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Address for correspondence: Laurent Poirel, Virologie, Hôpital de Bicêtre, 76 Rue du Général Leclerc, 94275 Le Kremlin-Bicêtre, Cedex, France; email: laurent.poirel@bct.aphp.fr

Aedes albopictus Mosquitoes, Yucatan Peninsula, Mexico

To the Editor: We collected Asian tiger mosquitoes, *Aedes albopictus* (Skuse), in Cancun in the Yucatan Peninsula of Mexico in September 2011. This mosquito is a nuisance biter of humans and a vector of numerous arboviruses, including those causing dengue, yellow fever, and chikungunya (1).

Ae. albopictus mosquitoes, which are native to Southeast Asia, emerged in the continental United States in 1985 and thereafter spread rapidly across the southeastern United States and into northern Mexico (2,3). These mosquitoes have also been found in the states of Tamaulipas, Coahuila, and Nuevo Leon in northern Mexico, Chiapas in southern Mexico, and south of Mexico in Guatemala and Belize (3–9). These findings are now complemented by our collection of *Ae. albopictus* mosquitoes from Cancun in Quintana Roo State, which with Yucatan and Campeche States compose the Yucatan Peninsula. A previous study of the mosquito fauna of Quintana Roo conducted in 2006 did not report any *Ae. albopictus* mosquitoes (10).

During September 2011, *Ae. albopictus* mosquitoes were collected from a cemetery in Cancun, which is located in the eastern part of the Yucatan Peninsula (21°8.53'N, 86°52.79'W) (Figure). The collection location was shaded by trees. Water in containers from which larvae were collected had an average temperature of 24.5°C and a pH of 8.5. The larval collection included ≈30 specimens of different developmental stages that were collected from vases and other artificial containers in the cemetery. The containers were examined as part of routine surveillance activities by Servicios Estatales de Salud de

Quintana Roo. Larvae suspected to be those of *Ae. albopictus* mosquitoes were reared to adults for identification, and a colony of *Ae. albopictus* mosquitoes from Cancun was established.

F₀ or F₁ adult specimens were confirmed to be *Ae. albopictus* mosquitoes by species identification at Servicios Estatales de Salud de Quintana Roo (Quintana Roo, Mexico), Universidad Autónoma de Yucatan (Merida, Mexico), and Colorado State University (Fort Collins, CO, USA). The initial mosquito larval collection was composed of 26 *Ae. albopictus*, 3 *Ae. aegypti*, and 1 *Culex* sp. In addition, 6 *Ae. albopictus* female mosquitoes were collected from the cemetery by landing catches.

Finding *Ae. albopictus* mosquitoes in Cancun was not surprising because these mosquitoes have been found in nearby Belize (9). Cancun is also a major port for ships carrying tourists and goods that originate in areas to which *Ae. albopictus* mosquitoes are endemic, including Florida and Texas. Nevertheless, the introduction of *Ae. albopictus* mosquitoes into Cancun and the high potential for establishment and spread across the Yucatan Peninsula has major public health implications.

The Yucatan Peninsula is hyperendemic for dengue, with all 4 dengue virus (DENV) serotypes circulating in this region. Should *Ae. albopictus* mosquitoes persist in this region, they may spread and come to play a secondary role to *Ae. aegypti* mosquitoes as local vectors of DENV. *Ae. albopictus* mosquitoes may also change local virus transmission dynamics. For example, DENV transmission may be intensified in rural areas because *Ae. albopictus* mosquitoes are more likely than *Ae. aegypti* mosquitoes to be found in this setting. *Ae. albopictus* and *Ae. aegypti* mosquitoes also may differ in their potential for vertical transmission of DENV, which could

