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Letter to the Editor

Household clustering of SARS-CoV-2 variant of concern B.1.1.7 (VOC-202012–01) in England

Following on from the paper published by Hui *et* al. on the emergence of a new possibly more transmissible variant in the UK of SARS-CoV-2 variant B1.1.7 (also referred to as VOC-2020–12–01 in the UK and herein referred to as the variant).[1] The variant coincided with a period of accelerated incidence during December 2020, leading to widespread alarm and immediate foreign travel restrictions.[2] First identified in the South East of England, the variant spread rapidly to other parts of the country, fuelling concerns of increased transmissibility. [3] We undertook a comparative analysis of household clustering to provide a rapid assessment of transmissibility of this variant against other sequenced cases. England benefits from a national collaborative sequencing effort known as COVID-19 Genomics UK (COG-UK); as of 8th February 2021, this comprised approximately 7% of confirmed cases, primarily based on samples from community testing. The presence of a sequenced case in a household is not an automated criterion for the selection of other cases' samples for sequencing, therefore providing an important opportunity to independently assess household clustering.

All cases from 1 October-15 December 2020 in England with a sequenced positive SARS-CoV-2 test result reported through the COG-UK consortium database were included.[4] Property classifications were obtained through address matching against Ordnance Survey reference database, providing a unique property reference number (UPRN) and basic land and property unit (BLPU) class. Household clusters were defined as a sequenced index case followed by one or more laboratory confirmed SARS-CoV-2 cases at the same private dwelling (UPRN) within 14 days. Private dwelling households were sub-divided into type of property such as detached, semi-detached, and terraced houses or self-contained flats using routine surveillance data so that diversity in households could be adjusted for in analysis. We excluded any households which had laboratory confirmed cases in the preceding 90 days (under the assumption that this would independently reduce the number of susceptible persons in a household and potential clustering effects), and households containing mixed sequencing results. To retain as many index cases as possible in the analysis, secondary cases were identified from national laboratory confirmed case data but not necessarily sequenced.

The number and proportion of variant (VOC-2020–12–01) and wild-type (non-variant) cases that were clustered within households were calculated. A logistic regression model was used to estimate odd ratios of clustering between the groups as well as age group, sex, Index of multiple Deprivation (IMD), race and ethnicity, region of residence, time period of testing (2-week period) and property type in bivariable and multivariable analyses, carried out in STATA 15.0 (STATA Corp,TX). All statistical tests had a threshold of $\alpha = 0.05$ (two-sided).

From 57,382 sequenced cases, 22,221 (38.8%) were single cases in a household and 15,837 (27.6%) identified as an index cases in a household cluster, Table 1). Crude analysis yielded increased odds of clustering with the variant (OR = 2.13, 95% CI 1.98–2.31) compared to wild-type, reduced to 88% higher odds (OR = 1.88, 95% CI 1.67 to 2.08, $p<0.001$) when adjusted for IMD, region, time, age, sex and race and ethnicity of the index case (Table 2). All covariates were strongly associated with household clustering, with higher odds of clustering in less deprived households and lower odds where the index case was age 70 years or older. Odds of clustering also increased over the period of the study. Household clustering was more likely in households with an index case of Asian ethnicity and less likely if the index case was of Black ethnicity, compared with index cases of white ethnicity.

Analysis of national data has shown that VOC-2020–12–01 variant cases were almost twice as likely to give rise to household clusters compared with wild type cases.

Household exposures are high risk with passive surveillance demonstrating high attack rates, providing an important indicator of transmissibility as household exposures are unlikely to differ between cases infected with different variants and their contacts. [5] This study benefits from the ability to link a large national sequencing dataset with residential address data during a period of time when both variants were circulating in the population. Limitation include the assumptions that subsequent cases at a residential address were most likely acquired within a household, i.e. no differential intra vs extra-household acquisition by variant type. Secondary attack rates were not estimated because test dates for subsequent cases in a household might reflect family members testing together rather than onset of illness. Data were not available to ascertain whether there were any (non-random) foci of sequencing in geographic areas where the new variant was known to be spreading, but these areas had large populations with both strains in circulation and estimates were adjusted for time and region. Cumulative sequencing coverage in England to week December 13th was 8%. [4]

Overall these findings are consistent with modelling which indicated that the variant increased the reproduction number by 73–81%

Declaration of Competing Interest

The authors declare no conflicts of interest

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Table 1
Characteristics of VOC-2020–12–01 variant within sporadic and primary case household clusters.

	Single case in household ($N = 22,221$)	Primary case of household cluster ($N = 15,837$)
Variant		
WT	20,987 (94.5)	14,069 (88.8)
202,012_01	1234 (5.5)	1768 (11.2)
Ethnicity of index case*		
White	17,799 (81.8)	12,058 (77.4)
Asian/Asian British	2138 (9.8)	2407 (15.5)
Black/Black British	738 (3.4)	367 (2.4)
Mixed	385 (1.8)	250 (1.6)
Other	708 (3.3)	492 (3.2)
Public Health England Centre region		
East Midlands	1578 (7.1)	528 (6.3)
East of England	2286 (10.3)	939 (11.2)
London	3678 (16.6)	1464 (17.5)
North East	1647 (7.4)	567 (6.8)
North West	4695 (21.2)	1681 (20.1)
South East	2192 (9.9)	927 (11.1)
South West	720 (3.2)	212 (2.5)
West Midlands	2011 (9.1)	774 (9.3)
Yorkshire and Humber	3392 (15.3)	1263 (15.1)
Time period†		
01/10 - 14/10	4192 (19.0)	1823 (12.1)
15/10 - 28/10	4866 (22.1)	2788 (18.3)
29/10 - 11/11	5775 (25.2)	4332 (26.5)
12/11 - 25/11	4450 (20.2)	3876 (25.5)
26/11 - 13/12	2750 (12.5)	2375 (15.6)
Age of index case (years)**		
<10	530 (2.4)	759 (4.8)
10 to 19	2735 (12.3)	1987 (12.6)
20 to 29	4967 (22.4)	2598 (16.4)
30 to 39	4214 (19.0)	2724 (17.2)
40 to 49	3240 (14.6)	2836 (17.9)
50 to 59	3054 (13.8)	2836 (17.9)
60 to 69	1631 (7.3)	1294 (8.2)
70 to 79	918 (4.1)	547 (3.5)
80+	937 (4.2)	250 (1.6)
Sex of index case^		
Male	10,258 (46.2)	7583 (48.0)
Female	11,926 (53.8)	8204 (52.0)

