2020/12/19 15:30	United Kingdom	[UK EWRS National Focal Point]()	Dear Colleagues, Please see an below an update on VUI202012/01 SARS-CoV-2 variant cluster in the UK Following the UK's initial notification of VUI202012/01 on 14 December 2020, we wish to share further information. As a result of preliminary modelling data and rapidly rising incidence rates in the parts of the country where this variant is being detected, the UK now considers that VUI-202012/01 demonstrates a significant increase in transmissibility compared to wild-type SARS-CoV2 and other variants in circulation. We hold this view with moderate confidence and are continuing to improve the modelling estimates and data available to us to refine our estimates and will share that information once we have this next week. We do not as yet have additional biological data as the virus is currently being grown in the laboratories, prior to formal experiments. We will continue to share further information as this becomes available. Best wishes, UK EWRS Team

Dear colleagues, Hereby the answers from the Netherlands: 1. Are you performing genomic surveillance of SARS-CoV-2 in order to be able to detect novel variants such as VUI202012/01? => Yes, at RIVM we perform the weekly national surveillance into the genetic signature of SARS-CoV-2 in samples (12-24 per lab per week) that are send in by 14 labs with good geographic coverage across the country. This is supplemented with sequencing information from outbreak clusters. Erasmus MC monitors SARS-CoV-2 at a monthly basis in additions to sequencing of outbreak clusters. We are in progress to collect all national data in one shared data-base. 2. What proportion of November cases were sequenced? => In the surveillance structure which was in start-up phase in November (so sequencing in outbreak context not included) RIVM collected approx. 250 sequences in November. ErasmusMC generated 26 sequences in November and 48 in December from outbreak clusters and monitoring activities. 3. Have you observed SARS-CoV-2 isolates similar to the new VUI202012/01 isolate recently reported by the UK? => Yes, RIVM observed in the national surveillance once a strain with exactly the same combination of variation. The sample was taken on 5 December 2020. 4. Have you observed variant SARS-CoV-2 variants carrying the N501Y mutation? => no 5. Any other detections of the previously reported cluster 5 variant from Denmark? => In the Netherlands there has been no detection of the exact combination of variations as described in the cluster 5 in Denmark. Best regards, on behalf of the Dutch EWRS team, 5.1.2e 5.1.2e

2020/12/19 12:09	Denmark	5.1.2e	Dear colleagues, Here are answers from Denmark: Are you performing genomic surveillance of SARS-CoV-2 in order to be able to detect novel variants such as VUI202012/01? Yes What proportion of November cases were sequenced? We sequenced 8096 samples through November of a total of 34555 cases (23.4%) Have you observed SARS-CoV-2 isolates

			similar to the new VUI202012/01 isolate recently reported by the UK? We have observed 10 cases of the variant since November 14. Have you observed variant SARS-CoV-2 variants carrying the N501Y mutation? N501Y is only observed in the VUI202012/01 variant. Any other detections of the previously reported cluster 5 variant from Denmark? No Best regards [redacted] Duty Officer, Danish EWRS Team	
2020/12/18 16:30	EC	[redacted] [redacted]	Dear EWRS colleagues, Please find attached, as informed in the HSC today, ECDC's threat assessment brief on the "Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom" prior to its publication. Best regards, SANTE EWRS	ECDC Threat Assessment Brief - Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom.pdf
2020/12/18 14:08	Germany	epialert ROBERT KOCH INSTITUTE	Dear colleagues, please find below the answers to the question from Germany: 1. Are you performing genomic surveillance of SARS-CoV-2 in order to be able to detect novel variants such as VUI202012/01? Yes 2. What proportion of November cases were sequenced? Unfortunately, we have no overview on the exact number of cases sequenced in Germany. However, we are aware of a total of 99 SARS-CoV-2 genome sequences from Germany from November in internal and public databases. 3. Have you observed SARS-CoV-2 isolates similar to the new VUI202012/01 isolate recently reported by the UK? No, we didn't. Still, we identified some sequences encoding distinctly S-P681H or S-H69del/S-V70del or S-Y144del. 4. Have you observed variant SARS-CoV-2 variants carrying the N501Y mutation? We did not identify a variant encoding the N501Y polymorphism, but we found one	

