Wolbachia in native populations of aedes albopictus (Diptera: Culicidae) from Yucatan Peninsula, Mexico

Henry Puerta-Guardo, Universidad Autónoma de Yucatán
Yamili Contreras-Perera, Universidad Autónoma de Yucatán
Silvia Perez-Carrillo, Universidad Autónoma de Yucatán
Azael Che-Mendoza, Universidad Autónoma de Yucatán
Guadalupe Ayora-Talavera, Universidad Autónoma de Yucatán
Gonzalo Vazquez Prokopec, Emory University
Abdiel Martin-Park, Universidad Autónoma de Yucatán
Dongjing Zhang, Zhongshan School of Medicine
Pablo Manrique-Saide, Universidad Autónoma de Yucatán

Journal Title: Journal of Insect Science
Volume: Volume 20, Number 5
Publisher: Oxford University Press | 2020-09-01, Pages 1-7
Type of Work: Article | Final Publisher PDF
Publisher DOI: 10.1093/jisesa/ieaa096
Permanent URL: https://pid.emory.edu/ark:/25593/vqrpb

Final published version: http://dx.doi.org/10.1093/jisesa/ieaa096

Copyright information:
© The Author(s) 2020. Published by Oxford University Press on behalf of Entomological Society of America.

This is an Open Access work distributed under the terms of the Creative Commons Attribution-NonCommercial 4.0 International License (https://creativecommons.org/licenses/by-nc/4.0/).

Accessed November 12, 2022 1:06 AM EST
Wolbachia in Native Populations of Aedes albopictus (Diptera: Culicidae) From Yucatan Peninsula, Mexico

Henry Puerta-Guardo,1 Yamili Contreras-Perera,1 Silvia Perez-Carrillo,1 Azael Che-Mendoza,1 Guadalupe Ayora-Talavera,2 Gonzalo Vazquez-Prokopec,3 Abdiel Martin-Park,1 Dongjing Zhang,4 Pablo Manrique-Saide,1,5 and UCBE-LCB Team1

1Unidad Colaborativa de Bioensayos Entomológicos (UCBE) y del Laboratorio de Control Biológico (LCB) para Ae. aegypti, Universidad Autónoma de Yucatán (UADY), Campus de Ciencias Biológicas y Agropecuarias, Km. 15.5 Carr. Mérida-Xmatkuil s.n., C.P. 97315, Mérida, Yucatán, Mexico, 2Centro de Investigaciones Regionales, Dr. Hideyo Noguchi, Universidad Autónoma de Yucatán (UADY), Merida, Yucatan, Mexico, 3Department of Environmental Sciences, Emory University, Atlanta, GA, 4Key Laboratory of Tropical Disease Control of the Ministry of Education, Sun Yat-sen University—Michigan State University Joint Center of Vector Control for Tropical Diseases, Zhongshan School of Medicine, Sun Yat-sen University, Guangzhou, China, and 5Corresponding author, e-mail: pablo_manrique2000@hotmail.com

Subject Editor: Blake Bextine

Received 26 May 2020; Editorial decision 17 August 2020

Abstract

This study reports the results of a molecular screening for Wolbachia (Wb) infection in Aedes albopictus (Skuse) populations recently established in the Yucatan Peninsula, Mexico. To do so, collections of free-flying adults with BG traps and emerged adults from eggs after ovitraps field collections were performed in three suburban localities of the city of Merida, Yucatan. Overall, local populations of Ae. albopictus present a natural Wb infection rate of ~40% (18 of 45). Wb infection was detected in both field-collected adults (76.5%, 13 of 17) and eggs reared (17.8%, 5 of 28) and in 37.3% (11/29) of females and 43.7% (7/16) of male Ae. albopictus mosquitoes. An initial screening for Wolbachia strain typing showed that native Ae. albopictus were naturally coinfected with both wAlbA and wAlbB strains. The knowledge of the prevalence and diversity of Wolbachia strains in local populations of Aedes mosquitoes is part of the baseline information required for current and future Wolbachia-based vector control approaches to be conducted in Mexico.

