

Session 3: Genomic surveillance

Portugal - on the experience for SARS-CoV-2 and influenza

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National Reference Laboratory for Influenza and Other Respiratory Viruses INSA

8th Joint WHO Europe & ECDC Annual European Influenza and COVID-19 Surveillance Meeting 5-7 October 2022







Influenza Networks

- Sentinel GP
- Emergency/obstetrician rooms
- Hospital
- Laboratory

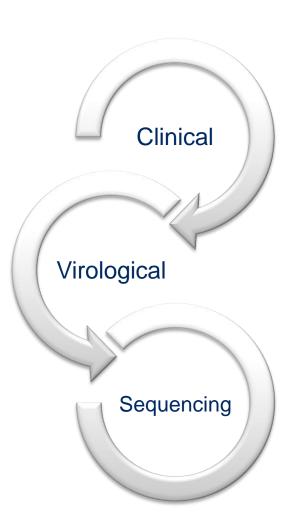
Influenza Sequencing

- First viruses of the season
- Weekly selection viruses
- ~ 96 virus/month
- All age groups, regions
- Vaccinated
- Severe cases
- Hospitalized
- Antiviral therapy
- Less frequent type/subtype

Pandemic period

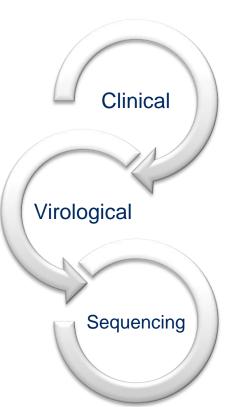
- increase global genomic sequencing capacities
- rapid sharing of sequence data and metadata

Integration of SARS-CoV-2 testing and sequencing should occur without compromising influenza surveillance



COVID-19 pandemic response

- improve the geographic and demographic representativeness
- timeliness of influenza and SARS-CoV-2 genetic sequence
- data in publicly accessible databases, Global Initiative on Sharing All Influenza Data (GISAID)
- monitor trend and prevalence of existing and emerging (co-) circulating genetic variants (clades) among samples from sentinel sites.



Influenza/SARS-CoV-2 Sequencing

Health Sentinel Units for respiratory disease

Samples tested for

SARS-CoV-2

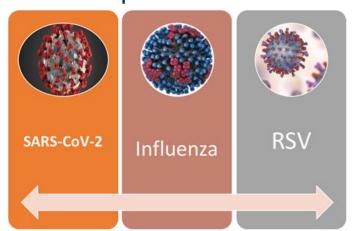
(laboratory network for COVID-19)



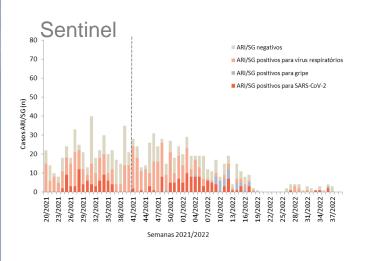
National Reference Laboratory, INSA

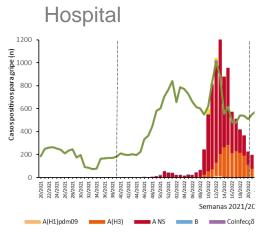
Sequencing

 All Influenza and SARS-CoV-2 positive rRT-PCR cycle-threshold (Ct) value of ≤30 5-10 samples /week/each site



Influenza Sequencing, 2021/2022

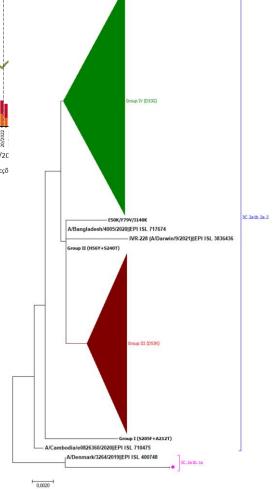




Quadro II — Caracterização genética dos vírus da gripe, detetados desde a semana 40/2021

| Subtipo/Linhagem | Grupo Filogenético | Nº de vírus |
|------------------|---|-------------|
| A (H1)pdm09 | A/Victoria/2570/2019 (H1N1)pdm09-like virus ⁽¹⁾ | 0 |
| | A/Guangdong-Maonan/SWL1536/2019 (H1N1)pdm09-like virus (2) | 10 |
| A(H3) | A/Cambodja/e0826360/2020 (H3N2)-like virus ⁽¹⁾ | 0 |
| | A/Bangladesh/4005/2020 (H3N2)-like virus ⁽²⁾ | 496 |
| | A/Denmark/3264/2019 (H3N2)-like virus ⁽²⁾ | 2 |
| B/Victoria | B/Washington/02/2019 (B/Victoria lineage)-like virus ⁽¹⁾ | 0 |
| | B/Austria/1359417/2021 (B/Victoria lineage)-like virus ⁽²⁾ | 6 |
| B/Yamagata | B/Phuket/3073/2013 (B/Yamagata lineage)-like virus (1) | 0 |
| TOTAL: | | 514 |

