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 Delta variant (B.1.617.2), first detected in India, has rapidly become the dominant variant in England. Early reports suggest this variant has an increased growth rate suggesting increased transmissibility. This study indirectly assessed differences in transmissibility between the emergent Delta variant compared to the previously dominant Alpha variant (B.1.1.7).

Methods

A matched case-control study was conducted to estimate the odds of household transmission (≥ 2 cases within 14 days) for Delta variant index cases compared with Alpha cases. Cases were derived from national surveillance data (March to May 2021). One-to-two matching was undertaken on geographical location of residence, time period of testing and property type, and a multivariable conditional logistic regression model was used for analysis.

Findings

In total 3,765 genomically sequenced index cases in household clusters were matched to 7,530 sporadic index cases (single case within a household). 5.8% (n=220) of cases in household clusters were confirmed Delta variant compared to 4.7% (n= 351) of sporadic cases. The odds ratio of household transmission was 1.64 among Delta variant cases (95% CI 1.26-2.13, p <0.001) compared to Alpha cases after adjusting for age, sex, ethnicity, index of multiple deprivation (IMD) and vaccination status of index case.

Interpretation

We found evidence of increased household transmission of SARS-CoV-2 Delta variant, potentially explaining its success at displacing Alpha variant as the dominant strain in England. With the delta variant now having been detected in many countries worldwide, the understanding of the transmissibility of this variant is important for informing infection prevention and control policies internationally.

Introduction

Following detection of the first SARS-CoV-2 cases in England in January 2020, by June 2021, the total number of laboratory confirmed coronavirus (COVID-19) cases in England exceeds 4 million. Following a dramatic second wave of COVID-19 cases in late 2020, a subsequent national lockdown was implemented alongside an accelerated immunisation programme. The number of new COVID-19 infections declined, and since March 2021 had remained at low and stable incidence. However, during this time, several emerging SARS-CoV-2 variants were detected in England.

SARS-CoV-2 variant B.1.617.2, classified by the World Health Organization (WHO) as 'Delta' variant (1) was initially detected in India in December 2020 (2) amidst a surge in COVID-19 cases and associated hospitalisations and deaths. By 1 June 2021, this variant had been detected in 54 countries (3). The first genomically confirmed case was detected in England in late March 2021 as part of the national programme for routine sequencing of SARS-CoV-2 cases. The Delta variant was initially declared a variant under investigation by Public Health England and then upgraded to a variant of concern on 06 May 2021 (4). Initially detected in specific localised outbreaks and in association with travel to India, by 10 June 2021, 16,242 genomically confirmed cases of Delta variant SARS-CoV-2 variant have been detected across England (5).

Surveillance and modelling data suggest the Delta variant has quickly become the dominant variant in England, usurping the formerly successful Alpha (B.1.1.7) variant. The Delta variant has by far highest growth rate of detected variants, reflecting both the biological properties of this variant and the context in which it is transmitting, and has been associated with increased risk of hospital admission compared to the Alpha variant (3, 6, 7). 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 Alpha variant, to assess its potential impact on the incidence in England.

Households are high risk settings for transmission of COVID-19 (8) and are an important factor in wider community spread (9). By assessing the extent to which the Delta variant results in onward transmission to household members compared to the Alpha variant, we can assess the role of increased transmissibility in the recent rise in COVID-19 infection and provide information vital to the national and international pandemic response.

Methods

Study design

A matched case-control study design was used to estimate the odds of transmission within households for Delta variant compared with Alpha variant 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.

Data sources

In accordance with statutory requirements, positive SARS-CoV-2 tests are notified to Public Health England's (PHE) Second Generation Surveillance System (SGSS), a laboratory reporting system.

Residential address information for each positive SARS-CoV-2 test was obtained from NHS summary care records, laboratory information management system (LIMS) or is self-reported at test booking. The LIMS address, supplied by the diagnosing laboratory, was preferentially utilised as this should reflect the address at time of testing, as opposed to the centrally-held NHS held address which may not be up to date or include temporary address changes. To facilitate identification of specific residential location and to obtain residential property types, cases were address matched against Ordnance Survey reference databases. These hold all UK addresses and provided a standardised Unique Property Reference Number (UPRN) and Basic Land and Property unit (BLPU) class for each case, facilitating the detection of cases residing at the same property and the identification of property type.

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

Outcome assessment

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

‘Controls’ were cases where no further SARS-CoV-2 cases were 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 house or flat. Matching was undertaken as a way to address potential inter-relationships between time, geography of residence and property type, and to minimise potential for confounding related to household size and regional variation in incidence rates, and local interventions.

Exposure assessment

Delta and Alpha 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 were sampled for whole genome sequencing (WGS) with 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 and controls who did not have a full 14 days of follow-up time were excluded from the analysis. Additionally, 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-primary case households, defined as more than one case having the same earliest positive specimen date, were also excluded.

Targeted testing was undertaken for close contacts of cases with a variant of concern, apart from the Alpha variant. As such, households identified as targeted for testing were excluded as this would bias case-finding (and therefore cluster detection) for Delta variant cases.