Key words: Wolbachia, Aedes albopictus, Aedes aegypti, wAlbA, wAlbB

Aedes (Stegomyia) albopictus (Skuse), commonly known as the ‘Asian tiger mosquito’, is considered a secondary but competent vector of arboviruses of great importance in public health including dengue (DENV), chikungunya (CHIKV; Bonizzoni et al. 2013), and Zika (ZIKV; McKenzie et al. 2019). Although it is native to Asia, it has invaded and colonized many countries in the Americas, Europe, and Africa (Battaglia et al. 2016, Kraemer et al. 2019). In Mexico, Ae. albopictus has been recorded in 16 states including Mexico City, Guanajuato, Jalisco, Coahuila, Chiapas, Hidalgo, Morelos, Nuevo León, Oaxaca, San Luis Potosí, Sinaloa, Tabasco, Tamaulipas, Veracruz, Yucatán, and Quintana Roo (Villegas-Trejo et al. 2010, Salomón-Grajales et al. 2012, Ortega-Morales et al. 2018, Contreras-Perera et al. 2019, Dávalos-Becerril et al. 2019, González-Acosta et al. 2020), but its geographical distribution is expected to increase because the macro- and micro ecological conditions suitable for its establishment, particularly throughout South Mexico (Pech-May et al. 2016, Yañez-Arenas et al. 2018).

Wolbachia (Rickettsiaceae) (hereafter called as Wb) are ubiquitous obligate bacterial endosymbionts that naturally infect ~20% of all insect species (Hilgenboecker et al. 2008). Wb is maternally transmitted in insects, and it is known to exert a profound impact on host biology, mainly at the reproductive level. The most common reproductive effect is called cytoplasmic incompatibility (CI). Wb-induced CI modulates the production of viable eggs once an uninfected female mates a Wb-infected male, whereas Wb-infected females can successfully breed with either infected or uninfected males (Werren et al. 2008).

Wb naturally infects many mosquito species including Ae. albopictus but not the primary dengue vector Aedes aegypti (Ross et al. 2020). Wb introduced into Ae. aegypti via transinfection can cause early embryonic arrest (CI) and egg hatch failure (Mains et al. 2019). Interestingly, Wb can also cause pathogen interference in Ae. aegypti as Wb-infected mosquitoes are less susceptible to be infected or coinfected with important arboviruses such as DENV, CHIKV, ZIKV, Mayaro virus, and yellow fever virus (Moreira et al. 2009, 2013), and Zika virus (ZIKV; McKenzie et al. 2019).
Walker et al. 2011, Aliota et al. 2016, Pereira et al. 2018). This has led to inundative field-releases of Wb-infected mosquitoes as a potential control strategy for Ae. aegypti, either by population suppression (Crawford et al. 2020) or by population replacement (World Mosquito Program 2017, Nazni et al. 2019, Ryan et al. 2019).

In Mexico, both Wolbachia-based approaches, one using Wb strain wMel (Wolbachia pipientis from Drosophila melanogaster; Dutra et al. 2015, Nguyen et al. 2015) for population replacement in Baja California, and another using wAlbB (Wolbachia pipientis from Ae. albopictus; Xi et al. 2005) for population suppression in Yucatan, are under initial phases of implementation and evaluation for the control of Ae. aegypti. Data on natural infection frequency are critical to evaluate the potential of using Wolbachia as a vehicle to modify insect vector populations (Turelli and Hoffmann 1999, Kitrayapong et al. 2002). However, the prevalence and characteristics of Wolbachia in natural mosquito populations are yet poorly known in Mexico.

Aedes albopictus was recently reported in the periphery of Merida, the capital of the state of Yucatan, and the city with the largest population and major epidemiological importance in the Peninsula of Yucatan for the transmission of DENV, CHIKV, and ZIKV (Contreras-Perera et al. 2019). Aedes albopictus is very soon expected to invade and coexist with populations of Ae. aegypti in Merida. Thus, this study showed the molecular screening for Wolbachia infection of field-collected adult Ae. albopictus mosquitoes in the suburban areas of Merida, Yucatan.

Materials and Methods

Study Area

Field collections of local Aedes populations (adults and eggs) were performed every week from April to December of 2019 at San Pedro Chimay (20°51′55″N 89°34′46″O), Hacienda Tahdzibichen (20°53′06″N 89°35′52″O), and Tekik de Regil (hereafter Tekik; 20°48′59″N 89°33′39″O), all suburban areas in the periphery of the city of Merida in the Peninsula of Yucatan (southeast Mexico; Fig. 1A). Sociodemographic features of these localities include an average of 1,200 inhabitants per locality with an average of 6 households and 31 inhabitants per hectare (INEGI 2016). They share similar urban and ecological landscapes such as type of housing and share large vegetated backyards with vegetation (coverage > 60%). The average altitude of the localities is 9 m above sea level. The climate is mainly warm with an annual average temperature of 26°–27°C (36°C max–18°C min), relative humidity of 70–75%, and two distinct climate phases during the year: a rainy season, from May/June to October with a rainfall of 882.5 mm, and a dry season, from November to April with rainfall of 167.9 mm (INEGI 2017).

