

# Molecular Characterization of the Four Serotypes (DENV-1, DENV-2, DENV-3 and DENV-4) of Dengue Virus Circulating in Ouagadougou, Burkina Faso

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## Abstract

**Background and Objectives:** Dengue is an arbovirosis caused by the dengue virus with 04 serotypes. The aim of the study was to characterise the four serotypes (DENV-1, DENV-2, DENV-3 and DENV-4) of the dengue virus circulating in Ouagadougou, Burkina Faso. **Methods:** This was a descriptive analytical study that included 2833 patients and was carried out from January 2021 to December 2022. Rapid diagnosis of dengue was performed using the “Dengue Duo (AgNS1/IgM/IgG)” kit (SD Biotec, Korea). Viral RNA was extracted using the QIAGEN RNA RNeasy Plus Mini Kit (Qiagen, Germany) and virus serotypes were identified using the DENGUE Real-TM Genotype PCR kit (Sacace biotechnologies, Italy). Platelet counts were also performed using the XN-1500 Sysmex. **Results:** The prevalence of acute infections (NS1Ag positive) by TDR was 5.7% (162/2833), with the peak of dengue virus infection occurring between October and November. On the other hand, the AgNS1+ samples tested by RT-PCR were 53.7% positive for dengue virus; this

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shows the extent of probable cross-reactions with rapid diagnostic tests and false positives. Serotype 1 accounted for 52.6%, 28.4% had serotype 3, 16.8% had serotype 2 and 2.1% had serotype 4. We found cases of co-infection with DENV-1 and DENV-2 in two patients, co-infection with DENV-1 and DENV-3 in three patients, co-infection with DENV-1 and DENV-4 in one patient, co-infection with DENV-3 and DENV-4 in one patient and co-infection with three serotypes, DENV-1, DENV-2 and DENV-3 in one patient. **Conclusion:** The study showed that all four serotypes of the dengue virus were circulating in Ouagadougou. Serotype 1 was predominant.

## Keywords

Dengue Virus, Serotypes, RT-PCR, Burkina Faso

## 1. Introduction

Dengue fever, also known as “tropical flu”, is the most widespread arbovirolosis in tropical and subtropical countries around the world [1]. Dengue is transmitted to humans by diurnal mosquitoes of the genus *Aedes subgenus* Stegomyia, particularly the species *Aedes aegypti* and *Aedes albopictus* [2] [3]. The global distribution of these two major vectors puts almost a third of the world’s human population at risk of infection whereas before 1970 [4], only nine countries had experienced severe dengue epidemics (OMS, 2021).

The dengue virus (DENV), the aetiological agent of dengue fever, belongs to the Flavivirus genus and the Flaviviridae family. It was first isolated in Japan and Hawaii in 1943 and 1945 respectively [5]. DENVs are grouped into four serotypes—DENV-1, DENV-2, DENV-3 and DENV-4—and are single-stranded RNA viruses with positive polarity. They are genetically related, with 65% - 70% sequence homology, but are antigenically distinct with great genetic diversity within the different serotypes [6]. Immunity is specific to the serotype and there is no cross-protection between serotypes [7]. In 2013, a fifth viral serotype, DENV-5, was isolated in Sarawak, Malaysian part of the island of Borneo. To date, it has not caused any human cases, as it follows a purely sylvatic cycle, unlike the other four serotypes, which follow the human cycle [8].

Dengue is a re-emerging infection, the incidence of which has increased over the last fifteen years, and poses a major threat to public health in low- and middle-income countries where the disease is endemic [9]. It causes an acute, febrile illness known as dengue fever (DF), which can progress to severe forms such as dengue haemorrhagic fever (DHF), which can develop into dengue shock syndrome (DSS), the outcome of which can be fatal. The mortality rate for dengue haemorrhagic fever varies from 1 to 40%, depending on the epidemic and the treatment used. Many factors, such as age, frailty, previous contact with the virus (primary or secondary infection), and the circulation of several serotypes in the country, influence the severity of the disease and the genetics of the host. Viremia and the concentration of

circulating NS1 protein also depend on the host's genotype [10].

According to the World Health Organisation (WHO), in 2019, the number of cases of dengue fever rose from 505 430 in 2000 to over 2.4 million in 2010 and 5.2 million [11] (OMS, 2021). In fact, 3.9 billion people, i.e. 40% to 50% of the world's population, are exposed to the risk of DENV infection, with 500 000 cases of severe forms per year and around 30 000 deaths [12]. It has been recorded in 34 African countries in recent decades [13] [14]. The rapid growth of urban areas in West Africa without appropriate sanitation plans is creating nests in which the vector *Aedes aegypti* proliferates, increasing the rate of exposure to dengue fever [15] [16]. The post-winter period is therefore a high-risk period for vector proliferation and infection [17].

