

Incident management team report conference outbreak – March 2020

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Abbreviations

COG-UK: COVID-19 Genomics UK

COVID-19: coronavirus disease 2019

CPH/CPHM: Consultant in Public Health/Consultant in Public Health Medicine

CROC: Centres and Regional Operations Cell

CTAS: Contact Tracing and Advisory Service

ECDC: European Centre for Disease Prevention and Control

EWRS: Early Warning and Response System

HPS: Health Protection Scotland

HPT: health protection team

IMT: incident management team

NICC: National Incident Coordination Centre

PAG: problem assessment group

PCR: polymerase chain reaction

PHE: Public Health England

PHEIC: public health emergency of international concern

PHS: Public Health Scotland

PPE: personal protective equipment

ROC: Regional Operations Cell

SARS-CoV-2: severe acute respiratory syndrome – coronavirus 2

SNP: single nucleotide polymorphisms

WGS: whole genome sequencing

WHO: World Health Organization

WoSSVC: West of Scotland Specialist Virology Centre

Summary

An outbreak of COVID-19 was identified in Scotland on 2 March 2020 following the detection of a case among 71 delegates who attended a conference in Edinburgh between 25 and 27 February 2020. The delegates were from Scotland, England, Northern Ireland, the Republic of Ireland and the Netherlands.

Twenty-three primary cases were linked to the conference and 16 secondary cases were subsequently identified.

Whole genome sequencing (WGS) of the severe acute respiratory syndrome – coronavirus 2 (SARS-CoV-2) virus isolated from cases was undertaken. This identified a particular sub-lineage B-S16 associated with the conference.

In Scotland, eight cases were directly linked to the conference (six primary and two secondary cases). A small number of other cases of the B-S16 sub-lineage were identified as well as a small number of cases with three or greater single nucleotide polymorphisms (SNP) differences from the outbreak sub-lineage. These samples were more closely associated with samples from other cases in other countries than the conference samples and therefore have been discounted as being directly linked to the conference. This sub-lineage B-S16 has not been detected in Scotland since April 2020. These WGS results strongly suggest that the actions taken by the incident management team (IMT) to manage the outbreak were successful in curtailing onward transmission.

The outbreak demonstrated the value of incorporating genomics with epidemiological data to help understand transmission within an outbreak and to identify if there has been any wider transmission into the community.

Background

The end of 2019 saw the emergence of a novel virus in China, severe acute respiratory syndrome – coronavirus 2 (SARS-CoV-2), which causes coronavirus disease 2019 (COVID-19). Clinical presentation may range from mild-to-moderate illness to pneumonia or severe acute respiratory infection and death. On 30 January 2020, the World Health Organization (WHO) declared the outbreak a public health emergency of international concern (PHEIC), as travel-related cases began to be identified around the world. WHO declared COVID-19 as a pandemic on 11 March 2020. The first confirmed cases were reported in the UK on 29 January and the first case reported in Scotland was on 1 March 2020.

The UK entered into a 'containment strategy' in January 2020 until 12 March 2020, when Scotland and the rest of the UK moved to the 'delay phase' of the pandemic. In this phase a number of measures were introduced to slow the spread of the virus and to reduce the impact on the healthcare systems. This included the closure of non-essential services on 16 March, leading to a national lockdown on 23 March. The lockdown required social distancing of 2 metres and all individuals to stay at home and work from home where possible, with only an hour of outdoor exercise, and trips for food shopping and medication allowed per day.

The COVID-19 Genomics UK (COG-UK) consortium was launched as part of the public health response in March 2020 to sequence and analyse SARS-CoV-2 across the UK. This is the first time that large-scale genomic epidemiology has been used to inform the public health response to a pandemic in the UK (1). To help prioritise finite sequencing resources, COG-UK developed a sampling strategy to concurrently enable broad population-level analysis, targeted analysis of specific populations and local priorities (1).

Outbreak investigation in Scotland

In Scotland, the investigation of outbreaks of infectious disease is undertaken in accordance with the guidance for the Management of Public Health Incidents (2). This latest version was updated during the pandemic but, in common with the prior version extant at the time of this incident, involves the establishment of an IMT.

It is the remit of the IMT to:

- reduce to a minimum the number of cases of illness by promptly recognising the incident, defining how cases have been exposed to the implicated hazard, identifying and controlling the source of that exposure, and preventing secondary exposure
- minimise mortality and illness by ensuring optimum health care for those affected
- inform the patients, actually or potentially exposed groups, staff and clinical and management colleagues, the public, their representatives and the media of the health risks associated with the incident and how to minimise these risks
- collect information which will be of use in better understanding the nature and origin of the incident and on how best to prevent and manage future incidents.

In general, where the focus of an outbreak and the cases are largely confined to a single NHS Board area, the health protection team (HPT) in the relevant NHS Board area is the lead organisation and the IMT is chaired by a Consultant in Public Health/Consultant in Public Health Medicine (CPH/CPHM) for the Board. Where the nature of the outbreak is more diffuse and/or cases are spread across a number of NHS Board areas and/or other parts of the UK, Public Health Scotland (PHS) and its predecessor organisation, Health Protection Scotland (HPS), take on the lead role for outbreak management coordination. In such outbreaks, the public health management of individual cases and contacts remains the responsibility of the relevant NHS Board and the follow-up of individual premises of interest remains the

responsibility of the relevant NHS Board/Local Authority Environmental Health department.

Conference outbreak

On 2 March 2020, HPS became aware of a confirmed case of COVID-19 who had attended a conference in Edinburgh.

The conference

The conference with 71 attendees was held in Edinburgh over three days, 25–27 February 2020. Some participants arrived at the conference hotel on the evening of 24 February. All participants departed by the evening of 27 February. Delegates were from Scotland, England, Northern Ireland, the Republic of Ireland and the Netherlands. All participants stayed at the conference hotel in Edinburgh and the conference was held within its own space in the hotel along with conference meals. Three social events were also held for conference attendees.

Conference IMT

Conference participants came from a number of Scottish NHS Boards, different regions of England, Northern Ireland, the Republic of Ireland and the Netherlands, and so HPS took on a coordinating role and convened a multi-agency IMT.

The IMT, chaired by HPS, met on 3 March and attendees included representatives from NHS Lothian, West of Scotland Specialist Virology Centre (WoSSVC), Public Health England (PHE) regional representatives and PHE National Incident Coordination Centre (NICC).

A problem assessment group (PAG) was held after the IMT on the evening of 3 March. This included HPS, NHS Lothian and NHS Ayrshire and Arran (the Board with the first identified conference case in Scotland) to discuss the local management aspects in detail.

For attendees who were resident outside of the UK, as is standard practice, communication was via PHE as the national focal point using the European Centre for Disease Prevention and Control (ECDC) Early Warning and Response System (EWRS). This is a system with restricted access for monitoring public health threats in the EU and the sharing of confidential information between ECDC and Member States (3). (Note at the time of the conference the UK was a member of the EU).

