Increased household transmission of COVID-19 cases associated with SARS-CoV-2 Variant of Concern B.1.617.2: a national case-control study

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Summary

Background

The SARS-CoV-2 B.1.617.2 variant (Delta) first detected in India, has rapidly become the dominant variant in England. Studies suggest this variant has increased growth rate and is more transmissible than the previous dominant B.1.1.7 (Alpha) strain. This study aimed to assess the difference in transmissibility in England between the emergent B.1.617.2 variant compared to B.1.1.7 variant.

Methods

A matched case-control study was conducted to estimate the odds of household transmission for B.1.617.2 index cases compared with B.1.1.7 SARS-CoV-2 index cases. Two-to-one matching was undertaken on the basis of geographical location of residence, time period of testing and property type, using a conditional logistic regression model.

Findings

3,765 genomically sequenced index cases in household clusters (≥ 2 cases in a household), were matched to 7,530 sporadic cases (single cases in a household). 5.8% (n=220) of index cases in household clusters had confirmed B.1.617.2 variant, compared to 4.7% (n= 351) of sporadic cases. The adjusted odds of household transmission was1.64 among index cases with B.1.617.2 variant (95%CI 1.26 to 2.13, p <0.001) compared to the B.1.1.7 variant after adjusting for age, sex, ethnicity, index of multiple deprivation (IMD) and vaccination status of index case.

Interpretation

Overall, we found increased household transmission of COVID-19 associated with B.1.617.2 compared to B.1.1.7. These findings show households are important settings for rapid transmission of the lineage B.1.617.2. With household settings being an important factor in wider community spread, strategies to prevent transmission in these settings are vital to control the COVID-19 pandemic.

Introduction

Following detection of the first SARS-CoV-2 cases in England in January 2020, by June 2021, the total number of laboratory confirmed COVID-19 cases in England has exceeded 3.9 million. Following a large wave of COVID-19 cases in late 2020 and subsequent national lockdown, the number of new COVID-19 infections declined, and since March 2021 had remained stable. Also, during this time, several emerging SARS-CoV-2 variants were detected in England.

SARS-CoV-2 variant B.1.617.2, classified by WHO as ‘Delta’ variant, was initially detected in India in December 2020 (1) amidst a surge in COVID-19 cases and associated hospitalisations and deaths. As of 1 June 2021, this variant has been detected in 54

countries (2). The first genomically confirmed case was detected in England in late March 2021 as part of the national routine sequencing of SARS-CoV-2 cases. The B.1.617.2 variant was initially declared a variant under investigation by Public Health England (PHE) and then upgraded to a variant of concern on 28 April 2021. Initially detected in specific localised outbreaks and associated with travel to India, by 10 June 2021 there were 16,242 of genomically confirmed cases of B.1.617.2 SARS-CoV-2 variant, increasingly community acquired, which are geographically spread across England (3).

Surveillance and modelling data suggest B.1.617.2 has quickly become the dominant variant in England. In England, the B.1.617.2 variant has by far highest growth rate, reflecting both the biological properties of this variant and the context in which it is transmitting (2, 4). The observed rapid spread of this variant in England and internationally necessitate investigation into the transmissibility advantage of this variant compared to the previously dominant variant, B.1.1.7, to assess its potential impact on the incidence in England.

Households are high risk settings for transmission of COVID-19 (5) and are an important factor in wider community spread (6). By assessing the extent to which B.1.617.2 results in onward transmission to household members compared to the previously dominant variant B.1.1.7, we can assess the relative transmissibility of this variant, and provide information vital to the national and international pandemic response.

Methods

Study design

A pair-matched case-control study design was used to estimate the odds of transmission within households for B.1.617.2 compared with B.1.1.7 SARS-CoV-2 cases.

