

Drivers of spread of *Aedes aegypti*-borne infections in Latin America



 
Organized by the International Society for Infectious Diseases in collaboration with the Sociedad Argentina de Infectología (SADI)

BUENOS AIRES, ARGENTINA
MARCH 1-4, 2018

18th International Congress on Infectious Diseases

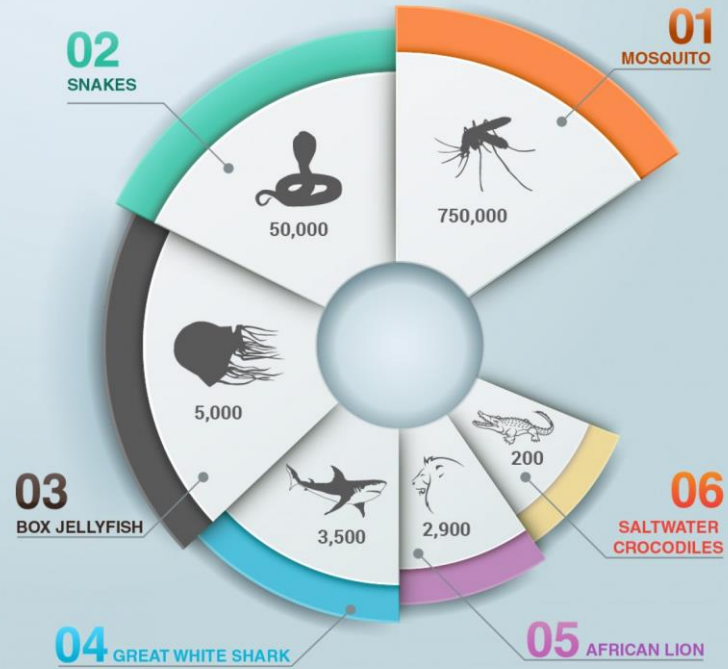
XVIII Congreso SADI

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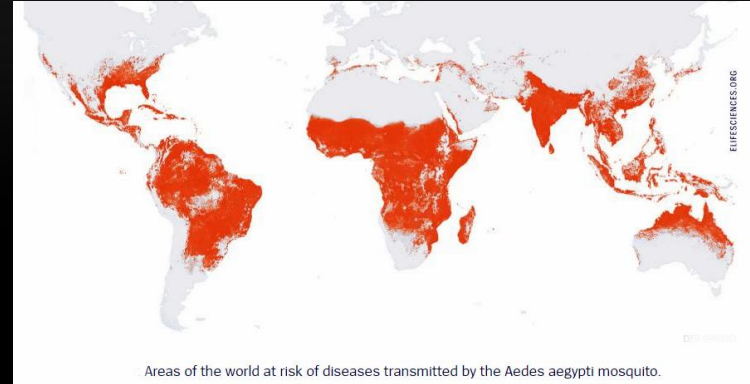
Jaime R. Torres , MD
Tropical Medicine Institute
Universidad Central de Venezuela



World's Most Dangerous Animals. (As per number of annual kills)



Dengue, Zika, Chikungunya
or Yellow Fever,
that is the question...



Areas of the world at risk of diseases transmitted by the *Aedes aegypti* mosquito.

Are some of us tastier than others...?

Why Do Some People Get Bitten More Than Others?

- How attractive you are to mosquitoes may be genetically based (about 85%, through gene control of body odor)
- Identical twins experience a similar number of mosquito bites while non-identical twins have a large disparity
- Movement and heat attract mosquitoes. Other factors include:

People with high concentrations of steroids or cholesterol on their skin surface	People who produce excess amounts of uric acid
People who give off more carbon dioxide, including pregnant women and those who are larger or overweight	People with Type O blood ⁸
People who are exercising, as this increases sweat, heat, lactic acid, and movement, all factors that lure in mosquitoes	Beer drinkers (for reasons that remain a mystery, drinking alcohol stimulates mosquito attraction) ⁹



Evolutionary transition from blood feeding to obligate nonbiting in a mosquito

Bradshaw et al. *PNAS*, Nov 2017

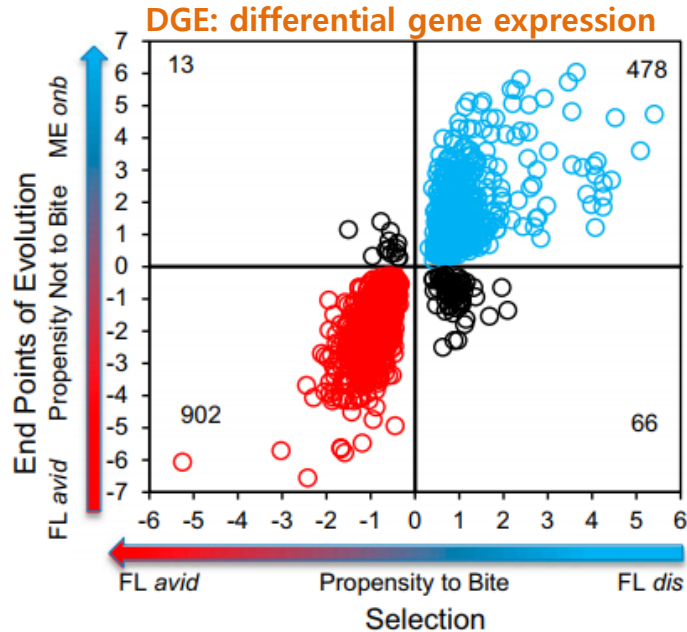


Fig. 2. *W. smithii*: DGE on the horizontal axis is associated with selection on blood feeding, and DGE on the vertical axis is associated with the evolution of nonbiting. The 902 biting genes are concentrated in the lower left; the 478 nonbiting genes are concentrated in the upper right. The orthogonal axis of 79 genes shows DGE not associated with selection on blood feeding.

If there is no bite, there is no disease transmission...

