

**To:** 5.1.2e 5.1.2e [5.1.2e]@rivm.nl  
**From:** 5.1.2e 5.1.2e  
**Sent:** Mon 1/18/2021 3:29:31 PM  
**Subject:** RE: voorstel reactie aan ECDC  
**Received:** Mon 1/18/2021 3:29:32 PM

Hoi 5.1.2e

Prima, alleen ben ik altijd bang voor de wedervraag 5.1.2i Iets als: 5.1.2i  
5.1.2i  
5.1.2i Maar misschien roept dat  
alleen maar meer vragen op. Kijk maar.

Verder nog twee kleine aanvullingen in rood.

Groeten

5.1.2e

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**From:** 5.1.2e 5.1.2e <5.1.2e@rivm.nl>  
**Sent:** Monday 18 January 2021 12:51  
**To:** 5.1.2e 5.1.2e <5.1.2e@rivm.nl>  
**Subject:** voorstel reactie aan ECDC  
**Importance:** High

Ha,

Ben benieuwd wat je er van vindt. Ik stuur de reactie natuurlijk met ons allen in cc. Hoop dat je snel kan kijken want ik vind het wel belangrijk dat de RRA van deze week niet gaat overdrijven qua aantallen...

Gr 5.1.2e

5.1.2i

5.1.2i

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**From:** 5.1.2e 5.1.2e <5.1.2e @ecdc.europa.eu>

**Sent:** dinsdag 12 januari 2021 09:08

**To:** 5.1.2e 5.1.2e <5.1.2e @rivm.nl>

**Subject:** RE: FYI prior to publication – ECDC Threat Assessment Brief entitled “Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom”

Dear 5.1.2i

After thinking more about your question I did an attempt o make a set of tables for this purpose (attached). We will most likely update our sequencing guidance doc with this information.

Let me know if you have any comments on this.

Best wishes,

5.1.2e

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**From:** 5.1.2e 5.1.2e <5.1.2e @rivm.nl>

**Sent:** 08 January 2021 12:02

**To:** 5.1.2e 5.1.2e <5.1.2e @ecdc.europa.eu>

**Subject:** RE: FYI prior to publication – ECDC Threat Assessment Brief entitled “Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom”

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Hj 5.1.2e

Thanks for you answer ( I already read it on monday but still needed to reply). It seems to me there is no rationale or caculations behind what is the needed sequencing level. We are going to try to do that ourselves. What are the questions and what does that mean for sequencing strategy.

Thanks 5.1.2e

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**From:** 5.1.2e 5.1.2e <5.1.2e @ecdc.europa.eu>

**Sent:** maandag 4 januari 2021 10:40

**To:** 5.1.2e 5.1.2e <5.1.2e @rivm.nl>

**Subject:** RE: FYI prior to publication – ECDC Threat Assessment Brief entitled “Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom”

Dear 5.1.2e

Sorry for not replying earlier, I took a few days off from all work-related issues over the new year.

I agree that it is not possible to base any conclusions on the percentage of sequences samples alone, the sampling strategy is also crucial.

The statement in the RRA (that only Denmark would be able to detect an emerging or introduced VOC at low levels with <30 days delay) is largely based on these factors and assumptions:

- The GISAID data reflects what is actually produced.
- The UK has a representative sequencing programme with approximately 5% of cases sequenced, it was successful in detecting this VOC at an early stage and follow its increase.
- ECDCs influenza sentinel guidance suggests sequencing 10% of cases to be able to catch the diversity of variants at a high enough resolution.
- The jump from Denmark to the other countries is about a factor of 10, it is likely that any reasonable cut-off for a representative sequencing programme would be in this interval.

In the RRA we also suggest that if representative sequencing at a level similar to the UK or Denmark (or Iceland, though they have not been submitting to GISAID) is not possible, a smarter sampling strategy needs to be employed to catch VOCs, and we outline some suggestions.

I think these issues needs to be discussed further, I do not see the RRA as a guidance document for sequencing programmes, and I agree with you that with more time we could have put more thought into this. I hope we will be able to discuss further in the ECOVID lab network in the near future.

Best wishes and happy new year,

5.1.2e

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**From:** 5.1.2e <5.1.2e@rivm.nl>

**Sent:** 30 December 2020 00:12

**To:** 5.1.2e <5.1.2e@ecdc.europa.eu>

**Subject:** RE: FYI prior to publication – ECDC Threat Assessment Brief entitled “Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom”

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Hi 5.1.2e

Thanks for the latest RRA.

