

Member State Information Session, 25 February 2021

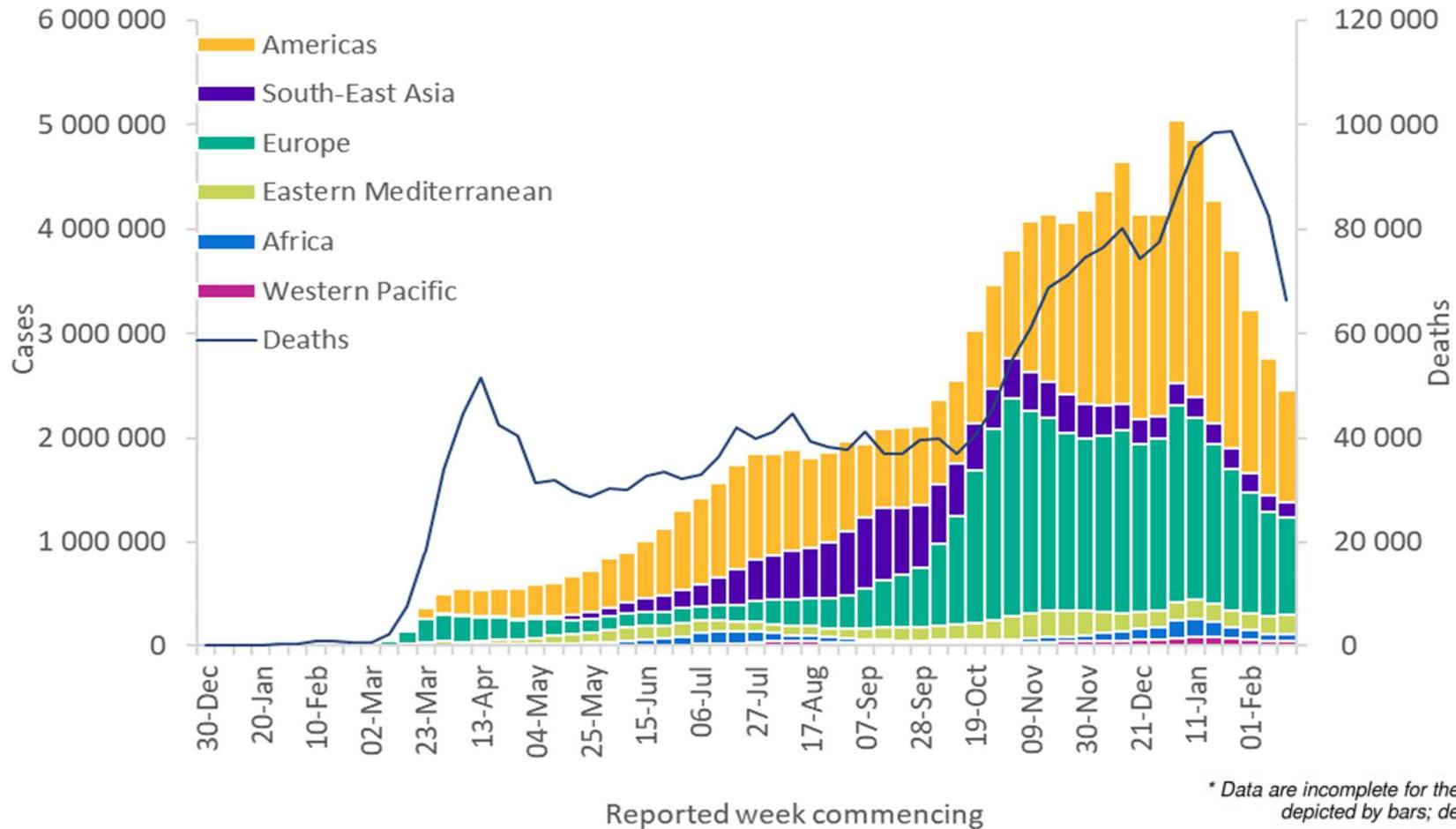


HEALTH
EMERGENCIES
programme

EPIDEMIOLOGICAL UPDATE

Global Situation: Weekly Overview

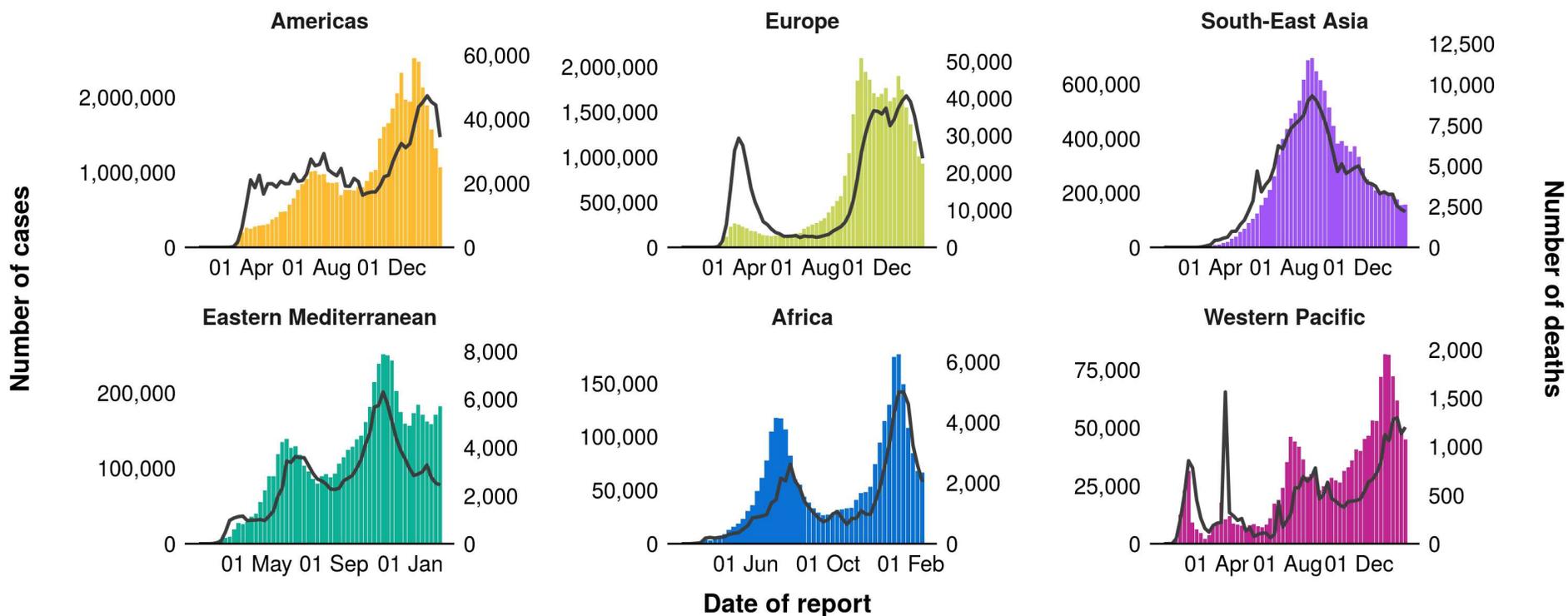
(as of 21 February 10H CET)



* Data are incomplete for the current week. Cases depicted by bars; deaths depicted by line.

