AUSTRALIA - BRAZIL

VIRTUAL RESEARCH COLLABORATION

2021 Edition on Covid-19 related research.

One-health: research and scenario in Brazil

INSTITUTIONAL SUPPORTER:

Programa Diplomacia Inovação

CO-ORGANIZATION:

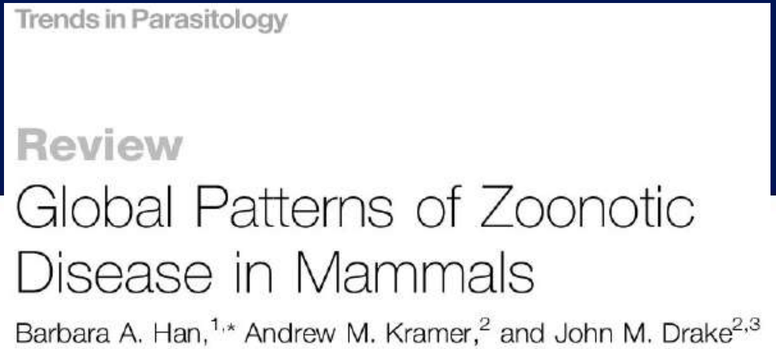
Australian Academy of Science

Academia Brasileira de Ciências

ORGANIZATION:

Australian Government
Department of Education, Skills and Employment

CONFAP

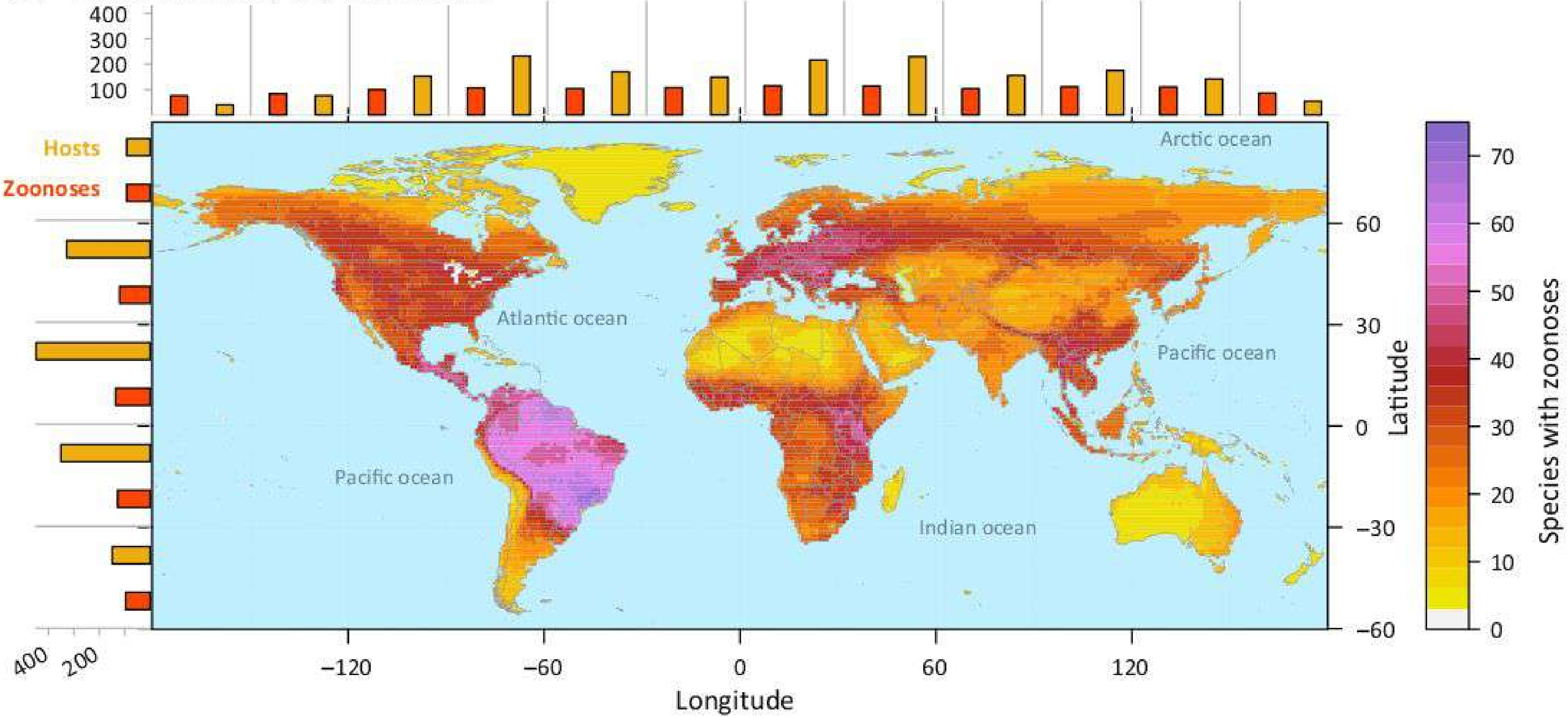


Trends in Parasitology

Review

Global Patterns of Zoonotic Disease in Mammals

Barbara A. Han,[1,*] Andrew M. Kramer,[2] and John M. Drake[2,3]



Trends in Parasitology

Figure 1. Geographic Ranges of Zoonotic Mammal Hosts. Mammal reservoirs of zoonotic diseases are globally distributed, with noteworthy hotspots in Amazonia and Eurasia. Overlapping geographic ranges of mammal species recognized to carry one or more zoonotic diseases, with counts of unique host species (gold bars) and unique zoonotic pathogens (red bars) found within 30° latitudinal and longitudinal bands. This map depicts 5007 total wild mammal species from 27 orders.

Beyond diversity loss and climate change: Impacts of Amazon deforestation on infectious diseases and public health

JOEL HENRIQUE ELLWANGER, BRUNA KULMANN-LEAL, VALÉRIA L. KAMINSKI, JACQUELINE MARÍA VALVERDE-VILLEGAS, ANA BEATRIZ G. DA VEIGA, FERNANDO R. SPILKI, PHILIP M. FEARNSIDE, LÍLIAN CAESAR, LEANDRO LUIZ GIATTI, GABRIEL L. WALLAU, SABRINA E.M. ALMEIDA, MAURO R. BORBA, VANUSA P. DA HORA & JOSÉ ARTUR B. CHIES

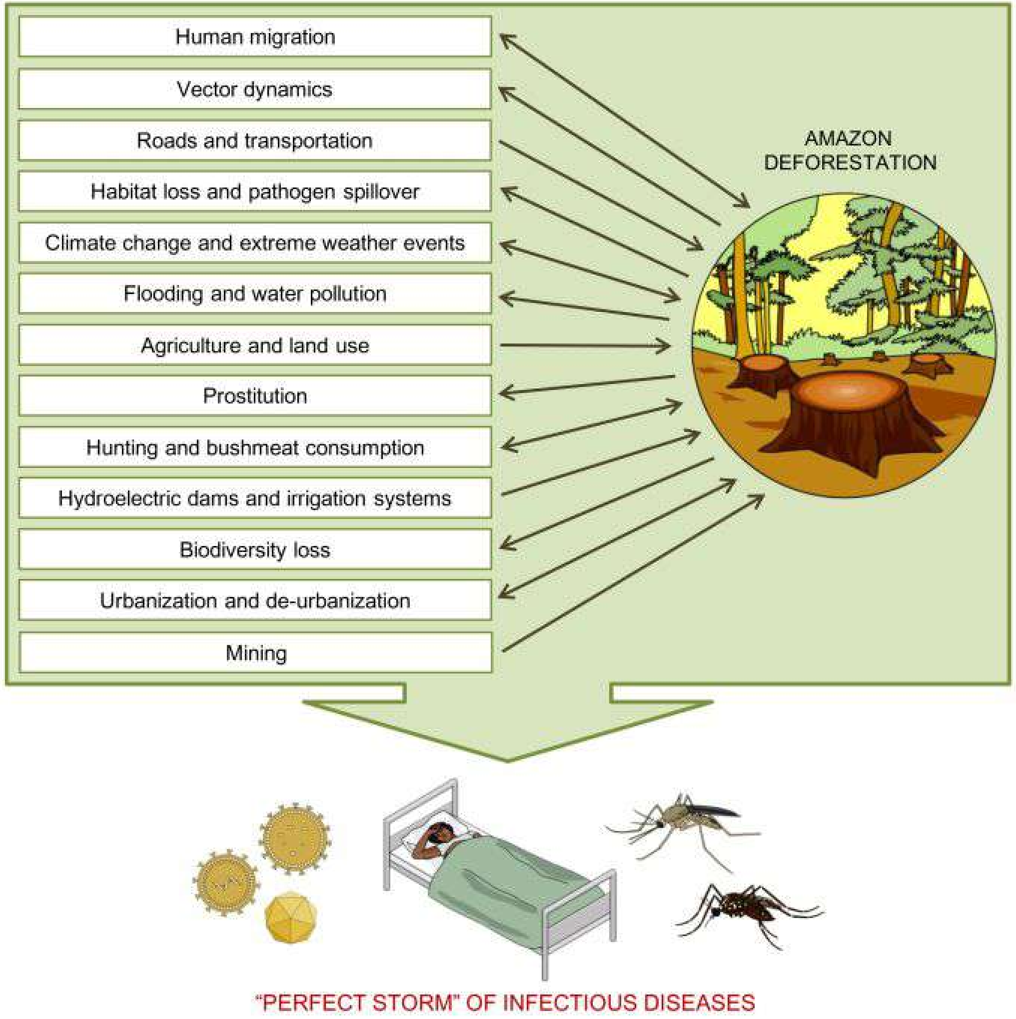
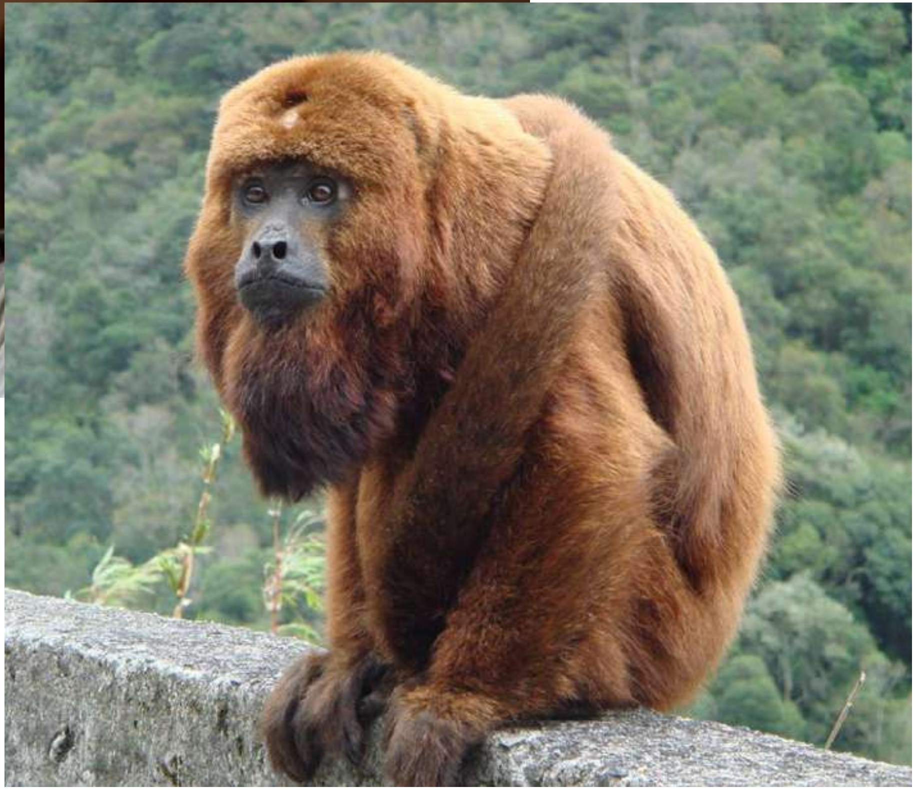


Figure 1. Problems and activities associated with Amazon deforestation and impacts on infectious diseases. The problems and activities associated with the emergence of infectious diseases can result from Amazon deforestation (e.g., floods and water pollution). In other situations, they act as promoters of deforestation (e.g., road construction and mining). Some factors are both consequences and causes of deforestation, as in the case of human migrations and urbanization, as represented by bidirectional arrows. This figure was created using *Mind the Graph* illustrations (available at www.mindthegraph.com).