- Identification of key genes responsible for the evolution of an obligate nonbiting lifestyle, provides the potential to mitigate mosquito-borne diseases
- At the genetic level, it might lead to the identification of universal nonbiting genes or to universal target genetic pathways in mosquitoes

ZIKA, CHIK, DENGUE AEDES COINFECTIONS



PLOS | NEGLECTED TROPICAL DISEASES June, 2017

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RESEARCH ARTICLE

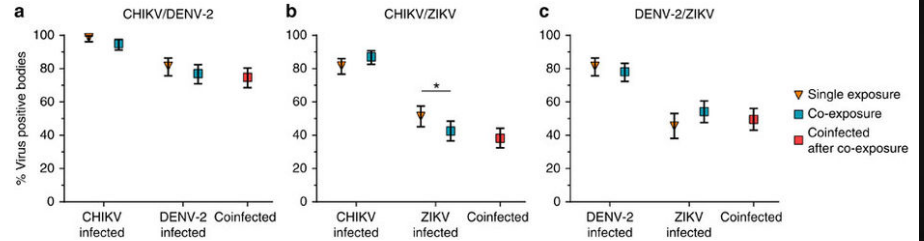
Mosquito co-infection with Zika and chikungunya virus allows simultaneous transmission without affecting vector competence of *Aedes aegypti*

Giel P. Goertz, Chantal B. F. Vogels, Corinne Geertsema, Constantianus J. M. Koenraadt, Gorben P. Pijlman

nature COMMUNICATIONS Ruckert C, et al. *Nature Communications* 2017, 8, Article number: 15412

Susceptibility of *Aedes aegypti* to arbovirus infection after single and dual exposure.

From: Impact of simultaneous exposure to arboviruses on infection and transmission by *Aedes aegypti* mosquitoes



Ae. aegypti mosquitoes were exposed to CHIKV, DENV-2 or ZIKV either individually or in combination by infectious bloodmeal. Infection rates for individual viruses after single exposure (yellow triangle) with CHIKV (a,b), DENV-2 (a,c) or ZIKV (b,c), and parallel co-exposures (blue square) with CHIKV/DENV-2 (a), CHIKV/ZIKV (b) and DENV-2/ZIKV (c) are





Evaluation of Simultaneous Transmission of Chikungunya Virus and Dengue Virus Type 2 in Infected *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae)

Nuckols J, et al

J Med Entomol, March 15, 2015

What Impacts a Vector's Ability to Transmit?

Zika virus alters the microRNA expression profile and elicits an RNAi response in *Aedes aegypti* mosquitoes

Miguel A. Saldaña , Kayvan Etebari , Charles E. Hart, Steven G. Widen, Thomas G. Wood, Saravanan Thangamani, Sassan Asgari , Grant L. Hughes 

Version 2 Published: July 17, 2017 • <https://doi.org/10.1371/journal.pntd.0005760>



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Original Article

MicroRNA levels are modulated in *Aedes aegypti* after exposure to Dengue-2

C. L. Campbell , T. Harrison, A. M. Hess, G. D. Ebel

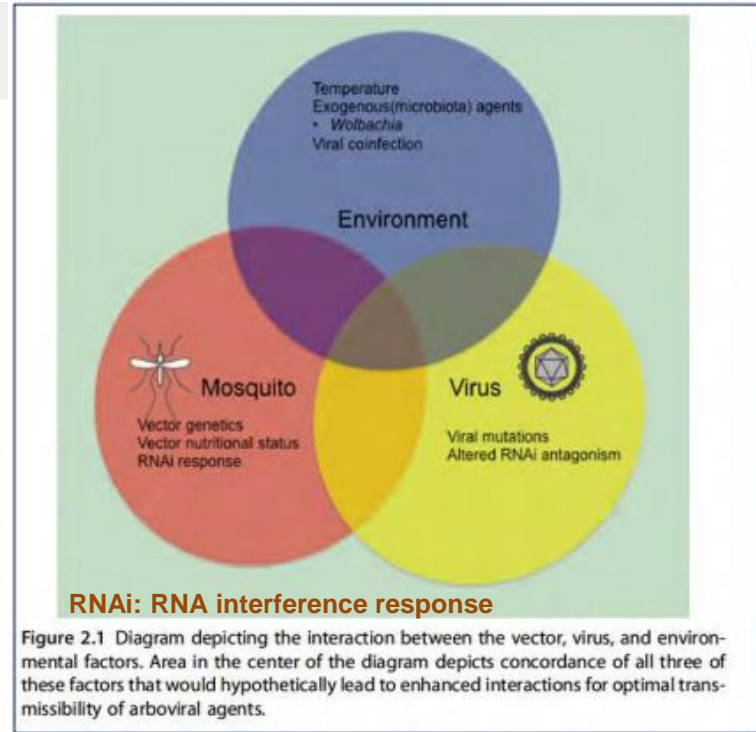
First published: 15 November 2013 [Full publication history](#)

Arbovirus Research Branch, Division of Vector-Borne Diseases, National Center for Emerging and Zoonotic Infectious Diseases, U.S. Centers for Disease Control and Prevention, Fort Collins, Colorado, USA
¹ Corresponding author: e-mail address: ahsult@cdc.gov