Case and contact management

The investigation and management of confirmed or suspected cases and contacts of cases was undertaken by the relevant NHS Board HPT in Scotland and regional PHE teams in England. Cases and contacts were managed as per the guidance extant at the time of the outbreak. Guidance has changed over the course of the pandemic to reflect the evolving epidemiology and science.

Case definitions

The case definitions applied by the IMT for primary and secondary cases were:

Primary case

A case of COVID-19 infection confirmed by polymerase chain reaction (PCR) with direct links to the conference or conference events.

Secondary case

A confirmed case of COVID-19 infection in someone with onset two or more days after a confirmed case that is a household or other close contact of a confirmed case and who did not attend the conference or conference events.

Molecular case definitions

The WGS was conducted after the initial outbreak investigation and therefore did not form part of the original case definitions. Based on sequencing results, a sub-lineage identified as B-S16 was identified among conference cases.

Epidemiological methods

At the time of the outbreak, all SARS-CoV-2 testing in Scotland was conducted by NHS laboratories and confirmed cases were reported to NHS Board HPTs by the laboratory. The positive laboratory confirmation was also shared with HPS via Electronic Communication of Surveillance in Scotland (ECOSS) (4). A similar system was in operation in England. In the early stages of the pandemic when case numbers were low, these positive confirmations were also reported real time by phone to ensure rapid public health action.

During this period of the pandemic, the UK was in the containment phase and all confirmed cases were actively followed up by the HPTs in Scotland to obtain detailed exposure and clinical information. This was also used to identify the contacts of these cases and advise either active or passive follow-up depending on the level of exposure, as described in the guidance. Active follow-up required immediate isolation for 14 days from exposure and daily contact by phone or SMS to check the contact had not developed any symptoms. Passive follow-up required self-monitoring of symptoms by contacts and immediate isolation if they became symptomatic. Testing was then arranged for any contacts who became symptomatic.

Information on cases identified as part of the conference outbreak was shared with HPS or PHE by the local teams and then collated by HPS to monitor and describe the outbreak.

Details of the conference delegates in Scotland were shared with the NHS Board HPT and advised to self-isolate for 14 days and to contact the HPT if they became symptomatic. In England, the 53 conference delegates were contacted through Contact Tracing and Advisory Service (CTAS) (Field Service South West) via a SMS

message advising them to self-isolate and contact NHS111 if they became unwell. They were not put under active surveillance. Their details were passed on to HPTs via the Regional Operations Cell (ROC) of PHE in case they later presented with symptoms.

The company organising the conference was proactive in communicating the management of any infection risk to their staff. After being informed of the first cases from the conference, the company advised all staff who attended the conference to self-isolate at home for 14 days. The company undertook decontamination of the workplaces of conference attendees.

For delegates attending the conference from the Netherlands or the Republic of Ireland, liaison with the relevant public health authorities was through PHE as the national focal point using the ECDC EWRS.

Epidemiological results

The data presented below is based on the information available to HPS from the HPTs in Scotland and PHE.

Table 1: Number of delegates attending the conference

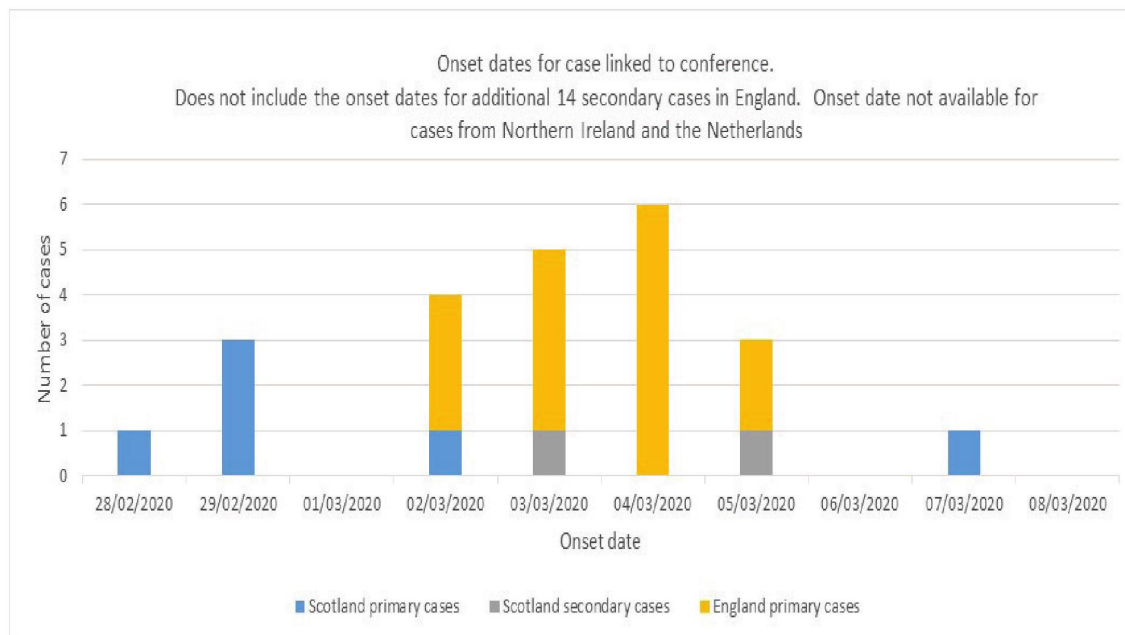
| Home residence for delegate | Number of delegates |
|-----------------------------|---------------------|
| England | 53 |
| Scotland | 10 |
| Northern Ireland | 3 |
| Republic of Ireland | 3 |
| The Netherlands | 2 |

Table 2: Cases epidemiologically linked to the conference

| Area of residence | Primary (attended the conference or directly linked to conference) | Secondary cases | Total |
|-------------------|--|-----------------|-------|
| Scotland | 6 | 2 | 8 |
| England | 15 | 14 | 29 |
| Northern Ireland | 1 | 0 | 1 |
| The Netherlands | 1 | 0 | 1 |
| Total | 23 | 16 | 39 |

PHE received information from the public health authorities in the Netherlands that they were aware of a conference delegate who was a case and that the onset of symptoms was after they returned to the Netherlands. Using their own risk assessment, the Dutch determined that the individual was not symptomatic in Scotland, and contact tracing was not required. However, later testimony from cases and contacts reported that the individual was symptomatic during the conference. (Based on a greater understanding of COVID-19 infection available now and cases being infectious when asymptomatic, the individual might have been contagious at the conference, even if deemed to be asymptomatic in the pre-symptomatic phase).

Figure 1: Date of onset for conference associated cases of COVID-19



Contacts of cases

In Scotland, 68 contacts were identified from the primary cases and followed up by the HPTs. In England, 253 contacts of cases were identified (median 8, range 1–104), which included workplace exposures.

