Geographical distribution of *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae) and genetic diversity of invading population of *Ae. albopictus* in the Republic of the Congo

[version 1; peer review: 2 approved]

Basile Kamgang 1, Theodel A. Wilson-Bahun 1,2, Helen Irving 3, Michael O. Kusimo 1, Arsene Lenga 2, Charles S. Wondji 1,3

1Medical Entomology, Centre for Research in Infectious Diseases, Yaounde, P.O. Box 13591, Cameroon
2Faculty of Science and Technology, Marien Ngouabi University, Brazzaville, Congo
3Liverpool School of Tropical Medicine, Liverpool, UK

**Abstract**

**Background:** The arbovirus vector, *Aedes albopictus*, originating from Asia, has recently invaded African countries, including the Republic of the Congo, where it was associated with a chikungunya outbreak. Up until now, little was known about its distribution in relation to the native *Aedes aegypti* and how the invasion will modify the epidemiology of arboviral diseases. Here, we assessed the current distribution of *Ae. albopictus* and *Ae. aegypti* in the Republic of the Congo and explored the genetic diversity of the invading species, *Ae. albopictus*.

**Methods:** Immature stages of *Aedes* were collected in nine locations in the Republic of the Congo in 2017 following a north-south transect and reared to adult stage. Adults were morphologically identified, counted and grouped according to species and location. Genetic diversity of *Ae. albopictus* was assessed by analyzing the cytochrome oxidase I (*COI*) gene.

**Results:** *Ae. albopictus* and *Ae. aegypti* were found together across the country in all the locations investigated. The invasive species is predominant over the native species in all locations except Brazzaville, suggesting that *Ae. albopictus* is displacing *Ae. aegypti* across Congo. When comparing the species distributions across the two largest cities, Brazzaville and Pointe Noire, *Ae. albopictus* was more prevalent than *Ae. aegypti* in the suburbs whereas the opposite situation was reported in the city centre. Mitochondrial DNA analysis revealed very low genetic diversity of *Ae. albopictus* with only three haplotypes recorded across the country supporting the recent introduction of this species in the Republic of the Congo. Phylogenetic tree analysis revealed that *Ae. albopictus* from Congo originated from other tropical Asian countries such as China, likely as a result of increasing trade links.

**Conclusion:** These findings are important for the implementation of vector control strategies and can serve as a foundation for further research on arboviral epidemiology.
control strategies and can serve as a foundation for further research on these vectors in the country.

Keywords
Aedes albopictus, Aedes aegypti, ecological distribution, arbovirus vectors, genetic diversity, Republic of Congo

Corresponding author: Basile Kamgang (kamgang_d@yahoo.fr)

Author roles: Kamgang B: Conceptualization, Data Curation, Formal Analysis, Funding Acquisition, Investigation, Methodology, Project Administration, Resources, Software, Supervision, Validation, Visualization, Writing – Original Draft Preparation, Writing – Review & Editing; Wilson-Bahun TA: Formal Analysis, Investigation, Methodology, Visualization, Writing – Review & Editing; Irving H: Data Curation, Formal Analysis, Writing – Review & Editing; Kusimo MO: Writing – Review & Editing; Lenga A: Supervision, Writing – Review & Editing; Wondji CS: Conceptualization, Funding Acquisition, Project Administration, Supervision, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: This work was supported by a Wellcome Trust Training Fellowship in Public Health and Tropical Medicine (204862) awarded to Basile Kamgang. The funders had no role in study design, data collection or analysis, decision to publish or preparation of the manuscript. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Copyright: © 2018 Kamgang B et al. This is an open access article distributed under the terms of the Creative Commons Attribution Licence, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

How to cite this article: Kamgang B, Wilson-Bahun TA, Irving H et al. Geographical distribution of Aedes aegypti and Aedes albopictus (Diptera: Culicidae) and genetic diversity of invading population of Ae. albopictus in the Republic of the Congo [version 1; peer review: 2 approved] Wellcome Open Research 2018, 3:79 (https://doi.org/10.12688/wellcomeopenres.14659.1)

