Mosquito-Borne Arboviruses Occurrence and Distribution in Central Africa

Subjects: Microbiology

Contributor: Natacha Poungou , Silas Lendzele Sevidzem , Aubin Armel Koumba , Christophe Roland Zinga Koumba , Phillipe Mbehang , Richard Onanga , Julien Zahouli Bi Zahouli , Gael Darren Maganga , Luc Salako Djogbénou , Steffen Borrmann , Ayola Akim Adegnika , Stefanie C. Becker , Jacques François Mavoungou , Rodrigue Mintsa Nguéma

Arboviruses represent a real public health problem globally and in the Central African subregion in particular, which represents a high-risk zone for the emergence and re-emergence of arbovirus outbreaks.

arboviruses mosquitoes epidemics transmission Central Africa

1. Occurrence of Arboviruses in the Central African Region

The six arboviruses of public health importance considered herein belonged to three genera: (i) *Alphavirus* (CHIKV); (ii) *Flavivirus* (DENV, WNV, YFV, ZIKV); (iii) *Phlebovirus* (RVFV). Of these six arboviruses reported to be circulating in the Central African region, CHIKV and DENV have been detected in all the countries of this region [1], and the other four appear to variably occur in the different countries as follows.

1.1. Angola

The available and relevant information on arboviruses and associated vectors for Angola was documented in 17 papers. The details on each arbovirus targeted herein are presented (**Table 1**) as follows.

DENV

Dengue circulation in Angola was first announced in the 1980s by infected travellers returning from Angola to the Netherlands [2]. In 2013, Angola reported its first locally acquired DENV cases [3]. During the 2013 epidemic, about 10% of cases and random cluster participants in Luanda, Angola’s capital city, displayed evidence of recent DENV infection [4]. Furthermore, the genetic study by Neto et al. [5] reported the circulation of DENV2 in Luanda. The detection of dengue during suspect outbreaks or in travelers in Angola was realised using three methods (rapid diagnostic tests, ELISA, and PCR/sequencing). A study conducted in the field used the rapid diagnostic kit (Dengue Duo, Standard Diagnostics) for the detection of the DENV non-structural protein 1 (NS1) (Morbidity and Mortality Weekly Report (MMWR) (http://www.cdc.gov/mmwr, accessed on 21 May 2023) (Ministry of Health Angola and the WHO). The non-structural protein (NSP) ELISA was also used to establish acute infections of DENV [3]. The Trioplex real-time RT-PCR was used to detect dengue, with the advantage that it is capable of differentiating ZIKV and discriminating CHIKV and DENV in coinfected individuals [6]. In addition, the nested PCR was conducted using primers targeting the C-prM region of DENV [7]. There is need for studies on vector competence of local potential mosquito populations for the transmission of DENV in hotspot areas.

YFV and CHIKV

In 1970 in Angola, outbreaks of YFV and CHIKV were reported [8]. The first YFV cases in Angola were reported in Luanda. On 13 April 2016, the WHO declared a YFV outbreak in Angola, and during the same period, the WHO also noted a case of RVFV in a man from China working in Luanda, the capital of Angola. Again, in May 2016, a 21 year old female traveller from Luanda to Tokyo tested positive for CHIKV. According to the distribution map proposed by Adam and Jassoy [1], Angola is endemic for YF and CHIKV. Although evidence of circulating YFV and CHIKV was established using high throughput diagnostic techniques in Angola, the issue of the lack of regular surveillance remains. The occurrence of CHIKV was confirmed using the Trioplex real-time RT-PCR [6][9]. The YFV cases were detected using RT-PCR, with primers targeting the 5′ non coding region, and positive samples were further tested using the pan-flavivirus RT-PCR, targeting the flavivirus NS5 gene region using specific primers (FU18993F and cFD29258R [10]. Additionally, although *Aedes*, *Anopheles* spp., and *Culex pipiens* vector compatibility was studied in Angola [11][12], an interesting study was conducted to show the implication of *Aedes* mosquitoes in the transmission of YFV during the 2016 outbreak [13].

1.2. Cameroon

All six medically important arboviruses targeted in this text have been reported in Cameroon (**Table 1**). This study found 58 papers published online on these arboviruses and associated vectors. The situation of the different arboviruses of Cameroon is as follows.

