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Sent:	February 23, 2021 8:57 AM
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Cc:	Clement Chris (NHQ-AC); VanDalen Madison (NHQ-AC)
Subject:	FW: WHO variant webinar
Attachments:	03.02. EPI-WIN webinar Variants.pdf

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Subject: WHO variant webinar

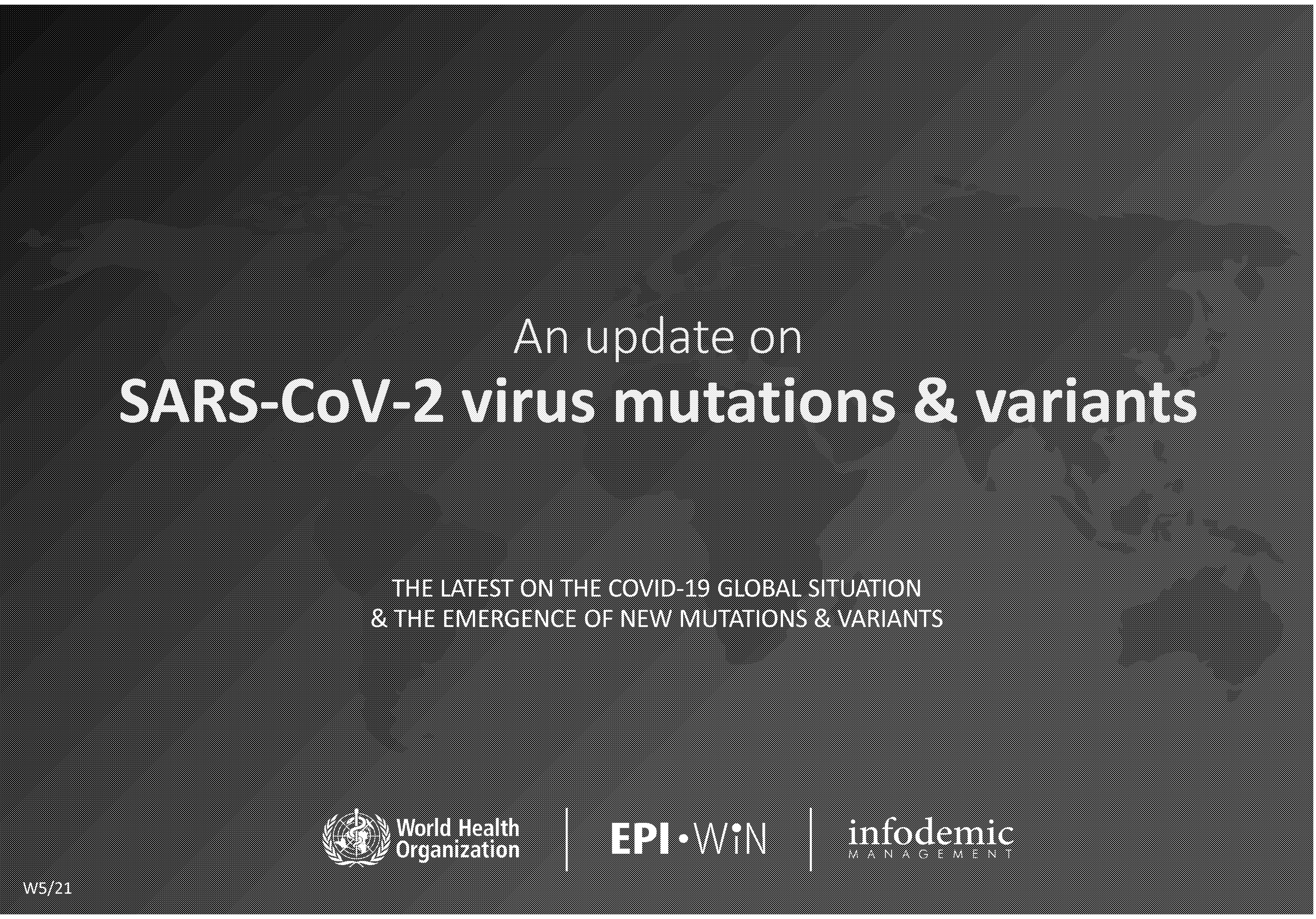
Commissioner,

I thought you might be interested in the WHO webinar on variants. For the most part the material has all been covered at morning ops but nice to have it all in one place.

The you tube link is below and the slides are attached.