**Introduction**

Arthropod-borne viral diseases such as dengue, zika and chikungunya have emerged or re-emerged in several countries of the world during the past decades. These viruses are transmitted to vertebrates, including humans, by the bites of infected mosquitoes that share the same ecological niche as the host organism. Indeed, two distinct ecological cycles, enzootic and urban epidemic cycles, have been well documented. The enzootic cycle occurs in the sylvan environment, involving non-human primates and wild mosquitoes, while urban epidemic cycle occurs in urban environments, implicating human beings and urban mosquitoes such as *Aedes aegypti* Linnaeus 1762 and *Aedes albopictus* (Skuse) 1894. Other potential modes of zika virus transmission to humans have been evoked notably via sexual intercourse or via blood donor. Both epidemic vectors, *Ae. aegypti* and *Ae. albopictus*, are found in sub-Saharan Africa, where *Ae. aegypti* is native. Two subspecies of *Ae aegypti*, *Ae. aegypti formosus* and *Ae. aegypti aegypti*, were formally identified by Mattingly in 1957. *Ae. aegypti formosus*, is a dark colored mosquito confined to African forests while *Ae. aegypti aegypti* is light-colored with white abdominal scales and is found in human-dominated habitats primarily outside Africa. Generally, *Ae. aegypti* collected in central Africa match *Ae. aegypti formosus*. While *Ae. albopictus* is a native of South East Asia, it has now invaded all the five continents during the past 30–40 years. This rapid global spread was caused mainly by sales and distribution of used tires across the world coupled with the ecological plasticity of the species, enabling its adaptation to various environments. *Ae. albopictus* was reported for the first time in Central Africa in early 2000 and is currently present in almost all central African countries, where it tends to supplant the indigenous species *Ae. aegypti* in human-domesticated environment. The predominance of *Ae. albopictus* over *Ae. aegypti* in sympatric areas has been shown to result from the higher mating competitiveness of *Ae. albopictus* over *Ae. aegypti*. Previous studies in Central Africa showed that both *Ae. aegypti* and *Ae. albopictus* can be found together in the same location and often share the same larval habitats. In this region, the immature stages of both species develop in stagnant water found mainly in peri-domestic containers such as used tires and discarded tanks. However, in the sympatric area, *Ae. albopictus* prefers containers surrounded by vegetation whereas *Ae. aegypti* prefers containers located in neighbourhoods with high building densities.

Dengue, zika and chikungunya were for a long-time considered to be rare in Central Africa, because only sporadic epidemics were reported in the rural environment, with isolation of the viruses in wild mosquitoes and humans. In the past decades, several outbreaks have been reported in this part of the world, notably a concurrent dengue/chikungunya outbreak in Gabon in 2007, with more than 20,000 cases of chikungunya, and a large chikungunya outbreak in 2011 in the Republic of the Congo with more than 11,000 cases. This suggests an epidemiological modification of arboviral diseases in the region. During these outbreaks, *Ae. albopictus* was established as the major vector particularly in Gabon, where zika was detected in this species. In Congo, both *Ae. aegypti* and *Ae. albopictus* were found to be positive for chikungunya virus, implicating both species in virus transmission. This investigation was the first to confirm the presence of *Ae. albopictus* in the Republic of the Congo. Since then, no study has been undertaken to compare the geographical distribution and prevalence of *Ae. aegypti* and *Ae. albopictus* in the Republic of the Congo as well as the genetic diversity of the invading species. Indeed, previous studies in Central Africa based on polymorphisms to the cytochrome oxidase subunit 1 (COI) gene indicated that *Ae. albopictus* populations in Cameroon are related to tropical rather than temperate or subtropical out-groups. However, the Central African Republic population segregated into two lineages: the first encompassed specimens from tropical areas including all the haplotypes from Cameroon and the second lineage encompassed temperate and subtropical areas, suggesting multiple sources of *Ae. albopictus*.

To improve entomological surveillance and the control of these arbovirus vectors in the Republic of the Congo, we present here the current nation-wide geographical distribution and prevalence of *Ae. aegypti* and *Ae. albopictus* in this country, and establish the genetic diversity of the invading population of *Ae. albopictus* using the COI gene.

