

**To:** [5.1.2e] [5.1.2e] [5.1.2e] @rivm.nl]  
**Cc:** [5.1.2e] [5.1.2e] [5.1.2e] @rivm.nl]; [5.1.2e] [5.1.2e] [5.1.2e] @rivm.nl]  
**From:** [5.1.2e] [5.1.2e]  
**Sent:** Thur 12/17/2020 2:37:37 PM  
**Subject:** RE: EWRS sante vragen aan UK over de covid-variant  
**Received:** Thur 12/17/2020 2:37:37 PM

2.

We hebben met afnemedatum in november 244 cases gesequenced in het kader van kiemsurveillance (dus de uitbraken niet meegeteld)

Totaal aantal positieven in NL in november??

Dit is de dezelfde als de N501Y volgens mij hebben we daar niet nog meer van Rest??

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

**Sent:** donderdag 17 december 2020 13:16

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

**Cc:** [5.1.2e] [5.1.2e] <[5.1.2e]@rivm.nl>; [5.1.2e] [5.1.2e] <[5.1.2e]@rivm.nl>

**Subject:** Fw: EWRS sante vragen aan UK over de covid-variant

**Importance:** High

**Sensitivity:** Confidential

Hoi,

er zijn heel veel parallele zaken die vandaag afmoeten ook ivm OMT morgen. Dus wederom een verzoek om assistentie:

@ [5.1.2e] kun jij onderstaande aanvullen? Kan jij ook contact opnemen met [5.1.2e] om te vragen of zij deze mutant aangetroffen hebben? We moeten NL-breed antwoorden in EWRS.

Thanks [5.1.2e]

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**From:** LCI Voorwacht

**Sent:** Thursday, 17 December 2020 13:00

**To:** [5.1.2e] [5.1.2e]

**Cc:** [5.1.2e] [5.1.2e] [5.1.2e] [5.1.2e]

**Subject:** FW: EWRS sante vragen aan UK over de covid-variant

Beste [5.1.2e]

In overleg met [5.1.2e] [5.1.2e] [5.1.2e] [5.1.2e], stuur ik u het volgende. EWRS santé heeft aan de hand van het bericht van de UK over de SARS-CoV-2 variant, onderstaande vragen gesteld aan alle EWRS-landen die hier informatie over hebben. Is het mogelijk om deze vragen voor zover mogelijk, te beantwoorden? Eventuele antwoorden kunnen teruggemaid worden naar de lci voorwacht ([5.1.2e]@rivm.nl) en dan zullen wij via EWRS het antwoord posten.

**De vragen van EWRS** [5.1.2e]

Dear EWRS colleagues,

Following the notification from the UK, would you be able to respond to the following questions?

1. Are you performing genomic surveillance of SARS-CoV-2 in order to be able to detect novel variants such as VUI202012/01?

**Yes, we perform a weekly surveillance into the genetic signature of SARS-CoV-2 in samples that are send in by 14 labs with good geographic coverage across the country. This is supplemented with information from outbreak studies.**

2. What proportion of November cases were sequenced?

xxxxxx

3. Have you observed SARS-CoV-2 isolates similar to the new VUI202012/01 isolate recently reported by the UK?

**Yes we have observed in our surveillance a strain with exactly the same mutations. The sample was taken on 5 December 2020.**

4. Have you observed variant SARS-CoV-2 variants carrying the N501Y mutation?

xxx

5. Any other detections of the previously reported cluster 5 variant from Denmark?

xx

Many thanks, Best regards,

5.1.2e

#### **Het bericht van de UK:**

Dear colleagues,

We would like to inform you that a SARS-CoV-2 variant has been identified through viral genomic sequencing in the United Kingdom, including in 1108 individuals in England (as of 13/12/2020). Although we are currently assessing the significance of this variant, we are providing an early alert due to its spike mutations and rapid spread. This variant is referred to in the United Kingdom as SARS-COV-2 VUI 202012/01 (Variant Under Investigation, year 2020, month 12, variant 01). It is defined by multiple spike protein mutations (deletion 69-70, deletion 144-145, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H) present. Following analysis

conducted in December, cases of VUI 2022012/01 were identified dating back to September, with a rapid increase in cases reported in November. Further epidemiological and virological investigations are underway to assess the transmissibility of this strain. N501Y is in the receptor binding domain. We are urgently investigating the neutralisation activity of sera from recovered and vaccinated patients against this variant. It should also be noted that the deletion at position 69/70 has been found to affect the performance of some diagnostic PCR assays with an S gene target. Genomic data has been uploaded to GISAID. We note small numbers of similar genomes have also been identified in other countries. Additional findings will be shared as soon as they are available.

Kind regards, UK EWRS team

Met vriendelijke groet,

5.1.2e 5.1.2e

Voorwacht LCI

Landelijke Coördinatie Infectieziektebestrijding (LCI)

RIVM- Centrum infectieziektebestrijding

W: [www.lci.rivm.nl](http://www.lci.rivm.nl)

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