Hospitalisations

All eight confirmed cases in Scotland were admitted to hospital as the extant policy in Scotland advised admission to a hospital infectious disease unit to support clinical management and infection control management, even if a case's clinical presentation did not require hospitalisation based on the severity of their symptoms. This policy was revised as more cases were identified and it was no longer practical or necessary for all cases to be admitted. The duration of hospitalisation ranged from 4 to 12 days, mean 7.1 days, median 7 days. There were no deaths associated with the outbreak.

Virology methods

Initial diagnosis

At the time of the outbreak, samples were tested in NHS laboratories for the detection of the SARS-CoV-2 virus. This was done using a diagnostic real-time PCR with reverse transcription to detect SARS-CoV-2-positive samples following nucleic acid extraction using the NucliSENS easyMAG and Roche MG96 platforms (5).

Sequencing and bioinformatic methods

Whole genome sequencing

Residual nucleic acid from extracts used for the diagnostic real-time PCR underwent whole-genome next-generation sequencing at the COG-UK sequencing laboratories at the MRC-University of Glasgow Centre for Viral Research and Edinburgh Royal Infirmary. Samples were sequenced using Oxford Nanopore technology. For more detailed methods see the description in da Silva Filipe et al (6).

Sequencing data

Consensus sequences with > 90% coverage were included. All consensus genomes are available from the WHO Global Influenza Surveillance and Response System Database (GISAID) (www.gisaid.org) and the COG-UK Consortium website (www.cogconsortium.uk/data/).

Phylogenetic analysis

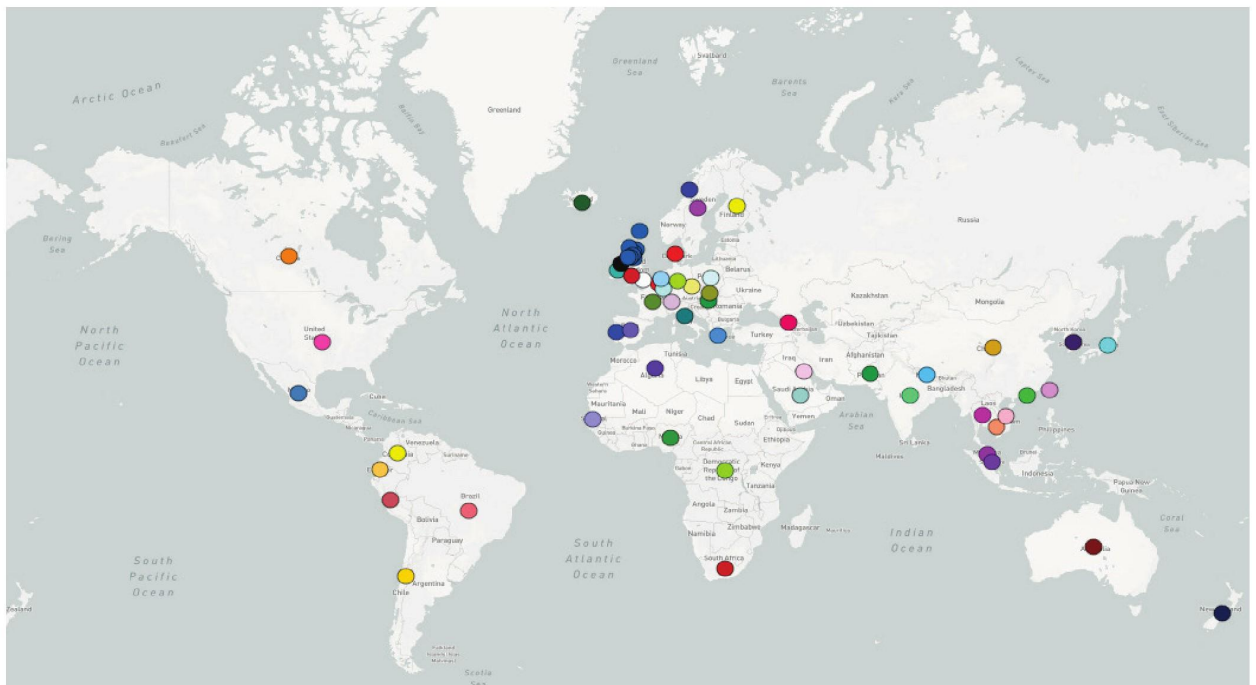
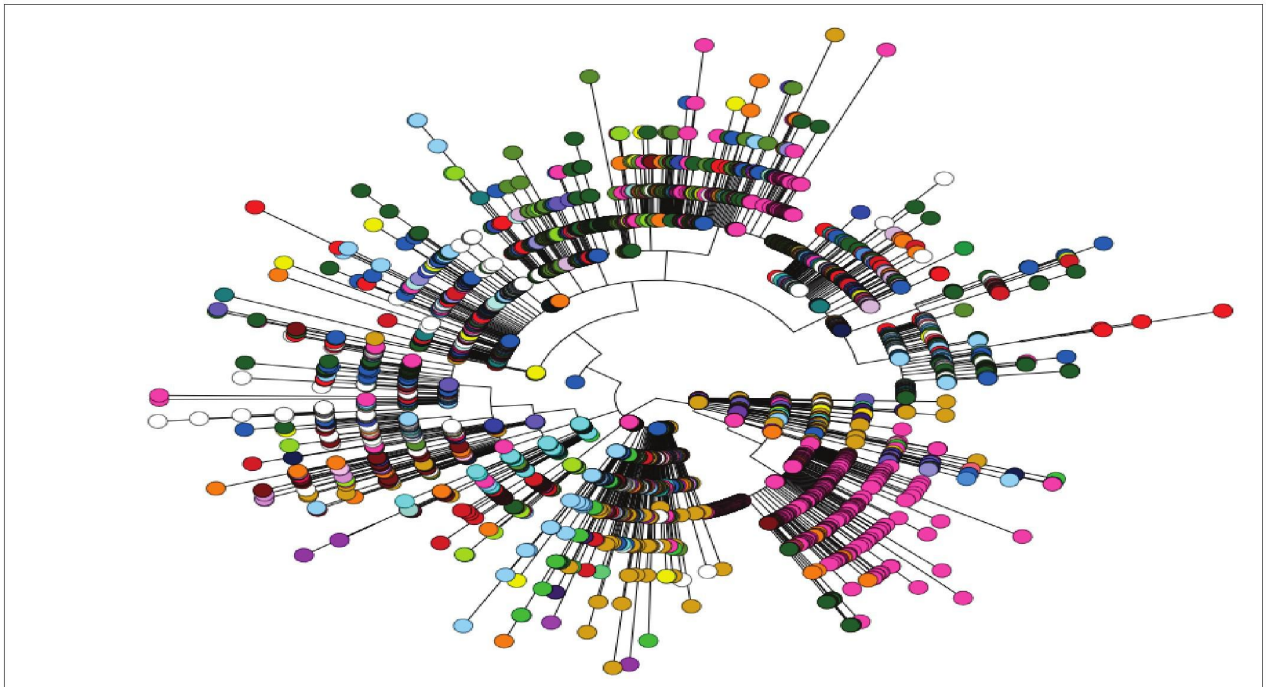
For more details of the phylogenetic methods see the description in da Silva Filipe et al (6).

