



RESEARCH ARTICLE

REVISED **Detection of Cell-Fusing Agent virus across ecologically diverse populations of *Aedes aegypti* on the Caribbean island of Saint Lucia [version 2; peer review: 2 approved, 1 approved with reservations]**

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V2 **First published:** 25 Jun 2020, 5:149
<https://doi.org/10.12688/wellcomeopenres.16030.1>
Latest published: 16 Dec 2020, 5:149
<https://doi.org/10.12688/wellcomeopenres.16030.2>

Abstract

Background. Outbreaks of mosquito-borne arboviral diseases including dengue virus (DENV), Zika virus (ZIKV), yellow fever virus (YFV) and chikungunya virus (CHIKV) have recently occurred in the Caribbean. The geographical range of the principal vectors responsible for transmission, *Aedes (Ae.) aegypti* and *Ae. albopictus* are increasing and greater mosquito surveillance is needed in the Caribbean given international tourism is so prominent. The island of Saint Lucia has seen outbreaks of DENV and CHIKV in the past five years but vector surveillance has been limited with the last studies dating back to the late 1970s. Natural disasters have changed the landscape of Saint Lucia and the island has gone through significant urbanisation.





Methods. In this study, we conducted an entomological survey of *Ae. aegypti* and *Ae. albopictus* distribution across the island and analysed environmental parameters associated with the presence of these species in addition to screening for medically important arboviruses and other flaviviruses.

Results. Although we collected *Ae. aegypti* across a range of sites across the island, no *Ae. albopictus* were collected despite traps being placed in diverse ecological settings. The number of *Ae. aegypti* collected was significantly associated with higher elevation, and semi-urban settings yielded female mosquito counts per trap-day that were five-fold lower than urban settings. Screening for arboviruses revealed a high prevalence of cell-fusing agent virus (CFAV).

Conclusions. Outbreaks of arboviruses transmitted by *Ae. aegypti* and *Ae. albopictus* have a history of occurring in small tropical islands and Saint Lucia is particularly vulnerable given the limited resources available to undertake vector control and manage outbreaks. Surveillance strategies can identify risk areas for predicting future outbreaks. Further research is needed to determine the diversity of

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version 2 (revision) 16 Dec 2020	 report		 report
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version 1 25 Jun 2020	 report	 report	

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current mosquito species, investigate insect-specific viruses, as well as pathogenic arboviruses, and this should also be extended to the neighbouring smaller Caribbean islands.

Keywords

Mosquitoes, arboviruses, *Aedes aegypti*, arbovirus surveillance

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Author roles: **Jeffries CL:** Conceptualization, Formal Analysis, Investigation, Methodology, Writing – Original Draft Preparation, Writing – Review & Editing; **White M:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Wilson L:** Formal Analysis, Investigation, Methodology, Writing – Review & Editing; **Yakob L:** Conceptualization, Formal Analysis, Investigation, Methodology, Project Administration, Supervision, Writing – Original Draft Preparation, Writing – Review & Editing; **Walker T:** Conceptualization, Formal Analysis, Funding Acquisition, Investigation, Methodology, Project Administration, Supervision, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: This work was supported by the Wellcome Trust through a Wellcome Trust/Royal Society grant awarded to TW [101285]. CLJ and TW were supported by this grant. Supplementary funding was also provided by the London School of Hygiene and Tropical Medicine and Bayer Pharmaceuticals awarded to MW and LW.

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

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How to cite this article: Jeffries CL, White M, Wilson L *et al.* **Detection of Cell-Fusing Agent virus across ecologically diverse populations of *Aedes aegypti* on the Caribbean island of Saint Lucia [version 2; peer review: 2 approved, 1 approved with reservations]** Wellcome Open Research 2020, 5:149 <https://doi.org/10.12688/wellcomeopenres.16030.2>

First published: 25 Jun 2020, 5:149 <https://doi.org/10.12688/wellcomeopenres.16030.1>

REVISED Amendments from Version 1

Our manuscript now includes the addition of an analysis of our trapping data using a negative binomial mixed effects model but significant associations remain the same. We have included trapping nights in Table 1 and an explanation of why a large amount of mosquitoes were collected at Soufriere Hospital. Additional CFAV sequences which became publicly available after the original analysis have now enabled a re-analysis to be carried out which has revealed our sequences are identical or very closely related to CFAV sequences from Guadeloupe potentially representing a Caribbean lineage of CFAV. We have adjusted our manuscript in all relevant areas to reflect this and replaced the previous Figure 3 and Figure 4 phylogenetic trees with a single updated phylogenetic tree (now Figure 3) from the re-analysis which incorporates additional more recently available sequences of CFAV for a more comprehensive comparison. We have now also included our % nucleotide homologies following re-analysis (*Underlying data*) and modified our conclusions to include some sentences on insect-specific flaviviruses.

Any further responses from the reviewers can be found at the end of the article

Introduction

Medically important arboviruses that cause human morbidity and mortality are predominantly transmitted by mosquitoes. There are more than 600 known arboviruses and related zoonotic viruses with more than 80 known to be human pathogens. Outbreaks of dengue virus (DENV), Zika virus (ZIKV), yellow fever virus (YFV) – all from the *Flavivirus* genus (Family: *Flaviviridae*); and chikungunya virus (CHIKV) – from the *Alphavirus* genus (Family: *Togaviridae*) are increasing¹ and there is potential for zoonotic viruses to spill-over into human populations. Arboviral disease transmission mostly occurs in tropical countries of Southeast Asia and South America and has a significant impact on developing countries². Annual DENV infections are estimated at 100–390 million per year³ and dengue is ‘re-emerging’ mostly due to the expansion of the geographical range of the principal mosquito vector, *Aedes (Ae.) aegypti*, through globalization and climate change^{2,4}. ZIKV is historically thought to be transmitted by *Ae. aegypti*. Local transmission in the Americas was first reported in early 2014⁵ and the latest update from the World Health Organisation (July 2019) reports that 87 countries and territories have had evidence of autochthonous ZIKV transmission⁶. YFV is also transmitted by *Ae. aegypti* and can result in large urban outbreaks and rapid spread to distant locations⁷ and is now endemic in Central American countries and several Caribbean Islands⁸. CHIKV is transmitted by *Ae. albopictus* (and to a lesser extent by *Ae. aegypti*) and has spread globally, with outbreaks in the mid 2000s in the Indian Ocean and India, and even in Europe in 2007⁹. Transmission of CHIKV has also been seen recently in the Americas and this rapid geographical expansion (in a similar way to DENV) is likely due to the expanding habitat of the mosquito vectors¹⁰.

Outbreaks of arboviral diseases including DENV¹⁰, YFV⁸, CHIKV¹¹ and ZIKV¹² have recently occurred in the Caribbean. The possibility of additional recent arbovirus transmission in the Caribbean must be considered given some infections result

in nearly indistinguishable clinical symptoms. For example, Mayaro virus (MAYV) is an *Alphavirus* closely related to CHIKV and has resulted in sporadic outbreaks in South America¹³. MAYV transmission is restricted to South and Central America where it is thought that non-human primates act as reservoir hosts and *Haemogogus* mosquitoes (eg. *H. janthinomys*) found in sylvatic jungle environments are responsible for human cases. Although human cases are strongly correlated with exposure to forest environments, urban transmission of MAYV must be considered given the association of cases and major cities infested with *Ae. aegypti*¹³. As the Caribbean is a destination for many international tourists, surveillance is needed for individual Caribbean islands to determine the risk of facilitating the spread of arboviral diseases. In particular, arboviruses transmitted by *Ae. aegypti* are considered important given that prevention predominantly relies on mosquito vector control.

Aedes aegypti was first identified in the Caribbean Islands in 1864¹⁴ and has remained present despite the Pan American Health Organization (PAHO) mosquito control campaign in the 1940s–1960s that was launched to eliminate urban yellow fever. *Aedes aegypti* was successfully eradicated in many countries including Brazil, Mexico and Guatemala¹⁵ but eradication was not achieved in other countries such as the USA, Suriname, Guyana, French Guyana, Venezuela and the Caribbean Islands. As the eradication campaign deteriorated in the early 1970s and 1980s, many countries became re-infested with *Ae. aegypti*^{16,17} and the geographical expansion of *Ae. aegypti* with urbanization resulted in the introduction of DENV to many countries¹⁸. With the exception of YFV, there are no currently available treatments or vaccines for arboviral diseases transmitted by *Ae. aegypti* and *Ae. albopictus*. Disease control is currently limited to traditional vector control strategies that rely on insecticides or destruction of larval breeding sites. In most DENV-endemic countries, ultra-low volume space spraying is recommended only during dengue outbreaks. However, widespread insecticide resistance has developed in *Ae. aegypti*, including high pyrethroid resistance rates in South America^{19–22} and further north in the Caribbean²³.

