



# ECDC RRA on Risk related to spread of new SARS-CoV-2 variants of concern in the EU/EEA

5.1.2e and 5.1.2e, ECDC  
NFP webinar, 28 January 2021

## SARS-CoV-2 variants of concern



- Viruses constantly change through mutation, and so the emergence of new variants is not unexpected
- Variations in SARS-CoV-2, due to evolution and adaptation processes, have been observed worldwide
- Variants considered “of concern”:
  - Increased transmissibility
  - Ability to evade the host immune response
  - Associated with deteriorating epidemiological situation in the areas where have recently become established

## ECDC rapid risk assessments on variants of concern (1)



RAPID RISK ASSESSMENT

**Detection of new SARS-CoV-2 variants related to mink**

12 November 2020

### Summary

Since April 2020, when the first SARS-CoV-2 infection was reported in the Netherlands in a mink and subsequently in a mink farm worker, it has been established that human-to-mink and mink-to-human transmission can occur [1].

### Variants of concern (VOC):

- Mink-related variants, including "Cluster 5" variant

## ECDC rapid risk assessments on variants of concern (2)



RAPID RISK ASSESSMENT

**Risk related to spread of new SARS-CoV-2 variants of concern in the EU/EEA**

29 December 2020

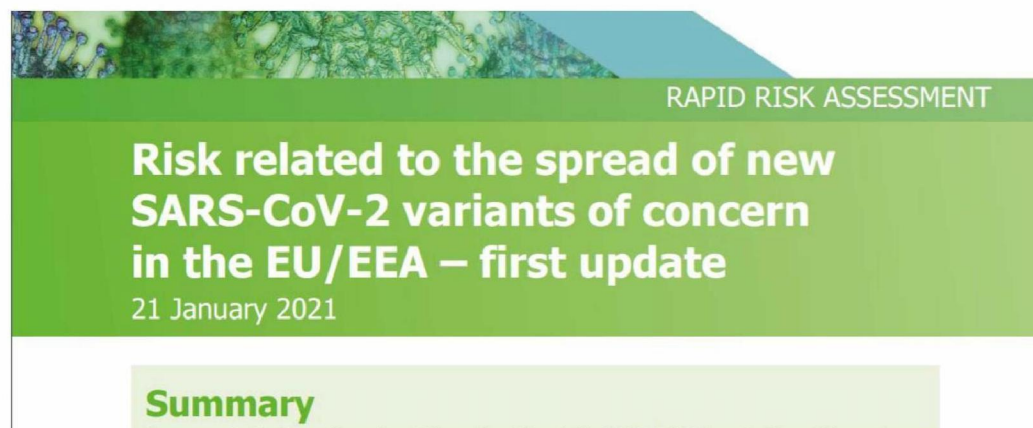
### Summary

Viruses constantly change through mutation, and so the emergence of new variants is an expected occurrence

### Variants of concern:

- VOC 202012/01 (first identified in the UK)

## ECDC rapid risk assessments on variants of concern (3)



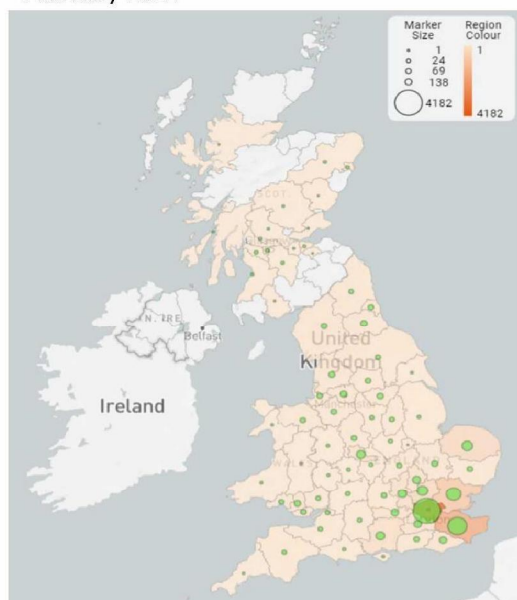
### Variants of concern:

- VOC 202012/01 (first identified in the UK)
- 501Y.V2 (first identified in South Africa)
- P.1 (first identified in Brazil, and in travellers from Brazil)

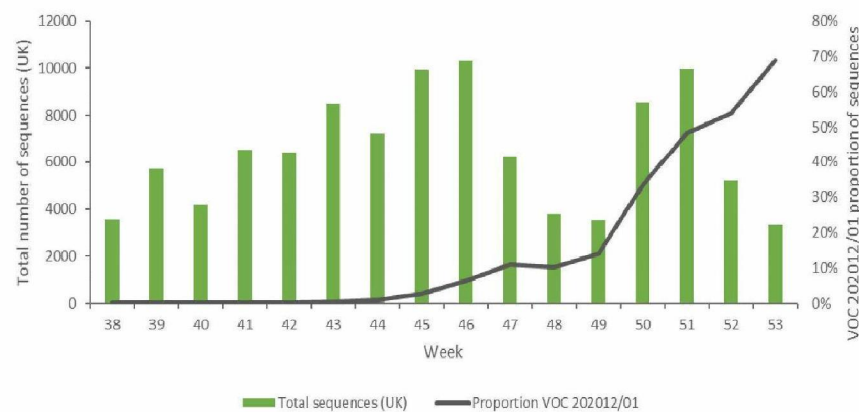
## Distribution VOC 202012/01 (lineage B.1.1.7), UK