Jenn

https://www.youtube.com/channel/UC-t0AL4GoNJYJOOtt2UhvMg



An update on

SARS-CoV-2 virus mutations & variants

THE LATEST ON THE COVID-19 GLOBAL SITUATION
& THE EMERGENCE OF NEW MUTATIONS & VARIANTS

World Health Organization | EPI·WiN | infodemic MANAGEMENT

W5/21

Current global situation

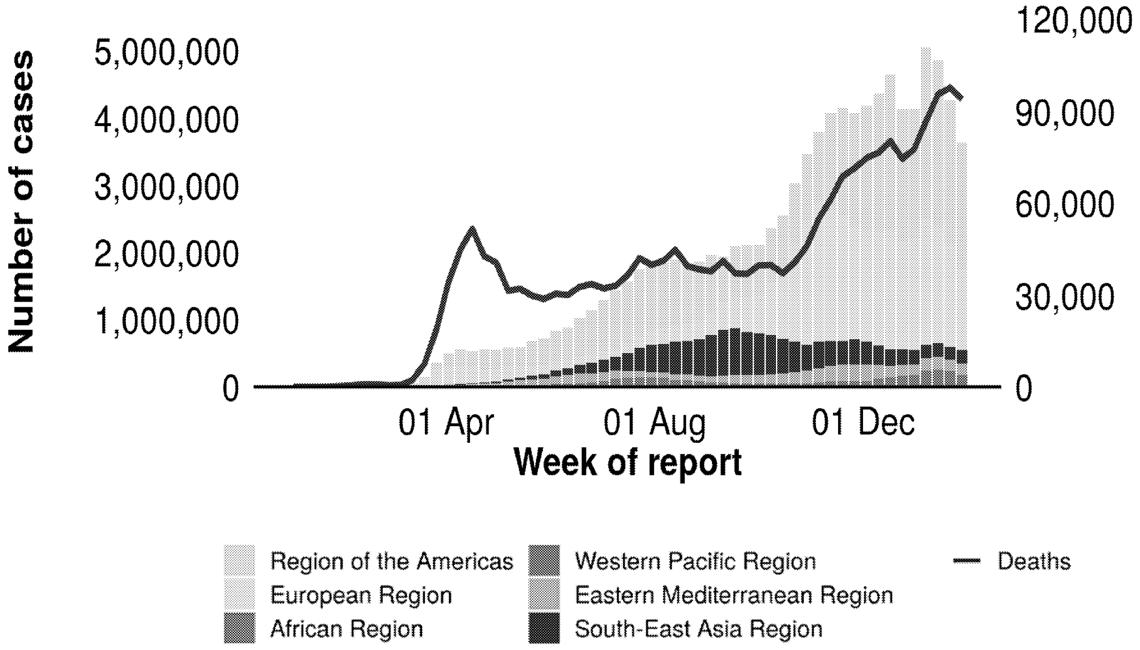
As of 31 January 2021, 10:00AM CEST

- **> 101 million cases**
- 5 countries with highest cumulative number of cases
  - United States of America
  - India
  - Brazil
  - Russian Federation
  - The United Kingdom

- **> 2.2 million deaths**
- 5 countries with highest cumulative number of deaths
  - United States of America
  - Brazil
  - Mexico
  - India
  - The United Kingdom

Current global situation

Cases reported to WHO as of 31 January 2021, 10:00AM CEST

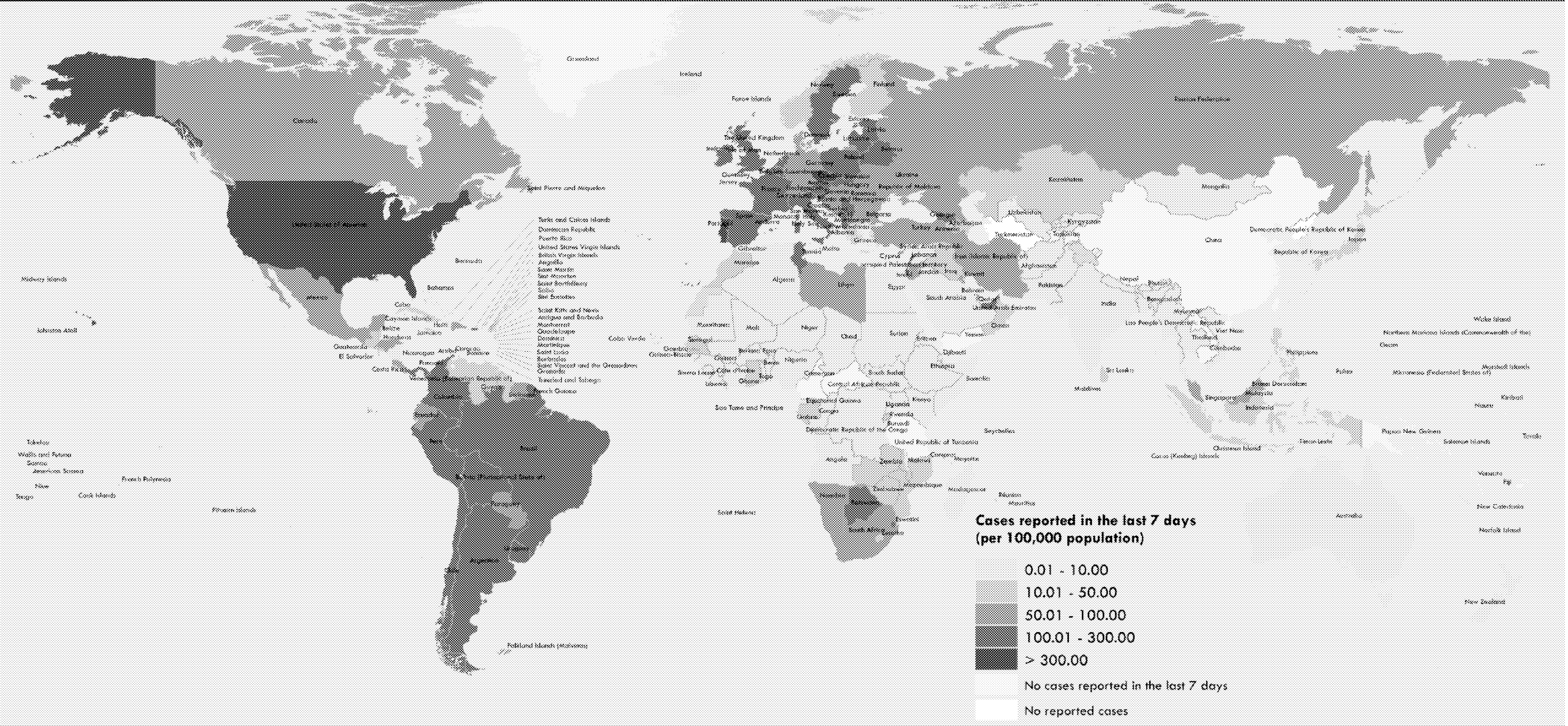


* Data are incomplete for the current week. Cases depicted by bars; deaths depicted by line

COVID-19 cases reported in the last 7 days

Per million population

FROM 25 to 31 JANUARY 2021, 10:00 AM CEST



Cases reported in the last 7 days
(per 100,000 population)

- ▨ 0.01 - 10.00
- ▨ 10.01 - 50.00
- ▨ 50.01 - 100.00
- ▨ 100.01 - 300.00
- ▨ > 300.00
- ☐ No cases reported in the last 7 days
- ☐ No reported cases

Data Source: *World Health Organization, United Nations Population Division (population prospect 2020)*
Map Production: *WHO Health Emergencies Programme*