Virology results

The phylogeny presented below is based on the analysis conducted in the summer of 2020 and was updated in summer 2021 for the preparation of this report. The analysis places the samples from conference-associated cases in the context of the wider phylogeny at that point in time. Over the rest of 2020 and 2021, the SARS-CoV-2 virus has continued to evolve and the phylogeny has expanded.

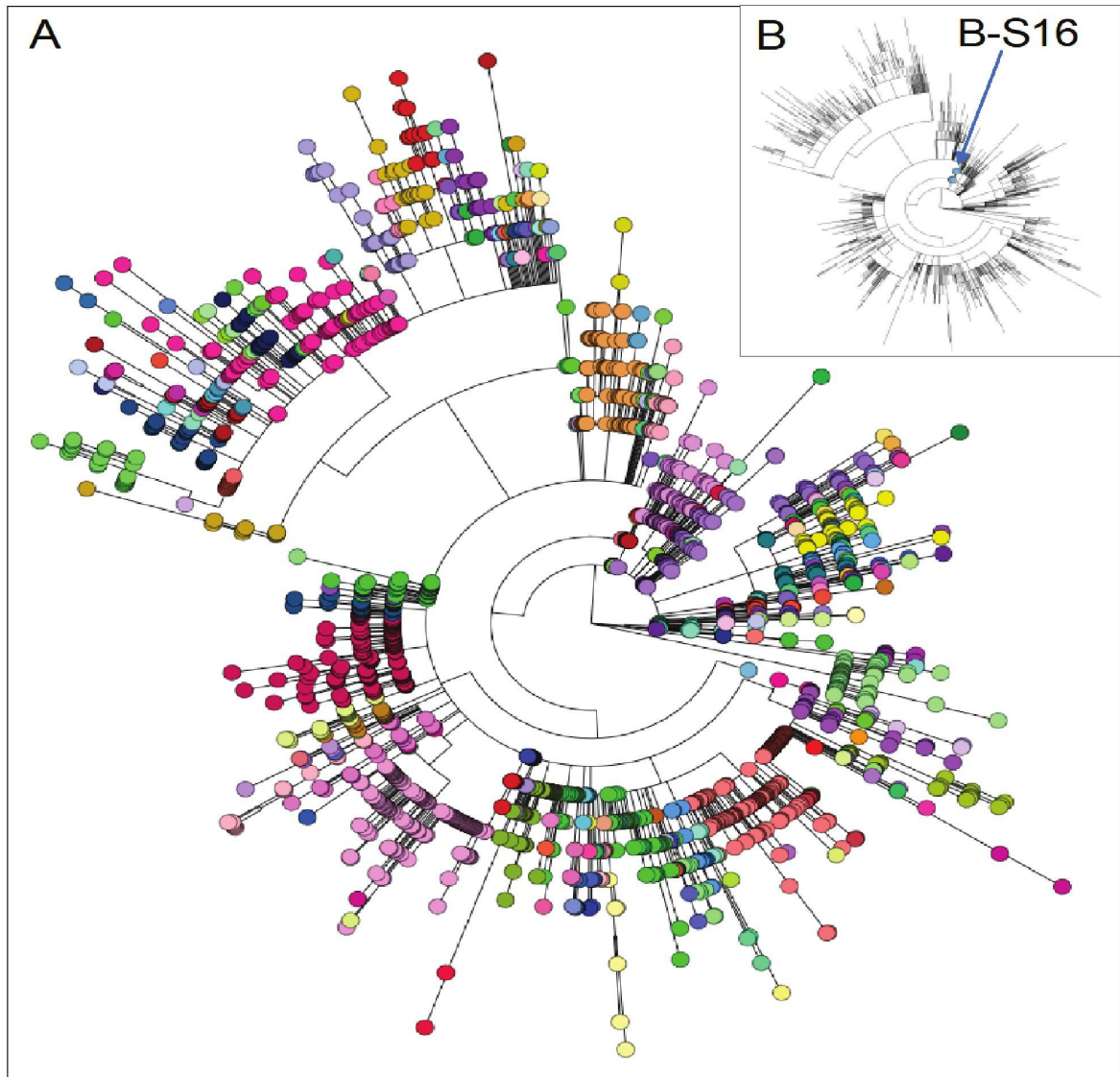
The phylogeny (Figure 2) shows different SARS-CoV-2 virus sequences from around the world, with each dot representing a sample. Dots on the same branch of the tree are more closely related. The core ancestor for these samples is near the centre – originating from Wuhan, China in late 2019. This demonstrates how as SARS-CoV-2 virus has spread around the world, and how it has evolved and acquired different mutations which allows it to be distinguished based on sequencing. This diversity also provides an indication when a virus is identified in Scotland of where the virus may have been imported from.

Figure 2: Global genome phylogeny illustrating the genetic relationship of virus sample – colour coded according to the country of origin (summer 2020).



The SARS-CoV-2 isolated and sequenced in Scotland are not a single lineage of the virus, but rather a diverse mix of different lineages imported from around the world. Figure 3A presents the genome phylogeny of the 1817 SARS-CoV-2 sequences identified in Scotland from 1 March to 10 May 2020, with samples coloured according to the viral sub-lineages that represent separate introductions into Scotland from the rest of the UK and worldwide.

Figure 3: Scottish SARS-CoV-2 genome phylogeny. A) Genome phylogeny of samples sequenced from Scotland 1 March to 10 May 2020 (1817 SARS-CoV-2 sequences) colour coded according to sub-lineages. B) Genome phylogeny showing the sub-lineage associated with the conference B-S16. An expanded phylogeny of the B-S16 sample is illustrated in Figure 4.



All the samples sequenced from the cases associated with the conference belong to a particular sub-lineage identified as B-S16 (Figure 3B). These show a small and discreet family tree. This information about samples associated with the conference enables the identification of any other samples not associated with the conference that have the same or very similar sequences to be identified and investigated.

An initial description of samples from the conference was described in the publication by da Silva Filipe et al (6). What follows is a more detailed description of the phylogenetic analysis that also include additional samples that were not available at the time of writing of the manuscript by da Silva Filipe et al (6), nor at the time of the original investigation that was conducted by HPS.

The samples from Scotland associated with the conference and the other sub-lineage B-S16 samples are shown in Figure 4. Most of the conference isolates highlighted in red on Figure 4 are genetically indistinguishable but an additional two have a unique mutation. Included in the conference samples is a case from the Netherlands who attended the conference and who was reported as symptomatic to the IMT from other cases/delegates but who had been reported to be asymptomatic at the conference to the public health authorities in the Netherlands (Oss_1363500).