Burkina Faso is considered by the WHO to be an endemic country, as it is one of 34 African countries where cases of dengue fever have been reported since 2000 [14]. The first dengue epidemic is thought to have occurred in 1925. A large number of cases were subsequently identified in the 1980 [18]. In 2013, three serotypes were isolated following an epidemic of dengue fever that shook the country [19]. Ouattara *et al.* reported that the prevalence of infection by the dengue virus was 23.5% in 2016 and 13.5% in 2016 [20]; Bello *et al.* found a prevalence of 5.4% between 2020 and 2021 [21]. Primary dengue infections were recorded at 85.5% from September to December in their study in Burkina Faso [22]. A new epidemic of dengue fever broke out in September-October 2023. In September 2023, the Ministry of Health and Public Hygiene, through the Hauts Bassins Regional Department of Health and Public Hygiene, reported 2 494 probable cases of dengue fever and 48 deaths in the region [23]. According to the WHO, Burkina Faso is the most affected country in the region in 2023, with a cumulative number of reported cases of 146,878 suspected cases, including 68,346 probable cases (positive rapid diagnostic test) and 688 deaths among suspected cases, representing a case-fatality rate of 0.5% [24].

Dengue fever is a real public health problem in Burkina Faso, so regular data on the serotypes of circulating dengue viruses, cases of infection and prevalence are essential for proper monitoring of any epidemics. The objectives of this study were to determine the diversity of dengue virus serotypes circulating in Ouagadougou, Burkina Faso, and to establish their prevalence.

## 2. Material and Methods

### 2.1. Type, Period, and Site of Study

This was a descriptive analytical study conducted over a period of 2 years (from 1st January 2021 to 31st December 2022) at the Hôpital Saint Camille de Ouagadougou (HOSCO) and the Biomolecular Research Centre (CERBA/LABIOGENE) in Ouagadougou, the capital of Burkina Faso.

### 2.2. Study Population and Sampling

Samples were collected from 2 833 patients (children and adults) of both sexes

who came to the HOSCO for a general medical consultation with a febrile syndrome accompanied by pain, or to the laboratory at HOSCO and CERBA for serological diagnosis of dengue fever. Patients who were seen during the study period and had at least two signs consistent with dengue fever were included. Patients with known pathology were not included in this study.

Patients' blood samples were taken from the elbow using EDTA (Ethylene Diamine Tetra-Acetic Acid) tubes. After centrifugation at 4000 g for 5 minutes, some of the plasma was used for serological diagnosis of dengue fever and the rest was stored at  $-40^{\circ}\text{C}$  for extraction of viral RNA for molecular characterisation of the different serotypes of the dengue virus.

### **2.3. Serodiagnosis of Dengue Fever**

Detection of the dengue virus was carried out by testing for DENV serological markers using the "Dengue Duo (NS1Ag+IgM/IgG) (SD Bioline, Standard Diagnostic Inc., Korea)" dengue determination test in accordance with the protocols provided by the manufacturers. Results were read between 15 and 20 minutes. Platelet counts were also performed using the XN-1500 Sysmex automated blood count system.

### **2.4. Extraction of Viral RNA**

Viral RNA was extracted using the QIAamp<sup>®</sup> Viral RNA Mini Kit, (Quiagen, Germany), according to the manufacturer's protocol. RNA purity and concentration were assessed using a Biodrop (Isogen Life Science, NV/S.A, Temse, Belgium). Extracts were stored at  $-80^{\circ}\text{C}$  until use.

### **2.5. Molecular Characterisation of the Dengue Virus (Dengue Genotyping by RT-PCR)**

Dengue virus genotyping was carried out by real-time RT-PCR using the Dengue Real-TM Genotype kit (Sacace Biotechnologies <https://sacace.com/new-dengue-virus-genotyping.htm>) in the SaCycler-96 Real Time PCR machine (Sacace Biotechnologies). The Dengue Real-TM Genotype kit is based on multiplex real-time amplification in a well of each sample. Each well contains primers directed against the four dengue genotypes (Denv 1, Denv 2, Denv 3, Denv 4).

PCR reactions were carried out in 25 $\mu\text{L}$  of reaction mixture containing 15  $\mu\text{L}$  of working solution (10  $\mu\text{L}$  of PCR-mix-FRT DV, 5  $\mu\text{L}$  of RT-PCR-mix-2-TM, 0.25  $\mu\text{L}$  of RT-G-mix-2, 0.5  $\mu\text{L}$  of Hot Start TaqF Polymerase, 0.25  $\mu\text{L}$  of MMLV Revertase) and 10  $\mu\text{L}$  of RNA (25 to 100 ng). PCR conditions were as follows : 1 cycle of  $50^{\circ}\text{C}$  for 30 minutes ; 1 cycle of  $95^{\circ}\text{C}$  for 15 minutes ; 5 cycles of  $95^{\circ}\text{C}$  for 10s,  $56^{\circ}\text{C}$  for 40s and  $72^{\circ}\text{C}$  for 20s ; and 40 cycles of  $95^{\circ}\text{C}$  for 10s,  $54^{\circ}\text{C}$  for 40s and  $72^{\circ}\text{C}$  for 20s.

### **2.6. Data Analysis**

Data were recorded using Microsoft Excel 2016. SPSS version 20.0 was used for

data analysis. The results were considered statistically significant at  $p \leq 0.05$ . The Odds Ratio (OR) and 95% confidence intervals (CI) were calculated to estimate the effect of patient sex and age on dengue virus infection using Epi Info 7.

## 2.7. Ethical Considerations

All study participants gave their free and informed consent, in accordance with the Helsinki declarations. This study has received the approval of the Ministry of Health of Burkina-Faso through its Health Research Ethics Committee (CERS) (Deliberation N°2017-01-004 and N°2021-12-295), as well as the institutional ethics committee of CERBA/LABIOGENE have approved this study.

