

cephalosporinases, usually only AmpC (9). Nevertheless, we hypothesize that *E. cloacae* complex contains genotypes with epidemic potential associated with increasing rates of carbapenem resistance observed in the VHA.

The scope of this study did not include molecular characterization, so we could not determine emerging genotypes or detect outbreaks at individual facilities. Also, non-uniform susceptibility testing and interpretation throughout the VHA may affect reporting of CRE. Although criteria for interpretation of carbapenem susceptibility changed during the past decade, the revised breakpoints do not appear to have a major effect on resistance rates in *Klebsiella* and *Enterobacter* spp., according to other surveillance data (10). Despite these limitations, the VHA may serve as a vantage point for detecting nationwide trends in antimicrobial drug resistance. Integration of susceptibility testing with molecular characterization at the VHA may help elucidate the changing epidemiology of CRE in the United States.

This work was approved by the Institutional Review Board at the Louis Stokes Cleveland Department of Veterans Affairs Medical Center.

This work was supported in part by the National Institutes of Health through the Clinical and Translational Science Collaborative of Cleveland (UL1TR000439), National Institute for Allergy and Infectious Disease (R01AI100560, R01AI063517, R21AI114508, and R01AI072219), and VA Research and Development Office (BX001974) and by the VISN 10 Geriatrics Research, Education and Clinical Center. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health or the Department of Veterans Affairs.

Dr. Wilson is a researcher at the Louis Stokes Cleveland Department of Veterans Affairs Medical Center in Cleveland, Ohio, USA. Her main research interest is the use of healthcare databases to study infectious diseases in the elderly.

References

- Guh AY, Bulens SN, Mu Y, Jacob JT, Reno J, Scott J, et al. Epidemiology of carbapenem-resistant *Enterobacteriaceae* in 7 US communities, 2012–2013. *JAMA*. 2015;314:1479–87. <http://dx.doi.org/10.1001/jama.2015.12480>
- Kiedrowski LM, Guerrero DM, Perez F, Viau RA, Rojas LJ, Mojica MF, et al. Carbapenem-resistant *Enterobacter cloacae* isolates producing KPC-3, North Dakota, USA. *Emerg Infect Dis*. 2014;20:1583–5. <http://dx.doi.org/10.3201/eid2009.140344>
- Hargreaves ML, Shaw KM, Dobbins G, Snippes Vagnone PM, Harper JE, Boxrud D, et al. Clonal dissemination of *Enterobacter cloacae* harboring *bla*_{KPC-3} in the upper midwestern United States. *Antimicrob Agents Chemother*. 2015;59:7723–34. <http://dx.doi.org/10.1128/AAC.01291-15>
- Chavda KD, Chen L, Fouts DE, Sutton G, Brinkac L, Jenkins SG, et al. Comprehensive genome analysis of carbapenemase-producing *Enterobacter* spp.: new insights into phylogeny, population structure, and resistance mechanisms. *MBio*. 2016;7:e02093-16. <http://dx.doi.org/10.1128/mBio.02093-16>
- US Department of Veterans Affairs. Health Services Research and Development. VA Informatics and Computing Infrastructure (VINCI) [cited 2016 Sep 8]. http://www.hsrd.research.va.gov/for_researchers/vinci/
- Park SO, Liu J, Furuya EY, Larson EL. Carbapenem-resistant *Klebsiella pneumoniae* infection in three New York City hospitals trended downwards from 2006 to 2014. *Open Forum Infect Dis*. 2016;3:ofw222. <http://dx.doi.org/10.1093/ofid/ofw222>
- van Duin D, Perez F, Rudin SD, Cober E, Hanrahan J, Ziegler J, et al. Surveillance of carbapenem-resistant *Klebsiella pneumoniae*: tracking molecular epidemiology and outcomes through a regional network. *Antimicrob Agents Chemother*. 2014;58:4035–41. <http://dx.doi.org/10.1128/AAC.02636-14>
- Gomez-Simmonds A, Hu Y, Sullivan SB, Wang Z, Whittier S, Uhlemann AC. Evidence from a New York City hospital of rising incidence of genetically diverse carbapenem-resistant *Enterobacter cloacae* and dominance of ST171, 2007–14. *J Antimicrob Chemother*. 2016;71:2351–3. <http://dx.doi.org/10.1093/jac/dkw132>
- Pecora ND, Li N, Allard M, Li C, Albano E, Delaney M, et al. Genomically informed surveillance for carbapenem-resistant *Enterobacteriaceae* in a health care system. *MBio*. 2015;6:e01030-15. <http://dx.doi.org/10.1128/mBio.01030-15>
- Rennie RP, Jones RN. Effects of breakpoint changes on carbapenem susceptibility rates of *Enterobacteriaceae*: results from the SENTRY Antimicrobial Surveillance Program, United States, 2008 to 2012. *Can J Infect Dis Med Microbiol*. 2014;25:285–7. <http://dx.doi.org/10.1155/2014/265981>