Further epidemiological investigation was undertaken into the other sub-lineage B-S16 samples that were not linked to the conference when they were identified on sequencing. As the sequencing results became available sometime after the conference this was based on the information collected from the cases at the time of their identification and management by the local HPTs.

- CVR118 – no identified connections to the conference, but did have overseas visitors a week before onset of symptoms.
- CVR817, GCVR-170BAF, GCVR-1712A9, GCVR-1713D3 and GCVR-17079C – no known connection to the conference or to conference delegates for these five cases and no connection identified between the cases, although two were resident in the same NHS Board and the other three cases were resident in the same NHS Board. These five cases had sample dates after the conference cases.

There were five sequences identified with three or more SNP differences from the conference samples, these are identified in Figure 4 as CVR304, CVR2052, CVR2732, CVR2734 and CVR2737. Using the wider international sequencing data, plausible explanations for their isolation in Scotland are given (Figure 5).

- CVR304: this sample is more closely related to a case from Finland than the other cases in Scotland.
- Samples CVR2732, CVR2734 and CVR2737 were not available when the original tree was built and are closely related to CVR2052 which is three SNPs different to the conference sequence. As CVR2052 is basal in the clade that contains these samples (Figure 4), and the English samples are basal to this, and are therefore ancestral to CVR2052, CVR2732, CVR2734 and CVR2052, it would suggest that the mutations in the Scottish samples only occurred after earlier mutations identified in cases in England. Thus these cases in Scotland were not directly related to the incident in Scotland but rather re-importations of this sequence into Scotland. There are known epidemiological links between samples CVR2052, CVR2732, CVR2734 and CVR2737.