## 3. Results

### 3.1. Socio-Demographic Characteristics

This study involved 2833 patients with clinical signs of suspected dengue who were referred to the medical laboratory for a diagnosis of dengue fever. The patients ranged in age from 0 to 87 years. The study population was made up of 59.3% women and 40.7% men. The 16 - 30 age group was the most represented (36.7%) (1040/2833). Children under 15 accounted for 18.8% (535/2833) of study population (**Table 1**).

**Table 1.** Socio-demographic characteristics of patients.

Gender	2021 - 2022		Age		p-value
	Number	Percentage (%)	Mean (years)	Standard deviation	
Men	1 152	40.7	29.95	18.48	0.62
Women	1 681	59.3	30.27	16.13	
<b>Total</b>	<b>2 833</b>	<b>100</b>	<b>30.14</b>	<b>17.12</b>	
<b>Age groups</b>					
0 - 15	535	18.88	7.40	4.37	
16 - 30	1 040	36.71	24.06	4.09	
31 - 45	827	29.19	36.77	4.36	
46 - 60	262	9.25	53.47	4.81	
>60	169	5.97	70.89	6.04	
<b>Total</b>	<b>2 833</b>	<b>100</b>	<b>30.14</b>	<b>17.12</b>	

### 3.2. Dengue Serological Profiles (Ag NS1, IgG and IgM Type Ac)

All three dengue virus markers (Ag NS1, Ac IgM, Ac IgG) were tested in patients with signs of dengue fever. In the study, 22.7% (644/2833) of patients were positive for one of the dengue serological markers. Of these patients, 5.71% (162/2833) had

a recent or acute dengue infection (NS1+), 1.09% (31/2833) had a primary acute infection (NS1+/IgM+) and 25.7% (728/2833) had a secondary infection or past exposure to the virus (IgG+). In addition, 3.35% (95/2833) had a late onset or recent secondary dengue infection (IgM+/IgG+). A prevalence of 0.95% (27/2833) of patients positive for all three markers was observed (NS1+/IgM+/IgG+) (**Table 2**).

**Table 2.** Prevalence of Ag NS1, IgG and IgM type Ac in patients.

DENV serology	NS1 Ag+ (%)	IgM+ (%)	IgG+ (%)
<b>Gender</b>			
Male (n = 1152)	92 (8.0)	53 (4.6)	269 (23.3)
Female (n = 1681)	70 (4.2)	64 (3.8)	459 (27.3)
Total (n = 2833)	162 (5.7)	117 (4.1)	728 (25.7)
$\chi^2$	17.84	1.15	5.85
<i>p</i> value	<0.0001*	0.030*	<0.016*
<b>Age group (years)</b>			
0 - 15 (n = 535)	12 (2.2)	19 (3.5)	78 (14.6)
16 - 30 (n = 1 040)	71 (6.8)	48 (4.6)	267 (25.7)
31- 45 (n = 827)	37 (4.5)	29 (3.5)	235 (28.4)
46 - 60 (n = 262)	22 (8.4)	10 (3.8)	83 (31.7)
>60 (n = 309)	8 (2.6)	11 (3.6)	65 (21.0)
Total (n = 2833)	162 (5.7)	117 (4.1)	728 (25.7)
$\chi^2$	26.26	2.01	45.42
<i>p</i> value	<0.0001*	0.734	<0.0001*

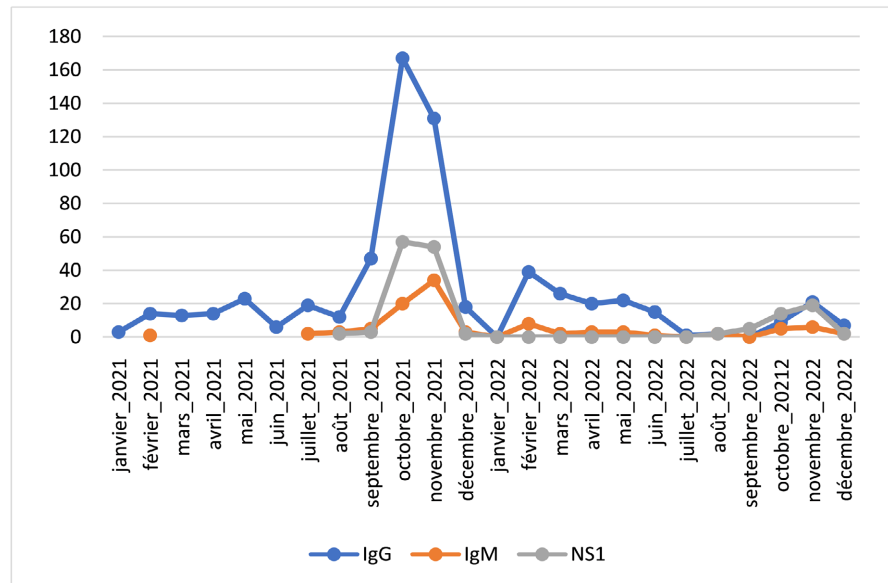
### 3.3. Trends in Dengue Virus Infection in the Population

The majority of suspected cases of dengue fever were recorded in October and November. Patients positive for the NS1Ag antigen during this period accounted for 88.88% (144/162) of positive patients in the entire study (**Figure 1**). **Figure 1** shows the changes in the three dengue virus markers (Ag NS1, Ac IgM, Ac IgG) as a function of month during the study period.