The volcanic island of Saint Lucia is located midway down the Eastern Caribbean Chain between Martinique and Saint Vincent and north of Barbados (Figure 1). The first cases of dengue in Saint Lucia were recorded in the 1980s and following Hurricane Thomas in 2011 another outbreak occurred. CHIKV was first introduced to Saint Lucia in 2014²⁴ but despite these outbreaks of major mosquito-borne arboviruses, vector surveillance has been limited and the last documented studies were carried out in 1976¹⁴. The landscape of Saint Lucia in many areas has changed over the past 40 years due to natural disasters and urbanisation, which has likely changed the distribution of arbovirus vectors. As the density and habitats of *Ae. aegypti* have expanded both in urban and rural areas of many tropical countries, we conducted an initial survey of *Ae. aegypti* and *Ae. albopictus* distribution and analysed any environmental parameters that were associated with the presence of these species. Female mosquitoes were screened for medically

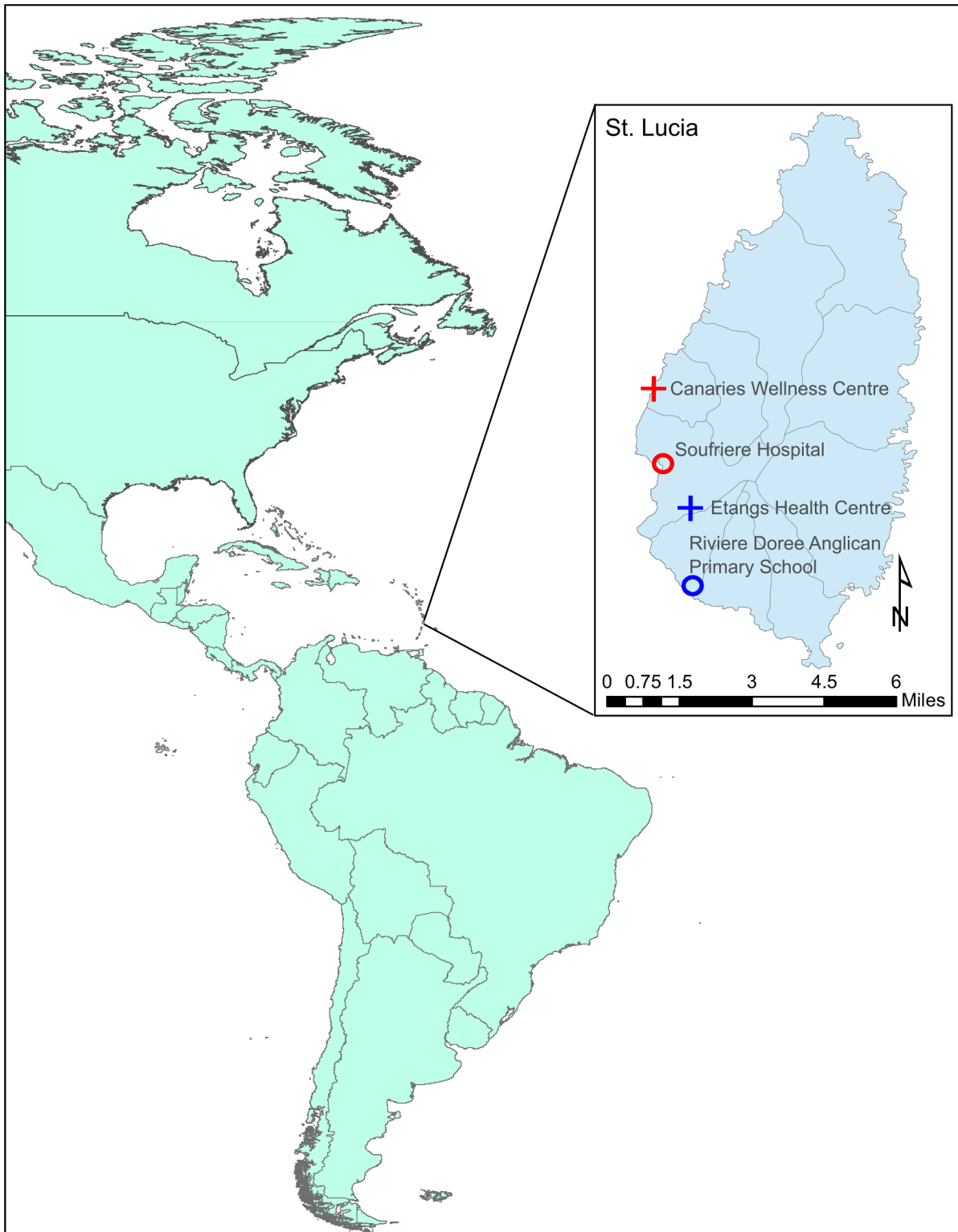


Figure 1. Sampling locations of the longer-term permanent mosquito traps on the island of Saint Lucia used throughout the duration of the study (July 2015). Maps were produced using ArcGIS® software (version 10.4.1) by Esri.

important arboviruses and other flaviviruses to investigate whether there was any evidence of infection.

Methods

Study sites and mosquito collection

Mosquito collections were carried out on the island of Saint Lucia (N 13° 54' 33.9984, W 60° 58' 44.0148) in July 2015. Saint Lucia has a population of ~166,000 people and is 27 miles long and 14 miles wide, with forest covering 77% of the island. The tropical climate includes a dry season (December to June) and a wet season (July to November). Biogents (BG) Sentinel 2.0 mosquito traps baited with BG lure® were used at various sites across the island (Supplementary Figure 1, *Extended data*)²⁵ during the beginning of the wet season. Site selection was undertaken based on geographical and environmental variation in urban and semi-urban areas across the island and factors based on island topology including forested areas, brackish water bodies, freshwater bodies and mangrove habitats in communities with previously high mosquito numbers recorded, gathered from local knowledge. In some locations traps were placed inside houses. Four longer-term permanent traps were connected to power supplies at Canaries Wellness Centre, Soufriere Hospital, Etangs Health Centre and the Riviere Doree Anglican Primary School (Figure 1) and traps were run for a period of 22–24 days with mosquitoes collected at 24-hour intervals. Four temporary traps powered by Power King®12-volt batteries were deployed at various locations across the island (Supplementary Figure 1, *Extended data*)²⁵ to collect mosquitoes over a 24-hour period. Due to logistical difficulties accessing all sites across the island, not all trapping days had four temporary traps running synchronously with the four longer-term permanent traps. EasyLog USB data loggers (EL-USB-2, LASCAR electronics Ltd.) were placed in permanent traps to record relative humidity and temperature at hourly intervals. Garmin eTrex® 20 hand-held GPS units (Garmin Ltd.) were used to determine co-ordinates of both permanent and temporary traps. Trapped mosquitoes were collected, killed on ice for genera morphological identification to identify individuals belonging to the *Aedes* genus using basic defining characteristics including patterns of light and dark scales on the abdomen and thorax and alternating light and dark bands on the legs. Larval dipping was undertaken at Soufriere Town, Choiseul Village, Marisule and Gros Islet to sample immature stages (larvae/pupae) from domestic containers (e.g. tanks and drums, discarded containers and tyres). Immature stages were reared and allowed to emerge in mosquito cages. Individual mosquitoes that were identified by morphology to be *Ae. aegypti* were placed in RNAlater and stored at -20°C to preserve RNA for molecular analysis.

RNA extraction and PCR analysis

A sub-sample of *Aedes* adult female mosquitoes were selected to maximise diversity of geographical trapping locations and pooled according to trap location and date of collection (1–3 females/pool) and RNA was extracted using Qiagen 96 RNeasy Kits (cat no. 74182) according to manufacturer's instructions after using a Qiagen Tissue Lyser II (Hilden, Germany) with 3mm stainless steel beads to homogenise

mosquitoes. RNA was eluted in 45 µl of RNase-free water and stored at -70°C. A Qiagen QuantiTect Reverse transcription Kit (cat no. 205314) was first used to remove any genomic DNA co-purified during the RNA extraction protocol and then reverse transcription was performed with random primers to generate cDNA from all RNA extracts according to manufacturer's instructions. Confirmation of species identification was undertaken using an internal transcribed spacer 1 (ITS1) real-time PCR assay that discriminates between *Ae. aegypti* and *Ae. albopictus*²⁶. Cycling conditions were as follows: 95°C for 15 minutes followed by 40 cycles of 95°C for 10 seconds, 55°C for 30 seconds, 72°C for 20 seconds. Amplification was followed by a dissociation curve (95°C for 10 seconds, 65°C for 60 seconds and 97°C for 1 second) to ensure the correct target sequence was being amplified.

