



80 ANOS
DE CONTRIBUIÇÃO À CIÊNCIA E À SAÚDE

OFICINA CONJUNTA UNASUR / CPLP DE ATUALIZAÇÃO CIENTÍFICA E TECNOLÓGICA
SOBRE FEBRE AMARELA E OUTRAS ARBOVIROSES EMERGENTES E REEMERGENTES
Outubro de 2017 - Rio de Janeiro

SOROPREVALÊNCIA DAS ARBOVIROSES NO BRASIL



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SECRETARIA DE
VIGILÂNCIA EM SAÚDE

MINISTÉRIO
DA SAÚDE



International Catalogue of Arboviruses, Including Certain Other Viruses of Vertebrates (Karabatsos, 1985)

n= 537/118 doença humana/ + 20 epidemia

1954 – 2016

- **18.000 isolamentos**
- **210 tipos de vírus**
- **165 isolados pela primeira vez no Brasil**
- **Pelo menos 110 novos para a ciência**
- **36 associados com doença em humanos**
- **Apenas 1 isolamento**

ESTUDOS ECO-EPIDEMIOLÓGICOS NA AMAZÔNIA BRASILEIRA



Belem-Brasilia



Santarem- Cuiaba



Carajás



Serra do Navio



Itaituba-Jacareacanga



Porto Trombetas



Transamazonia -1972

VIAGEM DE CAMPO

Captura de insetos hematófagos – solo



VIAGEM DE CAMPO

Captura de insetos hematófagos – Copa



VIAGEM DE CAMPO

Captura de insetos hematófagos – Armadilha CDC



VIAGEM DE CAMPO

Captura de aves silvestres – rede de neblina



VIAGEM DE CAMPO

Captura de animais silvestres – armadilhas



VIAGEM DE CAMPO

Humanos



Coleta de material na floresta de Uriboca (1954) para exame de febre amarela



Coleta de material na floresta de Uriboca (1954)
exame de febre amarela



LABORATÓRIO DE CAMPO



VIAGEM DE CAMPO

As dificuldades do trabalho de campo



Um dos aviões biplanos e monomotores, de asas de lona, do Correio Aéreo Nacional, para o piloto e um só passageiro, que quinzenalmente levava de Belém a Abaetetuba um a um dos membros da equipe que atuava com Evandro



Chegada de pesquisadores ao interior em canoas:
adversidades superadas para o avanço da ciência

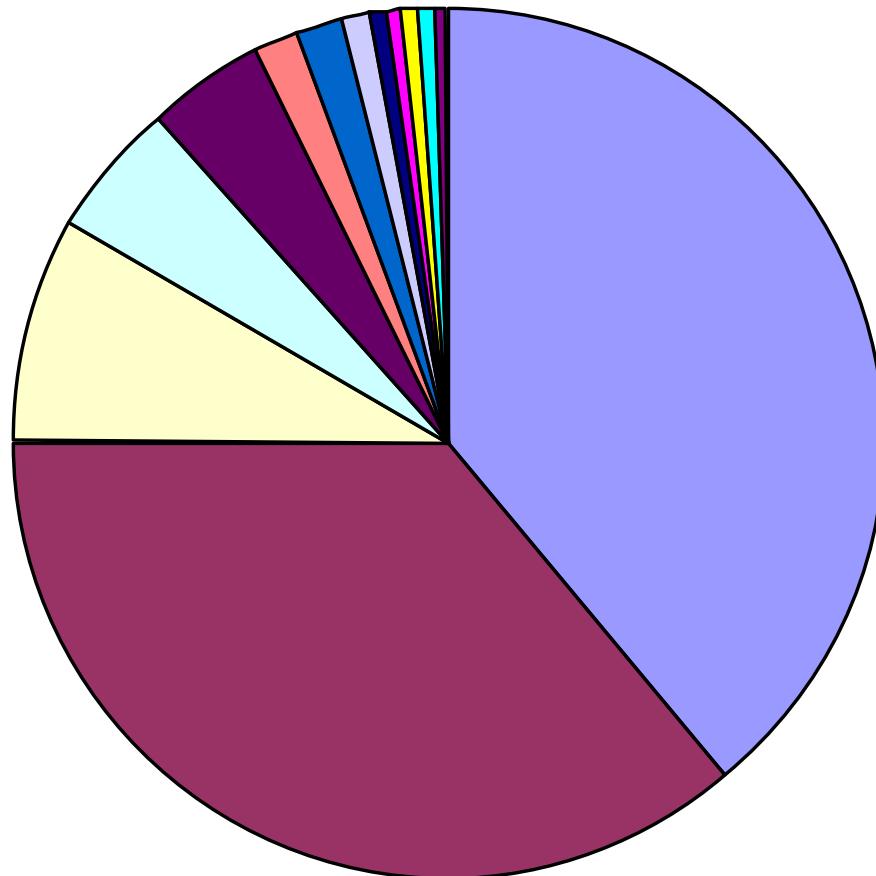


VIAGEM DE CAMPO

As dificuldades do trabalho de campo

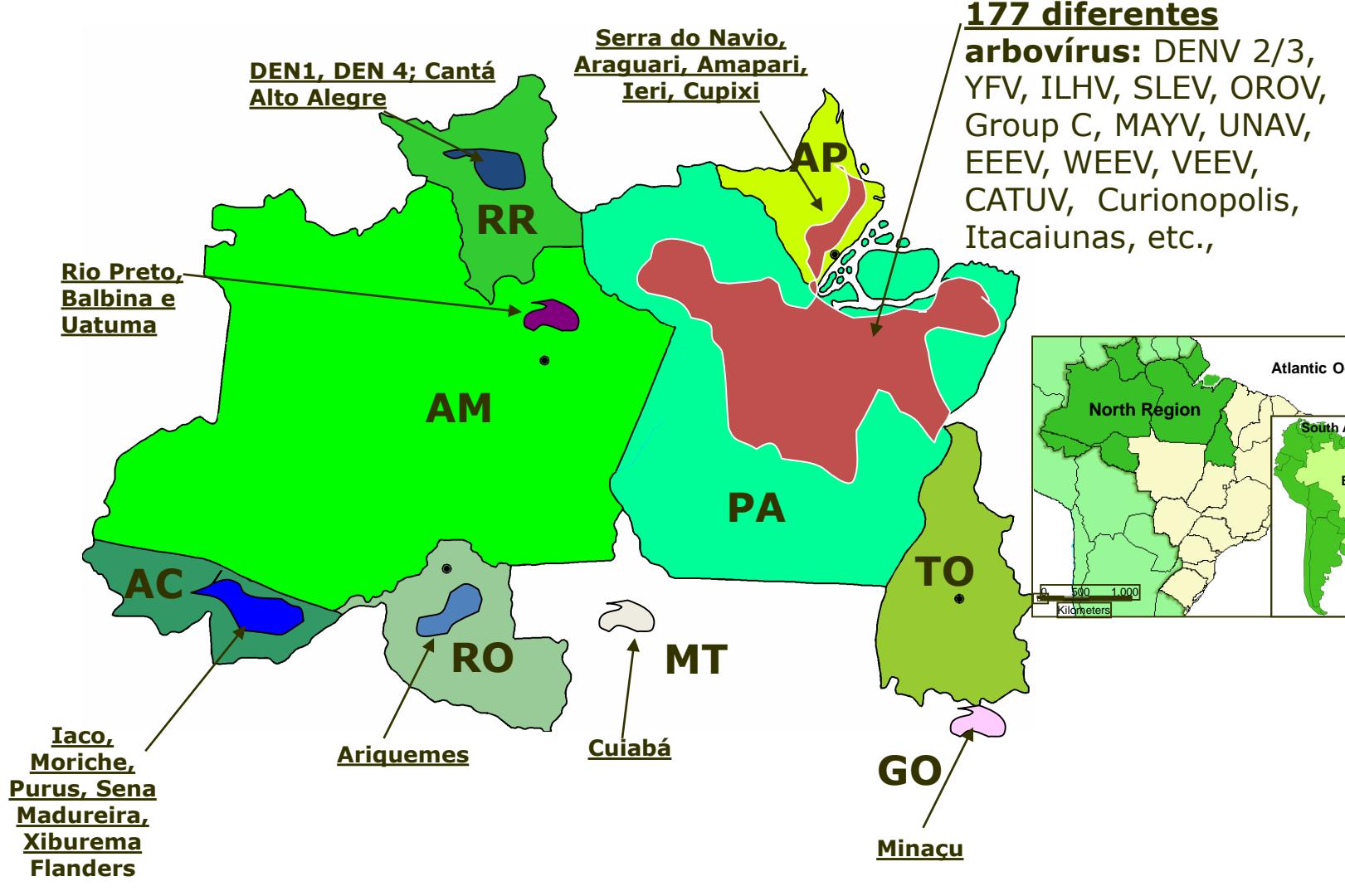


Distribuição dos 210 diferentes tipos de arbovírus e outros vírus isolados na Amazônia Brasileira por família viral



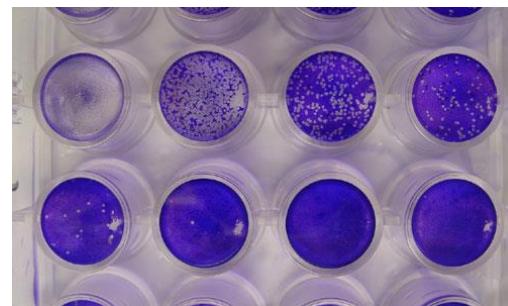
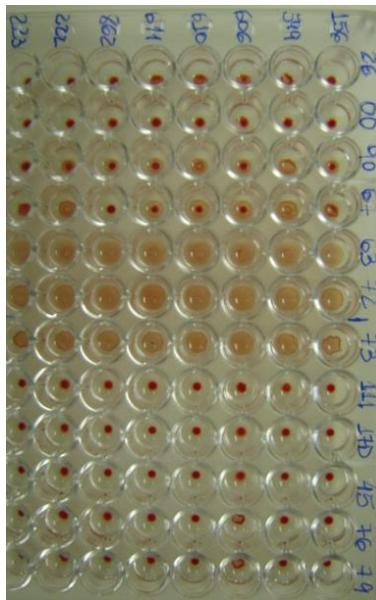
Family	(nº)
Bunyaviridae	(70)
Reoviridae	(66)
Rhabdoviridae	(17)
Togaviridae	(10)
Flaviviridae	(11)
Arenaviridae	(03)
Picornaviridae	(03)
Herpesviridae	(02)
Poxviridae	(01)
Orthomyxoviridae	(01)
Paramyxoviridae	(01)
Coronaviridae	(01)
Unclassified	(14)

Local de isolamento dos 210 Arbovírus, 1954-2010.