**Methods**

**Sampling sites**

Mosquitoes were collected in May and November 2017 in nine locations in the Republic of the Congo across the north-south transect (Table 1 and Figure 1). The Republic of the Congo is located in Central Africa, straddling the equator. Two main types of vegetation are found. The forest in the north, covering 60% of the national territory, and the savannah, which occupies the remaining parts of the country. There are three types of climate. The equatorial climate is found in the north of the country, characterized by high humidity and rainfall greater than 1,700 mm per year, with an average temperature between 24°C and 26°C. The humid tropical climate in the southwest, where annual average precipitation varies from 1,200 mm to 1,700 mm, with an average monthly temperature between 21°C and 27°C. The subequatorial climate, experienced at the plateau and basin regions, has an average annual rainfall of about 1,600 mm. Because the spread of *Aedes* mosquitoes mainly relies on human activities, sampling was focused on human-domesticated environments spread along the main communication networks, and trade routes throughout the country.

**Mosquito collection, rearing and identification**

In Brazzaville and Pointe Noire, the two most populated cities in the Republic of the Congo, the difference between downtown and suburban was examined during the investigation. In the other locations, however, samples were collected randomly throughout each city and pooled together. In each selected location, all containers with water were inspected and positive containers (with at least one *Aedes* larvae or pupae) were recorded. Immature stages of *Aedes* were collected, transported to the insectaries, pooled according to the location and reared to adult stage for morphological identification. G0 adults were stored
Table 1. Sampling sites in the Republic of the Congo.

<table>
<thead>
<tr>
<th>Location</th>
<th>Geographical coordinates</th>
<th>Altitude, m</th>
<th>Climate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brazzaville</td>
<td>S 4°19'38&quot; E 15°09'12&quot;</td>
<td>278</td>
<td>Subequatorial climate</td>
</tr>
<tr>
<td>Lefini</td>
<td>S 2°54'58&quot; E 15°37'56&quot;</td>
<td>314</td>
<td>Subequatorial climate</td>
</tr>
<tr>
<td>Ngo</td>
<td>S 2°29'14&quot; E 15°45'00&quot;</td>
<td>636</td>
<td>Subequatorial climate</td>
</tr>
<tr>
<td>Gamboma</td>
<td>S 1°52'27&quot; E 15°52'25&quot;</td>
<td>378</td>
<td>Subequatorial climate</td>
</tr>
<tr>
<td>Oyo</td>
<td>S 1°09'14&quot; E 15°58'21&quot;</td>
<td>297</td>
<td>Subequatorial climate</td>
</tr>
<tr>
<td>Owando</td>
<td>S 0°29'42&quot; E 15°54'41&quot;</td>
<td>275</td>
<td>Subequatorial climate</td>
</tr>
<tr>
<td>Makoua</td>
<td>S 0°00'23&quot; E 19°37'33&quot;</td>
<td>350</td>
<td>Equatorial climate</td>
</tr>
<tr>
<td>Ouesso</td>
<td>N 1°36'35&quot; E 16°02'58&quot;</td>
<td>339</td>
<td>Equatorial climate</td>
</tr>
<tr>
<td>Pointe Noire</td>
<td>N 4°48'19&quot; E 11°53'23&quot;</td>
<td>14</td>
<td>Tropical climate</td>
</tr>
</tbody>
</table>

Figure 1. Geographic distribution of *Ae. aegypti* and *Ae. albopictus* across the Republic of the Congo.
at -20°C for molecular and genetic analyses. The comparisons between the prevalence of *Ae. aegypti* and *Ae. albopictus* in each location, across the country were performed using multiple chi-square test.

Mitochondrial DNA analysis for *Ae. albopictus*

Genomic DNA was extracted from 20 whole *Ae. albopictus* per location (nine locations) using the Livak protocol as previously described. DNA extracts from each location were used as templates to amplify 700-bp fragment of COI gene. The sequences of primers used are: albCOIF 5’-TTTCAACAAT-CATAAGATATGG-3’ and albCOIR 5’- TAAACTTCTGGA TGACCAAAAAATCA-3’. Polymerase chain reaction (PCR) amplification was performed using a Gene Touch thermal cycler (Bulldog Bio, Portsmouth, USA), as described previously. PCR products were detected by agarose gel electrophoresis in Tris-Acid-EDTA buffer (TAE). The gel was prepared with Midori green, staining dye, and visualized with the aid of UV light. PCR products from each location with very good amplification were purified using the Exo-SAP protocol and sent to the Centre for Genomic Research (Liverpool, UK) for sequencing.