Address for correspondence: Federico Perez or Robert A. Bonomo, Louis Stokes Cleveland Department of Veterans Affairs Medical Center; 10701 East Blvd, Cleveland, OH 44106, USA; email: federico.perez@va.gov or robert.bonomo@va.gov

Vertical Transmission of Zika Virus by *Aedes aegypti* and *Ae. albopictus* Mosquitoes

Alexander T. Ciota, Sean M. Bialosuknia, Dylan J. Ehrbar, Laura D. Kramer

Author affiliations: Wadsworth Center, New York State Department of Health, Slingerlands, New York, USA (A.T. Ciota, S.M. Bialosuknia, D.J. Ehrbar, L.D. Kramer); State University of New York, School of Public Health, Albany, New York, USA (A.T. Ciota, L.D. Kramer)

DOI: <http://dx.doi.org/10.3201/eid2305.162041>

To determine the potential role of vertical transmission in Zika virus expansion, we evaluated larval pools of perorally infected *Aedes aegypti* and *Ae. albopictus* adult female mosquitoes; $\approx 1/84$ larvae tested were Zika virus-positive; and rates varied among mosquito populations. Thus, vertical transmission may play a role in Zika virus spread and maintenance.

Following the 2007 outbreak in Micronesia, Zika virus (*Flaviviridae*, *Flavivirus*) has continued to expand its distribution throughout the Pacific region and, since 2014, the Americas (1,2). The virus is primarily maintained by horizontal transmission between *Aedes aegypti* mosquitoes and humans, yet other *Aedes* spp. are also competent vectors (3). The extent to which Zika virus can utilize vertical transmission between mosquitoes (i.e., transmission from an infected adult female mosquito to her progeny) has not been adequately assessed after peroral infection. Such studies are required to accurately determine the potential role of vertical transmission in Zika virus expansion and maintenance.

Although previous studies have found that other flaviviruses, including West Nile (4), dengue (5), yellow fever (6), and St. Louis encephalitis (7), can undergo vertical transmission, such transmission is generally relatively inefficient, with filial infection rate (FIR) estimates ranging from 1/36 to 1/6,400 (8). A previous study estimated rates for Zika virus vertical transmission in *Ae. aegypti* mosquitoes to be 1/290, yet a reliable estimate for transmission in *Ae. albopictus* mosquitoes was not achieved (8). In addition, these estimates were based on intrathoracic inoculation of Zika virus rather than on assessment after infectious blood meal acquisition.

We exposed laboratory colonies of *Ae. aegypti* mosquitoes (collected in Posadas, Argentina, or Poza Rica, Mexico) and *Ae. albopictus* mosquitoes (obtained from Suffolk County, New York) to Zika virus through infectious blood meals and evaluated the mosquitoes' capacity to transmit the virus to progeny. For this study, we used the Zika virus strain ZIKV HND (Honduras 2016, GenBank accession no. KX906952), passaged once on C6/36 cells, and Zika virus PR (Puerto Rico 2015, GenBank accession no. KX087101.3), passaged 4 times on Vero cells and twice on C6/36 cells. Zika virus was propagated on C6/36 cells for 4 days, and freshly harvested supernatant was mixed 1:1 with sheep blood (Colorado Serum Company, Denver, CO, USA) and 2.5% sucrose.