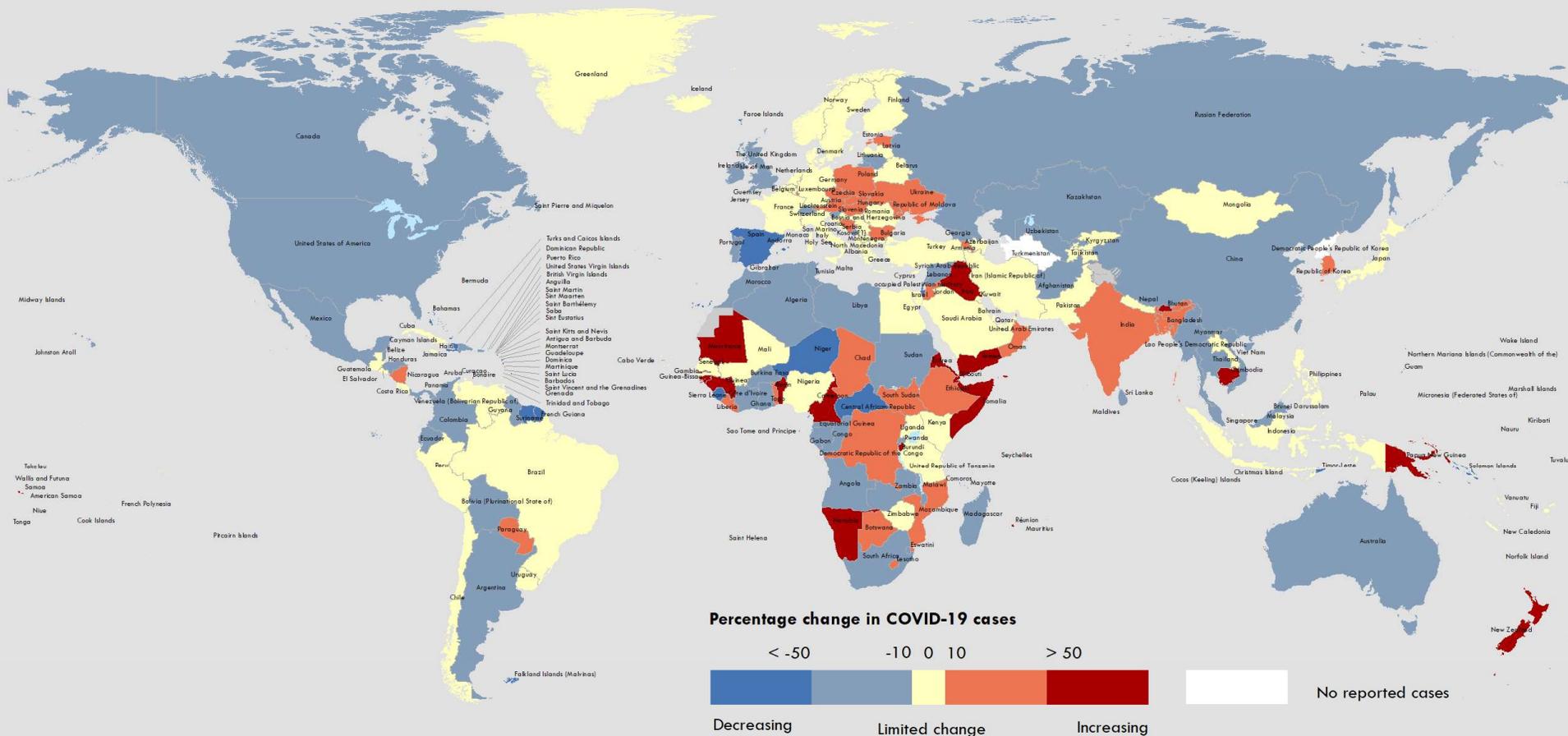
Weekly situation by WHO region

(as of 21 February 10H CET)



* Data are incomplete for the current week. Cases depicted by bars; deaths depicted by line. Note different scales for y-axes.

Percentage change in COVID-19 cases over the last seven days relative to the previous seven days (as of 21 February 2021 10:00AM CET)



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

Not applicable

0 2,500 5,000 km
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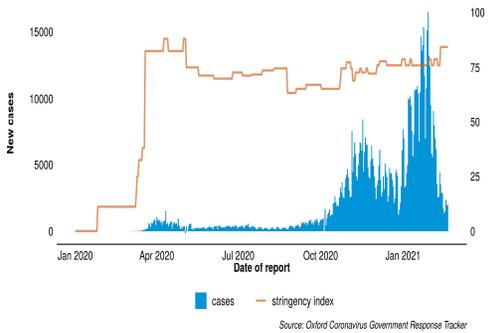
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Countries driving the decrease in cases

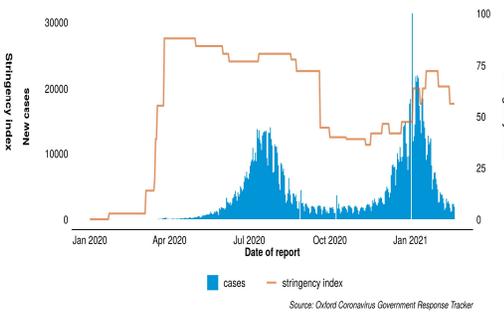
Country	Number of cases reported in week 7 (15 to 21 February)	Number of cases reported in week 3 (18 to 24 January)	% decrease in cases
United States of America	480,467	1259902	-61.9
Brazil	316,221	360428	-12.3
The United Kingdom	78569	260098	-69.8
Russian Federation	92843	151191	-38.6
France	131179	138288	-5.1
Mexico	51537	122555	-57.9
Colombia	31832	117239	-72.8
Spain	29764	109000	-72.7
Germany	51998	101418	-48.7
India	86711	96548	-10.2
Italy	84977	86452	-1.7
Portugal	12260	85053	-85.6
Indonesia	60650	80832	-25.0
South Africa	12304	79180	-84.5
Argentina	33128	70783	-53.2
Canada	20280	41700	-51.4
Japan	10035	38365	-73.8
Netherlands	26313	37381	-29.6
Israel	10644	29421	-63.8
Chile	23450	29154	-19.6

