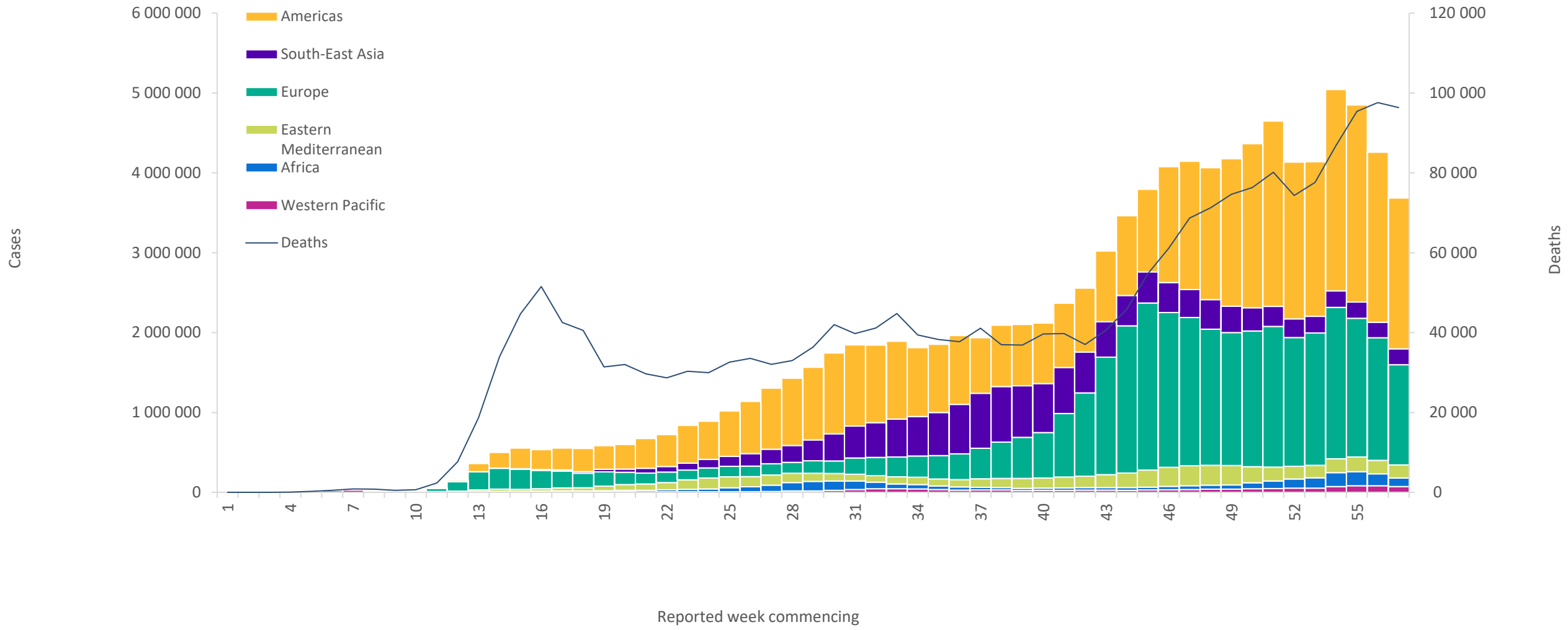
Emerging SARS-CoV-2 Variants

4 February 2021

Global Situation: Weekly Overview (as of week ending 31 Jan 2021)



SARS-CoV-2 Variants

- Jan-Feb 2020: SARS-CoV-2 with D614G substation
- August to September 2020: a mink-associated SARS-CoV-2 variant in Denmark
- 14 Dec 2020: SARS-CoV-2 Variant B.1.1.7 reported by the United Kingdom of Great Britain and Northern Ireland authorities
- 18 Dec 2020: SARS-CoV-2 variant B.1.351 reported by South African authorities
- 9 Jan 2021: SARS-CoV-2 variant P.1 reported by Japan from persons traveling from Brazil. Local transmission reported in Manaus, Amazonas State, Brazil.

Countries/territories/areas reporting lineage B.1.1.7 (situation as of 02 February 2021)

World Health Organization

Data Source: World Health Organization
Map Production: WHO Health Emergencies Programme

Not applicable

0 2,500 5,000 km

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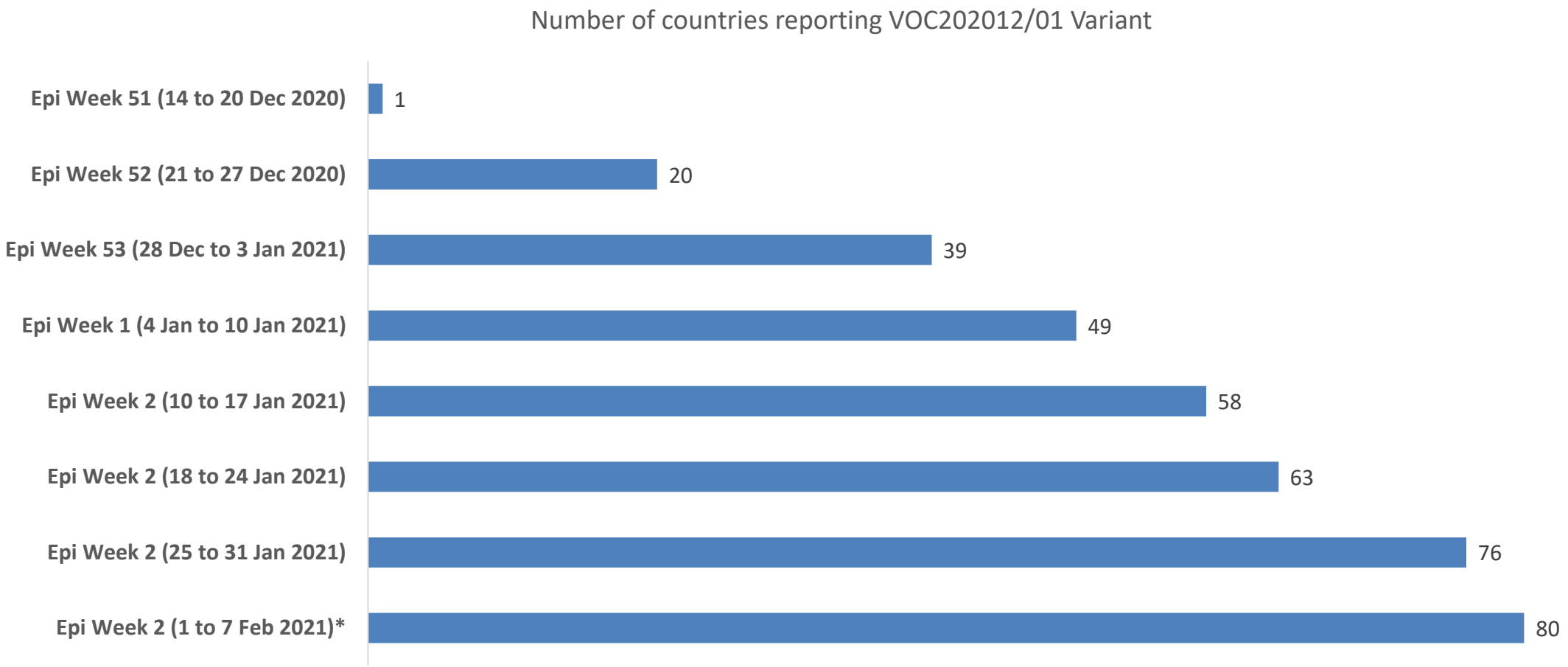
Countries reporting the SARS-CoV-2 B.1.1.7 Variant