			sequence with a N501T variation (hCoV-19/Germany/MV-Tv4-20-Tier-4/2020|EPI_ISL_491111|2020), which however does not resemble the UK variant in other specific positions. 5. Any other detections of the previously reported cluster 5 variant from Denmark? No In case you have further questions regarding this topic, please reach out to our colleague Dr. [redacted] ([redacted]@rki.de). Kinds regards, [redacted] [redacted] on behalf of the German EWRS Team
2020/12/18 11:04	Ireland	[redacted]	Dear Colleagues, Please see below answers: 1. Are you performing genomic surveillance of SARS-CoV-2 in order to be able to detect novel variants such as VUI202012/01? Yes. Whole-genome sequencing is performed employing the MinION Artic protocol. 2. What proportion of November cases were sequenced? To date, about 1% of November cases have been sequenced 3. Have you observed SARS-CoV-2 isolates similar to the new VUI202012/01 isolate recently reported by the UK? No 4. Have you observed variant SARS-CoV-2 variants carrying the N501Y mutation? No 5. Any other detections of the previously reported cluster 5 variant from Denmark? No Kind regards, [redacted] on behalf of Irish EWRS Team
2020/12/18 09:34	Sweden	[redacted]	Dear colleagues, here come the answers to your questions from Sweden. 1. Are you performing genomic surveillance of SARS-CoV-2 in order to be able to detect novel variants such as VUI202012/01? Yes 2. What proportion of November cases were sequenced? 0,02% 3. Have you observed SARS-CoV-2 isolates similar to the new VUI202012/01 isolate recently reported by the UK? No

			4. Have you observed variant SARS-CoV-2 variants carrying the N501Y mutation? No 5. Any other detections of the previously reported cluster 5 variant from Denmark? No Kind regards, the Swedish EWRS Team
2020/12/18 08:25	Slovenia	[redacted] [redacted]	Dear colleagues, please find enclosed information from Slovenia. We contacted two laboratories which perform genome sequencing in our country. Unfortunately, because of high work load, the laboratories are not able to provide recent data. All Slovenian sequences have been uploaded in GISAID with latest results dating in April 2020. 1.Are you performing genomic surveillance of SARS-CoV-2 in order to be able to detect novel variants such as VUI202012/01? No 2.What proportion of November cases were sequenced? None 3.Have you observed SARS-CoV-2 isolates similar to the new VUI202012/01 isolate recently reported by the UK? Not applicable 4.Have you observed variant SARS-CoV-2 variants carrying the N501Y mutation? 5.Any other detections of the previously reported cluster 5 variant from Denmark? Not applicable Kind regards, [redacted] [redacted] on behalf of Slovenian EWRS team
2020/12/17 22:12	Norway	[redacted] [redacted]	Dear SANTE EWRS team, below you find the response from Norway to your questions: 1. Yes we are performing genomic surveillance of SARS-CoV-2 2. Total cases in November: 15.484. Total samples analysed with WGS 187 (1.2%) (some still pending). Total cases October: 6.994. Total samples analysed with WGS 309 (4.4%) 3. No, we have not observed cases that match the profile of VUI202012/01. We

			have, however, several and increasing number of cases with a substitution in the S gene receptor binding domain, typically N439K and not N501Y, where a deletion of amino acids 69&70 appears to have occurred as secondary events within different outbreaks. Hence, we have more cases with both the substitution N439K and the deletions than we have cases with the N439K without the deletions. 4. None on the sequenced Norwegian SARS-CoV-2 viruses (n= 11.569) possess the S gene N501Y substitution 5. No cluster 5 variants from Denmark have been detected in Norway. However, the same deletion of aminoacids in position 69/70 is observed in several cases and increasing cases in November. Kind regards EWRS Norway
2020/12/15 15:17	EC	5.1.2e 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? 2. What proportion of November cases were sequenced? 3. Have you observed SARS-CoV-2 isolates similar to the new VUI202012/01 isolate recently reported by the UK? 4. Have you observed variant SARS-CoV-2 variants carrying the N501Y mutation? 5. Any other detections of the previously reported cluster 5 variant from Denmark? Many thanks, Best regards, SANTE EWRS
2020/12/14 16:19	United Kingdom	UK EWRS National Focal Point	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