CHIKV

In Cameroon, CHIKV was reported in most regions, with high prevalence reported in the northwest (51.4%) [14], and others recorded varing prevalence as follows: Littoral region (12.6–59.4%) [15]; Central region (3–59.4%) [14]; and South West region (4–63%) [16]. However, Cameroon has already been reported as a CHIKV-endemic area with high transmission risk [1]. The 2006, a CHIKV outbreak in Cameroon was confirmed via real-time RT-PCR and partial sequencing of the envelope gene [17]. During the 2006 CHIKV outbreak in the West region of Cameroon, the persistence of anti-CHIKV IgM antibodies was reported in the local population, and entomological studies revealed high relative abundance of *Aedes africanus* [18]. The risk of CHIKV emergence and re-emergence in the west region of Cameroon was supported by an entomological study that showed high species richness and abundance of competent vectors in this part of the country [19]. Interestingly, a study conducted at the border between Cameroon and Gabon showed that patients coming to seek health services in Kyé-ossi in Cameroon from the neighboring town of Gabon (Bitam) were diagnosed positive with CHIKV, indicating the possibility of cross-border transmission between the two countries [20]. The transmission risk of arboviruses at borders between central African countries needs to be studied.

DENV

Dengue was found in all the epidemiological studies for Cameroon and was detected in all the 10 regions of the country. The prevalence, by region, or reports of this virus is as follows: Littoral (3.8–68.3%) [21][22][23], Far North (6.7–14.36%) [24][25], West (6.14–14.36%) [25][26], Center (3–45.45%) [25][27], South West (2.5–74%) [16][28] and South (0.5–14.28%). Similar to CHIKV, Dengue is also endemic in the whole of Cameroon with high transmission risk [1]. The nationwide occurrence of DENV has been shown using several diagnostic methods (ELISA and PCR/sequencing). At the regional level, DENV was detected among inpatients using ELISA [29]. In the rural town of Kribi in the south region of Cameroon, MAC-ELISA and the CDC Trioplex real-time RT-PCR were used to show the circulation of DENV [30]. Moreover, the amplification of the partial *E* gene (expected band size of 250 bp) for DENV revealed the occurrence of this virus in the economic capital city (Douala) of Cameroon [21]. The trasmission risk of DENV in this town has already been proven by Kamgang et al. [31] where the two competent vectors (*Ae. aegypti* and *Ae. albopictus*) were identified and their vector roles established for three major towns of Cameroon (Garoua, Douala and Yaounde). Furthermore, a study in the political capital city (Yaounde) of Cameroon revealed high ecological adaptation of *Ae. aegypti* and *Ae. albopictus* and the potential risk for the transmission of arboviruses [32]. The vector ecology and competence of these two vectors of DENV has already been studied in Cameroon [19][31][33][34].

YFV

Yellow Fever Virus was detected in two hotspot regions with following prevalences notably: North (25.5%) region [35] and South West region (4–72%) [16][28]. YFV is endemic in Cameroon, with high risk of transmission [1]. It is important to add that the YFV outbreak in Garoua town of the North region of Cameroon was first identified via serology using the MAC-ELISA IgM test, and positive samples were airlifted to the WHO reference laboratory in Dakar, Senegal, for confirmation [35]. The circulation of YFV in this local population is not surprising; Kamgang et al. [31] already identified and established the role of competent *Aedes* vectors in this town. Furthermore, the analysis of laboratory tests results from 2010 to 2020 in Cameroon revealed sustained YFV transmission [36]. It should be noted that Cameroon has a national YFV surveillance system that is planned and implemented by the expanded programme on immunization (EPI) of the Ministry of Public Health, with support from foreign donors.

ZIKV

Most of the studies found online concerning the arboviruses of Cameroon frequently reported ZIKV. The prevalence differed in each region as follows: Southwest (11.4%) [28]; Littoral (10–26.2%) [3][24]; East (7.6%) [37]; Far North (2–4.8%) [37]; and Adamawa (2%) [37]. Zika virus has already been reported to be endemic in Cameroon and with high transmission risk [1]. The studies showing the burden of ZIKV in populations of the different regions of Cameroon were conducted using the CDC Trioplex real-time RT-PCR assay, which is capable of discriminating ZIKV from DENV/CHIKV [20]. In fact, it has already been reported via a transmission study that *Ae. aegypti* and *Ae. albopictus* are susceptible to infection and spread of ZIKV in Cameroon [38].