### 3.4. Prevalence of Dengue Virus Serotypes

Molecular characterisation of dengue serotypes was carried out by RT-PCR using the DENGUE Real-TM Genotype PCR kit (Sacace biotechnologies) on AgNS1 positive samples. The virus was identified in 53.7% (87/162) of these samples (**Table 3**). Serotype DENV-1 represented 52.6% with 46% of females and 54% of males, while DENV-2 represented 16.8% with 50% of males and 50% of females. DENV-3 was

detected in 28.4%, of which 59% were female and 40% male, while 2.1% had DENV 4, all of whom were female.

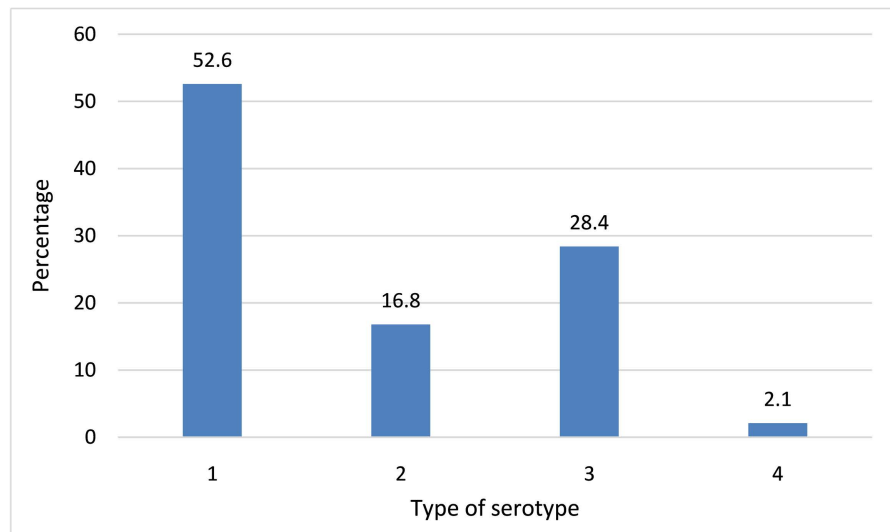


**Figure 1.** Trends in markers of dengue infection from 2021 to 2022, by month.

**Table 3.** Different dengue virus serotypes.

	DENV-1 n(%) = 50 (52.6)	DENV-2 n(%) = 16 (16.8)	DENV-3 n(%) = 27 (28.4)	DENV-4 n(%) = 2 (2.1)
<b>Gender</b>				
Male	27 (54.0)	8 (50.0)	11 (40.0)	0
Female	23 (46.0)	8 (50.0)	16 (59.0)	2 (100)
<b>Age (years)</b>				
0 - 15	8 (16.0)	0	3 (11.1)	0
16 - 30	24 (48.0)	9 (56.2)	13 (48.1)	1 (50.0)
>30	18 (36.0)	7 (43.7)	11 (40.7)	1 (50.0)
<b>Infection status</b>				
Acuteinfections NS1+/IgM-	31 (62.0)	12 (75.0)	14 (51.8)	2 (100)
Primary infections NS1+/IgM+	15 (30.0)	2 (12.5)	10 (37.0)	0
Secondary infections NS1-/IgM+/IgG+	7 (14.0)	2 (12.5)	8 (29.6)	0
<b>Hematology data</b>				
Hemoglobin (g/dL)	14.4 ± 1.5	14.0 ± 1.6	14.6 ± 20	11.9
Platelets (/L)	116.2 ± 25.7	116.0 ± 28.7	119.0 ± 11.4	137.0

All four (4) dengue serotypes investigated in our study were identified in patients. Considering multiple infections, serotypes were found 95 times in the 87 RT-PCR-positive patients (**Figure 2**).



**Figure 2.** Frequency of dengue serotypes found in patients.

Co-infections with two different serotypes were observed in 8.1% of patients and 1.1% had multiple infections with three serotypes (**Table 4**).

**Table 4.** Number of serotypes identified per person.

Serotype identified per person	Number	Percentage (%)
1	79	90.8
2	7	8.1
3	1	1.1
Total	87	100

#### 4. Discussion

A total of 2 833 patients were seen during the study period, the majority of whom were women (59.3%) and men (40.7%). This high representation of women could be explained by the fact that they are more frequent visitors to health facilities and also represent 51.7% of the general population of Burkina Faso according to the results of the 5th general population recension in Burkina Faso [25]. The results of this study are in line with those of a study carried out at HOSCO where Ouattara *et al.* revealed a percentage of 56.2% and 57.3% of women in 2016 and 2017 respectively [20], but slightly lower than the 69.2% of women found in another study in Ouagadougou [26]. The 16 - 30 age group accounted for 36.7% of the study population. This result is similar to that of Sondo *et al.* [27], who found that the 15 - 30 age group accounted for 40%, because the population of Burkina Faso

is itself predominantly young, according to the 5th general population and housing census of Burkina Faso.