Study population

Data on laboratory confirmed COVID-19 cases in England that have been genomically sequenced was extracted on 31 May 2021. The study population consisted of sequenced B.1.617.2 and B.1.1.7 SARS-CoV-2-positive cases who: a) had a first positive specimen date between March 18 2021 and May 17 2021, to allow for subsequent household cases to be detected; b) resided in a terraced, semi-detached or detached house or a flat and c) had no recorded history of foreign travel within 14 days preceding the specimen date. Individuals were included in the analysis if they were the only or earliest cases within a household.

Outcome assessment

Positive SARS-CoV-2 tests are required to be notified to Public Health England (PHE)'s Second Generation Surveillance System (SGSS), a laboratory reporting system. Residential address information for each positive SARS-CoV-2 test is obtained via the reporting laboratory and the NHS Spine (national electronic health record database). To obtain accurate information on residential setting, including to derive Unique Property

Reference Number (UPRN) and Basic Land and Property unit (BLPU) class, patients with positive SARS-CoV-2 tests were matched using address data in SGSS to reference databases held by PHE. The residential address held by the laboratory was preferentially used over the address on NHS Spine as this should better reflect the address at time of testing. BLPU classes were used to classify property type according to local authority data.

Household clusters were defined as 2 or more laboratory confirmed SARS-CoV-2 cases at the same private residential dwelling. This includes an initial sequenced index case followed by one or more laboratory confirmed cases in the household (based on UPRN) within 14 days of the index cases' positive specimen date. Secondary cases within a household were identified from all national laboratory confirmed case data regardless of whole genome sequencing data availability to optimise case ascertainment.

For the case-control study, cases were defined as the person within a household with the earliest positive test date (index case) and there were other cases reported within the household , and no SARS-CoV-2 cases had been reported in the household within the previous 90 days. Controls were index cases where there were no other SARS-CoV-2 cases reported in the household in the subsequent 14 days. Cases and controls were matched on a 1:2 ratio on the fortnight of specimen date, geography (lower tier local authority) and property type, that is, terraced, semi-detached or detached household or flat. Matching on time and geography was undertaken to minimise potential for confounding related to regional variation in the rapid rise in case rates. Matching on property type was undertaken to minimise potential confounding related to household size.

Exposure assessment

B.1.617.2 and B.1.1.7 variant cases were identified from sequencing information nationally co-ordinated by the COG-UK consortium and uploaded to the CLIMB (Cloud Infrastructure for Big Data Microbial Bioinformatics) database. PCR confirmed cases are sampled for whole genome sequencing (WGS) with approximately over 50% of laboratory confirmed cases in England sequenced during the study period (7). Sequences are assigned to Public Health England's single nucleotide and multinucleotide polymorphisms based variant definitions (8).

Exclusions

Cases that were non-B.1.617.2 or non-B.1.1.7 variant and cases that did not have a full 14 days of follow-up time were excluded. Any households that had laboratory confirmed cases in the preceding 90 days from the index case were excluded under the assumption that this would independently reduce the number of susceptible persons in a household and potential observed effects on transmission. Co-index households were defined as more than one case having the same earliest positive specimen date and were also excluded.

Currently targeted testing is undertaken for close contacts of cases with a variant of concern (VOC), apart from B.1.1.7, so any households identified as targeted for such testing were excluded as this would increase the potential observed transmissibility of B.1.617.2 cases. Address data from targeted testing operations were matched to

reference databases held by PHE to derive Unique Property Reference Number (UPRN) and any positive SARS-CoV-2 cases linked to these UPRNs were excluded.

Data on recent travel history for sequenced cases was collected via passenger locator forms, contact tracing advisory service (CTAS) dataset and enhanced follow up of cases with genomically confirmed variants of concern through local health protection teams. Travel status was defined as an index case traveling outside the UK and Ireland within 14 days preceding of the positive specimen date. To minimise the impact of potential bias introduced through different isolation guidance for travellers and non-travellers, including quarantine guidance and compulsory hotel quarantine for returning travellers, cases with travel history within 14 days were excluded from analysis.