WNV

The reports on WNV for Cameroon are scant, and it was only reported in the South West region of Cameoron, with a prevalence range of 3–82% [16]. It is clear from the study of Mayi et al. [19] on vector adaptability conducted in an area bordering the South West region of Cameroon that there was high species richness and diversity of WNV-competent vectors that could represent a transmission risk in the area. However, in the town of Garoua in the North region, a study identified competent vectors of RVFV and WNV [39].

1.3. Central African Republic

The CAR has been victim of attacks of 19 arboviruses in the past, and recently, 3 arboviruses were involved in fatal cases: in 1983, WNV was isolated in four patients; two serious cases of YFV occurred in 1985 and 1986; and from 1983 to 1986, RVFV was identified in patients who died from hemorrhagic fever [40]. The details on the different arboviruses are presented (**Table 1**) in the following paragrahs.

CHIKV

Genetic analysis by Tricou et al. [41] confirmed the circulation of CHIKV in the 1970s and 1980s. A serological survey of antibodies to arboviruses was carried out in the human population of the southeast part of CAR in April 1979, and CHIKV was detected to be actively circulating in adult population [42]. The distribution map of CHIKV by Adam and Jassoy [1] shows that CAR is an endemic country for this virus. It is necessary to underline here that CHIKV was frequently studied, and this could be due to the fact that major outbreaks were associated to it. The evidence of circulating CHIKV in CAR was conducted using PCR, where two sets of primers (E1-10145F/E1-11158R and E2-8458F/E2-9240R) were used to amplify the partial sequences of the structural polyprotein gene in the E1 and E2 coding region [43]. Furthermore, an entomological study supported the transmission risk of endemic CHIKV via anthropophilic *Ae. aegypti* and *Ae. albopictus* [44][45].

RVFV

An RVFV study conducted in cattle and humans in Bangui reported an overall seroprevalence of anti-RVFV IgM antibodies of 1.9% and that of IgG antibodies of 8.6%. IgM antibodies were found only during the rainy season, but the frequency of IgG antibodies did not differ significantly by season. No evidence of recent RVFV infection was found in 335 people considered at risk; however, 16.7% had evidence of past infection [46]. In another study conducted on cattle, it was found that antibodies to RVFV virus were found in about 8% of adult cattle [47]. The presence of antibodies of CHIKV in cattle indicates their possible role as a reservoir of the disease in Bangui.

YFV, DENV, and ZIKV

In the Central African Republic, since 2006, YFV cases have been notified in the provinces of Ombella-Mpoko, Ouham-Pende, Basse-Kotto, Haute-Kotto, and in Bangui, the capital, which is also an *Aedes* spp.-endemic area. However, the presence of the YFV vectors in the capital city of CAR represents a risk for the spread of the disease. To the best of our knowledge, little or no updated information on YFV, DENV, and ZIKV has been published on the burden of these arboviruses in CAR. However, a distribution map on these three arboviruses of public health concern by Adam and Jassoy [1] showed that CAR is an endemic country for these arboviruses and its vectors. Researchers noticed from the published information on arboviruses of CAR that more entomological studies were conducted to show potential spillover, but epidemiological evidence was scant, probably due to lack of diagnostic capacity and the health care priority being focused on other diseases. An interesting study from 1973 to 1983 in CAR revealed the vector competence status of several species of *Aedes*, *Culex*, and *Anopheles* in the spread of the six medically important arboviruses considered herein [48]. Moreover, updated information on competent vectors of arboviruses from 2006 to 2010 was reported [49]. Furthermore, the competent vectors of YFV were identified in CAR [50].

1.4. Chad

Three important arboviruses (DENV, YFV, and RVFV) have been reported to occur in Ndjamena (**Table 1**), the capital city of Chad. Only six papers were found eligible for Chad and were included in the study. The weak publication turnover of Chad could be due to the lack of diagnostic capacity as in most central African countries, where samples are usually sent for further confirmation outside the country, and due to the fact that health care priority is oriented towards other epidemics.