HEALTH

‘We didn’t expect this’: A historic yellow fever outbreak spreads in Brazil

By DOM PHILLIPS / APRIL 13, 2017
Photos by LIANNE MILTON FOR STAT



SCIENTIFIC REPORTS

OPEN

Potential risk of re-emergence of urban transmission of Yellow Fever virus in Brazil facilitated by competent *Aedes* populations

Received: 15 March 2017
Accepted: 23 May 2017
Published online: 07 July 2017

Dinair Couto-Lima[1,2], Yoann Madec[3], Maria Ignez Bersot[1], Stephanie Silva Campos[1], Monique de Albuquerque Motta[1], Flávia Barreto dos Santos[1], Marie Vazeille[2], Pedro Fernando da Costa Vasconcelos[4], Ricardo Lourenço-de-Oliveira[1] & Anna-Bella Failloux[2]

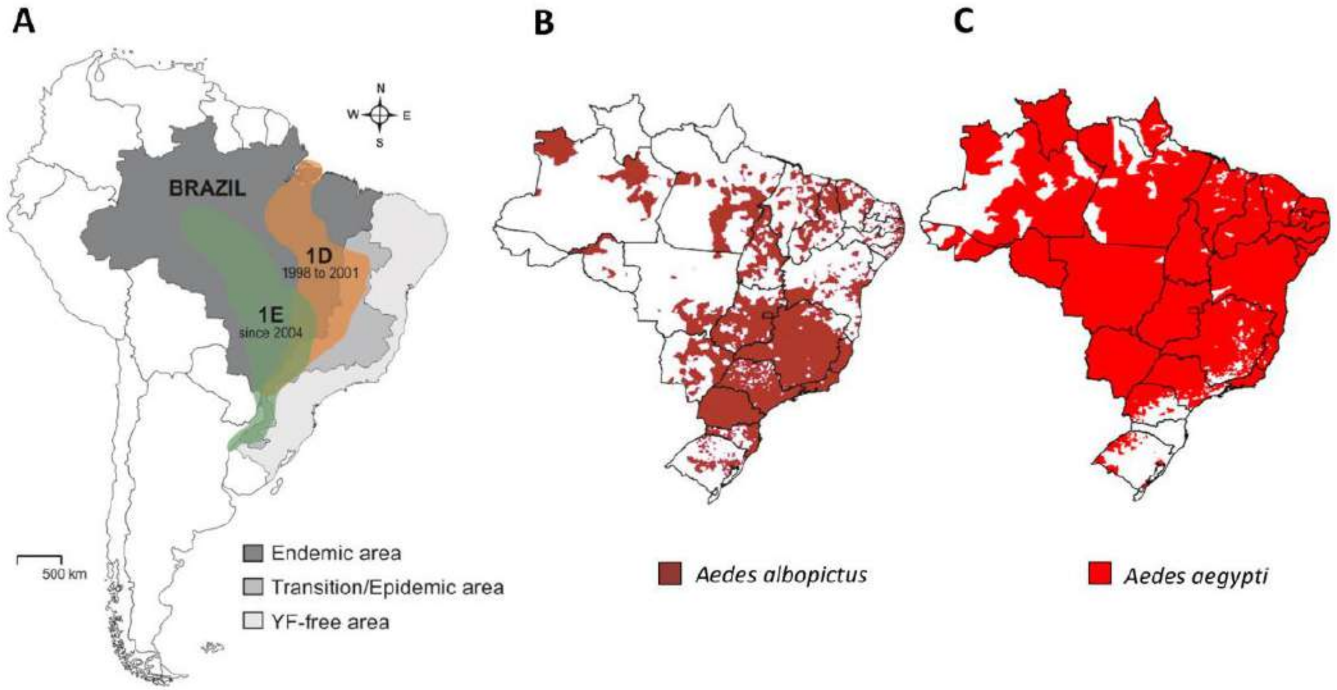


Figure 1. Geographic distribution of YFV strains (71016-1D and 4408-1E) (**A**), the mosquitoes *Ae. aegypti* (**B**) and *Ae. albopictus* (**C**) according to ref. 13. The map was created using software the CorelDraw X5 software (http://www.coreldraw.com/br/).

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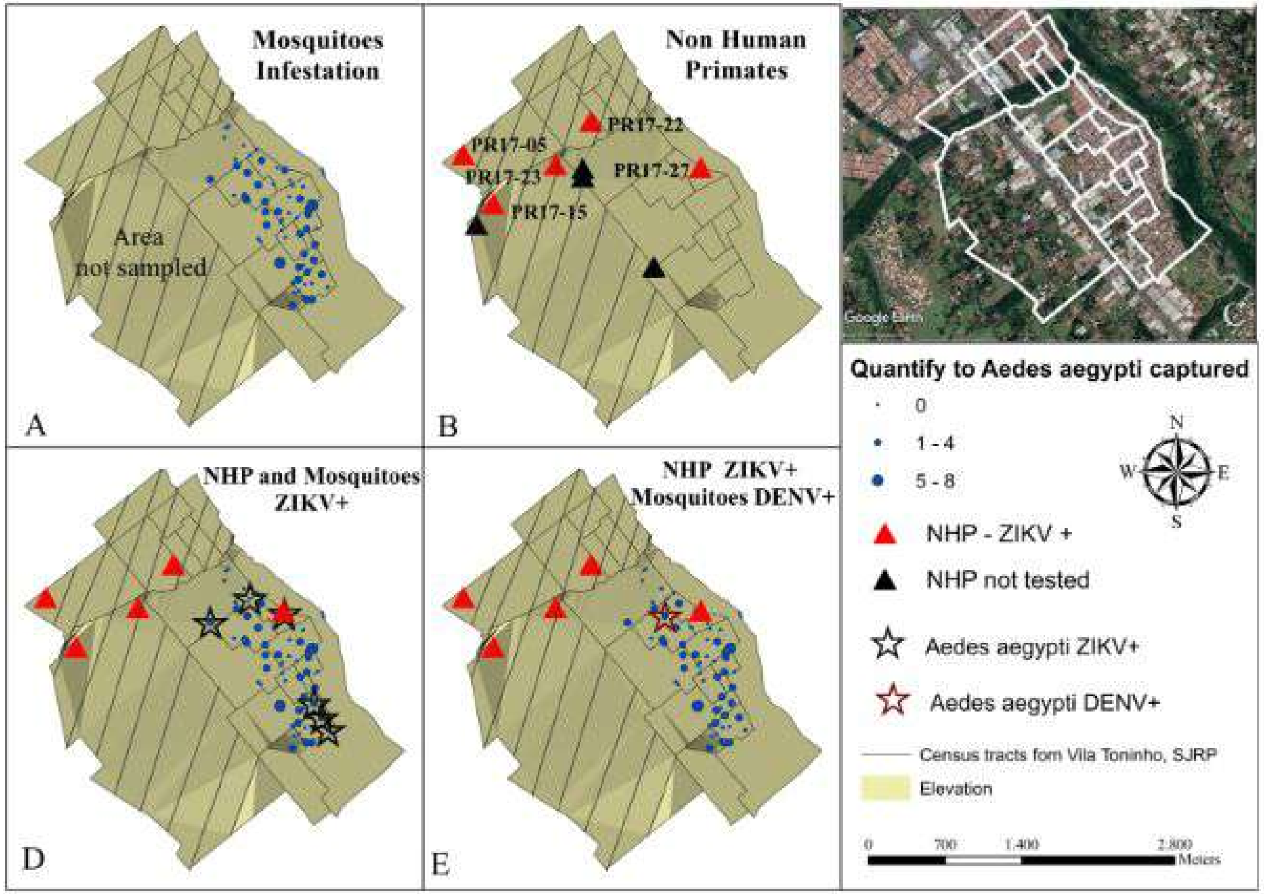

Figure 1. Geoprocessing map of the NHPs and mosquitoes captured in the Vila Toninho neighborhood. (**A**) Schematic representation of the area where mosquitoes are regularly collected in the Vila Toninho neighborhood. The hatched area represents the area where there is no specimen collection. The blue dots represent the collection points of the mosquitoes and the quantity of specimen collected. (**B**) Schematic representation of the collection points of the nine NHP found dead. The NHPs identified by ID PR 17-05, PR 17-15, PR 17–22, PR 17–23, PR 17–27 were analyzed and tested positive for ZIKV in one or more tissue samples and are represented by a red triangle. The black triangles represent the NHPs collected but not tested. (**C**) Satellite image of the Vila Toninho neighborhood. The boundary of the neighborhood is marked in white. Vegetation cover area can be seen in green surrounding the neighborhood. (**D**) Overlap of the area of the animals and mosquitoes collection. The ZIKV-positive PR 17–27 is overlapping with a ZIKV-positive *Ae. aegypti* mosquito pool. (**E**) Overlap of the areas of animas and mosquito collections with the presence of the DENV-positive *Ae. aegypti* mosquitoes (Vila Toninho satellite image by Google Earth Pro 7.3.1.4507 (64-bit) software. URL https://www.google.com/maps/@−20.84677,−49.34063,5682 m/data = !3m1!1e3). Map data: Google, 2018 DigitalGlobe.

SCIENTIFIC REPORTS

OPEN

Evidence of natural Zika virus infection in neotropical non-human primates in Brazil

Received: 19 March 2018
Accepted: 17 October 2018

Ana Carolina B. Terzian[1], Nathalia Zini[1], Lívia Sacchetto[2], Rebeca Froes Rocha[3], Maisa Carla Pereira Parra[1], Juliana Lemos Del Sarto[3], Ana Carolina Fialho Dias[3], Felipe Coutinho[3], Jéssica Rayra[3], Rafael Alves da Silva[1], Vivian Vasconcelos Costa[3], Natália Coelho Couto De Azevedo Fernandes[4], Rodrigo Réssio[4], Josué Díaz-Delgado[4], Juliana Guerra[4], Mariana S. Cunha[4], José Luiz Catão-Dias[5], Cintia Bittar[6], Andréia Francesli Negri Reis[7], Izalco Nuremberg Penha dos Santos[7], Andréia Cristina Marascalchi Ferreira[7], Lilian Elisa Arão Antônio Cruz[7], Paula Rahal[6], Leila Ullmann[8], Camila Malossi[8], João Pessoa de Araújo Jr[8], Steven Widen[9], Izabela Maurício de Rezende[2], Érica Mello[10], Carolina Colombelli Pacca[11], Erna Geessien Kroon[2], Giliane Trindade[2], Betânia Drumond[2], Francisco Chiaravalloti-Neto[12], Nikos Vasilakis[13], Mauro M. Teixeira[3] & Maurício Lacerda Nogueira[1]

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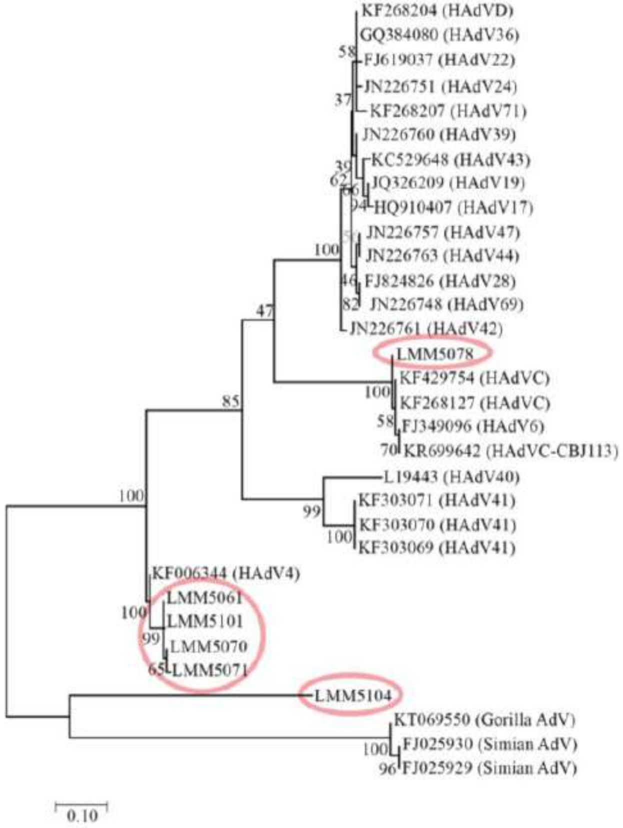
Molecular Detection of Human Adenovirus and Rotavirus in Feces of White-Eared Opossums

Paulo Q. Menezes,[1] Thassiane T. Silva,[1] Fernanda B. Simas,[1] Rodrigo K. Brauner,[1]
Paulo Bandarra,[1] Meriane Demoliner,[2] Ana K. A. Eisen,[2] Paula Rodrigues,[2]
Fernando R. Spilki,[2] Geferson Fischer,[3] and Silvia de O. Hübner[3]



EcoHealth 17, 326–332, 2020
https://doi.org/10.1007/s10393-020-01497-6

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2021 Edition on Covid-19 related research.

The origin, supply chain, and deforestation risk of Brazil's beef exports

Erasmus K. H. J. zu Ermgassen[a,b,1], Javier Godar[c], Michael J. Lathuillière[c], Pernilla Löfgren[c], Toby Gardner[c], André Vasconcelos[d], and Patrick Meyfroidt[a,b]

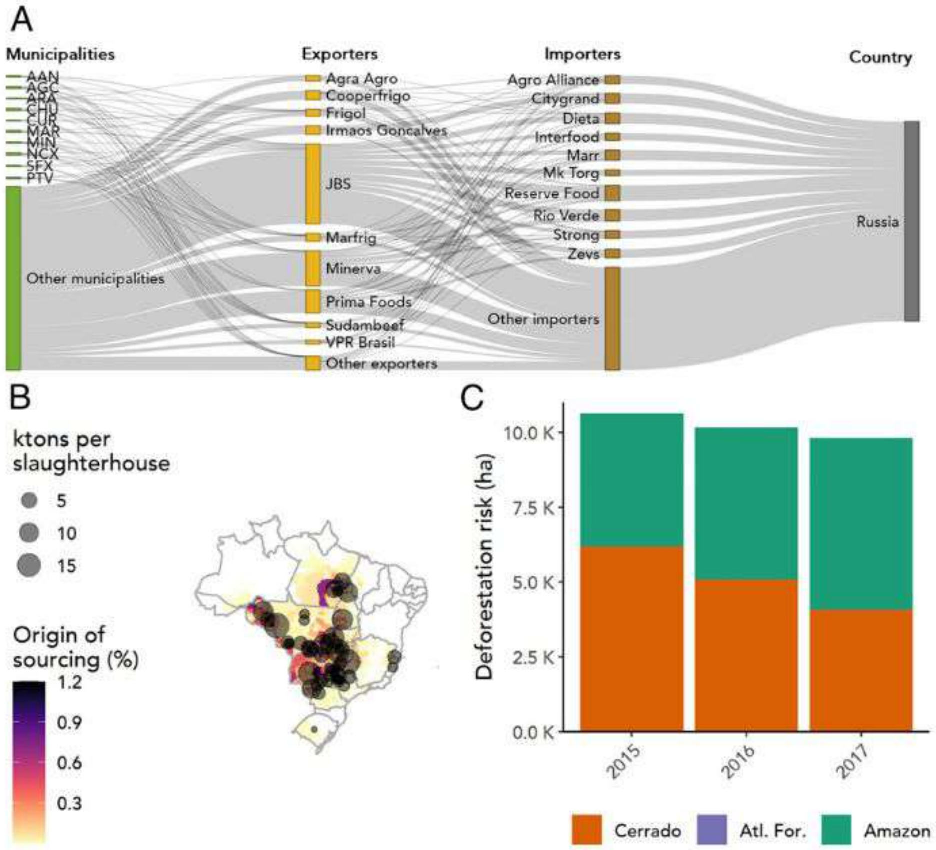

Fig. 1. Example trade flow for Brazilian beef to Russia, the third largest importer between 2015 and 2017. (*A*) The flow of exports in 2015 from municipalities where cattle were raised (shown in green), via intermediary exporting (orange) and importing companies (beige), into Russia (grey). The top 10 actors are displayed in each case. (*B*) The origin of these 2015 exports, per municipality and slaughterhouse (shown as gray circles). (*C*) Supply chain data can be crossed with indicator data, such as deforestation risk, to calculate the risks associated with each actor's sourcing, here shown per biome/year. Abbreviations: AAN, Agua Azul do Norte; AGC, Agua Clara; ARA, Alto Araguaia; CHU, Chupinguaia; CUR, Curionópolis; MAR, Marabá; MIN, Mineiros; NCX, Nova Crixas; SFX, São Felix do Xingu; PTV, Porto Velho; and Atl. For., Atlantic Forest.