Sequence data analysis

Sequences were manually corrected using BioEdit software version 7.2.1 (http://en.bio-soft.net/format/BioEdit.htm) and aligned using ClustalW, which is present in BioEdit software. Sequences were numbered based on the reference sequences downloaded in GenBank KU738429.1. The number of haplotypes (h), the number of polymorphism sites (S), haplotype diversity (Hd) and nucleotide diversity (π) were computed with DnaSP 5.10.01 (http://en.bio-soft.net/dna/dnasp.html). The statistical tests of Tajima, and Fu and Li were also estimated with DnaSP in order to establish non-neutral evolution and deviation from mutation-drift equilibrium. The different haplotypes detected were compared to previous sequences published in GenBank (Supplementary Table 1) that originated from China, Papua New Guinea, USA, Singapore, Taiwan, Malaysia, Hawaii, Christmas Islands, Japan, Solomon Islands, Timor Leste and Torres Strait Islands. The same COI region was sequenced at these various regions and the maximum likelihood phylogenetic tree was constructed using MEGA 7.0. Genealogical relationships between haplotype in this current study was assessed using TCS version 1.21 and tcsBU (http://cibio.up.pt/software/tcsBU) software.

Results

Containers inspected and prevalence of *Ae. aegypti* and *Ae. albopictus*

A total of 640 containers with water were investigated across the Republic of the Congo (Table 2). Among them, 42.9% were positive for immature stages of *Aedes*. Containers were classified into three main groups: domestic (flower pot and water storage tanks), peridomestic (used tires, discarded tanks and car wrecks) and natural (axil of plants). Used tires were the most prevalent habitat and most productive containers in all the locations, ranging from 18.1% in Pointe Noire to 100% in Lefini (Table 2). The presence of *Aedes* in other containers was very limited.

In total, 6,684 specimens of immature stages of *Aedes* were identified, comprising 72.24% of *Ae. albopictus*, 27.70% of *Ae. aegypti* and 0.06% (four specimens collected in Brazzaville downtown) that originated from China, Papua New Guinea, USA, Singapore, Taiwan, Malaysia, Hawaii, Christmas Islands, Japan, Solomon Islands, Timor Leste and Torres Strait Islands. The same COI region was sequenced at these various regions and the maximum likelihood phylogenetic tree was constructed using MEGA 7.0. Genealogical relationships between haplotype in this current study was assessed using TCS version 1.21 and tcsBU (http://cibio.up.pt/software/tcsBU) software.

Table 2. Containers prospected per location.

<table>
<thead>
<tr>
<th>Location</th>
<th>Axil of plants</th>
<th>Used tires</th>
<th>Car wrecks</th>
<th>Discarded tanks</th>
<th>Water storages</th>
<th>Flower pots</th>
<th>All</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>N (%)</td>
<td>N (%)</td>
<td>N (%)</td>
<td>N (%)</td>
<td>N (%)</td>
<td>N (%)</td>
<td>N (%)</td>
</tr>
<tr>
<td>Brazzaville downtown</td>
<td>1 (0.0)</td>
<td>59 (49.2)</td>
<td>3 (100)</td>
<td>10 (80.0)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>73 (54.8)</td>
</tr>
<tr>
<td>Brazzaville suburb</td>
<td>0 (NC)</td>
<td>69 (63.8)</td>
<td>0 (NC)</td>
<td>3 (0.0)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>72 (61.1)</td>
</tr>
<tr>
<td>Pointe Noire downtown</td>
<td>0 (NC)</td>
<td>61 (18.1)</td>
<td>0 (NC)</td>
<td>3 (33.3)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>64 (18.8)</td>
</tr>
<tr>
<td>Pointe Noire suburb</td>
<td>0 (NC)</td>
<td>56 (25.0)</td>
<td>0 (NC)</td>
<td>13 (46.2)</td>
<td>4 (50.0)</td>
<td>0 (NC)</td>
<td>73 (30.1)</td>
</tr>
<tr>
<td>Lefini</td>
<td>0 (NC)</td>
<td>3 (100)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>3 (100)</td>
</tr>
<tr>
<td>Ngo</td>
<td>0 (NC)</td>
<td>47 (38.3)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>47 (38.3)</td>
</tr>
<tr>
<td>Gamboma</td>
<td>0 (NC)</td>
<td>58 (37.9)</td>
<td>0 (NC)</td>
<td>2 (50)</td>
<td>1 (100)</td>
<td>0 (NC)</td>
<td>61 (39.3)</td>
</tr>
<tr>
<td>Oyo</td>
<td>0 (NC)</td>
<td>43 (48.8)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>43 (48.8)</td>
</tr>
<tr>
<td>Owando</td>
<td>0 (NC)</td>
<td>4 (25)</td>
<td>0 (NC)</td>
<td>8 (62.5)</td>
<td>0 (NC)</td>
<td>10 (10.0)</td>
<td>22 (31.8)</td>
</tr>
<tr>
<td>Makoua</td>
<td>0 (NC)</td>
<td>59 (54.2)</td>
<td>0 (NC)</td>
<td>10 (30)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>69 (50.7)</td>
</tr>
<tr>
<td>Ouesso</td>
<td>0 (NC)</td>
<td>97 (50.5)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>0 (NC)</td>
<td>97 (50.5)</td>
</tr>
<tr>
<td>All</td>
<td>1 (0.0)</td>
<td>556 (43.9)</td>
<td>3 (100)</td>
<td>65 (36.9)</td>
<td>5 (60.0)</td>
<td>10 (10.0)</td>
<td>640 (42.9)</td>
</tr>
</tbody>
</table>