There are 2 main testing routes for COVID-19 in the UK which are through hospital and public health laboratories for those with a clinical need as well as some healthcare workers (referred to as Pillar 1) and through wider population testing (referred to as Pillar 2), through both community testing sites and postal tests. Cases identified through Pillar 1 were excluded to omit individuals identified as SARS-CoV-2 positive while hospitalised and therefore minimise bias in terms of household transmission.

Covariates

A range of factors that may be associated with household transmission and risk of exposure to COVID-19, or specifically to either B.1.617.2 or B.1.1.7 were accounted for in the study. These factors included: age, sex, ethnicity, index of multiple deprivation (IMD) quintiles and vaccination status of the index case.

Vaccination status of index cases were obtained from a national vaccination register (the National Immunisation Management System, NIMS) and linked using patient NHS number.

Statistical Analysis

To initially assess differences between cases in household clusters and controls in terms of demographic characteristics not accounted for in the matching criteria, including in term of age, sex, ethnicity, history of foreign travel and vaccination status of index case, Chi-squared tests for trend were used.

A conditional logistic regression model was used to account for pair-matching within the data. The model for the association with variant and household transmission was adjusted for confounding by age, sex, ethnicity, index of multiple deprivation (quintiles) and vaccination status of index case.

In addition, an analysis including data for cases with travel history was used to assess the effects on the results. Interactions with history of foreign travel were explored but no evidence of this was found therefore the model was adjusted for history of foreign travel.

Results

Of the 143,285 positive SARS-CoV-2 reported cases during the study period (18 March to 17 May), 64,855 (45.3) were successfully genomically sequenced (for any variant).

We excluded 22,555 index cases with confirmed B.1.6.7.2 or B.1.1.7 variant with specimen dates between 18 March and 17 May as they did not meet eligibility or matching criteria. Of these, 2,588 confirmed B.1.6.7.2 index cases were excluded as they did not meet the eligibility criteria if they were tests carried out via Pillar 1 testing (as these tests are primarily conducted as part of hospital and travel associated testing), if they had recently travelled, or within households with multiple index cases. A further 2,017 confirmed B.1.6.7.2 index cases were excluded as they could not be matched as cases or control on the matching criteria. A total of 571 confirmed B.1.6.7.2 variant cases were included in the analysis (Table 1).

After applying eligibility criteria and pair matching, we obtained a sample of 11,295 individual index cases, this included 3,765 index cases in household clusters (hereafter referred to as cases in the case-control study) and 7,530 sporadic cases (defined as controls) (Table 1).

The index cases excluded from the analysis (n= 22,555) differed from those included in terms of variant, PHE centre of residence, age, sex, ethnicity and IMD (χ^2 p=<0.05) (S1 Table 1). A higher proportion of included cases were 10 to 19 years old compared to excluded cases (23.7%, 19.8%, respectively) and a lower proportion were over 70 (1.5%, 3.4%, respectively). A lower proportion of included cases were of Asian ethnicity (13.8%, 16.0%, respectively). A higher proportion of included cases were resident in Yorkshire and Humber compared to excluded cases (43.7% and 18.1%, respectively).

Study population

Females made up 52.0% (1,956) of cases and 51.7% (3,890) of controls. 23.7% of both cases and controls were aged between 10 to 19, with a slightly higher proportion of cases aged between 30-49 compared to controls (Table 1). The majority of the study population were of White ethnicity (78.1%, 8,823) with a higher proportion of Asian ethnicity (15.7%, 590) among cases compared to controls (12.8%, 964)). A large proportion of the study population resided in Yorkshire and Humber (43.7%, 4,932) and the North West (22.5%, 2,544), reflecting the location of geographic clusters of COVID-19 cases during the study period. The most common residential setting was terraced households (41.6%, 4,698)), followed by semi-detached (39.6%, 4,470). A higher proportion of cases were also unvaccinated compared to controls (72.8% vs 70.2%).

A higher proportion of cases had confirmed B.1.617.2 variant among the cases group (5.8%, 220), compared to those who were controls (4.7%, 351).