Figure 4: The conference and the sub-lineage B-S16 samples

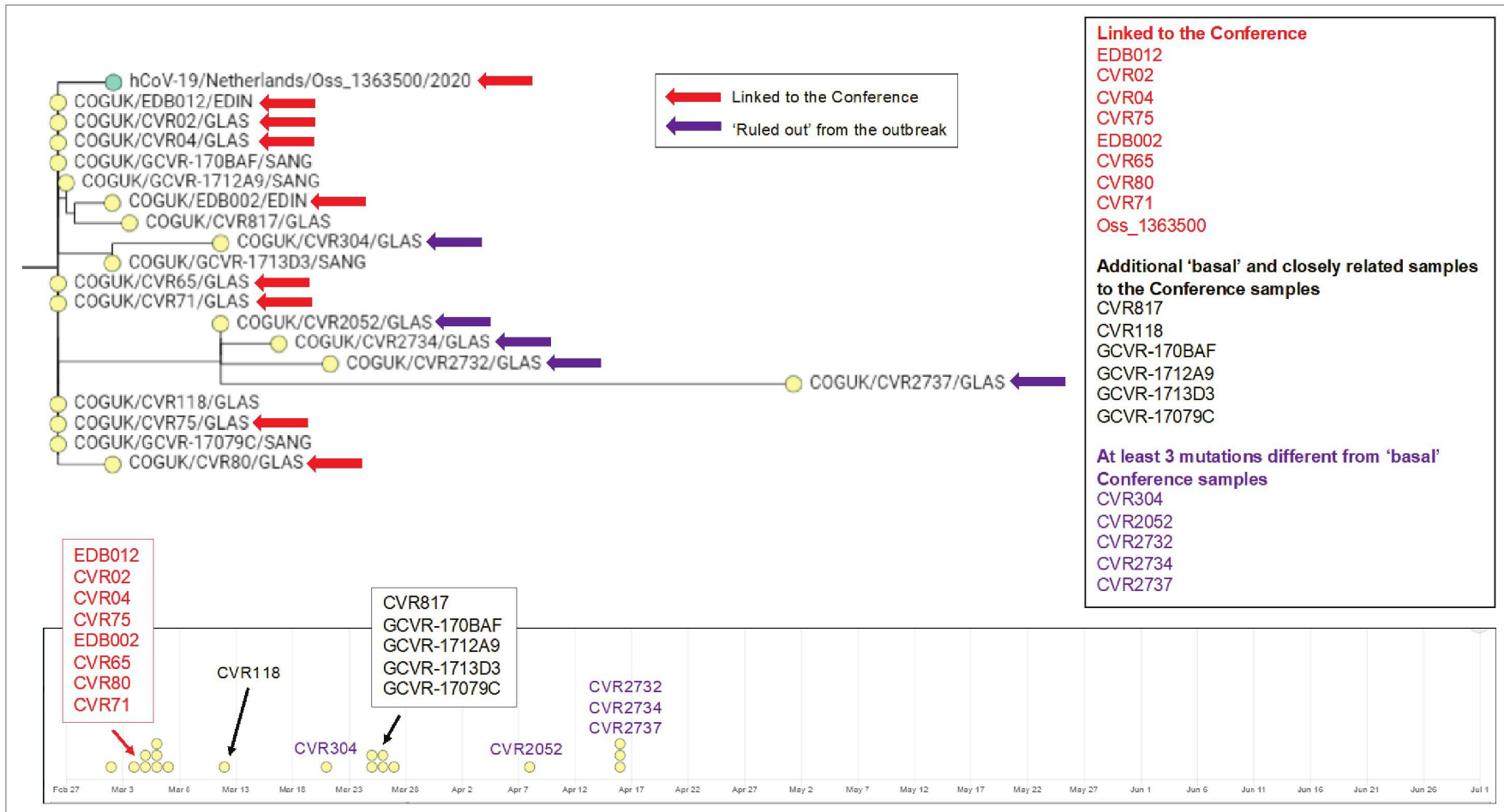


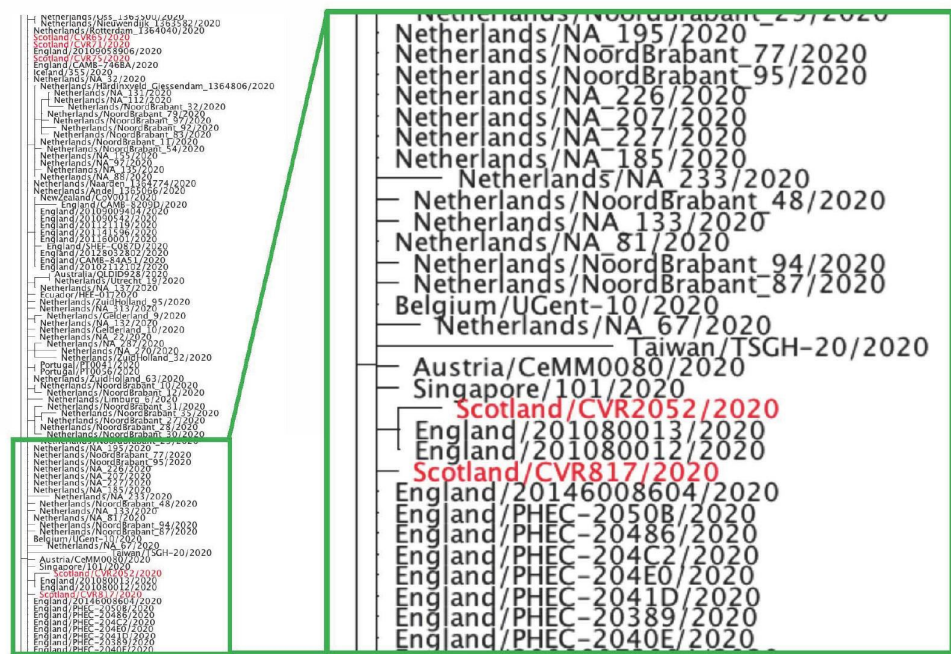
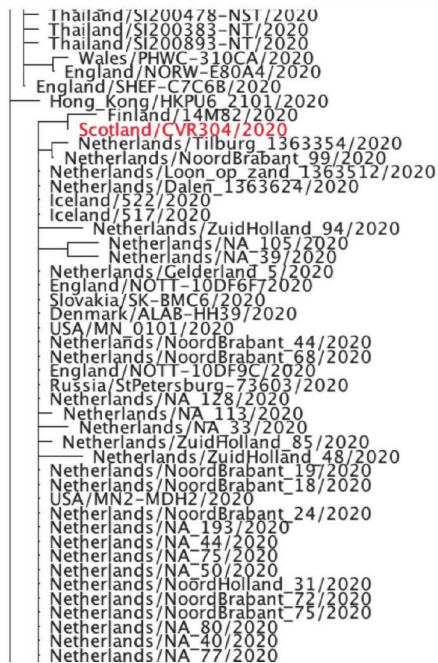
Figure 5: Phylogeny trees for samples with three mutations from the conference samples and placing them in an international context.

CVR304

3 SNP differences from conference samples
2 SNP differences from a Finnish sample

CVR2052

3 SNP differences from conference samples
2 SNP differences from English samples



It is important to note that since the identification of the sub-lineage B-S16 sequences associated with the conference in Scotland, this sub-lineage has not been subsequently identified in Scotland. This clearly demonstrates there was no wider undetected spread of this sub-lineage in Scotland and that the actions taken by the IMT to manage the outbreak were successful in curtailing onward transmission. These IMT actions were later bolstered by measures including national lockdown that ensured elimination of not just this but other lineages (while reducing their risk of re-introduction through travel restrictions). No more isolates with this sub-lineage were detected in Scotland after 17 April.

Analysis of the wider phylogenetic context of the Scottish samples demonstrated that sequences closely related to the sub-lineage B-S16 were found in England and also elsewhere in Europe, including the Netherlands. Figure 6 presents data from the sequencing of English samples and the identification of those of the B-S16 sub-lineage. Many of the samples on the basal branch are from the North East of England and London. There are also samples on the basal branch of the tree from the Netherlands (Figure 7).

Figure 6: English samples related to the B-S16 sub-lineage. Sixty-two samples were identified that were closely related to the B-S16 sub-lineage or closely related sub-lineages.