N, number of containers found with water; (%), percentage of positive containers; NC, not computed.
Mitochondrial DNA analysis of *Ae. albopictus*

In total, 127 specimens of *Ae. albopictus* from nine locations across the Republic of the Congo were analysed using the COI gene. Sequence analysis, based on 638 nucleotides, revealed a low polymorphism, with only two mutational sites defining three haplotypes namely H1, H2 and H3 (Figure 2B). Consequently, this resulted in low haplotype diversity (Hd=0.24) and nucleotide diversity (π=0.00005) indexes (Table 4). The most frequent haplotype, H1 (86.6%), was detected in all the locations. Supplementary Table 2 shows the haplotype distribution per location. The haplotypes H2 (10.2%) and H3 (3.2%) were found in three (Brazzaville, Oueso and Oyo) and two (Brazzaville and Lefini) locations, respectively (Table 4 and Figure 2). The dominant haplotype matches perfectly with the COI gene sequence deposited in GenBank that originated from China (KU738429.1). A higher genetic diversity was reported in Brazzaville where all the three haplotypes were reported. The haplotype network showed that each haplotype was separated from the others by one mutational step (Figure 2). Overall, Tajima’s D (D=-0.294) and Fu’s Fs (Fs=-0.024) statistics were negative, but not statistically significant. Phylogenetic tree generated and analysed based on 445 nucleotides previously published in GenBank showed that the Republic of the Congo’s haplotypes were closely related to the sequences from China, Singapore, Papua New Guinea and Christmas Island.

**Discussion**

This study has assessed the geographical distribution of *Ae. aegypti* and *Ae. albopictus* in the Republic of the Congo, revealing the co-occurrence of both species across the country. Analyses showed that the invasive species *Ae. albopictus* is the predominant species in all locations investigated except Brazzaville. The co-occurrence of *Ae. aegypti* and *Ae. albopictus* across the Republic of the Congo suggests that the environmental factors which prevail in the country are favourable for the development of both species. The presence of *Ae. albopictus* in the Republic of the Congo was confirmed in 2011 during the chikungunya outbreak in Brazzaville, suggesting its recent introduction. Indeed, previous studies in some central African countries such as Cameroon and Central Africa Republic showed that the co-occurrence of *Ae. aegypti* and *Ae. albopictus* is limited to the southern part of the country up to 6°N, suggesting that climate is a limiting factor for invasion. The predominance of the invading species, *Ae. albopictus*, over the indigenous species, *Ae. aegypti*, has been previously reported in areas where both species are found together in Central Africa. The ecological plasticity of *Ae. albopictus* has been suggested as the main cause of its adaptation to different environments, as well as its mating competitiveness in areas of sympatry with *Ae. aegypti*.