Arbovirus screening included the major arboviruses of public health importance, suspected or having the potential of being transmitted by *Ae. aegypti* / *Ae. albopictus* in the Caribbean: DENV, CHIKV, ZIKV, YFV and MAYV (Supplementary Table 1, *Extended data*)²⁵. In addition, Pan-Flavivirus PCR screening was undertaken that allows simultaneous detection of numerous flaviviruses using a conserved region of the NS5 gene²⁷. PCR reactions for all assays except ZIKV were prepared using 5 µl of Qiagen QuantiTect SYBR Green Master mix (cat no. 204145), a final concentration of 1 µM of each primer, 1 µl of PCR grade water and 2 µl template cDNA, to a final reaction volume of 10 µl. Prepared reactions were run on a Roche LightCycler® 96 System (product no. 05815916001) and PCR primer sequences are described in Supplementary Table 1 (see *Extended data*)²⁵. Cycling conditions were as follows: DENV, CHIKV, YFV and MAYV - 95°C for 15 minutes followed by 40 cycles of 95°C for 10 seconds, 55°C for 30 seconds, 72°C for 30 seconds; Pan-Flavivirus - 95°C for 15 minutes followed by 50 cycles of 95°C for 10 seconds, 60°C for 10 seconds, 72°C for 10 seconds. Amplification was followed by a dissociation curve (95°C for 10 seconds, 65°C for 60 seconds and 97°C for 1 second) to ensure the correct target sequence was being amplified. ZIKV screening was undertaken using a probe-based assay²⁸ that used 5 µl of Qiagen QuantiTect Probe PCR Kit (cat no. 204345), a final concentration of 1 µM of each primer, 1 µl of PCR grade water and 2 µl template cDNA, to a final reaction volume of 10 µl. Cycling conditions for ZIKV were 95°C for 15 minutes followed by 40 cycles of 95°C for 10 seconds, 55°C for 30 seconds, 72°C for 30 seconds. PCR results were analysed using the LightCycler® 96 software (Roche Diagnostics). Synthetic long oligonucleotide standards of PCR products were generated in the absence of biological virus cDNA positive controls and each assay included negative (no template) controls.

Sanger sequencing and phylogenetic analysis

Pan-Flavivirus PCR products were submitted to Source BioScience (Source BioScience Plc, Nottingham, UK) for PCR reaction clean-up, followed by Sanger sequencing to generate both forward and reverse reads. Sequencing analysis was carried out in MEGA7²⁹ as follows. Both chromatograms (forward and reverse traces) from each sample were manually checked,

edited, and trimmed as required, followed by alignment by ClustalW and checking to produce consensus sequences. Consensus sequences were used to perform nucleotide BLAST (NCBI) database queries. Maximum Likelihood phylogenetic trees were constructed from Sanger sequences as follows. The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura-Nei model³⁰. The tree with the highest log likelihood is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. The phylogeny test was by Bootstrap method with 1000 replications. Evolutionary analyses were conducted in MEGA7²⁹.

Statistical analysis

Count data analysis was conducted using a generalized linear model because the response variable (mosquito counts)

had a non-normal error distribution. Models were run using Stata MP (version 14, Stata Corp, College Station, TX, USA). Both Poisson and negative binomial link functions were used in analysis, with the superior model identified from visual inspection of fits (Supplementary Figure 2, *Extended data*)²⁵. A univariate analysis included elevation, humidity and temperature as continuous explanatory variables, and urbanisation level (urban or semi-urban) as a factor. Incident rate ratios (IRRs) and corresponding 95% confidence intervals were calculated.

Ethical approval

The study protocol was reviewed and approved by the Research Governance & Integrity Office of the London School of Hygiene and Tropical Medicine (LSHTM ethics no. 9308).

Results

A total of 3,701 adult mosquitoes were collected across the island of Saint Lucia over a four-week period using BG Sentinel 2 traps (Table 1). *Culex* was the dominant genus, comprising 78.7% of the total mosquitoes collected and the remaining 21.3% were morphologically identified as species within the *Aedes* genus. No *Ae. albopictus* females were collected in any of the locations despite traps being placed in diverse ecological settings. *Ae. aegypti* adults were collected

Table 1. Collection site locations and characteristics with total numbers of adult mosquitoes collected from each site.

Location of collection (trapping nights)	GPS coordinates		Elevation (m)	EcoZone Category (trap placement)	<i>Culex spp.</i>		<i>Ae. aegypti</i>		<i>Other Aedes spp.</i>	
	Latitude	Longitude			female	male	female	male	female	male
Canaries Wellness Centre (21)	N 13°54.291	W 061°04.084	4	Urban (outdoor)	162	75	93	16	46	7
Soufriere Hospital (21)	N 13°51.382	W 060°03.546	14	Urban (outdoor)	501	438	196	87	52	11
Etangs Health Centre (18)	N 13°50.120	W 061°01.628	289	Semi-Urban (outdoor)	77	25	34	1	14	0
Riviere Doree Anglican Primary School (21)	N 13°45.842	W 061°02.141	67	Semi-Urban (outdoor)	421	173	3	0	5	1
Monzie (1)	N 13°48.605	W 061°01.300	374	Rural (outdoor)	0	0	0	0	0	0
Roblot (1)	N 13°48.011	W 061°01.442	318	Semi-Urban (outdoor)	0	4	2	0	2	0
De Brioul (1)	N 13°47.991	W 061°01.427	308	Semi-Urban (outdoor)	1	0	0	0	2	0
Reunion (1)	N 13°46.353	W 061°02.510	84	Urban (outdoor)	20	6	1	0	1	0
Delcer (1)	N 13°46.948	W 060°58.182	199	Semi-Urban (indoor)	0	2	1	0	0	1

Location of collection (trapping nights)	GPS coordinates		Elevation (m)	EcoZone Category (trap placement)	<i>Culex spp.</i>		<i>Ae. aegypti</i>		<i>Other Aedes spp.</i>	
	Latitude	Longitude			female	male	female	male	female	male
Upper Augier (1)	N 13°44.680	W 060°57.390	33	Semi-Urban (outdoor)	11	18	0	0	4	0
Lower Augier (1)	N 13°43.678	W 060°57.229	25	Urban (indoor)	6	2	0	0	3	0
Desrisseaux (1)	N 13°45.209	W 060°59.553	86	Semi-Urban (outdoor)	0	1	0	0	0	0
Perriot (1)	N 13°46.214	W 060°58.776	162	Rural (indoor)	20	1	0	0	7	0
La Faruge (1)	N 13°44.196	W 060°58.233	17	Semi-Urban (outdoor)	0	0	0	0	0	0
Sauzay (1)	N 13°43.859	W 060°56.983	40	Semi-Urban (outdoor)	19	14	1	0	2	0
Laborie High Way (1)	N 13°44.927	W 060°58.852	44	Semi-Urban (outdoor)	1	0	0	0	0	0
Vieux- Fort Town (3)	N 13°43.510	W 060°56.868	13	Urban (outdoor)	0	0	0	0	0	0
Montete (2)	N 13°43.477	W 060°56.876	14	Urban (outdoor)	30	10	0	0	0	0
Fond Dor (1)	N 13°46.358	W 061°02.393	85	Urban (indoor)	50	97	1	0	0	0
Dennerly Highway (1)	N 13°46.525	W 061°02.329	102	Semi-urban (outdoor)	2	1	0	0	0	0
Micoud Village 1 (1)	N 13°49.186	W 060°53.816	12	Urban (outdoor)	7	10	5	0	2	0
Micoud Village 2 (1)	N 13°49.238	W 060°53.921	21	Urban (outdoor)	10	4	9	4	3	0
Micoud Highway (1)	N 13°49.228	W 060°53.873	10	Urban (outdoor)	40	14	4	0	10	1
Micoud Health Centre (1)	N 13°49.178	W 060°53.826	13	Urban (outdoor)	77	47	0	0	3	2
Fond Doux (1)	N 13°49.048	W 061°02.956	347	Forest-fringe (outdoor)	19	27	9	3	2	0
Choiseul Village (1)	N 13°46.474	W 061°02.994	15	Urban (outdoor)	36	27	2	4	0	0
Dugard (1)	N 13°48.547	W 061°01.373	315	Forested (outdoor)	2	1	0	0	0	0
Belle Plain (1)	N 13°49.243	W 061°01.664	466	Forest-fringe (outdoor)	0	0	0	0	0	0
Lamaze (1)	N 13°48.295	W 061°01.104	313	Forested (outdoor)	0	0	0	0	0	0
Montete (2)	N 13°54.663	W 060°53.463	12	Urban (indoor)	10	6	7	0	1	0
Vieux Fort Town (1)	N 13°54.563	W 060°53.633	15	Urban (outdoor)	3	0	0	0	0	0
La Ressource (1)	N 13°54.528	W 060°53.636	10	Rural (outdoor)	70	63	7	0	0	0