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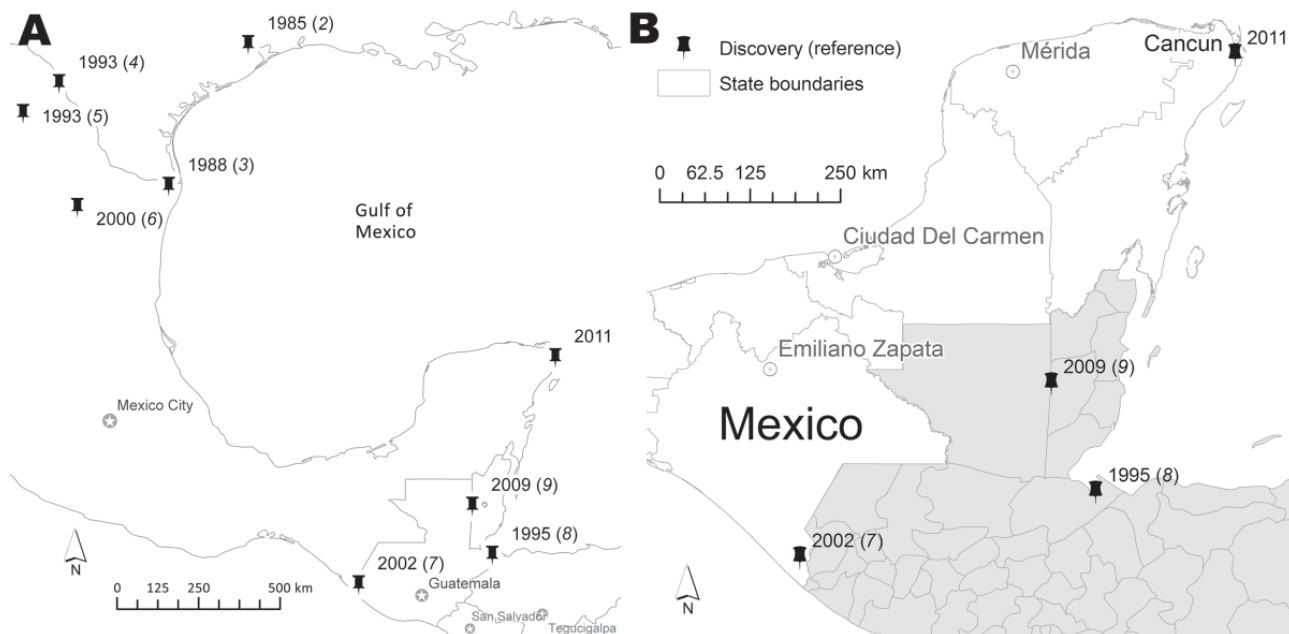


Figure. Notable locations (pushpins) in Mexico, the United States, and Central America where *Aedes albopictus* mosquitoes were collected and year of the first collection (reference) (A), including the current collection in 2011 from Cancun, Quintana Roo State, Mexico (B). Shaded areas indicate countries in Central America (Guatemala, Belize, Honduras, and El Salvador).

affect virus transmission dynamics, especially during interepidemic periods or parts of the year that have low mosquito activity and infrequent human–mosquito contact. Other concerns regarding introduction of *Ae. albopictus* mosquitoes into the Yucatan Peninsula are their role as an aggressive nuisance biter of humans, which may necessitate intensified mosquito control to protect the local tourist industry; and their potential role as a vector of chikungunya virus, which is a major threat to immunologically naive populations in the Americas should the virus emerge there.

Introduction of *Ae. albopictus* mosquitoes into the Yucatan Peninsula requires research on local biology of the mosquito and their potential role as an arbovirus vector in this part of Mexico. Studies are needed to determine how fine-scale spatial segregation of *Ae. albopictus* and *Ae. aegypti* mosquitoes might result from competition for containers that serve as larval development sites, from differential survival

related to container type, and from hydrologic microclimates or nutrient conditions. One possible scenario is for *Ae. albopictus* mosquitoes to outcompete and exclude *Ae. aegypti* mosquitoes from certain settings. Other issues include how effectively *Ae. albopictus* mosquitoes can transmit locally circulating DENV strains and, because this species bridges the transitional zone from urban to forested environments and may bite a wide range of mammals, what role it might play in the urban emergence of arboviruses that are currently restricted to sylvatic forest transmission cycles in the Yucatan Peninsula.

This study was supported in part by the National Institutes of Health/National Institute of Allergy and Infectious Diseases (International Collaborations in Infectious Disease Research Program U01-AI-088647).