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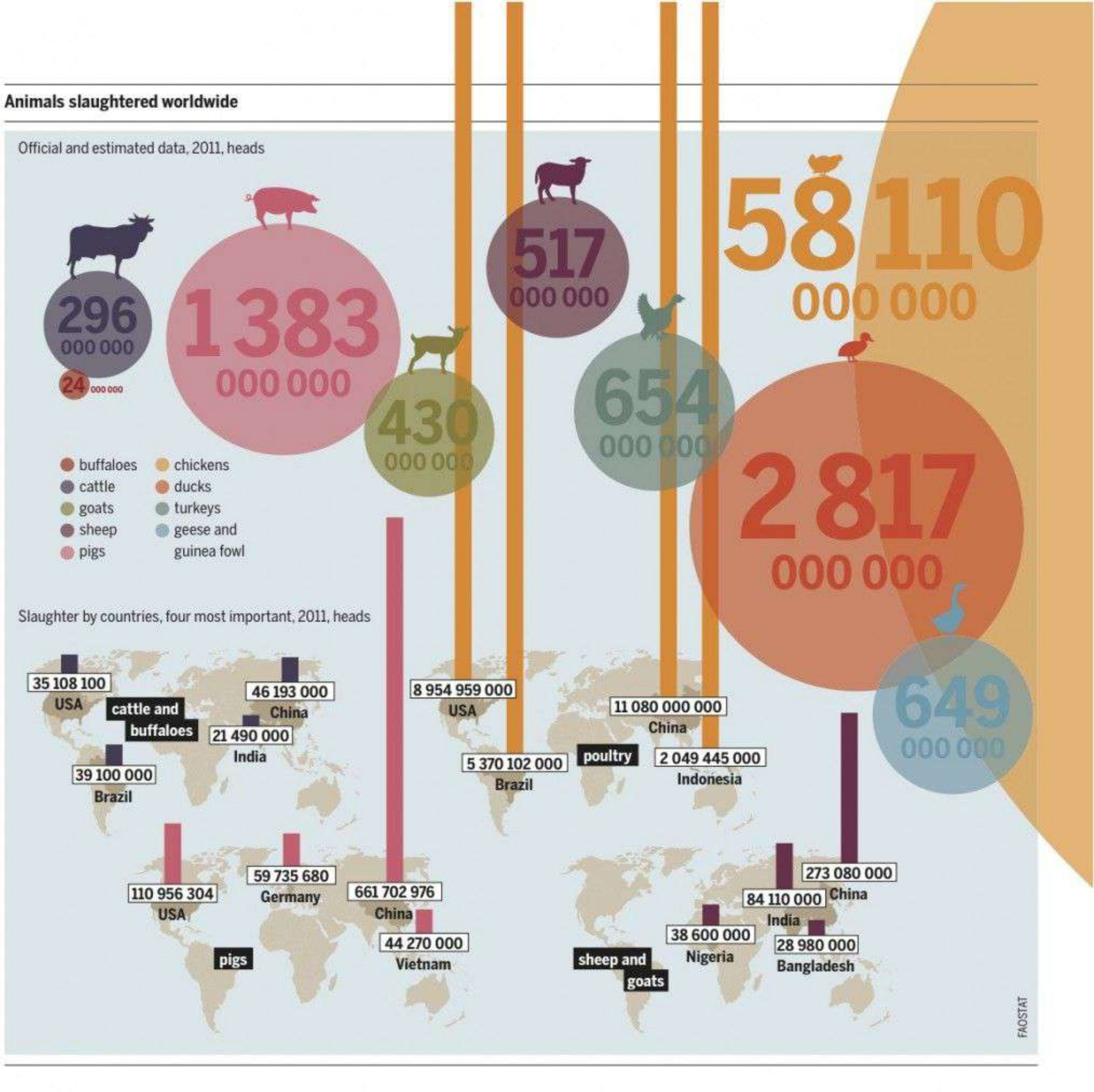

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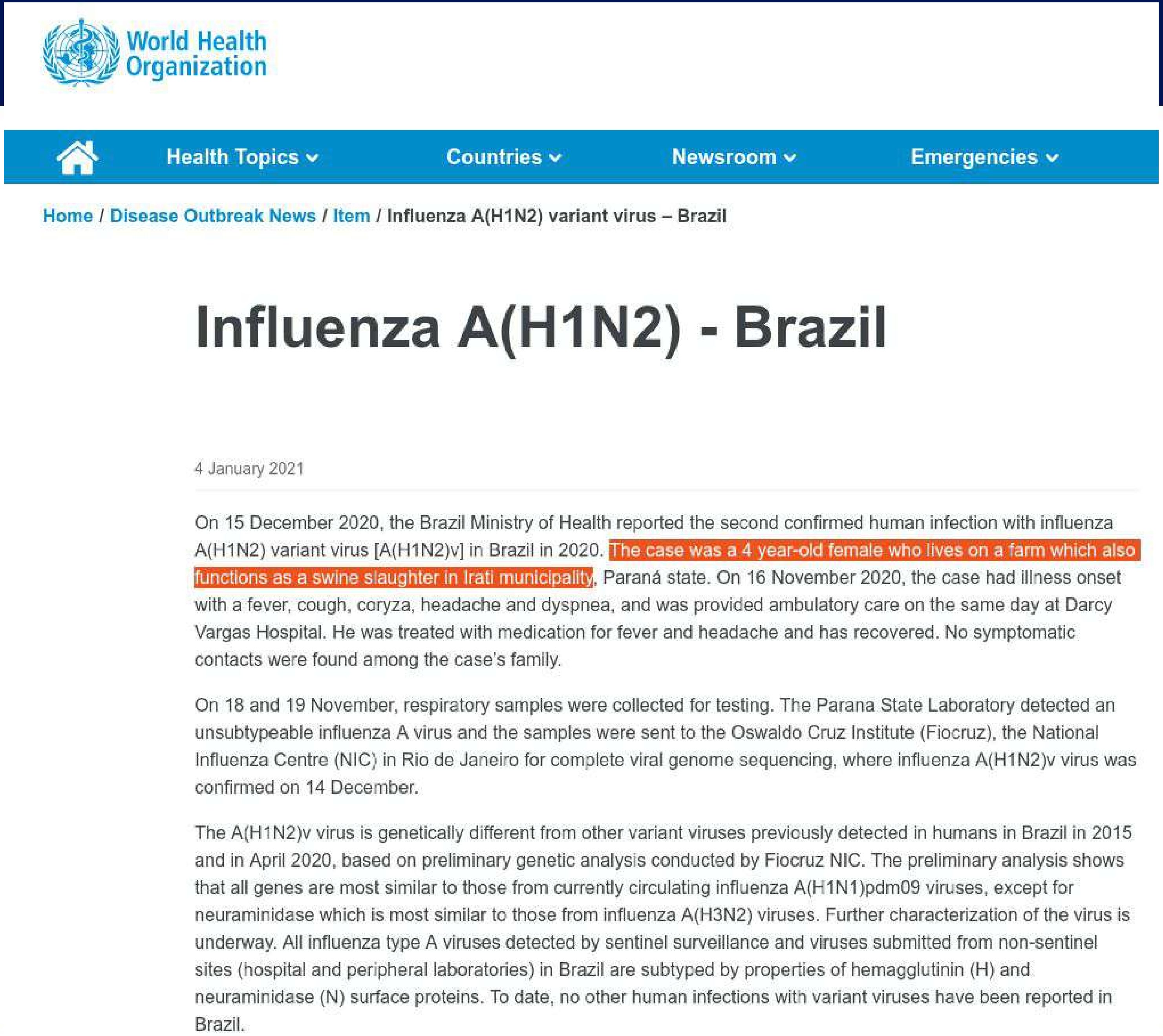


Influenza A(H1N2) - Brazil

4 January 2021

On 15 December 2020, the Brazil Ministry of Health reported the second confirmed human infection with influenza A(H1N2) variant virus [A(H1N2)v] in Brazil in 2020. The case was a 4 year-old female who lives on a farm which also functions as a swine slaughter in Irati municipality, Paraná state. On 16 November 2020, the case had illness onset with a fever, cough, coryza, headache and dyspnea, and was provided ambulatory care on the same day at Darcy Vargas Hospital. He was treated with medication for fever and headache and has recovered. No symptomatic contacts were found among the case's family.

On 18 and 19 November, respiratory samples were collected for testing. The Parana State Laboratory detected an unsubtypeable influenza A virus and the samples were sent to the Oswaldo Cruz Institute (Fiocruz), the National Influenza Centre (NIC) in Rio de Janeiro for complete viral genome sequencing, where influenza A(H1N2)v virus was confirmed on 14 December.

The A(H1N2)v virus is genetically different from other variant viruses previously detected in humans in Brazil in 2015 and in April 2020, based on preliminary genetic analysis conducted by Fiocruz NIC. The preliminary analysis shows that all genes are most similar to those from currently circulating influenza A(H1N1)pdm09 viruses, except for neuraminidase which is most similar to those from influenza A(H3N2) viruses. Further characterization of the virus is underway. All influenza type A viruses detected by sentinel surveillance and viruses submitted from non-sentinel sites (hospital and peripheral laboratories) in Brazil are subtyped by properties of hemagglutinin (H) and neuraminidase (N) surface proteins. To date, no other human infections with variant viruses have been reported in Brazil.

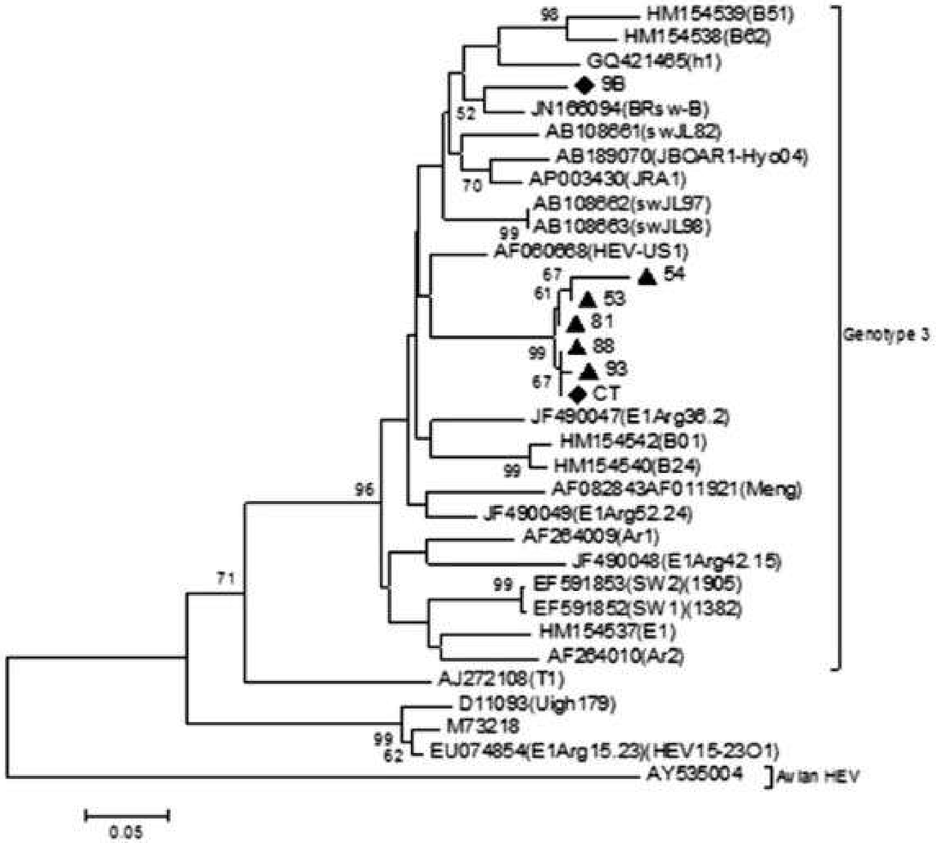
Food Environ Virol (2016) 8:200–205
DOI 10.1007/s12560-016-9243-7

ORIGINAL PAPER

Hepatitis E Virus in Surface Water, Sediments, and Pork Products Marketed in Southern Brazil