Countries with >50% decrease in cases in the past 4 weeks

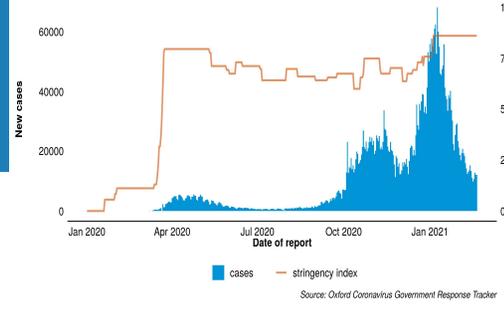
Response: Portugal



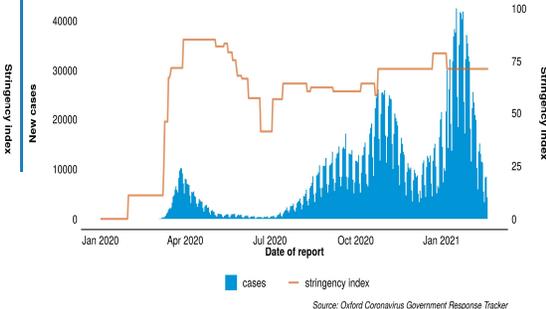
Response: South Africa



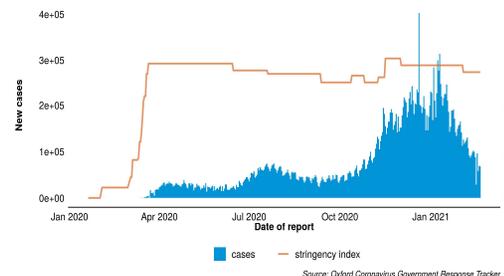
Response: United Kingdom



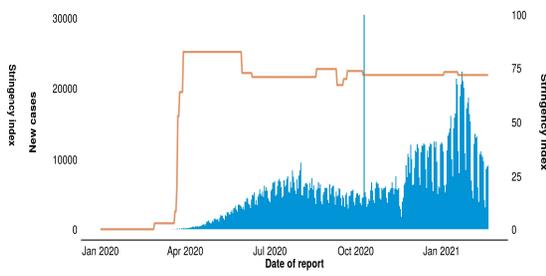
Response: Spain



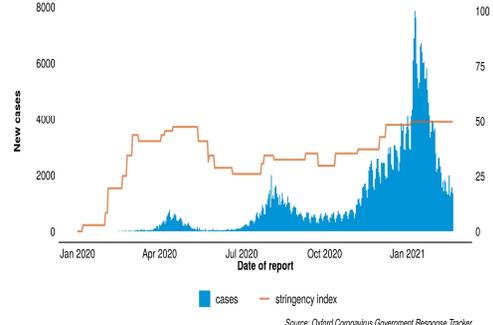
Response: United States of America



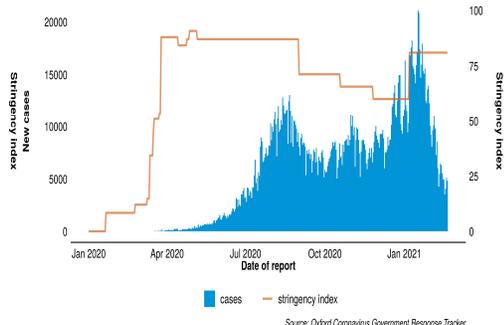
Response: Mexico



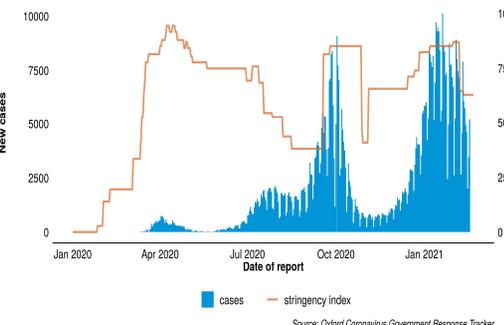
Response: Japan



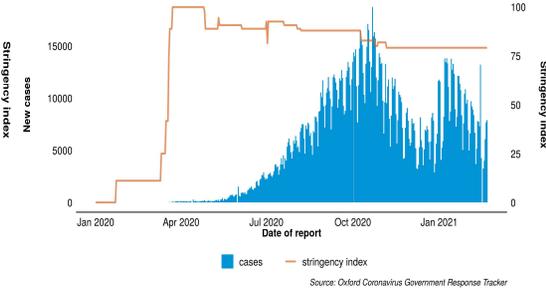
Response: Colombia



Response: Israel



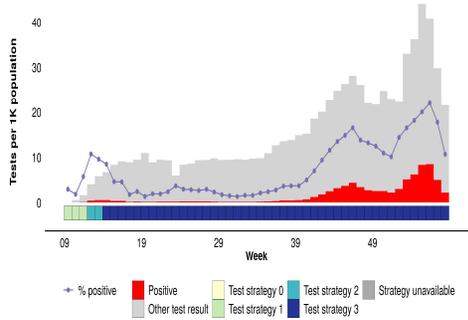
Response: Argentina



TPR of countries with >50% decrease in cases in the past 4 weeks

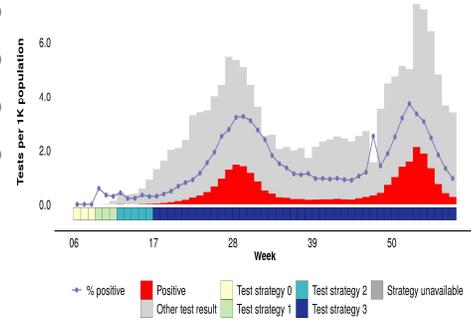
Portugal

total tests as of Feb 14: 7,844,783 (samples tested)



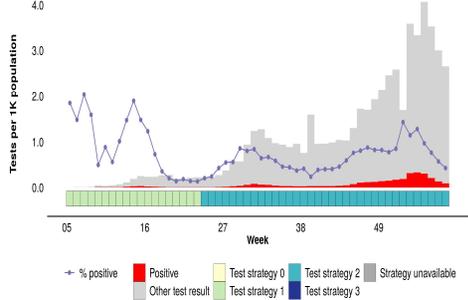
South Africa

total tests as of Feb 14: 8,697,066 (people tested)



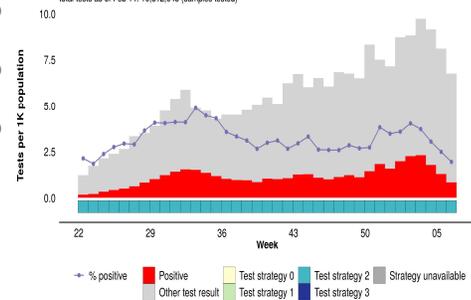
Japan

total tests as of Feb 14: 7,086,119 (people tested)



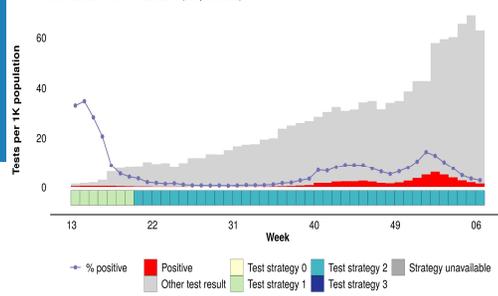
Colombia

total tests as of Feb 14: 10,812,043 (samples tested)



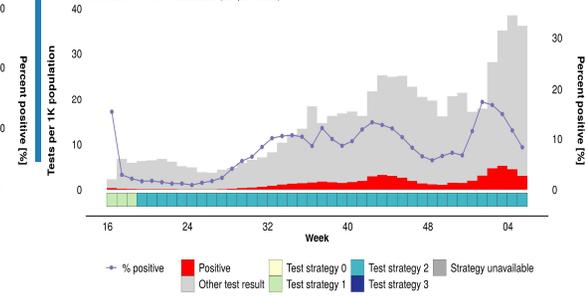
United Kingdom

total tests as of Feb 14: 79,338,077 (samples tested)



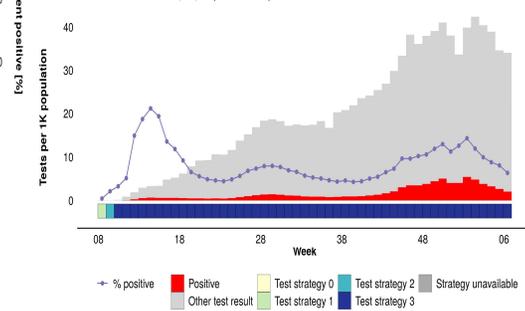
Spain

total tests as of Feb 07: 29,965,252 (samples tested)



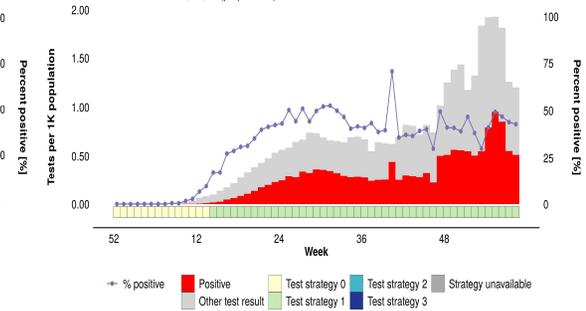
United States of America

total tests as of Feb 14: 335,086,712 (unknown units)



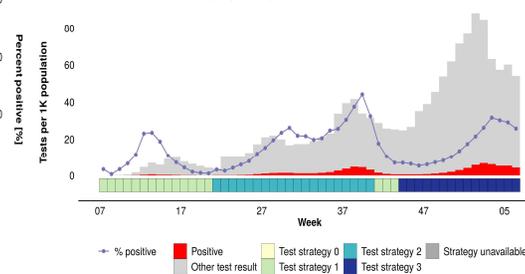
Mexico

total tests as of Feb 14: 4,712,973 (people tested)



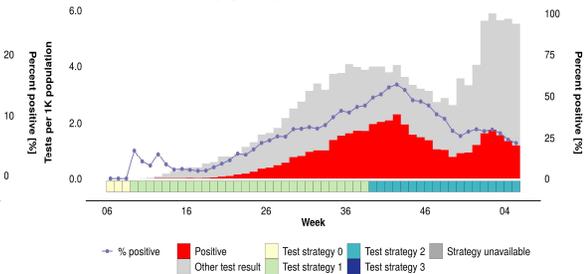
Israel

total tests as of Feb 14: 12,167,002 (samples tested)