In both major cities where samples were analysed according to peri-urban and downtown environment, results revealed the predominance of *Ae. aegypti* in downtown areas but less in peri-urban areas. Similar findings to these were reported previously in Central Africa. These observations are consistent with former studies indicating the segregation of habitats in sympatric areas according to urban environmental gradients as well as its mating competitiveness in areas of sympatry with *Ae. aegypti*, suggesting its recent introduction. Indeed, previous studies in some central African countries such as Cameroon and Central Africa Republic showed that the co-occurrence of *Ae. aegypti* and *Ae. albopictus* is limited to the southern part of the country up to 6°N, suggesting that climate is a limiting factor for invasion. The predominance of the invading species, *Ae. albopictus*, over the indigenous species, *Ae. aegypti*, has been previously reported in areas where both species are found together in Central Africa. The ecological plasticity of *Ae. albopictus* has been suggested as the main cause of its adaptation to different environments, as well as its mating competitiveness in areas of sympatry with *Ae. aegypti*.

### Table 3. Prevalence of *Aedes aegypti* and *Aedes albopictus* according to the location.

<table>
<thead>
<tr>
<th>Location</th>
<th><em>Ae. aegypti</em></th>
<th><em>Ae. albopictus</em></th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brazzaville downtown</td>
<td>611 (95.62%)</td>
<td>153 (13.72%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Brazzaville suburb</td>
<td>249 (14.96%)</td>
<td>28 (4.38%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Pointe Noire downtown</td>
<td>116 (22.97%)</td>
<td>122 (11.25%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Pointe Noire suburb</td>
<td>249 (14.96%)</td>
<td>104 (41.43%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Makoua</td>
<td>249 (14.96%)</td>
<td>249 (14.96%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Oyo</td>
<td>20 (30.30%)</td>
<td>20 (30.30%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Owando</td>
<td>249 (14.96%)</td>
<td>249 (14.96%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>All</td>
<td>1162 (93.03%)</td>
<td>561 (93.03%)</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>
Figure 2. Genetic diversity of the COI gene across Congolese populations of *Ae. albopictus*. (A) Haplotype network showing the genealogic relationships between three haplotypes detected across Congo. The pie chart represents the proportion of each haplotype per site. (B) COI haplotypes found across the Republic of the Congo. Only polymorphic positions are shown and are numbered with reference (Ref) to the published *Ae. albopictus* sequences for COI (JF309317; China). Dots represent identity with respect to the reference. The numbers above nucleotides indicate the position where mutations were found. *GenBank accession number shown in brackets.


<table>
<thead>
<tr>
<th>Locality</th>
<th>N</th>
<th>H</th>
<th>S</th>
<th>Haplotypes</th>
<th>H</th>
<th>D</th>
<th>D*</th>
<th>F*</th>
<th>Fs</th>
<th>F*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brazzaville</td>
<td>14</td>
<td>H1, H2, H3</td>
<td>2</td>
<td>0.692</td>
<td>0.0014 (0.890)</td>
<td>1.127&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.935&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.0005 (0.890)</td>
<td>0.612&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>1.021&lt;sup&gt;ns&lt;/sup&gt;</td>
</tr>
<tr>
<td>Lefini</td>
<td>15</td>
<td>H1, H3</td>
<td>2</td>
<td>0.133</td>
<td>0.0004 (0.266)</td>
<td>-1.490&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>-1.873&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.235&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>-1.844&lt;sup&gt;ns&lt;/sup&gt;</td>
<td></td>
</tr>
<tr>
<td>Ngo</td>
<td>12</td>
<td>H1</td>
<td>0</td>
<td>0.000</td>
<td>0.0000 (0.000)</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
</tr>
<tr>
<td>Gamboma</td>
<td>14</td>
<td>H1</td>
<td>0</td>
<td>0.303</td>
<td>0.0005 (0.303)</td>
<td>-0.195&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.752&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.297&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.533&lt;sup&gt;ns&lt;/sup&gt;</td>
<td></td>
</tr>
<tr>
<td>Oyo</td>
<td>12</td>
<td>H1, H2</td>
<td>1</td>
<td>0.303</td>
<td>0.0000 (0.303)</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
</tr>
<tr>
<td>Owando</td>
<td>11</td>
<td>H1</td>
<td>0</td>
<td>0.000</td>
<td>0.0000 (0.000)</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
</tr>
<tr>
<td>Makoua</td>
<td>14</td>
<td>H1</td>
<td>0</td>
<td>0.000</td>
<td>0.0000 (0.000)</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
</tr>
<tr>
<td>Ouessso</td>
<td>15</td>
<td>H1, H2</td>
<td>1</td>
<td>0.514</td>
<td>0.0008 (0.5143)</td>
<td>1.376&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.701&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>1.253&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.906&lt;sup&gt;ns&lt;/sup&gt;</td>
<td></td>
</tr>
<tr>
<td>Pointe Noire</td>
<td>20</td>
<td>H1</td>
<td>0</td>
<td>0.000</td>
<td>0.0000 (0.000)</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
<td>NC</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>127</td>
<td>3</td>
<td>2</td>
<td>0.246</td>
<td>0.0005 (0.2952)</td>
<td>-0.294&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.662&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>-0.0238&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>0.417&lt;sup&gt;ns&lt;/sup&gt;</td>
<td></td>
</tr>
</tbody>
</table>