Location of collection (trapping nights)	GPS coordinates		Elevation (m)	EcoZone Category (trap placement)	<i>Culex spp.</i>		<i>Ae. aegypti</i>		Other <i>Aedes spp.</i>	
	Latitude	Longitude			female	male	female	male	female	male
Vieux- Fort Town (2)	N 13°46.472	W 061°02.255	108	Urban (outdoor)	1	0	0	1	0	0
Mongouge (1)	N 13°44.981	W 060°56.621	11	Rural (outdoor)	2	0	1	4	0	0
Beanfield (1)	N 13°45.007	W 060°59.701	10	Semi-urban (outdoor)	0	0	0	0	0	0
Dugard (1)	N 13°44.830	W 060°57.863	38	Semi-urban (indoor)	32	29	47	10	2	0
Palmiste (1)	N 13°48.110	W 061°01.772	281	Urban (indoor)	5	1	0	0	0	0
Laborie Town (1)	N 13°51.561	W 061°03.394	54	Urban (indoor)	6	14	6	1	0	0
Sapphaire (1)	N 13°45.497	W 061°01.055	57	Urban (outdoor)	1	0	0	1	0	0
Dennery Village (1)	N 13°46.616	W 061°00.770	138	Semi-urban (outdoor)	12	3	4	1	0	0
Piaye (1)	N 13°48.276	W 061°00.787	292	Semi-urban (outdoor)	11	14	14	5	2	4
Saltibus (1)	N 13°46.251	W 061°01.412	92	Semi-urban (indoor)	11	5	5	2	0	0
Rainforest (1)	N 13°50.345	W 060°58.563	321	Forested (outdoor)	48	0	0	0	0	0
Richfond (1)	N 13°56.086	W 060°55.320	35	Rural (indoor)	23	8	0	0	0	0
Castries City (1)	N 14°00.765	W 060°59.096	16	Urban (indoor)	1	1	1	0	1	0
Ford St Jacques (3)	N 13°49.138	W 061°02.631	338	Semi-Urban (outdoor)	12	15	0	1	0	0

in 26/46 trap locations, with the largest number of females being collected at Soufriere Hospital (n=196) and Canaries Wellness Centre (n=93), where permanent traps were running for the duration of the collection period (Figure 2). The average number of female *Ae. aegypti* collected over a 24-hour period across all trap locations was 3.09. A particularly high number of *Ae. aegypti* were collected during a 24-hour period from Dugard (47 females and 10 males, comprising 47.5% of the total collection) using a trap placed indoors in a semi-urban area (Table 1; Supplementary Figure 1, Extended data)²⁵. In contrast, low numbers of *Ae. aegypti* were collected using the permanent trap at Riviere Doree Anglican Primary School, with *Ae. aegypti* comprising 0.5% (n=5) of the collection and an average of 0.13 female mosquitoes per 24 hours of trapping.

A generalized linear model (GLM) was used to analyse the associations between the counts of female *Ae. aegypti* (combining

counts from both the temporary traps and permanent traps) and four independent variables: peak daily temperature, peak daily humidity, trap elevation and ecological zone (semi-urban or urban). Plotting count frequencies against alternative, competing models, assuming either a Poisson or a negative binomial distribution, clearly demonstrated the superiority of a negative binomial model in fitting the data distribution (Supplementary Figure 2, Extended data)²⁵. Exponentiation of the coefficients resulting from a GLM (negative binomial family) produced the IRR associated with the independent variables. Here, IRR can be interpreted as the ratio of counts per trap-day associated with the tested variable. These are described along with 95% confidence intervals in Table 2. No significant association was found with temperature. Because previous studies have shown a non-monotonic association between *Ae. aegypti* and temperature (i.e. *Ae. aegypti* thrive at a non-trivial optimal temperature)³¹, we subsequently attempted to fit a more complex (quadratic) function between these variables but this did

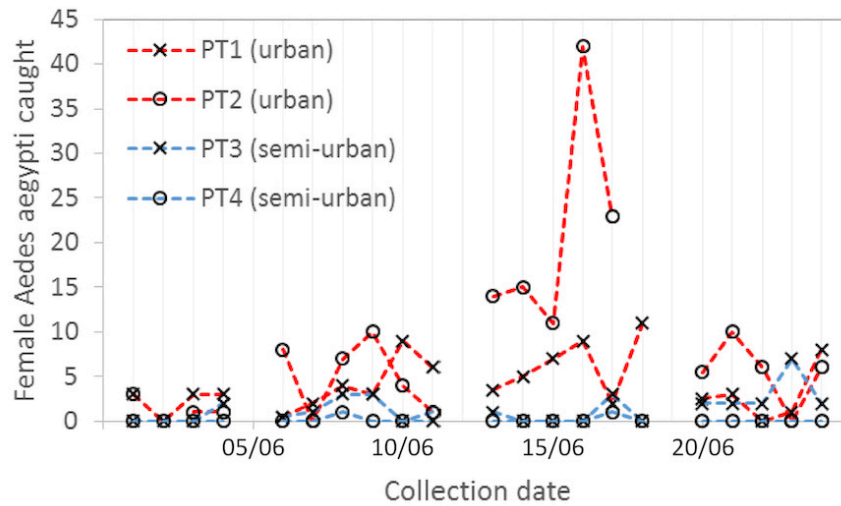


Figure 2. Population dynamics of local female *Ae. aegypti* mosquitoes caught from the four longer-term traps positioned in field sites detailed in Figure 1.

Table 2. Incidence rate ratios (IRRs) and corresponding 95% confidence intervals resulting from univariate generalized linear models with negative binomial link function.

Environmental variable	IRR	Std. Err.	z	P>z	95% Confidence interval	
elevation	1.012516	0.004744	2.65	0.008	1.00326	1.021858
humidity	1.005635	0.01621	0.35	0.727	0.974361	1.037913
temperature	1.039605	0.089212	0.45	0.651	0.878666	1.230023
semi-urban	0.188336	0.046641	-6.74	0.000	0.115914	0.306008

not improve model fit ($p=0.850$). Higher counts were significantly associated with higher elevation although the effect size was small; and semi-urban settings yielded female mosquito counts per trap-day that were five-fold lower than urban settings. We tested for interactions between all covariates but none were found to be significant. We also used a negative binomial mixed effects model to account for the potential additional random effect of trap site and found the same significant associations (Supplementary Table 2, *Extended data*)²⁵.

A sub-sample of adult female *Ae. aegypti* mosquitoes ($n=381$) collected from BG traps were screened for arboviruses. No evidence was seen for infection of the major medically important arboviruses that have historically been transmitted by *Ae. aegypti*. However, the presence of a *Flavivirus* closely related to cell-fusing agent virus (CFAV) was detected in 15.6% (7/45) individuals screened from Soufriere Hospital, 13.3% (2/15) of individuals screened from Etangs Health Centre, 33% (1/3) screened from Micoud Village, 50% (1/2) individuals from Micoud Highway and 50% (2/4) individuals from Piaye (Supplementary Figure 3 and Supplementary

Table 3, *Extended data*)²⁵. We also detected this *Flavivirus* in adult females that had been reared from larval collections (Supplementary Table 3, *Extended data*)²⁵. Phylogenetic analysis indicated the *Flavivirus* sequences obtained were identical to, or closely matched to, CFAV NS5 sequences, particularly sequence obtained from *Ae. aegypti* specimens collected in Guadeloupe in 2016 (GenBank accession number: LR694081), revealing they are potentially forming a Caribbean strain of CFAV (Figure 3 and Jeffries *et al.* qPCR and sequencing data file, *Underlying data*)²⁵. This phylogenetic analysis also confirmed these *Flavivirus* sequences cluster with other insect-specific flaviviruses (ISFs) and are separate from pathogenic flaviviruses such as DENV, ZIKV and YFV (Figure 3).