TESTES SOROLÓGICOS

1. Inibição da hemaglutinação – IH
2. Neutralização viral – Camundongos e PRNT
3. Elisa



QUADRO CLÍNICO

SINTOMÁTICAS	Síndrome clínica	Genero/Grupo antigênico	Arbovírus
SINTOMÁTICAS	Febril	Alphavirus – A	MUCV, PIXV
		Flavivirus – B	BSQV, ILHV, DENV, CPCV
		Orthobunyavirus - C	CARV, APEUV, MTBV, MURV, ORIV, ITQV, NEPV
		Orthobunyavirus – Califórnia	GROV
		Orthobunyavirus - Anopheles A	TCMV
		Orthobunyavirus – Guamá	CATUV, GMAV
		Phlebovirus - Phlebotomus	ALEV, CDUV, MBIV, SNTV
		Orthobunyavirus- Simbu	OROV
		Bunyamwera	XINV
		Vesiculovirus – VSV	PIRYV*, JURV
	Febril exantemática	Alphavirus – A	MAYV, CHIKV
		Flavivirus – B	DENV, ZIKV
		Orthobunyavirus - Simbu	OROV
Assintomáticas	Neurológica	A	EEEV, WEEV, VEEV subtipo IF *, CHIKV
		B	WNV, ROCV, SLEV, DENV, ZIKV
		Bunyamwera	TUCV
	Hemorrágica	Flavivirus – B	DENV, YFV

TESTE DE IH – 36 ARBOVÍRUS

- Amostras: humanos e animais domésticos e silvestres

<i>Alphavirus</i> (7)	<i>Vírus encefalite equina Leste</i> <i>Vírus encefalite equina Oeste</i> <i>Vírus Mayaro</i> <i>Vírus Chikungunya</i>	<i>Vírus mucambo</i> <i>Vírua Aurá</i> <i>Vírus Pixuna</i>
<i>Flavivirus</i> (13)	<i>Vírus febre amarela</i> <i>Vírus dengue (4 sorotipos)</i> <i>Vírus Zika</i> <i>Vírus Ilhéus</i> <i>Vírus encefalite Saint Louis</i>	<i>Vírus Rocio</i> <i>Vírus Bussuquara</i> <i>Vírus Cacipacoré</i> <i>Vírus Naranjal-Like</i> <i>Vírus West Nile</i>
<i>Orthobunyavirus</i> (13)	<i>Vírus Maguari</i> <i>Vírus Tacaima</i> <i>Vírus Caraparú</i> <i>Vírus Oropouche</i> <i>Vírus Catú</i> <i>Vírus Utinga</i> <i>Vírus Belém</i>	<i>Vírus Itaqui</i> <i>Vírus Apeú</i> <i>Vírus Murucutú</i> <i>Vírus Oriboca</i> <i>Vírus Guaroa</i> <i>Vírus Marituba</i>
<i>Phlebovirus</i> (3)	<i>Vírus Icoaraci</i> <i>Vírus Bujaru</i>	<i>Vírus Urucuri</i>

Serological survey for arboviruses in Juruti, Pará State, Brazil

CIA E

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Lívia Medeiros Neves Casseb¹

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Lívia Carício Martins¹

Jennifer Oliveira Chiang¹

Sueli Guerreiro Rodrigues¹

Pedro Fernando da Costa Vasconcelos¹

Tabela 1

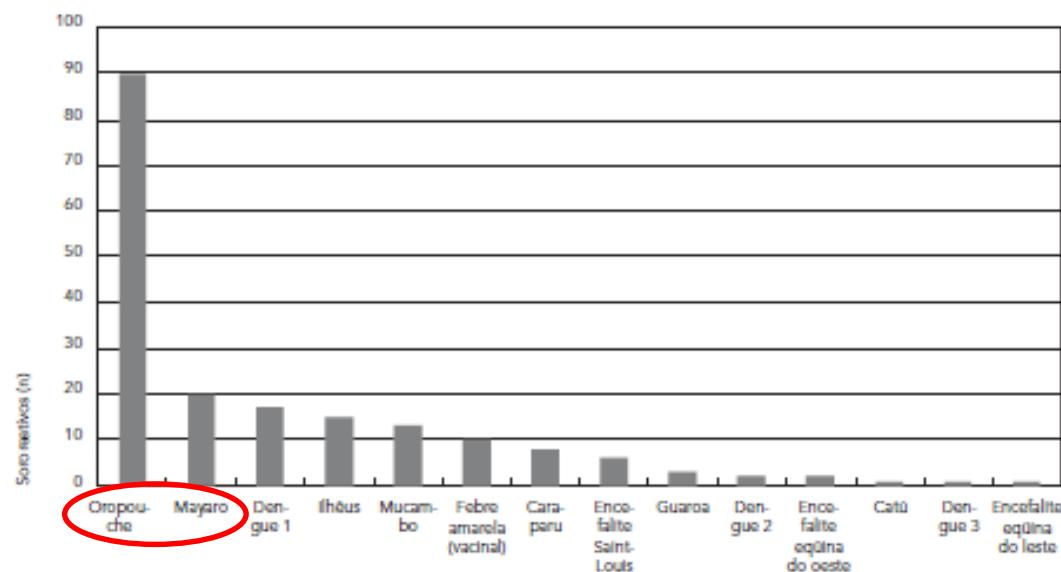
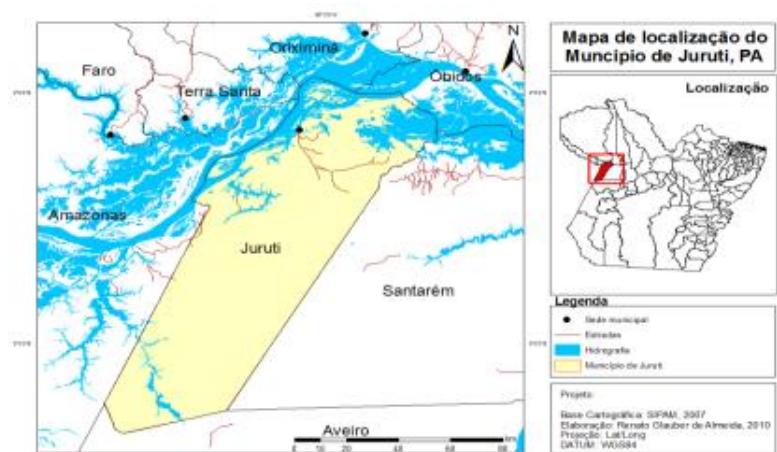
Prevalência de anticorpos totais para arbovírus em soros de humanos.

Famílias virais	Positivos	Total	
	n	%	%
Togaviridae	41	6,11	2,57
Bunyaviridae	116	17,29	7,26
Flaviviridae	379	56,48	23,73
Rações mistas	135	20,12	8,45
Togaviridae + Bunyaviridae	13	1,94	0,81
Togaviridae + Flaviviridae	41	6,11	2,56
Togaviridae + Bunyaviridae + Flaviviridae	13	1,94	0,81
Flaviviridae + Bunyaviridae	68	10,13	4,28
Positivos	671		41,02
Negativos	926		58,98
Total	1.597		

**1.597 soros de humanos
Fevereiro de 2007 a abril de 2008**

Figura 2

Respostas monotípicas detectadas pela presença de anticorpos inibidores da hemaglutinação a partir de soros de humanos.



Serological survey for arboviruses in Juruti, Pará State, Brazil

CIA E TECNOLOGIA A SERVIÇO DA SAÚDE PÚBLICA

Tabela 2

Avaliação sorológica por captura de IgM (MAC ELISA) em soros de humanos.

	Febre amarela	Dengue	Mayaro	Oropouche
Positivo	0	20	5	23
Negativo	1.597	1.577	97	90
Não testado	0	0	1.495	1.484
Total	1.597	1.597	1.597	1.597

Tabela 3

Inquérito sorológico pela presença de anticorpos inibidores da hemaglutinação a partir de soros de animais silvestres.

Animal	Espécie	Negativos	Positivos	Resultado da inibição da hemaglutinação
Aves	<i>Phlegopsis n. pareensis</i>	71	1	Vírus Ilhéus, Rocio e encefalite Saint Louis
	<i>Geotrygon montana</i>	0	1	Vírus da febre amarela, Ilhéus, encefalite Saint Louis e Rocio
	<i>Thamnophilus aethiops</i>	0	1	Vírus da febre amarela, Ilhéus, encefalite Saint Louis e Rocio
	<i>Conopophaga roberti</i>	0	1	Vírus da encefalite Saint Louis e Cacicaporé
	<i>Schiffornis tuldinus</i>	0	1	Vírus da encefalite Saint Louis
	<i>Xiphorhynchus ocellatus</i>	0	1	Vírus da encefalite Saint Louis
	<i>Myrmothera companisona</i>	0	1	Vírus da encefalite Saint Louis
Roedor	<i>Proechimis gulanensis</i>	2	0	Negativo
	<i>Proechimis longicaudatus</i>	0	0	Negativo
Marsupial	<i>Didelphis marsupialis</i>	5	0	Negativo
	<i>Metachirus filander</i>	0	0	Negativo
	<i>Didelphis albiventris</i>	0	0	Negativo
Total		78	7	

Ecoepidemiology of arboviruses in the influence area of Cuiabá-Santarém Highway (BR 163), Pará State, Brazil