The results of the rapid serological diagnosis of dengue fever, which tested for the three markers of the dengue virus (Ag NS1, Ac IgM, Ac IgG), revealed that 5.71% (162/2 833) of patients had a recent or acute infection with dengue fever (NS1+). In the study, 22.7% (644/2 833) of patients were positive for one of the serological markers of dengue. This percentage is higher than the 2.42% reported in 2020 by Ilboudo *et al.* [28]. In contrast, another study reported that 40.1% of patients positive for one of the dengue serological markers [20]. These results confirm that the dengue virus is circulating in the population of Burkina Faso.

PCR results on AgNS1+ samples confirmed the presence of the virus in 53.7% (87/162). Dieng *et al.* characterised the dengue virus in 15.6% (27/173) of patient samples collected by qRT-PCR [29]. Molecular diagnosis is still the most specific method for detecting the dengue virus, but cross-reactivity with rapid diagnostic tests and false positives can occur.

The DENGUE Real-TM Genotype PCR Kit from Sacace biotechnologies used for characterisation enabled us to identify the four dengue serotypes (DENV1-DENV2-DENV3-DENV4) in our study. In Bali, all four dengue serotypes were found [30].

Serotype 1 predominated over the other three serotypes of the dengue virus with 52.6% (50/87), followed by serotype 3 with 28.4% (27/87). Serotypes 2 and 4 represented 16.8% (16/87) and 2.1% (2/87) respectively of the serotypes found. Our results are similar to those of Dieng *et al.* in 2017 who found a predominance of serotype 1 of the dengue virus (96.15% of the study population) in the town of Louga in Senegal [31] and Dhanao *et al.* which also show a predominance of serotype 1 [32]. However, in Burkina Faso Targanada *et al.* found that serotype 2 was predominant with 57.8% [33]. This difference could be explained by the different sample collection areas, population trends and the environment.

In our study, serotypes 2 and 3 accounted for 16.8% and 28.4% respectively. This confirms that serotypes 2 and 3 of the dengue virus are still circulating in the population. These serotypes 2 and 3 had already been found during a study of dengue fever in Burkina Faso in 2016 [33]. Serotype 2 of the dengue virus has been shown to be endemic in Burkina Faso [34]. Two cases of dengue due to serotype 4 have been identified. Ridde *et al.* also reported serotype 4 in 3 patients [19]. Serotype 4 of the dengue virus is rarely implicated in dengue infections.

We reported eight cases of co-infection, including co-infection with serotypes 1 and 2; 1 and 3; 1, 2 and 3; 1 and 4; and 4 and 3. Our results are similar to those of Figueiredo *et al.* in Brazil in 2011, who reported the presence of co-infection with serotypes 1 and 4 [35] and co-infections of the dengue virus with serotypes 1 and 2; 1 and 3 by Dhanao *et al.* [32]. A study on the presence of co-infection of dengue viruses carried out on the population of New Delhi revealed cases of co-infection by serotypes 1 and 2 of the dengue virus [36]. In Senegal, the co-circulation of Denv-2 and Denv-3 with a re-emergence of Denv-3 at the large religious

gathering in Touba was reported in 2018 [37]. We note that cases of co-infection are found in hyper-endemic areas where several serotypes of the dengue virus co-circulate. The risk factors for dengue infection and co-infection include the virulence of the virus and the density of the vector in the area [35]. The dengue virus vectors *Aedes aegypti* and *Aedes albopictus* can both carry two serotypes of the dengue virus [38] which they can transmit to humans by bite. In Benin, in the departments of Oueme and Plateau, Denv1, Denv2 and Denv3 have been detected in *Aedes aegypti* and *Aedes albopictus* [39]. Co-infection may also occur if the patient is bitten within a short space of time by two different mosquitoes carrying different serotypes of the virus. The occurrence of these co-infections is therefore natural and results from the endemicity of the dengue virus in Burkina Faso, where serotypes 2, 3 and 4 have been observed since 2013.

The study found cases of thrombocytopenia, but no association between thrombocytopenia and dengue virus infection. Thrombocytopenia is thought to be a biological sign of dengue virus infection and one of the classic features of severe dengue fever [40] which is why it is used as a criterion for diagnosis [41]. Dhanoa *et al.* in 2016 found that patients co-infected with serotype 2 had a higher frequency of thrombocytopenia. In the same study, they found that cases of co-infection with serotypes 1 and 2 were accompanied by thrombocytopenia [32]. Thrombocytopenia was observed in haemorrhagic forms of dengue fever in the infectious diseases department of the University Hospital Yalgado Ouédraogo in Burkina Faso [42]. The low platelet rate was also reported in a study [43]. One of the limitations of the study was that we did not have access to the patients' clinical records to establish the relationship between the course of the disease and the serotypes identified, as well as the size of our sample.

Burkina Faso, like many other African countries, faces a number of challenges when it comes to differential diagnosis, detection and notification of cases to ensure proper treatment and, above all, epidemiological surveillance of possible epidemics of arboviroses such as dengue and chikungunya. The results of this study established the prevalence of dengue fever, confirmed the circulation of the virus in Burkina Faso and detected the four serotypes of dengue fever.