F. H. Heldt[1] · R. Staggmeier[1] · J. S. Gularte[1] · M. Demoliner[1] · A. Henzel[1] ·
F. R. Spilki[1]

Fig. 1 Neighbor-joining phylogenetic reconstruction based on partial sequences of the HEV ORF1 gene, showing samples detected in the present study (marked with *black triangles*), compared to reference strains, a control sample, and a recent isolate from Rio Grande do Sul (Vasconcelos et al. 2015; *black diamonds*). A homologous avian HEV sequence was included as an outgroup



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Isolation and characterization of a pandemic H1N1 influenza virus in pigs in Brazil[1]

Rejane Schaefer[2], Janice R.C. Zanella[2], Liana Brentano[2], Amy L. Vincent[3], Giseli A. Ritterbusch[2], Simone Silveira[2], Luizinho Caron[2] and Nelson Mores[2]

ABSTRACT.- Schaefer R., Zanella J.R.C., Brentano L., Vincent A.L., Ritterbusch G.A., Silveira S., Caron L. & Mores N. 2011. **Isolation and characterization of a pandemic H1N1 influenza virus in pigs in Brazil.** *Pesquisa Veterinária Brasileira 31(9):761-767.* Embrapa Swine and Poultry Research Center, BR153, Km110, Vila Tamanduá, Concórdia, SC 89700-000, Brazil. E-mail: rejane@cnpsa.embrapa.br

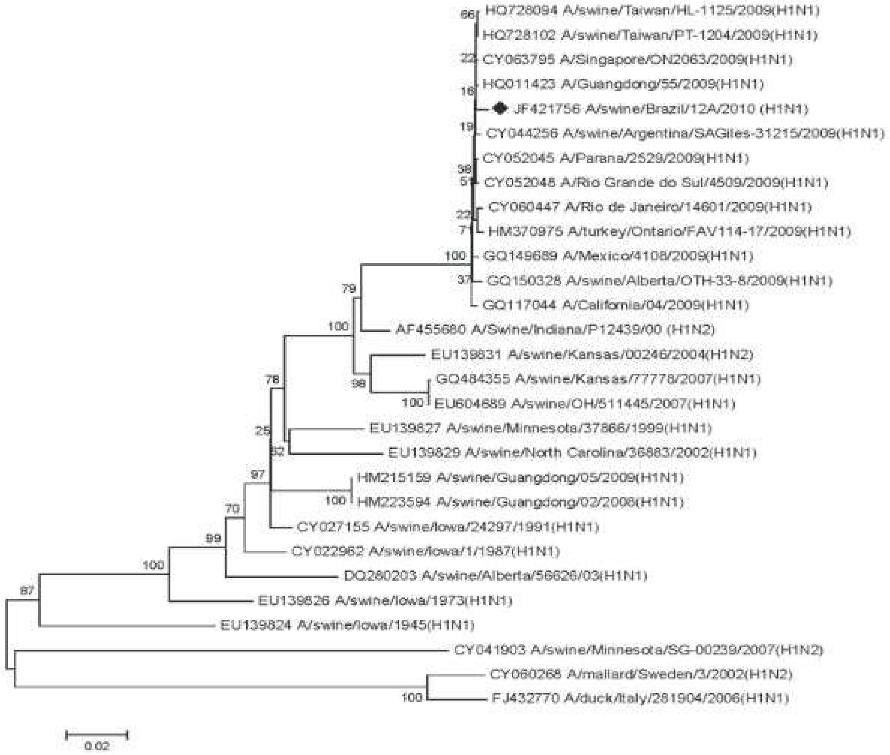

Fig.3. Nucleotide phylogenetic tree of HA gene segment from H1N1 and H1N2 influenza A virus isolates from swine, human and avian origin. The swine influenza viruses were representative from previous and current isolates from North America and Eurasia. Diamond shaped symbol indicate the H1N1 influenza virus isolate sequenced in this study. The tree was inferred using the Neighbor-Joining method.

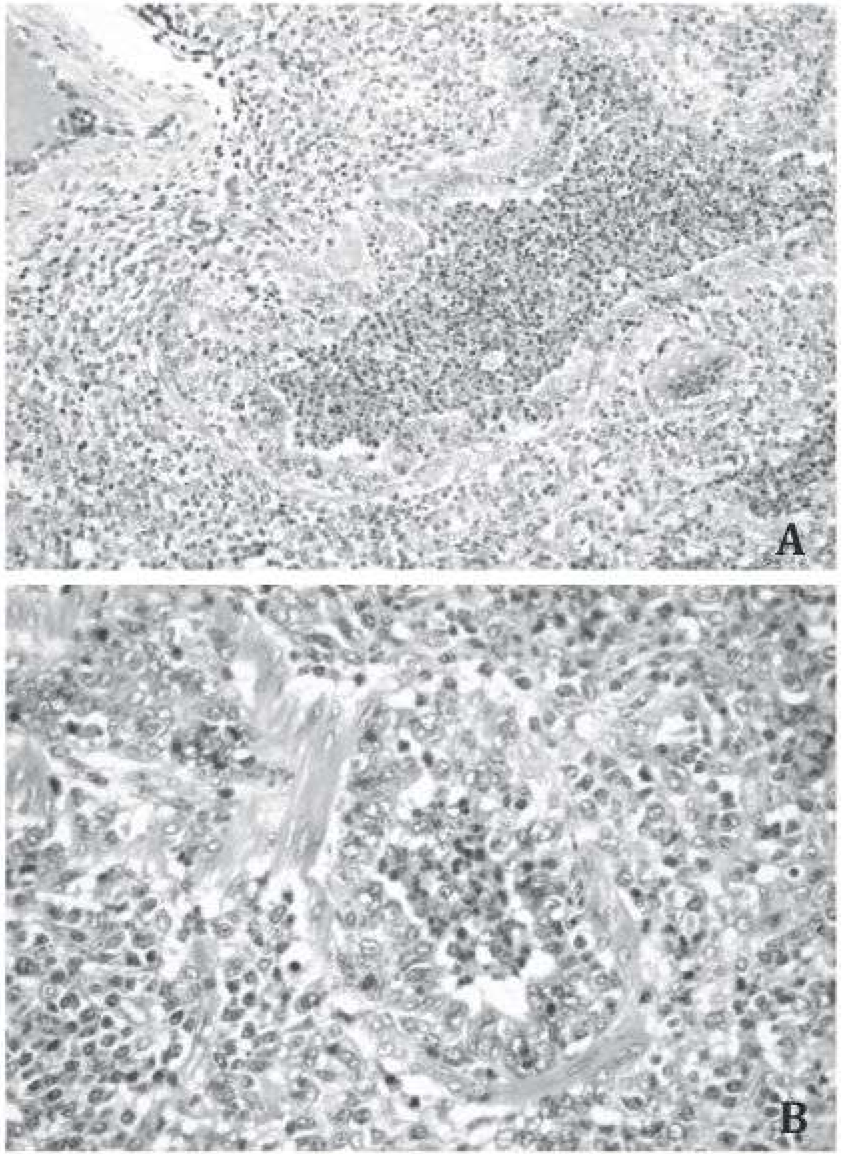

Fig.1. (**A**) Intense inflammatory exudate obliterates the lumen of the bronchiole. The surrounding parenchyma is infiltrated by moderate numbers of lymphocytes. Hematoxylin and eosin. (**B**) Higher magnification of an affected bronchiole. The lumen is infiltrated by numerous neutrophils. Hematoxylin and eosin.


frontiers
in Public Health

ORIGINAL RESEARCH
published: 22 July 2020
doi: 10.3389/fpubh.2020.00318

Using Surveillance of Animal Bite Patients to Decipher Potential Risks of Rabies Exposure From Domestic Animals and Wildlife in Brazil

Julio A. Benavides[1,2,3,4]*, *Jane Megid*[3], *Aline Campos*[5] and *Katie Hampson*[4]

[1] Facultad de Ciencias de la Vida, Universidad Andrés Bello, Santiago, Chile, [2] Centro de Investigación para la Sustentabilidad, Facultad de Ciencias de la Vida, Universidad Andrés Bello, Santiago, Chile, [3] Department of Veterinary Hygiene and Public Health, São Paulo State University, Botucatu, Brazil, [4] Institute of Biodiversity, Animal Health and Comparative Medicine, College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow, United Kingdom, [5] Programa Estadual de Controle e Profilaxia da Raiva, Health Secretary of Rio Grande Do Sul, Porto Alegre, Brazil

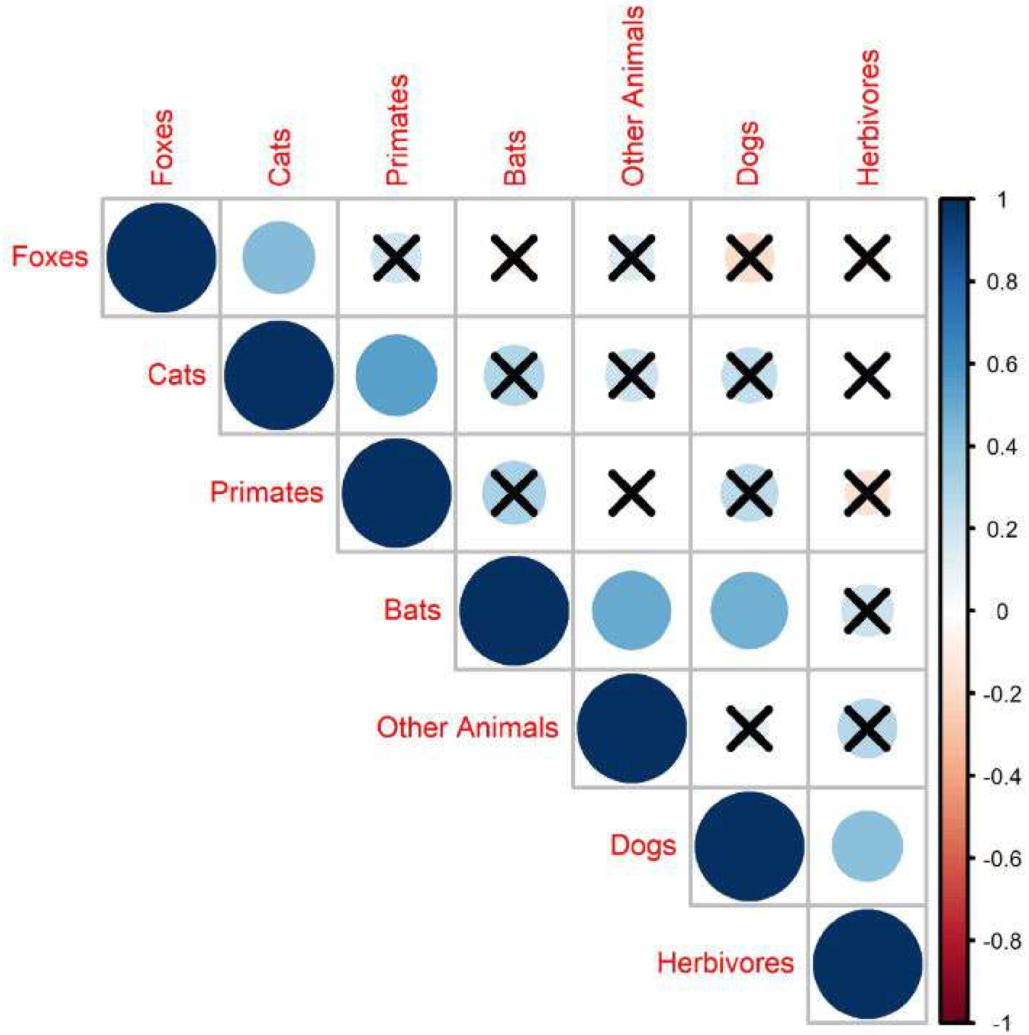

FIGURE 2 | Correlation in bite incidence across states. Circle size is proportional to the value of the Spearman's correlation rho. Blue colors indicate a positive correlation and red colors a negative correlation. Crosses over circles indicate that the relationship was not statistically significant.

