

Fundação Oswaldo Cruz (Fiocruz) Oswaldo Cruz Foundation

The use of non-invasive clinical specimens as a tool for epidemiological surveillance of Zika virus

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Ministério da Saúde

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NATIONAL REFERENCE	STATE
ANTHRAX	RJ
CHAGAS DISEASE	RJ,MG,PE
BACTERIAL DIARRHOEAL DISEASES	RJ
SCHISTOSOMIASIS	RJ,MG
FILARIASIS	RJ,PE
INFLUENZA	RJ
VIRAL HEPATITIS	RJ,BA
HIDATIDOSIS	RJ
LEISHMANIASIS	RJ,MG,PE,B A
LEPTOSPIROSIS	RJ
SYSTEMIC MYCOSIS	RJ
PLAGUE	PE
POLIOMYELITIS	RJ
RICKETTSIOSIS	RJ
TUBERCULOSIS	RJ
RUBELLA/MEASLES	RJ
AIDS	RJ
LEPROSY	RJ
SARS	RJ
24 D'	

24 Diseases

50 Reference Laboratories

7 Outpatient clinics



Algorithm for testing of microcephaly suspected samples



Source: Ministry of Health, Brazil



Flavivirus Laboratory

Regional Reference Center for Dengue, Zika, Yellow Fever and Chikungunya diagnosis

Ana Maria Bispo de Filippis, PhD - Lab Head Rita Maria R. Nogueira, PhD - Research Scientist Patrícia C Sequeira, PhD - Research Scientist Marcos C Mendonça, PhD - Research Scientist Maria Angélica Mares-Guia, PhD - Research Scientist Eliane M de Araújo, *MSc - Research Associate* Simone A Sampaio, MSc - Research Associate Leda M Santos, BsC - Research Associate Jose Carlos Silva, BsC - Research Associate Carolina Santos, BsC - Research Associate Everton Rodrigues, BsC - Research Associate Marcele Santos, BsC - Research Associate Sheila Cheles, BsC - Biosafety officer

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Visiting Scholars:

Raquel Medialdea-Carrera – PhD student/ University of Liverpool Ravi Mehta – MD/ University of Liverpool

Scientific advisor: David Brown





Flavivirus Laboratory international colaborations:



Zika virus in Brazil

Whole viral genome sequencing





The green outer circle corresponds to the complete Brazilian Zika virus genome isolated from the amniotic fluid of patient 1. 10 793 bases were sequenced. The red circle corresponds to the Senegal (KF383118.1) strain of Zika virus and the blue circle corresponds to the Uganda strain (NC_012532.1). The percentage deviation in GC content between the Brazilian Zika virus and the reference Zika virus is represented along the Zika virus genome by the varying heights of the black bars. The innermost (black) circle corresponds to the reference genome (French Polynesia, KJ76791.1). Genome shared identity between each strain and the reference genome are shown as percentages. BLAST=basic local alignment search tool.



Figure 4: Maximum likelihood phylogeny of Brazilian Zika virus, other Flaviviridae genomes, and an alphavirus genome

Brazilian Zika virus (in red) was isolated from the amniotic fluid of patient 1, whose fetus was diagnosed with microcephaly. Approximate likelihood-ratio test and Bayesian inference support values are shown at nodes. Chikungunya is an alphavirus; all other viruses are from the Flaviviridae family. DENV=dengue virus. JEV=Japanese encephalitis virus. YFV=yellow fever virus. ZIKV=Zika virus.



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Samples from suspected ZIKV cases, 2015-2016











ZIKV Detection in Alternative Samples

Specimen	Days after the first symptoms	Result RT-qPCR
Urine	0-18 days	Positive
Saliva	4 - 9 days	Positive
Amniotic fluid	20 weeks	Positive
Breast milk	3- 20 days	Positive
Semen	4 - 16 days	Positive
Vaginal secretion	3- 23 days	Positive
Cerebrospinal fluid (CSF)	4-9 days	Positive

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Molecular diagnosis

Genetic and Serologic Properties of Zika Virus Associated with an Epidemic, Yap State, Micronesia, 2007

Robert S. Lanciotti," Olga L. Kosoy," Janeen J. Laven," Jason O. Velez," Amy J. Lambert," Alison J. Johnson," Stephanie M. Stanfield," and Mark R. Duffy"

Primer	Genome position †	Sequence (5' 3')	Sensitivity, no. copies	Specificity
ZIKV 1086	1086-1102	CCGCTGCCCAACACAAG		
ZIKV 1162c	1162-1139	CCACTAACGTTCTTTTGCAGACAT	25	ZIKV
ZIKV 1107-FAM	1107-1137	AGCCTACCTTGACAAGCAGTCAGACACTCAA		

Gold standard for molecular diagnosis of ZIKV

	No of positive samples (real-time RT- PCR)	Average day post infection	Ct value range (real-time RT- PCR)
Serum	16	3 rd	26 - 37
Saliva	13	5 th	28 - 38
Urine	16	8 th	28 - 38
TOTAL	45		



Percentage of ZIKV RNA detection in serum, urine and saliva







Correlation between the type of clinical specimens and ZIKV detection







Correlation between days after initial onset of symptoms and ZIKV RNA detection in serum







Correlation between days after initial onset of symptoms and ZIKV RNA detection in urine







The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Persistence of Zika Virus in Body Fluids — Preliminary Report

Gabriela Paz-Bailey, M.D., Ph.D., Eli S. Rosenberg, Ph.D., Kate Doyle, M.P.H., Jorge Munoz-Jordan, Ph.D., Gilberto A. Santiago, Ph.D., Liore Klein, M.S.P.H., Janice Perez-Padilla, M.P.H., Freddy A. Medina, Ph.D., Stephen H. Waterman, M.D., M.P.H., Carlos Garcia Gubern, M.D., Luisa I. Alvarado, M.D., and Tyler M. Sharp, Ph.D.

Clinical specimen	Range of days of ZIKV RNA detection
Serum	14-54
Urine	8-39
Semen	34-81

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Final considerations:

- Urine and saliva are useful non-invasive clinical specimens for ZIKV RNA detection;
- Prolonged ZIKV RNA detection in urine and saliva samples are important features for diagnosis and prevention of ZIKV;
- ZIKV RNA detection rates range from 30 to 37% in serum, urine and saliva samples;
- ZIKV RNA has been detected in serum, urine, saliva, semen, breast milk, amniotic fluid, vaginal secretion and CSF;
- The use of non-invasive clinical specimens collection for ZIKV diagnosis means an extra tool for epidemiological surveillance.
- Whole genome sequencing of viral RNA from different clinical specimen of one single patient will shed light into viral compartmentalization.



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Thank you

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