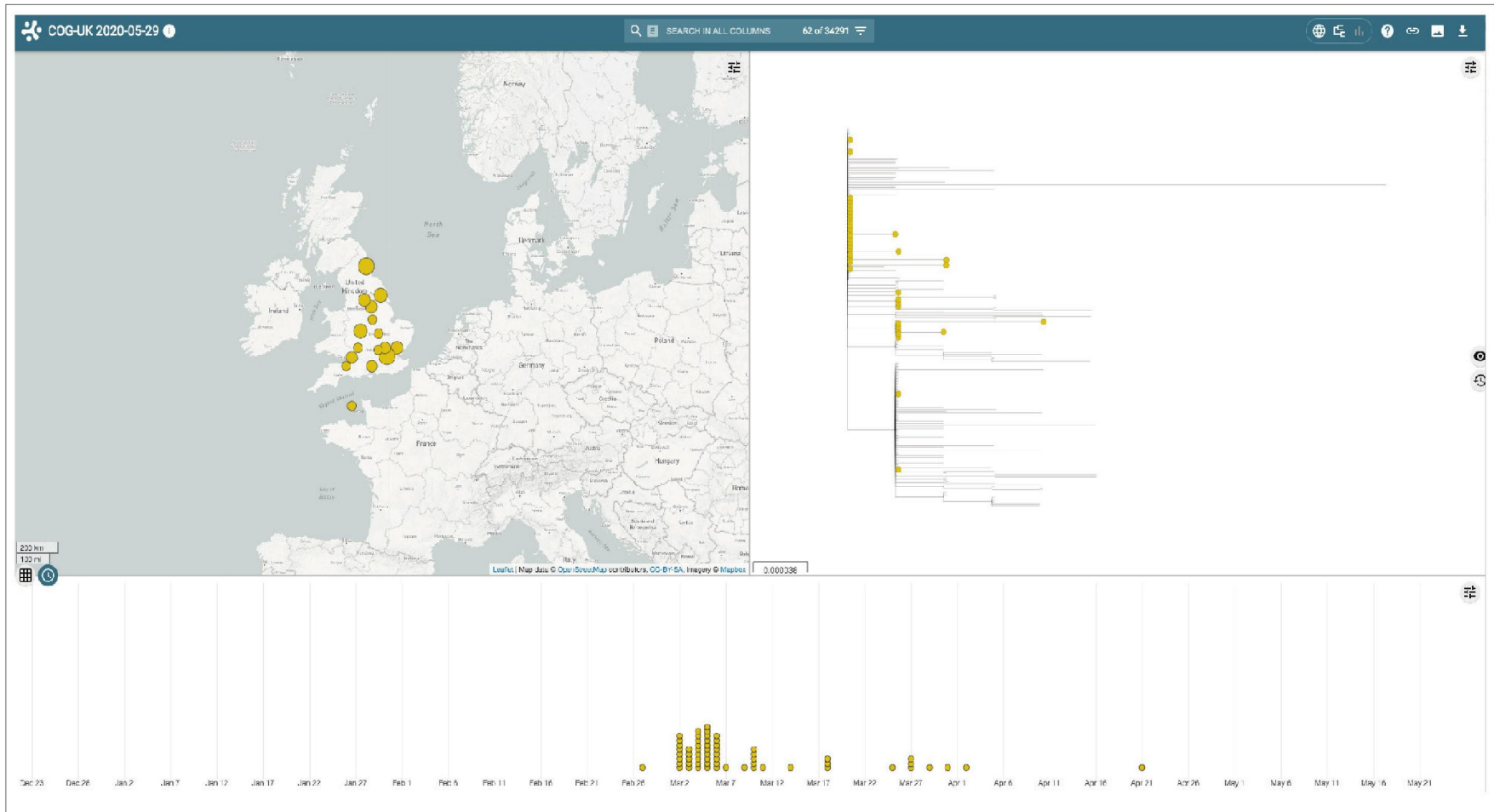
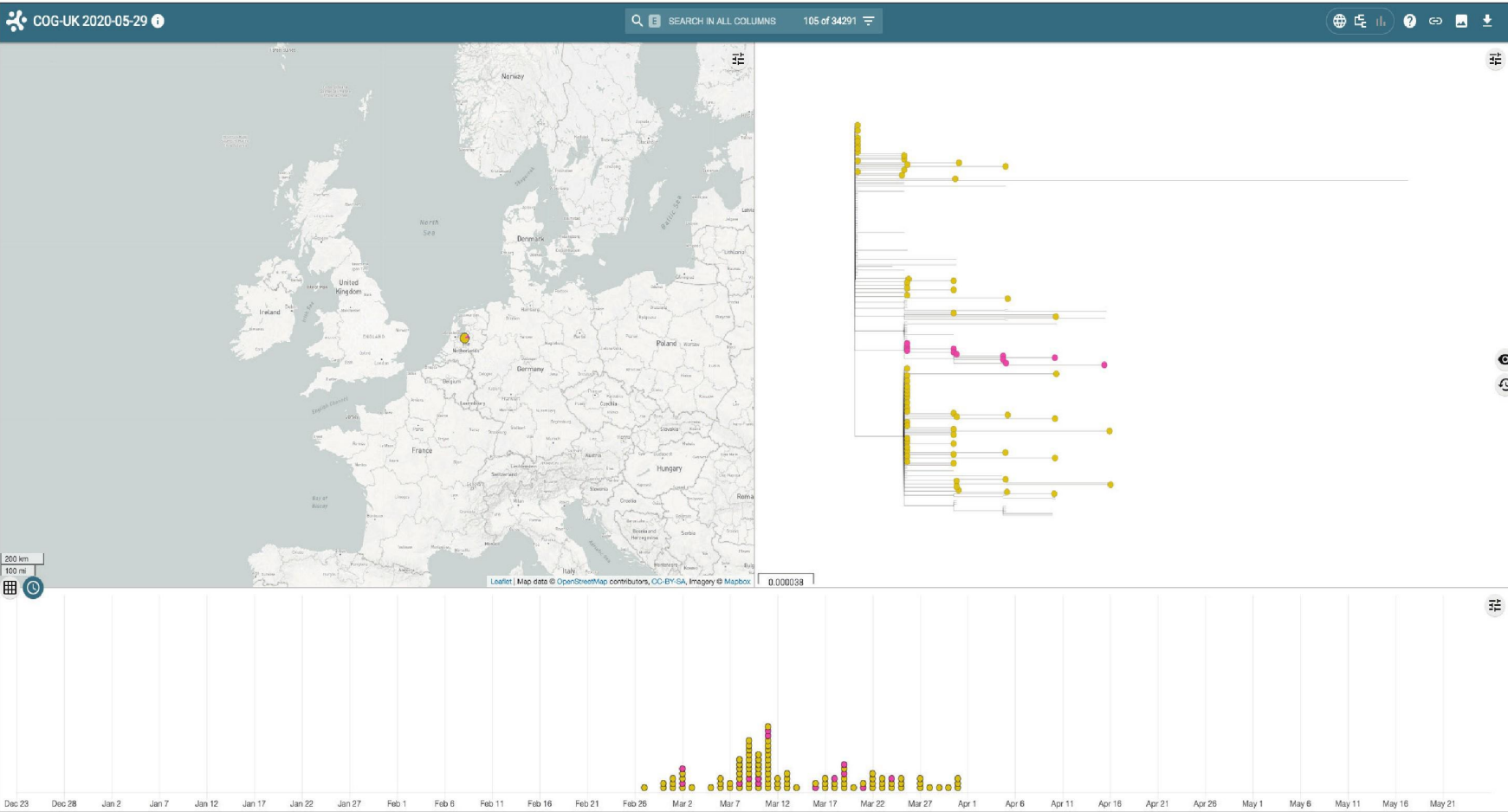


Figure 7: Dutch samples related to the B-S16 sub-lineage. One hundred and five samples were identified that were closely related to the B-S16 sub-lineage or closely related sub-lineages.



Virology conclusions

The source of the outbreak cannot be definitively determined. However, evidence supports the likelihood that the virus was introduced from outside of Scotland. This represents one of several hundreds of introductions of SARS-CoV-2 into Scotland from February 2020 and there is no evidence of community transmission of this sub-lineage, which was not detected in Scotland after April 2020.

Control measures

The coordination of national and international aspects of the outbreak was undertaken by HPS. The management of individual cases and their contacts was undertaken by local HPTs. Good liaison with the company allowed identification and communication with those personnel at risk and facilitated the risk assessment process.

In the early stages of the pandemic, cases were often managed in hospital to support infection control management and reduce the potential for household transmission.

The daily active follow-up by HPTs of close contacts of confirmed cases supported the rapid identification and testing of contacts who developed symptoms and enforced compliance with self-isolation.

NHS Lothian provided advice to the conference hotel and other venues on the requirements for any deep cleaning and use of personal protective equipment (PPE) by those undertaking the cleaning. This took cognizance of the then UK national infection prevention and control guidance which recognised that COVID-19 environmental risk was restricted to a period of 72 hours after the last exposure. NHS Lothian undertook risk assessments for individuals involved in working at the conference and conference social events. NHS Boards (or their equivalent in other countries outside Scotland) undertook further local risk assessment for cases and their contacts for their residents.

The company provided advice to all its premises where staff had worked after returning from the conference, in particular those where an attendee was identified as a case. The company conducted a deep clean at all premises and put additional cleaning measures in places across their premises, including at high contact points. Additional cleaning was conducted on sites as new cases were detected.

Communications

- The company proactively communicated with all staff who attended the conference as soon as they became aware of the initial cases. They advised all staff who attended the conference to self-isolate at home for 14 days following departure from the conference and for symptomatic individuals to be tested.
- NHS Board HPTs contacted all confirmed cases and contacts and provided advice regarding self-isolation and testing in accordance with the extant guidance.
- Information on the outbreak was shared with the NHS Boards HPTs and Scottish Government by HPS.
- Information was provided to NHS24 to support any calls they received regarding the conference or from those working at the conference venue.
- Communication with the Republic of Ireland and the Netherlands was via EWRS and PHE as the national focal point.
- Following additional sequencing analysis, an update on the sequencing was included in the First Minister's media briefing on 9 June 2020 and PHS included information on the sequencing in a news article on its website on 10 June (7).