Mosquito Collection and Rearing

Aedes adults were collected using outdoor BG-sentinel traps (20–30 traps per locality) for 24 h/periods, one per week), as part of the routine surveillance for control of Ae. aegypti in the suburban communities of Merida performed by the Collaborative Unit for Entomological Bioassays (UCBE) and the Universidad Autonoma de Yucatan (UADY). According to the CDC and other studies, BG-sentinel traps are currently the most used and the gold-standard adult traps for the sampling, monitoring, and surveillance of outdoor Aedes and Culex species in field trials (Li et al. 2016, CDC 2018). Collected specimens were transported to UCBE-UADY for their identification using standard taxonomic keys (Rueda 2004). As part of the vector control program protocol in Mexico, corroboration and validation of larvae and adult specimens of mosquitoes is supported by the National Reference Center at the Instituto de Diagnóstico y Referencia Epidemiológicos (InDRE) of the Ministry of...
Health in Mexico. Voucher specimens are deposited at the Colección Entomológica Regional (CER)—Universidad Autónoma de Yucatán (UADY). All *Ae. albopictus* were separated from *Ae. aegypti*, which is also present in the localities. *Aedes* eggs were collected using ovitraps (approximately one ovitrap per Ha) in each locality and served weekly. Paper strips with eggs were sent to the LCB-UADY for mosquito rearing following standard operating procedures of the LCB-UADY. Briefly, eggs were incubated for embryo development (48 h) at room temperature. Larvae were reared and fed 6% larvae feeding solution (Food product for tilapia [Biofingerlin]: yeast powder [Pranat Ultra], 9:1, respectively) in plastic containers with water. Pupae obtained were maintained within BugDorm-1 Insect Rearing Cages. Adults emerged were maintained for 24 h under standard insectary conditions at 80 ± 5% humidity, 26 ± 1°C, and 12/12 light/dark cycle. Then, specimens were cold immobilized for taxonomic classification and stored at −20°C until further analyses.

**DNA Extraction and PCR Screening for Wolbachia Infection**

Total genomic DNA from individual adult mosquitoes was extracted using a Blood and Tissue DNAEasy Kit (Qiagen, Hilden, Germany) following the manufacturer’s instructions with some in-house modifications. Briefly, individual adult mosquitoes were firstly disinfected inside sterile Eppendorf tubes (70% ethanol) at room temperature (2 h) and later mechanically homogenized using a sterile pestle and electric homogenizer after adding the lysis buffer from the DNA extraction kit (Qiagen). After elution, DNA was quantified using a nanodrop (Thermo Scientific) and stored at −20°C until further analyses. To detect *Wolbachia* infection in *Aedes* mosquitoes, an initial set of primers was used to specifically amplify the 16S rRNA from *Wolbachia* as previously described: 16-2F (5′-AGCTTCGAGTGAAACCAATTC-3′) and 16-2R (5′-GAAGATAATGACGGTACTCAC-3′) PCR product size (bp) ~1,000 Multistrain Simoes et al. (2011). An end point PCR protocol was performed using a Mastercycler EP Gradient-Thermal-Cycler (Eppendorf) and Taq DNA polymerase recombinant kit including PCR buffer (10×), MgCl₂ (50 mM), dNTPs mix (10 mM), forward and reverse primers (10 μM), Taq DNA polymerase (5 U/μl), RNAse/DNAse-free water, and forward and reverse primers (10 μM) to amplify DNA genome from *Wolbachia* strain A and B described as follows: primers 328F (5′-CCAGCAGATACTATTGCG-3′) and 691R (5′-AAAAATTAAACGCTACTCCA-3′) for *wAlbA* strain, and primers 183F (5′-AAGGACCGAAGTTCTAGT-3′) and 691R (describe above) for *wAlbB*. Amplification parameters were established as described above for 16-2 primers. DNA extracted from *Ae. aegypti* mosquitoes either *Wb* free (*wAlbID*) or *Wb* strain B infected (*wAlbIB*) was used as negative and positive controls for the PCR assay, respectively, following published protocols (Xi et al. 2005). These two sets of primers amplify a DNA fragment ranging from 400 to 600 bp depending on the individual *Wb* strain.

**Results and Discussion**

In total, 45 *Ae. albopictus* adult mosquitoes (64% female–36% male), among which was 17 captured with BG-sentinel traps and 28 reared from field-collected eggs using ovitraps, were examined for *Wb* infection by PCR from the three localities (Fig. 1A–D). The trapping *Ae. albopictus* mosquitoes in both adult and egg stages provide further evidence of the early invasion of this mosquito species in the suburban areas of the municipality of Merida (Salomón-Grajales et al. 2012, Ortega-Morales et al. 2018, Contreras-Perera et al. 2019).