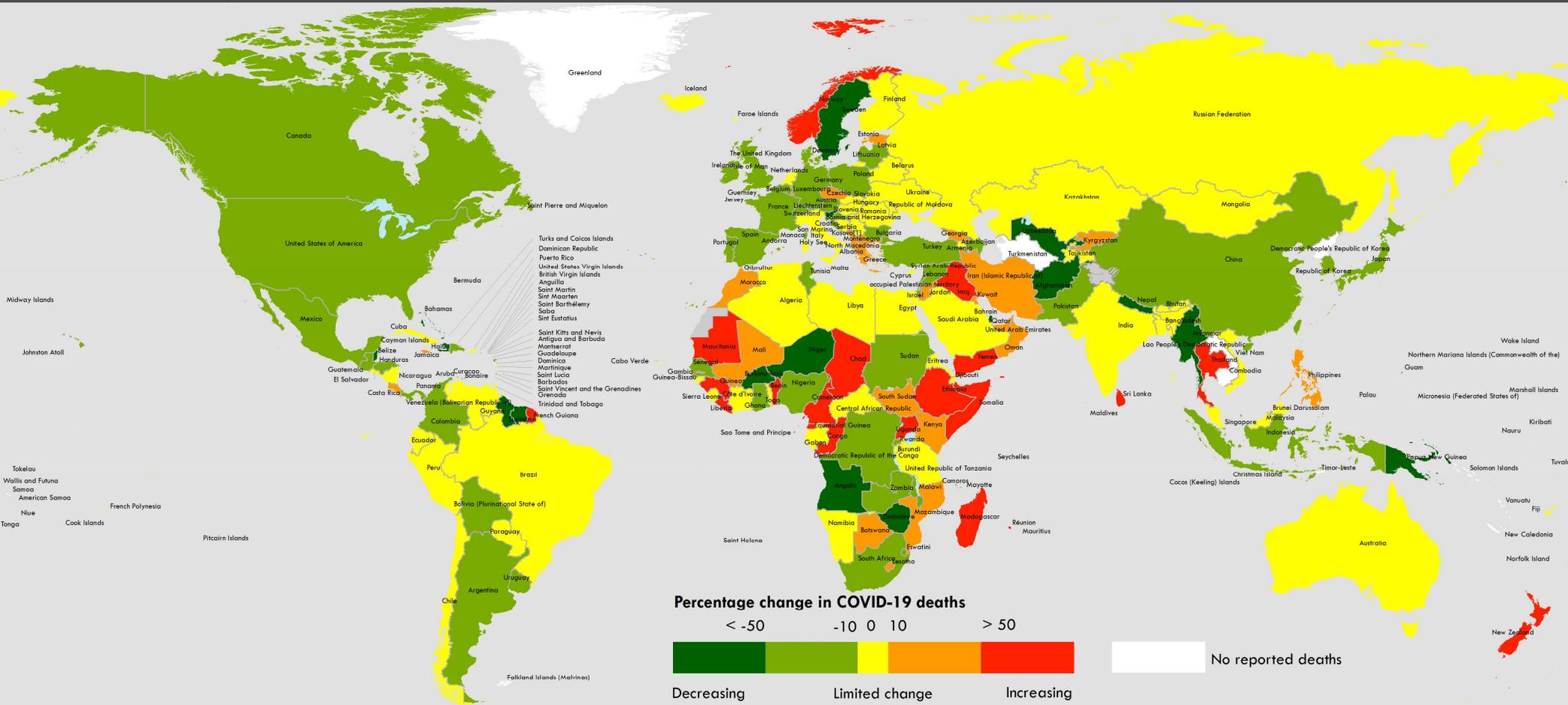


Argentina

total tests as of Feb 07: 5,688,694 (samples tested)



Percentage change in COVID-19 deaths over the last seven days relative to the previous seven days (as of 21 February 2021 10:00AM CET)



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

Not applicable

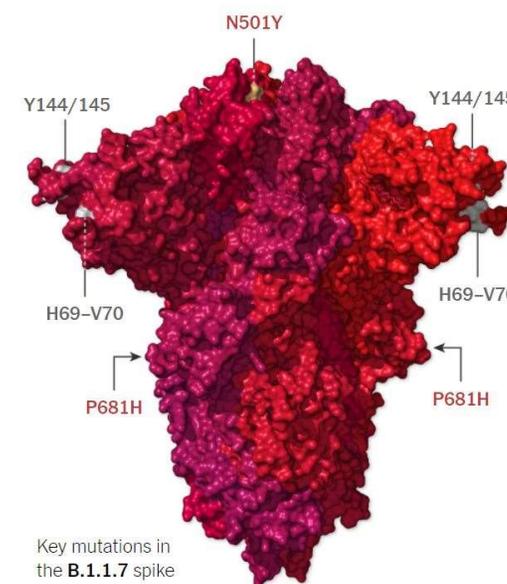
0 2,500 5,000 km
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VARIANT UPDATE

B.1.1.7, 20I/501Y.V1, **VOC202012/01**

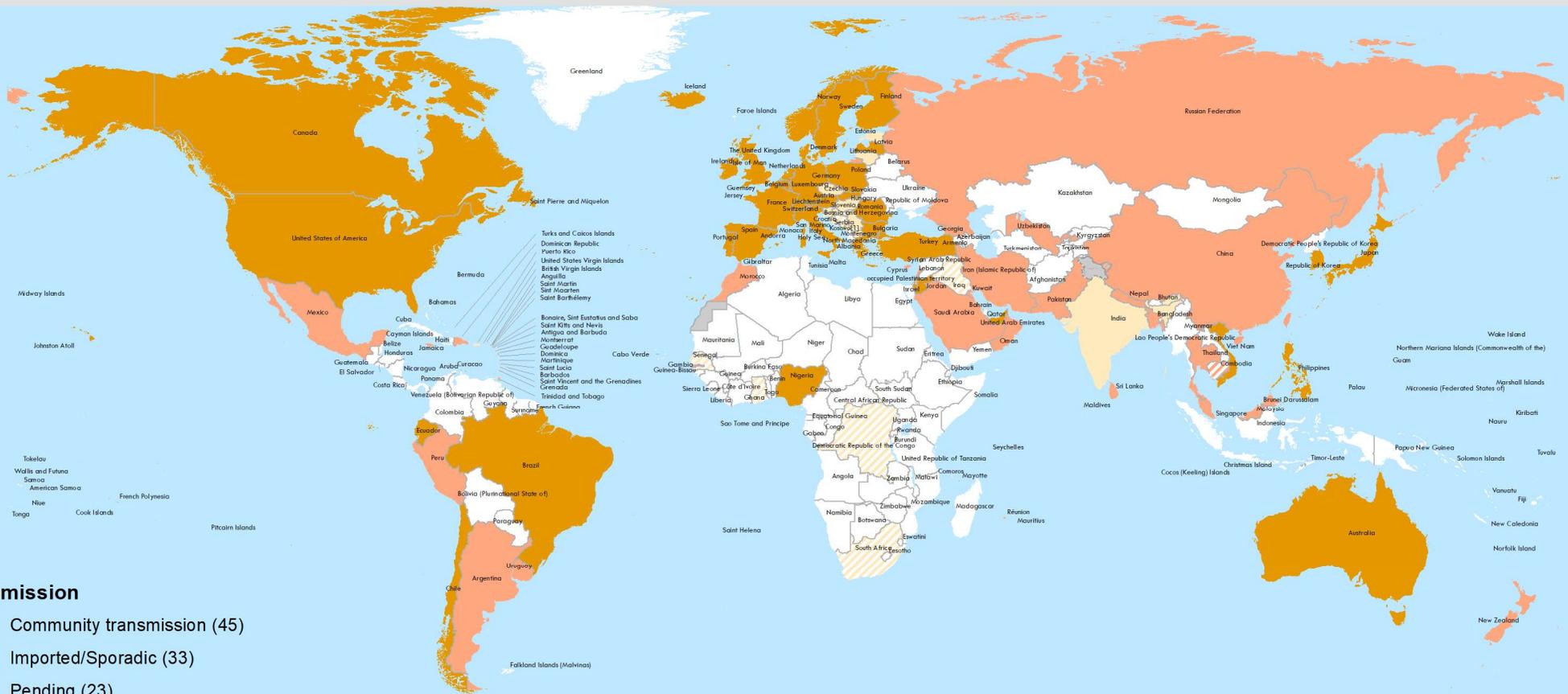
First detected by	United Kingdom
First appearance	20 September 2020
Key mutations	H69/V70 deletion; Y144 deletion; N501Y; A570D; D614G; P681H; S106/G107/F108 deletion in NSP6
Transmissibility*	Increased (43%-82%), increased secondary attack rate (10% to 13%)
Severity*	Likely associated with an increased risk of hospitalisation and death compared to infection with non-VOC viruses.
Neutralization capacity*	Slight reduction but overall neutralizing titers remained above the levels expected to confer protection
Potential impacts on vaccines*	No significant impact on Moderna, Pfizer-BioNTech, and Oxford-AstraZeneca
Potential impacts on diagnostics*	S gene target failure. No impact on Ag RDTs observed
Countries reporting cases (community transmission) as of 23 Feb	101 (45)



<https://www.nytimes.com/interactive/2021/health/coronavirus-variant-tracker.html>

**Generalized findings as compared to non-VOC viruses. Based on emerging evidence from multiple countries, including non-peer-reviewed preprint articles and reports from public health authorities and researchers – all subject to ongoing investigation and continuous revision.*

Countries/territories/areas reporting lineage B.1.1.7 (situation as of 22 February 2021)



Transmission

- Community transmission (45)
- Imported/Sporadic (33)
- Pending (23)