Could you explain to me why ecdc states in the latest RRA that denmark (with 13% sequencing of pos cases) has enough coverage. What is this conclusion based on? Why is 13% enough and not 7% or 5% or 1%? It makes no sense to me and I see no evidence to base this conclusion on.

It is not the % that matters for VOC monitoring but how samples are selected. For all you know countries largely sequence outbreak while you need random sampling with good geographic coverage from both clinical care setting and population screening set up (testing lanes).

I really would like to understand what the rationale is for statements on what % of pos cases needs to be sequenced to answer what specific questions.

Thanks 5.1.2e

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**Van:** 5.1.2e <5.1.2e@ecdc.europa.eu>

**Datum:** 19 december 2020 om 11:49:26 CET

**Aan:** 5.1.2e <5.1.2e@rivm.nl>

CC: [redacted] <[redacted]@ecdc.europa.eu> [redacted] <[redacted]@ecdc.europa.eu> [redacted] [redacted] <[redacted]@rivm.nl> [redacted] <[redacted]@rivm.nl> [redacted] <[redacted]@rivm.nl> [redacted] <[redacted]@rivm.nl> [redacted] <[redacted]@rivm.nl>

**Onderwerp:** RE: FYI prior to publication – ECDC Threat Assessment Brief entitled “Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom”

Thank you [redacted] for the rapid response.

Best wishes,

[redacted]

Den 19 dec. 2020 11:45 skrev [redacted] <[redacted]@rivm.nl>:

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HI,

We will put the info in EWRS as well. One case in our weekly national surveillance of the genetic make-up of SARS2 circulating in the Netherlands, sampled on 5 December. We had a delay with submission in GISAID, next year we will upload on a more real-time basis. Yes you can share this.

Best [redacted]

**From:** [redacted] <[redacted]@ecdc.europa.eu>

**Sent:** zaterdag 19 december 2020 11:34

**To:** [redacted] <[redacted]@rivm.nl>

**Cc:** [redacted] <[redacted]@ecdc.europa.eu> [redacted] <[redacted]@ecdc.europa.eu> [redacted] <[redacted]@rivm.nl> [redacted] <[redacted]@rivm.nl> [redacted] <[redacted]@rivm.nl>

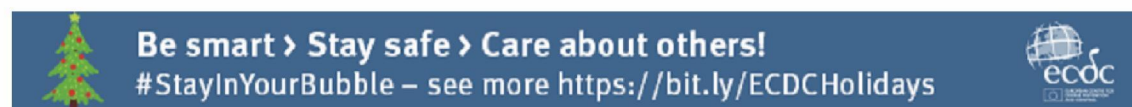
**Subject:** RE: FYI prior to publication – ECDC Threat Assessment Brief entitled “Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom”

Dear [redacted]

Thank you for the information, how many cases and when were they detected? Can this be shared in the ECDC Threat Assessment to be published on Monday?

Best wishes,

[redacted]



[redacted]  
[redacted]  
Phone: [redacted]  
[redacted]@ecdc.europa.eu

**European Centre for  
Disease Prevention and Control (ECDC)**

Gustav III:s boulevard 40, 169 73 Solna, Sweden

Phone: [redacted]

[www.ecdc.europa.eu](http://www.ecdc.europa.eu)

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Den 19 dec. 2020 11:31 skrev [5.1.2e](#) [5.1.2e](#) <[5.1.2e](#) [@rivm.nl](#)>

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Hi,

We found the exact same strain in the Netherlands in the Amsterdam area on 5 December 2020. We have not been able to upload it to GISAID yet.

Best wishes [5.1.2e](#)

From [5.1.5](#) <[5.1.5](#) [@ecdc.europa.eu](#)>

Sent: vrijdag 18 december 2020 16:24

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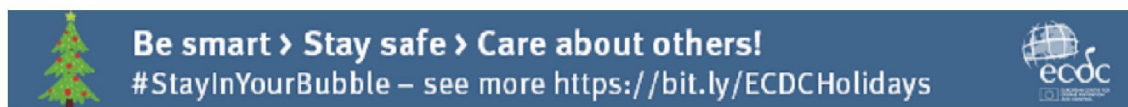


ECDC plans to publish an edited version of this Threat Assessment Brief on its website on Monday 21 December.

Warmest regards,

5.1.2e

ECDC Response Duty Officers



**European Centre for Disease Prevention and Control (ECDC)**

Gustav III:s boulevard 40, 169 73 Solna, Sweden

Phone 5.1.2e

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