Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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Letter to the Editor

Observations of SARS-CoV-2 variant of concern B.1.1.7 at the UK's largest hospital trust

To the editor,

The outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has placed unprecedented strain on health-care services, leading to 134,125,854 cases and more than 2905,412 deaths worldwide, as of 09/04/21.[1] Globally it has been observed that more transmissible variants develop.[2] Since October, one such variant of concern (VOC) (SARS-CoV-2 20B/GR clade; VOC-202012/01; lineage B.1.1.7) has been described in the UK.[3] B.1.1.7 appears to have substantially increased transmissibility compared to other variants and has quickly become the dominant variant in much of the UK.[4] A report by the Office for National Statistics suggested that people infected with B.1.1.7 are more likely to have a cough, sore throat, fatigue, or myalgia than those infected with other variants.[5] Furthermore, preliminary data indicate that infection with VOC B.1.1.7 is associated with an increased risk of death compared with other variants.[4] At University Hospitals Birmingham (UHB) NHS Foundation Trust, we undertake whole genome sequencing on a substantial proportion of our SARS-CoV-2 positive samples. Here, we report our observations and outcomes of VOC-202012/01 B.1.1.7 infected patients admitted to UHB during December 2020.

UHB is one of the largest Trusts in the UK, covering 4 NHS hospital sites, treating over 2.2 million patients per year and housing one of the largest single critical care units in the world. UHB's patient testing programme detects SARS-CoV-2 RNA from nasopharyngeal swabs/sputum using molecular platforms including Panther, Hologic, M2000, Abbott and Cepheid, GeneXpert,. Positive samples were collected from new admissions from the 15th to 31st December 2020 and then subjected to whole-genome sequencing at the University of Birmingham. Lineages were assigned with Pangolin.[6] To understand the impact of the VOCs: VOC-202012/01 B.1.1.7 and B.1.351, clinical details for patients whose samples resulted in an assignment of lineage were collected. This included: hospital length of stay, ethnicity, age, sex, critical care admission, critical care length of stay, treatment given for COVID-19 (dexamethasone or remdesivir), oxygen and ventilatory support, death, comorbidities and presenting symptoms. Multiple logistic, linear and quasipoisson regression models were used to examine the role of variants and patient characteristics such as age and sex and clinical outcomes. Statistical modelling was performed using R.[7]

SARS-2 positive samples from 152 patients were assigned a lineage following whole genome sequencing - 79 belonging to the B.1.1.7 lineage, 1 to the South African VOC B.1.351 and 72 to other variants (Fig. 1). During the study period, 52.3% of positive samples were the UK 'Kent' variant (B.1.1.7), 40.2% the 'Spanish' variant (B.1.177), and one South African variant (B.1.351) (Fig. 1). During December, there was a steady increase in the proportion of B.1.1.7 detected at UHB (18% and 63% in weeks 50 and 52 respectively) (Fig. 1). A quasipoisson regression model fitted to the number of patient isolates with COVID-19 demonstrated a significant interaction between collection date and B.1.1.7, leading to a significant increase in the recovery of B.1.1.7 (but not other variants) as time progressed ($p = 0.0077$). The following non-significant observations were made between the other variants vs B.1.1.7 and B.1.351 (Table 1); for the former, total length of stay was longer, length of stay on critical care was shorter, the proportion of patients on critical care was lower, the proportion of patients who died was higher and patients were older. A multiple logistic regression suggests that VOCs are significantly associated with the probability of developing a cough when compared to a similar patient with one of the other variants, with an odds ratio of 2.19 ($p = 0.0443$).