In this study, using a universal set of primer nucleotides to amplify a sequence of the *Wb* 16S rDNA gene (Table 1), we initially assessed the circulation of *Wb* in native *Ae. albopictus* mosquitoes from all the localities, either from field-caught and free-flying adults or those reared from eggs (Fig. 2). This initial PCR assay resulted in the amplification of approximately 1,000 base pairs long DNA fragment, identified as positive for *Wb* infection (Fig. 2A), as it has been previously reported (Simoes et al. 2011, Carvajal et al. 2019).

Overall *Wb* infection rate in *Ae. albopictus* from all the localities was 40% (18/45; 37.9% of females, 43.7% of males; Table 2, Fig. 2A and B). Average *Wb* infection rate by locality was 13.3% and varied between localities (Table 2; Fig. 2E), with Tekik showing

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Nucleotide sequence (5′–3′)</th>
<th>PCR product size (bp)</th>
<th>Wolbachia strain</th>
<th>Reference(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>16-2F</td>
<td>AGTTCGGATGAACCAACATTTC</td>
<td>~1,000</td>
<td>Multistrain</td>
<td>Simoes et al. (2011)</td>
</tr>
<tr>
<td>16-2R</td>
<td>GAAAGATGACGGTACTCAC</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>328F</td>
<td>CCAGCAGATACTATTGCG</td>
<td>~300–400</td>
<td>A</td>
<td>Zhou et al. (1998); Ahmad et al. (2017)</td>
</tr>
<tr>
<td>691R</td>
<td>AAAATTAACGCTACTCCA</td>
<td>~500–600</td>
<td>B</td>
<td>Zhou et al. (1998); Ahmad et al. (2017)</td>
</tr>
</tbody>
</table>
the highest percentage of Wb infection (>60%) of all mosquitoes tested in that site (33.3% males, 33.3% females; Fig. 2). The overall Wb infection rate (40%) found in this study lies between several field surveys around the world using field-collected specimens, which have found variable frequency rates of Wb infection ranging from 11 to 100% (Kitrayapong et al. 2002, de Albuquerque et al. 2011, Zhang et al. 2014, Noor Afizah et al. 2015, Ahmad et al. 2017, Guo et al. 2018, Martin et al. 2019, Hu et al. 2020).

A 76.5% (13/17) of all adult mosquitoes directly captured in the field were positive for Wb infection. However, only few adults of Ae. albopictus reared from field-collected eggs (17.8%, 5/28) showed the presence of Wb genome. Wb are intracellular bacterium that can be vertically transmitted from infected females to their offspring (transovarial transmission) and considered its primary mode of dissemination within host species (Werren et al. 2008). Particularly in eggs, the density of Wb infection can be affected under certain environmental circumstances such as high temperature or prolonged light exposure, which reduced the ability of Wb to invade and persist in the mosquito populations (Ross et al. 2019). Nevertheless, our results showed that vertical transmission of Wb occurs in wild populations of Ae. albopictus in the suburban areas of Merida.

Although the natural infection of wild Ae. albopictus with Wb was expected, so far only one single report exists describing the circulation of Wb in mosquitoes of Mexico. Roblero-Andrade et al. (2019) reported Wb infections from free-flying Ae. albopictus populations collected from cemeteries in Chiapas, Southeast of Mexico. In total, 42% (135/343) of females collected were positive for Wb infection; however, only one male mosquito was tested in the study and this was Wb negative. Additionally, large variability in the infection rates (7.7%–100%) was also observed and no identification of the infecting Wb strain was performed (Roblero-Andrade et al. 2019). Our study in Yucatan we found similar rates of overall Wb infection in total adults Ae. albopictus (40%) and total females (37.9%) screened; and we provide information on the Wb infection rate of male Ae. albopictus mosquitoes for the first time in Mexico.

Naturally occurring populations of Ae albopictus can be single-infected or coinfected with two types of Wb strains known as wAlbA (supergroup A) and wAlbB (supergroup B; Werren et al. 1995,
Here, a set of five mosquito samples were further analyzed by PCR to amplify a segment of the *wsp* gene to determine which strain of *Wb* was circulating in these populations of *Ae. albopictus* of Yucatan. We identified strains A and B as the infecting *Wb* endosymbiont of *Ae. albopictus* (Fig. 3A and B). All samples analyzed showed an amplification product with a molecular size lower than 400 bp corresponding to *Wb* strain A (Fig. 3A, lanes 2–6), and four of these samples (Fig. 3B, lanes 2–5) showed an amplification fragment for *Wb* strain B (approx. 500 bp). These results indicate that coinfection with *Wb* strains A and B occurs in *Ae. albopictus* of Yucatan.