Household Transmission

In the single variable analysis, the odds of household transmission was 1.66 among those with B.1.617.2 variant (95%CI 1.28-2.14, p <0.001) compared to those with B.117 variant. After adjusting for age, sex, ethnicity, IMD and vaccination status of index case, evidence

of this association remained with the adjusted odds of household transmission 1.64 among those with B.1.617.2 variant (95%CI 1.26-2.13, p <0.001).

Differences in the odds of household transmission were also seen between age and ethnicity groups in both single variable and multivariable models (Table 2). The adjusted odds of household transmission among those with an index case aged <10 years old were 1.46 times those aged 30 to 39 (95%CI 1.23 to 1.75, p < 0.001). The odds of household transmission were increased when an index case was of Asian ethnicity (aOR 1.30, 95%CI 1.14 to 1.47, p < 0.001) and less likely when an index case was of Black ethnicity (aOR 0.73, 95%CI 0.56 to 0.95, p 0.02), compared with index cases of White ethnicity.

A supplementary analysis also including index cases who had known foreign travel within 14 days preceding the specimen date (n= 11,901) also found strong evidence of an association between household transmission and the B.1.617.2 variant with the crude odds ratio of transmission 1.67 among those with B.1.617.2 variant compared to those with B.117, and an adjusted odds ratio of 1.68 after adjustment for age, sex, ethnicity, IMD and vaccination status (95% CI 1.31 to 2.14, p <0.001).

Discussion

This study found a 64% increase in the odds of household transmission associated with infection with B.1.617.2 SARS-CoV-2 variant compared to B.1.1.7, following adjustment for the index cases' vaccination status, as well as sex, ethnicity, IMD and age group. This study provides early real-world evidence of the effect B.1.617.2 variant on household transmission. The findings support existing evidence that B.1.617.2 has a substantially increased transmissibility advantage over the B.1.1.7 variant which has contributed to the rapid increase in the number of B.1.617.2 cases in the UK over the study period and the level of increase is consistent with estimates of increased transmission to close contacts (2, 4, 9).

This study also found evidence of increased household transmission among households with an index case of Asian ethnicity, a finding which is consistent with studies of the previously dominant B.1.1.7 variant (10). These results add important new evidence to help understand the underlying reasons for this increased susceptibility to COVID-19 infection, and possibly reflect differences in household composition and inter-household mixing between ethnic groups, such as more common large or multi-generational households.

This study benefits from utilising multiple national-level surveillance datasets and allowing enrichment of COVID-19 case data with genomic sequencing results, residential address data and travel information to create a large sample of cases and controls for inclusion in the analysis.

This analysis covers a period of time when both B.1.617.2 and B.1.1.7 variants were circulating in the population, allowing comparison of risk with sufficient power to detect a difference in transmission. By the end of May 2021, B.1.617.2 had become the dominant SARS-CoV-2 virus in England, accounting for over 90% of all new cases (2).

Due to the extensive genomic surveillance in England and resulting high sequencing coverage during the period studied, over 50% of positive COVID-19 cases during this time were genomically sequenced. Therefore, the sequenced cases included in this study are likely representative of the population testing positive for COVID-19, increasing the generalisability of the results, although it must be noted that the sampling strategy for sequencing is not random. Some effects of this non-random sampling were addressed by removing households that received targeted testing.

The inclusion of vaccination status data further strengthens this study. By linking COVID-19 case data to vaccination data we were able to partially adjust for the effect of vaccination on onward transmission to secondary cases. This adjustment is an important factor in assessing transmissibility, as other studies have shown vaccination is effective in reducing secondary cases within households with a symptomatic index case (5). However, our assessment of this effect in this study was limited as the majority of cases included in the analysis were unvaccinated.

There are several limitations to this study. Firstly, by applying matching criteria, to minimise confounding and identify a study cohort of over 11,000 cases, we excluded 34,568 sequenced cases that could not be matched. We found that the demographic profile of the sequenced cases that were excluded differed from those included in terms of key characteristics such as age, ethnicity and vaccination status, therefore introducing a potential level of bias in the findings.