Verification

- Under verification

Not applicable



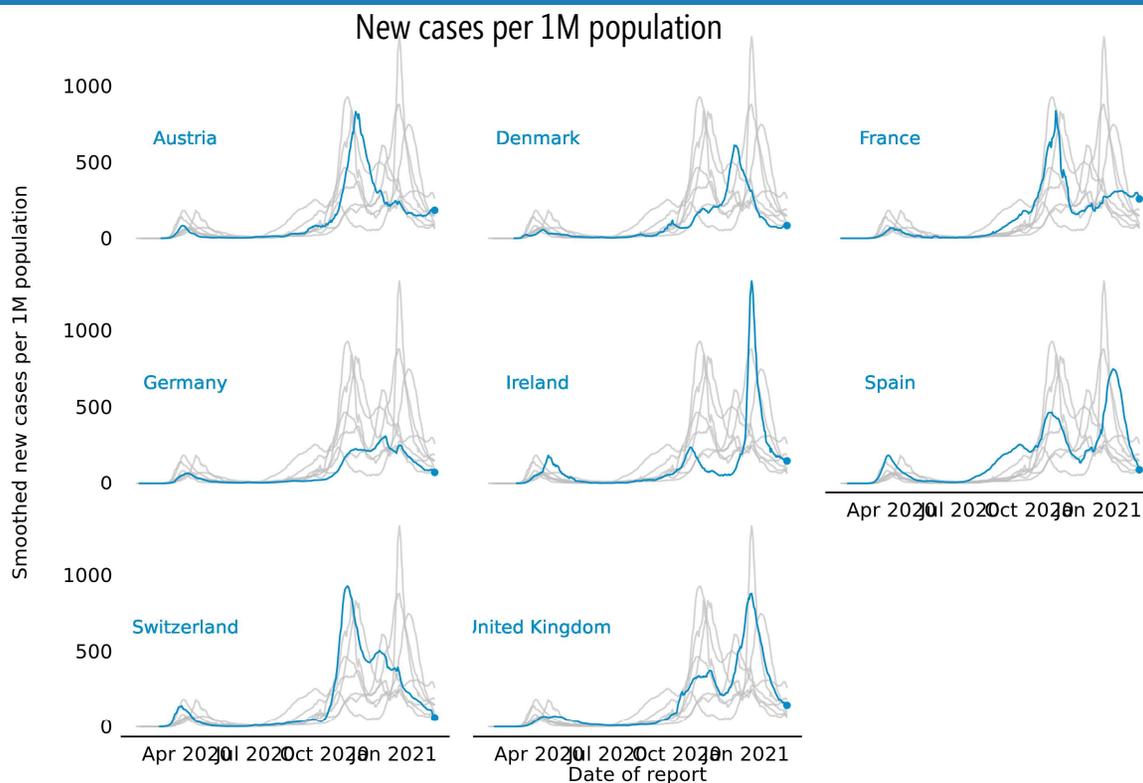
Data Source: World Health Organization
Map Production: WHO Health Emergencies Programme

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Countries reporting community transmission of VOC202012/01

- Where community transmission has been reported, predominantly decreasing trends in new case, hospitalizations, deaths over the past 4 weeks
- Implementation of PHSM has reduced transmission

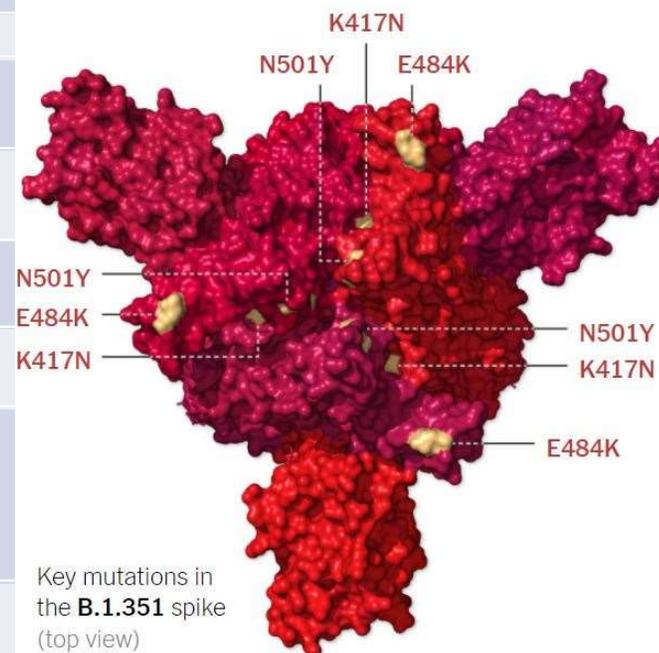


Data taken from COVID Intel database on 2021-02-25.
The lines and associated text show the trend in incidence of COVID-19 cases.

B.1.351, 20H/501Y.V2, VOC202012/02

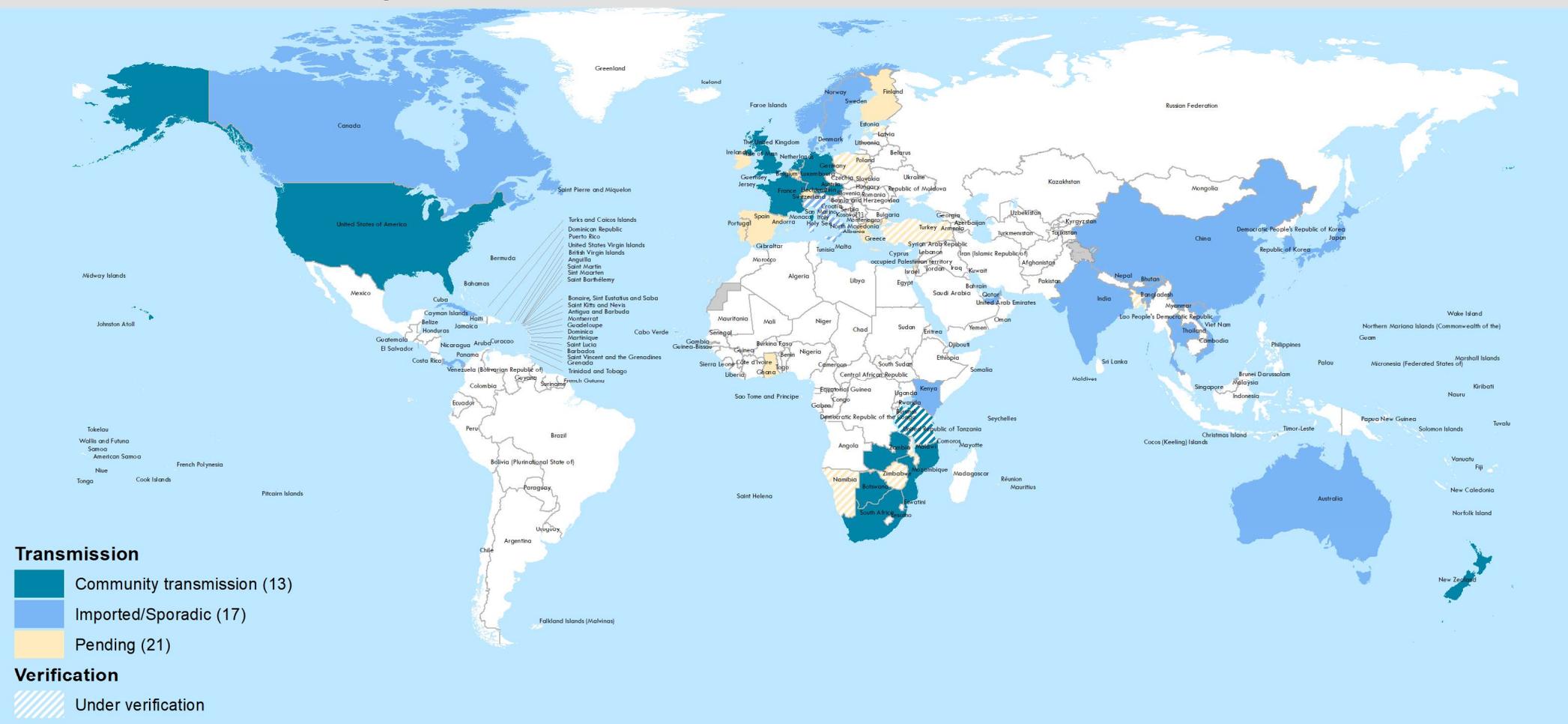
First detected by	South Africa
First appearance	Early August 2020
Key mutations	L242/A243/L244 deletion; N501Y; D614G; E484K; K417N; S106/G107/F108 deletion in NSP6
Transmissibility*	Increased [1.50 (95% CI: 1.20-2.13) times more transmissible than previously circulating variants]
Severity*	No impact reported to date, no significant change in-hospital mortality
Neutralization capacity*	Decreased, suggesting potential increased risk of reinfection
Potential impacts on vaccines*	Reduction in the neutralizing activity, but impact on protection against disease or relative importance of other immune response mechanisms (e.g., T/B-cells), not fully known. Potentially decreased based on small, prelim studies.
Potential impacts on diagnostics*	None reported to date.
Countries reporting cases (community transmissions) as of 23 Feb	51 (13)

*Generalized findings as compared to non-VOC viruses. Based on emerging evidence from multiple countries, including non-peer-reviewed preprint articles and reports from public health authorities and researchers – all subject to ongoing investigation and continuous revision.