As expected, the DNA used as positive control obtained from *Ae. aegypti* previously infected with *Wb* strain B (*wMIDB*) showed an amplification fragment for *wAlbB*, but not *wAlbA* (Fig. 3A and B, lane 8). No amplicon was obtained when genomic DNA obtained from the native *Ae. aegypti* strain (*wtMID*) was used (Fig. 2A, lanes 10–11). The lack of any amplification product confirmed that the native populations of *Ae. aegypti* mosquitoes in the localities included in the study are not hosting *Wb* strains.

**Table 2. Wolbachia infection of individual adult *Aedes albopictus* mosquitoes collected in distinct suburban areas of Merida, Yucatan**

<table>
<thead>
<tr>
<th>Study sites</th>
<th>Sample type&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Sex (no. of individuals)</th>
<th><em>Wolbachia</em> infection (no. of PCR + individuals)</th>
<th><em>Wolbachia</em> infection rate (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tekik</td>
<td>Free-flying adults from BG traps</td>
<td>F 3, M 1</td>
<td>Total 9</td>
<td>F 3, M 1, Total 6</td>
</tr>
<tr>
<td></td>
<td>Adults emerged from eggs</td>
<td>F 0, M 5</td>
<td>Total 9</td>
<td>F 0, M 2</td>
</tr>
<tr>
<td>SPCH</td>
<td>Free-flying adults from BG traps</td>
<td>F 6, M 1</td>
<td>Total 24</td>
<td>F 4, M 1, Total 8</td>
</tr>
<tr>
<td></td>
<td>Adults emerged from eggs</td>
<td>F 9, M 8</td>
<td>Total 17</td>
<td>F 0, M 3</td>
</tr>
<tr>
<td>HT</td>
<td>Free-flying adults from BG traps</td>
<td>F 6, M 0</td>
<td>Total 12</td>
<td>F 4, M 0, Total 4</td>
</tr>
<tr>
<td></td>
<td>Adults emerged from eggs</td>
<td>F 5, M 1</td>
<td>Total 6</td>
<td>F 0, M 0</td>
</tr>
<tr>
<td>Total</td>
<td>Free-flying adults from BG traps</td>
<td>F 29, M 16</td>
<td>Total 45</td>
<td>F 11, M 7, Total 18</td>
</tr>
</tbody>
</table>

<sup>a</sup>F, female; M, male; Tekik, Tekik de Regil; SPCH, San Pedro Chimay; HT, Hacienda Tahdzibichen.
<sup>b</sup>Field-collected free-flying adults (collected at BG traps).
<sup>c</sup>Field-collected adults emerged from eggs (collected in the field with ovitraps).
<sup>d</sup>Estimated from *Wolbachia* positive females or males and the total of mosquitoes captured per locality.
<sup>e</sup>Estimated from total of *Wolbachia* positive (female/male) mosquitoes and the total of mosquitoes tested.

*Fig. 3. Molecular characterization of Wolbachia strains infecting adult *Aedes albopictus* mosquitoes of the suburban areas of Merida, Yucatan. PCR amplification of *Wb* DNA genome from total genomic DNA extracted from individual *Ae. albopictus* mosquitoes using two set of primers specific for *Wb* strain A (A) and B (B). A representative image showing a group of five positive samples (lanes 2–7). An amplicon of 400 and 500 bp was considered positive for *Wb* infection with strain A and B, respectively; positive control: genomic DNA from *Aedes aegypti* infected with *Wb* strain B (*wMIDB*; *Xi* et al. 2005; lane 8); negative control: genomic DNA from wild-type *Ae. aegypti* (*Wb* free) from Yucatan (*wtMID*; lane 9); DNA marker of 100 bp (lanes 1 and 10).*
Acknowledgments

We acknowledge the field-surveillance team at UCBE for species determination and mosquito sampling. We also like to thank Dr. Zhiyong Xi at Michigan State University and Sun Yat-sen University for kindly donating *Aedes aegypti* mosquitoes artificially infected with the *Wolbachia* strain B, used as a positive control in the molecular characterization and validation of *Wolbachia* infection in *Aedes albopictus* of Yucatan by PCR. Abdel Martin-Park is supported by the Catedras-CONACYT program. Research funding was provided by Fondo Mixto CONACyT (Mexico)–Gobierno del Estado de Yucatan (Project YUC-2017-03-01-556) and USAID (Project AID-OAA-F-16-00082).

Author Contributions


Conflict of Interest

The authors declare no conflicts of interest.

References Cited