Additionally, we did not have information on household size, which is likely to have an effect on the estimates of transmissibility. For example, some controls (sporadic cases) will have lived alone and have no chance of onward transmission within their residence and therefore becoming a household cluster. However, we were unable to identify and exclude these cases in the analysis. Further studies of household transmission that includes denominators of all individuals in the household and their vaccination status are needed to provide improved estimates of household transmission and allow for the calculation of household secondary attack rates.

This analysis is specific to residential households and excluded outbreaks occurring other residential settings susceptible to SARS-CoV-2 outbreaks such as prisons or care homes, or in other vulnerable populations such as homeless people. As data is based on residential address, we were also not able to include outbreaks in education or occupational settings. Care must therefore be taken when applying conclusions form this study to other such settings.

Conclusions

Overall, we found increased household transmission of COVID-19 associated with B.1.617.2 compared to B.1.1.7. Improving the understanding of the level of transmissibility of new variants can help inform UK and international infection prevention and control policies and improve pandemic planning. Our study shows that households are important settings for rapid transmission of the lineage B.1.617.2 and with household settings being an important factor in wider community spread, it is vital to maintain policies to prevent transmission in these settings to control the COVID-19 pandemic.

Table 1. Characteristics of cases and controls

	Controls		Cases			
	Count	Percent	Count	Percent	χ^2	p-value
Total	**7,530**		**3,765**			
VARIANT						
B.1.617.2	351	4.66	220	5.84	7.3	0.007
B.1.1.7	7,179	95.34	3,545	94.16		
Household type						
Terraced	3132	41.59	1566	41.59	N/A	N/A
Semi-detached	2,980	39.58	1,490	39.58		
Detached	914	12.14	457	12.14		
Flat	504	6.69	252	6.69		
Specimen date (2-week period)						
w/c 15th Mar 2021	2402	31.90	1201	31.90	N/A	N/A
w/c 29th Mar 2021	2,048	27.20	1,024	27.20		
w/c 12th Apr 2021	1,206	16.02	603	16.02		
w/c 26th Apr 2021	1,312	17.42	656	8.71		
w/c 10th May 2021	562	7.46	281	7.46		
PHE Centre						
East Midlands	710	9.43	355	9.43	N/A	N/A
East of England	282	3.75	141	3.75		
London	278	3.69	139	3.69		
North East	510	6.77	255	6.77		
North West	1,696	22.52	848	22.52		
South East	80	1.06	40	1.06		
South West	44	0.58	22	0.58		
West Midlands	642	8.53	321	8.53		
Yorkshire and Humber	3288	43.67	1,644	43.67		
Age						
<10	379	5.03	300	7.97	97	<0.001
10-19	1,782	23.67	892	23.69		
20-29	1,597	21.21	591	15.70		
30-39	1,582	21.01	869	23.08		
40-49	1,075	14.28	616	16.36		

	Controls		Cases			
	Count	Percent	Count	Percent	χ^2	p-value
50-59	698	9.27	336	8.92		
60-69	287	3.81	119	3.16		
70+	130	1.73	42	1.12		
Sex						
Female	3,890	51.66	1,956	51.95	0.09	0.77
Male	3,640	48.34	1,809	48.05		
Ethnicity						
Asian	964	12.80	591	15.70	33.4	<0.001
Black	229	3.04	78	2.07		
Mixed	163	2.16	80	2.12		
Other	221	2.93	146	3.88		
White	5,953	79.06	2,870	76.23		
IMD (quintile)						
1	3,015	40.04	1,527	40.56	2.82	0.588
2	1,581	21.00	817	21.70		
3	1201	15.95	558	14.82		
4	1,049	13.93	521	13.84		
5	684	9.08	342	9.08		
Vaccination status of index case						
Unvaccinated	5,286	70.20	2,741	72.80	12.9	0.012
<21 days post dose 1	515	6.84	264	7.01		
>= 21 days post dose 1	1,027	13.64	472	12.54		
>= 14 days post dose 2	51	0.68	19	0.50		
Unknown	651	8.65	349	9.27		