Advances in Virus Research, Volume 89

ISSN 0065-3527

<http://dx.doi.org/10.1016/B978-0-12-800172-1.00002-1>



OTHER FACTORS INVOLVED IN SPREAD OF AEDES AEGYPTI-BORNE DISEASES

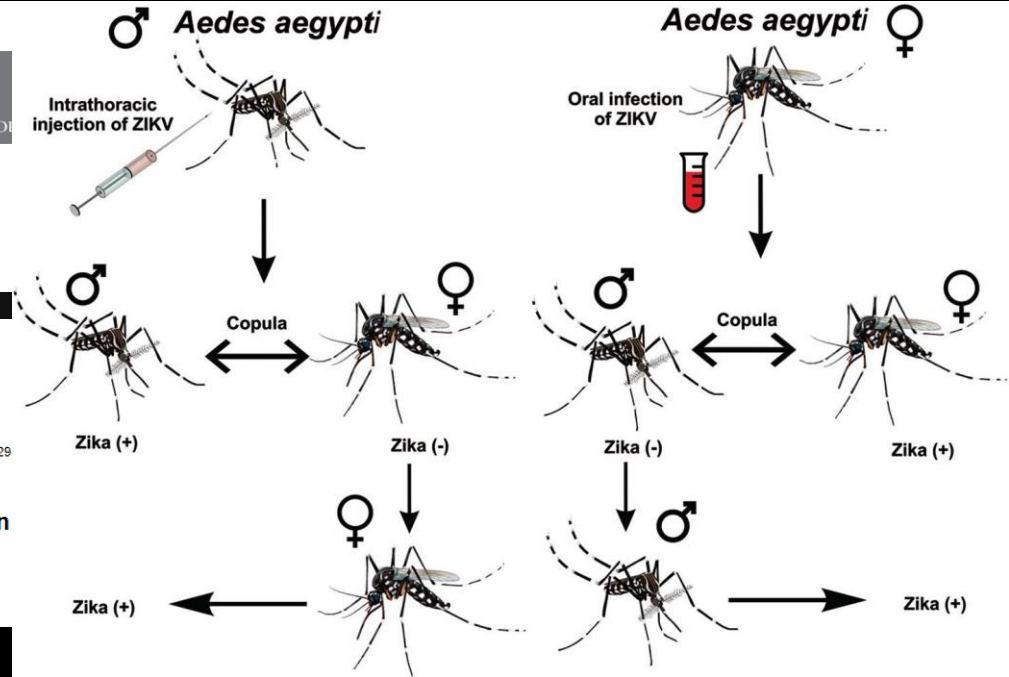


Mem Inst Oswaldo Cruz. 2018 Jan; 113(1): 56-61.
Published online 2017 Nov 27. doi: 10.1590/0074-02760170329

First evidence of Zika virus venereal transmission in *Aedes aegypti* mosquitoes

Martin Grunhill^{1,2} and Michael Boots³

PMCID: PMC5710150



PMCID: PMC484229

a virus in

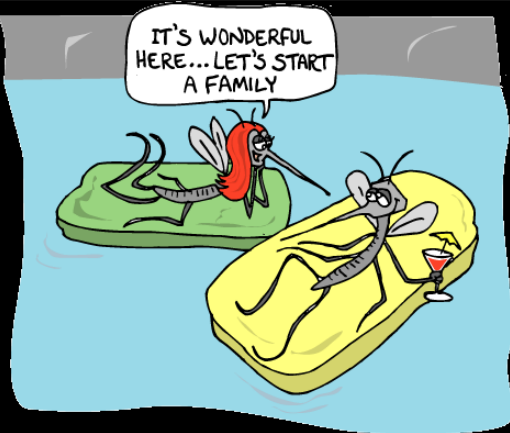
Somchai



Parasit Vectors. 2016; 9: 227.
Published online 2016 Apr 23.

Vertical transmission of Zika virus in *Aedes aegypti*

Jakkrawarn Chompoonsri,
Sangkitporn, and Padet S



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Published Date: 2017-01-30 15:30:04
Subject: PROESP/A. aegypti - Argentina: dispersión pasiva por transporte humano
Archive Number: 20170130-400106

Aedes AED/PT1 - ARGENTINA: DISPERSIÓN PASIVA POR TRANSPORTE HUMANO

Un comunicado de ProMED-mail
http://www.promedmail.org
ProMED-mail es un programa de la
Sociedad Internacional de Enfermedades Infecciosas
http://www.isid.org

Fecha: 20 de Enero del 2017
Fuente: Yahoo Noticias
https://es-us.news.yahoo.com/mosquito-dengue-viaja-ruta-2-16285593.html
(Editado por Jaime Torres y Jorge Gonzalez)

El movimiento de camiones, colectivos y autos por la ruta 2, la principal vía de conexión entre Buenos Aires y Mar del Plata, no sólo transporta mercaderías y turistas. De acuerdo a un grupo de científicos, los vehículos también favorecen a la dispersión a lo largo de esa arteria del mosquito *Aedes aegypti*, el vector del dengue, la fiebre chikungunya, el Zika y la fiebre amarilla urbana.

El trabajo demuestra la "necesidad urgente" de implementar controles sanitarios en aquellas rutas en donde se produce un gran desplazamiento de personas. aseguró la doctora Corina Berón, científica del CONICET en el Instituto de Investigaciones en Biodiversidad y Biotecnología (INBIOTEC), con sede en Mar del Plata y que cuenta con el apoyo de la Fundación para Investigaciones Biológicas Aplicadas (FIBA).

Entre 2009 y 2012, el grupo de Berón relevó especies de mosquitos existentes en Mar del Plata y alrededores, y no detectó la presencia del *Aedes aegypti*, a pesar de que ya era una especie abundante en las ciudades de Buenos Aires y La Plata. Sin embargo, todo indica que la especie ya en camino a la costa.

En 2002 el profesor Gustavo Rossi del Centro de Estudios Parasitológicos y de Vectores (CEPAVE), dependiente del CONICET y de la Universidad Nacional de La Plata (UNLP) – y colaboradores publicaron el registro de esta especie por primera vez en Chasicomús, a 130 km de la Capital Federal. En los meses de 2011, también se constató la presencia del vector en Lacarua, a 30 km de Chasicomús, y un año después, ya se lo encontraba en Castelli y Dolores, distante 55 km de Lacarua. "En otras palabras, se observó que con el paso del tiempo las poblaciones del mosquito colonizaban localidades cada vez más hacia el sur", indicó Berón.

La científica de Mar del Plata puntualizó que *Aedes aegypti*, tiene un rango de vuelo en su vida que varía entre 10 y 800 metros. "Que esta población de insectos haya logrado desplazarse casi 60 kilómetros en un año indica una rápida dispersión pasiva producto del transporte humano", enfatizó.

Aedes DISPERSAL BY VEHICLES

- Argentina: average vector passive dispersal of >60 km a year by automotive vehicles

[PLoS Negl Trop Dis](#). 2016 Sep; 10(9): e0004839.