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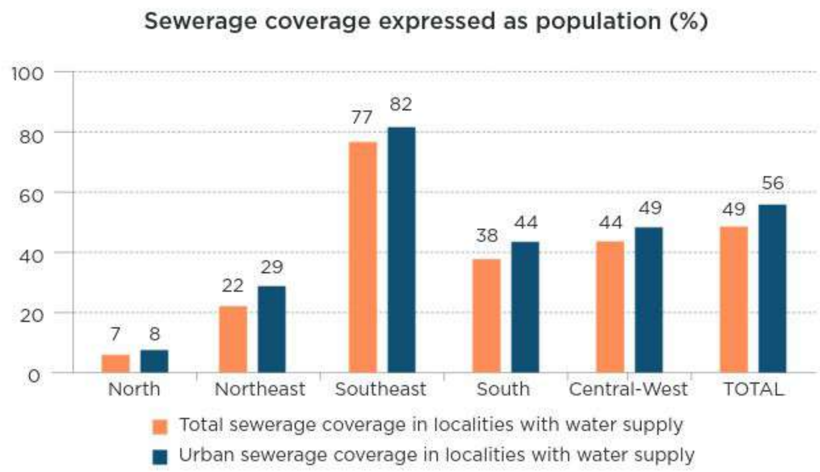
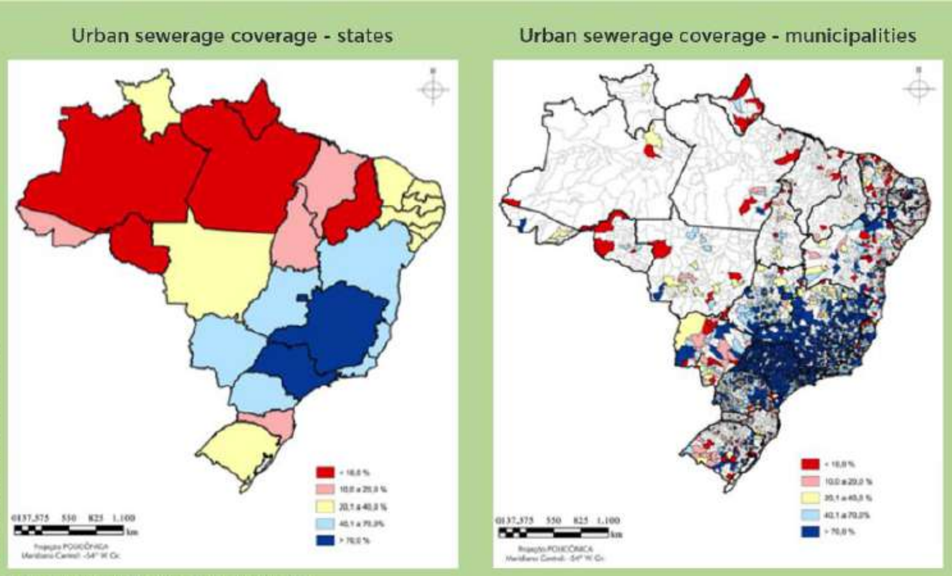
Fig. 9. Percentage of population (total and urban) connected to a sewage collection system, according to region and in Brazil, as a whole, in 2013



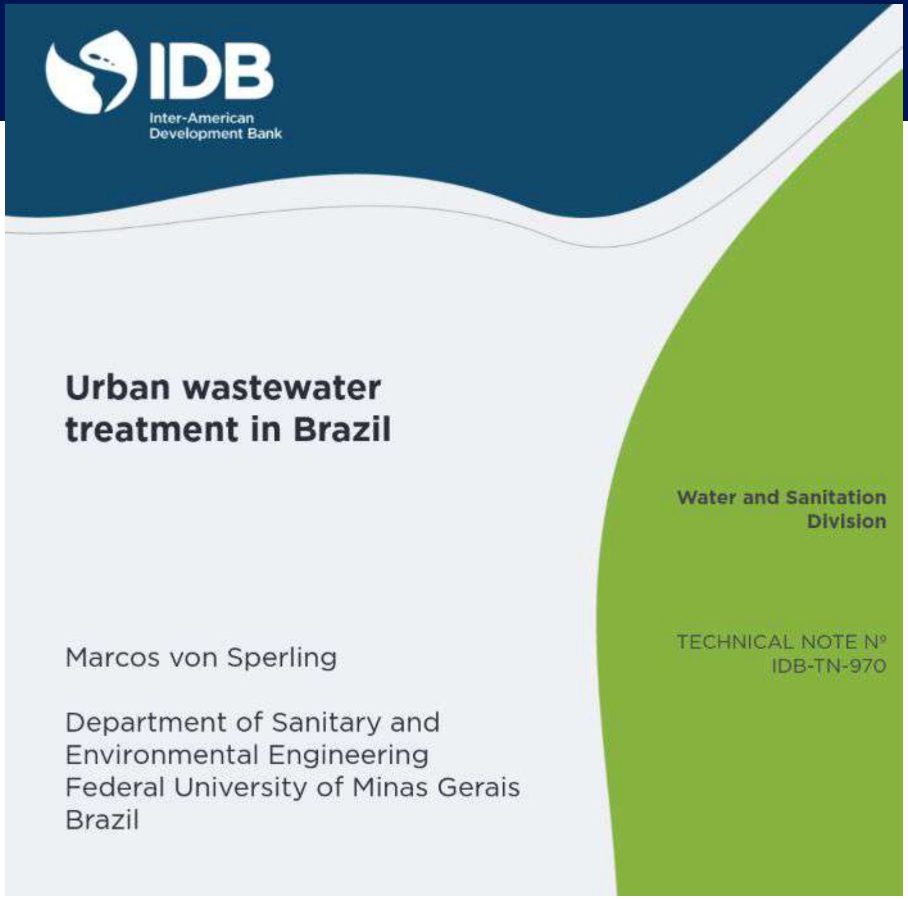
Left bars: total population connected to sewers divided by total population in municipalities that have water supply
Right bars: urban population connected to sewers divided by urban population in municipalities that have water supply

Source: graph made with data from SNIS (2014)

Fig. 10. Percentage of urban population connected to a sewage collection system, according to region and in Brazil, as a whole, in 2013



Top: statistics per state of the federation
Bottom: statistics per municipalities. Municipalities in white: no response to the questionnaires
Source: adapted from SNIS (2014)



Urban wastewater treatment in Brazil

Water and Sanitation Division

TECHNICAL NOTE Nº IDB-TN-970

Marcos von Sperling

Department of Sanitary and Environmental Engineering
Federal University of Minas Gerais
Brazil

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Original Paper | Published: 18 January 2016

Viruses Surveillance Under Different Season Scenarios of the Negro River Basin, Amazonia, Brazil

Carmen Baur Vieira, Adriana de Abreu Corrêa, Michele Silva de Jesus, Sérgio Luiz Bessa Luz, Peter Wyn-Jones, David Kay, Marta Vargha & Marize Pereira Miagostovich

Food and Environmental Virology **8**, 57–69 (2016) | Cite this article

497 Accesses | **27** Citations | Metrics

ELSEVIER

New Microbes and New Infections
Volume 29, May 2019, 100519

Original article

'Don't put your head under water': enteric viruses in Brazilian recreational waters

V. Girardi [1], M. Demoliner [1], J.S. Gularte [1], F.R. Spilki [1]

ELSEVIER

Science of The Total Environment
Volume 586, 15 May 2017, Pages 304-312

Enteric viruses and adenovirus diversity in waters from 2016 Olympic venues

Rodrigo Staggemeier, Tatiana M.S. Heck, Meriane Demoliner, Rute G.F. Ritzel, Nicole M.S. Röhnelt, Viviane Girardi, Carolina A. Venker, Fernando R. Spilki

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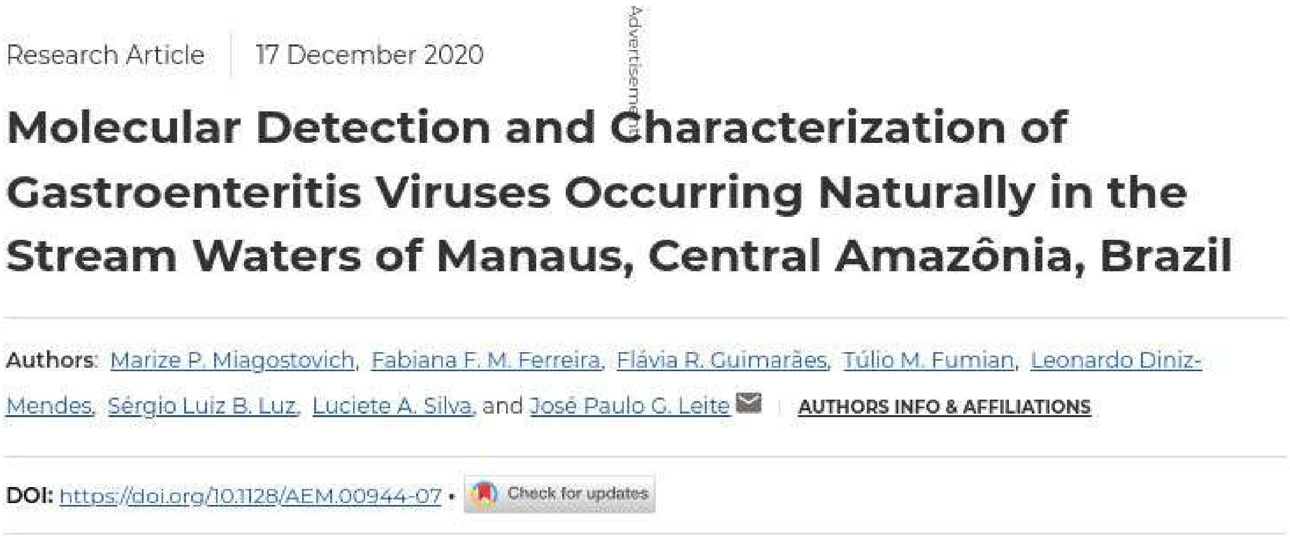


Research Article | 17 December 2020

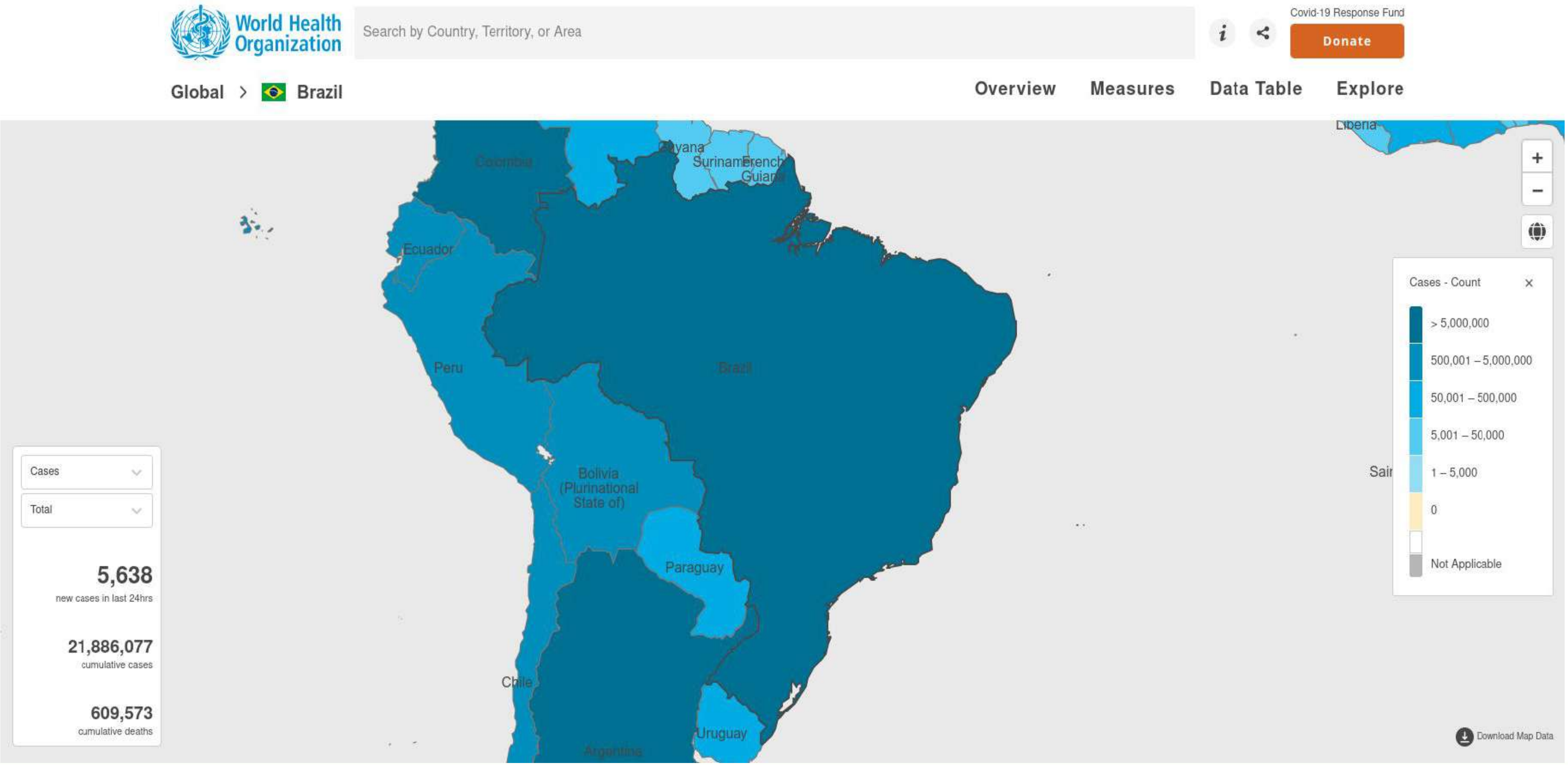
Advertisement

Molecular Detection and Characterization of Gastroenteritis Viruses Occurring Naturally in the Stream Waters of Manaus, Central Amazônia, Brazil

Authors: Marize P. Miagostovich, Fabiana F. M. Ferreira, Flávia R. Guimarães, Túlio M. Fumian, Leonardo Diniz-Mendes, Sérgio Luiz B. Luz, Luciete A. Silva, and José Paulo G. Leite | **AUTHORS INFO & AFFILIATIONS**

DOI: https://doi.org/10.1128/AEM.00944-07 • Check for updates

Covid-19 in Brazil



5,638
new cases in last 24hrs

21,886,077
cumulative cases

609,573
cumulative deaths

Brazilian Network of COVID-19 -omics

Rede Nacional de ômicas de COVID-19

para identificação de fatores associados à dispersão da epidemia e severidade.