Discussion

Entomological indices including the abundance of adult mosquitoes are often used to assess the risk of disease transmission and this, in turn, influences vector control strategies. The lack of surveillance studies, to our knowledge, for major vectors of arboviruses of public health importance on the island of Saint Lucia needed to be addressed, given the recent outbreaks of

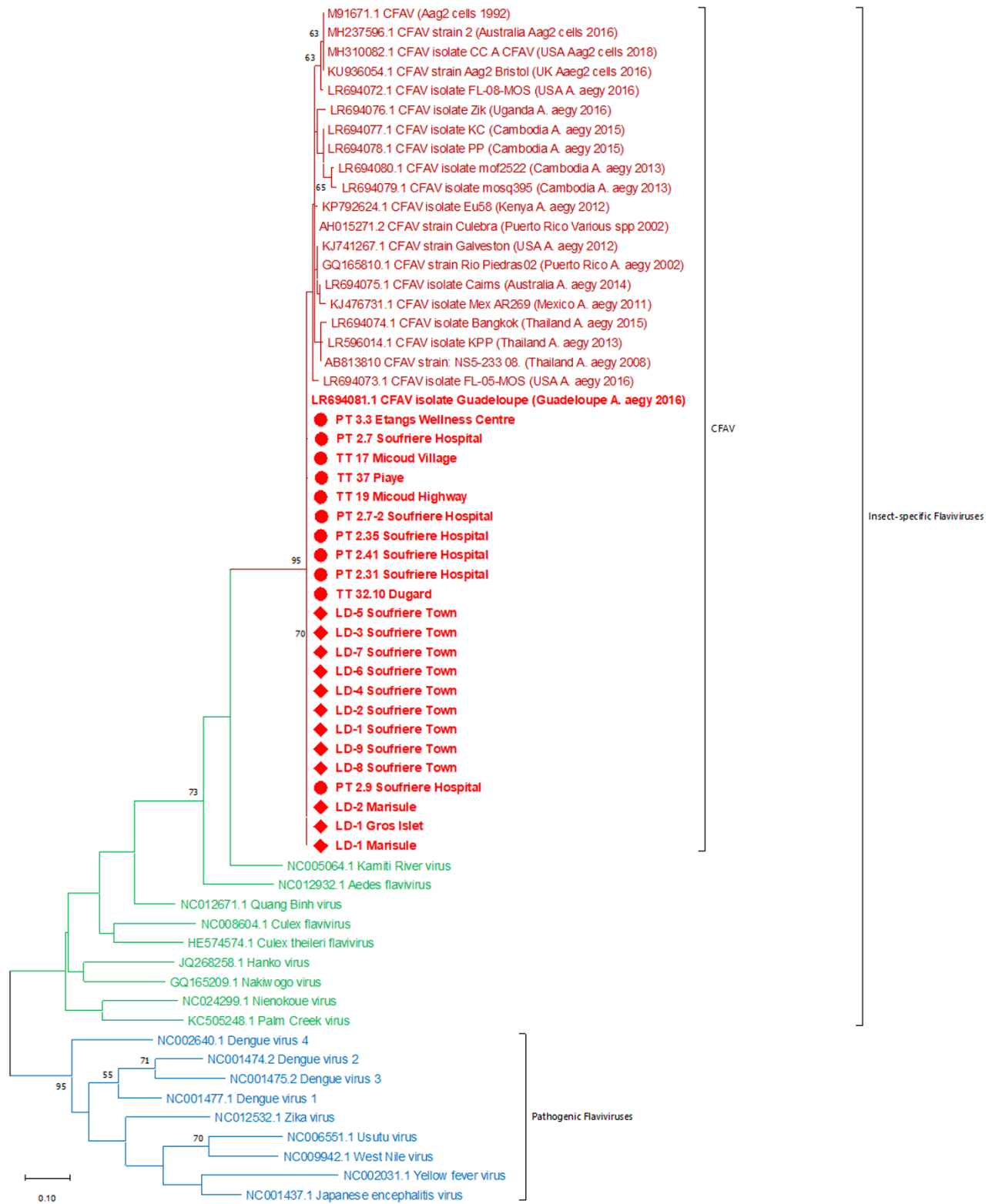


Figure 3. Maximum Likelihood molecular phylogenetic analysis of selected *Flavivirus* NS5 partial sequences showing the *Flavivirus* sequences from Saint Lucia *Ae. aegypti* clustering alongside other cell-fusing agent virus (CFAV) sequences, within the insect-specific flaviviruses group. Sequences generated in this study are shown with node markers, circular markers for *Flavivirus* sequences obtained from adult female *Ae. aegypti* and diamond markers for those obtained from larval collections. The tree with the highest log likelihood (-2701.53) is shown. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 62 nucleotide sequences. There was a total of 166 positions in the final dataset.

arboviruses such as DENV, CHIKV and ZIKV in the Caribbean and surrounding regions. The principal vector of these arboviral diseases, *Ae. aegypti*, is highly invasive and is now present in much of the Americas including the USA⁵. In this study, we collected adult mosquitoes to determine the geographical distribution of *Ae. aegypti* across the island of Saint Lucia and to determine any correlation with environmental variables. BG Sentinel 2 traps were selected as these traps were redesigned to provide increased durability in field conditions and were recently shown to be effective at trapping *Aedes* species³². The durability of traps was particularly important for the four permanent traps that were used for approximately 24 days. Adult collections indicate that *Ae. aegypti* is present throughout the island of Saint Lucia and population densities are significantly higher in urban areas compared to semi-urban or rural settings. We also demonstrated that adult counts were positively correlated to elevation.

The comparatively larger number of mosquitoes collected at Soufriere hospital is likely due to this trapping location having several optimal characteristics for *Ae. aegypti*. Firstly, the trap was placed in the hospital garden which is located in the centre of an urban area with a high abundance of available human hosts for blood feeding. Secondly, breeding sites resulting from the accumulation of rainwater in animal troughs and deep gutters lining the edges of roads were in close proximity. The trapping of a high number of *Ae. aegypti* (47 females and 10 males) during a 24-hour period from Dugard using a trap placed indoors in a semi-urban area suggests an interesting behavioural observation. The biology and behaviour of *Ae. aegypti* in the Caribbean has not been extensively studied but previous work on a Trinidad strain using human landing catches revealed the periodicity consisted of 90% arriving during daylight and twilight and 10% during the night³³. This study included both urban and rural sites and a consistently larger number of mosquitoes were collected outside vs. inside houses. Light intensity was also significantly correlated with mosquito landing patterns³³. The trapping of *Ae. aegypti* inside houses in Saint Lucia could indicate a change in behavior, with mosquitoes biting indoors during the night in houses with lights on (an anecdotal observation that occurred during our study). Indoor resting of *Ae. aegypti* has recently been documented in Mexico³⁴, which has implications for control methods. Other studies in the Caribbean have also shown that high temperatures in open environments can result in *Ae. aegypti* breeding in underground sites³⁵ and indoor oviposition has been demonstrated^{36,37}.

Confirmation of the presence of *Ae. aegypti* on the island of Saint Lucia is not particularly surprising given this species is widespread throughout the Caribbean and is now widespread in the Americas^{4,5}. The association with urban environments in Caribbean Islands is seen with the most common breeding sites being drums/barrels, uncovered tanks and cisterns, brick holes, flower pots, used tyres and utility manholes³⁸. Saint Lucia now provides the ideal environment for *Ae. aegypti* due to recent changes in the climate. The El Niño period in 2009 – 2010 introduced dry hot periods and provided an environment that was not conducive for mosquito production. Water conservation has become a critical issue for Saint

Lucia and the majority of the water supply comes from surface runoff collected in rivers, streams and dams. Rain water is collected and stored haphazardly and inappropriately in various containers such as water tanks, drums, and buckets, creating ideal breeding grounds for this species¹. This study was undertaken during the commencement of the wet season with the average rainfall in June and July 2015 being 37.1mm and 175.8mm, respectively. This indicates that greater mosquito abundance is likely throughout later stages of the wet season and follow-up studies should be undertaken to determine this. Clearly climatic patterns resulting in unpredictable rainfall will provide ideal breeding grounds (unpolluted water in artificial and natural containers) for *Ae. aegypti* in Saint Lucia³⁵.

Aedes albopictus was not identified in the mosquitoes collected in our study despite many traps being set in or near forested areas. The range of *Ae. albopictus* has expanded to Europe, USA and many South American countries⁴. In the Caribbean, this species was first reported in the Dominican Republic³⁹ and has also been recently found in Jamaica⁴⁰ and implicated in CHIKV transmission in Haiti in the eastern Caribbean⁴¹. Therefore, recent outbreaks of CHIKV on Saint Lucia and neighbouring Caribbean islands suggest that there might be a possibility that *Ae. albopictus* may also play a role in the spread of the disease. With *Ae. albopictus* present in the US to the north and the Cayman Islands to the south, Saint Lucia is clearly considered at risk for establishment of *Ae. albopictus*⁴². *Aedes albopictus* has also been shown to harbour Eastern equine encephalitis virus (EEEV)⁴³, highlighting the potential transmission risk of additional arboviruses. The traditional ways of importing *Ae. albopictus* through the trade of tyres is also a possible source of introduction for this species. Although Saint Lucia has signed onto the International Health Regulations (IHR) 2005, to prevent and control the international spread of disease, port surveillance systems are not fully implemented and might not be sufficient to monitor containers present on ships and ensure that they are fumigated before they arrive in port. Saint Lucia is also faced with the problem of tyre disposal where there is no functional shredding equipment, which is of great concern, particularly so because tyres in landfills are in close proximity to urban communities.