PMCID: PMC5008820

Published online 2016 Sep 1. doi: [10.1371/journal.pntd.0004839](#)

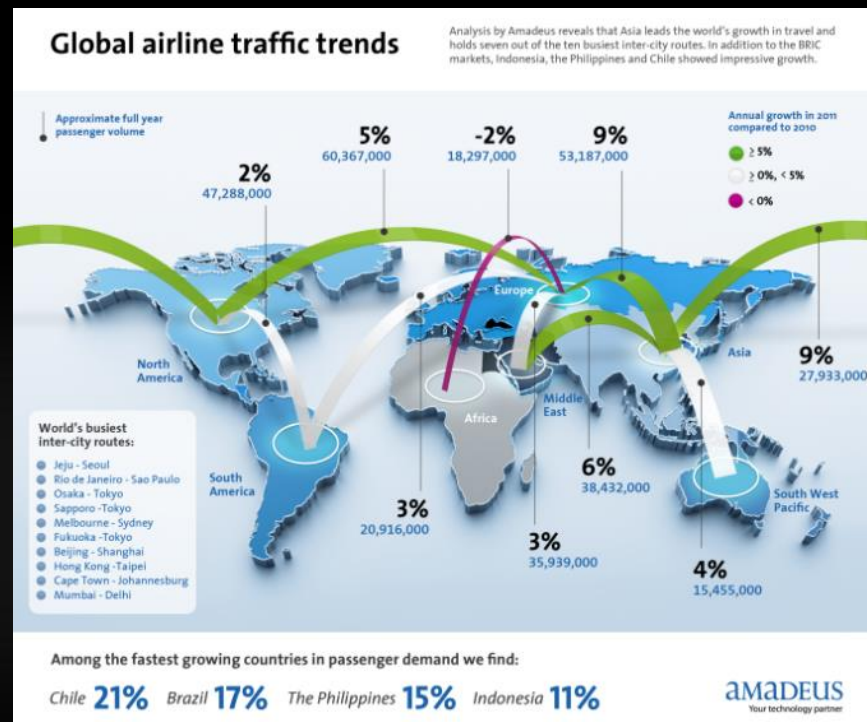
Genetic Evidence of Expansion by Passive Transport of *Aedes (Stegomyia) aegypti* in Eastern Argentina

[Leonardo M. Díaz-Nieto](#)^{1,2} [Marina B. Chiappero](#)³ [Clara Díaz de Astarloa](#)^{1,2} [Araldo Maciá](#)⁴ [Cristina N. Gardenal](#)³ and [Corina M. Berón](#)^{1,2,*}



GLOBALIZATION AND VECTOR-BORNE DISEASES

> 1.3 billion international
travelers, globally
World Bank, 2017



- Modern contributing factors to the rapid expansion of vector-borne disease include globalization of travel and trade, associated with vector accommodating trends in modern human settlement and suitable climate conditions
- The contributions of increased mobility, both of vector and human populations, may be the most important variable to explain the recent increase in dengue transmission

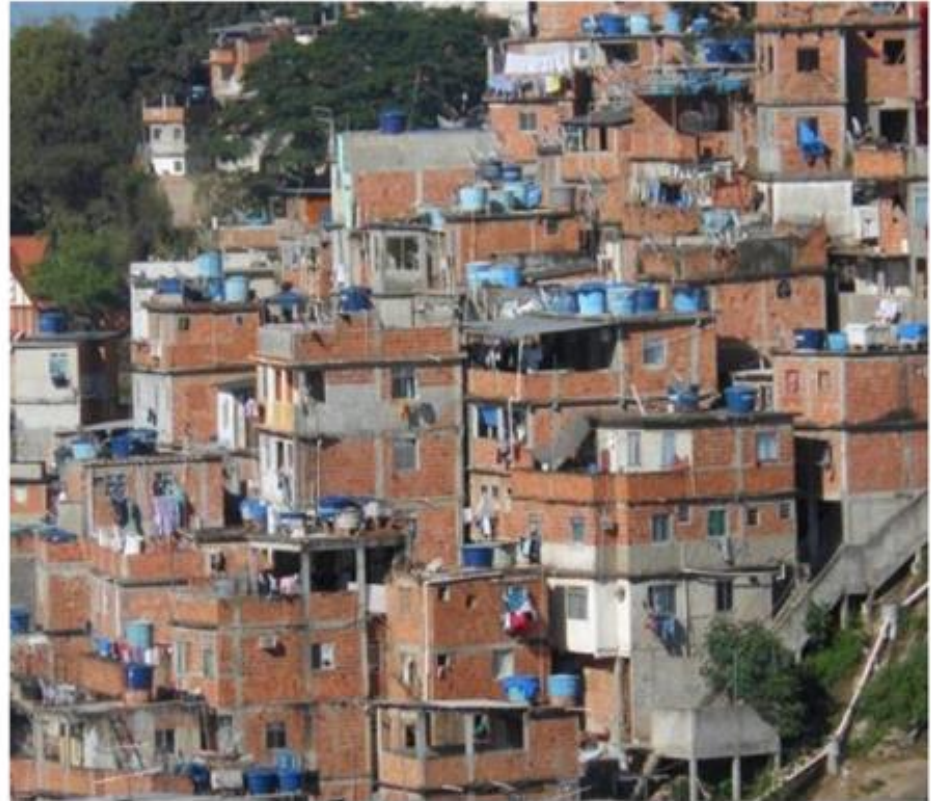
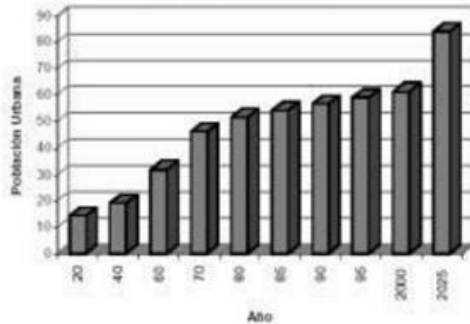
- Historically, the increase in the number of cases of DH/DF has been correlated closely with the growth of urban human population. In addition, complacency by health authorities, as well as lack of public health resources for research, surveillance, prevention and control programs
- The increased epidemic activity caused by several viral serotypes increases the rate of genetic variation of the virus, thus increasing the probability of emergence of strains of viruses or genotypes with greater potential for epidemic or virulence, an important risk factor for severe dengue