IMD = Index of Multiple Deprivation (1= least deprived, 5 = most deprived)

Table 2. Results of univariate and fully adjusted multivariate conditional logistic regression models

	Household Transmission			
	Univariate OR (95% CI)	**Univariate P value**	**Multivariate OR (95% CI)**	**Multivariate P value**
Variant				
B.1.617.2	1.66(1.28-2.14)	<0.001	1.64(1.26-2.13)	<0.001
B.1.1.7	1.00	base	1.00	base
Sex				
Female	1.00	base	1.00	base
Male	0.99(0.91-1.07)	0.769	0.97(0.89-1.05)	0.415
Age group				
<10	1.46(1.23-1.74)	<0.001	1.46(1.23-1.75)	<0.001
10-19	0.92(0.82-1.03)		0.92(0.81-1.04)	
20-29	0.67(0.59-0.76)		0.67(0.59-0.76)	
30-39	1.00		1.00	
40-49	1.05(0.92-1.2)		1.05(0.92-1.19)	
50-59	0.88(0.75-1.03)		0.9(0.76-1.06)	
60-69	0.76(0.61-0.96)		0.79(0.62-1.01)	
70+	0.59(0.41-0.85)		0.65(0.45-0.95)	
Ethnicity				
Mixed	1.04(0.79-1.36)	<0.001	1.01(0.77-1.34)	<0.001
Asian	1.33(1.18-1.51)		1.30(1.14-1.47)	
Black	0.73(0.56-0.95)		0.73(0.56-0.95)	
White	1.00		1.00	
Other	1.39(1.12-1.72)		1.42(1.14-1.76)	
IMD quintile				
1-most deprived	1.1(0.97-1.25)	0.546	1.07(0.94-1.21)	0.694
2	1.12(0.98-1.28)		1.11(0.97-1.27)	
3	1.00		1.00	
4	1.07(0.92-1.24)		1.08(0.93-1.25)	
5-least deprived	1.07(0.9-1.27)		1.07(0.9-1.27)	
Vaccination status of index case				
<21 days post dose 1	0.99(0.85-1.16)	0.010	1.01(0.85-1.2)	0.012
>=21 days post dose 1	0.88(0.79-1.00)		0.94(0.81-1.08)	
>=14 days post dose 2	0.71(0.41-1.21)		0.76(0.44-1.31)	
Unvaccinated	1.00		1.00	
Unknown	0.79(0.68-0.92)		0.77(0.66-0.9)	

Declarations

Conflicts of interest or competing interests
The authors have no relevant financial or non-financial conflicts of interest to disclose.

Availability of data and material
Data are incorporated into the article and material contained within. Individual level data cannot be shared due to ethical or privacy reasons.

Code availability
Custom code using Stata15.

Authors' contributions
AV and HA were the principal investigators and led the writing of this report. HA, AV, MK, JF, KT and GD made significant contributions to conception of the study design. All authors contributed to the interpretation of results and critical review.

Ethics 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.

Consent to participate
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.

Consent for publication
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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Supplementary material

Supplementary Table 1. Characteristics of excluded index cases and included index cases