DENV

Information on dengue in Chad is not documented and no available evidence on its occurrence was found for the period from 1993 to 2023, but the distribution map of Adam and Jassoy [1] indicates the presence of this arbovirus in this country. The occurrence of competent mosquito vectors have already been reported in the DENV outbreak areas of Chad, and this portrays the risk for the transmission of arboviruses [51].

YFV

A low prevalence (0.28%) of YF was obtained from jaundice patients in Ndjamena from 2015 to 2020 during a non-outbreak period [52]. Chad has also been reported to be a yellow-fever-endemic area with high transmission risk [1]. It is important to add that the detection of YFV was carried out by MAC-ELISA-CDC [52].

RVFV

This is a zoonotic febrile disease that affects livestock and humans and was first reported in Chad in 1967 [53] and in the same period in Cameroon; since then, this disease has spread beyond the subregion. Apart from this preliminary report, another report by Durand et al. [54] revealed a prevalence rate of 4% in French troops. The evidence of circulating RVFV among these French soldiers was carried out using ELISA and confirmed via real time PCR/sequencing using primers targeting the L, M, and S regions of the genome [54]. In fact, the competent vectors of this arbovirus have already been reported [51].

1.5. Democratic Republic of Congo

YFV

Following the indepence of the DRC in 1960, YF epidemics have been reported in all 26 provinces of the country. A two-year survey (2013 to 2014) reported a YFV prevalence of 31.5% among children in the DRC [55]. From 5 December 2015 to November 2016, a large YF outbreak affected Angola and the DRC, with 7334 suspected cases, of which 962 have been confirmed, and 393 deaths were reported to the WHO as of 28 October 2016 [56][57]. According to the updated distribution map of Adam and Jassoy [1], the DRC is a YF-endemic area with high transmission risk [57][58]. A recent report on YF in the DRC was conducted in Kinshasa, its capital city, with a seroprevalence range of 6–73% [55][59] (**Table 1**). The occurrence of YFV in the capital city of this country was not astonishing, as it is known that densely populated cities, where high densities of mosquitoes coexists with city inhabitants, are a favouratble milieu for an epidemic of massive proportions. Moreover, the existence of a high density of competent *Aedes* vectors of YFV, already identified in the DRC, is the major driver of major epidemics [60].

CHIKV

In the last two decades, Kinshasa, the capital of the DRC, experienced CHIKV epidemics in the years 1999 and 2000, with an estimated 50,000 reported cases [61]. In addition, also in Kinshasa, another outbreak occurred in 2012 [62]. Apart from Kinshasa, other provinces where CHIKV has been reported are Kisangani [63] and Matadi [60]. According to the *Aedes* spp. and the CHIKV distribution maps published in Adam and Jassoy [1], the DRC is a CHIKV-endemic area with high transmission risk [58]. The evidence for the occurrence and spread of CHIKV in the DRC was obtained through high-throughput diagnostic approaches such as PCR/sequencing, where a CHIKV-specific RT-qPCR was performed using primers targeting a 77 bp portion of the non-structural protein 1 (NSP-1), as described by Planning and collaborators [60]. An entomological investigation led to the identification of *Ae. albopictus* as the primary vector of CHIKV [60]. Similarly, another study used primers that rather targeted the E1/3′UTR region, as evidence of the re-emergence of CHIKV in DRC [64]. The principal vector involved in CHIKV transmission in the DRC has been reported to be *Ae. albopictus* [65][66].

DENV

Dengue fever virus is one of the common mosquito-borne viruses in the DRC, and cases of this disease has been reported in some hotspot provinces such as Kisangani [63] and Kinshasa [55][62][67][68] via seroepidemiological studies [55][69]. Furthermore, serotyping information on the circulating DENV in the DRC was not available until a survey reported 16 DENV-1 and DENV-2 cases from 2003 to 2012 [70]. Genetic analysis revealed that the DENV-1 strain that caused the 2013 epidemic in Angola also circulated in the DRC in 2015 [71]. Three serotypes of DENV (DENV-1, DENV-2, and DENV-3) have been recorded in the DRC, the most frequent being serotype DENV-1 [55]. In Kisangani, DENV co-circulated with CHIKV during the WNV outbreak of 1998 [63]. In Kinshasa, co-occurrence of dengue and chikungunya was reported during the 2012 outbreak [62]. To conclude, the DENV updated map for sub-Saharan Africa (SSA), published in Adam and Jassoy [1], shows that the DRC is a DENV-endemic area with high transmission risk [58]. The evidence of DENV in the population was confirmed via PCR/sequencing, where the DENV-1 was detected using pan-flavivirus nested RT-PCR with primers targeting the non-structural protein 5 (NS5) gene [71]. Similarly, another study for the confirmation of DENV-1 rather used specific primers targeting the *E* gene [67]. The circulation of DENV-1 was not surprising, as entomological studies reported the presence of competent vectors in the DRC [65][66].

