

database used would require optimization with addition of reference spectra for the organism and its close relatives (e.g., *B. thailandensis*). *B. pseudomallei*, although different from other *Burkholderia* spp. in its pathogenicity and epidemiology, is not easily discriminated from *B. thailandensis* or *B. cepacia* complex by using phenotypic tests (10).

In summary, infection with *B. pseudomallei* should be considered in patients with pneumonia after travel to the Baja Peninsula in Mexico, and especially after an extreme weather event. Because of risk for transmission to laboratory workers and the potential for *B. pseudomallei* to be used for bioterrorism, clinical laboratories should perform only limited work up of suspected isolates before referring them to a public health laboratory for definitive identification.

Acknowledgment

We used the Multi-Locus Sequence Typing website (<http://www.mlst.net>) at Imperial College London, developed by David Aanensen and supported by the Wellcome Trust.

References

1. Currie BJ, Dance DA, Cheng AC. The global distribution of *Burkholderia pseudomallei* and melioidosis: an update. *Trans R Soc Trop Med Hyg.* 2008;102(Suppl 1):S1–4. [http://dx.doi.org/10.1016/S0035-9203\(08\)70002-6](http://dx.doi.org/10.1016/S0035-9203(08)70002-6)
2. Inglis TJ, Rolim DB, Sousa AQ. Melioidosis in the Americas. *Am J Trop Med Hyg.* 2006;75:947–54.
3. Centers for Disease Control and Prevention. Melioidosis: risk of exposure, January 26, 2012 [cited 2014 Dec 19]. <http://www.cdc.gov/melioidosis/exposure/index.html>
4. Currie BJ. Melioidosis: evolving concepts in epidemiology, pathogenesis, and treatment. *Semin Respir Crit Care Med.* 2015;36:111–25. <http://dx.doi.org/10.1055/s-0034-1398389>
5. Schweizer HP, Limmathurtsakul D, Peacock SJ. New insights from the 7th World Melioidosis Congress 2013. *Emerg Infect Dis.* 2014;20:e131737.
6. Wiersinga WJ, Currie BJ, Peacock SJ. Melioidosis. *N Engl J Med.* 2012;367:1035–44. <http://dx.doi.org/10.1056/NEJMra1204699>
7. Gee JE, Allender CJ, Tuanvok A, Elrod MG, Hoffmaster AR. *Burkholderia pseudomallei* type G in Western Hemisphere. *Emerg Infect Dis.* 2014;20:682–4. <http://dx.doi.org/10.3201/eid2004.130960>
8. Pitman MC, Luck T, Marshall CS, Anstey NM, Ward L, Currie BJ. Intravenous therapy duration and outcomes in melioidosis: a new treatment paradigm. *PLoS Negl Trop Dis.* 2015;9:e0003586. <http://dx.doi.org/10.1371/journal.pntd.0003586>
9. Lipsitz R, Garges S, Aurigemma R, Baccam P, Blaney DD, Cheng AC, et al. Workshop on treatment of and postexposure prophylaxis for *Burkholderia pseudomallei* and *B. mallei* infection, 2010. *Emerg Infect Dis.* 2012;18:e2. <http://dx.doi.org/10.3201/eid1812.120638>
10. Zong Z, Wang X, Deng Y, Zhou T. Misidentification of *Burkholderia pseudomallei* as *Burkholderia cepacia* by the Vitek 2 system. *J Med Microbiol.* 2012;61:1483–4. <http://dx.doi.org/10.1099/jmm.0.041525-0>

Address for correspondence: Jennifer W. Cheng, Department of Infectious Disease, Rush University Medical Center, 600 S Paulina St, Ste 143, Chicago, IL 60612, USA; email: jennifer.w.cheng@gmail.com

Zika Virus Outbreak, Bahia, Brazil

Gubio S. Campos, Antonio C. Bandeira, Silvia I. Sardi

Authors affiliations: Federal University of Bahia, Salvador, Bahia, Brazil (G.S. Campos, S.I. Sardi); Hospital Aliança, Salvador (A.C. Bandeira)

DOI: <http://dx.doi.org/10.32301/eid2110.150847>

To the Editor: Zika virus (ZIKV) is a mosquito-borne flavivirus related to yellow fever virus, dengue virus (DENV), and West Nile virus (WNV). It is a single-stranded positive RNA virus (10,794-nt genome) that is closely related to the Spondweni virus and is transmitted by many *Aedes* spp. mosquitoes, including *Ae. africanus*, *Ae. luteocephalus*, *Ae. hensilli*, and *Ae. aegypti*. The virus was identified in rhesus monkeys during sylvatic yellow fever surveillance in the Zika Forest in Uganda in 1947 and was reported in humans in 1952 (1).

