SARS-CoV-2 Genomic Surveillance in Brazil

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Real-time virus genome sequencing: maximizing public health impact

**Effective genomic surveillance requires** high quality samples and metadata and substantial investment in terms of staff, equipment, reagents, bioinformatic infrastructure, and effective collaboration between scientific community and stakeholders.

**Untargeted sequencing**  
Pathogen identification, understand origins of viral outbreaks  
Metagenomics human and non-human samples

**Targeted sequencing**  
Design of diagnostics, therapeutics, phenotypic changes (e.g., Alpha, Omicron)  
Targeted sequencing of Δ69–70, extensive experimental work  
Investigate transmission clusters & complement epi (e.g., outbreaks in hospitals, travelers)  
Non-random, dense cluster & community sequencing

**Population sequencing**  
Large-scale patterns, drivers and assess detection (e.g., $R$, pop size, dispersal patterns)  
Random population (representativity) sequencing

Adapted from WHO SARS-CoV-2 Sequencing Guidelines 2021 (courtesy of Nuno Faria)
Disparities in SARS-CoV-2 global genomic surveillance

Turn around time and number of sequences are important to detect new variants in real time.

ITpS (Instituto Todos pela Saúde)

**Instituto Todos pela Saúde (ITpS)** is a non-profit organization created in Feb 2021.

**Objective** – Collaborate in the development of an epidemiological surveillance system to prepare Brazil to face future outbreaks.

Articulate networks to obtain relevant scientific information to help the country in public health decision-making.

Website: [https://www.itps.org.br](https://www.itps.org.br) | Coordinator: Jorge Kalil | Initial Funding: Itau Bank
Evolution of the number of SARS-CoV-2 genomes in Brazil

- Over 183,000 complete genome sequences (15 Oct’22)
- Over 34.6 million reported cases (0.53% sequenced)
- 54 days from sample collection to GISAID deposition

Anderson Brito et al. *Nature Communications* 2022 | Courtesy Anderson Brito ITPS
Epidemic virus: Number of full-length genome from Brazil

<table>
<thead>
<tr>
<th>Virus</th>
<th>No. Brazil Genomes in GenBank or GiSAID</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yellow fever</td>
<td>195</td>
</tr>
<tr>
<td>Dengue 1-4</td>
<td>281</td>
</tr>
<tr>
<td>St. Louis encephalitis virus</td>
<td>1</td>
</tr>
<tr>
<td>West Nile</td>
<td>5</td>
</tr>
<tr>
<td>Zika</td>
<td>76</td>
</tr>
<tr>
<td>Mayaro virus</td>
<td>24</td>
</tr>
<tr>
<td>Venezuelan equine encephalitis virus</td>
<td>0</td>
</tr>
<tr>
<td>Chikungunya</td>
<td>78</td>
</tr>
<tr>
<td>Influenza</td>
<td>1182</td>
</tr>
</tbody>
</table>

Nuno Faria & Darlan Candido Imperial College
Heterogeneity in sequencing platforms used

ONT Nanopore

Ion Torrent

Illumina

Anderson Brito et al. *Nature Communications* 2022 | Courtesy Anderson Brito ITPS
(1) Brazil-UK CADDE Research Collaboration

Coordinators: Ester Sabino and Nuno Faria | Website: caddecenter.org | Funding: FAPESP and Medical Research Council
COVID-19 in Amazonas, Brazil, was driven by the persistence of endemic lineages and P.1 emergence


(2) FioCruz Genomic Network

Coordinators: Marilda Siqueira | Website: https://www.genomahcov.fiocruz.br/a-rede | Funding: Brazilian Ministry of Health
(3) CoronaOmica Network

CoronaOmica BR
MCTI

1. Universidade Federal de Santa Maria – RS
2. Universidade Federal de Santa Catarina – SC
3. Instituto de Medicina do Rio Grande do Sul – RS
4. Universidade Federal do Rio de Janeiro – RJ
5. Universidade Federal do Rio Grande do Sul – RS
6. Universidade Federal de Minas Gerais – MG
7. Universidade Federal de Pernambuco – PE
8. Instituto Nacional de Pesquisas da Amazônia – AM
9. Instituto Federal de Educação, Ciência e Tecnologia de Minas Gerais – MG
10. Instituto Federal de Educação, Ciência e Tecnologia de Goiás – GO
11. Instituto Federal de Educação, Ciência e Tecnologia de Pernambuco – PE
12. Instituto Federal de Educação, Ciência e Tecnologia de Alagoas – AL
13. Instituto Federal de Educação, Ciência e Tecnologia de Bahia – BA
14. Instituto Federal de Educação, Ciência e Tecnologia de Alagoas – AL
15. Instituto Federal de Educação, Ciência e Tecnologia de Alagoas – AL
16. Instituto Federal de Educação, Ciência e Tecnologia de Alagoas – AL
17. Instituto Federal de Educação, Ciência e Tecnologia de Alagoas – AL