Marcio Roberto Teixeira Nunes ¹

Taciana Fernandes Souza Barbosa ¹

Lívia Medeiros Neves Casseb ¹

Joaquim Pinto Nunes Neto ¹

Nazaré de Oliveira Segura ¹

Hamilton Antônio de Oliveira Monteiro ¹

Eliana Vieira Pinto ¹

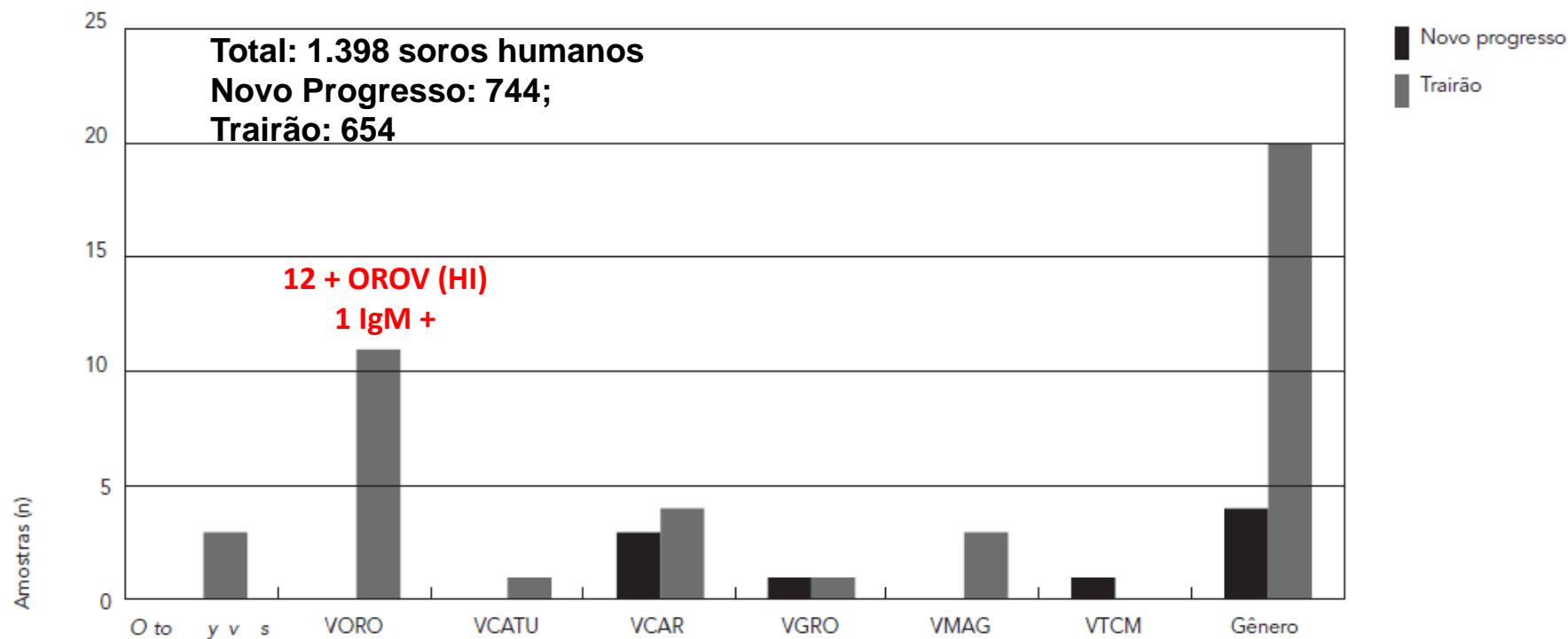
Samir Mansour Casseb ¹

Jennifer de Oliveira Chiang ¹

Lívia Caricio Martins ¹

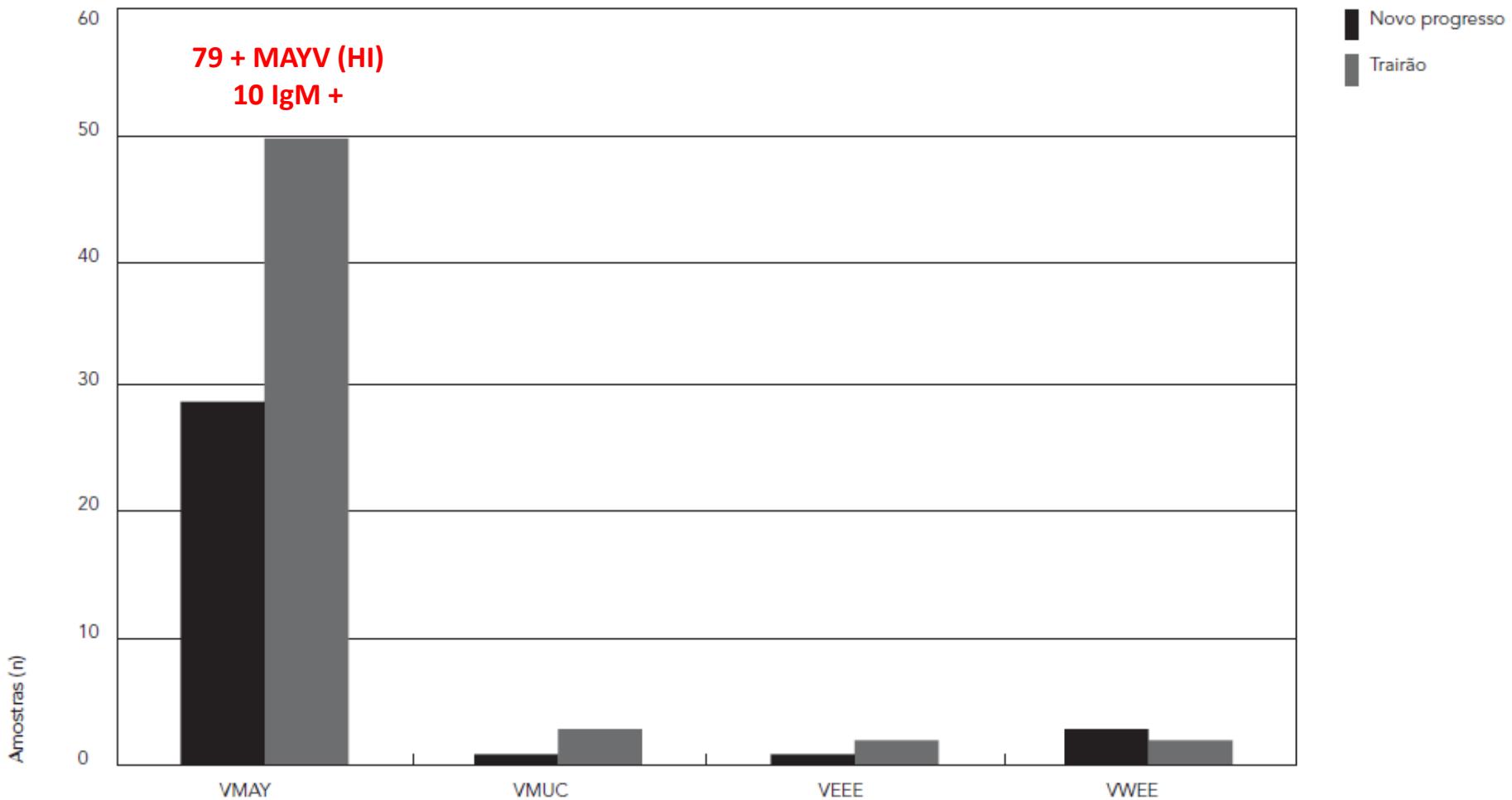
Daniele Barbosa de Almeida Medeiros ¹

Pedro Fernando da Costa Vasconcelos ¹



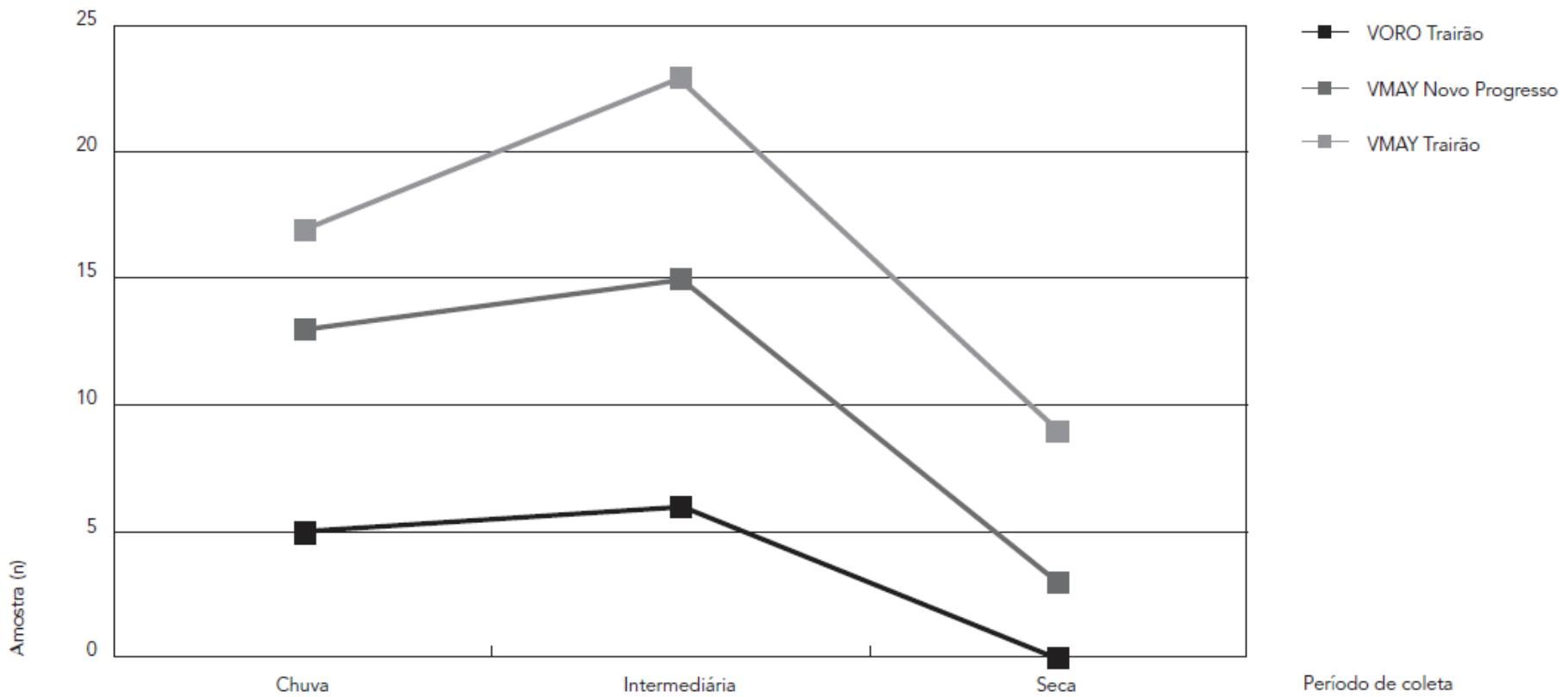
Ecoepidemiology of arboviruses in the influence area of Cuiabá-Santarém Highway (BR 163),
Pará State, Brazil