## 5. Conclusion

This study made it possible to characterise the serotypes of the dengue virus circulating in Burkina Faso. All four serotypes of the dengue virus are circulating in Ouagadougou, with serotype 1 predominating. Cases of co-infection by all four serotypes have been detected. A dengue epidemic resurfaced in Burkina Faso in August-September 2023. Arbovirose surveillance and warning systems need to be strengthened to control the spread of infection and, if possible, the introduction of the dengue vaccine. The development of antivirals and vaccines offers hope of improving the management of dengue fever.

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SOTB wrote the first draft of the manuscript and revised the different versions of

the manuscript ASAT, YJRB, WSKY, PB, OFK, FT, TMZ and FWD collected the data and revised the different versions of the manuscript. AAZ, AD and JS designed the work and revised the different versions of the manuscript.

## Conflicts of Interest

The authors declare that they have no conflicts of interest.

## References

- [1] Ayukekbong, J.A., Oyero, O.G., Nnukwu, S.E., Mesumbe, H.N. and Fobisong, C.N. (2017) Value of Routine Dengue Diagnosis in Endemic Countries. *World Journal of Virology*, **6**, 9-16. <https://doi.org/10.5501/wjv.v6.i1.9>
- [2] Bello, S.O.T., Zoure, A.A., Ouattara, A.K., Somda, D., Nadembega, C., Obiri-Yeboah, D., *et al.* (2024) Geographical Distribution of Arboviruses, *Aedes aegypti* and *Aedes albopictus* Vectors and Their Resistance to Insecticides in Africa—A Systematic Review. *Advances in Entomology*, **12**.
- [3] Santos, A.C.M.d., de Moura, E.L., Ferreira, J.M., Santos, B.R.C.d., Alves, V.d.M., de Farias, K.F., *et al.* (2016) Meta-Analysis of the Relationship between TNF- $\alpha$  (–308G/A) and IL-10 (–819C/T) Gene Polymorphisms and Susceptibility to Dengue. *Immunological Investigations*, **46**, 201-220. <https://doi.org/10.1080/08820139.2016.1248560>
- [4] Baum, A., Sachidanandam, R. and García-Sastre, A. (2010) Preference of RIG-I for Short Viral RNA Molecules in Infected Cells Revealed by Next-Generation Sequencing. *Proceedings of the National Academy of Sciences*, **107**, 16303-16308. <https://doi.org/10.1073/pnas.1005077107>
- [5] Wilder-Smith, A., Murray and Quam, M. (2013) Epidemiology of Dengue: Past, Present and Future Prospects. *Clinical Epidemiology*, **5**, 299-309. <https://doi.org/10.2147/cep.s34440>
- [6] Chen, R. and Vasilakis, N. (2011) Dengue—Quo tu et quo vadis? *Viruses*, **3**, 1562-1608. <https://doi.org/10.3390/v3091562>
- [7] Wilder-Smith, A., Ooi, E., Vasudevan, S.G. and Gubler, D.J. (2010) Update on Dengue: Epidemiology, Virus Evolution, Antiviral Drugs, and Vaccine Development. *Current Infectious Disease Reports*, **12**, 157-164. <https://doi.org/10.1007/s11908-010-0102-7>
- [8] Taylor-Robinson, A. (2016) A Putative Fifth Serotype of Dengue—Potential Implications for Diagnosis, Therapy and Vaccine Design. *International Journal of Clinical & Medical Microbiology*, **1**, 1-2. <https://doi.org/10.15344/2456-4028/2016/101>
- [9] Adam, A. and Jassoy, C. (2021) Epidemiology and Laboratory Diagnostics of Dengue, Yellow Fever, Zika, and Chikungunya Virus Infections in Africa. *Pathogens*, **10**, Article No. 1324. <https://doi.org/10.3390/pathogens10101324>
- [10] Chau, T.N.B., Quyen, N.T.H., Thuy, T.T., Tuan, N.M., Hoang, D.M., Dung, N.T.P., *et al.* (2008) Dengue in Vietnamese Infants—Results of Infection-Enhancement Assays Correlate with Age-Related Disease Epidemiology, and Cellular Immune Responses Correlate with Disease Severity. *The Journal of Infectious Diseases*, **198**, 516-524. <https://doi.org/10.1086/590117>
- [11] Roy, S.K. and Bhattacharjee, S. (2021) Dengue Virus: Epidemiology, Biology, and Disease Aetiology. *Canadian Journal of Microbiology*, **67**, 687-702. <https://doi.org/10.1139/cjm-2020-0572>
- [12] Achee, N.L., Grieco, J.P., Vatandoost, H., Seixas, G., Pinto, J., Ching-NG, L., *et al.*