Infectious blood meals were offered to 4- to 7-day-old female mosquitoes, and weekly noninfectious blood meals were offered after the first oviposition. Eggs laid during the second oviposition and beyond were collected and hatched for subsequent testing. Third- to fourth-instar larvae were collected in pools of 5 and processed by homogenization and centrifugation. After RNA extraction, we used Zika virus-specific quantitative reverse transcription PCR (9) to determine adult infection (indicated by positive bodies), dissemination (indicated by positive legs), viral load, and

Table. Vertical transmission of Zika virus in *Aedes* spp. mosquitoes*

Species/ population	Zika virus strain	Cycle	Blood meal titer, log ₁₀ PFU/mL	% Infected (diss)†	Mean body titer, log ₁₀ PFU/mL	Total no. pools	No. individual mosquitoes	dpi	Zika virus positive	FIR‡ (95% CI)
<i>Ae. aegypti</i>										
Mexico	ZIKV HND	All§	8.9	90.9 (95.0)	7.6	26	130	11–18	1	7.7 (0.5–36.9)
Argentina	ZIKV HND	All§	9.3	100 (100)	6.6	28	136	11–38	2	14.9 (2.7–8.3)
Combined¶	ZIKV HND	OV2				29	141	11–22	1	7.1 (0.4–4.0)
		OV3				23	115	18–38	2	17.7 (3.2–57.2)
		OV4				2	10	38	0	<94.6 (6.6–495.8)
Combined¶	ZIKV HND	All§	9.1#	95.5 (97.5)	7.4	54	266	11–38	3	11.5 (3.0–30.8)
Argentina	ZIKV PR	OV1				24	120	36–38	2	17.0 (3.1–54.8)
		OV2				15	75	43–52	0	<13.3 (0.8–63.6)
		OV3				4	18	60–62	0	<55.8 (3.4–262.5)
		OV4				7	35	63	1	28.5 (1.7–34.8)
Combined	ZIKV PR	All§	9.1	100 (100)	7.7	50	248	36–63	3	12.3 (3.3–33)
Combined	Combined**	All§	9.1#	96.9 (98.3)	7.5	104	514	11–63	6	11.9 (4.9–4.6)
<i>Ae. albopictus</i>										
New York	ZIKV HND	All§	8.9	100 (93.3)	7.1	17	85	11–63	1	11.8 (0.7–56.2)

*Diss, disseminated; dpi, days post infection; FIR, filial infection rate; ZIKV HND, Zika virus Honduras 2016; OV, oviposition; ZIKV PR, Zika virus Puerto Rico.

†Percentage of infected with Zika virus-positive legs.

‡No. Zika virus positive/1,000 larvae.

§Combines data from all hatched eggs.

¶Data for both mosquito populations are combined.

FIR, which was calculated by using a maximum-likelihood estimate (PoolInfRate 4.0; Centers for Disease Control and Prevention, Atlanta, GA, USA).

We tested 104 *Ae. aegypti* pools; 6 were Zika virus–positive, indicating a FIR of 11.9 (range 4.9–24.6; Table). This value equates to a ratio of $\approx 1:84$, which is substantially higher than that found by Thangamani et al., as well as ratios historically measured for flaviviruses (4–8). Although just 17 pools of *Ae. albopictus* were tested, 1 pool was positive, which equates to a similar FIR (11.8 [range 1.7–134.8]; Table) and establishes that *Ae. albopictus* mosquitoes are capable of vertical transmission of Zika virus in the laboratory.

Although the bypassing of the midgut during inoculation generally results in higher levels of vertical transmission, we fed mosquitoes high virus doses (8.9–9.3 log₁₀ PFU/mL), resulting in >93% of disseminated infections and development of high viral titers in individual mosquitoes, averaging 7.1 (*Ae. albopictus*) to 7.5 (*Ae. aegypti*) log₁₀ PFU/mosquito (Table). Although the likelihood that eggs were derived from mosquitoes with disseminated infections is high, the rate of vertical transmission (proportion of infected mosquitoes transmitting to progeny) could not be determined. Future studies assessing infection status and FIR of individual mosquitoes will help clarify the extent of individual variability in vertical transmission efficiency. In addition, we tested larvae rather than adults, and it is likely that transtadial transmission is not completely efficient, so further studies are required to fully evaluate transmission potential of adults infected via vertical transmission. We observed a trend of increasing vertical transmission with time and additional egg laying, similar to what has been reported for West Nile virus (10). This finding suggests that survival and gonotrophic cycles could be key determinants of success of vertical transmission in nature. Finally, our results demonstrate population-specific differences, with the FIR of the population from Argentina more than twice that of the population from Mexico (Table), suggesting that particular populations may have increased capacity for maintenance through vertical transmission. Although we did not measure differences between ZIKV HND and ZIKV PR, evaluating additional strains could help clarify the influence of viral genotype on vertical transmission efficiency.