SERVIÇO DA SAÚDE PÚBLICA



Ecoepidemiology of arboviruses in the influence area of Cuiabá-Santarém Highway (BR 163), Pará State, Brazil

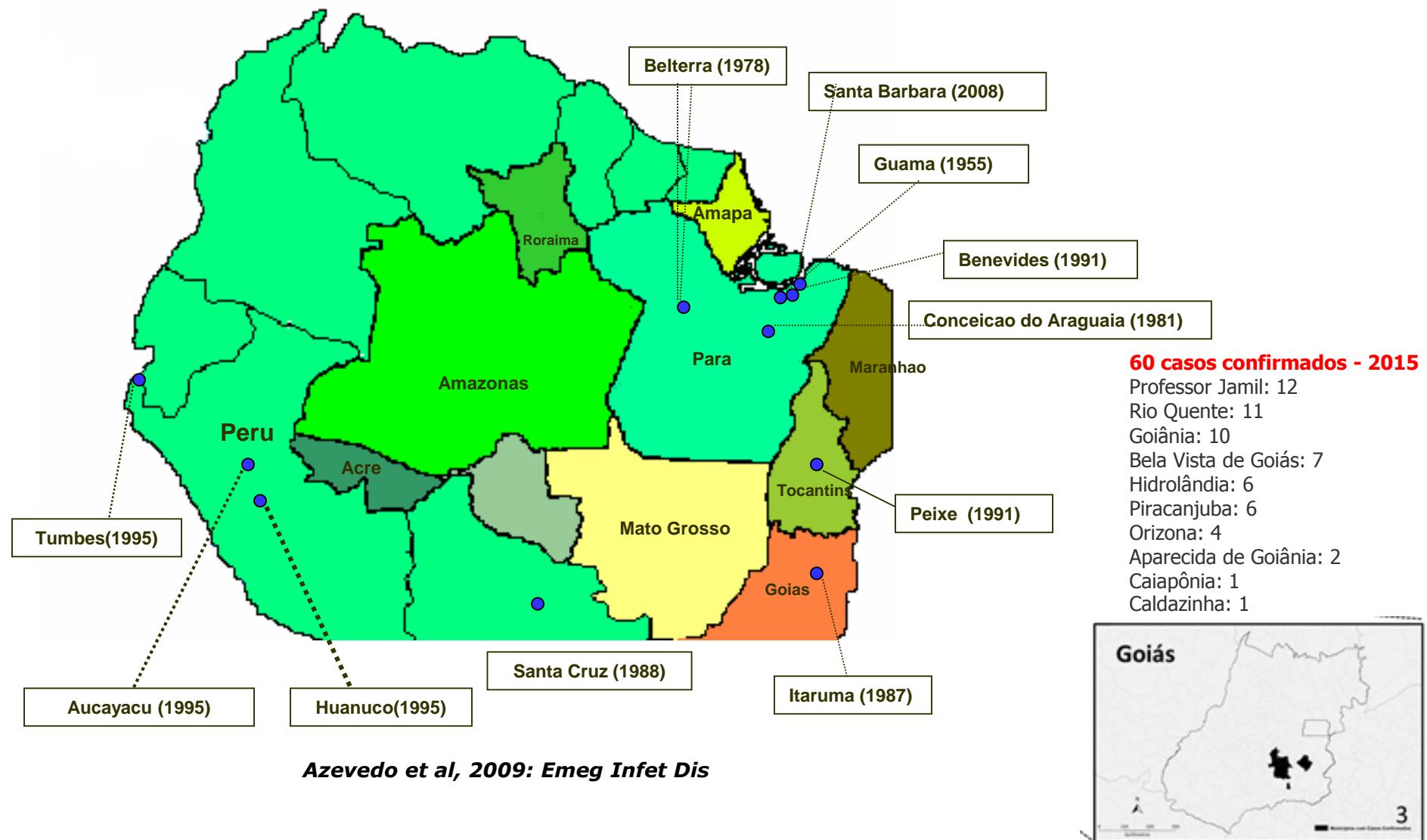
SERVIÇO DA SAÚDE PÚBLICA



- *Togaviridae – Alphavirus* – Grupo antigênico A;
- Relacionado ao vírus Chikungunya;
- Semelhante quadro clínico;
- Transmissão ciclo urbano: *Aedes aegypt*
- Diagnóstico laboratorial

PRINCIPAIS EPIDEMIAS MAYV NA REGIÃO AMAZÔNICA

1955-2008



Mayaro Fever Virus, Brazilian Amazon

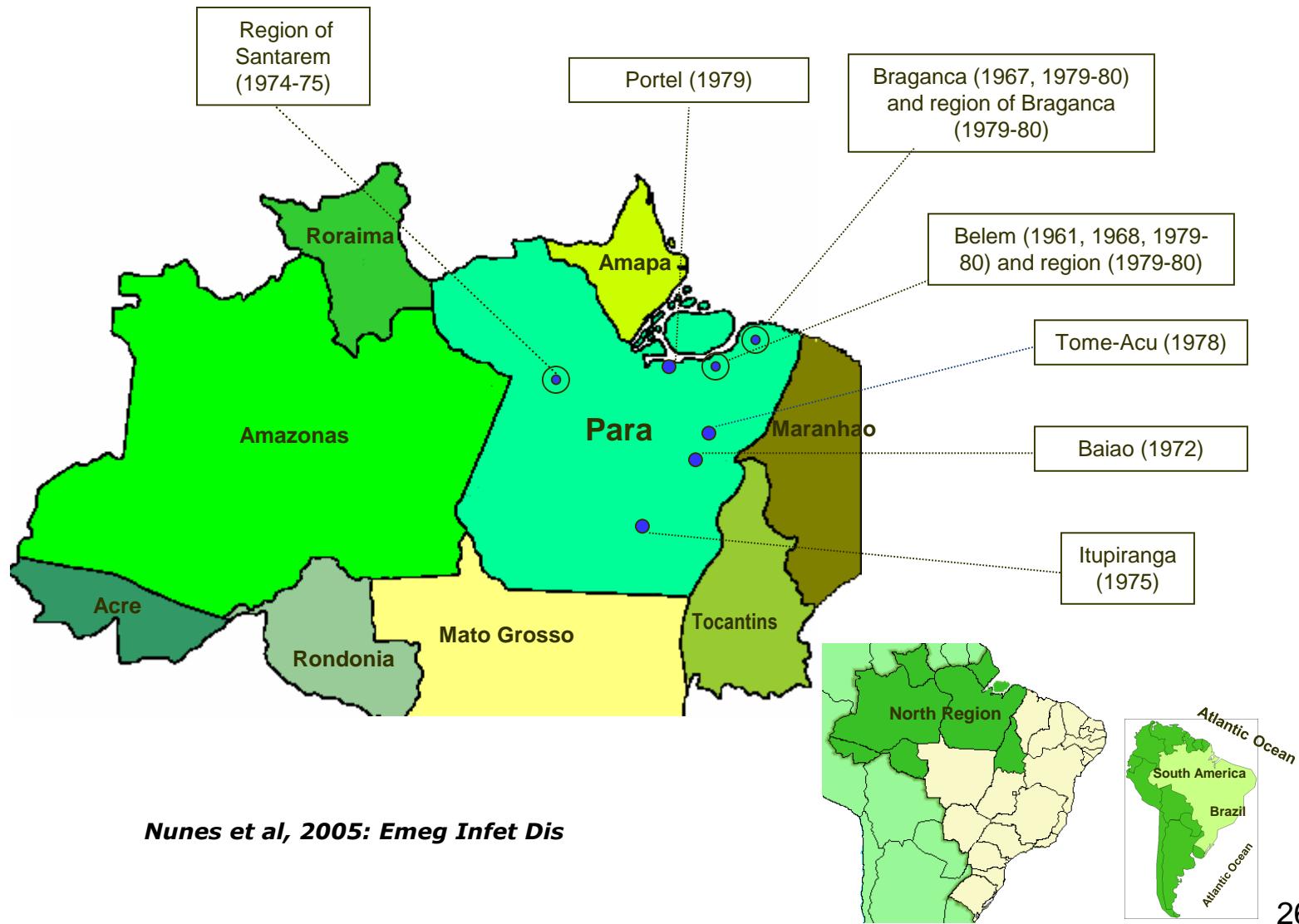
Raimunda S.S. Azevedo, Eliana V.P. Silva,
Valéria L. Carvalho, Sueli G. Rodrigues,
Joaquim P. Nunes Neto, Hamilton A.O. Monteiro,
Victor S. Peixoto, Jannifer O. Chiang,
Márcio R.T. Nunes, and Pedro F.C. Vasconcelos

In February 2008, a Mayaro fever virus (MAYV) outbreak occurred in a settlement in Santa Barbara municipality, northern Brazil. Patients had rash, fever, and severe arthralgia lasting up to 7 days. Immunoglobulin M against MAYV was detected by ELISA in 36 persons; 3 MAYV isolates sequenced were characterized as genotype D.