UHB has seen the largest number of COVID-19 cases in the country compared to other hospital Trusts: between 01/03/20–09/04/21, the Trust had 13,677 cases of COVID-19. In our small data set, B.1.1.7 was associated with younger age, an increased proportion of patients being admitted to critical care for longer periods but the association wasn't statistically significant. Whilst numbers of patients were relatively low, no increase in mortality was observed. Interestingly, significantly more patients infected with B.1.1.7 presented with a cough which could be a factor contributing to the increased transmission observed with this variant. This concurs with the report issued by the Office for National Statistics.[5] The NERVTAG report on B.1.1.7 suggests an increase in transmission of up to 71% in comparison to other circulating variants of SARS-CoV-2.[4] This is probably why the emergent new variant has contributed to UHB's record number of inpatients, which reached a peak of 1067 on 24th January, with 165 of those patients being on critical care. Gregson et al., (2020) showed that when a patient coughs, the average particle number is higher than that of someone talking, singing or shouting.[8] This could partly explain why more transmission is seen with B.1.1.7. This is an important observation, as heightened transmissibility of this new variant may result in a more prolonged period of increased incidence within healthcare institutions due to nosocomial spread. Importantly, UHB have seen more outbreaks within the acute setting in January 2021 when the new variant became the dominant strain. Further work is warranted to observe the effect of the new variant on nosocomial outbreaks and the conversion rate of contacts exposed to patients infected with B.1.1.7.

Finally, it will be important to monitor the proportion of new variant cases in hospital settings, both within patients and healthcare workers. Technologies such as whole genome sequencing are useful to pick up new variants quickly, especially with the emergence of other VOCs such as B.1.351 in South Africa and P1 in Brazil. In our dataset we were able to identify the South African variant B.1.351 in one of our patients, where normally this would

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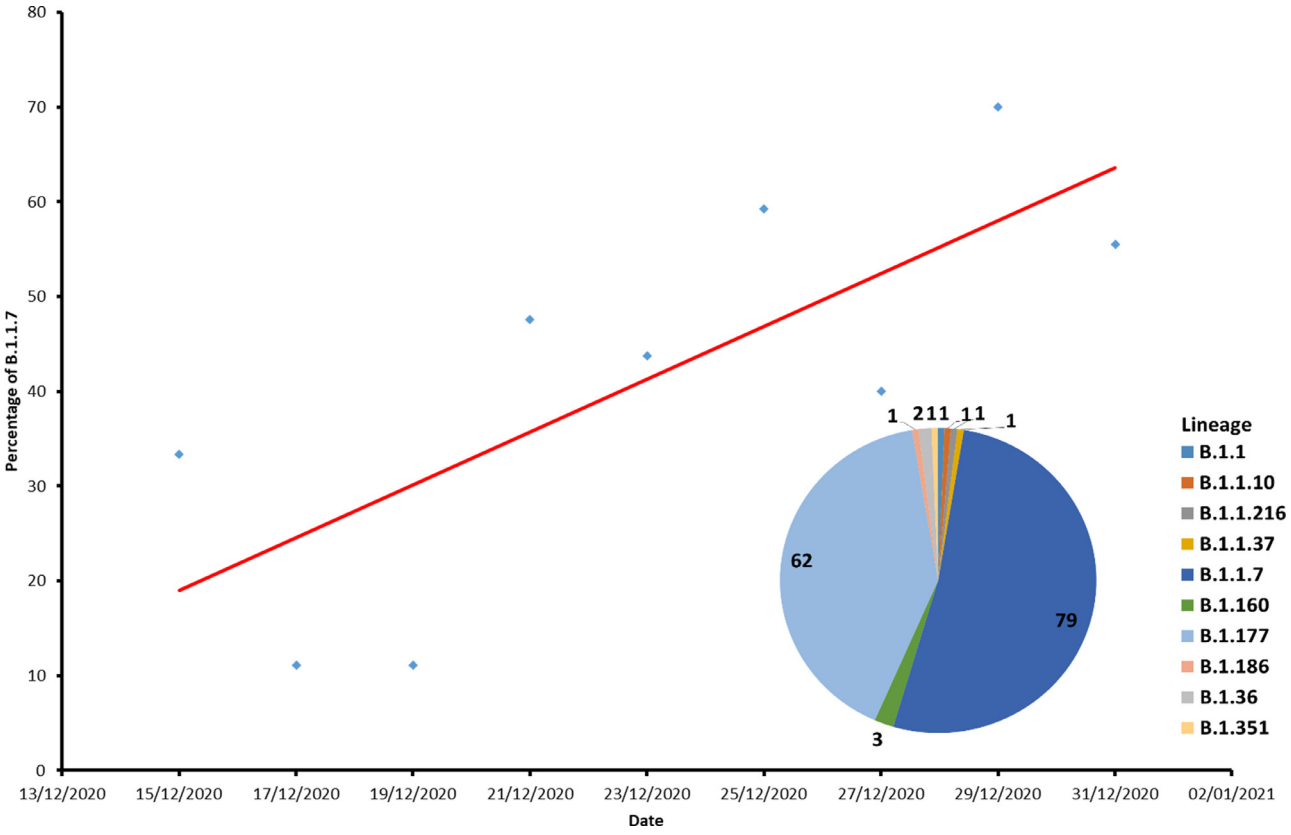

