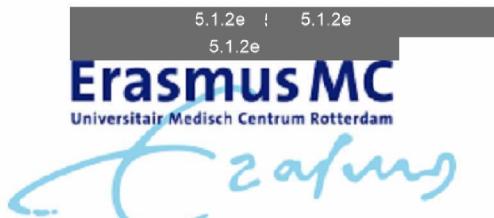


To: 5.1.2e 5.1.2e 5.1.2e 5.1.2e | 5.1.2e @rivm.nl]
From: LCI Voorwacht
Sent: Tue 12/15/2020 11:41:24 AM
Subject: FW: UK covid19: early alert due to its spike mutations and rapid spread
Received: Tue 12/15/2020 11:41:25 AM

From: 5.1.2e <5.1.2e@erasmusmc.nl>
Sent: dinsdag 15 december 2020 11:14
To: LCI Voorwacht <5.1.2e@rivm.nl>; 5.1.2e <5.1.2e@rivm.nl>; 5.1.2e <5.1.2e@rivm.nl>
Subject: Re: UK covid19: early alert due to its spike mutations and rapid spread

Ja bekend, en besproken in who context. Is nog wat voorbarig. Is vergelijkbaar met de discussie over varinten in nertsen



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From: LCI Voorwacht <5.1.2e@rivm.nl>
Sent: 15 December 2020 11:12
To: 5.1.2e <5.1.2e@rivm.nl>; 5.1.2e <5.1.2e@rivm.nl>; 5.1.2e <5.1.2e@erasmusmc.nl>
Subject: UK covid19: early alert due to its spike mutations and rapid spread

Beste collega's,

Graag zouden we onderstaand bericht van het Verenigd Koninkrijk met u willen delen. Deze mail is puur informatief bedoeld. Mocht deze informatie al bekend zijn bij u, dan kunt u deze mail als niet verzonden zien.

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 202012/01 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

Landelijke Coördinatie Infectieziektebestrijding (LCI)

RIVM- Centrum infectieziektebestrijding

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