N, number of sequences; S, number of polymorphic sites; H, haplotype; Hd, haplotype diversity; π, nucleotide diversity; k, mean number of nucleotide differences; D, Tajima statistic; D* and F*, Fu and Li statistics; Fs, Fu statistic; NC, not computed; ns, not significant.
the main productive for both *Ae. aegypti* and *Ae. albopictus*. However, the current study targeted mainly garages and tire shops to increase the chances of discovering immature *Aedes*.

The presence and predominance of *Ae. albopictus* across the Republic of the Congo can increase the risk of mosquito-borne arboviral diseases since *Ae. albopictus* has been found competent to transmit about 22 arboviruses. Notably, the emergence of dengue and chikungunya viruses in the human dominated environment in central Africa coincides with the invasion of *Ae. albopictus* in this area where it was found as the main vector. During previous studies in central Africa, *Ae. albopictus* was found to be infected by zika virus in natural conditions. It was also demonstrated that *Ae. albopictus* from Bangui in Central African Republic is able to transmit enzootic chikungunya virus strains.

A very low polymorphism of *Ae. albopictus* discovered in the Republic of the Congo in this study is in agreement with the previous studies using the *COI* gene in areas newly colonised by this species including some Central African countries. This low polymorphism is consistent with the recent introduction from a founder *Ae. albopictus* population or could be related to ubiquitous *Wolbachia* infection in populations of this species, as suggested previously. Brazzaville, the capital city of the Republic of the Congo would be probably the main entry point of *Ae. albopictus* in the country, as higher levels of polymorphism (all the three haplotypes recorded) were detected at this location. For instance, *Ae. albopictus* was reported for the first time in the Republic of the Congo in Brazzaville during a chikungunya outbreak which occurred in the country. Phylogenetic analysis showed that the haplotype sequences from the Republic of the Congo are very close to the sequences isolated from populations originating from China, New Papua Guinea, Singapore and Christmas Islands. Primers used in this current study were not the same as those used in the previous study in Cameroon, Central African Republic and Sao Tome island. Therefore, the haplotypes in the current study cannot be compared with those detected in

---

**Figure 3.** Molecular phylogenetic analysis using the Maximum Likelihood method. The evolutionary history was inferred using the Maximum Likelihood method based on the Tamura 3-parameter model. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. There was a total of 445 positions in the final dataset.
Central Africa. Nevertheless, these data indicate that the population of *Ae. albopictus* found in Central Africa probably originated from other tropical regions as previously suggested[5,26,40]. It will be interesting to perform other studies at macro-geographic scale using other markers such as double-digest restriction-site-associated DNA sequencing to assess the genetic structure and the level of the gene flow between these populations.

**Conclusion**

To our knowledge, this is the first study assessing the distribution of *Ae. aegypti* and *Ae. albopictus* in the Republic of the Congo since *Ae. albopictus* was reported in 2011. Both species were found across the country with *Ae. albopictus* predominating in almost all locations. Low genetic polymorphism of *Ae. albopictus* indicated a recent introduction into the country. The spread of the invading species across the country could change the epidemiology of arboviral diseases in the Republic of the Congo. Thus, it will be important to assess urgently, the vector competence of both *Aedes* species from the Republic of the Congo to prevent several emergence or re-emergence of arboviruses such as dengue, zika and yellow fever viruses. Assessing the susceptibility profile of these species to insecticide will be an important information needed to prepare the country against potential future outbreaks.

**Data availability**

Sequence for *Aedes albopictus* haplotype H1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial, GenBank accession number MH025948: http://identifiers.org/ncbi/gi/1402399558.


Sequence for *Aedes albopictus* haplotype H3 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial, GenBank accession number MH025950: http://identifiers.org/ncbi/gi/1402399562.