Fig. 1. The pie chart within the graph shows proportion of variants seen at UHB and the graph itself shows the increasing proportion (as a percentage) of B.1.1.7 at UHB during December 2020.
Note: The pie chart within the Figure shows the proportion of variants seen at UHB during December. Numbers in the pie chart represent actual numbers. The line chart shows the percentage increase of B.1.1.7 from 15th – 31st December. The red line in the chart represents a trend line. The blue diamonds represent percent of B.1.1.7 vs other variants.

Table 1
Data of other variants vs VOCs B.1.1.7 & B.1.351.

Variant	Number	Mean LoS days	Mean critical care LoS days	Proportion patients admitted to critical care	Proportion patients died	Mean age	Proportion of patients with a cough
Other	72	11.51	15.25	0.111	0.21	64.39	0.38
VOCS	80	9.56	18.93	0.19	0.18	58.2	0.59*

Key:.
LoS – length of stay, * P <0.05.

not have been detected. This has enabled Public Health England (PHE) to undertake contact tracing on this patient and implement surge testing in the community.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Availability of data and material

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Declaration of Competing Interests

None.

References

1. Johns Hopkins University and Medicine. Coronavirus COVID-19 global cases by the center for systems science and engineering (CSSE) at Johns Hopkins University (JHU). Available at: https://coronavirus.jhu.edu/map.html (last accessed 9th April 2021).
2. Sabino EC, Buss LF, Carvalho MPS, et al. Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. *Lancet* 2021;**397**:P452–5 10273.
3. Tang JW, Tambyah PA, Hui DSC. Emergence of a new SARS-CoV-2 variant in the UK. *J Infect* 2020;**28**.

4. NERVTAG UK. Meeting on SARS-CoV-2 variant under investigation VUI-2020 12/01. Available at https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/955239/NERVTAG_paper_on_variant_of_concern__VOC__B.1.1.7.pdf (last accessed 9th April 2021).
5. Office for National Statistics. (COVID-19) infection survey: characteristics of people testing positive for covid-19 in England. 27 Jan 2021. Available at: https://www.ons.gov.uk/peoplepopulationandcommunity/healthandsocialcare/conditionsanddiseases/articles/coronaviruscovid19infectionsinthecommunityinengland/characteristicsofpeopletestingpositiveforcovid19inengland27january2021 (last accessed 9th April 2021).
6. Rambaut A, Holmes ED, Hill V, et al. A dynamic nomenclature proposal for SARS–CoV-2 to assist genomic epidemiology. Nat Microbiol 2020;**5**:1403–7.
7. R version 4.0.4 (2021-02-15) – The R Foundation for statistical computying.
8. Gregson FKA, Watson NA, Orton CM, et al. Comparing the respirable aerosol concentrations and particle size distributions generated by singing, speaking and breathing. Aerosol Sci Technol 2020 Available at: https://doi.org/10.1080/02786826.2021.1883544 (last accessed 9th April 2021).

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