▨ Not applicable

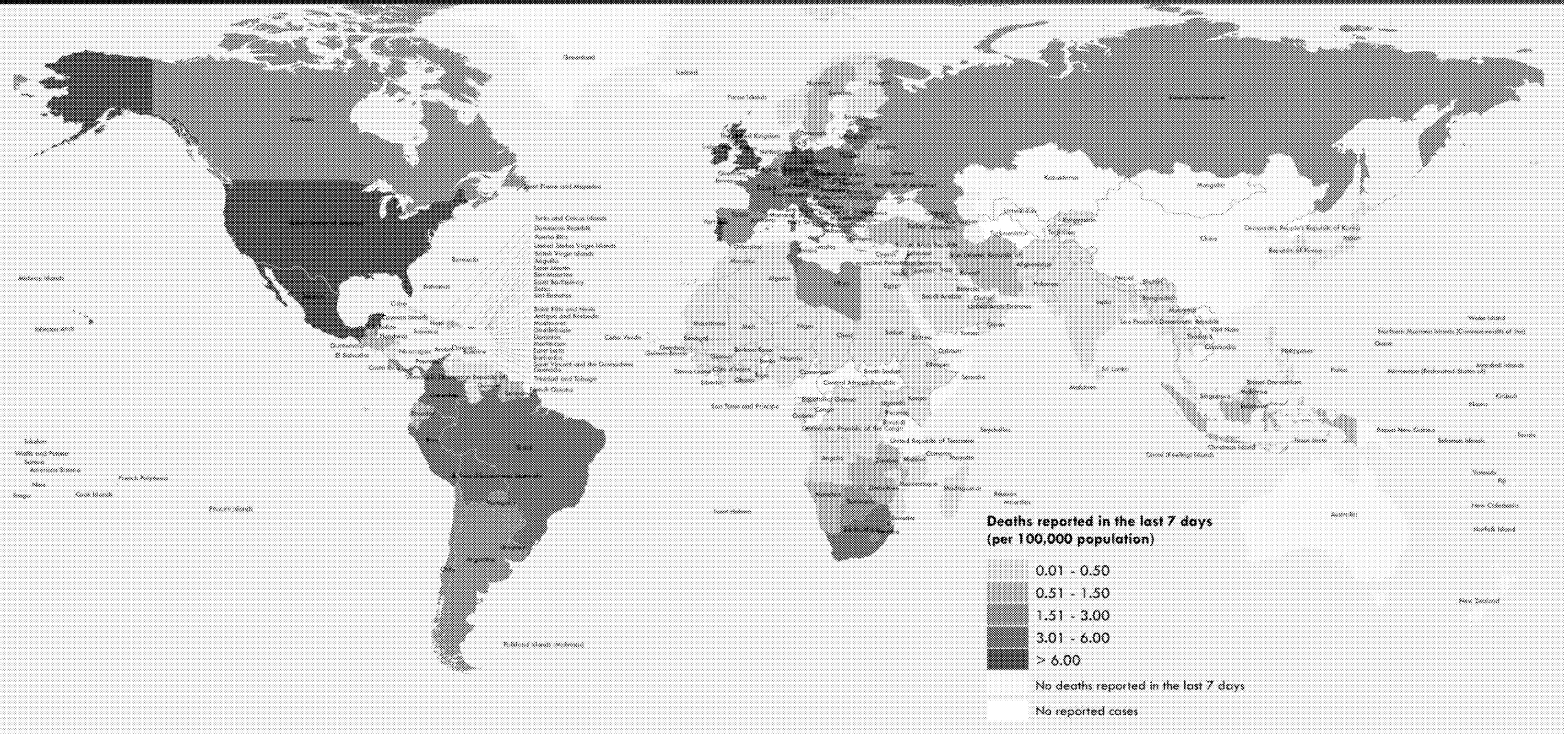
0 2,500 5,000 km

The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement. [1] All references to Kosovo in this document should be understood to be in the context of the United Nations Security Council resolution 1244 (1999). Number of cases of Serbia and Kosovo (UNSCR 1244, 1999) have been aggregated for visualization purposes. Data for Bonaire, Sint Eustatius and Saba have been disaggregated and displayed at the subnational level.

COVID-19 deaths reported in the last 7 days

Per million population

FROM 25 to 31 JANUARY 2021, 10:00 AM CEST



Deaths reported in the last 7 days (per 100,000 population)

- ▨ 0.01 - 0.50
- ▨ 0.51 - 1.50
- ▨ 1.51 - 3.00
- ▨ 3.01 - 6.00
- ■ > 6.00
- ▨ No deaths reported in the last 7 days
- □ No reported cases

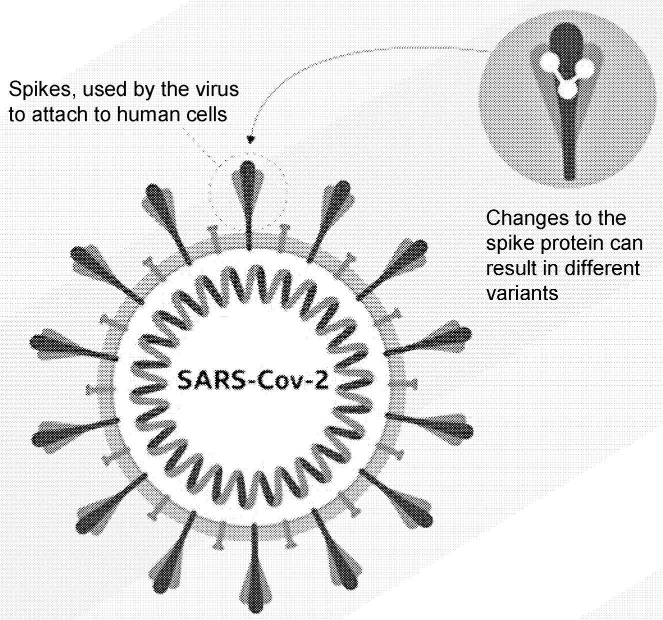
***Data Source**: World Health Organization,*
United Nations Population Division (population prospect 2020)
***Map Production**: WHO Health Emergencies Programme*

▨ Not applicable

0 2,500 5,000 km

All viruses change over time

- **It is normal for viruses to change over time through mutations. The emergence of new variants is to be expected**
  - most mutations have no impact on the virus itself
  - some may be harmful to the virus's survival
  - few may result in an advantage to the virus and can make it more transmissible, increase disease severity or influence efficacy of therapeutics or vaccines
  - When these variants increase the risk to human health they are considered to be **variants of concern (VOC)**
- **The potential for virus mutations increases with the frequency of human and animal infections**
- **SARS-CoV-2, tends to change more slowly than other RNA virus such as influenza viruses**