ZIKV

Only a few studies present relevant information on the burden and distributon of Zika in the DRC, and only one study reported on its occurrence. A serological study from 2013 to 2014 showed a prevalence rate of 3.5% for ZIKV antibodies in sud-Ubangi [55]. Another study by [70], for the period 2003 to 2011, showed a negative test result for ZIKV using the polymerase chain reaction (PCR) method. The occurrence of Zika virus in the DRC has also been shown in the updated distribution map for ZIKV for SSA [1].

RVFV

In 1998, in the Kisangani area of the DRC, RVF has was reported in humans with a low prevalence of 4% [63]. As a zoonotic arbovirus, it has also been reported in domestic animals such as cattle, where in 2009, a seroprevalence of 20% was reported in this animal species in Katanga [72]. Moreover, a seroprevalence rate range of 2–16% among cattle was reported in the Nord-Kivu, Sud-Kivu, and Ituri provinces from the Eastern region [73]. A transmission risk study conducted in 2014 revealed that *Aedes* mosquitoes harbored RVFV [74].

WNV

From the available information on WNV of the DRC, only one paper presents relevant information on clinical cases of the disease, and this was in 1998, when a high seroprevalence of 66% was reported in Kisangani [63]. Other information on this virus has been obtained from research on wild animals to establish their potential epizootiological role in its spread to humans, where WNV antibodies were detected in Haut-Uelé Province in chimpanzee [75], bufalo, and elephant in the Garamba National Park [73].

1.6. Equatorial Guinea

The available and relevant information on arboviruses and associated vectors for Equatorial Guinea (EG) was documented in only four papers. The weak publication frequency in EG could be due to the lack of diagnostic facilities, as in most central African countries, where samples are mostly sent for further confirmation outside the country, and also due to the fact that the health care priority is oriented towards other epidemics. It is important to add that the use of less sensitive and specific techniques, such as rapid diagnostic tests and ELISAs, could lead to the under-reporting of the occurrence and burden of some key arboviruses in many African countries. The details on each arbovirus are presented (**Table 1**) as follows.

CHIKV, DENV, and YFV

From the best of our knowledge, the only arboviruses that have been reported in EG are CHIKV, DENV, and YFV. Chikungunya was first detected in 2002 and 2003 [76]. In 2006, one of the three travelers returning from EG was diagnosed as positive for CHIKV in Spain [77]. Inaddition, EG is known to be CHIKV-endemic [1]. Similarly, only one study presents the distribution map of DENV and YFV of EG, and it shows that the country is endemic for the two arboviral types [1]. The PCR/sequencing techniques provided evidence for the circulation of CHIKV, where sequences of amplified fragments corresponding to 195 bp of the non-structural protein 4 gene of alphaviruses identified a homogenous cluster of this arbovirus in the 2002 and 2006 outbreaks [77]. In order to obtain a sequence with more phylogenetic information, primers designed by Powers et al. were used to amplify a fragment of a region of the envelope 1 (E1) gene often used for CHIKV phylogenetic analysis [77]. During major arboviral outbreak periods, entomological reports showed the wide spread of *Ae. albopictus* vectors in Bioko in EG [78].

1.7. Gabon

In Gabon, arboviruses and associated vectors have been reported in 39 papers. The publication trend has evolved positively for epidemiological studies, with a high number registered in 2022. All six arboviruses of public health concern have been identified (**Table 1**), but their prevalence and distribution differed with each province as follows.