The detection of *Flavivirus* sequences identical, or closely related to CFAV in diverse ecological populations of *Ae. aegypti* across the island of Saint Lucia suggests the potential for undiscovered and widespread viruses in the Caribbean which may have implications for vector potential and transmission of pathogenic arboviruses. A large study was undertaken in Trinidad, screening more than 185,000 mosquitoes representing 46 species, and 85 different viruses were isolated⁴⁴. The isolation of Mucambo virus (MUCV), (a Venezuelan equine encephalitis complex subtype IIIA), follows a history of isolating *Alphaviruses* from mosquitoes in Trinidad⁴⁵. More recently, high prevalence of a Phasi Charoen-like virus was reported in *Ae. aegypti* in Grenada⁴⁶, suggesting a high diversity of unknown viruses are present in Caribbean populations of *Ae. aegypti*. A potentially novel strain of CFAV was discovered in *Ae. aegypti* populations from Mexico⁴⁷ and CFAV was detected in *Ae. aegypti* populations from Kenya⁴⁸. The year

after our specimens were collected, *Ae. aegypti* specimens from Guadeloupe were collected which resulted in CFAV sequences being identified in the population from this nearby Caribbean island⁴⁹. Several studies have shown the potential for mosquito-specific viruses to interfere with arboviruses^{50–52}. Interestingly, CFAV infection significantly enhanced replication of DENV (and vice versa) in *Ae. aegypti* Aag2 mosquito cells⁵³. Furthermore, a study looking at ZIKV replication in *Ae. aegypti* and *Ae. albopictus* cell lines suggested that insect-specific viruses (including CFAV) may interfere with ZIKV, DENV and La Crosse virus replication⁵⁴. Further studies are needed to determine if this occurs in field settings by determining the prevalence of mosquito-specific viruses in mosquito populations. Newly described viruses/viral sequences allow a more comprehensive understanding of virus evolution and virus-host interactions and could also contribute to efforts to target both insects and pathogens⁵⁵. CFAV has been shown to be vertically transmitted in *Ae. aegypti* lab colonies, suggesting the possibility of using CFAVs and closely related ISFs for control of medically important arboviruses⁵⁶. The presence of insect-specific viruses in *Ae. aegypti* might be underestimated given a recent study suggested up to 27 insect-specific viruses (23 currently uncharacterized) in populations from Cairns (Australia) and Bangkok (Thailand)⁵⁷. The question remains as to whether insect-specific viruses like CFAV have not yet gained the ability to infect vertebrates and therefore become arboviruses or whether they have lost this ability⁵⁸. Phylogenetic studies focused on the *Flavivirus* E gene would suggest CFAV is a basal lineage that diverged prior to the separation of mosquito and tick-borne flaviviruses⁵⁹. Our results indicate the presence of CFAV but it has been shown that some *Flavivirus* genome-integrated sequences can be transcribed and therefore caution must be taken to assume the presence of an active *Flavivirus* infection⁶⁰. Furthermore, *Flavivirus*-related integrated DNA sequences were detected in wild *Ae. aegypti* mosquitoes most likely resulting from preceding infection by the corresponding RNA viruses⁶¹. As we removed genomic DNA during our reverse transcription step then this is less likely to have been the source of the *Flavivirus* sequences detected in this study. Caution must be taken as our *Flavivirus* sequences were short partial NS5 sequences from Pan-*Flavivirus* PCR products, limiting the phylogenetic analysis possible. However, the matching of our sequences to CFAV NS5 sequence from Guadeloupe (where genome sequences were obtained)⁴⁹ adds weight to the potential for a Caribbean lineage of CFAV being present in these *Ae. aegypti* populations. Full genome sequencing of these new isolates from Saint Lucia would provide much greater confidence on the phylogeny and level of genetic diversity and would allow further comparisons to CFAV infections in geographically diverse *Ae. aegypti* populations⁶¹. This is particularly important given insect-specific viruses are now being considered for mosquito control strategies including CFAVs in *Ae. aegypti*⁶².

Conclusions

The impact of arboviral diseases is increasing due to the expanding geographical range of many mosquito species, particularly *Ae. aegypti* and *Ae. albopictus*. As most arboviral diseases occur in sporadic epidemics, vector control options are often

limited to the use of insecticides that are becoming less effective due to insecticide resistance. As re-emerging arboviral diseases such as DENV and ZIKV continue to spread geographically, the fight to eradicate or reduce the transmission potential of *Ae. aegypti* is increasing in importance. Although we found no evidence of human arboviruses through screening, the detection of sequences which appear to be CFAV, an insect-specific *Flavivirus*, warrants further investigation, particularly given that these viruses can affiliate phylogenetically with flaviviruses that infect vertebrates and they may influence the transmission potential of pathogenic flaviviruses⁶⁰. Outbreaks of arboviral diseases, including DENV, CHIKV and ZIKV, have a history of occurring in small tropical islands. ZIKV emerged for the first time outside of Africa and Asia in Yap State in Micronesia and then a large outbreak in French Polynesia was followed by transmission in other Pacific islands⁶³. Small Islands Developing States (SIDS) and territories such as Saint Lucia are particularly vulnerable to arboviral disease outbreaks for several reasons⁶⁴. Natural disasters are more frequent and these change the geographical landscape, allowing rapid mosquito proliferation. SIDS often lack safe water supplies and sanitation and local governments have limited resources to undertake vector control and manage outbreaks. An increasing ability for travel between SIDS and continental regions facilitates the spread of arboviruses to previously unexposed populations. For these reasons, surveillance strategies need to be monitored, risk areas need to be mapped out and epidemic trends recorded for predicting future outbreaks. For the Caribbean island of Saint Lucia, further research is needed to determine the diversity of current mosquito species and investigate the presence of viruses within these species, and this should also be extended to the neighbouring smaller Caribbean islands.

Data availability

Underlying data

Open Science Framework: Detection of Cell-Fusing Agent virus across ecologically diverse populations of *Aedes aegypti* on the Caribbean Island of Saint Lucia. <https://doi.org/10.17605/OSF.IO/DACKS25>.

This project contains the following underlying data:

- Jeffries *et al.* qPCR and sequencing data file.xlsx
- Jeffries *et al.* Mosquito trapping data.xlsx

Extended data

Open Science Framework: Detection of Cell-Fusing Agent virus across ecologically diverse populations of *Aedes aegypti* on the Caribbean Island of Saint Lucia. <https://doi.org/10.17605/OSF.IO/DACKS25>.

- Supplementary Table 1 (PCR gene targets and primer sequences for the screening analysis undertaken on *Ae. aegypti* mosquito cDNA)
- Supplementary Table 2 (Negative binomial mixed effects model)
- Supplementary Table 3 (qRT PCR results of Pan-Flavi NS5 screening of *Ae. aegypti* samples)

- Supplementary Figure 1 (Map of Saint Lucia showing the location of BG Sentinel 2 traps used in the study)
- Supplementary Figure 2 (The observed proportions along with the Poisson and negative binomial probabilities for the count type variable using 'nbvargr' function in Stata).
- Supplementary Figure 3 (qRT PCR fluorescence and melting temperatures of Pan-Flavi NS5 positive samples)

Data are available under the terms of the [Creative Commons Zero "No rights reserved" data waiver](#) (CCO 1.0 Public domain dedication).

Acknowledgements

We would like to thank all the villagers in Saint Lucia who participated in the fieldwork.

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Open Peer Review

Current Peer Review Status:   

Version 2

Reviewer Report 07 April 2021

<https://doi.org/10.21956/wellcomeopenres.18175.r43154>

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Lícia Natal Fernandes 

Institute of Tropical Medicine, University of São Paulo, São Paulo, Brazil

The article is about an entomological survey conducted in Sant Lucia, a Caribbean island. Association between some environmental parameters and the counts of female *Aedes aegypti* mosquitoes was performed and a screening of arbovirus was also carried out. Higher counts of *Aedes aegypti* were significantly associated with elevation and mosquito counts in semi-urban settings were lower than urban settings. Nucleotide sequences of cell fusing agent virus, a insect specific flavivirus, was detected with a high prevalence in *Aedes aegypti* pools. It was very important to perform such study considering the island where the study took place has the potential for occurrence of arbovirus outbreaks.

This is a well written article and only minor changes are suggested, as follows.

In the first paragraph authors say: "YFV is also transmitted by *Ae. aegypti* and can result in large urban outbreaks and rapid spread to distant locations". In order to avoid confusion I would say something like: "YFV is also transmitted by *Ae. aegypti* in the urban circle of transmission, what can result in large urban outbreaks and rapid spread to distant locations where population has not been vaccinated yet".

In my opinion, citation of Figure 1 should be removed from the last paragraph of the introduction chapter because its title mentions the traps, which are only described in the methods. Therefore, the citation should be placed only in methods.

It would have been more appropriate to use a taxonomic key to separate mosquitoes *Aedes* from other mosquitoes. However I believe results are correct as the authors confirmed the morphology results by molecular biology based on the ITS1 gene.