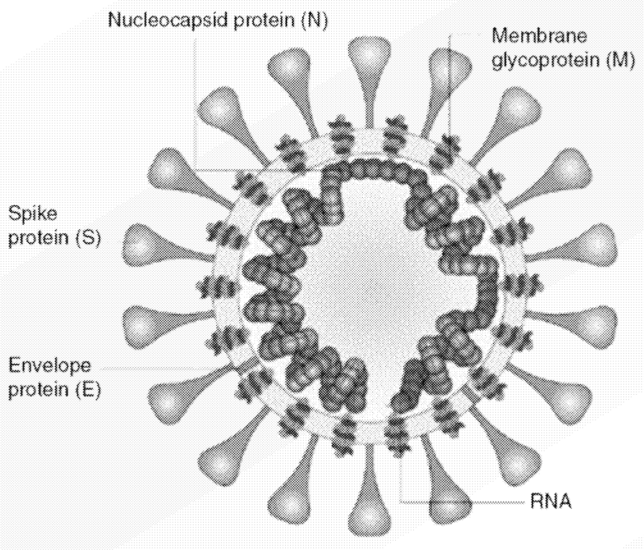
Spikes, used by the virus to attach to human cells

Changes to the spike protein can result in different variants

New emerging SARS-CoV-2 variants

- **New SARS-CoV-2 variants:**
  - Variant that emerged in Denmark in September 2020 related to mink farming
  - Variant detected in the United Kingdom in December 2020
  - Variant detected in South Africa in December 2020
  - Variant detected in Japan on 9th January 2021 among persons coming back from Brazil

- All these variants involve **genetic mutations coding for the spike protein**
- The spike protein of SARS-CoV-2 is targeted by most vaccines currently approved or in development; mutations of the spike protein are therefore closely monitored



Nature Reviews | Microbiology

What do we mean by mutations, variants and strains?

- **Mutation** refers to the actual change in the genomic sequence
  - The role of most individual mutations is still unclear and is being studied
  - Key mutations for viral evolution concern the **spike protein region.** Spike proteins stick up from the virus and give it the so characteristic "crown" appearance. In order to invade the host the spikes latch onto human cells. The spike's **Receptor Binding Domain** recognizes and binds to the host receptor, the angiotensin converting enzyme (ACE), and is also the primary target of the immune response
  - How we refer to mutations is illustrated by the following example:
    - **D614G** means that the amino acid at position 614 of the spike protein, normally an aspartic acid (referred to as D) has been replaced by glycine (referred as G)
- **Variants** are genomes that differ in sequence. Variants can differ by 1 mutation or many
- **Strain** is a variant that has a demonstrably different phenotype (e.g., a difference in antigenicity, transmissibility, or virulence).

Drivers of the emergence of variants for SARS-CoV2

Main drivers for the emergence of new variants[1]:

- **Natural selective pressure from antibodies**

  Variants that confer a competitive advantage with respect to viral replication, transmission, or can escape from immunity will increase in frequency, and outcompete other circulating viruses

- **Chance events or "founder effect"**

  Occurs when a variant takes off not because it is more infectious, but by chance, mutations were carried by one or more of the ancestors or it benefitted from more favorable conditions for its spread (early superspreading events, high risk population groups…)

- **The interplay of natural selection and chance events shapes virus evolution**

Other potential mechanisms for viral evolution for SARS-CoV2:

- **Species-jumping event or host shifts**

  When a pathogen invades and establishes in a new host species (major source of emerging diseases)

- **Persistent infections in immunocompromised hosts[2]**

  Increased genetic diversity and potential elevated rates of evolution compared to acute infections

- **Mutations affecting the proofreading function**

  Which could lead to a higher number of mutations in a shorter time period

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1. Genetic Variants of SARS-CoV-2—What Do They Mean?
2. Persistence and Evolution of SARS-CoV-2 in an Immunocompromised Host

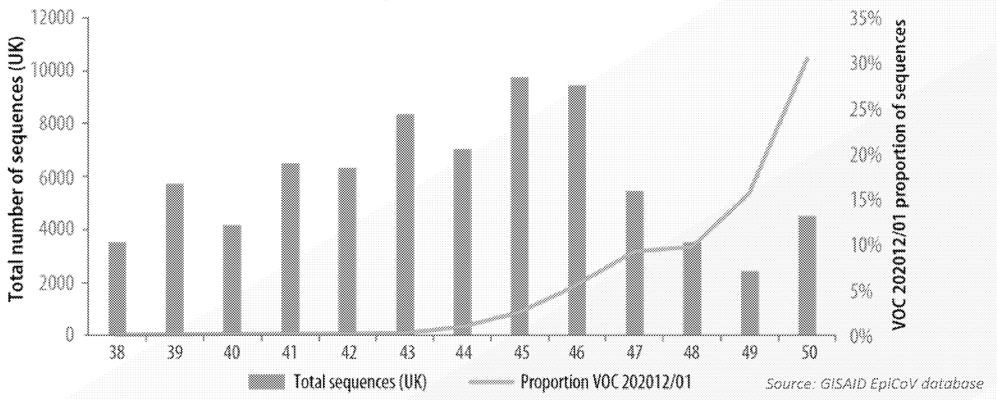
SAR-CoV-2 variant emerged among mink in Denmark

- A SARS-CoV-2 variant referred to as the 'Cluster 5' variant was linked to infection among farmed mink
- This variant was subsequently transmitted to humans
- In response to the outbreak in mink and to stop the spread of the 'Cluster 5' variant, 17 million mink were culled in Denmark in November 2020
- Danish authorities have identified only 12 human cases of the 'Cluster 5' variant and it does not appear to have spread more widely

https://science.sciencemag.org/content/371/6525/172

The variant detected in the United Kingdom

Fraction of SARS-CoV-2 sequences classified as VOC 202012/01 per week in the UK



Source: GISAID EpiCoV database

- On 14 December 2020, authorities of the United Kingdom reported a variant referred to as **SARS-CoV-2 VOC 202012/01** (Variant of Concern, year 2020, month 12, variant 01)
- This variant has an unusually large number of mutations involving 17 mutations on the spike protein
- SARS-CoV-2 VOC 202012/01 has become the predominant variant circulating in the UK

https://www.gov.uk/government/publications/investigation-of-novel-sars-cov-2-variant-variant-of-concern-20201201