Distribution of VOC 202012/01 cases confirmed by sequencing, UK, 1 September 2020 to 9 January 2021



Proportion of UK SARS-CoV-2 sequences classified as VOC 202012/01 per week, and total sequences per week from the UK



- First identification traced back to September 2020
- Large number of mutations, including on the spike protein
- Currently the predominant variant circulating in the UK
- As of 19/01/21, approx. 16 800 VOC 202012/01 cases

## Transmissibility and severity of VOC 202012/01



- Substantially increased transmissibility, compared to other variants
- Initial assessment reported no significant difference in risk of hospitalisation or death
- Based on new analyses, there is a “realistic possibility” of increased risk of death compared to other variants
- The absolute risk of death per infection remains low and transmissibility is main concern

## **501Y.V2 (lineage B.1.351)**



- December 2020, South Africa reported emergence and rapid spread of 501Y.V2
- Earliest detection traced back to October 2020
- Detected in about 25 countries in the world (as of 21 Jan 2021)
- Multiple spike protein changes including 3 mutations in the receptor binding domain

## **Variant P.1 (formerly P.1.1.28)**

- January 2021, Brazil reported emergence and rapid spread in Manaus (Amazonas)
- Reported simultaneously in travellers from Brazil in Japan and S. Korea
- Suspected association with very large increase in COVID-19 cases in Amazonas
- Multiple spike protein changes including 3 mutations in the receptor binding domain

## Detection VOC 202012/01 (green) and 501Y.V2 (red)

As of 21 January 2021

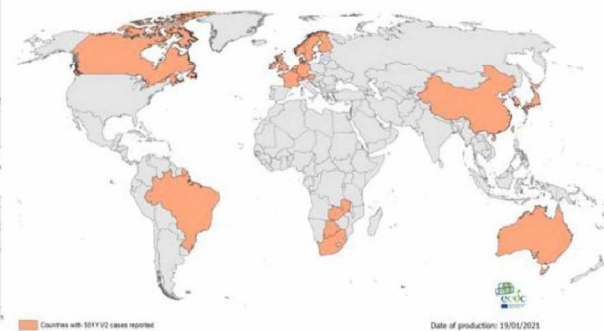


### VOC 202012/01 in world

In addition to UK,  
+/- 2 000 cases in 60 countries

### VOC 202012/01 in EU/EEA

In addition to UK,  
+/- 1 300 cases in 23 countries



### 501Y.V2 in world

+/- 550 cases in 23 countries

### 501Y.V2 in EU/EEA

27 cases in 10 countries

## Transmissibility and severity of 501Y.V2 and P.1

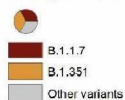


- 501Y.V2:
  - Preliminary results: 501Y.V2 may also have increased transmissibility
  - Uncertain whether 501Y.V2 causes a change in disease severity
  - Suspicions about increased risk of reinfection or breakthrough infections
- P.1:
  - Little known at this stage

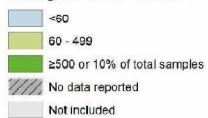
## Samples with published genomic sequence



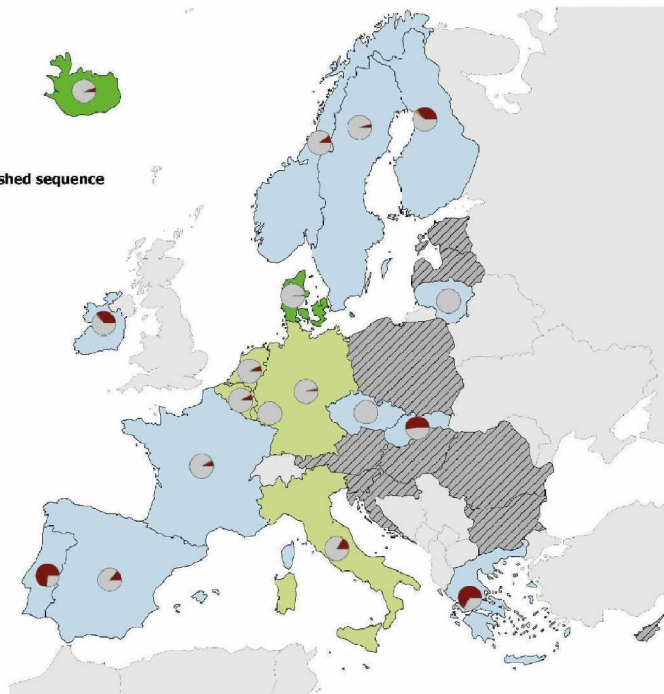
**Proportion of samples collected with a published sequence during week 49-2020 to 53-2020**