**Competing interests**

No competing interests were disclosed.

**Grant information**

This work was supported by a Wellcome Trust Training Fellowship in Public Health and Tropical Medicine (204862) awarded to Basile Kamgang.

*The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.*

**Acknowledgments**

We thank the people living around all the sampling sites for their cooperation during the field investigations.

**Supplementary material**

**Supplementary Table 1. Outgroup sequences used for phylogenetic analysis.**

Click here to access the data.

**Supplementary Table 2. H1, H2 and H3 haplotype distribution per location.**

Click here to access the data.

**References**


Open Peer Review

Current Peer Review Status: ✔ ✔

Version 1

Reviewer Report 07 August 2018

https://doi.org/10.21956/wellcomeopenres.15961.r33442

© 2018 Boyer S. This is an open access peer review report distributed under the terms of the Creative Commons Attribution Licence, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Sébastien Boyer
Unit of Medical Entomology, Institut Pasteur of Cambodia, Phnom Penh, Cambodia

The study is important and essential in the Public Health domain, especially in the Republic of Congo where data on vectors are missing, and where doing field study is not that easy. Even knowing it is difficult to do field studies, from a scientific point of view, there is no replicate in this experiment. The authors went into the field one time in May 2017 and one time in November 2017. It should not be count as two independent samples of the same sites, but it should be considered as one sample during one season, and one sample during the other season. It is better to have a representation of the geographic distribution in both seasons to observe if there is a variation than to have some chi-square tests that are not really useful here. It didn’t deserve the study. As I mentioned earlier, I truly think that the data are important here, including the percentage of positive container for each species, but is should be presented per season also, with no replicate.

For representing the data illustrated in the Figure 2, it should be better to represent it by chart by city. Here we didn’t see very well what is the percentage of H1, H2 and H3 in Brazzaville for example. It is the same problem for the proportion of H1 and H2 in Ouesso, H1 and H2 in Oyo and H1 and H3 in Lefini. By the way, it is very interesting to observe that these 3 haplotypes are nearby Asia and SouthEast Asia haplotypes.

In total, the study is well realized, and the conclusions are directly dependent of the results. But I suggest 2 only minor changes regarding the presentation of the results, especially for the sampling in May and November. I also suggest to replace the Figure 2 by a map with the % of each haplotype (circle or histograms) on each city.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes
Are sufficient details of methods and analysis provided to allow replication by others? 
Partly

If applicable, is the statistical analysis and its interpretation appropriate? 
Not applicable

Are all the source data underlying the results available to ensure full reproducibility? 
Partly

Are the conclusions drawn adequately supported by the results? 
Yes

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Medical Entomology

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

---

**Author Response 07 Aug 2018**

**Basile Kamgang,** Centre for Research in Infectious Diseases, Yaounde, Cameroon

Thank you so much for your comments. Mosquitoes were sampled in May in 8 locations (Brazzaville, Lefini, Ngo, Owando, Makoua, Ouessou, Oyo and Gamboma, and in November in Pointe Noire only) corresponding to rainy season in each location. Precision was made in the manuscript.

The number of haplotypes detected per city is presented in supplement Table S2.

**Competing Interests:** No competing interests were disclosed.

---

**Reviewer Report 23 July 2018**

https://doi.org/10.21956/wellcomeopenres.15961.r33460

© 2018 Konan Y. This is an open access peer review report distributed under the terms of the Creative Commons Attribution Licence, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

**Yao Lucien Konan**

Vector Control Department, National Institute of Public Hygiene, Abidjan, Cote d'Ivoire

The work is clearly written in a precise way with recent references used. At the method level, it should be noted the months of mosquito collection were indicated without the seasonal correspondence in the different localities.

In the results, the authors mention productivity of used tires while the larvae and pupae found in the different containers inspected were not counted. They must replace "productive" with "positive".
Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Author Response 23 Jul 2018

**Basile Kamgang**, Centre for Research in Infectious Diseases, Yaounde, Cameroon

I agree with the reviewer that the season was not indicated. Mosquitoes were collected in May and November 2017 corresponding to the rainy season in nine locations in the Republic of the Congo across the north-south transect.

It is true that the number of pupae and larvae has not been counted, but the number of mosquitoes emerging from each type of larval habitat has been counted.

**Competing Interests:** No competing interests were disclosed.