Gubler and Meltzer, *Adv Virus Res* 1990, 53, 35–70

Population growth and uncontrolled/unplanned urbanization

Percentage of urban population in Latin America



<http://www.ub.es/geocrit/sn/sn-194-101.htm> [ISSN: 1138-9788]
<http://www.ub.edu/geocrit/sn/sn-194-101.htm>

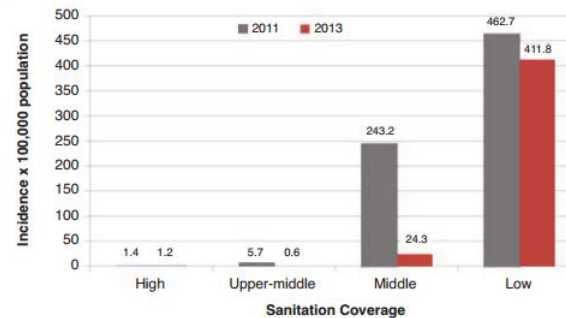
SOCIOECONOMIC DRIVERS

Social and economical drivers:

Lack of access to drinking water and drainage system

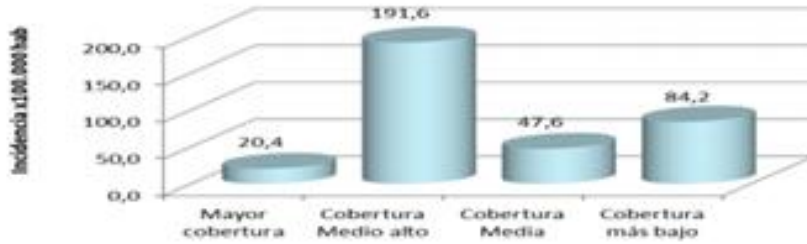


Dengue incidence in the Americas according to sanitation coverage, 2011 and 2013



DENGUE DRIVERS LATIN AMERICA

Dengue incidence in The Americas according to % of urban population with access to an improved source of drinking water



Dengue incidence in countries in the Americas region, according to per capita, INB in US\$

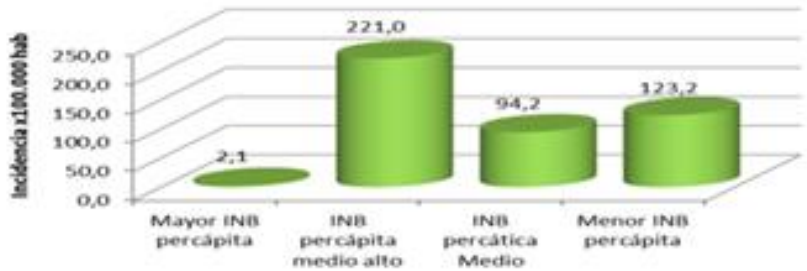
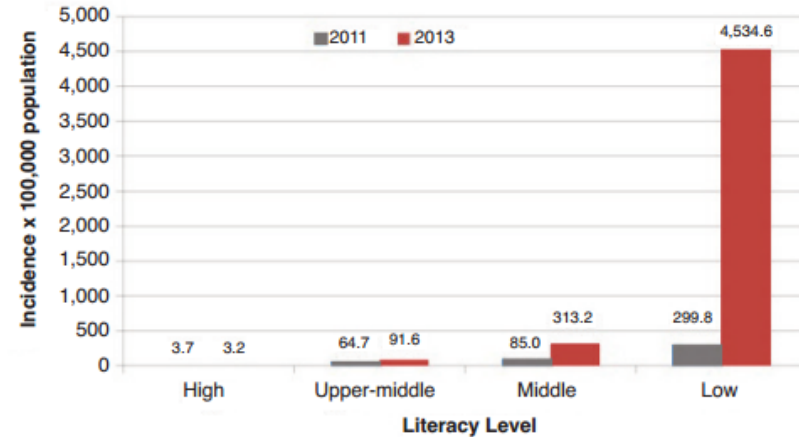


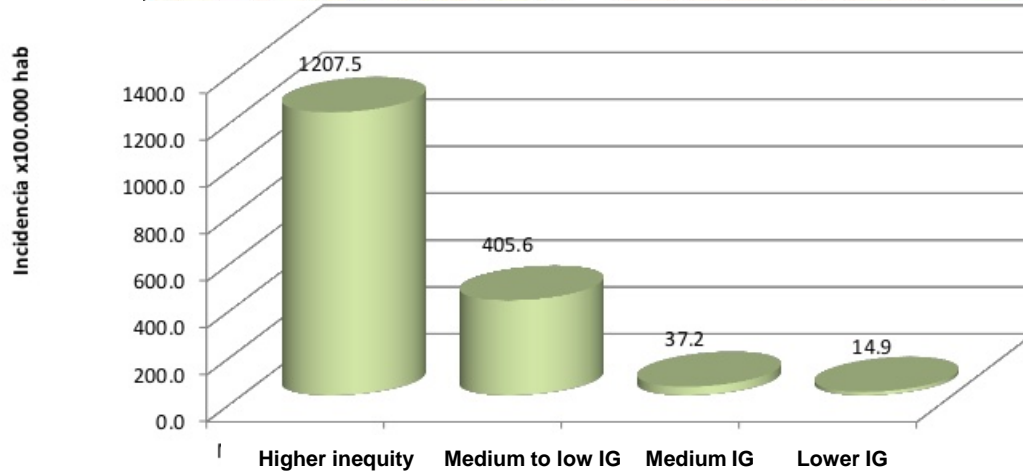
Figure 8B. Dengue incidence in the Americas according to literacy level, 2011 and 2013



Source: World Bank. Indicators. <http://datos.bancomundial.org/indicador/SH.STA.ACSN.UR>

Social drivers involved in the transmission of dengue

Level of inequity



Dengue incidence in The Americas according to GINI index, 2013

País	IG
Honduras	57,0
Colombia	55,9
Brasil	54,7
Paraguay	52,4
Chile	52,1
Panamá	51,9
Costa Rica	50,7
Ecuador	49,3
El Salvador	48,3
Perú	48,1
México	47,2
República Dominicana	47,2
Uruguay	45,3
Argentina	44,5

IG:

0 = absolute equity in income

100 = absolute inequity

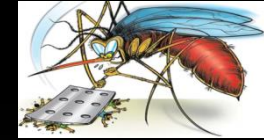
Table 5. Multivariate logistic regression model of risk factors associated with living in a hot spot household.