In 2007, an outbreak of ZIKV was reported in Yap Island, Federated States of Micronesia (2). ZIKV also caused a major epidemic in the French Polynesia in 2013–2014 (3), and New Caledonia reported imported cases from French Polynesia in 2013 and reported an outbreak in 2014 (4).

A new challenge has arisen in Brazil with the emergence of ZIKV and co-circulation with others arboviruses (i.e., DENV and chikungunya virus [CHIKV]). We report ZIKV infection in Brazil associated with a recent ongoing outbreak in Camaçari, Bahia, Brazil, of an illness characterized by maculopapular rash, fever, myalgias/arthritis, and conjunctivitis.

On March 26, 2015, serum samples were obtained from 24 patients (Table) at Santa Helena Hospital in Camaçari who were given a presumptive diagnosis of an acute viral illness by emergency department physicians. These patients were given treatment for a dengue-like illness, and blood samples were obtained for complete blood counts and serologic testing by using an ELISA specific for IgG and IgM against DENV.

Serum samples were analyzed at the Federal University of Bahia by reverse transcription PCR (RT-PCR) to detect DENV, CHIKV, WNV, Mayaro virus, and ZIKV. In brief, serum samples were subjected to RNA extraction by using the QIAamp Viral RNA Mini Kit (QIAGEN, Hilden, Germany). RNA was reverse transcribed by using the SuperScript II Reverse Transcription Kit (Invitrogen, Carlsbad, CA, USA) and subjected to PCRs specific for DENV (5) CHIKV (6), WNV (7) and Mayaro virus (8). A positive RT-PCR for a partial region of the envelope gene with primers ZIKVENF and ZIKVENVR (positions

Table. Characteristics of 24 patients with positive and negative results for infection with Zika virus, Brazil, 2015

Reverse transcription PCR result for Zika virus (no.)	Mean (SD) patient age, y	Patient sex, F/M	No. (%)			
			Rash	Fever	Myalgia	Headache
Positive (7)	33 (15)	6/1	6 (85.7)	3 (43)	4 (57.1)	3 (43)
Negative (17)	31 (8.5)	12/5	12 (70.6)	6 (35.3)	9 (53)	11 (64.7)

1538–1558 and 1902–1883, respectively) (9) was considered indicative of ZIKV infection. PCR products (362 bp) were sequenced at the ACTGene Analises Moleculares, Alvorada, Rio Grande do Sul (Porto Alegre, Brazil), and sequences were deposited in GenBank under accession nos. KR816333–KR816336.

All patients were negative by RT-PCR for DENV, Mayaro virus, and WNV. Samples from 7 (29.2%) patients were positive by RT-PCR for ZIKV (369-bp fragment) and from 3 (12.5%) patients for CHIKV (305-bp fragment). There was no simultaneous detection of ZIKV and CHIKV. Most (85.7%) patients positive for ZIKV were women; they had a median age of 28 years and no history of international travel. Patients positive for ZIKV sought medical care after a 4-day (range 1–5 days) history of rash, myalgias, arthralgias, or fever. Three patients had IgG against DENV, which is consistent with a previous DENV infection, and none of the 7 ZIKV-positive patients had a positive response for DENV.

Mean laboratory findings for patients with acute ZIKV infection were a leukocyte count of 3,750 cells/mm³ (range 2,790 cells/mm³–6,150 cells/mm³) and a platelet count of 180,000 platelets/mm³ (range 151,000 platelets/mm³–274,000 platelets/mm³). The mean C-reactive protein level was 16.3 mg/L (range 0.9 mg/L–19.7 mg/L). Sign and symptom duration was 1–5 days, and most patients had a maculopapular rash, myalgias, fever, and headache. Arthralgia was seen less frequently.

