ahidjo. Serological Evidence of Zika Virus Circulation in Burkina Faso. Pathogens. 2022; doi:10.3390/pathogens11070741.
19. Ouattara CA, Traore S, Traore TI, Sangare I, Meda CZ,Savadogo LG. Tendances épidémiologiques et stratégies de lutte contre la dengue au Burkina Faso de 2013 à 2020: une revue systématique. Sci Tech. 2022;45:137–51.
20. Tinto B. Le risque arboviral au Burkina Faso: caractérisation et surveillance. Thèse de doctorat à l'université de Montpellier; 2023. ⟨NNT : 2022UMONT045⟩.

21. Centers for Disease Control and Prevention. Test serologique pour le virus de la dengue. Centre National des maladies infectieuses émergentes et zoonotiques. https://www.cdc.gov/dengue/hcp/diagnosis-testing/serologic-tests-for-dengue-virus.html (2025). Consulté le 18 Janvier 2026
22. Statistique Canada. Categories d'âge - groupes établis selon le cycle de vie. https://www.statcan.gc.ca/fr/concepts/definitions/age2 (2024).Consulté le 10 Février 2026
23. Institut National de la Statistique et de la Démographie du Burkina Faso. Tableau de bord démographique 2022. https://www.insd.bf/sites/default/files/2024-02/TBD%202022_VF_2023 (2023) .Consulté le 29 Décembre 2025
24. Traore BS. Surveillance Epidemiologique de la Dengue au centre d' Infectiologie Charles Merieux de janvier à décembre 2019. Thèse de doctorat à l'universite des Sciences, des Techniques des Technologies de Bamako; 2021.
25. Sondo KA, Gnamou A, Diallo I, Ka D, Zoungrana J, Diendéré EA, Fortes L, Poda A, Ly D, Ouedraogo AG, Ouedraogo LW, Nikiema V, Niliema C, Kagone WCJ, Zida A, Sawadogo G, Koussoube D, Yameogo I, Sangare L, Ouedraogo M, Ki-Zerbo GA, Ehui E, Ndour CT, Ouedraogo M, Drabo YJ. Descriptive study of complications of dengue during the 2016 outbreak in Ouagadougou, Burkina Faso. Pan African Med J One Heal. 2022;7.
26. Ouattara AK, Toyin Bello SO, Ouédraogo A, Traoré L, Djigma FW, Simporé J. Predominance of DENV-3 among patients in Ouagadougou, Burkina Faso. J Vector Borne Dis. 2025; doi:10.4103/JVBD.JVBD_68_24.
27. Ouédraogo JCRP, Ilboudo S, Compaoré TR, Bado P, Nitiéma M, Ouédraogo WT, Ouedraogo S, Zeba M, Tougma A, Ouedraogo GG, Ouedroago N, Ouedraogo S, Savadogo LGB. Determinants and prevalence of symptomatic dengue fever among adults in the Central Region of Burkina Faso: a hospital-based cross-sectional study. BMC Infect Dis. 2024; doi:10.1186/s12879-023-08932-3.
28. Belemviré M. Dengue au Burkina Faso : Clarification sur le traitement et les soins. https://www.bulletinsante.net/dengue-au-burkina-faso-clarification-sur-le-traitement-et-les-soins/ (2023). Consulté le 18 Janvier 2026.
29. Herath JMMK, Abeyasundara HTK, De Silva WAPP, Weeraratne TC, Karunaratne SHPP. Weather-Based Prediction Models for the Prevalence of Dengue Vectors Aedes aegypti and Ae. albopictus. Genet Res (Camb). 2022; doi.org/10.1155/2022/4494660.
30. Gainor EM, Harris E, LaBeaud AD. Uncovering the Burden of Dengue in Africa: Considerations on Magnitude, Misdiagnosis, and Ancestry. Viruses. 2022; doi:10.3390/v14020233.
31. Manigart O, Ouedraogo I, Ouedraogo HS, Sow A, Lokossou VK. Dengue epidemic in Burkina Faso: how can the response improve? The Lancet. 2024; doi:10.1016/S0140-6736(23)02803-9.
32. Runge-Ranzinger S, McCall PJ, Kroeger A, Horstick O. Dengue disease surveillance an updated systematic literature review. Tropical Med Int Health - 2014; doi.org/10.1111/tmi.12333.