Timeline

| Date | Event |
|---------------------|---|
| 24 February 2020 | Some participants arrive at conference hotel |
| 25-27 February 2020 | Conference in Edinburgh |
| 27 February 2020 | All participants left the venue |
| 1 March 2020 | First COVID-19 case confirmed in Scotland. The case was not connected to the conference |
| 2 March 2020 | PHS alerted by the Netherlands of a confirmed case following attendance at the conference |
| 2 March 2020 | Conference raised as any other competent business at daily PHE ROC meeting attended by HPS. Following the identification of the case, reported international public health agency |
| 2 March 2020 | Meeting between NICC, Centres and Regional Operating Cell (CROC) Chair and HPS |
| 3 March 2020 | First confirmed case in Scotland linked to conference identified |
| 3 March 2020 | First confirmed case in England linked to conference identified |
| 3 March 2020 | HPS chaired IMT |
| 3 March 2020 | NHS Lothian, NHS Ayrshire and Arran and HPS PAG |
| 4 March 2020 | HPS chaired IMT |
| 13 March 2020 | Self-isolation for conference attendees ends (14 days since end of the conference) |
| 09 June 2020 | Scottish Government daily briefing CMO outlined genetic work undertaken. CMO explained the specific viral lineage associated with the conference had been eradicated in Scotland |
| 10 June 2020 | PHS publish news item on website about the IMT in advance of the paper on sequencing analysis from Scotland |

Discussion

This was the first identified outbreak of COVID-19 in Scotland and was subject to considerable media scrutiny. The availability of WGS data provided an opportunity to further understand this event.

In Scotland, in addition to the eight cases directly linked to the conference (six primary and two secondary cases), there were a small number of other cases of the B-S16 sub-lineage identified and a small number of cases with three or more SNPs difference from the outbreak sub-lineage. These were more closely associated with samples from other cases in other countries and have been discounted as being directly linked to the conference. This sub-lineage has not been detected in Scotland since April 2020. This suggests that the actions taken by the IMT to manage the outbreak were successful in curtailing onward transmission. These IMT actions were later bolstered by measures including national lockdown that ensured elimination of not just this but other lineages (while reducing their risk of re-introduction through travel restrictions).

The follow-up of the primary cases linked to the conference identified a total of 16 secondary cases. In accordance with the guidance in place at the time of the outbreak, contacts were only tested if they were/became symptomatic. We now know that some infected individuals will present asymptomatically or with mild non-typical COVID-19 symptoms (8–11). It is possible that asymptomatic cases among conference delegates or close contacts of primary cases may not have been detected as a result of the testing policy in place at the time of the outbreak.

Analysis of the SARS-CoV-2 sequences in Scotland from March 2020 by da Silva Filipe et al. (6) estimated that SARS-CoV-2 was introduced to Scotland on at least 283 occasions during February and March 2020. A similar estimate of 307 was obtained from subsequent analysis by Lycett et al (12). The strains introduced into Scotland were diverse, representing much of the global distribution of lineages, with the majority fitting within the lineage B. Lineages A.2 and A.5 were the most prevalent A lineages; both prevalent in Spain. An increase in the number of sequences with the B.1, B.1.1, B.2 and B lineages coincided with the number of returning travellers from Italy and other parts of Europe in the first half of March,

while the second half of March showed a rise in sequences within the A.2 lineage, coinciding with returning travellers from Spain and other parts of the UK (6).

Based on the production of time-scaled phylogeny trees, the authors (da Silva Filipe et al) inferred that the first introductions of SARS-CoV-2 in Scotland dated back as far as 19 February. This indicates that community transmission was likely to have occurred undetected up to 1–2 weeks earlier than the first detected cases (6). This hypothesis is consistent with a study published by the Scottish Blood Transfusion Service which detected anti-SARS-CoV-2 neutralising antibodies in blood donations in March 2020. Considering the 14–28 day incubation period before seroconversion, it is concluded that it is likely that the virus began circulating in Scotland in late February 2020 (13).

The fact that multiple introductions of SARS-CoV-2 seeded the first wave of the pandemic in the UK is also reported using UK wide phylogenetic analysis showing >1000 lineages were imported into the UK, with the rate of appearance of new lineages initially high and then declining throughout March and April. The authors concluded that the UK's first epidemic wave resulted from the concurrent growth of many hundreds of independently introduced transmission lineages, and that the introduction of non-pharmaceutical interventions was followed by the apparent extinction of lineages in a size-dependent manner (14).

A similar pattern of multiple introductions into Scotland was observed for the second wave. Analysis by Lycett et al (12) of sequences available to 21 October 2020, showed that most of the latter were novel lineages, rather than persisting wave one lineages. While some of the wave two lineages were re-introductions from other parts of the UK, the majority were introductions from outside the UK.

This was the first recognised COVID-19 outbreak in Scotland and provided a unique opportunity to assess the value of incorporating genomics with epidemiological data to help understand transmission within an outbreak and postulate the origins of viral introductions into a setting. The benefits have since been shown many times over during the pandemic, both within Scotland and in the rest of the UK in a range of settings (15–18). The sequencing has also proved indispensable in supporting the wider understanding of transmission dynamics, rates of epidemic growth, importation

of cases and the emergence and tracking of variants. However, the utility of sequencing to support outbreak investigations requires sufficiently high coverage of cases from outbreaks and timeliness of results.

Conclusion

The detection of 23 persons directly linked to the conference is clear evidence of person-to-person transmission within the conference/conference social events, and the 16 secondary cases shows limited onward transmission outside the conference setting. A particular sub-lineage B-S16 was associated with conference cases. This sub-lineage was not detected in Scotland after April 2020.

Lessons learned

- Dissemination of real-time learning about COVID-19 is crucial to inform subsequent management of incidents.
- Good engagement with companies can have a key role in facilitating the public health risk assessment process.
- Strengthening the national communication process between public health and local authorities is needed to ensure confidence in the effectiveness of public health interventions.
- The critical importance of WGS in understanding the epidemiology of COVID-19.
- The importance of the international collaboration in dealing with outbreaks of infection.
- The sustained pressures and intensive working practices developed during the COVID-19 pandemic makes the production of high-quality, timely reports challenging.

Recommendations and progress

- HPS and its successor PHS have used the National Incident Coordination meetings with the NHS Boards to share experiences
- Early and continued liaison with companies with clear lines of communication is important to ensure the effectiveness of the public health response.
- HPS has since become part of PHS and embraced closer working with local authorities to facilitate the strengthening of this communication process.
- Scottish Government and the UK Government have invested in WGS which will have legacy beyond COVID-19 for a range of infections.
- PHS is working closely with its devolved administration colleagues to support the post-Brexit arrangements for international reporting of incidents and outbreaks, building on its international health regulations requirements through WHO.
- Scottish Government has invested in COVID-19 response by NHS Boards and PHS to support this response and provide a legacy for future pandemic responses.
- Future revision of the “Management of Public Health Incidents guidance” (2) approach should consider whether interim IMT reports dealing with the factual accounts of the incident are supplemented by later reports incorporating WGS findings.

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