In the Results, authors say "No *Aedes albopictus* females were collected", what gives the impression that males might have been collected. So I think it would be more appropriate to say that no *Aedes albopictus* were collected.

It's not clear how many adults from collected larvae were analysed, if they were processed in pools or individually. Also, it would be very interesting to add information on the larvae collection (frequency of collection and kinds of breeding sites sampled – natural or artificial or both).

In the last paragraph of the results, authors begin saying the number of mosquitoes analysed (381), but when they talk about the positive results for PCR, it seems that information is given in number of mosquito pools. It would be important to have the number of mosquito pools analysed in the text, together with the number of positive pools. Also, it should be informed that positivity is given in number of pools and not in number of individual mosquitoes, if that really is the case. As mosquitoes were processed in pools, it's not possible to know the real number of positive mosquitoes, therefore authors should consider to calculate and inform the minimum infection rate.

One limitation of the study is the fact that very small nucleotide sequences were analysed, nonetheless this is very well discussed by the authors, that even comment on the importance of sequencing the entire genome of the virus detected.

Authors found significantly association between counts of *Aedes aegypti* and elevation although do not discuss it. If any explanation for that is available, it would be very important to be in the text.

- Figure 1 – extended material says: “yellow pins represent semi-permanent traps”. Is it correct or would it be “permanent traps” instead of “semi-permanent traps”?

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?

I cannot comment. A qualified statistician is required.

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.

Reviewer Expertise: Entomology / Molecular biology applied to detection of protozoans and viruses in mosquitos.

I confirm that I have read this submission and believe that I have an appropriate level of

expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 05 January 2021

<https://doi.org/10.21956/wellcomeopenres.18175.r41856>

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Jandouwe Villinger 

International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya

The issues of the original version of the manuscript have now been sufficiently addressed.

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.

Reviewer Expertise: Molecular entomology of mosquito- and tick-borne diseases.

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

Version 1

Reviewer Report 23 October 2020

<https://doi.org/10.21956/wellcomeopenres.17585.r40686>

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Marco Neira 

The Cyprus Institute, Nicosia, Cyprus

Major Revisions:

By comparing Table 1 with the mosquito trapping data available on the supplementary files, it would seem that most locations sampled with temporary traps were only sampled for a single day, with a single trap each, while locations sampled with permanent traps had a much higher number of trapping nights. If this was the case, the authors should address whether this style of sampling is appropriate for performing the type of statistical analysis presented in the paper. In any case, I suggest they include in Table 1 the number of trapping nights for each location.

The data shown in Figure 2 and Table 1 suggest that one of the permanent trapping sites (Soufriere Hospital) consistently produced much higher yields than any of the other sites, including those sampled with temporary traps. However, the authors don't discuss potential explanations for this phenomenon, or the ways in which this fact could (or not) create bias on their data analysis. I suggest they revise the discussion addressing these observations.

As the authors correctly point out, the detection of flavivirus-like RNA in a mosquito could very well be the product of a transcribed cell silent agents (CSA) integrated in the insect's genome sometime in the past. While it is certainly possible that a novel, extant virus could be the source of such CSA, it is also possible that the sequences obtained by the authors represent a CSA originating from a known virus and subsequently mutated after insertion in the mosquito genome. Alternatively, the sequences could correspond to a CSA derived from an extinct virus. In any case, I think that in the absence of a full viral genome, the authors should be more careful about their claim of having identified a novel insect-specific virus.

The 'Conclusions' section discusses aspects such as the spread of arboviral diseases, the limited options available for vector control, the history of Zika outbreaks (among other), which are at best tangentially related to the paper's original results. I recommend that the authors re-write this section, presenting conclusions that are actually related to their original work.

Minor Revisions:

Throughout the paper, please italicize scientific names.

Introduction:

- The authors state that "22 countries and territories have now been identified to have autochthonous transmission", which could be interpreted as being a global tally of countries reporting Zika transmission. However, this number (a) corresponds exclusively to the Americas, and (b) represents an outdated figure. The latest figures available from the Pan-American Health Organization (available [here](#)) indicate that just within the Americas, 48 countries and territories have reported mosquito-borne Zika transmission. Considering that earlier on the paper the authors provide global data for the epidemiology of dengue, I would recommend revising this figure to reflect updated global data on Zika distribution.

One potential source is the World Health Organization's Zika Epidemiology Update (available [here](#)).

- The authors state that “widespread insecticide resistance has developed in *Ae. aegypti*, including high pyrethroid resistance rates in South America and further north in the Caribbean”. To back up this statement, the authors cite a single paper focused on resistance found on a specific location in Brazil, and one paper focusing on a location in the Caribbean. I would recommend that the authors increase the number of citations to better represent the actual spread of pyrethroid resistance in the region. Suggestions include:
Fonseca-Gonzalez *et al.* (2011)¹
Rawlins SC (1998)²
Ryan SJ *et al.* (2019)³

Methods:

- The authors should provide a clearer summary of their trapping strategy. In the current text, they state that trapping was performed using four permanent traps and four temporary traps, for what can be understood as a total of eight traps per each 24-hour period. However, mosquito trapping data available on the supplementary files suggests that on most dates only six or less traps were used.
- Please specify which taxonomic key was used to separate mosquito genera. If no specific key was used, please provide a complete list of characters used to sort specimens by genus.
- The legend in Figure 1 makes reference to an inset showing a “representative BG Sentinel 2 trap placed in the Des Cartier rainforest”. However, the actual figure does not contain any inset showing a representative trap.
- Please specify what kind of primers were used for reverse-transcription reaction.

Discussion:

- In the first paragraph of the discussion, the sentence “The principle vector of these arboviral diseases...” should be changed to “The principal vector of these arboviral diseases...”.

References

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3. Ryan SJ, Mundis SJ, Aguirre A, Lippi CA, et al.: Seasonal and geographic variation in insecticide resistance in *Aedes aegypti* in southern Ecuador. *PLoS Negl Trop Dis.* **13** (6): e0007448 [PubMed Abstract](#) | [Publisher Full Text](#)

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

Partly

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

Partly

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

Partly

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

I cannot comment. A qualified statistician is required.

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

Yes

Are the conclusions drawn adequately supported by the results?

No

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Medical entomology, mosquito biology, mosquito control, vector/pathogen interaction, mosquito molecular physiology, insect transgenesis.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 15 Dec 2020

Thomas Walker, London School of Hygiene & Tropical Medicine, Keppel Street, London, UK

Response to reviewer 2

Many thanks Marco for your thorough and thoughtful review. Our responses are shown below in bold.

Major Revisions:

By comparing Table 1 with the mosquito trapping data available on the supplementary files, it would seem that most locations sampled with temporary traps were only sampled for a single day, with a single trap each, while locations sampled with permanent traps had a much higher number of trapping nights. If this was the case, the authors should address whether this style of sampling is appropriate for performing the type of statistical analysis presented in the paper. In any case, I suggest they include in Table 1 the number of trapping nights for each location.

Yes this is correct and why we described some as temporary and others as permanent. We repeated our statistical analysis using a negative binomial mixed effects model (as opposed to a generalized linear model) to account for the potential additional random effect of trap site (repeat sampling from the permanent traps but not the temporary traps) and the results remained relatively unchanged. We found a

statistically increased mosquito count for higher elevations and for urban (vs semi-urban) areas but no statistical association between counts and either humidity or temperature. As these significant associations are the same, the results of this analysis are now presented in Supplementary Table 2, *extended data*). We have also now included the trapping nights for each location in Table 1.

The data shown in Figure 2 and Table 1 suggest that one of the permanent trapping sites (Soufriere Hospital) consistently produced much higher yields than any of the other sites, including those sampled with temporary traps. However, the authors don't discuss potential explanations for this phenomenon, or the ways in which this fact could (or not) create bias on their data analysis. I suggest they revise the discussion addressing these observations.

Soufriere Hospital did indeed produce higher yields and we have added three sentences at the start of the second paragraph in the discussion to show how the trapping location had several optimal characteristics for *Ae. aegypti*.

As the authors correctly point out, the detection of flavivirus-like RNA in a mosquito could very well be the product of a transcribed cell silent agents (CSA) integrated in the insect's genome sometime in the past. While it is certainly possible that a novel, extant virus could be the source of such CSA, it is also possible that the sequences obtained by the authors represent a CSA originating from a known virus and subsequently mutated after insertion in the mosquito genome. Alternatively, the sequences could correspond to a CSA derived from an extinct virus. In any case, I think that in the absence of a full viral genome, the authors should be more careful about their claim of having identified a novel insect-specific virus.

We agree and have modified the end of our discussion to provide a more balanced view. Additional CFAV sequences which became publicly available after the original analysis have now enabled a re-analysis to be carried out which has been incorporated into the latest version of the manuscript, with relevant areas updated.