RedeVírus MCTI

CORONA-ÔMICA BR

BIG DATA
INTELIGÊNCIA ARTIFICIAL

BANCO DE DADOS

TRIAGEM DE AMOSTRAS

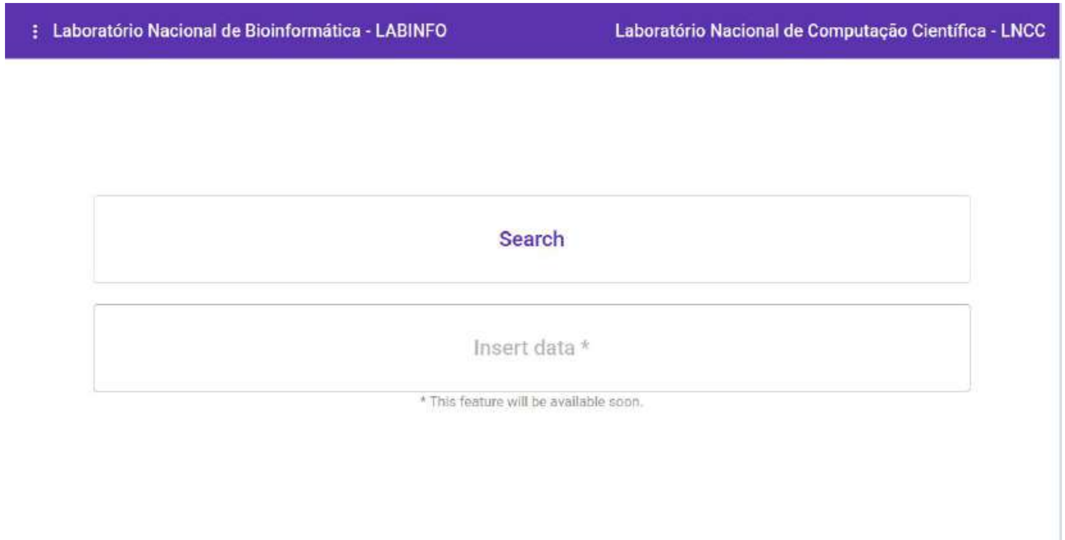
CENTROS DE GENÔMICA

SEQUENCIAMENTO

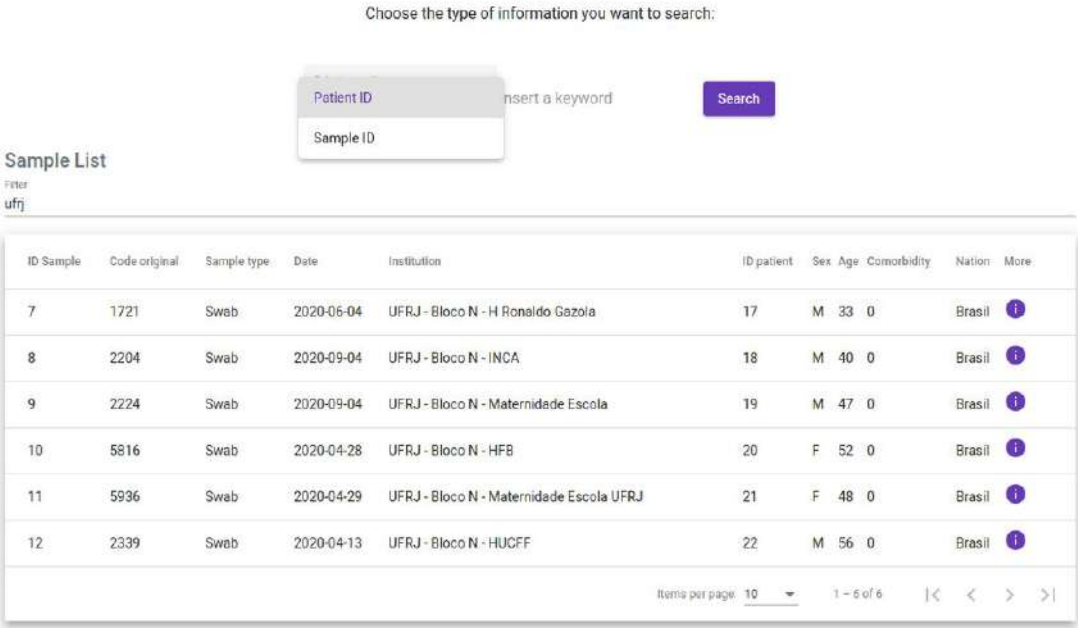
- Genômica Viral
- Metagenômica
- Exoma
- Transcriptomica

RedeVírus MCTI

Clinical data x genomics data



* This feature will be available soon.


Choose the type of information you want to search:

Sample List

Filter: ufrj

ID Sample	Code original	Sample type	Date	Institution	ID patient	Sex	Age	Comorbidity	Nation	More
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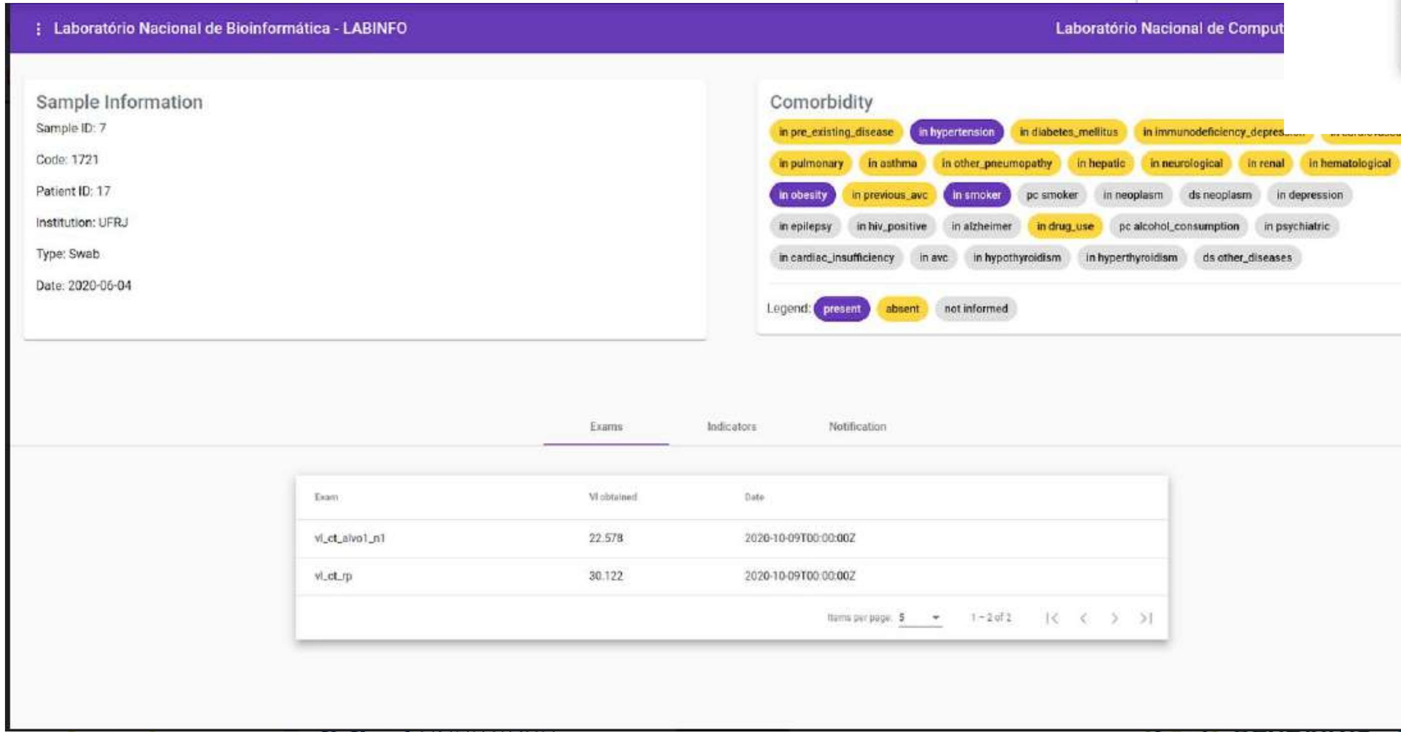
8	2204	Swab	2020-09-04	UFRJ - Bloco N - INCA	18	M	40	0	Brasil	●
9	2224	Swab	2020-09-04	UFRJ - Bloco N - Maternidade Escola	19	M	47	0	Brasil	●
10	5816	Swab	2020-04-28	UFRJ - Bloco N - HFB	20	F	52	0	Brasil	●
11	5936	Swab	2020-04-29	UFRJ - Bloco N - Maternidade Escola UFRJ	21	F	48	0	Brasil	●
12	2339	Swab	2020-04-13	UFRJ - Bloco N - HUCFF	22	M	56	0	Brasil	●

Items per page: 10 1 – 6 of 6



Sample Information

Sample ID: 7

Code: 1721

Patient ID: 17

Institution: UFRJ

Type: Swab

Date: 2020-06-04

Comorbidity

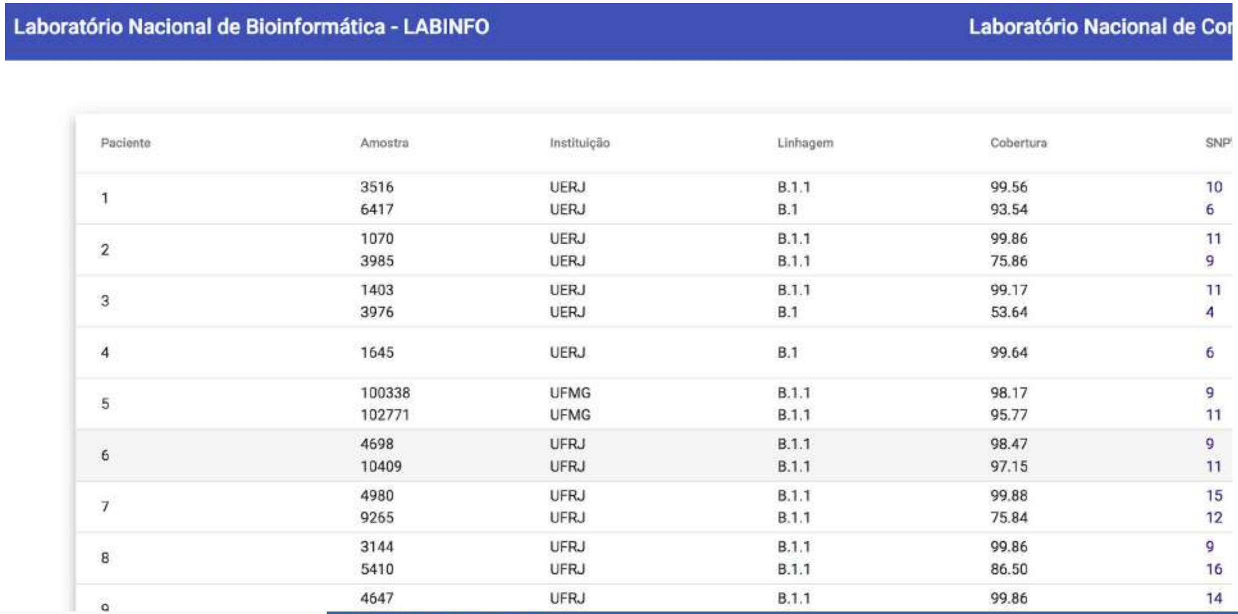
in pre_existing_disease · in hypertension · in diabetes_mellitus · in immunodeficiency_depres… · in pulmonary · in asthma · in other_pneumopathy · in hepatic · in neurological · in renal · in hematological · in obesity · in previous_avc · in smoker · pc smoker · in neoplasm · ds neoplasm · in depression · in epilepsy · in hiv_positive · in alzheimer · in drug_use · pc alcohol_consumption · in psychiatric · in cardiac_insufficiency · in avc · in hypothyroidism · in hyperthyroidism · ds other_diseases

Legend: present · absent · not informed

Exam	Vl obtained	Date
vl_ct_alvo1_n1	22.578	2020-10-09T00:00:00Z
vl_ct_rp	30.122	2020-10-09T00:00:00Z

Items per page: 5 1 – 2 of 2

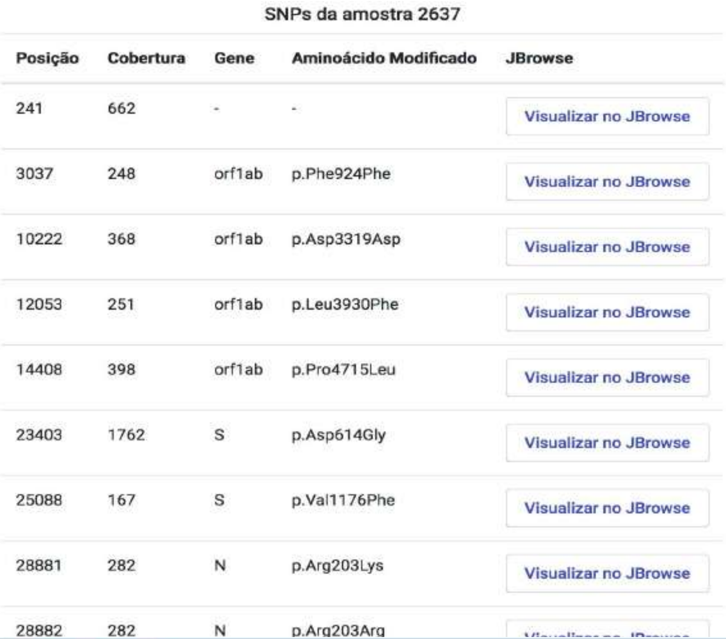
Variant analysis



Laboratório Nacional de Bioinformática - LABINFO

Laboratório Nacional de Cor

Paciente	Amostra	Instituição	Linhagem	Cobertura	SNP
1	3516 6417	UERJ UERJ	B.1.1 B.1	99.56 93.54	10 6
2	1070 3985	UERJ UERJ	B.1.1 B.1.1	99.86 75.86	11 9
3	1403 3976	UERJ UERJ	B.1.1 B.1	99.17 53.64	11 4
4	1645	UERJ	B.1	99.64	6
5	100338 102771	UFMG UFMG	B.1.1 B.1.1	98.17 95.77	9 11
6	4698 10409	UFRJ UFRJ	B.1.1 B.1.1	98.47 97.15	9 11
7	4980 9265	UFRJ UFRJ	B.1.1 B.1.1	99.88 75.84	15 12
8	3144 5410	UFRJ UFRJ	B.1.1 B.1.1	99.86 86.50	9 16
9	4647	UFRJ	B.1.1	99.86	14