ZIKV infections were assessed by sequencing partial ZIKV envelope gene regions of isolates. Phylogenetic analysis rooted with Spondweï virus showed that ZIKV sequences obtained belonged to the Asian lineage and showed 99% identity with a sequence from a ZIKV isolate from French Polynesia (KJ776791) (10).

We report ZIKV infection in Brazil in association with an ongoing outbreak of an acute maculoexantematic illness. Although the patient population samples were not randomly selected, 42% (10/24) of the patients were positive for ZIKV (n = 7) or CHIKV (n = 3) and had maculopapular rash, fever, myalgias and headache. After detection of ZIKV in Bahia, many cases have been identified in other states (<http://www.promedmail.org>, archive no. 20152015602.343.1158).

Cases of infection with DENV, CHIKV, and ZIKV in Brazil and elsewhere will make diagnosis based on clinical

and epidemiologic grounds unreliable. These issues show the need for laboratory confirmation of these arboviral infections. More studies are needed to address the effects of these concurrent arboviruses infections in Brazil.

This study was supported by Fundação de Amparo a Pesquisa do Estado da Bahia.

References

- Dick GW, Kitchen SF, Haddock AJ. Zika virus. I. Isolations and serological specificity. *Trans R Soc Trop Med Hyg.* 1952;46:509–20. [http://dx.doi.org/10.1016/0035-9203\(52\)90042-4](http://dx.doi.org/10.1016/0035-9203(52)90042-4)
- Duffy MR, Chen T-H, Hancock WT, Powers AM. 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>
- Cao-Lormeau VM, Roche C, Teissier A, Robin E, Berry AL, Mallet HP, et al. Zika virus, French Polynesia, South Pacific, 2013. *Emerg Infect Dis.* 2014;20:1085–6. <http://dx.doi.org/10.3201/eid2011.141380>
- Dupont-Rouzeyrol M, O'Connor O, Calvez E, Daures M, John M, Grangeon JP, et al. Co-infection with zika and dengue viruses in 2 patients, New Caledonia, 2014. *Emerg Infect Dis.* 2015;21:381–2.
- Lancioti RS, Calisher CH, Gubler DJ, Chang G, Vorndam AV. Rapid detection and typing of dengue viruses from clinical samples by using reverse transcriptase polymerase chain reaction. *J Clin Microbiol.* 1992;30:545–51.
- Edwards CJ, Welch SR, Chamberlain J, Hewson R, Tolley H, Cane PA, et al. Molecular diagnosis and analysis of chikungunya virus. *J Clin Virol.* 2007;39:271–5. <http://dx.doi.org/10.1016/j.jcv.2007.05.008>
- Chowdhury P, Kham SA, Dutta P, Topno R, Mahanta J. Characterization of West Nile virus (WNV) isolates from Assam, India: insights into the circulating WNV in northeastern India. *Comp Immunol Microbiol Infect Dis.* 2014;37:39–46. <http://dx.doi.org/10.1016/j.cimid.2013.10.006>
- Mourão MP, Souza Bastos M, Figueredo RP, Gimaque JB, Galusso Edos S, Kramer VM, et al. Mayaro fever in the city of Manaus, Brazil, 2007–2008. *Vector Borne Zoonotic Dis.* 2012;12:42–5.
- Faye O, Faye O, Dupressoir A, Weidmann M, Ndiaye M, Sall AA. One-step RT-PCR for detection of Zika virus. *J Clin Virol.* 2008;43:96–101. <http://dx.doi.org/10.1016/j.jcv.2008.05.005>
- Baronti C, Piorowski G, Charrel RN, Boubis L, Leparç-Goffart I, de Lamballierie X. Complete sequence of Zika virus from a French Polynesia outbreak in 2013. *Genome Announc.* 2014;2:e00500–14. <http://dx.doi.org/10.1128/genomeA.00500-14>

Address for correspondence: Silvia I. Sardi, Laboratório de Virologia, Instituto de Ciências da Saúde, Universidade Federal da Bahia, Av. Reitor Miguel Calmon, s/n 40110-100-Vale do Canela, Salvador, Bahia, Brazil; email: sissardi@yahoo.com.br