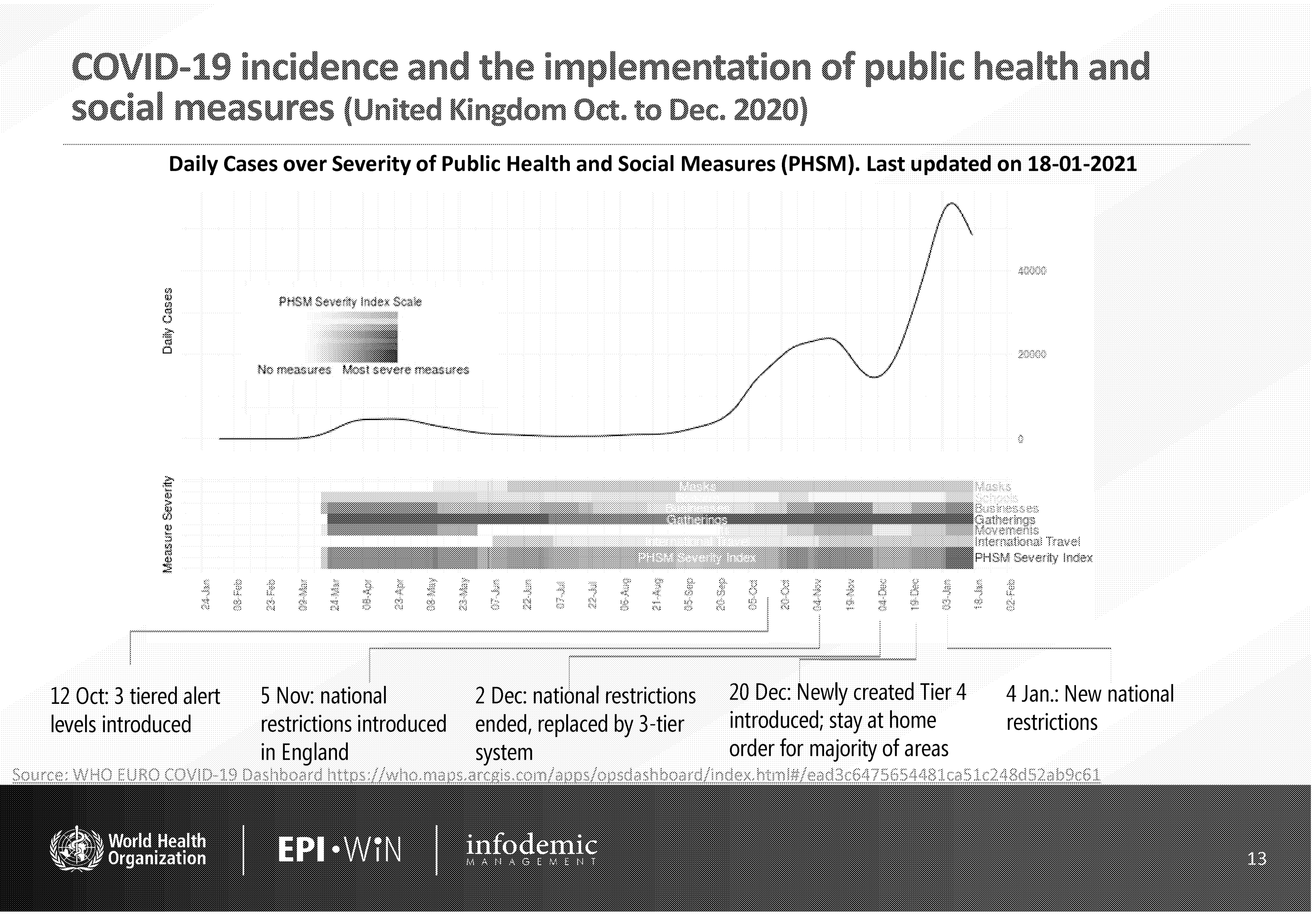
The variant detected in the United Kingdom

Countries, territories and areas reporting SARS-CoV-2 VOC 202012/01 as of 2 February 2021

On the 2nd February, **80 countries have reported VOC**, yet most countries lack sequencing capacity so the variant is likely spreading undetected in many places.

https://www.gov.uk/government/publications/investigation-of-novel-sars-cov-2-variant-variant-of-concern-20201201
https://www.who.int/publications/m/item/weekly-epidemiological-update---2-february-2021

Source: WHO



COVID-19 incidence and the implementation of public health and social measures (United Kingdom Oct. to Dec. 2020)

Daily Cases over Severity of Public Health and Social Measures (PHSM). Last updated on 18-01-2021

12 Oct: 3 tiered alert levels introduced

5 Nov: national restrictions introduced in England

2 Dec: national restrictions ended, replaced by 3-tier system

20 Dec: Newly created Tier 4 introduced; stay at home order for majority of areas

4 Jan.: New national restrictions

Source: WHO EURO COVID-19 Dashboard https://who.maps.arcgis.com/apps/opsdashboard/index.html#/ead3c6475654481ca51c248d52ab9c61

What do we know so far on the VOC 202012/01 behavior

Higher transmissibility but no evidence of increased severity

- Scientists have concluded that available evidence indicates the VOC has a **substantial transmission advantage**[1]
- As of Jan. 5th, contact tracing data indicated **higher attack rates** among contacts, **increasing from 11.0% for the wild virus contacts to 14.7% for those from VOC**[2]
- Preliminary studies indicate there may be association between infection with the variant and increased viral load, but this needs to be further studied[3]
- A matched cohort study to inform a preliminary assessment, found no statistically significant difference in hospitalization and 28-day case fatality between cases of VOC and wild-type virus2

Table: Cohort study on variant cases frequency matched to wild-type on a 1:1 basis by age group, sex, upper tier local authority (UTLA) of residence and two-week time-period for specimen date

	VOC 202012/01	Wild type s	P value
Hospital admission	16 (0.9%)	26 cases (1.5%)	0.162
28-day case fatality	12 (0.9%)	10 (0.7%)	0.65