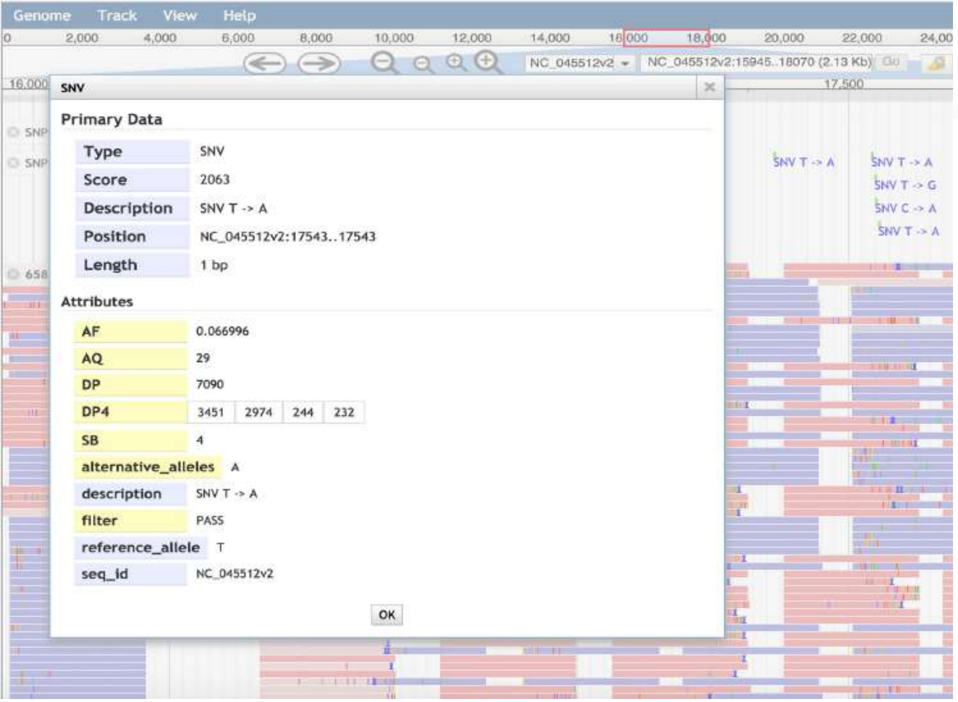


SNPs da amostra 2637

Posição	Cobertura	Gene	Aminoácido Modificado	JBrowse
241	662	-	-	Visualizar no JBrowse
3037	248	orf1ab	p.Phe924Phe	Visualizar no JBrowse
10222	368	orf1ab	p.Asp3319Asp	Visualizar no JBrowse
12053	251	orf1ab	p.Leu3930Phe	Visualizar no JBrowse
14408	398	orf1ab	p.Pro4715Leu	Visualizar no JBrowse
23403	1762	S	p.Asp614Gly	Visualizar no JBrowse
25088	167	S	p.Val1176Phe	Visualizar no JBrowse
28881	282	N	p.Arg203Lys	Visualizar no JBrowse
28882	282	N	p.Arg203Arg	Visualizar no JBrowse

Available Tracks

☑ SNPs 3517
☑ SNPs 6585
☑ SNPs Low Freq 3517
☑ SNPs Low Freq 6585
☐ 3517
☑ 3517 Coverage
☐ 6585
☑ 6585 Coverage
☑ Reference



SNV

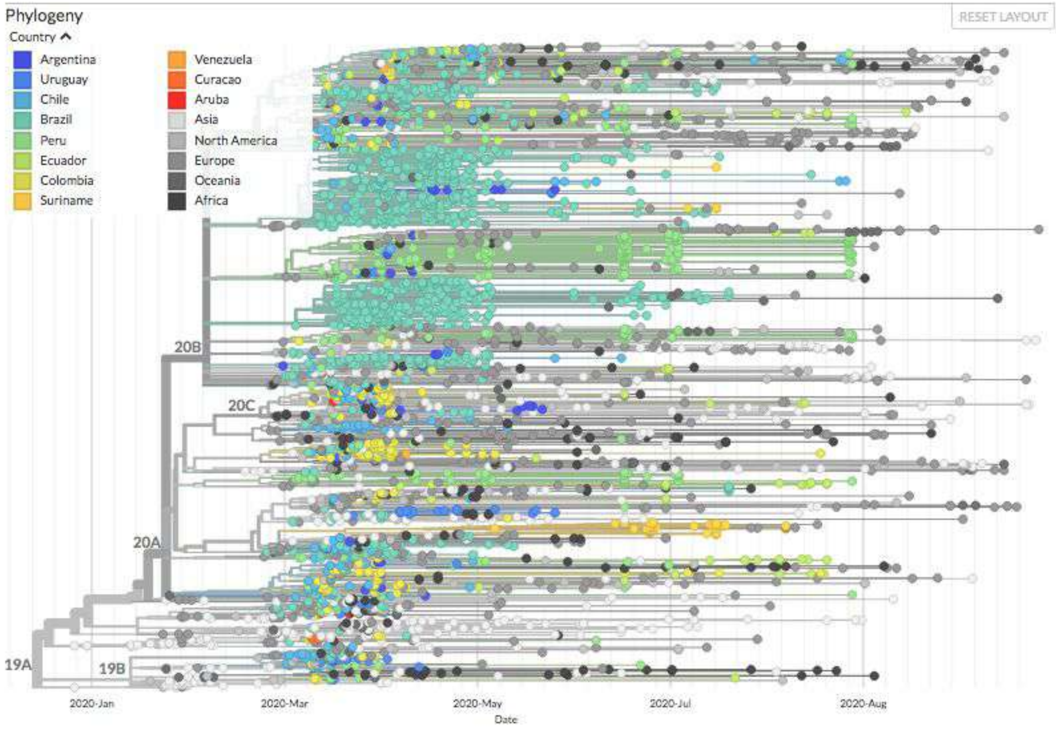
Primary Data

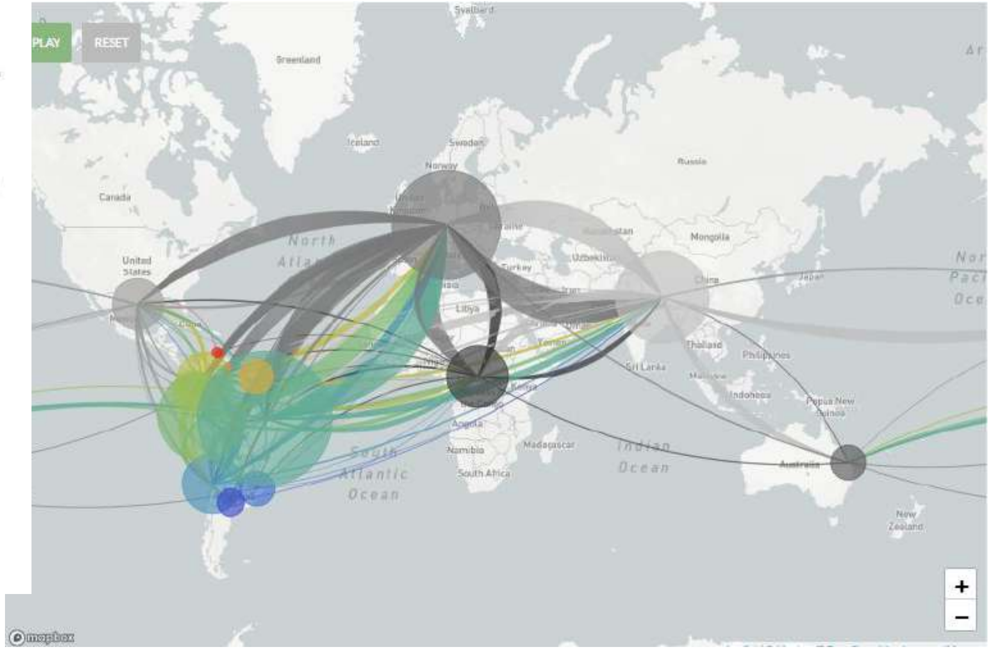
Type	SNV
Score	2063
Description	SNV T -> A
Position	NC_045512v2:17543..17543
Length	1 bp

Attributes

AF	0.066996
AQ	29
DP	7090
DP4	3451 2974 244 232
SB	4
alternative_alleles	A
description	SNV T -> A
filter	PASS
reference_allele	T
seq_id	NC_045512v2

Publicly Available Information





www.corona-omica.br-mcti.lncc.br/resultados

Other activities

- Continued efforts for sequencing, surveillance of the emergence and spread of variants
- Molecular modelling RBD
- *In vitro* studies > neutralization by sera convalescent and vaccinated individuals
- *In vivo* studies > animal models
- Patients -*omics* studies
- Generation of revertant clones
- Expansion of the Network and capacity building

RedeVírus MCTI Corona-ômica BR MCTI

National network of epidemiological surveillance of coronavirus SARS-CoV-2 and other emerging pathogens in bats, birds and other forest reservoirs in the context of *One Health*

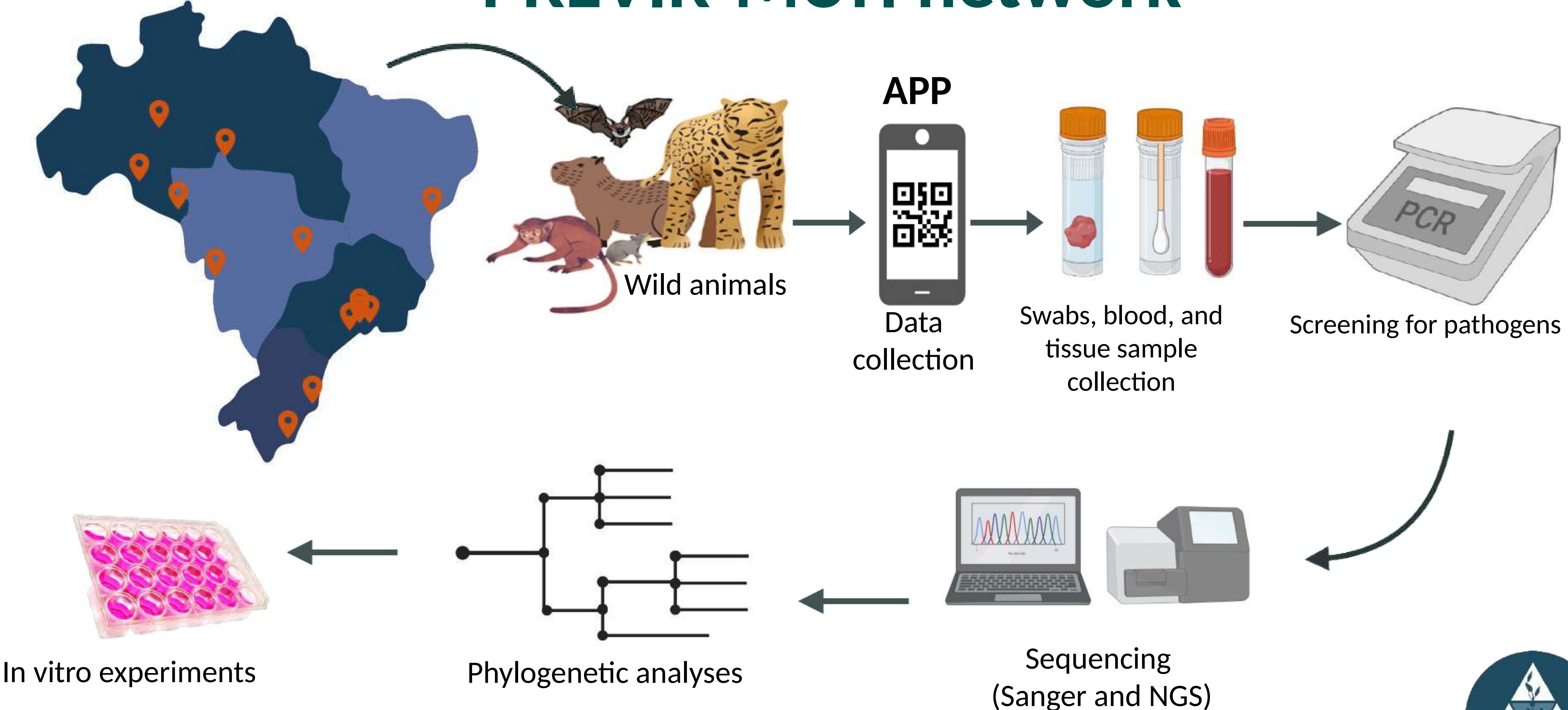
This project works to achieve the following UN SDGs:

RedeVírus MCTI

PREVIR MCTI

- Coordinators: Clarice Weis Arns (IB-UNICAMP), Edison Luiz Durigon (ICB-USP), Helena Lage Ferreira (FZEA-USP)