<https://www.nytimes.com/interactive/2021/health/coronavirus-variant-tracker.html>

Countries/territories/areas reporting lineage B.1.351 (situation as of 22 February 2021)



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

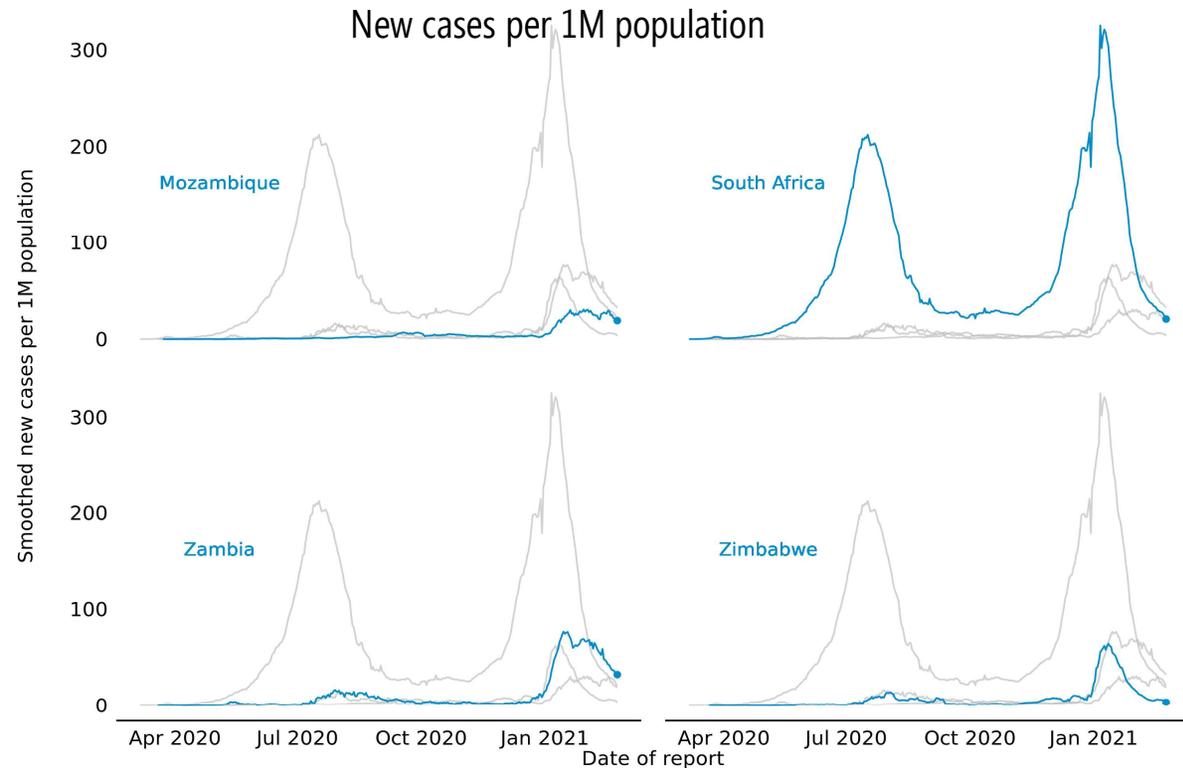


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Countries reporting community transmission of B.1.351

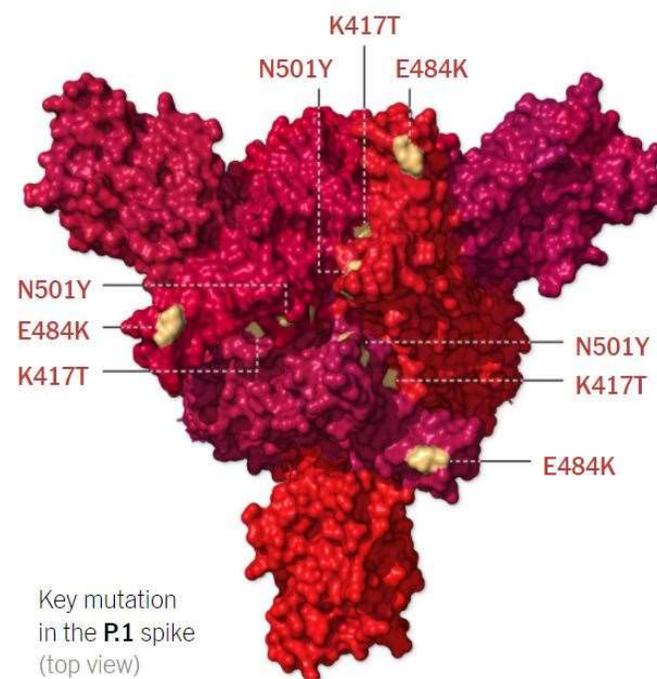
- Observed declines in incidence, hospitalizations, deaths in South Africa and most neighbouring countries
- Implementation of PHSM has reduced transmission



Data taken from COVID Intel database on 2021-02-25.
The lines and associated text show the trend in incidence of COVID-19 cases.

B.1.128.P.1, 20J/501Y.V3

First detected by	Brazil / Japan
First appearance	December 2020
Key mutations	N501Y; D614G; E484K; K417N; S106/G107/F108 deletion in NSP6
Transmissibility*	Suggested to be increased
Severity*	Under investigation, no impact reported to date
Neutralization capacity*	Potential decrease, small number of reinfections reported
Potential impacts on vaccines*	Under investigation
Potential impacts on diagnostics*	None reported to date
Countries reporting cases (Community transmission) as of 23 Feb	29 (3)



<https://www.nytimes.com/interactive/2021/health/coronavirus-variant-tracker.html>

**Generalized findings as compared to non-VOC viruses. Based on emerging evidence from multiple countries, including non-peer-reviewed preprint articles and reports from public health authorities and researchers – all subject to ongoing investigation and continuous revision.*

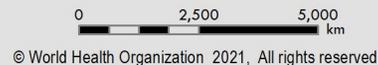
Countries/territories/areas reporting lineage P.1 (situation as of 22 February 2021)



- Transmission**
- Community transmission (3)
 - Imported/Sporadic (18)
 - Pending (8)
- Verification**
- Under verification
 - Not applicable



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

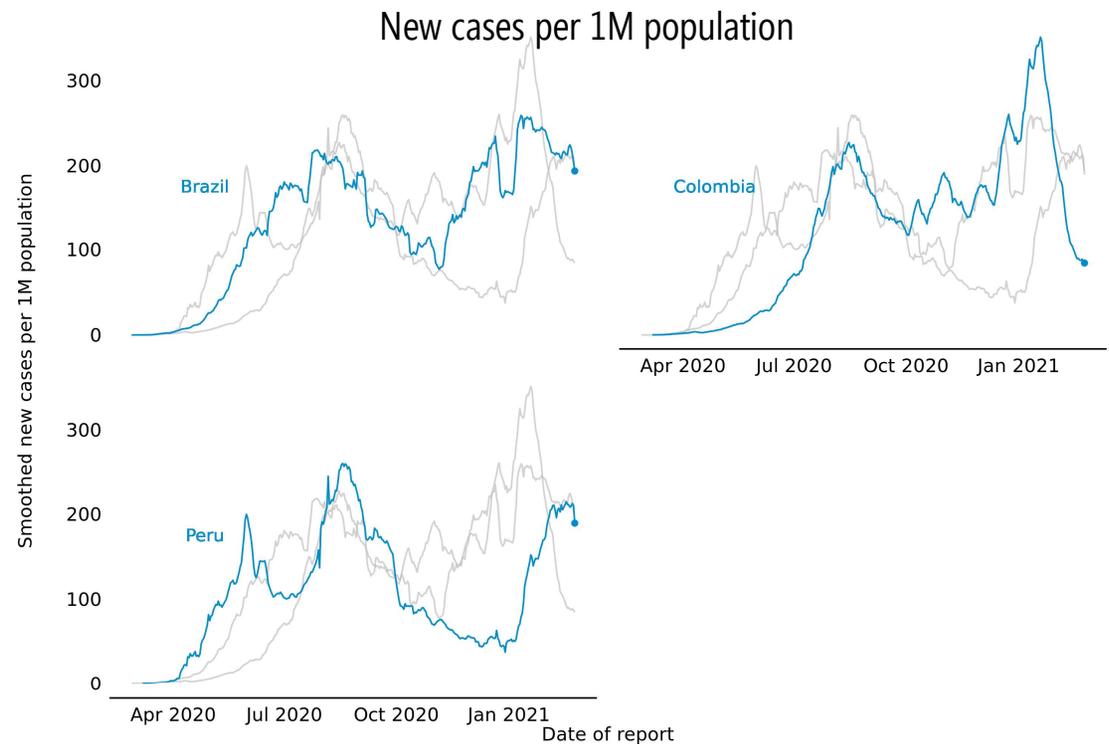


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Countries reporting community transmission of variant P.1

- Incidence rates in Brazil remains elevated, and increasing in Peru
- These countries have highly heterogenous epidemiological patterns, and the relative contribution of variant P.1, as well as potential impact on the effectiveness of PHSM and countermeasures requires further investigation.