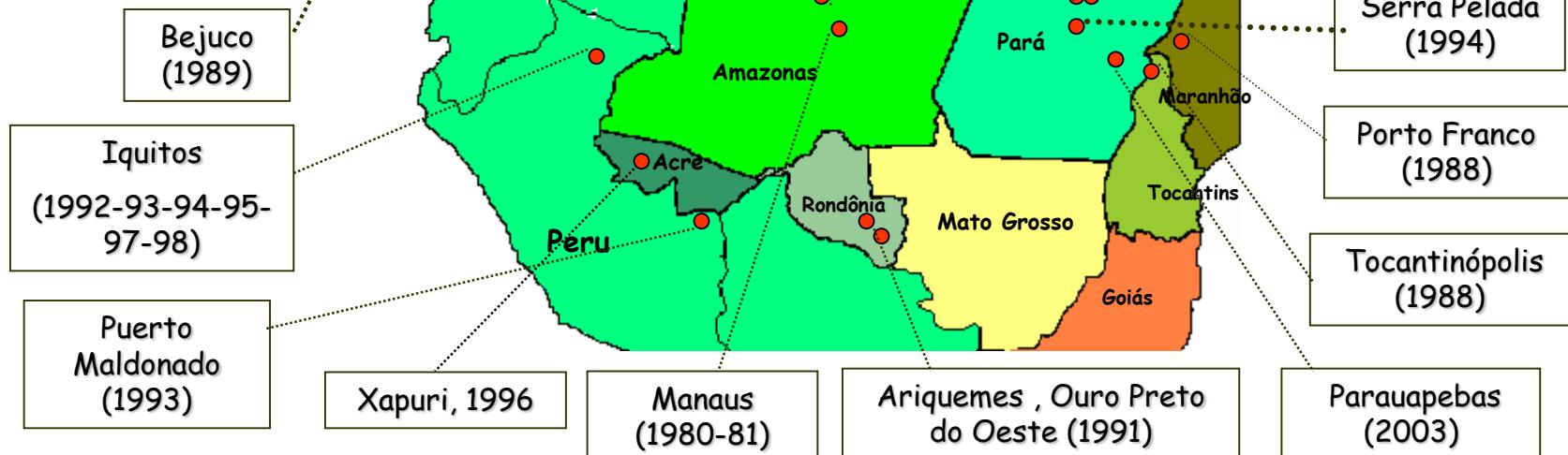
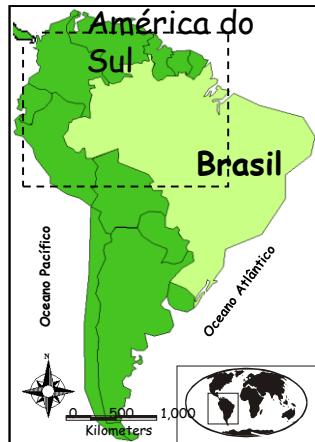
Febre do Oropouche: epidemias 1961 a 1980

MS-SECRETARIA DE VIGILÂNCIA EM SAÚDE



Febre do Oropouche: epidemias 1980 e 2009

MS-SECRETARIA DE VIGILÂNCIA EM SAÚDE



Reemergence of Oropouche Fever, Northern Brazil

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 Márcio Roberto Teixeira Nunes,*
 Jannifer Oliveira Chiang,* Gilberta Bensabath,*
 Helena Baldez Vasconcelos,* Ana Yecé das
 Neves Pinto,* Lívia Carício Martins,*
 Hamilton Antônio de Oliveira Monteiro,*
 Sueli Guerreiro Rodrigues,*
 and Pedro Fernando da Costa Vasconcelos*

Oropouche fever has reemerged in Parauapebas and Porto de Moz municipalities, Pará State, Brazil. Serologic analysis (immunoglobulin M-ELISA) and virus isolation confirmed Oropouche virus (OROV) in both municipalities. Nucleotide sequencing of 2 OROV isolates from each location indicated genotypes I (Parauapebas) and II (Porto de Moz) in Brazil.



Figure 1. Map of Brazil showing locations where Oropouche fever outbreaks were identified up to 2003–2004.

Oropouche Virus Isolation, Southeast Brazil

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 Lívia Carício Martins,*
 Sueli Guerreiro Rodrigues,*
 Jannifer Oliveira Chiang,*
 Raimunda do Socorro da Silva Azevedo,*
 Amelia P.A. Travassos da Rosa,†
 and Pedro Fernando da Costa Vasconcelos*

An Oropouche virus strain was isolated from a novel host (*Callithrix sp.*) in Arinos, Minas Gerais State, southeastern Brazil. The virus was identified by complement fixation test and confirmed by reverse transcription-polymerase chain reaction. Phylogenetic analysis identified this strain as a genotype III isolate previously recognized only in Panama.



Figure 1. Map of the Arinos region, where the strain BeAn 626998 was isolated from a sylvatic monkey of the genus *Callithrix*.

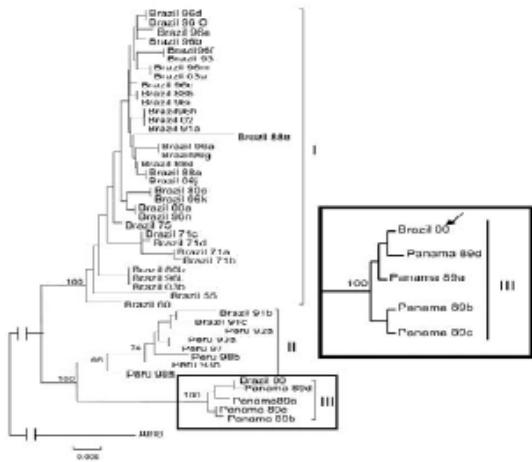
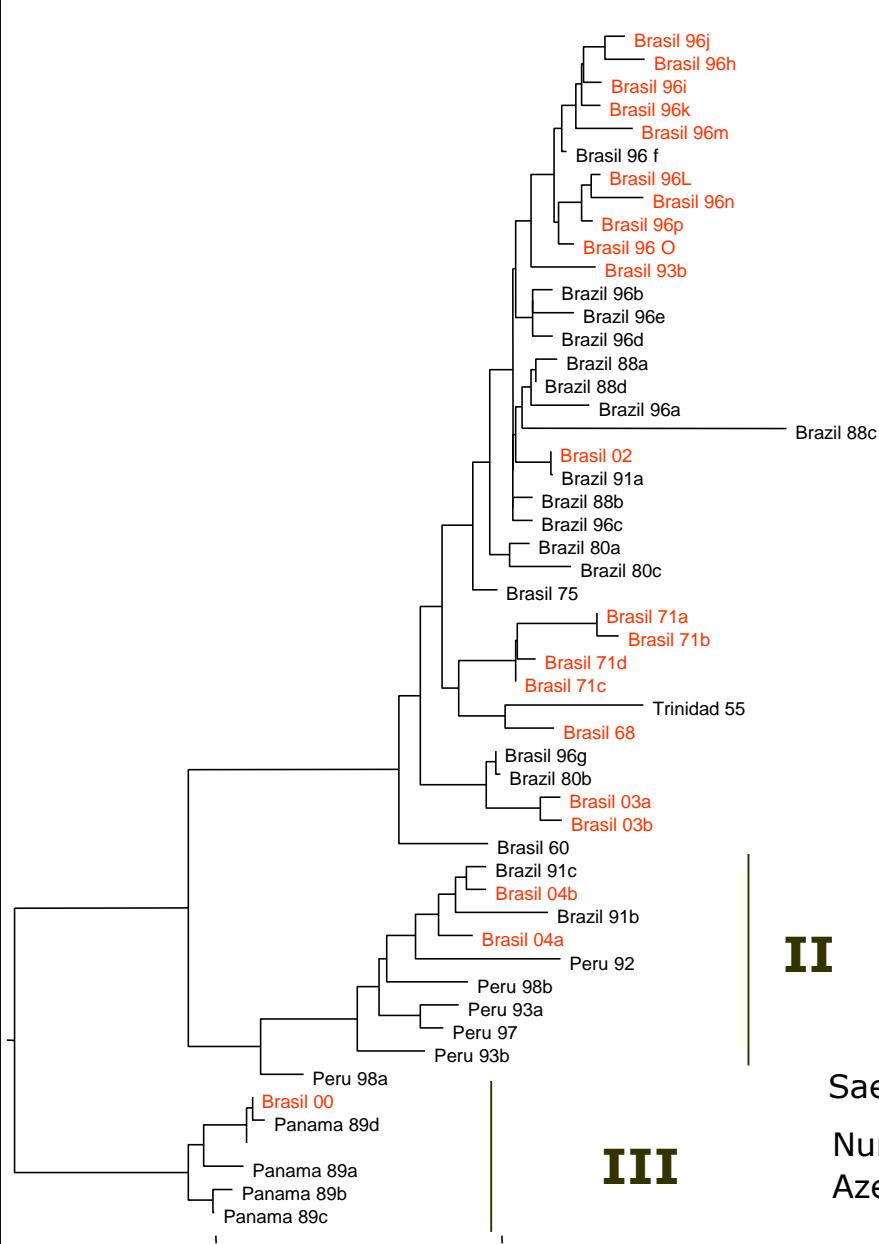
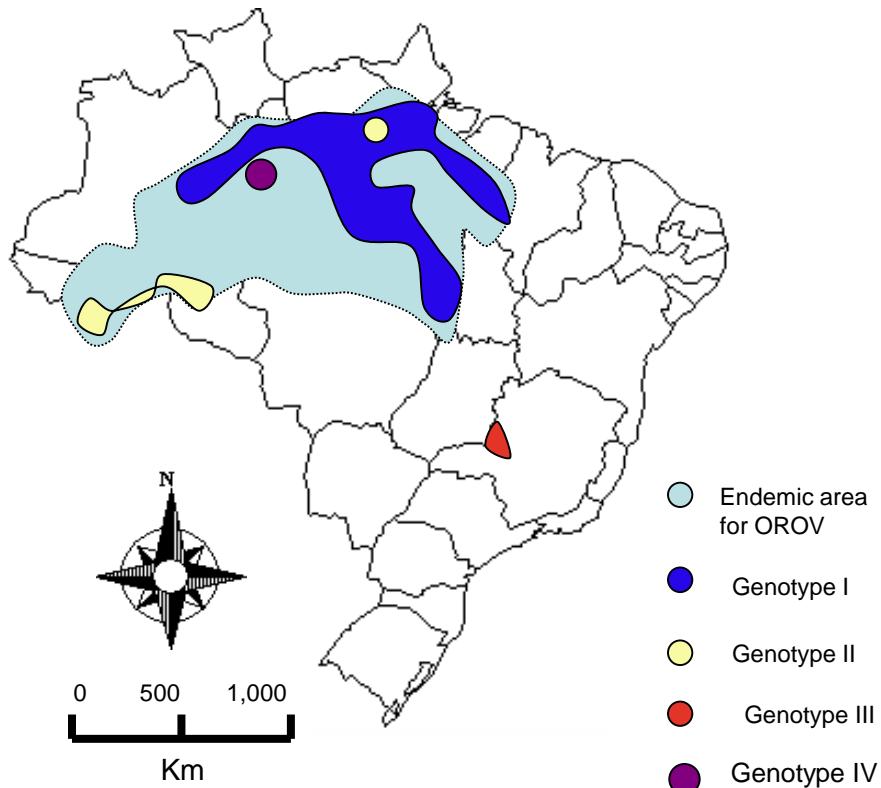


Figure 2. Phylogeny of Oropouche virus (OROV) strains isolated from different sources and periods by using the neighbor-joining and maximum parsimony methods. Bootstrap values were assigned over each internal branch nodes, and highest values were indicated by continuous arrows showing the presence of at least 3 lineages or genotypes (I, II, and III) of OROV. Bootstrap values for the 3 representative genotypes (indicated by black arrow) are placed over each respective branch node. The black arrow indicates the position of the strain BeAn 626998 (Brazil 00) in the tree. The Almo N genome nucleotide sequence was used as an outgroup to root the tree. The scale bar represents 5% nucleotide sequence divergence.