The 'Conclusions' section discusses aspects such as the spread of arboviral diseases, the limited options available for vector control, the history of Zika outbreaks (among other), which are at best tangentially related to the paper's original results. I recommend that the authors re-write this section, presenting conclusions that are actually related to their original work.

We agree and have modified our conclusions to include some sentences on insect-specific flaviviruses. However, confirmation of a wide distribution of *Ae. aegypti* on the island of St Lucia as part of our entomology survey and screening for human arboviruses undertaken does (in our opinion) relate to the possibility for future arboviral outbreaks.

Minor Revisions:

Throughout the paper, please italicize scientific names.

We have done this.

Introduction:

- The authors state that “22 countries and territories have now been identified to have autochthonous transmission”, which could be interpreted as being a global tally of countries reporting Zika transmission. However, this number (a) corresponds exclusively to the Americas, and (b) represents an outdated figure. The latest figures available from the Pan- American Health Organization (available here) indicate that just within the Americas, 48 countries and territories have reported mosquito-borne Zika transmission. Considering that earlier on the paper the authors provide global data for the epidemiology of dengue, I would recommend revising this figure to reflect updated global data on Zika distribution. One potential source is the World Health Organization’s Zika Epidemiology Update (available here).

Many thanks for pointing this out and we have updated our figures based on the last available WHO update (July 2019).

- The authors state that “widespread insecticide resistance has developed in *Ae. aegypti*, including high pyrethroid resistance rates in South America and further north in the Caribbean”. To back up this statement, the authors cite a single paper focused on resistance found on a specific location in Brazil, and one paper focusing on a location in the Caribbean. I would recommend that the authors increase the number of citations to better represent the actual spread of pyrethroid resistance in the region. Suggestions include: Fonseca-Gonzalez *et al.* (2011)¹ , Rawlins SC (1998)² , Ryan SJ *et al.* (2019)³

Many thanks for these suggestions to better represent pyrethroid resistance and we have incorporated these references.**Methods:**

- The authors should provide a clearer summary of their trapping strategy. In the current text, they state that trapping was performed using four permanent traps and four temporary traps, for what can be understood as a total of eight traps per each 24-hour period. However, mosquito trapping data available on the supplementary files suggests that on most dates only six or less traps were used.

Yes that is correct and this was due to logistical difficulties accessing all sites across the island so not all trapping days had four temporary traps running synchronous with the four longer-term permanent traps. Our methods have now been modified for clarity.

- Please specify which taxonomic key was used to separate mosquito genera. If no specific key was used, please provide a complete list of characters used to sort specimens by genus.

In our methods we have the following sentences:

‘Trapped mosquitoes were collected, killed on ice for genera morphological identification to identify individuals belonging to the *Aedes* genus using basic defining characteristics including patterns of light and dark scales on the abdomen and thorax and alternating light and dark bands on the legs.’

We then used ITS1 real-time PCR assays that discriminates between *Ae. aegypti* and *Ae. albopictus*.

- The legend in Figure 1 makes reference to an inset showing a “representative BG

Sentinel 2 trap placed in the Des Cartier rainforest". However, the actual figure does not contain any inset showing a representative trap.

Thank you for pointing this out – this was error from a previous figure version and we have removed this reference to the trap from the figure legend.

- Please specify what kind of primers were used for reverse-transcription reaction.

We have added in the methods that random primers are used with the QuantiTect Reverse transcription Kit

- Discussion: In the first paragraph of the discussion, the sentence "The principle vector of these arboviral diseases..." should be changed to "The principal vector of these arboviral diseases..."

Thank you for spotting this error and we have amended this

Competing Interests: No competing interests were disclosed.

Reviewer Report 14 July 2020

<https://doi.org/10.21956/wellcomeopenres.17585.r39242>

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Jandouwe Villinger 

International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya

This is a generally well written manuscript on a study surveying mosquito viruses in St Lucia. Although no arboviruses were detected, they found a 19% prevalence of Aedes-specific flaviviruses. There is a general lack in the literature of information on individual prevalence of insect-specific flaviviruses in mosquito populations. Therefore, their infection rate data could be highlighted more in the paper

My main concern is that the authors are likely over interpreting their finding of a new Aedes-specific flavivirus (AeFV) sequence as a novel insect-specific flavivirus. Just a few CFAV sequences and only one other AeFV sequence are included in the phylogenetic analyses. CFAV is part of a clade of AeFVs that are broadly distributed and show variation. The Saint Lucia AeFV seem to fall within the expected variation of AeFVs, if not even CFAVs. At the very least the sequence they found simply represents a new strain of AeFV associated with *Aedes aegypti* in St. Lucia. Percent nucleotide homologies are not given, so I cannot fully judge, but these are likely a St. Lucia lineage of CFAV. It would also be useful if there were GenBank accession numbers associated with the study's ISF sequences so that their phylogenies can be independently assessed and the sequences can be used in future analyses of ISF variation/evolution.

Please consider the recent papers:

Patterson *et al.* (2020)¹.

Baidaliuk *et al.* (2020)².

Minor comments:

- The authors should ensure that conventions are followed and that genus and species names are italicized (double check all '*Ae. aegypti*' and '*Alphavirus*').
- It is not clear to me why Figure 3 is required as the same information is fully represented in Figure 4. I think that Figure 3 can be removed.

References

1. Patterson EI, Villinger J, Muthoni JN, Dobel-Ober L, et al.: Exploiting insect-specific viruses as a novel strategy to control vector-borne disease. *Curr Opin Insect Sci.* 2020; **39**: 50-56 [PubMed Abstract](#) | [Publisher Full Text](#)
2. Baidaliuk A, Lequime S, Moltini-Conclois I, Dabo S, et al.: Novel genome sequences of cell-fusing agent virus allow comparison of virus phylogeny with the genetic structure of *Aedes aegypti* populations. *Virus Evol.* 2020; **6** (1): veaa018 [PubMed Abstract](#) | [Publisher Full Text](#)

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

Partly

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?

No

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

No

Are the conclusions drawn adequately supported by the results?

No

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Molecular entomology of mosquito- and tick-borne diseases.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 15 Dec 2020

Thomas Walker, London School of Hygiene & Tropical Medicine, Keppel Street, London, UK

Response to reviewer 1

Many thanks Jandouwe for your thoughtful review. Our responses are shown below in bold:

My main concern is that the authors are likely over interpreting their finding of a new Aedes-specific flavivirus (AeFV) sequence as a novel insect-specific flavivirus. Just a few CFAV sequences and only one other AeFV sequence are included in the phylogenetic analyses. CFAV is part of a clade of AeFVs that are broadly distributed and show variation. The Saint Lucia AeFV seem to fall within the expected variation of AeFVs, if not even CFAVs. At the very least the sequence they found simply represents a new strain of AeFV associated with *Aedes aegypti* in St. Lucia. Percent nucleotide homologies are not given, so I cannot fully judge, but these are likely a St. Lucia lineage of CFAV. It would also be useful if there were GenBank accession numbers associated with the study's ISF sequences so that their phylogenies can be independently assessed and the sequences can be used in future analyses of ISF variation/evolution.

Please consider the recent papers: Patterson *et al.* (2020), Baidaliuk *et al.* (2020)

We agree that although we included all relevant sequences that we were able to obtain at the time of original analysis, on which we based our original results and conclusions, there have since been further CFAV sequences made publicly available. We have therefore undertaken a reanalysis which now indicates our sequences are identical or very closely related to the CFAV sequence from Guadeloupe (From Baidaliuk *et al.* 2020)¹ and alongside this sequence may potentially form a Caribbean lineage of CFAV. We have adjusted our manuscript in all relevant areas to reflect this and replaced the previous Figure 3 and 4 phylogenetic trees with a single updated phylogenetic tree (now Figure 3) from the re-analysis which incorporates additional more recently available sequences of CFAV for a more comprehensive comparison.

We have now also included our % nucleotide homologies following re-analysis, in addition to further sequencing analysis information, within the Jeffries *et al.* qPCR and sequencing analysis file in the *Underlying data*.

As we sequenced products from a Pan-flavivirus PCR assay which detects a wide range of viruses², we obtained sequences less than 200bp and therefore Genbank unfortunately will not accept these. However, as stated in the underlying data section, raw sequence data is available at <https://doi.org/10.17605/OSF.IO/DACKS>.

Minor comments:

- The authors should ensure that conventions are followed and that genus and species names are italicized (double check all '*Ae. aegypti*' and '*Alphavirus*').

We have checked and corrected our manuscript for these conventions.

- It is not clear to me why Figure 3 is required as the same information is fully represented in Figure 4. I think that Figure 3 can be removed

We agree and as mentioned above we have removed both the previous Figure 3 and 4