Final model of risk factors for dengue hot spots at household level (n = 1983)

	OR	CI ₉₅	P-value
Domestic worker/housewife			
No	1	-	-
Yes	2.86	1.45–5.64	0.002
Type of housing			
House/Apartment/ other	1	-	-
Rancho ^a	13.55	5.40–34.02	<0.001
Number of persons per household			
1–6	1	-	-
≥7	0.42	0.24–0.76	0.004
Water storage in containers			
No	1	-	-
Yes	1.95	1.09–3.52	0.024
Litter outdoors			
No	1	-	-
Yes	2.37	1.38–4.08	0.002
Use of repellent			
No	1	-	-
Yes	2.03	1.17–3.51	0.011

^aIn Venezuela, the word “rancho” is used to define a “shack”, an informal substandard type of housing typical of slum areas.

doi:10.1371/journal.pntd.0005317.t005



POVERTY AS A RISK FACTOR FOR DENGUE

Vicenti M, et al. *PLoS Negl Trop Dis* 2017, 11 (1): e0005317



Other drivers involved

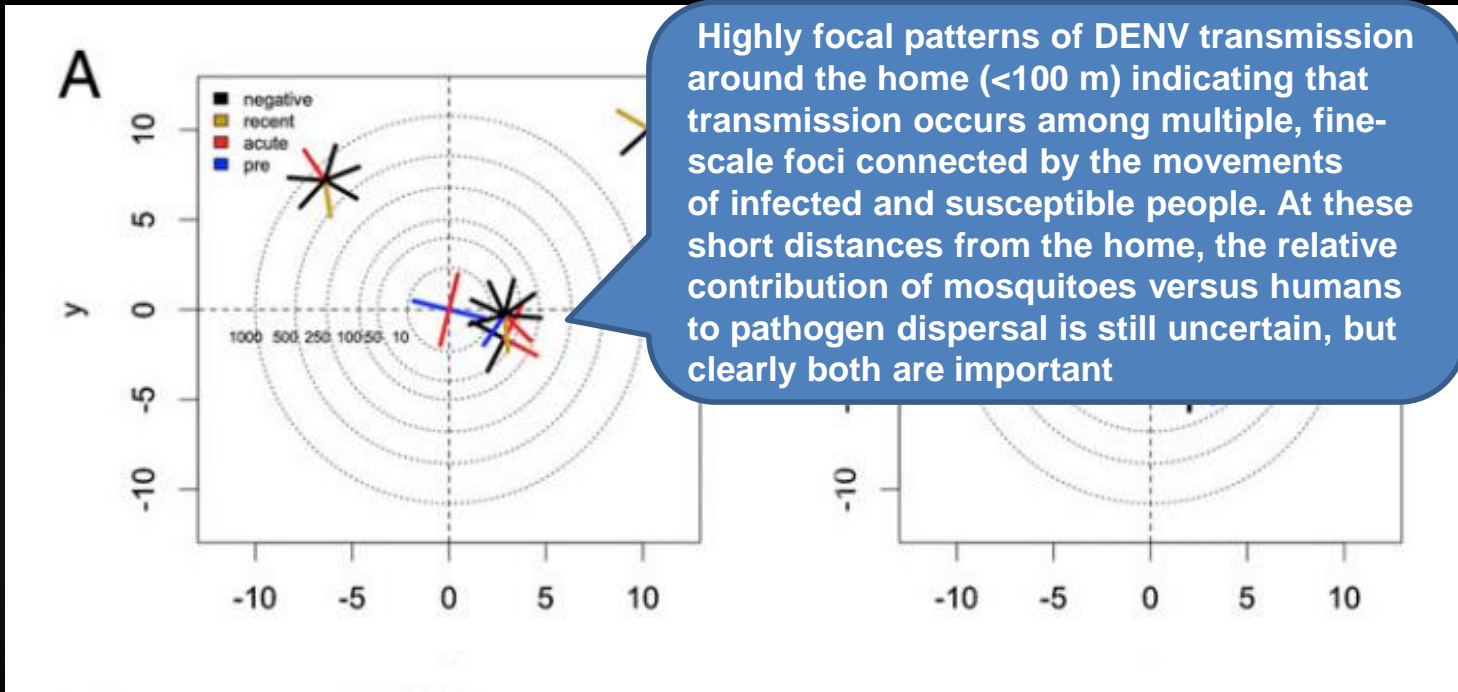
- Technical failures of the national vector control programs (i.e., lack of proper training and/or human and material resources)
- Absence of national policies (or inadequate application) in the correct use of insecticides
- Lag in availability of new molecules (insecticides) for the health sector

32% Incidence
77% seroprevalence



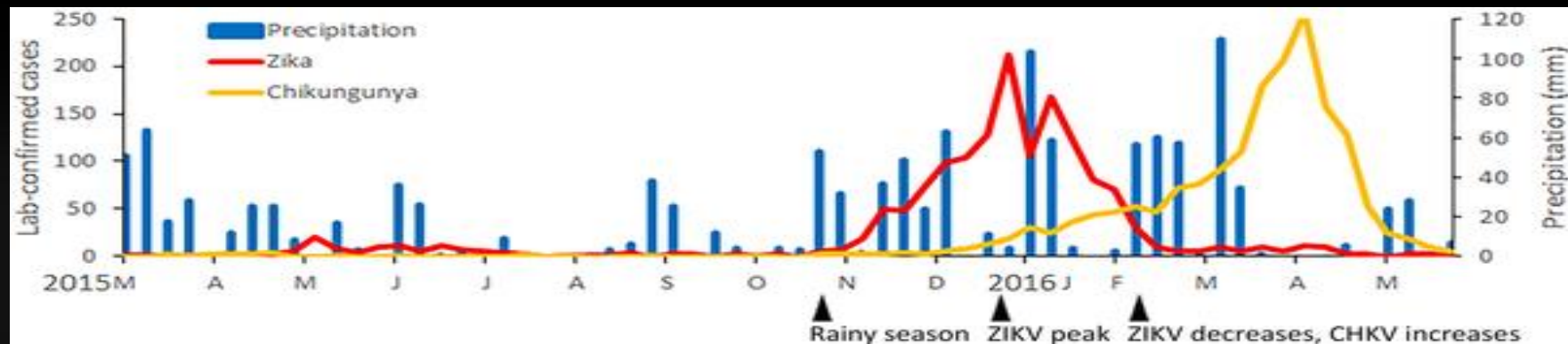
4% Incidence
39% seroprevalence

- Dengue endemicity and seroprevalence between neighboring border cities in Northern Mexico and Southern Texas, where climatic suitability is similar, in 2005, n=276 participants
- Socioeconomic and behavioral factors including income, water storage, usage of air-conditioning, waste disposal, and cross-border travel differed sustainably, as did dengue prevalence