* Race ethnicity data were missing for 453 (2.0%) and 263 (1.7%) of sporadic and cluster primary case, respectively. Race and ethnicity data were provided by the testing laboratory or obtained from hospital records. Broad race and ethnicity categories are based on Office for National Statistics (ONS) standard categories. Race and ethnicity data were used to obtain an unadjusted estimate, and assess trends.

† A further 188 (0.9%) single and 633 (4.0%) index cases were counted on 14/12–15/12 and were not included in multivariable analysis adjusted for 2-week time period.

** Age data were unavailable for 3 (0.01%) and 6 (0.04%) for sporadic and cluster primary case, respectively.

^ Data on sex were unavailable for 37 (0.2%) and 50 (0.3%) for sporadic and cluster primary cases, respectively.

Author contributions

DC & TL were the principal investigators, DC led the writing of this report. All authors assisted with the design the study. DC undertook a background literature review and drafted the letter. All authors contributed to the interpretation of results and critical review of the letter.

Ethical approval

All data were collected within statutory approvals granted to Public Health England for infectious disease surveillance and control. Information was held securely and in accordance with the Data Protection Act 2018 and Caldicott guidelines.

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This analysis was classified as surveillance undertaken as part of PHEs legal responsibility to monitor COVID-19 and was fully compliant with all current regulatory requirements.

Table 2
Bivariable and multivariable analysis for association of VOC-2020–12–01 variant with household clustering.

	Bivariable results Odds Ratio (95% CI)	p-value	Multivariable results* Adjusted Odds Ratio (95% CI)	p-value
Variant	2.13 (1.98–2.31)	<0.001	1.88 (1.67–2.08)	<0.001
Per Index of Multiple Deprivation decile	1.03 (1.02–1.04)	<0.001	1.02 (1.01–1.03)	<0.001
Ethnicity of index case				
White	1.00 (reference)	<0.001	1.00 (reference)	<0.001
Asian/Asian British	1.62 (1.50–1.76)		1.65 (1.52–1.79)	
Black/Black British	0.76 (0.65–0.88)		0.85 (0.72–1.00)	
Mixed	0.89 (0.73–1.10)		1.00 (0.81–1.24)	
Other	1.01 (0.88–1.17)		1.09 (0.94–1.27)	
Public Health England Centre region				
East Midlands	1.00 (reference)	<0.001	1.00 (reference)	<0.001
East of England	1.12 (1.06–1.36)		1.06 (0.93–1.21)	
London	1.18 (1.05–1.33)		1.22 (1.08–1.39)	
North East	1.05 (0.92–1.21)		1.11 (0.96–1.28)	
North West	1.05 (0.93–1.19)		1.09 (0.97–1.23)	
South East	1.21 (1.07–1.37)		1.03 (0.90–1.25)	
South West	0.90 (0.75–1.09)		1.02 (0.84–1.23)	
West Midlands	1.16 (1.01–1.32)		1.06 (0.93–1.21)	
Yorkshire and Humber	1.12 (0.99–1.26)		1.09 (0.96–1.23)	
Time period				
01/10 - 14/10	1.00 (reference)	<0.001	1.00 (reference)	<0.001
15/10 - 28/10	1.08 (0.99–1.18)		1.05 (0.96–1.15)	
29/10 - 11/11	1.47 (1.36–1.59)		1.39 (1.28–1.51)	
12/11 - 25/11	1.41 (1.29–1.54)		1.30 (1.19–1.42)	
26/11 - 13/12	1.62 (1.48–1.78)		1.32 (1.19–1.43)	
Property type				
Detached	1.00 (reference)	<0.001	1.00 (reference)	<0.001
Semi-detached	0.97 (0.90–1.04)		0.95 (0.86–1.03)	
Terraced	0.88 (0.82–0.94)		0.85 (0.78–0.92)	
Flat	0.53 (0.48–0.58)		0.50 (0.44–0.54)	
Age of index case (years)				
<10	1.00 (reference)	<0.001	1.00 (reference)	<0.001
10 to 19	0.82 (0.69–0.95)		0.83 (0.69–0.99)	
20 to 29	0.69 (0.58–0.81)		0.74 (0.62–0.88)	
30 to 39	0.86 (0.73–1.02)		0.90 (0.76–1.06)	
40 to 49	1.11 (0.94–1.13)		1.12 (0.94–1.33)	
50 to 59	1.17 (0.98–1.38)		1.19 (1.00–1.41)	
60 to 69	0.97 (0.81–1.16)		0.99 (0.82–1.19)	
70 to 79	0.70 (0.57–0.86)		0.73 (0.59–0.90)	
80+	0.34 (0.27–0.44)		0.37 (0.29–0.47)	
Sex of index case (male vs. female)	1.10 (1.04–1.16)	<0.01	1.09 (1.04–1.15)	0.01

* adjusted for all variables in table.

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