Figures

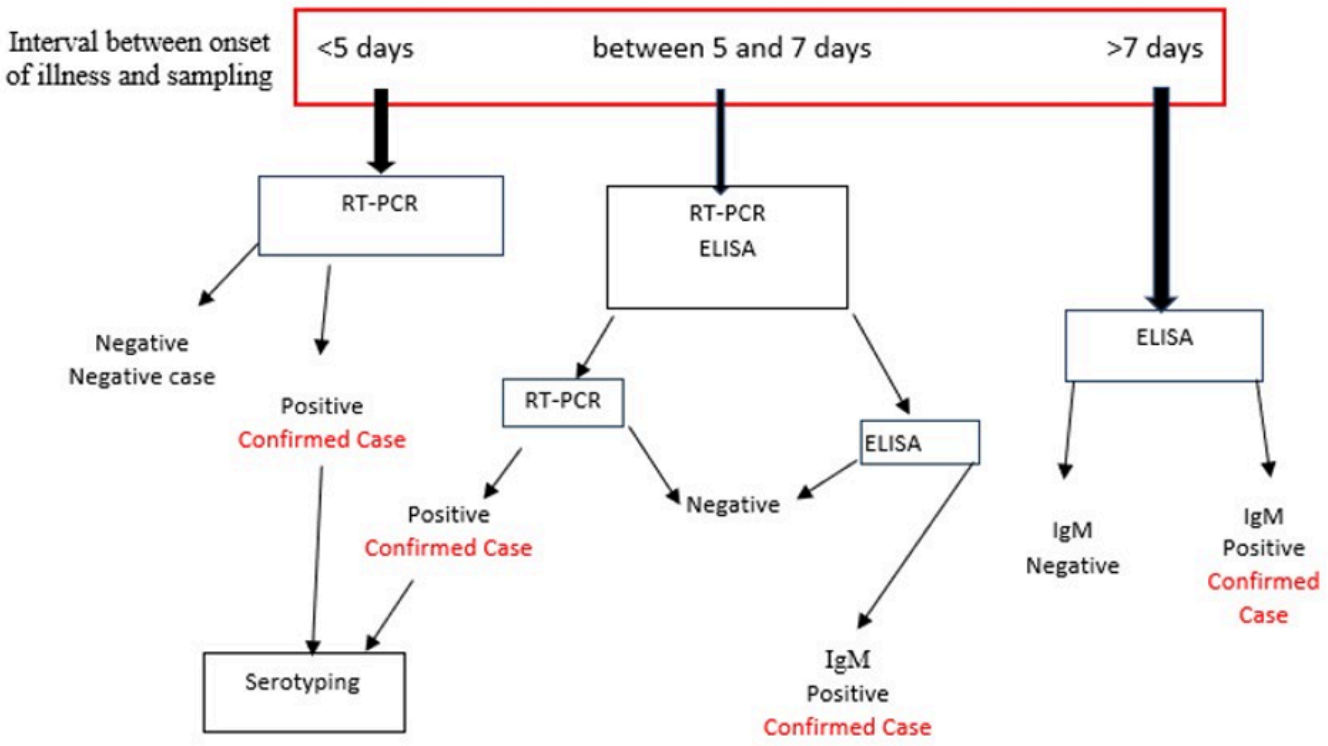


Figure 1

Algorithm for Dengue Diagnostics at LNR-FHV (Source: LNR-FHV Document, 2024)

Diagnostic algorithm for dengue according to the interval between symptom onset and sample collection. Samples collected within 5 days are tested by RT-PCR; between 5 and 7 days, RT-PCR is complemented by ELISA IgM; after 7 days, ELISA IgM alone is performed. Positive results confirm the case and allow serotyping, while negative results indicate non-confirmation.