As of 02 February 2021



*Current Epidemiological week, Data as of 02 February.
Data above includes both confirmed and under verification reports

Proportion of B.1.1.7 cases among tested samples in select countries

	United Kingdom	Ireland	Sweden	France	Spain	Denmark
Epi Week 51 14 to 20 Dec 2020	63%	8%	-	-	0.5%	-
Epi Week 52 21 to 27 Dec 2020	71%	16%	-	-	-	-
Epi Week 53 28 Dec 2020 to 3 Jan 2021	76%	26%	-	-	-	2.4%
Epi Week 1 4 to 10 Jan 2021	81%	46%	-	**3.3%**	-	4%
Epi Week 2 11 to 17 Jan 2021	86%	58%	-	-	4%	**7.4%**
Epi Week 3 18 to 24 Jan 2021	**89.9%**	**63%**	**11%**	-	**9%**	-
Date of last update	24 Jan, 2021	28 Jan, 2021	02 Feb, 2021	27 Jan, 2021	26 Jan, 2021	24 Jan, 2021
Source	Public Health England	Department of Health, Ireland (Slides from the NPHET press briefing - Thursday 28 January)	Media – The local.se Media - Xinhuanet Public Health Agency of Sweden	Sante Public France	MoH Spain	Statens Serum Institut

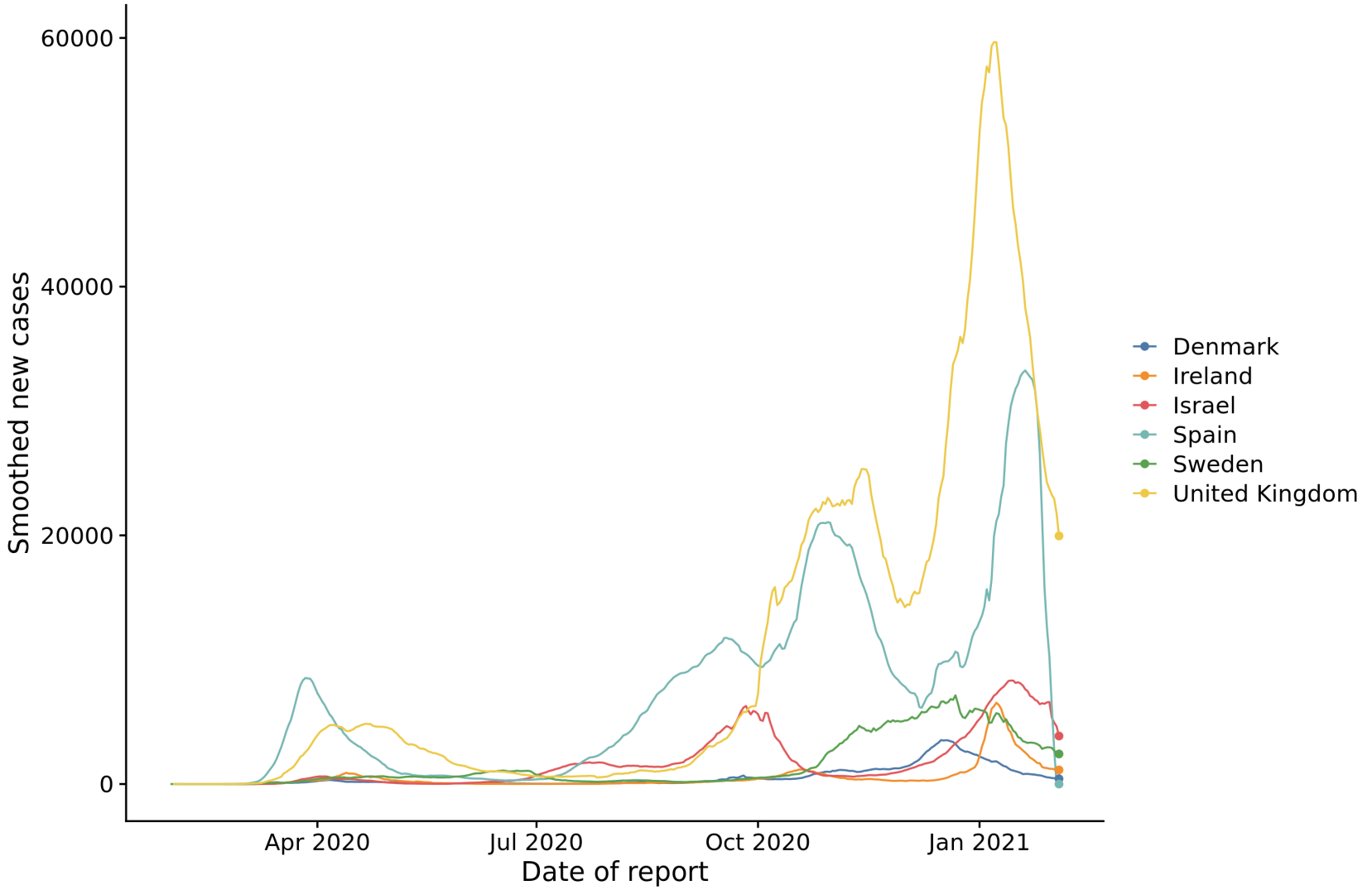
Features of B.1.1.7

- Increased transmissibility
- Possibility that infection with B.1.17 associated with an increased risk of death compared to infection with other variants (preliminary data from the UK)
- S gene target failure for diagnostics, but other targets no compromised
- Currently no evidence about changes in neutralizing activity
- Currently no evidence to show reduced effectiveness of vaccines

https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/955239/NERVTAG_paper_on_variant_of_concern__VOC__B.1.1.7.pdf
https://www.biorxiv.org/content/10.1101/2021.01.25.427948v1; https://www.biorxiv.org/content/10.1101/2021.01.18.426984v1;
https://www.medrxiv.org/content/10.1101/2021.01.19.21249840v1; https://www.biorxiv.org/content/10.1101/2021.01.15.426911v1
https://investors.modernatx.com/node/10841/pdf