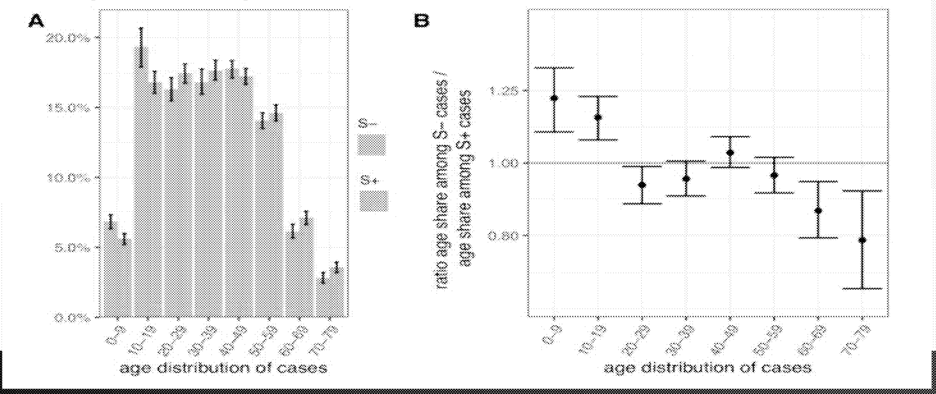
- **There is currently no evidence that this variant causes more severe disease or higher mortality**[4]
  - Available evidence suggest the variant does not escape neutralizing antibodies from natural immunity[5]
  - Vaccinations are therefore likely to protect from this strain but this remains to be evaluated, neutralization assays with antibodies originating from vaccination immunity are currently underway

1. NERVTAG/SPI-M Extraordinary meeting on SARS-CoV-2 variant of concern 202012/01 (variant B.1.1.7)
2. Investigation of novel SARS-CoV-2 variant Variant of Concern 202012/01 Technical briefing 2
3. S-variant SARS-CoV-2 is associated with significantly higher viral loads in samples tested by ThermoFisher TaqPath RT-QPCR
4. Estimated transmissibility and severity of novel SARS-CoV-2 Variant of Concern 202012/01 in England
5. Impact of B.1.1.7 variant mutations on antibody recognition of linear SARS-CoV-2 epitopes

Are children more at risk of the VOC 202012/01 variant?

- SARS-CoV2 wild virus, as it emerged, has manifested a reduced ability to infect children. In particular, children under 10 have been relatively spared from infection and its most severe effects,
- It is highly likely that the VOC enhanced transmissibility also affects children, however the size effect in different age groups is still unknown
- Preliminary data suggest a slight shift in infection rates, with a statistically significant largest share of under 20s among reported VOC than non VOC[1,2,3]
    - ➢ However, this finding is likely influenced by the lockdown period, with lockdown in force but schools open
    - ➢ Further research is ongoing on how the VOC affects different age-groups

Figure :
A. Analysis of age distribution of the new strain of Coronavirus (S-) as compared to wild virus (S+)
B. ratio age share among S- / S+ cases[1]

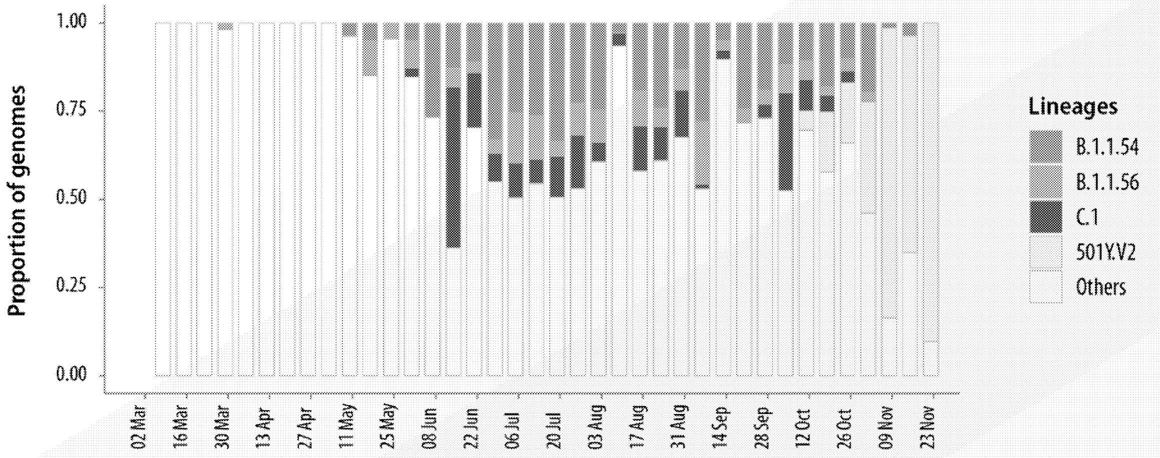


1. Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data
2. NERVTAG/SPI-M Extraordinary meeting on SARS-CoV-2 variant of concern 202012/01 (variant B.1.1.7)
3: We have entered a dangerous new phase of the pandemic. Andrew Hayward

World Health Organization | EPI•WiN | infodemic MANAGEMENT

Another variant emerges in South Africa

Graph: Frequency & distribution of SARS-CoV-2 lineages circulating in South Africa over time

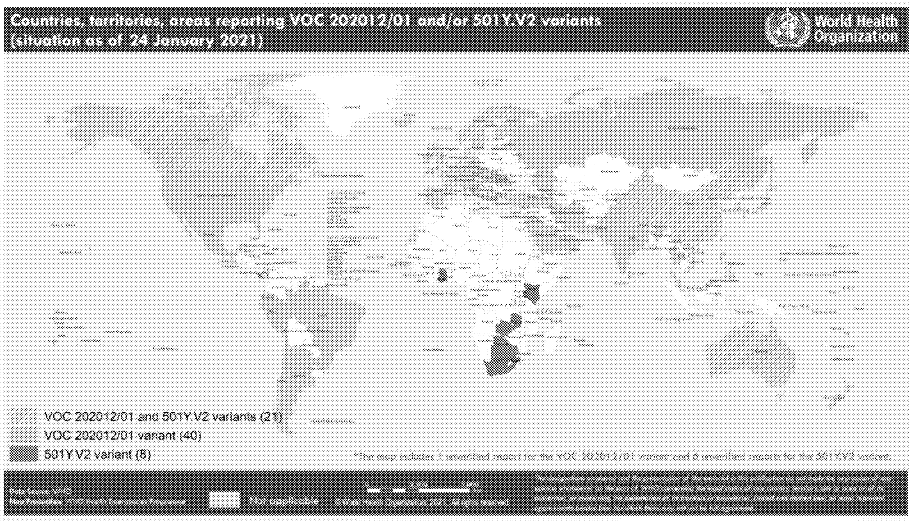


- On 18 December 2020, authorities of South Africa reported a variant referred to as **SARS-CoV-2 Variant 501Y.V2, lineage B.1.351**
- This variant 501Y.V2 has largely replaced other SARS-CoV-2 viruses circulating in South Africa
- As of 27 January 2021, Variant **501Y.V2 reported in 41 countries, territories and areas**

https://www.gov.uk/government/publications/investigation-of-novel-sars-cov-2-variant-variant-of-concern-20201201
https://www.who.int/publications/m/item/weekly-epidemiological-update---2-february-2021