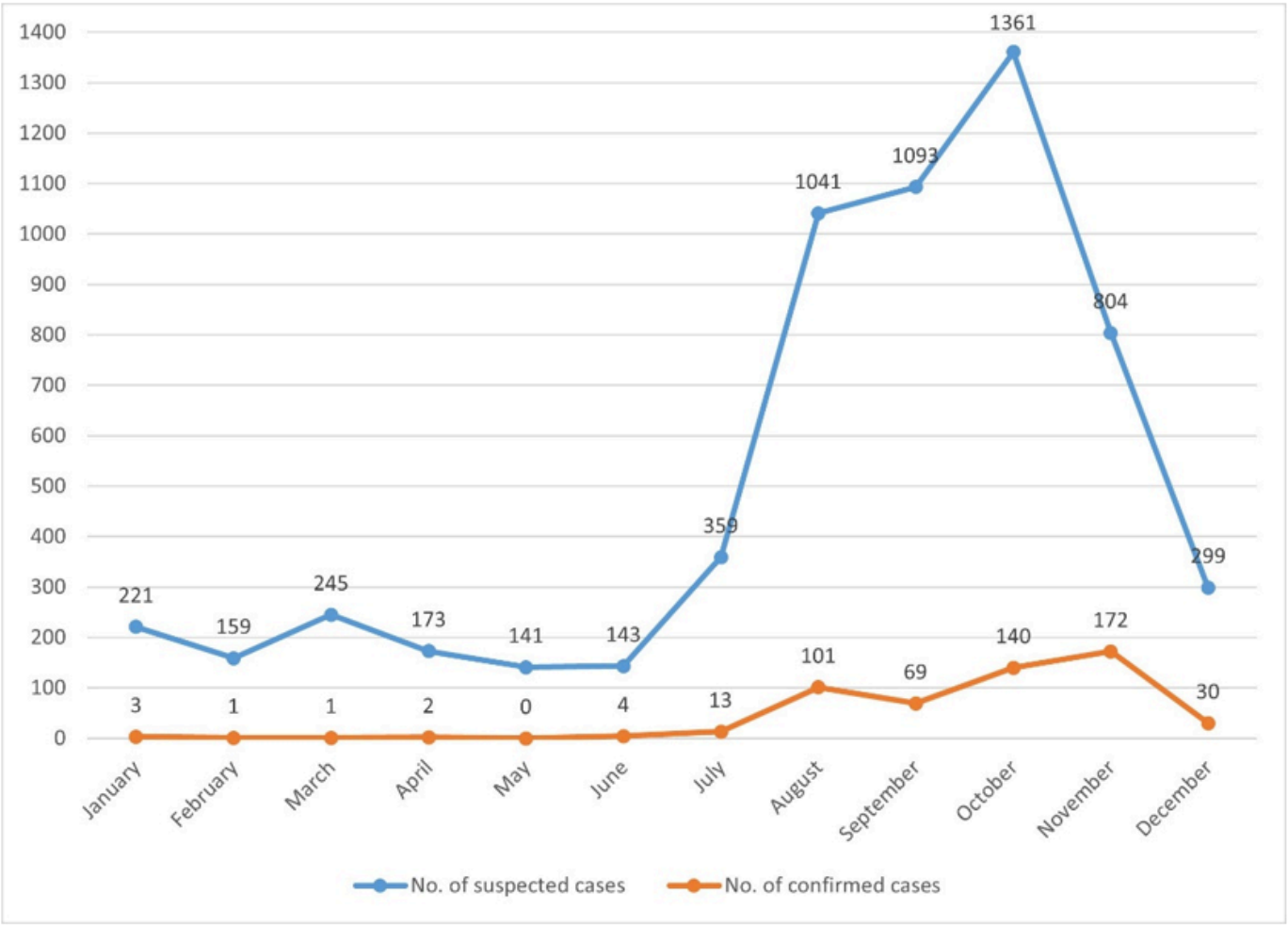


Figure 2

Monthly and Seasonal Distribution of Dengue Cases in Burkina Faso in 2024.

Monthly trends of suspected and confirmed dengue cases in Burkina Faso, 2024. The blue line represents suspected/probable cases, while the orange line shows confirmed cases. A sharp increase is observed from July, with suspected cases peaking in October and confirmed cases peaking in November, followed by a decline in December.