Together, these results indicate that Zika virus has a relatively high capacity for being transmitted vertically by both *Ae. aegypti* and *Ae. albopictus* mosquitoes. Although the mechanism of vertical transmission with flaviviruses is generally thought to be infection of eggs during oviposition, rather than transovarial transmission (5), these rates suggest that further investigation into Zika virus tropism in mosquitoes is warranted.

Acknowledgments

We thank the members of the Wadsworth Center Arbovirus Laboratory insectary staff for assistance with this project and the

Wadsworth Center tissue and media facility for supplying cells and media for these studies. We are also grateful to V. Micieli, Centro de Estudios de Parasitología y Vectores, for supplying *Ae. aegypti* mosquitoes collected in Posadas, Argentina; to G. Ebel, Colorado State University, for *Ae. aegypti* mosquitoes collected in Poza Rica, Mexico; and to I. Rochlin, Suffolk County Health Department, for *Ae. albopictus* mosquitoes obtained from Suffolk County, New York.

The construction of the Wadsworth Center Arbovirus Laboratory insectary facilities was partially funded by the National Institutes of Health (NIH) grant C06-RR-17715.

Dr. Ciota is deputy director of the Arbovirus Laboratory, Wadsworth Center, New York State Department of Health. His primary research interests are arbovirus evolution and vector–virus interactions.

References

- Duffy MR, Chen TH, Hancock WT, Powers AM, Kool JL, Lanciotti RS, et al. Zika virus outbreak on Yap Island, Federated States of Micronesia. *N Engl J Med*. 2009;360:2536–43. <http://dx.doi.org/10.1056/NEJMoa0805715>
- Rabaan AA, Bazzi AM, Al-Ahmed SH, Al-Ghath MH, Al-Tawfiq JA. Overview of Zika infection, epidemiology, transmission and control measures. *J Infect Public Health*. 2016;S1876–0341(16)30063–6.
- Weger-Lucarelli J, Rückert C, Chotiwan N, Nguyen C, Garcia Luna SM, Fauver JR, et al. Vector competence of American mosquitoes for three strains of Zika virus. *PLoS Negl Trop Dis*. 2016;10:e0005101. <http://dx.doi.org/10.1371/journal.pntd.0005101>
- Nelms BM, Fechter-Leggett E, Carroll BD, Macedo P, Klueh S, Reisen WK. Experimental and natural vertical transmission of West Nile virus by California *Culex* (Diptera: Culicidae) mosquitoes. *J Med Entomol*. 2013;50:371–8. <http://dx.doi.org/10.1603/ME12264>
- Rosen L, Shroyer DA, Tesh RB, Freier JE, Lien JC. Transovarial transmission of dengue viruses by mosquitoes: *Aedes albopictus* and *Aedes aegypti*. *Am J Trop Med Hyg*. 1983;32:1108–19.
- Monath TP. Yellow fever: an update. *Lancet Infect Dis*. 2001;1:11–20. [http://dx.doi.org/10.1016/S1473-3099\(01\)00016-0](http://dx.doi.org/10.1016/S1473-3099(01)00016-0)
- Nayar JK, Rosen L, Knight JW. Experimental vertical transmission of Saint Louis encephalitis virus by Florida mosquitoes. *Am J Trop Med Hyg*. 1986;35:1296–301.
- Thangamani S, Huang J, Hart CE, Guzman H, Tesh RB. Vertical transmission of Zika virus in *Aedes aegypti* mosquitoes. *Am J Trop Med Hyg*. 2016;95:1169–73. <http://dx.doi.org/10.4269/ajtmh.16-0448>
- Lanciotti RS, Kosoy OL, Laven JJ, Velez JO, Lambert AJ, Johnson AJ, et al. Genetic and serologic properties of Zika virus associated with an epidemic, Yap State, Micronesia, 2007. *Emerg Infect Dis*. 2008;14:1232–9. <http://dx.doi.org/10.3201/eid1408.080287>
- Ciota AT, Ehrbar DJ, Maccachiero AC, Van Slyke GA, Kramer LD. The evolution of virulence of West Nile virus in a mosquito vector: implications for arbovirus adaptation and evolution. *BMC Evol Biol*. 2013;13:71. <http://dx.doi.org/10.1186/1471-2148-13-71>

Address for correspondence: Alexander T. Ciota, Arbovirus Laboratory, Wadsworth Center, New York State Department of Health, 5668 State Farm Rd, Slingerlands, NY 12159, USA; email: alexander.ciota@health.ny.gov