**Jaime Salomón-Grajales,
Gerardo V. Lugo-Moguel,
Víctor R. Tinal-Gordillo,
Jorge de La Cruz-Velázquez,
Barry J. Beaty, Lars Eisen,
Saul Lozano-Fuentes,
Chester G. Moore,
and Julián E. García-Rejón**

Author affiliations: Servicios Estatales de Salud, Quintana Roo, Mexico (J. Salomón-Grajales); Departamento de Vectores de la Jurisdicción Sanitaria No 2, Quintana Roo (G.V. Lugo-Moguel, V.R. Tinal-Gordillo, J. de La Cruz-Velázquez); Colorado State University, Fort Collins, Colorado, USA (B.J. Beaty, L. Eisen, S. Lozano-Fuentes, C.G. Moore); and Universidad Autónoma de Yucatan, Yucatan, Mexico (J.E. García-Rejón)

DOI: <http://dx.doi.org/10.3201/eid1803.111626>

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Address for correspondence: Lars Eisen, Department of Microbiology, Immunology, and Pathology, Colorado State University, Infectious Disease Annex, 1690 Campus Delivery, Fort Collins, CO 80523, USA; email: lars.eisen@colostate.edu

Prevalence of Nontuberculous Mycobacteria Infection, China, 2004–2009

To the Editor: Pulmonary nontuberculous mycobacteria (NTM) diseases share clinical signs with tuberculosis (TB), causing a clinical dilemma with regard to therapy for patients with these diseases (1). In the past 30 years (post-AIDS era), NTM have increasingly been associated with pulmonary diseases in humans (2). Recent studies in urban areas of the People's Republic of China have shown that the prevalence of NTM (isolation rate of NTM among all mycobacteria) is increasing; for example, prevalence in Shanghai increased from 4.26% in 2005 to 6.38% in 2008 (3). To investigate NTM prevalence in rural areas of China, we evaluated the NTM isolation rates, species distribution, and drug-resistance profiles through a population-based TB sentinel surveillance study in Shandong Province, the second largest province in China. The study protocol was approved by the Institutional Review Board of Shandong Provincial Chest Hospital (Jinan, Shandong, China).

Clinical samples were collected through the ongoing sentinel TB surveillance project, which first began in 7 counties in Shandong Province in 2004 and expanded to 13 counties in 2008. Of the total surveillance population, rural populations accounted for ≈80%. Each sample collected in this study was identified only by a unique participant number. Each surveillance site sent sputum samples from all patients with suspected TB to the TB Reference Laboratory of Shandong Provincial Chest Hospital for mycobacterial culture, drug-susceptibility testing, and species identification.

From January 1, 2004, through December 31, 2009, *Mycobacteria*

spp. were isolated from sputum specimens from 3,949 patients with suspected pulmonary TB. Of these patients, mean age ± SD was 48.7 ± 20.4 years (range 1–92 years), 74.6% were male, and 300 were being re-treated for TB.

Identification of *Mycobacteria* spp. was first conducted by conventional biochemical testing—p-nitrobenzoic acid and 2-thiophene carboxylic acid hydrazide testing—following a standard protocol (4). *Mycobacteria* spp. were further identified by 16S rRNA gene sequence analysis (MicroSeq ID Microbial Identification Software, version 2.0; Applied Biosystems, Foster City, CA, USA) to the species level as described (5). Drug-susceptibility testing was performed according to standard procedures recommended by the World Health Organization, and quality control was conducted by inter-laboratory confirmation testing by reference laboratories recognized by the World Health Organization in South Korea and in Hong Kong Special Administrative Region, China (6,7). The drug panel included 4 first-line anti-TB drugs: isoniazid, rifampin, streptomycin, and ethambutol.

The conventional biochemical testing of the 3,949 *Mycobacteria* spp. strains identified 68 NTM strains, among which the 16s rRNA gene sequence analysis confirmed 64 (1.6%) NTM strains and identified 3 *M. tuberculosis* complex strains and 1 *Nocardia glanders* strain. Among the 64 NTM strains, 52 (81.2%) were *M. intracellulare*, 5 (7.8%) were *M. kansasii*, 3 (4.7%) were *M. fortuitum*, 2 (3.1%) were *M. chelonae*, 1 (1.6%) was *M. gordonae*, and 1 (1.6%) was *M. scrofulaceum*. The first-line anti-TB drug resistance rates of the 64 NTM strains were 100% for isoniazid, 98.4% for streptomycin, 78.1% for rifampin, and 51.6% for ethambutol (Table). Among the 3,949 *Mycobacteria* spp. strains, 163 (4.1%) were resistant to at least isoniazid and

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