**Weekly average of samples collected with a published sequence during week 49-2020 to 53-2020**



**Countries not visible in the main map extent**



Source: GISALD EpiCoV data™. Administrative boundaries: © EuroGeographics  
The boundaries and names shown on this map do not imply official endorsement or acceptance by the European Union. ECDC. Map produced on: 22 Jan 2021

## Risk assessment



- The **risk** associated with the introduction and community spread of VOC's is assessed to be "**high-very high**", based on:
  - Probability* of introduction and community spread of VOC, and particularly SARS-CoV-2 VOC 202012/01, in the EU/EEA countries is assessed as **very high**
  - Impact* of introduction and community spread of variants of concern, and particularly SARS-CoV-2 VOC 202012/01, in the EU/EEA countries is assessed as **high**

Impact \ Probability	None	Very low	Low	Moderate	High	Very high
Very low	None	Very low risk	Low risk	Low risk	Low risk	Low-moderate risk
Low	None	Low risk	Low risk	Low risk	Low-moderate risk	Moderate risk
Moderate	None	Low risk	Low risk	Low-moderate risk	Moderate risk	High risk
High	None	Low risk	Low-moderate risk	Moderate risk	High risk	High-very high risk
Very high	None	Low-Moderate risk	Moderate risk	Moderate-high risk	High-very high risk	Very high risk

## Options for response



- **Surveillance, testing and detection of the emerging variants**
  - Timely, targeted and representative sequencing of community cases
- **Non-pharmaceutical interventions**
  - **Community measures**
    - Physical distancing, telework, avoid mass gathering, social bubbles
  - **Shielding medically and socially vulnerable populations**
  - **Considerations for school settings**
- **Contact tracing**
- **Vaccination**
- **Hospital and healthcare preparedness**

## Options for response - Surveillance, testing and detection of the emerging variants



- Timely, targeted and representative sequencing of community cases
- Laboratory preparedness should be among the current high priorities
  - diagnostic pre-screening for variants of concern
  - human and material resources
  - **increase sequencing capacity** by making use of all possible sequencing capacity (from clinical, diagnostic, academic and commercial laboratories, or requesting assistance from ECDC)

## Options for response - NPIs



- **Community measures**
  - Telework; mass gatherings; social bubbles; high-risk businesses (e.g. bars and restaurants); curfews
  - Risk communication to overcome 'COVID-19 fatigue'
  - Support vulnerable and underprivileged populations to enable them to comply with physical distancing measures
- **Shielding medically and socially vulnerable populations**
  - LTCF residents + Populations living in confined structures (e.g. prisons, migrant centres)
- **Considerations for school settings**
  - COVID-19 mainly affected by levels of community transmission
  - School closures are a measure of last resort.
  - Should initially be arranged for children in the older age groups
  - Review other NPI measures, while also strengthening in-school measures to reduce risk of transmission in schools

## Options for response – Measures for travellers



### Principles

- Slowing down introduction could prevent triggering larger outbreaks
- Can only complement; cannot replace implementation of community measures

### Measures

- Non-essential travels should be avoided
- Restrictions on travel for those with active infection
- Testing and quarantining of travellers coming from areas with higher incidence of new variants / high level of community transmission
- Insufficient evidence to exempt travellers with proof of vaccination from quarantine and/or testing
- Consider implementing similar measures at the sub-national level
- Applicable to all travellers, irrespective of the means of transportation

## Options for response - Vaccination



- **Monitoring breakthrough infections following vaccination**
  - Breakthrough infections occurring >14 days after vaccination should be investigated, prioritised for sequencing and then reported
  - Unknown if adjustments of vaccination schedules will be needed due to variants
  - Level of cross-protection could vary for different variants, particularly 501Y.V2 variant
- **Accelerating vaccination campaigns**
  - Accelerate roll-out programmes to protect those most at risk from severe disease, and reduce the burden on health systems
- **Vaccine effectiveness studies**
  - Continue surveillance and sequencing to provide vaccine product-specific effectiveness results and variant-specific vaccine effectiveness results

## Points for discussions



Obstacles in reducing timeliness and increasing proportion of community cases undergoing sequencing

Obstacles in implementing NPIs to anticipate the increase in cases due to the increased transmissibility of the VOCs

System in place to monitor breakthrough infections



**Thank you for your attention**

**Figure 7.** Average time from sample collection to sequence publication (A) and percentage of cases reported with sequence (B) in the GISAID EpiCoV database, for samples collected between 1 September 2020 and 27 December 2020, per EU/EEA country having submitted sequenced cases during the period, and the UK