REPORTING AND DEFINING VARIANTS

Proposed working definitions and actions

Variant of interest (VOI):

- A SARS-CoV-2 isolate that is phenotypically changed compared to a reference isolate or that has a genome with mutations that lead to amino acid changes associated with established or suspected phenotypic implications;

AND

- has been identified to cause community transmission/multiple COVID-19 case clusters, or has been detected in multiple countries;

OR

- is otherwise assessed to be a VOI by WHO in consultation with the WHO SARS-CoV-2 Virus Evolution Working Group (VEWG).

1. Phenotypic changes include changes in the epidemiology, antigenicity, or virulence or changes that have a negative impact on diagnostics, vaccines, therapeutics or public health and social measures. WHO will provide guidance on amino acid changes with established or suspected phenotypic implications, and may be informed by a database on key amino acid changes, or as reported in the scientific literature.

2. See [WHO Public health surveillance for COVID-19: interim guidance](#) for definitions

Actions for potential VOIs:

• Member States:

- Inform WHO by VOI-associated cases (person, place, time, clinical and other relevant characteristics) through established WHO Country or Regional Office reporting channels.
- Submit full genome sequences and metadata to public database
- Perform field investigations to improve understanding of the potential impacts of the VOI (epidemiology, severity, effectiveness of countermeasures, or other relevant characteristics).

• WHO:

- Assessment by WHO SARS-CoV-2 VEWG. If meets criteria, and if meets criteria, designation as VOI.
- If determined necessary, coordinate lab investigations with Member States and partners.
- Review global epidemiology of VOI.
- Monitor and track global spread of VOI.

Proposed working definitions and actions

Variant of concern (VOC):

- A VOI (as defined above) that, through a comparative assessment, has been demonstrated to be associated with:
 - Increase in transmissibility or change in the epidemiology;
 - Increase in virulence or change in disease presentation; or
 - Decrease in effectiveness of available diagnostics, vaccines, therapeutics, or public health and social measures.

Actions:

- **WHO for a potential VOC:**
 - Assessment and if meets criteria, designation as VOC.
 - Assessment by VEWG and, if determined necessary, coordinate lab investigations with Member States and Partners.
 - Conduct rapid risk assessment as warranted.
 - Communicate new designations and findings to Member States and public
 - Evaluate WHO guidance and update, if necessary.
- **Member States, if a VOC is identified:**
 - Report initial cases/clusters to WHO through IHR mechanism.
 - Submit complete genome sequences and associated metadata to a publicly available database.
 - Where capacity exists and in coordination with the international community, perform field investigations to improve understand of the potential impacts of the VOC on COVID-19 epidemiology, severity, effectiveness of countermeasures, or other relevant characteristics.
 - Perform laboratory assessments on the impact of the VOC on diagnostic methods, immune responses, antibody neutralization or other relevant characteristics, when such lab capacity is available.

WHO resources and updates

Resources

- [COVAX Statement on New Variants of SARS-CoV-2](#)
- [SARS-CoV-2 genomic sequencing for public health goals: Interim guidance, 8 January 2021](#)
- [Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health](#)
- [Q&A on Coronavirus disease \(COVID-19\): Virus Evolution](#)

Updates

- Disease Outbreak News - [SARS-CoV-2 Variants](#)- 29 December 2020
- [Weekly Epidemiological Updates](#) – From 12 January to date

Monitoring and assessing SARS-CoV-2 variants and their impact



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Overall objectives and principles

- Objectives

- Coordinate the components of a global harmonized mechanism for monitoring and assessing SARS-CoV-2 variants and their impact
- Identify critical priorities, thresholds, and triggers for decision-making
- Enhance the multi-disciplinary coordination mechanism to collect, analyze, and share data to inform decision-making
- Leverage and enhance existing technical networks, systems, and expert groups

- Principles

- *Evidence-based*: Decisions and communications will be evidence-based, transparent, and consistent.
- *Sustainability*: Member States will be supported to develop and strengthen sustainable and agile capacities, which can be adapted to new threats.
- *Equity*: Equity is a key consideration in analysis, development, and communication of recommendations.
- *Partnerships*: Stronger and more effective collaboration and coordination across WHO and with external partners is necessary.

Two elements of the approach

1. Risk monitoring & assessment framework

- Highlight various elements that we need to consider for decision-making
- Will guide data collection, sharing, analysis

2. Coordination mechanism

- Architecture for who contributes, when, and on what

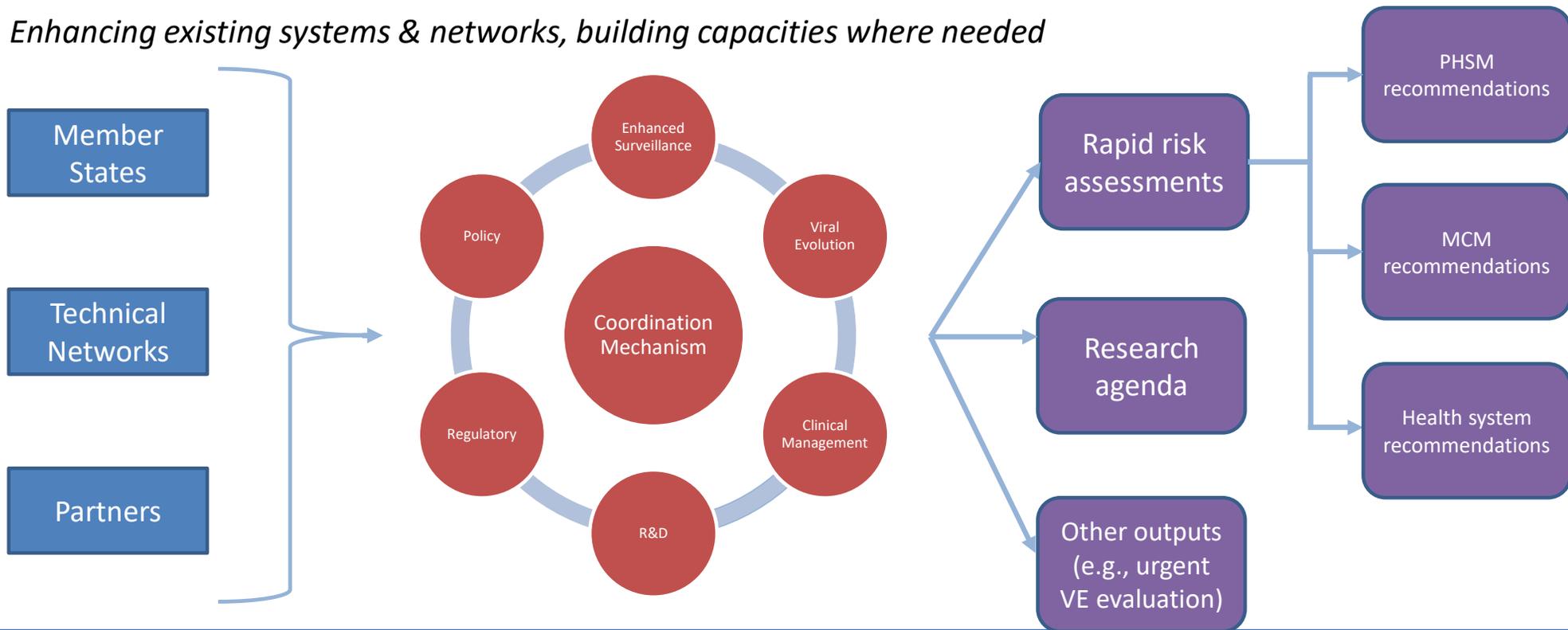
System is already established – many components are in progress, need to enhance them for longer term and more sustainable use

A globally coordinated risk monitoring & assessment framework necessary

- Variants are expected, but not every variant of interest will be of concern
 - Important to identify and assess variants, and communicate accordingly
- Need to evaluate the impact of SARS-CoV-2 variants on public health and social measures, vaccination programmes, medical countermeasures, health systems
 - Globally-coordinated response is essential, including any changes to diagnostics, therapeutics, or vaccines and vaccination policies and strategies (if needed)
- An integrated framework can identify what decisions must be made and what data will support the decision-making

Monitoring and assessing SARS-CoV-2 variants

Enhancing existing systems & networks, building capacities where needed



Quick update: WHO guidance on SARS-CoV-2 sequencing

SARS-CoV-2 genomic sequencing for public health goals

Interim guidance
8 January 2021



Key messages:

- Global surveillance of SARS-CoV-2 genetic sequences and related metadata contributes to the COVID-19 outbreak response. This contribution includes tracking the spread of SARS-CoV-2 geographically over time and ensuring that mutations that could potentially influence pathogenicity, transmission or countermeasures (such as vaccines, therapeutics and diagnostics) are detected and assessed in a timely manner.
- While the cost and complexity of genetic sequencing have dropped significantly over time, effective sequencing programmes still require substantial investment in terms of staff, equipment, reagents and bioinformatic infrastructure. Additionally, effective collaboration is needed to ensure that generated data are of good quality and are used in a meaningful way.
- Countries are encouraged to rapidly deposit SARS-CoV-2 sequences in a public database in order to share them with the scientific community for public health purposes. Investments in a tiered global sequencing network for SARS-CoV-2 will contribute to the development of resilient, high-quality global sequencing programmes for the detection and management of other outbreak pathogens in the future.