Phylogeny of Oropouche virus based on Nucleocapsid gene (693nt), 1955-2005



Circulating Genotypes in Brasil



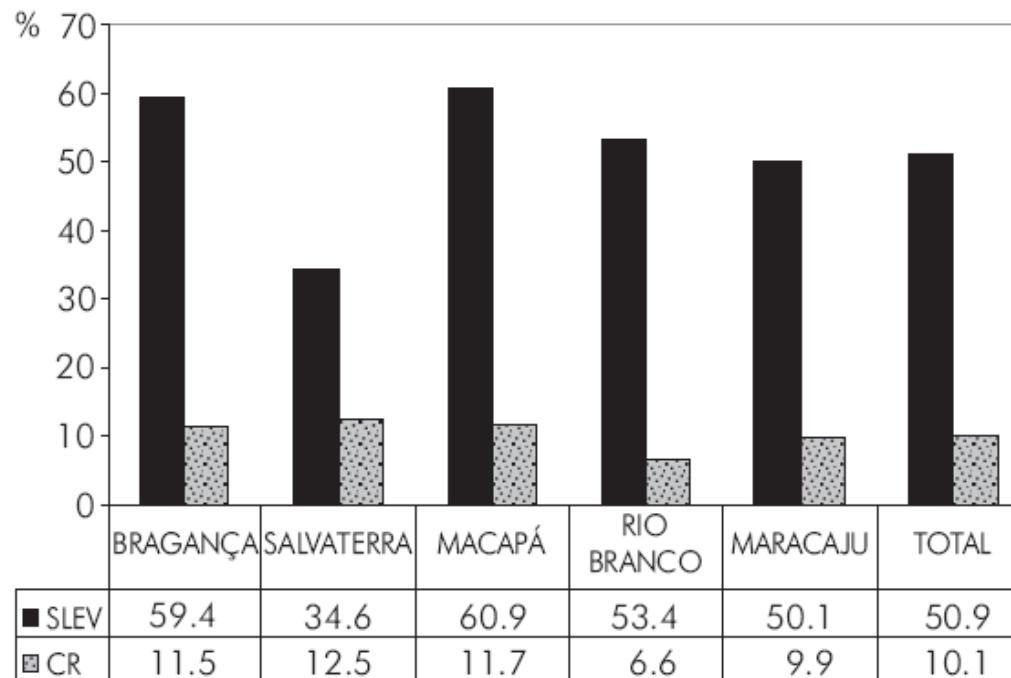
Saeed et al., J Gen Virol, 2000

Nunes et al Emerg Infect Dis, 2005
Azevedo et al Emerg Infect Dis, 2007

Epidemiology of Saint Louis encephalitis virus in the Brazilian Amazon region and in the State of Mato Grosso do Sul, Brazil: elevated prevalence of antibodies in horses

Epidemiologia do vírus da encefalite Saint Louis na Amazônia brasileira e no Estado do Mato Grosso do Sul, Brasil: elevada prevalência de anticorpos em equinos

Epidemiología del virus de la encefalitis de San Luis en la Amazonia brasileña y en el Estado de Mato Grosso do Sul (Brasil): alta prevalencia de anticuerpos en equinos



CR – cross-reactivity; SLEV – Saint Louis encephalitis virus.

Figure 3 – Percentage of equine serum samples presenting neutralizing antibodies (PRNT) against SLEV and cross-reactivity according to municipality



SHORT REPORT

Open Access

Seroprevalence of flaviviruses antibodies in water buffaloes (*Bubalus bubalis*) in Brazilian Amazon

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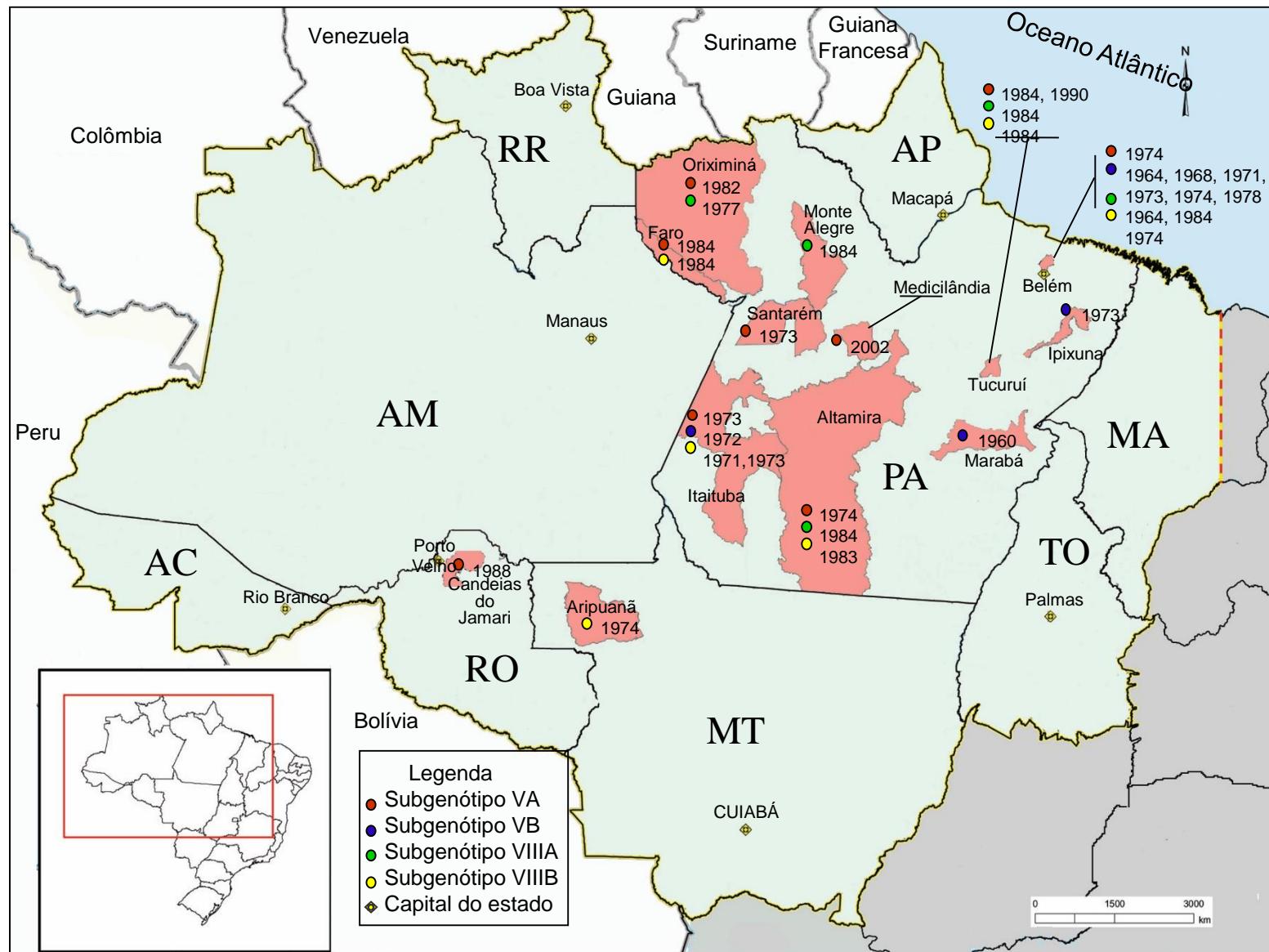
Table 1 Prevalence of hemagglutination-inhibition antibodies against antigens of six flaviviruses in serum samples of water buffaloes from different regions of Pará state, Brazilian Amazon

Virus	Water Buffaloes (n = 654)					
	HR	%HR	MR	%MR	TR	%TR
SLEV	65	9.94	82	12.54	147	22.48
ILHV	48	7.34	25	3.82	73	11.16
YFV	14	2.14	9	1.37	23	3.51
ROCV	11	1.68	2	0.30	13	1.99
BSQV	2	0.30	4	0.61	6	0.92
CPCV	8	1.22	0	0	8	1.22

HR: heterotypic reactions, MR: monotypic reactions, TR: total reactions, SLEV: Saint Louis encephalitis virus, ILHV: Ilheus virus, YFV: yellow fever virus, ROCV: Rocio virus, BSQV: Bussuquara virus, CPCV: Cacipacore virus.

SLEV: Distribuição na Amazônia Brasileira

MS-SECRETARIA DE VIGILÂNCIA EM SAÚDE



SAINT LOUIS ENCEPHALITIS VIRUS IN MATO GROSSO, CENTRAL-WESTERN BRAZIL

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SUMMARY

The dengue virus (DENV), which is frequently involved in large epidemics, and the yellow fever virus (YFV), which is responsible for sporadic sylvatic outbreaks, are considered the most important flaviviruses circulating in Brazil. Because of that, laboratorial diagnosis of acute undifferentiated febrile illness during epidemic periods is frequently directed towards these viruses, which may eventually hinder the detection of other circulating flaviviruses, including the Saint Louis encephalitis virus (SLEV), which is widely dispersed across the Americas. The aim of this study was to conduct a molecular investigation of 11 flaviviruses using 604 serum samples obtained from patients during a large dengue fever outbreak in the state of Mato Grosso (MT) between 2011 and 2012. Simultaneously, 3,433 female *Culex* spp. collected with Nasci aspirators in the city of Cuiabá, MT, in 2013, and allocated to 409 pools containing 1-10 mosquitoes, were also tested by multiplex semi-nested reverse transcription PCR for the same flaviviruses. SLEV was detected in three patients co-infected with DENV-4 from the cities of Cuiabá and Várzea Grande. One of them was a triple co-infection with DENV-1. None of them mentioned recent travel or access to sylvatic/rural regions, indicating that transmission might have occurred within the metropolitan area. Regarding mosquito samples, one pool containing one *Culex quinquefasciatus* female was positive for SLEV, with a minimum infection rate (MIR) of 0.29 per 1000 specimens of this species. Phylogenetic analysis indicates both human and mosquito SLEV cluster, with isolates from genotype V-A obtained from animals in the Amazon region, in the state of Pará. This is the first report of SLEV molecular identification in MT.