PHSM appears to be working in countries with local transmission of B.1.1.7

- UK, Denmark, Ireland, Spain, Sweden, and Israel where local transmission of B.1.1.7 has been reported have reported decreasing trends in new cases over the past two weeks
- Implementation of PHSM has reduced transmission



Data taken from COVID Intel database on 2021-02-03.
The lines and associated text show the trend in COVID-19 cases.

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Countries/territories/areas reporting lineage B.1.351 (situation as of 02 February 2021)

World Health Organization

Data Source: World Health Organization
Map Production: WHO Health Emergencies Programme

Not applicable

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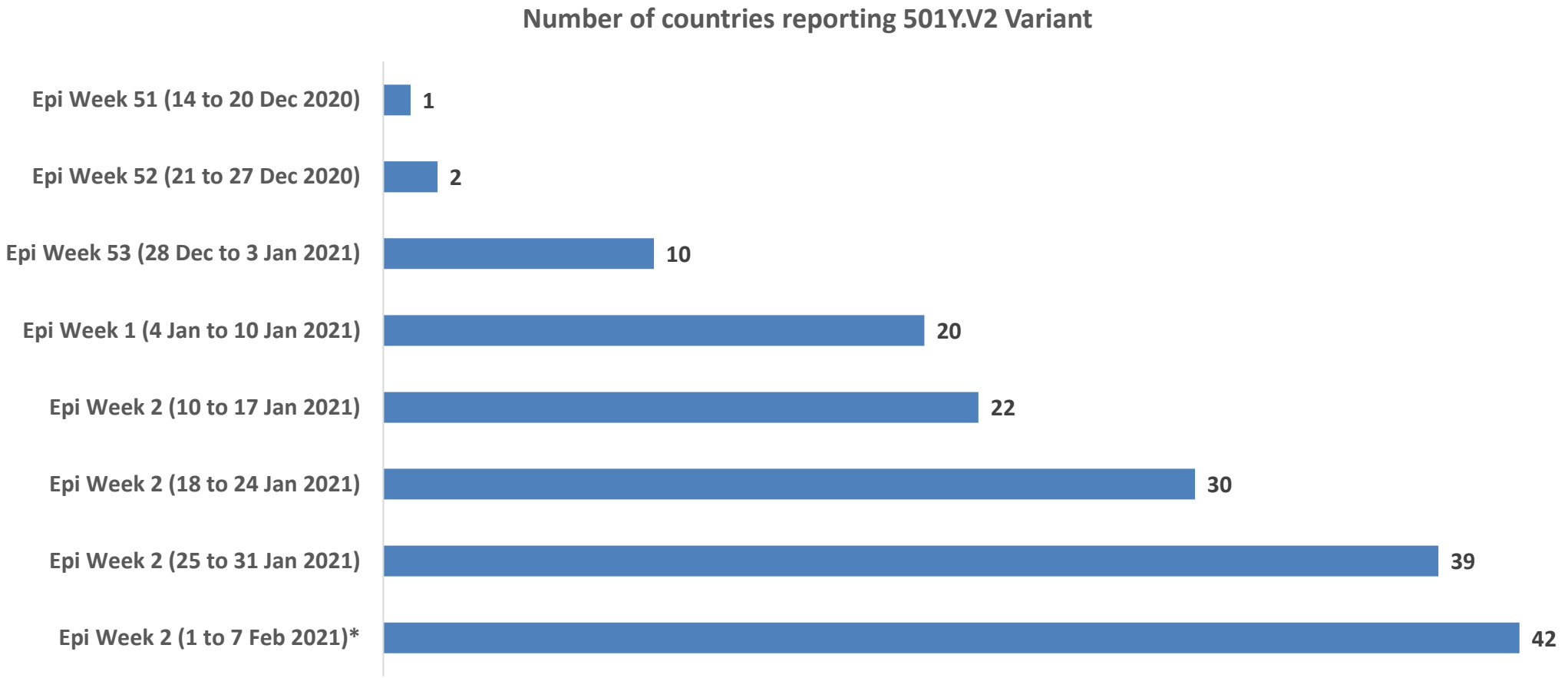
Countries reporting the SARS-CoV-2 B.1.351 Variant