- (2019) Alternative Strategies for Mosquito-Borne Arbovirus Control. *PLOS Neglected Tropical Diseases*, **13**, e0006822.  
<https://doi.org/10.1371/journal.pntd.0006822>
- [13] Gyasi, P., Bright Yakass, M. and Quaye, O. (2023) Analysis of Dengue Fever Disease in West Africa. *Experimental Biology and Medicine*, **248**, 1850-1863.  
<https://doi.org/10.1177/15353702231181356>
- [14] Malisheni, M., Khaiboullina, S.F., Rizvanov, A.A., Takah, N., Murewanhema, G. and Bates, M. (2017) Clinical Efficacy, Safety, and Immunogenicity of a Live Attenuated Tetravalent Dengue Vaccine (CYD-TDV) in Children: A Systematic Review with Meta-Analysis. *Frontiers in Immunology*, **8**, Article No. 863.  
<https://doi.org/10.3389/fimmu.2017.00863>
- [15] Weetman, D., Kamgang, B., Badolo, A., Moyes, C., Shearer, F., Coulibaly, M., *et al.* (2018) Aedes Mosquitoes and Aedes-Borne Arboviruses in Africa: Current and Future Threats. *International Journal of Environmental Research and Public Health*, **15**, Article No. 220. <https://doi.org/10.3390/ijerph15020220>
- [16] Stoler, J., al Dashti, R., Anto, F., Fobil, J.N. and Awandare, G.A. (2014) Deconstructing “Malaria”: West Africa as the Next Front for Dengue Fever Surveillance and Control. *Acta Tropica*, **134**, 58-65. <https://doi.org/10.1016/j.actatropica.2014.02.017>
- [17] Ouattara, C.A., Traore, S., Sangare, I., Traore, T.I., Meda, Z.C. and Savadogo, L.G.B. (2022) Spatiotemporal Analysis of Dengue Fever in Burkina Faso from 2016 to 2019. *BMC Public Health*, **22**, Article No. 462.  
<https://doi.org/10.1186/s12889-022-12820-x>
- [18] Gonzalez, J., Du Saussay, C., Gautun, J., McCormick, J. and Mouchet, J. (1985) Dengue in Burkina Faso (Ex-Upper Volta): Seasonal Epidemics in the Urban Area of Ouagadougou. *Bulletin de la Société de Pathologie Exotique et de ses Filiales*, **78**, 7-14.
- [19] Ridde, V., Agier, I., Bonnet, E., Carabali, M., Dabiré, R., Druetz, T., Fournet, F., Ly, A., Ocampo, C. and Parra, B. (2014) La Dengue Au Burkina Faso: Pas de panique mais soyons prudents. 1-4.
- [20] Ouattara, K., Nadembega, C., Diarra, B., Yonli, A., Obiri-yeboah, D., Belemnegre, M., *et al.* (2017) Serological Diagnosis in Suspected Dengue Cases at Saint Camille Hospital of Ouagadougou: High Prevalence of Infection among Young Adults Aged 15 to 30 Years. *International Journal of Recent Advances in Multidisciplinary Research*, **4**, 3299-3304.
- [21] Bello, S.O.T., Houkpevi, A., Zackari, S., Tapsoba, A.S.A., Zoure, A.A., Ilboudo, P.D., *et al.* (2022) Epidemiology of Dengue in Patients with Febrile Syndrome at Saint Camille Hospital, Ouagadougou, Burkina Faso from 2020 to 2021. *African Journal of Clinical and Experimental Microbiology*, **23**, 398-406.  
<https://doi.org/10.4314/ajcem.v23i4.8>
- [22] Donatien, K., Hien, Y.E., Salam, S., Yacouba, N.K., Denise, I.P., Nikiéma, A.R., *et al.* (2023) Seroepidemiological Study of Dengue Virus Infection Suspected Cases in Burkina Faso. *Journal of Biosciences and Medicines*, **11**, 47-56.  
<https://doi.org/10.4236/jbm.2023.111006>
- [23] MSHP, M. de la S. et de l'Hygiène P. (2023) Réponse sanitaire à un flambée de cas de dengue dans la région des Hauts-Bassins, Burkina Faso, Septembre 2023.
- [24] WHO (2023) Bulletins d'information sur les flambées épidémiques. Dengue—Situation Mondiale.  
<https://www.who.int/fr/emergencies/disease-outbreak-news/item/2023-DON498>
- [25] INSD (2022) Projections Démographiques De 2007 À 2020.