PREVIR-MCTI network



Wild animals

APP

Data collection

Swabs, blood, and tissue sample collection

Screening for pathogens

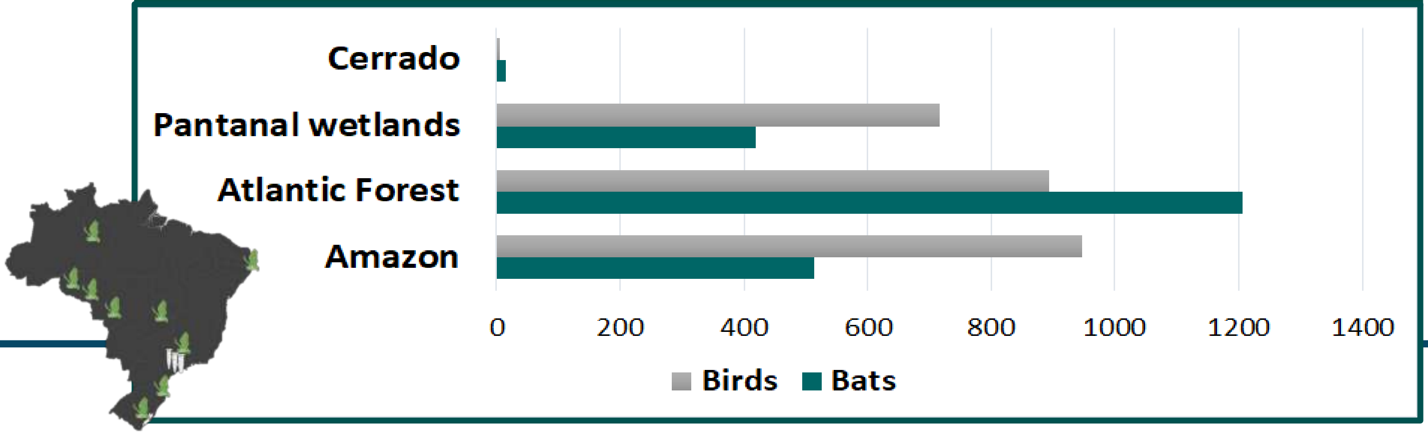
Sequencing (Sanger and NGS)

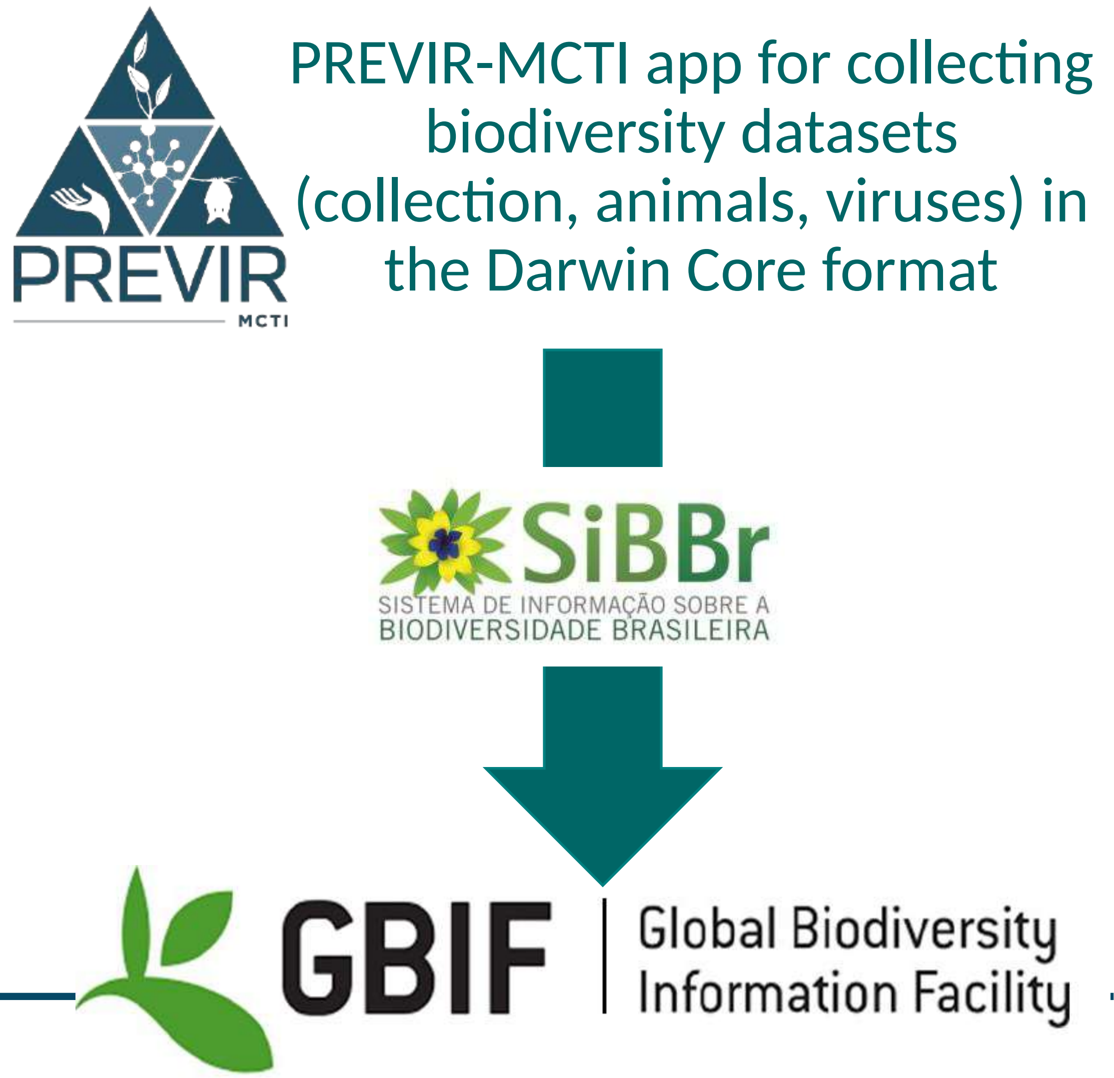
Phylogenetic analyses

In vitro experiments

Ecosurveillance of viruses in wild animals from Brazilian domains (Amazon, Atlantic Forest, Cerrado, and Pantanal wetlands)

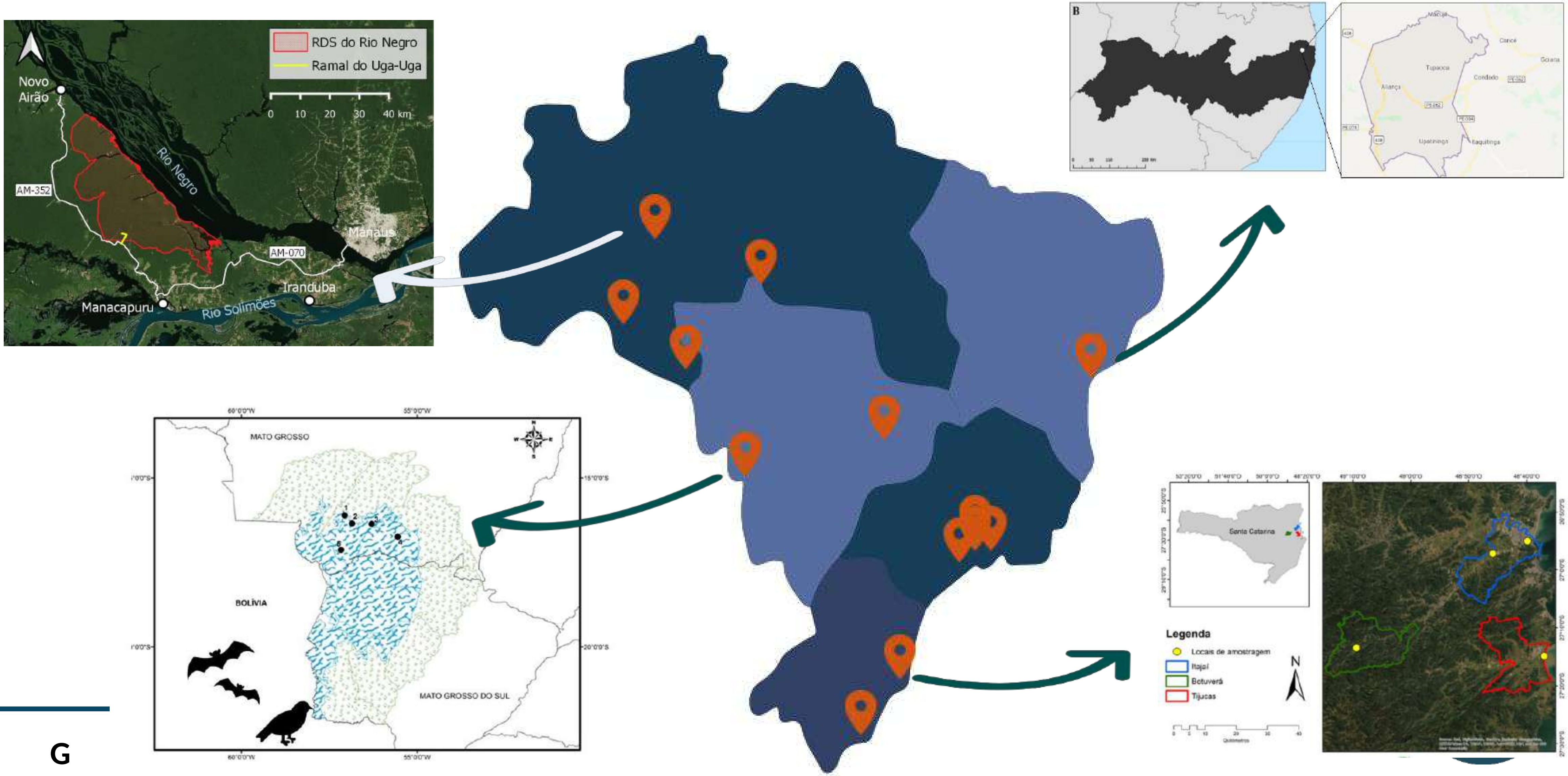
2153 bats and 2562 birds sampled from 11/2020 to 10/2021





PREVIR-MCTI app for collecting biodiversity datasets (collection, animals, viruses) in the Darwin Core format

Where are we?


RDS do Rio Negro
Ramal do Uga-Uga
0 10 20 30 40 km
Novo Airão
AM-352
Rio Negro
Manaus
AM-070
Iranduba
Manacapuru
Rio Solimões
B
0 50 110 220 km
Macuje
Camcé
Goiana
Tupaoca
Condado
Aliança
PE 062
PE 052
PE 034
PE 074
408
Upatininga
Itaquitinga
60°0'0"W
55°0'0"W
MATO GROSSO
15°0'0"S
20°0'0"S
BOLÍVIA
MATO GROSSO DO SUL
1
2
3
4
5
52°20'0"O
51°40'0"O
50°0'0"O
48°20'0"O
49°10'0"O
48°0'0"O
48°50'0"O
48°40'0"O
Santa Catarina
Legenda
Locais de amostragem
Itajaí
Botuverá
Tijucas
N
0 5 10 20 30 40
Quilômetros

Alphacoronaviruses detected in 46 samples from seven bat species collected in Atlantic forest *

545 tested swab samples

PE
Aliança


Sturnira lillium
(n=7)


Carollia perspicillata
(n=10)


Artibeus lituratus
(n=1)


Phyllostomus discolor
(n=16)


P. hastatus
(n=01)


Dermanura cinerea
(n=01)

SP
São Lourenço da Serra


Sturnira lillium
(n=3)


Diphylla ecaudata
(n=1)

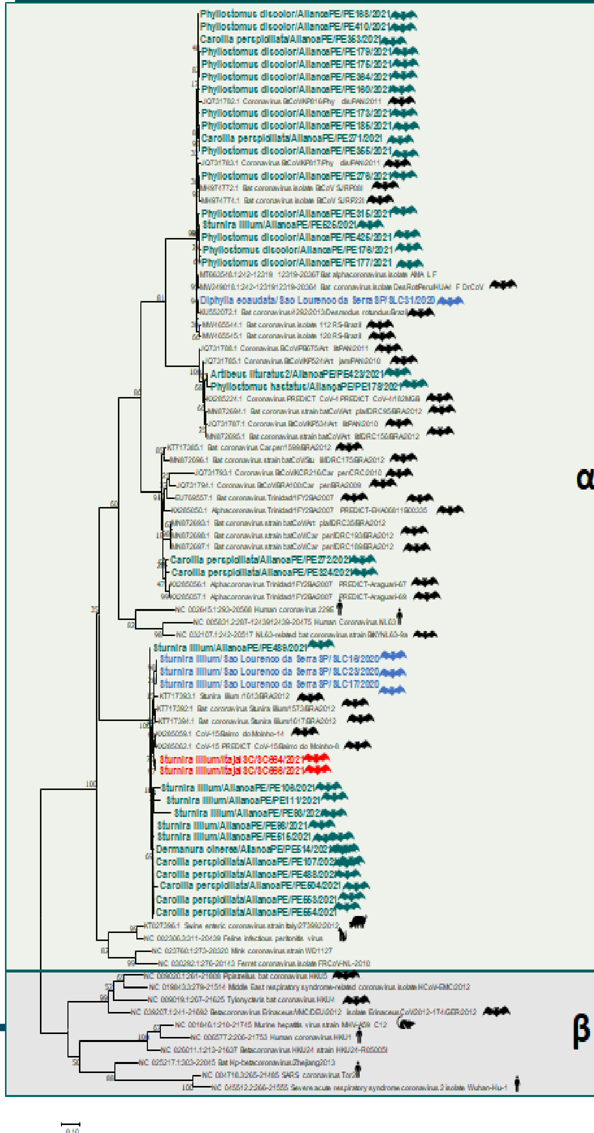
Hematophagous (vampire) bat

SC


Sturnira lillium
(n=3)


Artibeus lituratus
(n=3)

High diversity of alphacoronaviruses in bats



AUSTRALIA - BRAZIL

VIRTUAL RESEARCH COLLABORATION

2021 Edition on Covid-19 related research.

THANK YOU / OBRIGADO

INSTITUTIONAL SUPPORTER:

Programa Diplomacia Inovação

CO-ORGANIZATION:

Australian Academy of Science

105 anos ACADEMIA BRASILEIRA DE CIÊNCIAS

ORGANIZATION:

Australian Government
Department of Education, Skills and Employment

CONFAP

15 Anos