As of 02 February 2021



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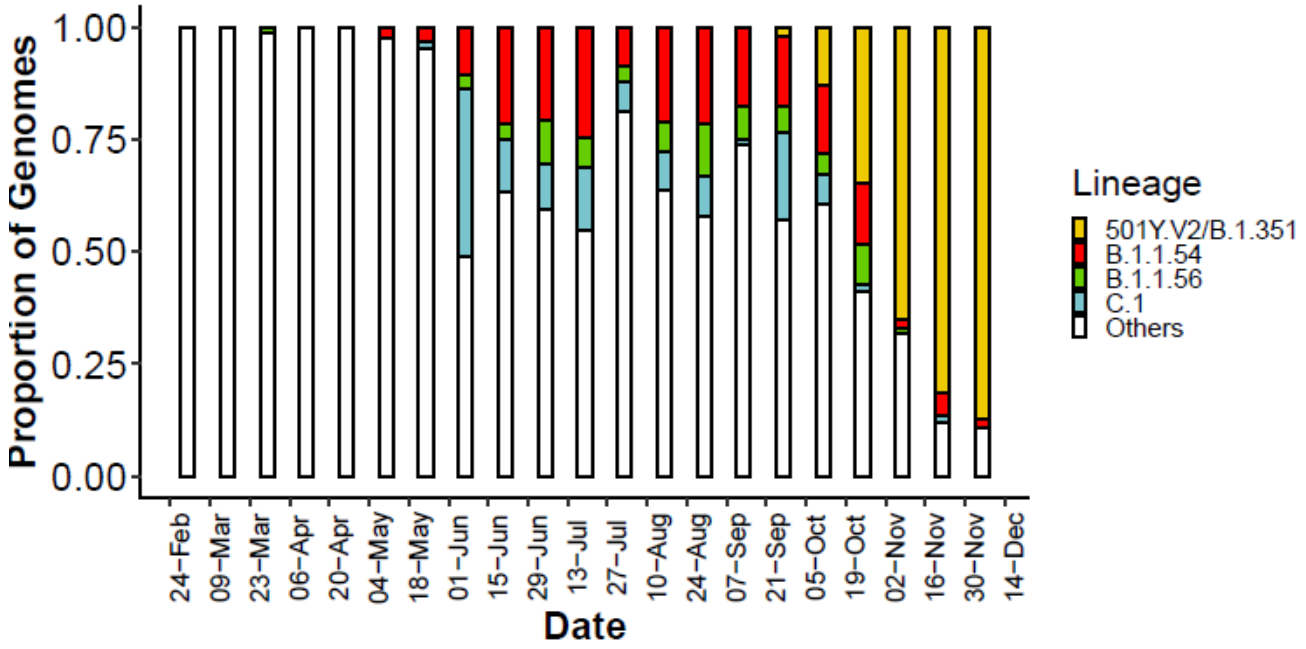
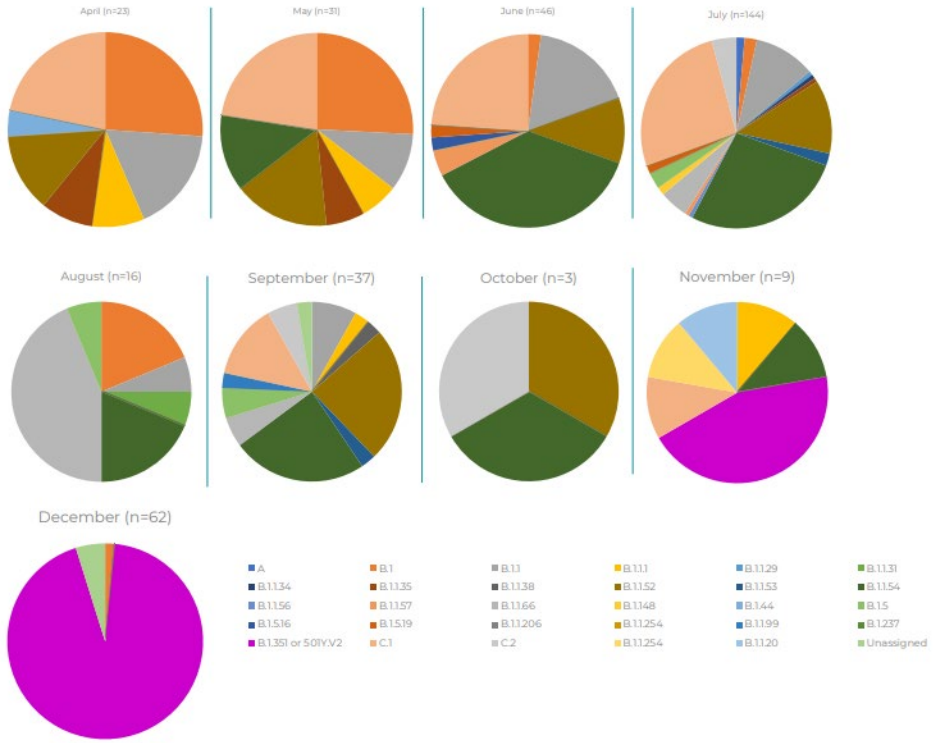
B.1.351 has become dominant in four provinces in South Africa

Genomes sequenced from the provinces of Eastern Cape, Western Cape, KwaZulu-Natal



Source: Network for Genomic Surveillance South Africa (NGS-SA) led by Professor Tulio de Oliveira

SARS-CoV-2 lineage distribution by month in Gauteng



https://www.nicd.ac.za/wp-content/uploads/2021/01/Dominance-of-the-SARS-CoV-2-501Y.V2-lineage-in-Gauteng-South-Africa-1.pdf

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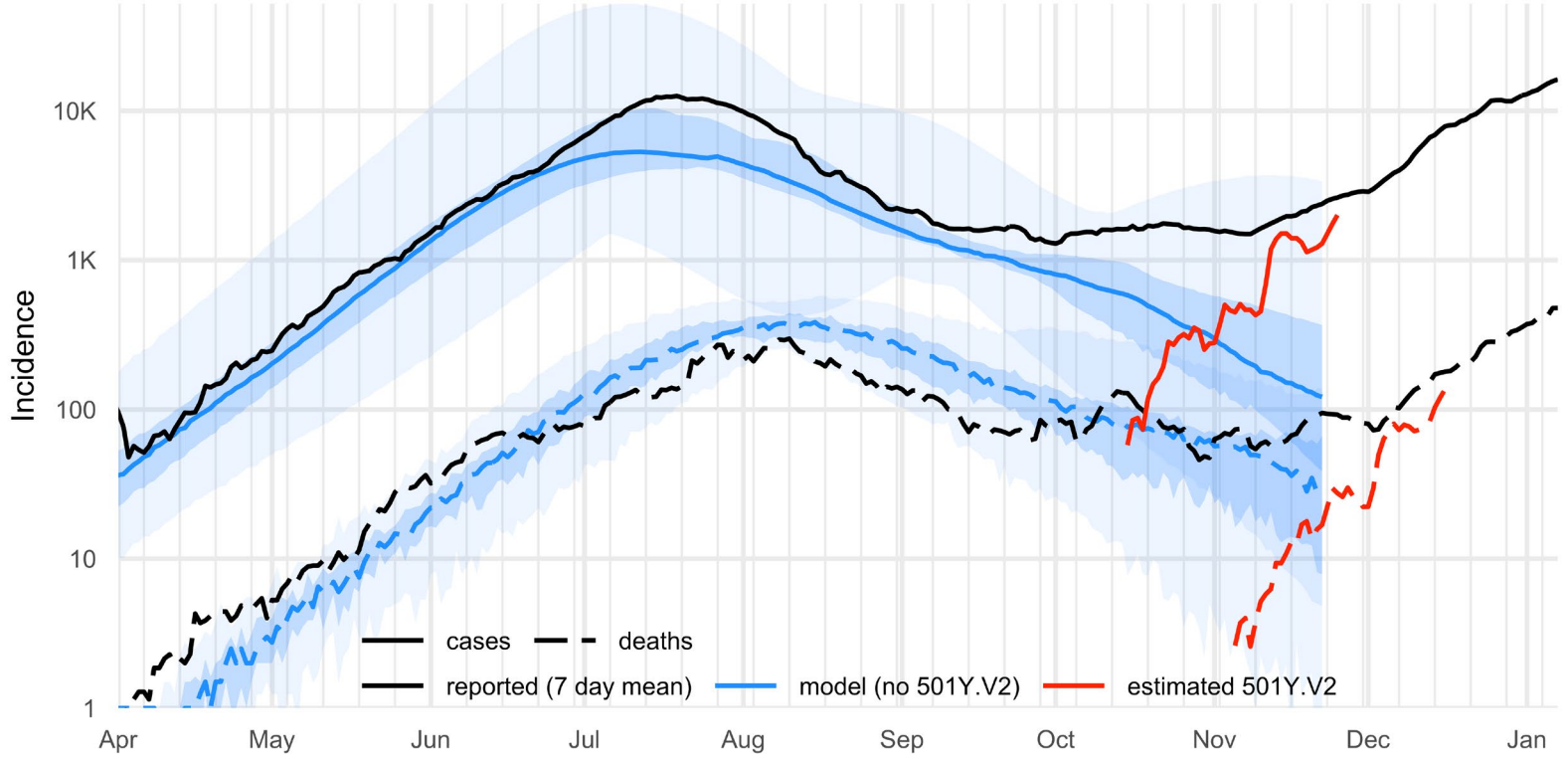
Increased transmissibility of B.1.351