- [26] Lim, J.K., Seydou, Y., Carabali, M., Barro, A., Dahourou, D.L., Lee, K.S., *et al.* (2019) Clinical and Epidemiologic Characteristics Associated with Dengue during and outside the 2016 Outbreak Identified in Health Facility-Based Surveillance in Ouagadougou, Burkina Faso. *PLOS Neglected Tropical Diseases*, **13**, e0007882. <https://doi.org/10.1371/journal.pntd.0007882>
- [27] Sondo, K.A., Gnamou, A., Diallo, I., Ka, D., Zoungrana, J., Diendéré, E.A., *et al.* (2022) Etude descriptive des complications de la dengue au cours de la flambée de 2016 à Ouagadougou au Burkina Faso. *Pamj-Oh*, **7**.
- [28] Ilboudo, D.P., Zohoncon, T.M., Hien, Y.E., Ouattara, A.K., Traore, L., Ouermi, D., *et al.* (2022) Dengue Immunological Markers Evolution at Saint Camille Hospital in Ouagadougou (HOSCO) Burkina Faso. *Pakistan Journal of Biological Sciences*, **25**, 254-262. <https://doi.org/10.3923/pjbs.2022.254.262>
- [29] Dieng, I., Ndiaye, M., Ndione, M.H.D., Sankhe, S., Diagne, M.M., Sagne, S.N., *et al.* (2022) Molecular Characterization of Circulating Dengue Virus 2 during an Outbreak in Northern Senegal's Saint-louis Region in 2018. *Journal of Medical Virology*, **95**, e28347. <https://doi.org/10.1002/jmv.28347>
- [30] Megawati, D., Masyeni, S., Yohan, B., Lestardini, A., Hayati, R.F., Meutiawati, F., *et al.* (2017) Dengue in Bali: Clinical Characteristics and Genetic Diversity of Circulating Dengue Viruses. *PLOS Neglected Tropical Diseases*, **11**, e0005483. <https://doi.org/10.1371/journal.pntd.0005483>
- [31] Dieng, I., Diarra, M., Diagne, M.M., Faye, M., Dior Ndione, M.H., Ba, Y., *et al.* (2021) Field Deployment of a Mobile Biosafety Laboratory Reveals the Co-Circulation of Dengue Viruses Serotype 1 and Serotype 2 in Louga City, Senegal, 2017. *Journal of Tropical Medicine*, **2021**, Article ID: 8817987. <https://doi.org/10.1155/2021/8817987>
- [32] Dhanoa, A., Hassan, S.S., Ngim, C.F., Lau, C.F., Chan, T.S., Adnan, N.A.A., *et al.* (2016) Impact of Dengue Virus (DENV) Co-Infection on Clinical Manifestations, Disease Severity and Laboratory Parameters. *BMC Infectious Diseases*, **16**, Article No. 406. <https://doi.org/10.1186/s12879-016-1731-8>
- [33] Tarnagda, Z., Cissé, A., Bicaba, B.W., Diagbouga, S., Sagna, T., Ilboudo, A.K., *et al.* (2018) Dengue Fever in Burkina Faso, 2016. *Emerging Infectious Diseases*, **24**, 170-172. <https://doi.org/10.3201/eid2401.170973>
- [34] Letizia, A.G., Pratt, C.B., Wiley, M.R., Fox, A.T., Mosore, M., Agbodzi, B., *et al.* (2022) Retrospective Genomic Characterization of a 2017 Dengue Virus Outbreak, Burkina Faso. *Emerging Infectious Diseases*, **28**, 1198-1210. <https://doi.org/10.3201/eid2806.212491>
- [35] Figueiredo, R.M.P.d., Naveca, F.G., Oliveira, C.M., Bastos, M.d.S., Mourão, M.P.G., Viana, S.d.S., *et al.* (2011) Co-Infection of Dengue Virus by Serotypes 3 and 4 in Patients from Amazonas, Brazil. *Revista do Instituto de Medicina Tropical de São Paulo*, **53**, 321-323. <https://doi.org/10.1590/s0036-46652011000600004>
- [36] Tazeen, A., Afreen, N., Abdullah, M., Deebe, F., Haider, S.H., Kazim, S.N., *et al.* (2016) Occurrence of Co-Infection with Dengue Viruses during 2014 in New Delhi, India. *Epidemiology and Infection*, **145**, 67-77. <https://doi.org/10.1017/s0950268816001990>
- [37] Dieng, I., Fall, C., Barry, M.A., Gaye, A., Dia, N., Ndione, M.H.D., *et al.* (2022) Re-emergence of Dengue Serotype 3 in the Context of a Large Religious Gathering Event in Touba, Senegal. *International Journal of Environmental Research and Public Health*, **19**, Article No. 16912. <https://doi.org/10.3390/ijerph192416912>
- [38] Thavara, U., Siriyasatien, P., Tawatsin, A., Asavadachanukorn, P., Anantapreecha, S., Wongwanich, R., *et al.* (2006) Double Infection of Heteroserotypes of Dengue Viruses

- in Field Populations of *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae) and Serological Features of Dengue Viruses Found in Patients in Southern Thailand. *Southeast Asian Journal of Tropical Medicine and Public Health*, **37**, 468-476.
- [39] Padonou, G.G., Konkon, A.K. and Sovi, A. (2023) Detection of DENV-1, DENV-3 and DENV-4 Serotypes in *Ae. aegypti* and *Ae. albopictus*, and Epidemic Risk in the Departments of Oueme and Plateau.
- [40] Chaturvedi, U.C., Nagar, R. and Shrivastava, R. (2006) Dengue and Dengue Haemorrhagic Fever: Implications of Host Genetics. *FEMS Immunology & Medical Microbiology*, **47**, 155-166. <https://doi.org/10.1111/j.1574-695x.2006.00058.x>
- [41] Fragnoud, R., Paranhos-Baccalà, G. and Bedin, F. (2014) Severe Dengue: From Pathogenicity Hypotheses to Pronostic Tools. *Virologie (Montrouge)*, **18**, 59-74. <https://doi.org/10.1684/vir.2014.0561>
- [42] Mamoudou, S. and Boushab, B.M. (2016) Formes hémorragiques de Dengue observées dans le service des maladies infectieuses du CHU Yalgado Ouédraogo, Burkina Faso. *Pan African Medical Journal*, **23**, Article No. 168. <https://doi.org/10.11604/pamj.2016.23.168.9234>
- [43] Umakanth, M. (2018) Case Series of Seronegative Dengue Hemorrhagic Fever. *OALib*, **5**, e4805. <https://doi.org/10.4236/oalib.1104805>