Background

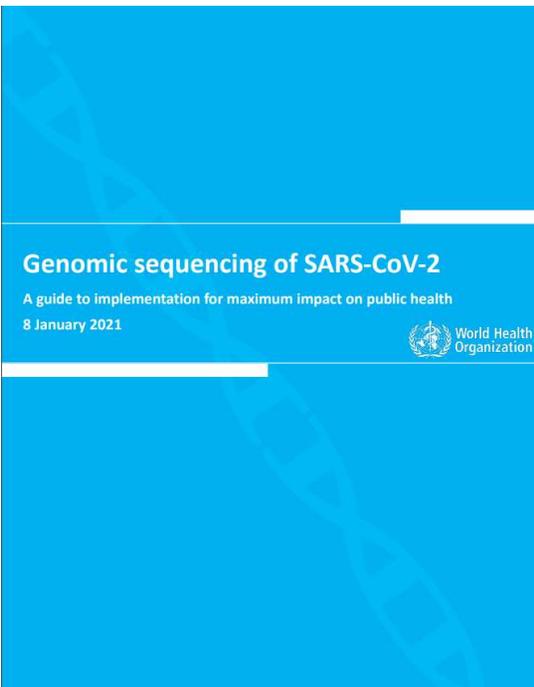
Over the last decade, genetic sequence data (GSD) of pathogens have come to play a pivotal role in the detection and management of infectious disease outbreaks, supporting the development of diagnostics, drugs and vaccines, and informing the outbreak response (1–11). With the emergence of the novel coronavirus, later named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the importance of GSD has been further underlined. More than 280 000 full genome sequences have been shared via publicly accessible databases within a year of the initial identification of SARS-CoV-2 (12). Near real-time analysis of data has directly impacted the public health response (12–16). The public health objectives of SARS-CoV-2 genomic sequencing are listed in Table 1.

The growing understanding of how sequence information can contribute to improved public health is driving global investments in sequencing facilities and programmes. The falling cost and complexity of generating GSD provides opportunities for expanding sequencing capacity; however, challenges to widespread implementation remain, and sequencing capacity and data are not evenly distributed around the world, with overrepresentation of SARS-CoV-2 GSD from high-income countries.

Table 1. Public health objectives of SARS-CoV-2 genomic sequencing

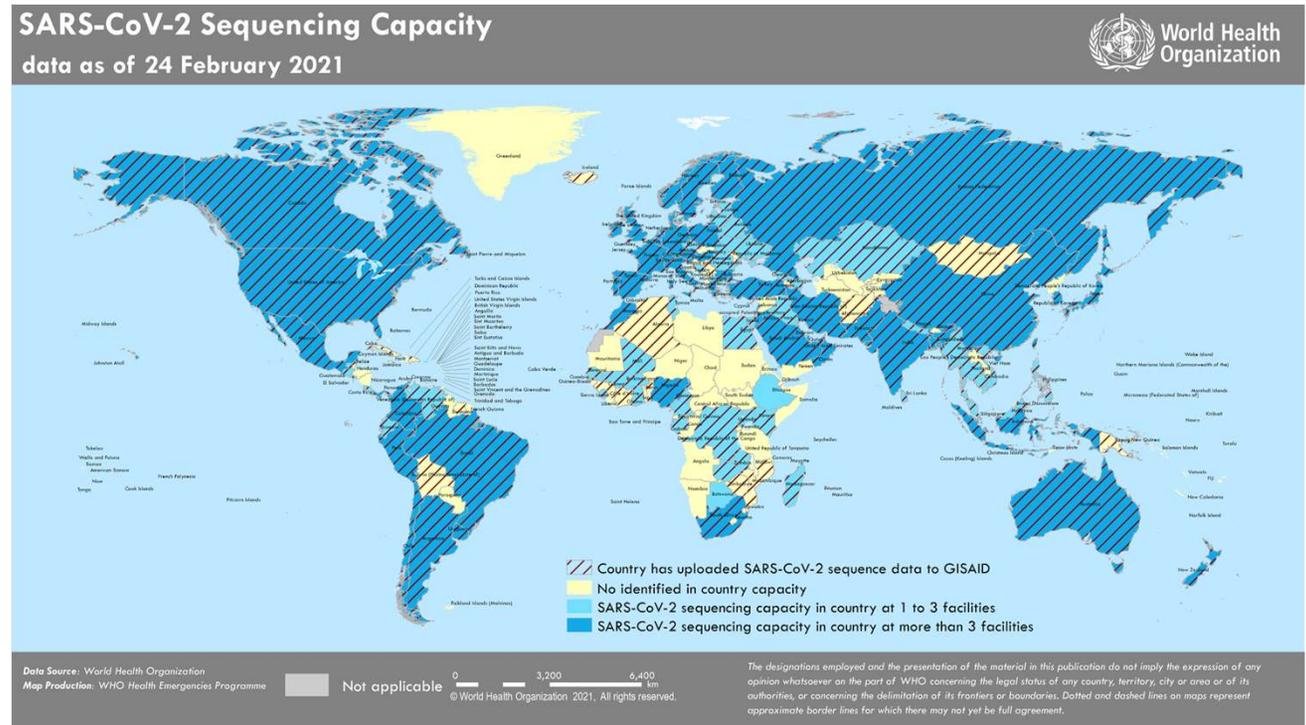
Activities that require a limited effort and once achieved might need either no sequencing or occasional sequencing for follow-up	Activities that require sustained sequencing activities over a longer period of time
<p>Identify SARS-CoV-2 as the causative agent of disease.</p> <ul style="list-style-type: none"> Develop diagnostics for SARS-CoV-2. Support the development of therapies and vaccines. Investigate date of introduction into humans and investigate SARS-CoV-2 origin (ongoing). <p>Research</p> <ul style="list-style-type: none"> Evaluate and improve understanding of this phenomenon. On the individual level, differentiate between prolonged infection and reinfection. 	<p>SARS-CoV-2 evolution and its impact on:</p> <ul style="list-style-type: none"> Change in viral behaviour (phenotypic change), e.g. transmissibility or pathogenicity. Immunity (from vaccines or natural infection). Diagnostics (e.g. molecular, serology, antigen assays). Therapeutic interventions (e.g. monoclonal antibodies). <p>Monitor viral movement and activity:</p> <ul style="list-style-type: none"> Investigate geographic spread and reintroductions between populations. Investigate outbreaks in specific settings and populations (e.g. in hospitals). Track zoonotic reintroduction in both directions over the species barrier. Monitor environmental and waste water. Support clinical surveillance by quantifying the period of transmission and evaluating efforts, and by estimating the transmission level in the population.

- Practical considerations when implementing a sequencing programme
- Data sharing recommendations
- Applications of genomics to COVID-19
- Practical guidance on technical aspects (logistics, biosafety, technology selection, bioinformatics protocols and analysis tools)
- Checklist for setting up a programme



Global SARS-CoV-2 Sequencing Capacities

- **Globally:**
 - **523,778** WGS in GISAID
 - **134/194 (69%)** countries submitted WGS
 - **5%** of sequences with metadata
- **GISRS:**
 - At least **61% GISRS labs** submitted WGS to GISAID
 - **95 labs from 78 countries**
 - **32 GISRS labs** support sequencing for other GISRS and non-GISRS labs



Next steps

- Definitions and actions required for SARS-CoV-2 VOI/VOC
- Nomenclature for VOC
- Coordination of Research and Development on variants
 - Transmission, severity, potential impacts on diagnostics, therapeutics and vaccines
- Information Sharing
 - WHO Weekly Situation Rep
 - EIS/DON
 - Guidance
 - MS Briefings
- Global Consultations
- Partner Coordination