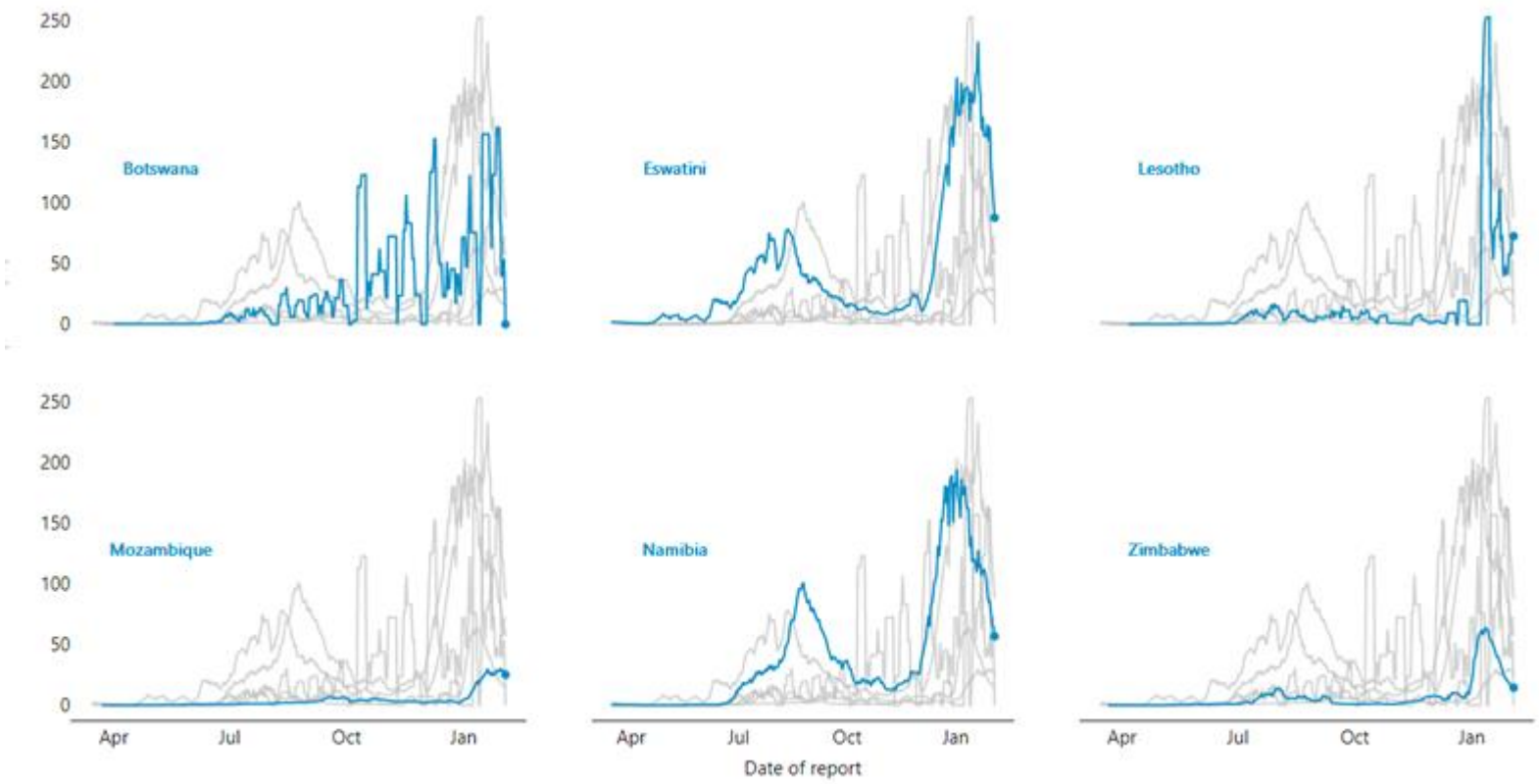
Estimates that B.1.351 is 1.50 (95% CrI: 1.20-2.13) times as transmissible as previously circulating variants



Source: Pearson et al,. https://cmmid.github.io/topics/covid19/sa-novel-variant.html

Epidemiology of COVID-19 in countries neighbouring South Africa

- A number of countries neighbouring South Africa experienced sharp increases in case numbers from mid December similar to the one observed in South Africa
- Unknown exact burden of the B.1.351 variant due to limited sequencing capacity
- Implementation of PHSM has reduced transmission