	Exclusions		Inclusions			
	Count	Percent	Count	Percent	χ^2	p-value
Total	**22,555**		**11,295**			
VARIANT						
B.1.617.2	2,588	11.47	571	5.06	366.47	<0.001
B.1.1.7	19,967	88.53	10,724	94.94		
PHE Centre						
East Midlands	2956	13.11	1065	9.43	35,00.00	<0.001
East of England	2118	9.39	423	3.75		
London	2535	11.24	417	11.57		
North East	1401	6.21	765	6.77		
North West	4961	22.00	2,544	22.52		
South East	1657	7.35	120	1.06		
South West	563	2.50	66	0.58		
West Midlands	2235	9.91	963	8.53		
Yorkshire and Humber	4071	18.05	4,932	43.67		
Missing	58	0.26	0	0.00		
Age						
<10	1291	5.72	679	6.01	166.7	<0.001
10-19	4471	19.82	2,674	23.67		
20-29	4607	20.43	2,188	19.37		
30-39	4901	21.73	2,451	21.70		
40-49	3349	14.85	1,691	14.97		
50-59	2185	9.69	1,034	9.15		
60-69	985	4.37	406	3.59		
70+	766	3.40	172	1.52		
Sex						
Female	11379	50.45	5,846	51.76	5.15	0.023
Male	11176	49.55	5,449	48.24		
Ethnicity						
Asian	3609	16.00	1,555	13.77	57.61	<0.001
Black	702	3.11	307	2.72		
Mixed	489	2.17	243	2.15		

	Exclusions		Inclusions			
	Count	Percent	Count	Percent	χ^2	p-value
Other	940	4.17	367	3.25		
White	16815	74.55	8,823	78.11		
IMD (quintile)						
1	6,627	29.38	4,542	40.21	461.04	<0.001
2	5008	22.20	2398	21.23		
3	4052	17.96	1759	15.57		
4	3709	16.44	1,570	13.90		
5	3101	13.75	1,026	9.08		
Unknown	58	0.26	0	0.00		

Supplementary Table 2. Results of univariate and fully adjusted multivariate conditional logistic regression models

	Household transmission			
	Univariate OR (95% CI)	**Univariate P value**	**Multivariate OR (95% CI)**	**Multivariate P value**
Variant				
B.1.617.2	1.63(1.28-2.07)	<0.001	1.68(1.31-2.15)	<0.001
B.1.1.7	1.00	base	1.00	base
Sex				
Female	1.00	base	1.00	base
Male	0.98(0.91-1.06)	0.593	0.96(0.89-1.04)	0.349
Age group				
<10	1.41(1.19-1.67)	<0.001	1.4(1.18-1.66)	<0.001
10-19	0.95(0.84-1.06)		0.94(0.84-1.06)	
20-29	0.7(0.62-0.79)		0.69(0.61-0.78)	
30-39	1.00		1.00	
40-49	1.05(0.92-1.19)		1.05(0.93-1.2)	
50-59	0.86(0.74-1)		0.89(0.75-1.05)	
60-69	0.72(0.57-0.9)		0.76(0.6-0.97)	
70+	0.65(0.47-0.92)		0.71(0.49-1.01)	
Ethnicity				
Mixed	1.03(0.79-1.36)	<0.001	0.99(0.75-1.3)	<0.001
Asian	1.29(1.15-1.46)		1.35(1.19-1.53)	
Black	0.73(0.57-0.94)		0.73(0.57-0.95)	
White	1.00		1.00	

	Household transmission			
	Univariate OR (95% CI)	**Univariate P value**	**Multivariate OR (95% CI)**	**Multivariate P value**
Other	1.4(1.14-1.73)		1.39(1.12-1.73)	
IMD quintile				
1-most deprived	1.09(0.96-1.23)	0.748	1.05(0.93-1.19)	0.894
2	1.08(0.94-1.23)		1.06(0.93-1.21)	
3	1.00		1.00	
4	1.05(0.91-1.21)		1.05(0.91-1.22)	
5-least deprived	1.08(0.91-1.27)		1.08(0.91-1.28)	
Vaccination status of index case				
<21 days post dose 1	0.97(0.83-1.13)	0.019	0.99(0.83-1.17)	0.108
>=14 days post dose 2	0.76(0.45-1.29)		0.81(0.47-1.4)	
>=21 days post dose 1	0.87(0.77-0.98)		0.92(0.8-1.06)	
Unvaccinated	1.00		1.00	
Unknown	0.83(0.71-0.95)		0.83(0.71-0.96)	
History of foreign travel				
Not Travelled	1.00	base	1.00	base
Travelled	0.58(0.45-0.74)	<0.001	0.5(0.38-0.65)	<0.001

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