CHIKV

This virus was reported in the whole of Gabon [79], and two important outbreaks occurred in 2007 and 2010 [80] in the Estuaire province of the capital city (Libreville) of Gabon. In Libreville, the prevalence range was 3–86% [81], followed by Haut-Ogooue (45.2–62.3%) [80], and then Ogooue-Lolo (28.7%) [82]. Recent reports on CHIKV are from the Moyen-Ogooue province, with a prevalence range of 0.6–61.2% [28][83]. Chikungunya is endemic in Gabon, with high transmission risk [1]. The evidence of circulating CHIKV in Gabon was confirmed using high-throughput PCR/sequencing using specific primers (OP16 and OP17) [84]. Another study targeted the *E*1 gene for CHIKV, as well as the 3′UTR region, during the 2007 and 2010 CHIKV/DENV outbreaks in Libreville, the capital city of Gabon [82]. It is important to underline that the 2010 arbovirus outbreak in Gabon was driven by CHIKV and DENV [79][83]. This period (2007 and 2010) was characterised by the invasion and wide spread of competent *Aedes* vectors in Libreville [85][86][87].

DENV

Similar to CHIKV, DENV in Gabon was identified in all the regions surveyed [79][88] and has been reported to be endemic [1]. The DENV hotspot areas are Moyen-Ogooue (12.3–88.24%) [89][90][91], Haut-Ogooue (12.2%) [80], and Estuaire (4–21.4%) [81]. The evidence of DENV-2 circulation in Gabon by PCR/sequencing was carried out using primers to amplify the envelope (E) gene (758 bp; genome position 1503–2260 nt). Similarly, consensus DENV-1 and DENV-3 PCR fragments of the *E* gene corresponding to a 472 bp fragment of DENV-1 (genome position 1234–1705 nt) and to a 935 bp fragment of DENV-3 (genome position 1256 to 2190 nt) were amplified [88]. Another study was conducted to show the evidence of DENV-3 having amplified the full length of the envelope gene (1479 bp) [90]. Entomological studies found that *Ae. aegypti* and *Ae. albopictus* were associated with CHIKV and DENV-2 [81][92]. In 2021, the re-emergence of DENV, CHIKV, and ZIKV was established via

PCR/sequencing using primers targeting the envelope of dengue virus serotype 1 (1485 bp). The updated entomological studies in both urban [93][94] and sylvan environments [95] showed high density and species richness of *Aedes* mosquito vectors in Gabon. Another interesting finding in Gabon was that which identified genes underlying specific resistance of DENV-1 and DENV-3 in *Ae. aegypti* [87].

RVFV, YFV, WNV, and ZIKV

The reports on RVFV, YFV, WNV, and ZIKV for Gabon are scant; only one paper reported the presence of these four arboviruses, and only in the Moyen-Ogooue province, with varying prevalences: YFV (60.7%); ZIKV (40.3%); WNV (25.3%); and RVFV (14.3%) [89]. The evidence from serology/RT-PCR tests shows the recent circulation of the six medically important arboviruses considered in this study [89]. The evidence of circulating ZIKV was made through PCR/sequencing, where the non-structural protein 3 (1851 bp) was targeted, and then further screening targeted non-structural proteins (772 bp) and envelope (750) genes of ZIKV [96]. Moreover, the evidence of circulating ZIKV in Gabon was made by amplifying the *E* and *NS3* region using specific primer sequences already published for *E* genes (ZIK-ES1/ZIK-ER1, ZIK-ES2/ZIK-ER2) and *NS3* genes (ZIK-NS3FS/ZIK-NS3FR and ZIK-X1/ZIK-X2), and the entomological part of this study revealed *Ae. albopictus* as the primary vector [97]. It is important to state that the RVFV reported in Gabon was only confirmed via serology and the presence of competent vectors [98].

1.8. The Republic of the Congo

The available and relevant information on arboviruses and associated vectors for the RoC was documented in 10 papers. Evidence of the circulating arboviruses in the RoC was based on rapid diagnostic tests, ELISA, and RT-PCR/sequencing. It is known that the sensitivity and specificity of any rapid antibody (IgG or IgM) ELISA or RT-PCR could be of limited value during the initial phase of the transmission window of the disease, as the level of viraemia and IgM antibody titres may be below the limits of detection [99]. The details is presented (**Table 1**) as follows.