Features of B.1.351

- Potentially increased transmission
- Studies of a limited number of patients using pseudo virus and live attenuated virus from South Africa have shown that the B.1.351 **variant may be less susceptible to antibody neutralization**:
  - Activity was either lost or reduced in blood samples of patients with natural infection with previous variants circulating earlier in the pandemic.
- Preliminary in vitro studies using sera from individuals vaccinated with Moderna or Pfizer-BioTech vaccines showed either equivalent or reduction in neutralizing titers to the 501Y.V2 variant compared to previous variants tested, however, **neutralizing titres remain above the levels expected to be protective.**
- Out of an abundance of caution, Moderna is investigating the potential use of an **additional booster dose** to increase neutralizing titres against emerging variants and beginning to evaluate an **emerging variant booster candidate vaccine**.

https://www.biorxiv.org/content/10.1101/2021.01.25.427948v1
https://www.biorxiv.org/content/10.1101/2021.01.15.426911v1 https://www.biorxiv.org/content/10.1101/2021.01.07.425740v1.full.pdf
https://investors.modernatx.com/node/10841/pdf
https://www.biorxiv.org/content/10.1101/2021.01.18.427166v1; https://www.medrxiv.org/content/10.1101/2021.01.26.21250224v1

Countries/territories/areas reporting lineage P.1 (situation as of 2 February 2021)

World Health Organization

Data Source: *World Health Organization*
Map Production: *WHO Health Emergencies Programme*

Not applicable

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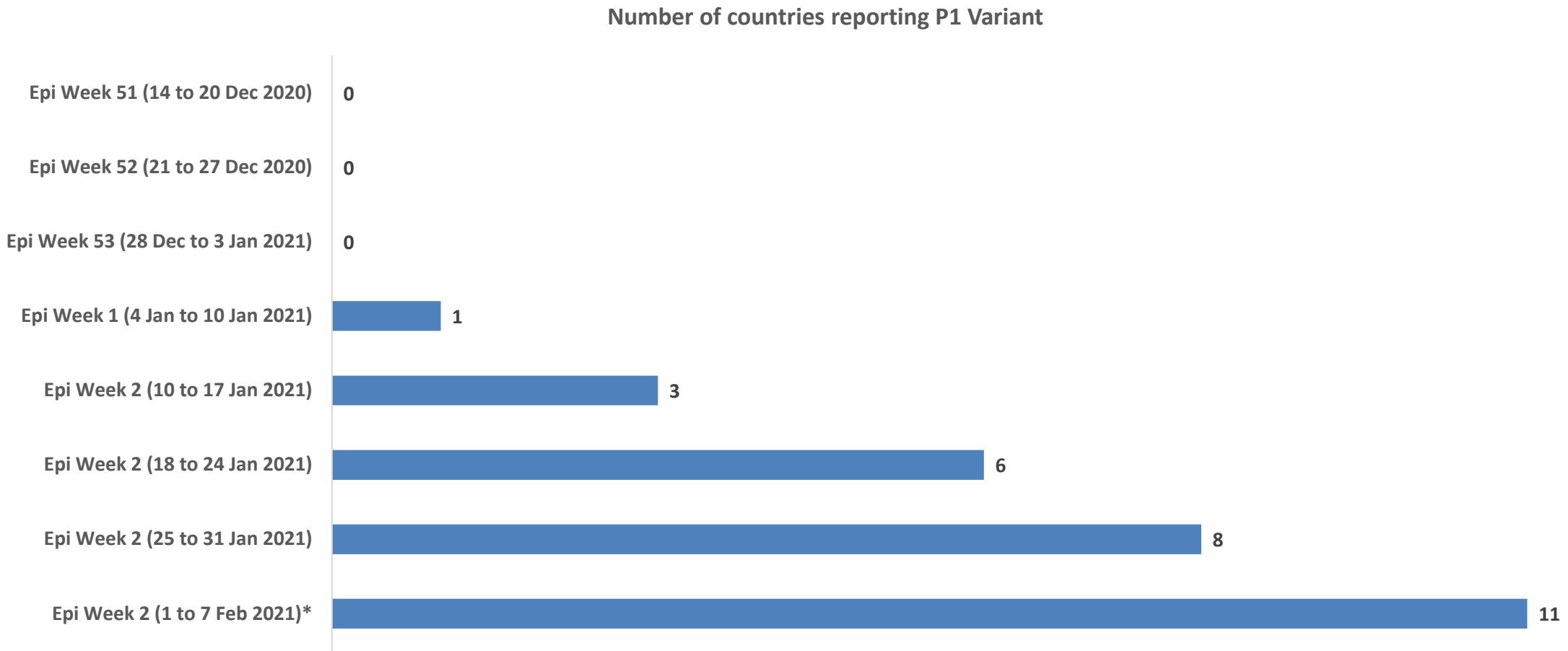
Countries reporting the SARS-CoV-2 P1 Variant

As of 02 February 2021



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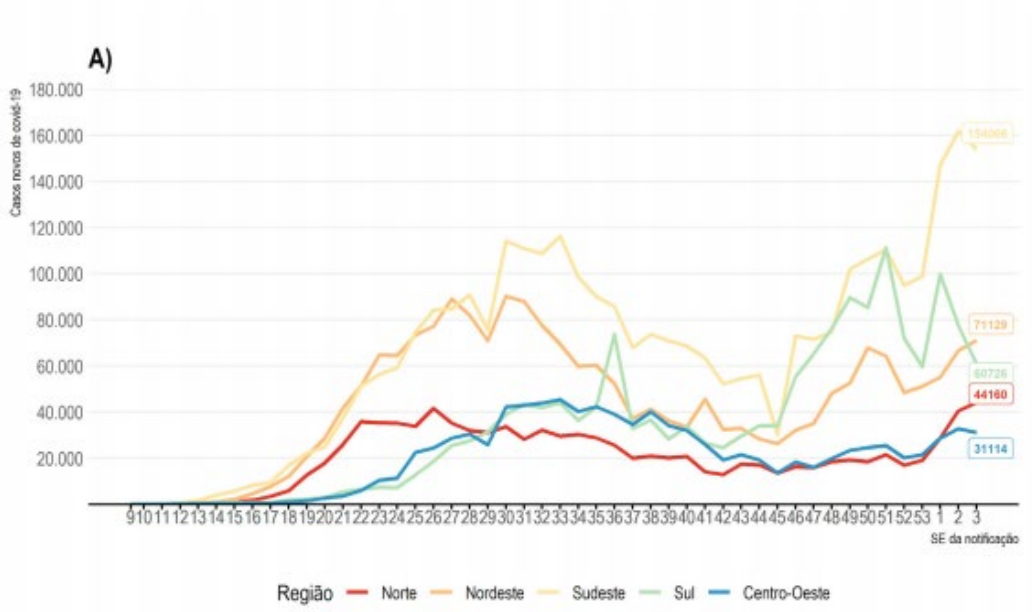
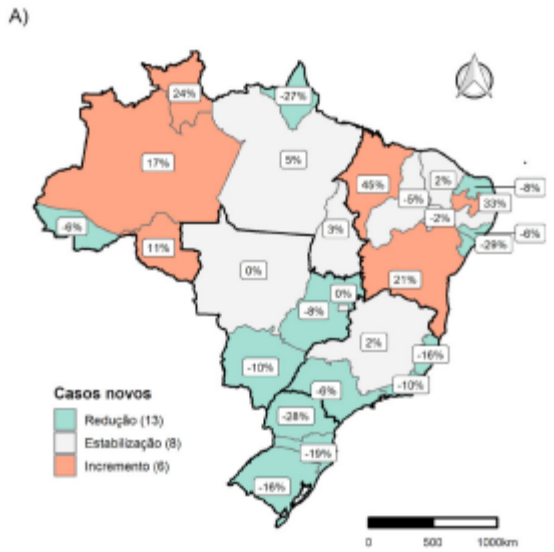
Spread of P.1 variant in Amazonas as cases surge across Brazil