DENV-infection risk among contacts. Diagrams A and B show two clusters plotted in relative space (index house is at the center). Each segment represents one participant, color indicates serological status.. (A) DENV+ cluster ($\sigma = 1.1$). (B) DENV- cluster ($\sigma = -0.71$). Both clusters were initiated in the same neighborhood, in the same week of the second season of transmission in Iquitos, Peru.

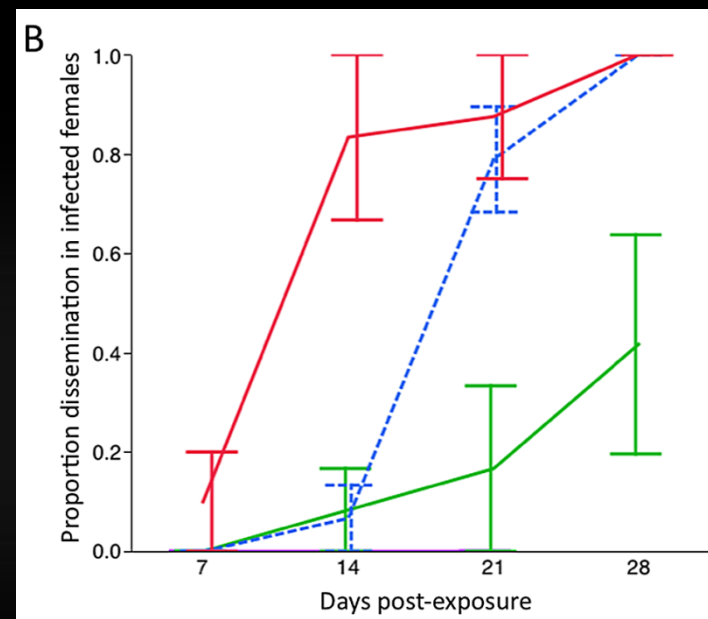
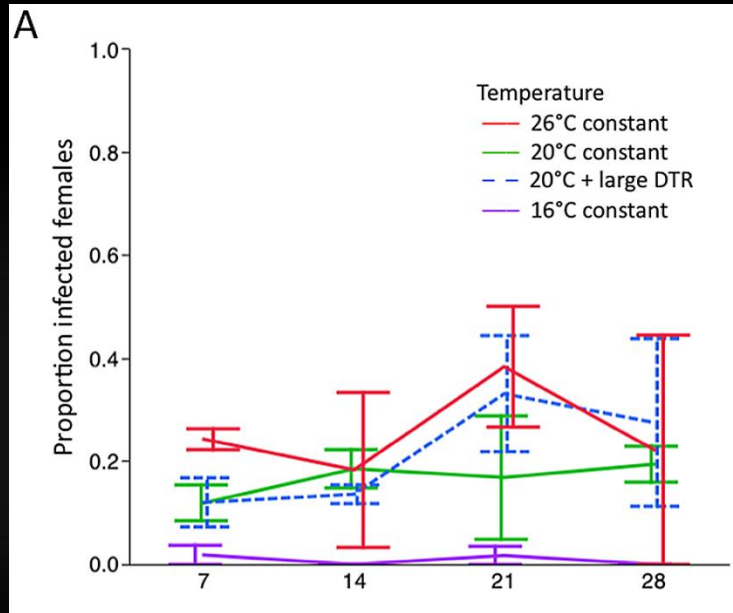
Fig 2. Confirmed cases of ZIKV and CHIKV per week in the state of Rio de Janeiro, March 2015 to May 2016 (LABFLA data set).



Rainfall appears to precede ZIKV and CHIKV epidemics suggesting that an early warning system based on weather that predicts these outbreaks 3-4 weeks in advance would provide policy-makers and clinicians a warning to prepare countermeasures, which could lead to improved prognoses for ZIKV patients

The incubation period of CHIKV in *Aedes aegypti* is 2–4 days whereas that of ZIKV is at least 10 days

Proportion of *Ae. aegypti* with a detectable infection after being held at low temperatures