Increased transmissibility of variants detected in the UK & South Africa

- Preliminary analysis shows that both variants of the virus may spread more easily and infect more people[1,2,3]
- An increase in COVID-19 cases can put pressure on the health system and can lead to an increase in hospitalizations and deaths
- However, the mode of transmission of the virus variants has not changed and the same preventive measures continue to be effective and should continue to be implemented[4]



Countries and territories reporting VOC 202012/01 and/or 501Y.V2 variants

Source: WHO

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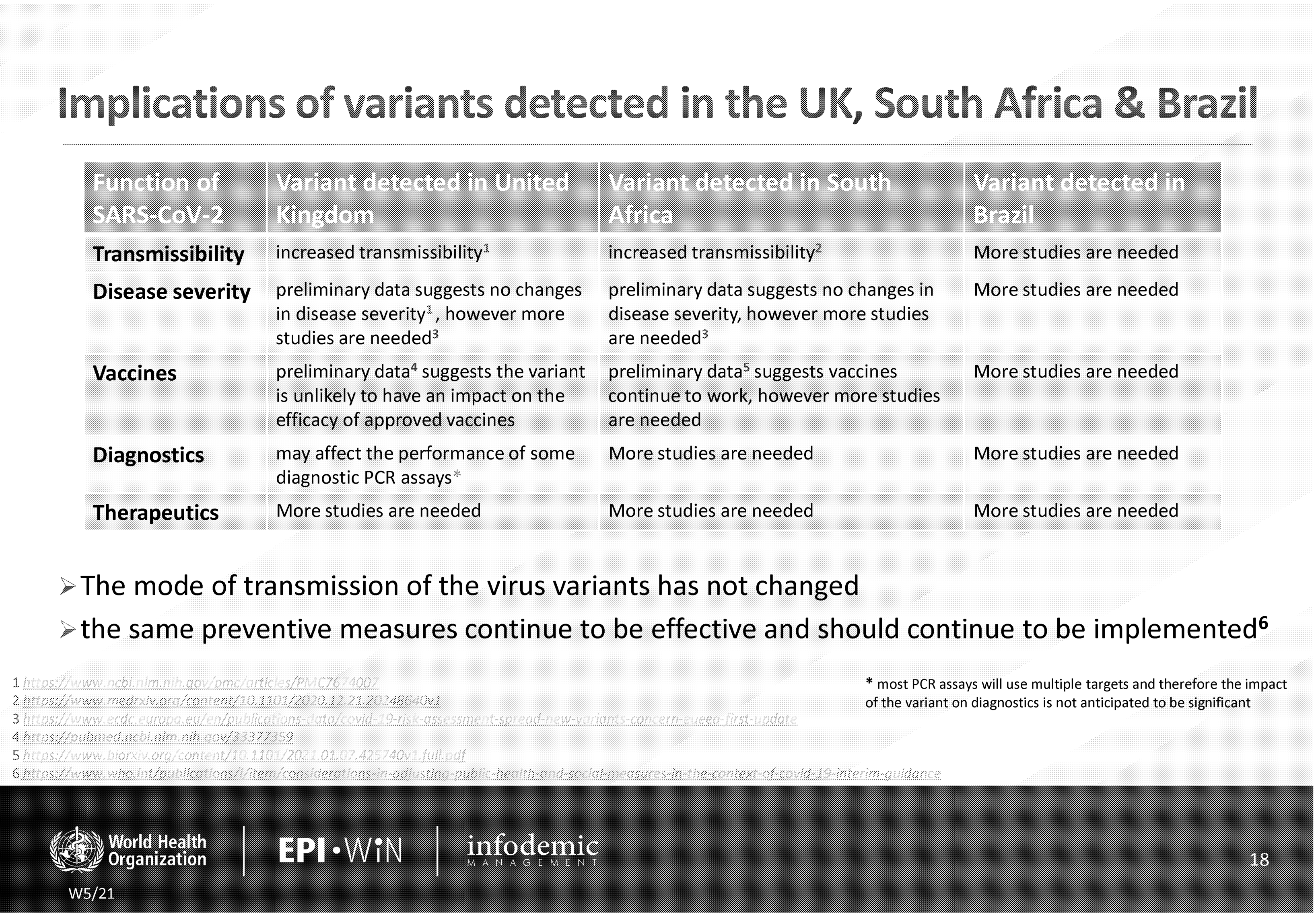
[1] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7674007/

[2] https://www.medrxiv.org/content/10.1101/2020.12.21.20248640v1

[3] https://jamanetwork.com/journals/jama/fullarticle/2775006?alert=article#_=

[4] https://www.who.int/publications/i/item/considerations-in-adjusting-public-health-and-social-measures-in-the-context-of-covid-19-interim-guidance



Implications of variants detected in the UK, South Africa & Brazil

Function of SARS-CoV-2	Variant detected in United Kingdom	Variant detected in South Africa	Variant detected in Brazil
Transmissibility	increased transmissibility[1]	increased transmissibility[2]	More studies are needed
Disease severity	preliminary data suggests no changes in disease severity[1], however more studies are needed[3]	preliminary data suggests no changes in disease severity, however more studies are needed[3]	More studies are needed
Vaccines	preliminary data[4] suggests the variant is unlikely to have an impact on the efficacy of approved vaccines	preliminary data[5] suggests vaccines continue to work, however more studies are needed	More studies are needed
Diagnostics	may affect the performance of some diagnostic PCR assays*	More studies are needed	More studies are needed
Therapeutics	More studies are needed	More studies are needed	More studies are needed