^{(1) -} grupo que inclui vírus geneticamente semelhantes ao contemplado na vacina do Hemisfério Norte para a época 2021/2022



^{(2) -} grupo que inclui vírus geneticamente diferentes ao contemplado na vacina do Hemisfério Norte para a época 2021/2022

Influenza/SARS-CoV-2 Sequencing

COVID-19 lab. network



Selection of positive Swabs

43 Public + 96 private + 34 academy



WGS Sequencing

All positive rRT-PCR cycle-threshold (Ct) value of ≤30

SNP PCR (SARS-CoV-2)

Monitoring new VOC spread



National Reference Laboratory INSA

- Influenza5 samples/week/each lab
- SARS-CoV-2~520 samples/week

2022/2023 Influenza/SARS-CoV-2 Sequencing

- GP sentinel network (~55)
- Sentinel Health Units (~55)
- Hospital laboratory network (42)

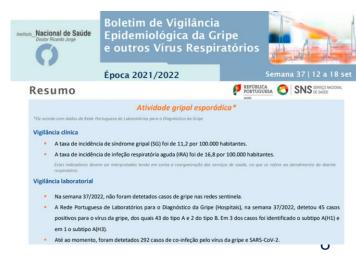


10% resident population
All regions (mainland, Islands)
ARI case def.
Vacination flu/Covid-19
HCW
medical appointments/statins
smoking habits
RAT COVID-19

Sequencing

- All positive rRT-PCR cycle-threshold (Ct) value of ≤30
- Influenza ~96 virus /month
- ➤ SARS-CoV-2 ~520 virus/week
- *RSV WGS sequencing

Virus characterization, vaccine viruses, new clades/variants



2022/2023 SARS-CoV-2 Sequencing

Hospital laboratory network Public + Private + Academia

Variants monitoring
Complement sentinel surveillance
Geographical coverage

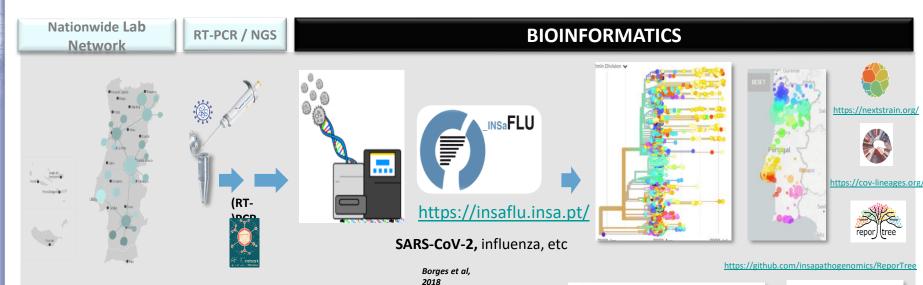
Sequencing

- All positive rRT-PCR cycle-threshold (Ct) value of ≤30
- SARS-CoV-2 ~520 virus/week



Genomic surveillance of SARS-CoV-2 in Portugal

https://insaflu.insa.pt/covid19/

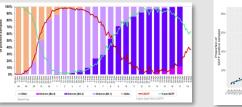


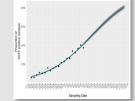
Genome Medicine 10: 46

<u>WGS</u>

Nationwide weekly surveys

- Positive samples (all Regions) are sent to the National Institute of Health (INSA) for sequencing
- Since, June 2021: ~520 sequences / week, covering ~140
 municipalities per week





https://insaflu.insa.pt/covid1

(Release on 8 April 2020)

SGTF

Monitoring based on TaqPath data provided by large laboratories dispersed accross the country, when needed



Genomic surveillance of SARS-CoV-2 in Portugal

https://insaflu.insa.pt/covid19/

Open data sharing and reporting







PT / EN

Weekly reports every Tuesdays

Genetic diversity of the novel coronavirus SARS-CoV-2 (COVID-19) in Portugal

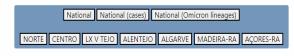
Download - Latest situation report

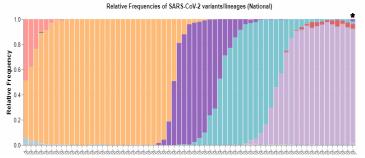
The Portuguese National Institute of Health [Instituto Nacional de Saude Doutor Ricardo Jorge (INSA)] is coordinating a national project to monitor the spread of the pandemic novel coronavirus SARS-CoV-2 in Portugal using whole-genome sequencing (WGS) data, in collaboration with a nationwide network of hospitals/labs.

SARS-CoV-2 genome sequence data was obtained through next-generation sequencing (NGS) and bioinformatics analyses using the INSaFLU platform. Up to the current date, INSA analysed 41147 SARS-CoV-2 genome sequences.

More details about the study (click here)

The interactive graphs show the evolution of the weekly relative frequency of the SARS-CoV-2 variants/lineages at national and regional levels.











Thank you Q&A

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