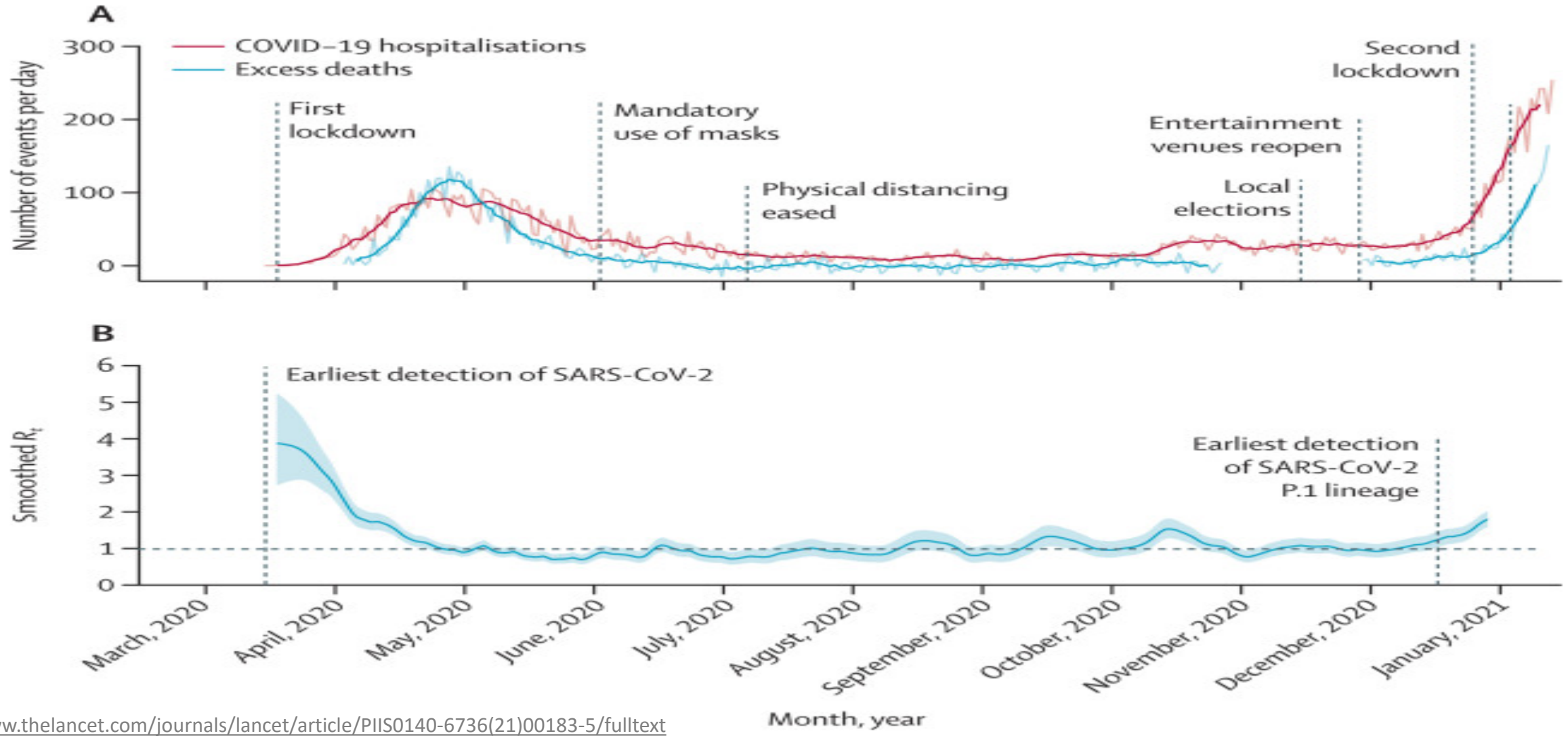
- P.1 variant first identified in a patient sample on 4 December 2020
- The P.1 variant has been identified in 10 additional municipalities in Amazonas in addition to Manaus.
- Sequencing of over 85 SARS-CoV-2 samples from Amazonas found the P.1 variant increased from 0% in November 2020 to 51% in December 2020 then reached 91.4% as of 24 January 2021.





https://virological.org/t/sars-cov-2-reinfection-by-the-new-variant-of-concern-voc-p-1-in-amazonas-brazil/596/3; https://www.gov.br/saude/pt-br/media/pdf/2021/janeiro/28/boletim_epidemiologico_covid_47_28jan21_seg.pdf

Resurgence in cases despite high levels of previous infection, Manaus, Brazil



https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(21)00183-5/fulltext
https://www.biorxiv.org/content/10.1101/2020.12.31.425021v1.abstract; https://virological.org/t/sars-cov-2-reinfection-by-the-new-variant-of-concern-voc-p-1-in-amazonas-brazil/596/3

Features of P.1

- High attack rate in Manaus above expected to be above herd immunity threshold
  - As of October 2020, 76% of blood donors in Manaus had been infected with SARS-CoV-2
- However, there was an unexpected sharp increase in COVID-19 hospital admissions in January 2021
- E484K mutation, present in P.1 variant, has been identified in several people who have been reinfected in Brazil and has been shown to reduce neutralization (in-vitro) by polyclonal antibodies in convalescent sera
- Further studies are needed to determine whether waning immunity, immune escape, or increased transmissibility play a role in the resurgence despite high levels of previous infection.