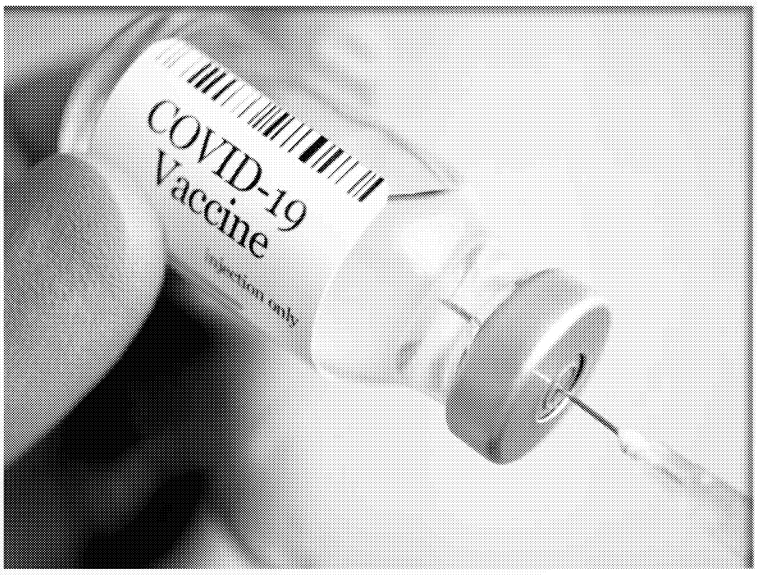
- The mode of transmission of the virus variants has not changed
- the same preventive measures continue to be effective and should continue to be implemented[6]

1 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7674007
2 https://www.medrxiv.org/content/10.1101/2020.12.21.20248640v1
3 https://www.ecdc.europa.eu/en/publications-data/covid-19-risk-assessment-spread-new-variants-concern-eueea-first-update
4 https://pubmed.ncbi.nlm.nih.gov/33377359
5 https://www.biorxiv.org/content/10.1101/2021.01.07.425740v1.full.pdf
6 https://www.who.int/publications/i/item/considerations-in-adjusting-public-health-and-social-measures-in-the-context-of-covid-19-interim-guidance

* most PCR assays will use multiple targets and therefore the impact of the variant on diagnostics is not anticipated to be significant

Monitoring of SARS-CoV-2 variants

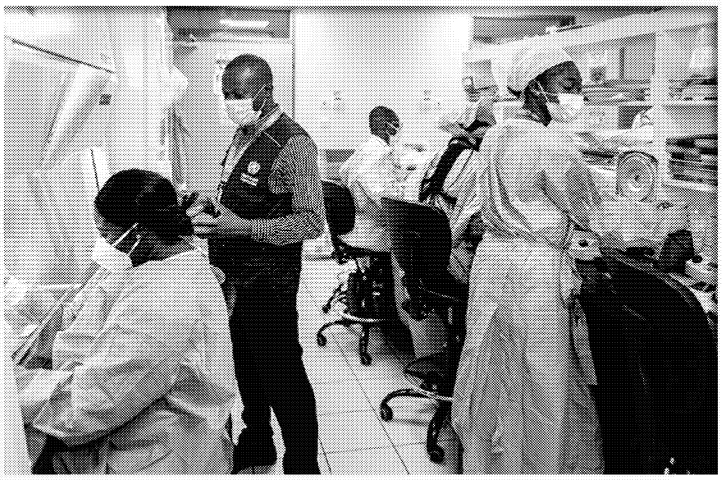
- **Virus mutations or variants are being monitored** from the start of the COVID-19 pandemic through the Global Initiative on Sharing Avian Influenza Data (GISAID) sequencing database
- **WHO routinely assesses if variants of SARS-CoV-2 have an impact on**
  - ➢ Virus transmissibility
  - ➢ Disease severity
  - ➢ Efficacy of diagnostics, therapeutics and vaccines
- WHO performs a risk assessment for **variants of concern** to determine if there will be public health implications



https://www.who.int/news/item/15-01-2021-statement-on-the-sixth-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-coronavirus-disease-(covid-19)-pandemic

Global response to the emergence of new variants

- Countries with adequate capacity are sequencing samples in order to understand if and how widely these new variants are circulating
- **WHO SARS-CoV-2 Virus Evolution Working Group** is collaborating with researchers and governments to assess and better understand the results of studies on these variants
- **WHO is working with countries to:**
  - **Strengthen surveillance systems** to evaluate virus variations
  - **Establish genetic sequencing capacity** where possible
  - **Provide access to international sequencing services**, so countries can send samples for sequencing and analysis



Source: WHO

Assessing new SARS-CoV-2 variants

What questions should be asked?

- How did the variant achieve prominence, through natural selection or chance events?
- If the evidence suggests natural selection, which mutation(s) are being selected?
- What is the adaptive benefit of these mutations?
- What effect do these mutations have on transmissibility and spread, antigenicity, or virulence?
- What impact do specific mutations have on the utility of diagnostics and medical countermeasures?

Genetic Variants of SARS-CoV-2—What Do They Mean?

Key messages

- **Mutations – it is normal** for the virus to evolve over time, and important to track changes to the virus if it has an impact on the transmission , the severity or the medical countermeasures
- **Uncertainty** – it is an evolving situation. There is still a lot of unknown about the new variants. The scientific community is working collaboratively to accelerate the generation of new knowledge. explain the global/national scientific process to educate the public
- **Maintain the preventive measures**[1] -
  - there is no change in modes of transmission . Use the same measures to protect yourself and the others
- **Avoid stigmatization –** use appropriate variant names not associated with locations as this may stigmatize individuals and goods from those locations
- **Communication for specific target groups**
  - For ***individuals who have a low perception of risk***, discourage risky behaviours such as social gatherings especially in crowded, close spaces where there is no physical distancing.
  - Remind ***vulnerable populations*** that they are a high risk population and to stay vigilant

[1] https://www.who.int/publications/i/item/considerations-in-adjusting-public-health-and-social-measures-in-the-context-of-covid-19-interim-guidance

Thank you

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