Funding: Brazilian Ministry of Science and Technology

 Coordinates: Fernado Spilki | Website: http://www.corona-omica.rj.lncc.br/
Genomic epidemiology of the SARS-CoV-2 epidemic in Brazil

The high numbers of COVID-19 cases and deaths in Brazil have made Latin America an epicentre of the pandemic. SARS-CoV-2 established sustained transmission in Brazil early in the pandemic, but important gaps remain in our understanding of virus transmission dynamics at a national scale. We use 15,215 near-complete genomes sampled from 27 Brazilian states and bordering country Paraguay. From March to November 2020, we detected co-circulation of multiple viral lineages that were linked to multiple importations (predominantly from Europe). After November 2020, we detected large, local transmission clusters within the country. In the absence of effective restriction measures, the epidemic progressed, and in January 2021 there was emergence and onward spread, both within and abroad, of variants of concern and variants under monitoring, including Gamma (P.1) and Zeta (P.2). We also characterized a genomic overview of the epidemic in Paraguay and detected evidence of importation of SARS-CoV-2 ancestor lineages and variants of concern from Brazil. Our findings show that genomic surveillance in Brazil enabled assessment of the real-time spread of emerging SARS-CoV-2 variants.
(5) Seq-BR – Magalu & Mulheres do Brasil

- Designed in May 2021
- First Phase: Training between March and September 2022
- Second Phase (ongoing): 100 seq/month/Brazilian State Capital performed locally
- Third Phase: wastewater sewage genomic surveillance

Participating states, no. sequences

No. SARS-CoV-2 sequences per state

Coordinators: Ester Sabino and Jaqueline Goes | Funding: Magalu
(6) Genov Network

- Convenient residual diagnostic samples from large private laboratory network

<table>
<thead>
<tr>
<th>Brazilian Region</th>
<th>No. (GISAID, 15 Sep 2022)</th>
<th>% cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>SOUTH</td>
<td>2,912</td>
<td>16.8</td>
</tr>
<tr>
<td>SOUTHEAST</td>
<td>3,463</td>
<td>20.0</td>
</tr>
<tr>
<td>MID-WEST</td>
<td>2,461</td>
<td>14.2</td>
</tr>
<tr>
<td>NORTHEAST</td>
<td>1,884</td>
<td>10.9</td>
</tr>
<tr>
<td>NORTH</td>
<td>147</td>
<td>0.8</td>
</tr>
<tr>
<td>SÃO PAULO CITY</td>
<td>3,716</td>
<td>21.4</td>
</tr>
<tr>
<td>RIO DE JANEIRO CITY</td>
<td>2,763</td>
<td>15.9</td>
</tr>
<tr>
<td><strong>TOTAL</strong></td>
<td><strong>17,346</strong></td>
<td><strong>100</strong></td>
</tr>
</tbody>
</table>
How to improve turn around time?

Data from private laboratories

Turn around time: 7 days

Data from ThermoFischer PCR: SGTF vs SGTP

Data from all results: PCR+ rate
ITpS (Instituto Todos pela Saúde)

Monitoramento da variante Ómicron
(de 01/05/2022 a 29/10/2022)

Relatório 22
Semana de 23/10 a 29/10
Taxa de positividade: 17%

Caso com perfil SxIF (Ómicron BA.4/BA.5 e subunidades) por semana, desde 15/05/2022 (RT-PCR Thermo Fisher)

Porte de dosagem

Monitoramento de patógenos respiratórios
(de 01/02/2022 a 15/10/2022)

Positividade de testes para COVID-19
(de 01/05/2022 a 29/10/2022)

Website: https://www.itps.org.br | Coordinator: Jorge Kalil | Initial Funding: Itaú Bank
Conclusions

• Brazil has dramatically expanded the capacity to perform SARS-CoV-2 full-length genome sequencing across the country through state and private funding initiatives.
• Genomic diversity of other epidemic viruses remains poorly understood.
• Median: 54 days - date of collection to submission to GISAID.
• Still a long delay between sample collection, sequence and information to the public for SARS-CoV-2, but even longer for other viruses.
• Need to organize the several initiatives to improve cost/effectiveness and sustainability of targeted and untargeted (metagenomic) virus sequencing.