CHIKV

In January 2019, an outbreak of CHIKV fever was reported near Pointe-Noire. This study found a novel CHIKV strain and established the presence of the A226V substitution and close relation with *Aedes aegypti*-associated Central Africa chikungunya strains [100]. Similarly, in 9 February 2019, during the CHIKV outbreak, investigations found two new CHIKV sequences of the East/Central/South African (ECSA) lineage, clustering with the recent enzootic sub-clade 2, showing the A226V mutation. Entomological surveys reported one *Ae. albopictus* pool to be RT-PCR positive [101]. The establishment of the occurrence of CHIKV in the RoC was conducted using two methods (rapid diagnostic test (RDT) and RT-PCR/sequencing). The RDT for specific IgG and IgM detection (STANDARD F Chikungunya IgM/IgG FIA SD BIOSENSOR, Chungcheongbuk, Republic of Korea) was used, and RT-PCR/sequencing was conducted using primers designed by referring to the sequences of the Pakistan-07/2016 CHIKV isolate complete genome [101]. Moreover, the evidence of the CHIKV 2011 outbreak in the RoC was obtained via RT-PCR, where primers previously designed to sequence the LR2006 OPYI CHIKV strain were used to generate PCR products [102]. *Aedes albopictus* was identified to be the primary vector of CHIKV in the RoC [101]. The re-emergence of CHIKV in the RoC was due to the wide spread and dense population of *Ae. albopictus*, as already reported [103].

DENV

Although DENV is one of the frequently reported arboviruses in the Central African subregion, to the best of our knowledge, no relevant information has been presented on its burden and occurrence in the RoC. However, the distribution map of DENV for SSA by Adam and Jassoy [1] clearly shows that the RoC is endemic for this virus and its *Aedes* spp. Vectors [103].

ZIKV

The lone study reporting the occurrence of ZIKV in the RoC was conducted on 386 serum specimens from volunteer blood donors in 2011 from rural and urban areas of the Republic of the Congo. The result of this study showed a low ZIKV seropositivity rate (1.8%) [104]. The occurrence of competent vectors (*Ae. aegypti* and *Ae. albopictus*) of ZIKV is evidence of risk for its transmission in the RoC [105].

2. Distribution of Arboviruses in the Central African Subregion

Chikungunya and Dengue were the most frequently detected of the six studied arboviruses of medical importance. Indeed, some countries have already witnessed historic epidemic waves of CHIKV; for instance, in Cameroon in 2006, in Gabon (2007 to 2010), in Congo Brazzaville in 2011, and in the DRC in 2019. The circulating arboviruses in the different Central African countries are presented in **Table 1**. The widespread distribution of CHIKV and DENV could be attributed to the suitable ecological variables for its vectors, and, of course, it has already been reported that DENV is the most prevalent of all arboviruses [106][107]. Although RVFV cases have already been reported in clinical cases in countries such as Chad, CAR, Gabon, and the DRC, data are still scant, but in a country such as Cameroon, information is mostly available for animal species (cattle, sheep, and goats) [108][109]. The free circulation of livestock and people in the Central African regional corridor could be the main driver of the circulating strains of major arboviruses in countries of this region [28]. The circulation of RVFV in domesticated ruminants in countries of this region could indicate a possible risk of human exposure to zoonotic strains [110]. Moreover, information on WNV was also poorly documented, with clinical cases reported in Cameroon, Gabon, and the Democratic Republic of Congo. Moreover, information on WNV in animals is scant and needs to be documented. The detection discrepancies between countries could be multifactorial, as follows: (i) lack of knowledge; (ii) low or lack of diagnostic capacity; and (iii) poor surveillance systems. The lack of data from the Central African subregion makes it difficult to generate robust and quality field epidemiological and entomological information that could inform us of the patterns and drivers of arthropod-borne diseases transmission [111][112].

Table 1. Occurrence and burden of major arboviruses in different countries of the Central African subregion from January 1993 to June 2023.