Serologic evidence of the recent circulation of *Saint Louis encephalitis virus* and high prevalence of equine encephalitis viruses in horses in the Nhecolândia sub-region in South Pantanal, Central-West Brazil

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Fernanda Marciano Burlandy¹, Michele Murta¹, Aiesca Oliveira Pellegrin²,
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Major Article

Revista da Sociedade Brasileira de Medicina Tropical 47(3):280-286, May-Jun, 2014
<http://dx.doi.org/10.1590/0037-8682-0083-2014>



Serological evidence for Saint Louis encephalitis virus in free-ranging New World monkeys and horses within the upper Paraná River basin region, Southern Brazil

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Carmen Lúcia Scortecci Hilst^[6], Lucas M. Aguiar^[7], Gabriela Ludwig^[8],
Fernando de Camargo Passos^[9], Lineu Roberto da Silva^[10], Selwyn Arlington Headley^[11]
and Italmar Teodorico Navarro^[11]

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TROPICAL DISEASES

Isolation of Saint Louis Encephalitis Virus from a Horse with Neurological Disease in Brazil

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Abstract

St. Louis encephalitis virus (SLEV) is a causative agent of encephalitis in humans in the Western hemisphere. SLEV is a positive-sense RNA virus that belongs to the *Flavivirus* genus, which includes West Nile encephalitis virus, Japanese encephalitis virus, Dengue virus and other medically important viruses. Recently, we isolated a SLEV strain from the brain of a horse with neurological signs in the countryside of Minas Gerais, Brazil. The SLEV isolation was confirmed by reverse-transcription RT-PCR and sequencing of the E protein gene. Virus identity was also confirmed by indirect immunofluorescence using commercial antibodies against SLEV. To characterize this newly isolated strain *in vivo*, serial passages in newborn mice were performed and led to hemorrhagic manifestations associated with recruitment of inflammatory cells into the central nervous system of newborns. In summary this is the first isolation of SLEV from a horse with neurological signs in Brazil.

Infection with Saint Louis encephalitis virus in the city of Ribeirao Preto, Brazil: report of one case



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Marilia Farignoli Romeiro, Luiza Antunes de Castro-Jorge,
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SUMMARY

Saint Louis encephalitis virus (SLEV) is a mosquito-borne flavivirus from the Americas. In this report we describe aspects of the laboratory diagnosis of a patient with an acute febrile illness induced by SLEV that was initially diagnosed as dengue by positive IgM-ELISA. Infection with this virus is probably not rare in Brazil, but cases remain undiagnosed. It is necessary to improve the surveillance system, including laboratories, for the diagnosis of SLEV in Brazil.

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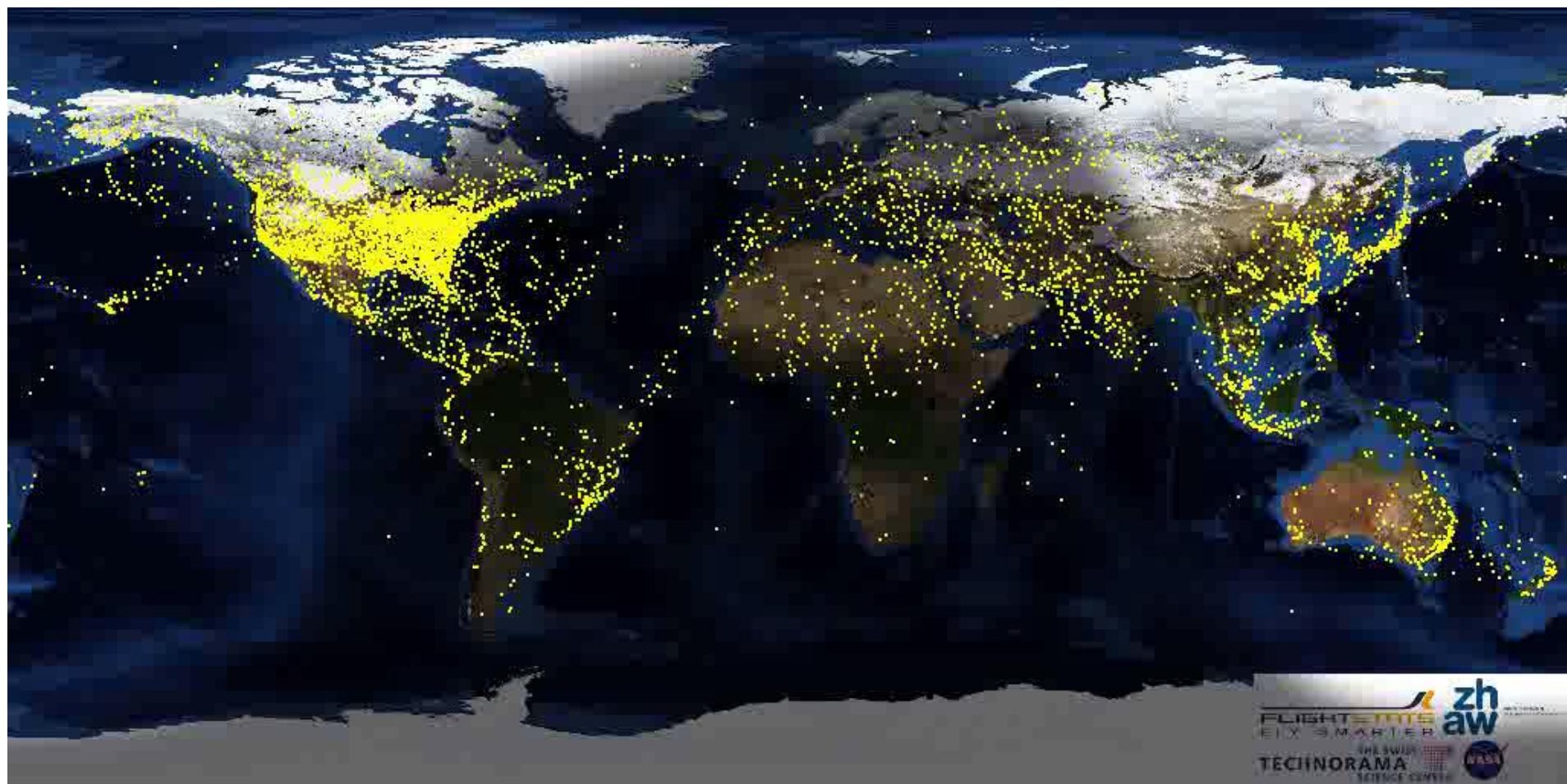
FATORES ASSOCIADOS COM A RE/EMERGÊNCIA DE ARBOVÍRUS

- Crescimento da população;
- Urbanização sem planejamento;
- Derrubada de floresta;
- Construção de estradas na floresta;
- Construção de hidrelétricas;
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- Transporte x dispersão dos arbovírus
- Mutações e rearranjos genéticos
- Turismo ecológico



Projeto Salobo/Marabá -VALE

Global Airline Routes

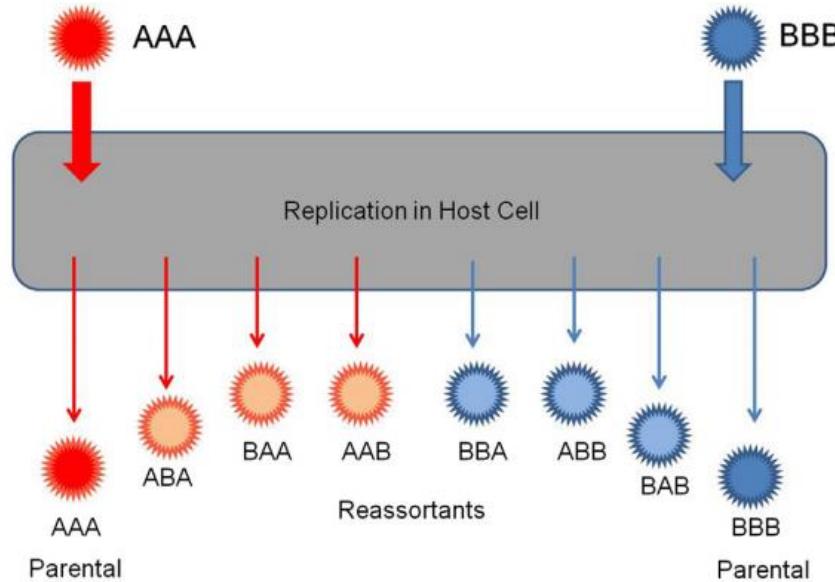


24 Hour Global Air Traffic Simulation

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REARRANJO GENÉTICO - BUNYAVIRIDAE



Ngari Virus Is a Bunyamwera Virus Reassortant That Can Be Associated with Large Outbreaks of Hemorrhagic Fever in Africa

Sonja R. Gerrard,^{1,2} Li Li,³ Alan D. Barrett,³ and Stuart T. Nichol^{1*}

Schmallenberg Virus as Possible Ancestor of Shamonda Virus

Katja V. Goller,¹ Dirk Höper,¹ Horst Schirrmeier,
Thomas C. Mettenleiter, and Martin Beer

Schmallenberg virus (SBV), an orthobunyavirus of the Simbu serogroup, recently emerged in Europe and has been suggested to be a Shamonda/Sathuperi virus reassortant. Results of full-genome and serologic investigations indicate that SBV belongs to the species *Sathuperi virus* and is a possible ancestor of the reassortant Shamonda virus.