Establishing a risk monitoring framework to evaluate SARS-CoV-2 VOCs

- **Components of framework**
  - Surveillance: Epidemiological; Molecular diagnostic testing; Monitor virus circulation with genomic sequencing, including virus evolution and phylogenetics
  - Research studies on potential variants of interest (VOI) and variants of concern (VOCs)
    - Protein modelling studies
    - Laboratory Studies (*in vivo and in vitro*)
    - Modelling and epidemiological studies
  - Evaluation impact of evolution on available and future diagnostics, therapeutics and vaccines

  → All information feeding into WHO Rapid Risk Assessments

- **Principals for success**
  - Robust framework and assessment; building from/enhancing existing systems
  - Regular communication
  - Strong collaboration
  - Increased capacities for sequencing and bioinformatics
  - Platforms to support sequences and phylogenetics
  - Clear, consistent and evidence-based communications and actions

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Risk Monitoring Framework for SARS-CoV-2 Variants

Member States, Partners, Technical Networks

Draft for input/in development

Enhanced surveillance & analyses

- Epidemiologic, Virologic
- Genomic Sequencing (SARS-CoV-2, GISRIS, etc./pubic, private, commercial, vet)

Sharing of data & analyses

- Samples and related materials (WHO BioHub)
- Genetic sequences and meta data
- Supporting platforms for visualization and analyses
- Phylogenetics and Bioinformatics

WHO Virus Evolution Working Group

- Strengthen mechanisms to identify and prioritize (potential) relevant mutations
- Identify relevant mutations early and study the potential impacts related to viral characteristics and effectiveness of available and future countermeasures
- Evaluate possible mitigation strategies to reduce the negative impact of mutations
- Study the impact of specific mutations (including laboratory-controlled in vitro and in vivo studies of mutants)
- VOC risk assessment of impact - *in development with VEWG and partners* (e.g. TIPRA-like)

Coordinated research on transmission, severity, impacts on diagnostics, therapeutics & vaccines

- R&D Blueprint for Epidemics working groups (animal models, diagnostics, therapeutics, vaccines)
- External partners and manufacturers
- In vivo/in vitro studies; protein modelling, modelling and epidemiology studies

R&DBlueprint
Powering research to prevent epidemics

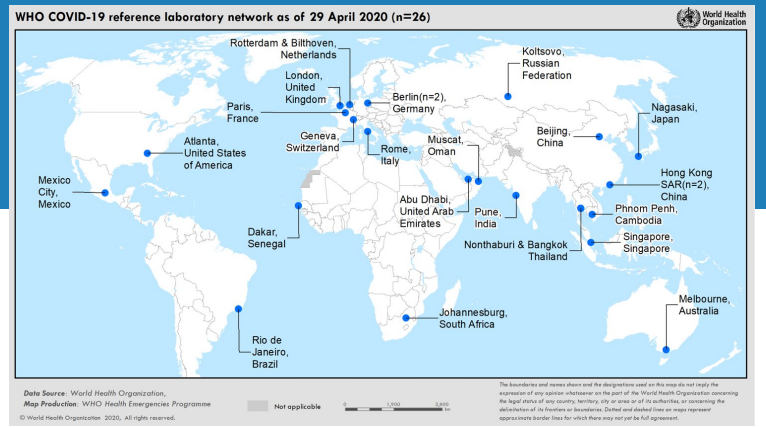
Revision/modifications to available and future diagnostics, therapeutics, vaccine composition

- *Building vaccine composition framework (To be developed)*

Regular WHO Rapid Risk Assessments related to mutations, variants of interest and variants of concern

Enhancing existing networks: SARS-CoV-2; GISRIS; R&D Blueprint for Epidemics

Increasing capacities



- **Increasing strategic testing and "intelligent" sequencing**
  - Increasing Ag based RDT use
  - Increasing sequencing capacities worldwide
    - Leveraging existing/building systems (GISRIS, polio, influenza, TB/HIV…)
    - In country academic, private, commercial sequencing capacities; vet labs
    - External support – SARS-CoV-2 reference lab, GISRIS, AFRO/Africa CDC, countries with additional capacities
  - GISRIS Sequencing guidance (*pending*)

- **SARS-CoV-2 Risk Monitoring Framework**
  - Seeking input partners
  - Increasing sequence sharing; phylogenetics and bioinformatics
  - Support platforms for sequences, meta-data & analyses
  - Nomenclature discussions – organized by WHO with partners
  - Risk Framework - SARS-CoV-2 Virus Evolution Working Group (e.g., TIPRA-like)
  - Research studies to evaluate transmissibility, severity, impact on diagnostics, therapeutics and vaccines
  - Strong links with WHO R&D Blueprint for epidemics research agenda on variants and vaccines

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SARS-CoV-2 Nomenclature

- 3 main nomenclatures currently in existence (GISAID, Nextstrain, Pango).
- Each nomenclature system has a different purpose and associated advantages and disadvantages (evolutionary biology <> public health).
- IHR(2005) EC and VEWG: need to come up with a standardized nomenclature for the different variants based on their genetic sequence. The nomenclature should be easily understood and not include country names to avoid geopolitical issues.
- First call with three nomenclature groups and other experts in the field on 2 Feb and follow up call scheduled early next week.
- Looking into a mechanism that designates variants of concern; linking it with the three existing nomenclature systems; and labeling these with an innocuous, easy to pronounce name.

WHO Updates - SARS-CoV-2 variants

SARS-CoV-2 mink-associated variant strain – Denmark

- Disease Outbreak News – 6 Nov, and 3 Dec 2020

SARS-CoV-2 VOC 202012/01 initially identified in UK

- Disease Outbreak News –SARS-CoV-2 Variant – United Kingdom of Great Britain and Northern Ireland- 21 December 2020

SARS-CoV-2 variant reported by Japan ex-Brazil

- WHO News Update 9 January 2020

All variants of concern

- Disease Outbreak News - SARS-CoV-2 Variants- 29 December 2020
- Weekly Epidemiological Updates – 12, 19, 27 January, 2 February 2021