Country	Site (Region, Province, City)	Arbovirus	Diagnosis	Proportions (%)	References
Gabon	Estuaire	CHIKV	P, S, S	3–86	[80][81][84]
		DENV	P, S, S	4–21.4	[80][81][84]
	Moyen Ogooue	CHIKV	S + P, S, S	0.6–61.2	[83][89][113]
		DENV	S + P, S, S + P, S + P	12.3–88.24	[83][89][90][91]
		RVFV	S + P	14.3	[89]
		YFV	S + P	60.7	[89]
		WNV	S + P	25.3	[89]
		ZIKV	S + P	40.3	[89]
	Haut Ogooue	CHIKV	p	45.2–62.3	[82]
		DENV	P	12.2	[82]
	Ogooue Lolo	CHIKV	P	28.7	[82]
	Woleu Ntem	CHIKV	P	0.5	[20]
	nationwide	CHIKV	P, P	35.6–86	[79][114]
		DENV	P, P	0.2–94.8	[79][88]
	212–220 villages	DENV	S	0.5	[115]
		RVFV	S	3.3	[98]
Cameroon	East	ZIKV	S	7.6	[37]
	Littoral	CHIKV	S	12.6–59.4	[14][15]
		DENV	S + P + R, S + P + R, P, P, S + R, R + S, R + P	3.9–68.3	[15][21][22][23][24][25][27]
		ZIKV	S + P + R, S	10–26.2	[15][37]
	South	DENV	P, S + P	0.5–14.28	[20][116]
	North	YFV	S	25.5	[35]
	Far North	DENV	S + P + R, S + P + R	6.7–14.36	[24][25]
		ZIKV	S	2–4.8	[37]
	Adamawa	DENV	S + R, R	4.7–6.89	[27][29]
		ZIKV	S	2	[37]
	West	CHIKV	S + P	15.7	[26]
		DENV	S + R, S +R, S + P, P + R	6.14–14.36	[24][25][26][27]

Country	Site (Region, Province, City)	Arbovirus	Diagnosis	Proportions (%)	References
	Center	CHIKV	S, S + P + R, S + P	3–59.4	[14][15][17]
		DENV	S + P + R, S + R, S + R, P + R, S + P	3–45.45	[15][17][24][25][27]
		ZIKV	S	3.3	[37]
	North West	CHIKV	S	51.4	[18]
	South West	CHIKV	S, S	4–63	[16][28]
		ZIKV	S	11.4	[28]
		DENV	S, S	2.5–74	[16][28]
		YFV	S	4–72	[16]
		WNV	S	3–82	[16]
Democratic Republic of Congo	Matadi	CHIKV	S + P + R	83.2	[60]
	Kisangani	WNV	S	66	[63]
		CHIKV	S	34	[63]
		DENV	S	3	[63]
		RVFV	S	4	[25]
	kinshasa	DENV	S, R, P, S + P + R, S + P	0.4–8.1	[55][62][67][68][70]
		YFV	S, S + P	6.0–73	[55][59]
		CHIKV	S, R, S + P, S, P, P	0.1–49.7	[55][62][64][70][117][118]
	Sud-Ubangi	ZIKV	S	3.5%	[55]
Republic of the Congo	Brazzaville	CHIKV	P, S + P	11.7–71	[102][119]
	Pointe-Noire		P, S + P	-	[100][101]
	-	ZIKV	S	1.8	[104]
	-	DENV	S + P	-	[1]
Angola	Luanda	DENV	P, P + R, S + P	11.1–94.4	[5][9][120]
		CHIKV	P, P	7	[5][121]
	13 provinces	YFV	S	70	[122]
Equatorial Guinea	Bata	CHIKV	P	1.1–33.3	[77]
Chad	N'Djamena	YFV	S + P, S + R	0.28	[1][52]
		RVFV	P	4	[54]
		DENV	S + P	-	[1]
Central African Republic	Bangui	YFV	S + P	6.5	[123]
		RVFV	P	1.9–16.7	[46]
		CHIKV	P	-	[41]

Chikungunya virus (CHIKV); dengue Virus (DENV); Zika Virus (ZIKV); yellow fever Virus (YFV); Rift Valley fever virus (RVFV); West Nile virus (WNV). (-) not available; RNA detection (P); rapid diagnostic test (R); serology (S); serological and RNA detection in the same paper (S + P); serology, RNA detection, and rapid diagnostic test (S + P + R). The order of tests separated by commas in the diagnosis column corresponds to the references in the square brackets of the references column.

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