REVIEW ARTICLE
‘Schmallenberg virus’ – a novel orthobunyavirus emerging in Europe

M. BEER^{1*}, F. J. CONRATHS² AND W. H. M. VAN DER POEL³

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Two novel epistatic mutations (E1:K211E and E2:V264A) in structural proteins of Chikungunya virus enhance fitness in *Aedes aegypti*



CrossMark

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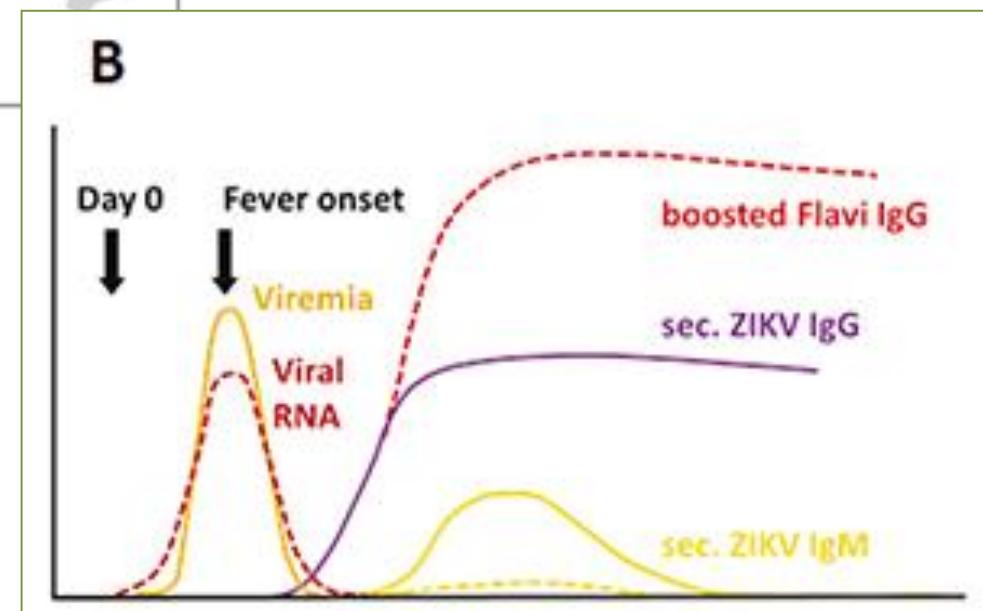
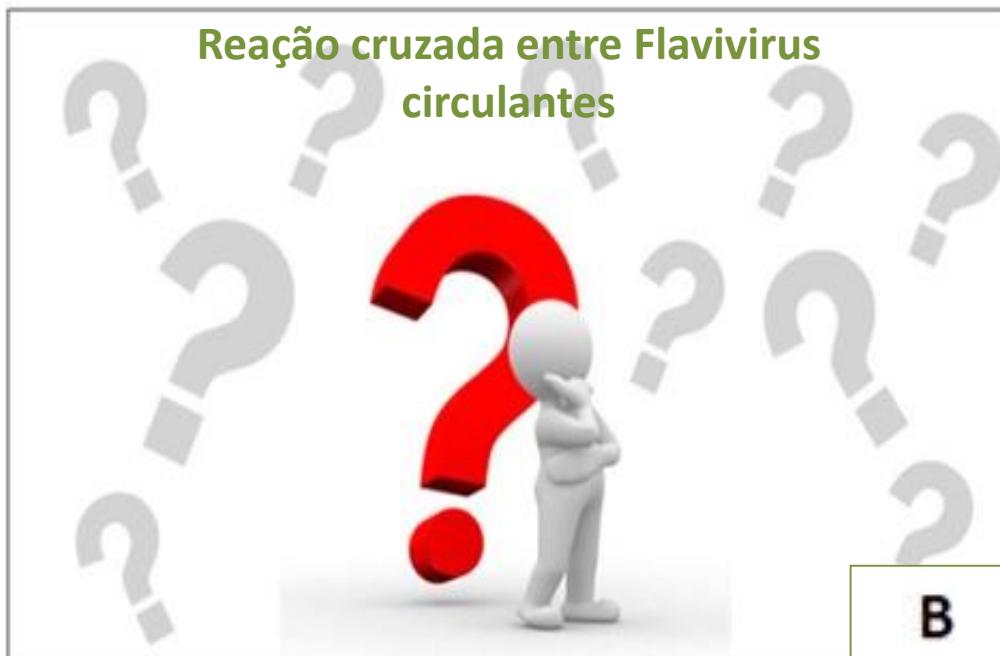
ABSTRACT

Expansion of CHIKV outbreaks with appearance of novel mutations are reported from many parts of the world. Two novel mutations viz. E1:K211E and E2:V264A in background of E1:226A are recently identified from *Aedes aegypti* dominated areas of India. In this study, the role of these mutations in modulation of infectivity, dissemination and transmission by two different *Aedes* species was studied. Mutations were sequentially constructed in CHIKV genome and female *Ae. aegypti* and *Aedes albopictus* mosquitoes were orally infected with eight different CHIKV mutants. Double mutant virus containing E1:K211E and E2:V264A mutations in background of E1:226A revealed remarkably higher fitness for *Ae. aegypti*, as indicated by significant increase in virus infectivity (13 fold), dissemination (15 fold) and transmission (62 fold) compared to parental E1:226A virus. These results indicate that adaptive mutations in CHIKV are leading to efficient CHIKV circulation in *Ae. aegypti* endemic areas, contributing and sustaining the major CHIKV outbreaks.

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DESAFIOS DO DIAGNÓSTICO LABORATORIAL

MS-SECRETARIA DE VIGILÂNCIA EM SAÚDE



Conclusões

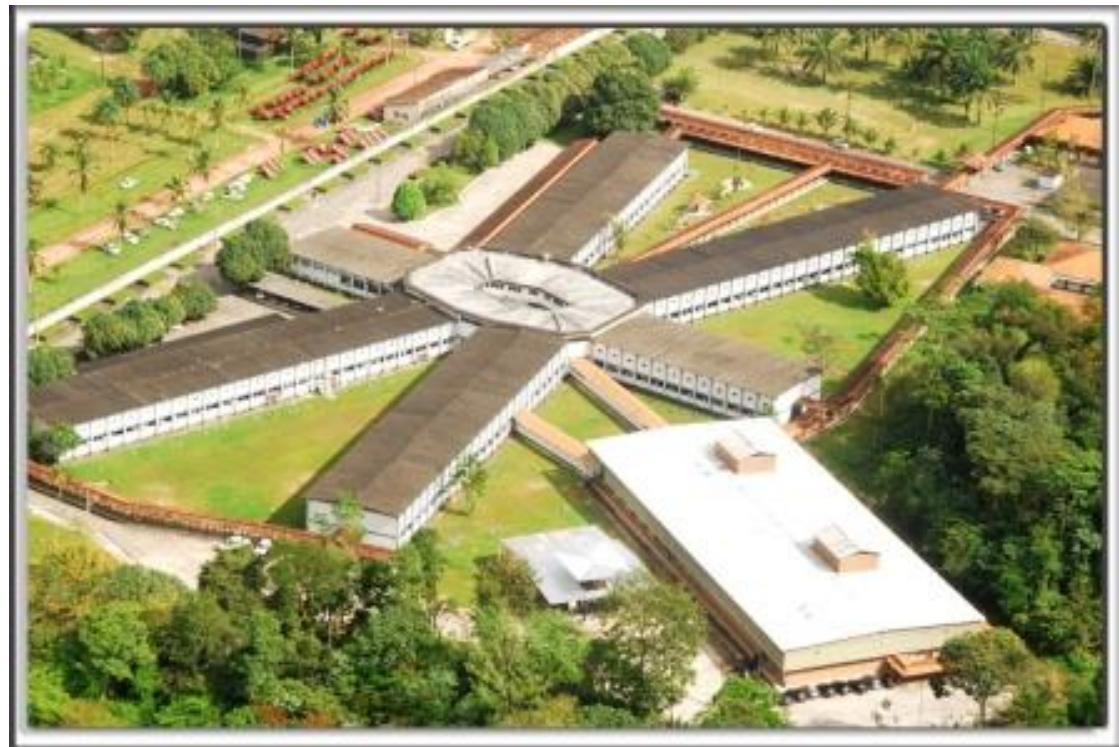
- Conhecimento:
 - Importâncias dos estudos de soroprevalência e ecoepidemiológicos;
 - Estar atento para surtos/epidemias que estão ocorrendo em outros países – Dispersão;
- Diagnóstico diferencial para outros arbovírus;

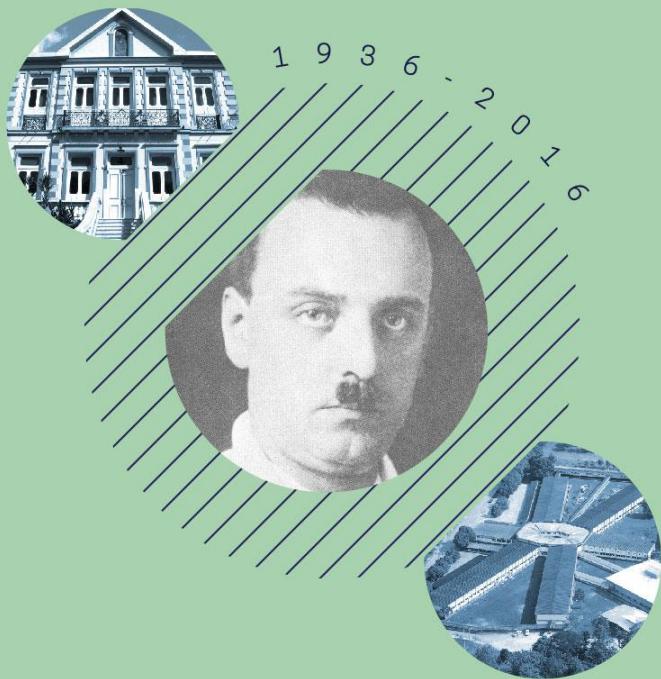
Qual?
Quando?
Onde?



SEÇÃO DE ARBOVIROLOGIA E FEBRES HEMORRAGICAS – INSTITUTO EVANDRO CHAGAS

- **3 Lab Sorologia**
 - HI
 - Elisa
 - Hantavirus
- **2 lab isolamento viral**
 - Cultura de células
 - Camundongos
- **Lab Biologia molecular**
- **Lab Entomologia**
- **Lab Raiva**
- **Lab NB3**





MUITO OBRIGADO!