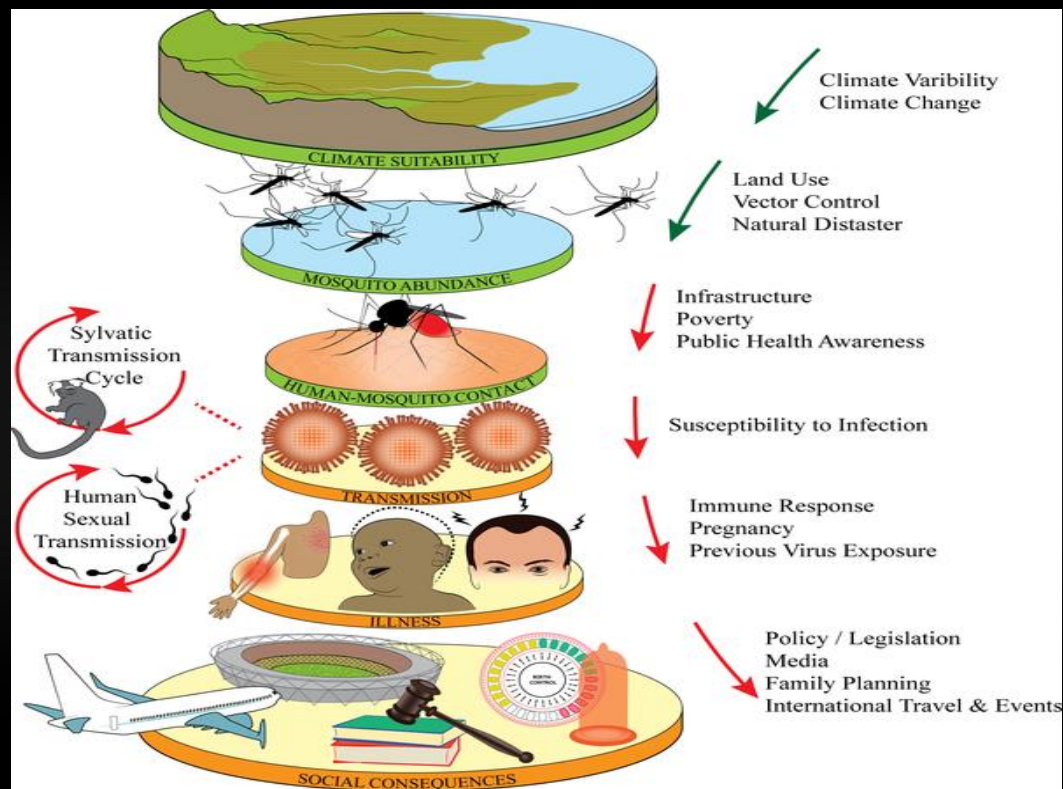


- Increased infection and transmission rates at higher temperatures, as well as altered infection rates and extrinsic incubation period (EIP) in response to fluctuating temperatures and diurnal temperature range (DTR)
- DTRs have been shown to enhance DENV infection rates and reduce EIPs at low temperatures, but decrease infection rates (and not affect DENV EIP) at higher temperatures

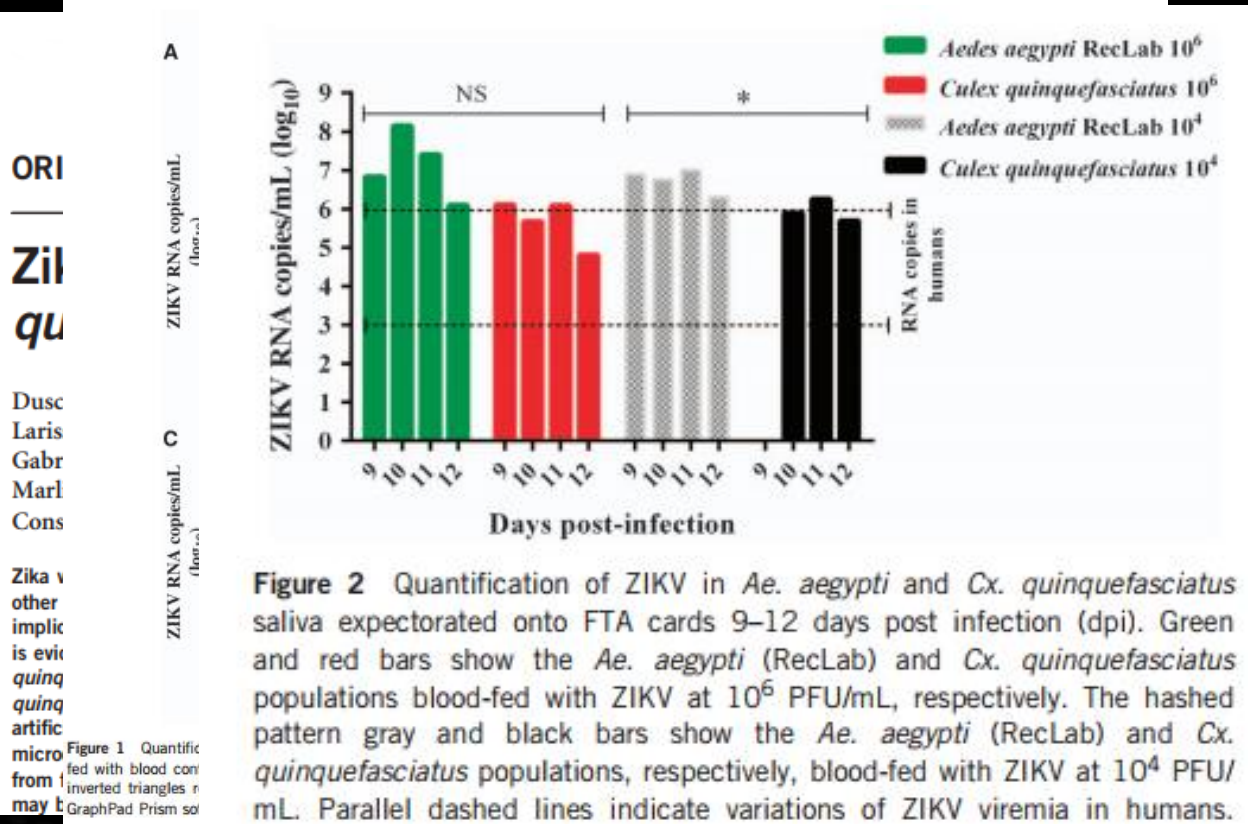
Carrington L, et al. *PLOS Neglected Tropical Diseases*, April 25, 2013

Hierarchy of factors that influence ZIKV transmission, illness, and social consequences.

Climate suitability, mosquito abundance & human–mosquito contact partly determine rates of ZIKV transmission, which causes illness in some cases. Social consequences depend on both actual and perceived risks of illness



CULEX AS NATURAL VECTOR OF ZIKA VIRUS?



GENERAL CONCLUSIONS

- The individual role played by climate change in the resurgence of *Aedes aegyti*-transmitted infections remains uncertain
- The contributions of increased mobility, both of vector and human populations due to globalization factors, such as travel and trade, associated with vector accommodating trends in modern human settlements, may be the most important variable to explain the recent increase in *Aedes*-borne diseases
- To better understand the likely impact of climate change on VBDs, it is important to view climate-driven disease systems as complex socio-ecological dynamical systems

THANKS...GRACIAS!