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, case with history of traveling outside the UK in the 14 days preceding diagnosis were excluded from analysis. 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.

There are 2 main testing routes for COVID-19 in the UK: tests carried out by hospital and public health laboratories, which can include testing of those presenting to healthcare services (referred to as Pillar 1) and wider population testing (referred to as Pillar 2), which includes both community testing sites and postal tests. While not exclusively hospitalised patients, cases identified through Pillar 1 were omitted to minimise bias in terms of household transmission for those identified as SARS-CoV-2 positive while hospitalised, which would not contribute to household transmission and therefore dilute the estimated difference in transmission risk between variants.

Statistical Analysis

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

To assess the impact of using a limited number of cases and controls in the matched design, an additional sensitivity analysis was carried out fitting a logistic regression model using all index cases prior to matching that met the inclusion and exclusion criteria.

In addition, a supplementary analysis including those cases and controls with a recorded travel history was used to assess the effects on the results.

Results

During the study period (18 March to 17 May), of the genomically sequenced cases, there were 6,361 and 57,099 identified as Delta and Alpha variants respectively, representing 97.9% of all sequenced cases in total in England during this period.

We excluded 22,555 index cases with confirmed Delta or Alpha variant with specimen dates between 18 March to 17 May 2021 as they did not meet the inclusion, exclusion or matching criteria. Of these, 2,588 Delta variant index cases were excluded as they did not specifically meet the eligibility criteria, namely they were tests carried out via Pillar 1 (primarily conducted as part of hospital and travel associated testing), they had recently travelled, or were co-primary cases (multiple index cases). A further 2,017 Delta variant index cases were excluded as they could not be matched to a case or control. A total of 571 confirmed Delta variant cases were included in the matched case-control analysis (Table 1).

After applying eligibility and 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 ('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 (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% v 3.4%). A lower proportion of included cases were of Asian ethnicity (13.8% vs 16.0%). 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 to 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 were 1.66 among those with Delta variant (95%CI 1.28-2.14, p <0.001) compared to those with Alpha variant. After adjusting for age, sex, ethnicity, IMD and vaccination status of index case,

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

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

In the sensitivity analysis without restriction to matching criteria, logistic regression models including all eligible index cases found the crude odds of transmission was 1.53 among those with the Delta variant compared to those with the Alpha variant (95% CI 1.40-1.67, p <0.001). With adjustment for property type, fortnight of specimen date, lower tier local authority of residence, age, sex, ethnicity, index of multiple deprivation (IMD) and vaccination status of index case, the adjusted odds of transmission were similar to the matched analysis at 1.62 for the Delta compared to the Alpha variant (95% CI 1.45-1.81, p <0.001) (Supplementary Table 2).

A supplementary matched 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 Delta variant with the crude odds ratio of transmission 1.67 among those with Delta variant compared to those with the Alpha variant , and an adjusted odds ratio of 1.68 after adjustment for age, sex, ethnicity, IMD and vaccination status (95% CI 1.31-2.14, p <0.001) (Supplementary Table 3).

Discussion

Our study found a 64% increase in the odds of household transmission associated with infection with SARS-CoV-2 Delta variant compared to Alpha, 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 of Delta variant on household transmission. The findings support existing evidence that the Delta variant has a substantially increased transmissibility advantage over the Alpha variant, which has contributed to the rapid increase in the number of Delta variant cases in the UK over the study period and may explain the rapid surge in cases seen in other countries where this variant has been observed (3, 6, 10).

This study also found evidence of increased household transmission in households with an index case of Asian ethnicity, a finding consistent with studies of the previously dominant Alpha variant (11). These results add important new evidence to help understand the underlying reasons for increased susceptibility to COVID-19 infection, and possibly reflect differences in household composition and inter-household mixing between ethnic groups, with specific groups more likely to live in large or multi-generational households.

The strength of this study is the comprehensive genomic sequencing programme in England co-ordinated by COG-UK which delivers large scale, rapid, whole genome

sequencing of SARS-CoV-2 cases allowing for surveillance, early detection of variants and the increased understanding of viral transmission, both nationally and internationally.

With over 50% of positive COVID-19 cases sequenced during the study period, the sequenced cases included in this study are likely representative of the population testing positive for COVID-19. This increases the generalisability of the results, despite the sampling strategy for sequencing not being random. However, some effects of this non-random sampling were addressed by removing households that received targeted testing.

This analysis covers a period of time when both Delta and Alpha 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, Delta had become the dominant SARS-CoV-2 virus in England, accounting for over 90% of all new cases (3).

The inclusion of vaccination data further strengthens this study. By linking COVID-19 case data to vaccination status 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 in households with a symptomatic index case (8). However, our assessment of this effect was limited as most cases included in the analysis were unvaccinated.

This study also benefits from the enrichment of COVID-19 case data with residential address data and travel information to create a large sample of cases and controls for inclusion in the analysis.

There are several limitations to this study. Firstly, 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 becoming a household cluster However, we were unable to identify and exclude these cases in the analysis but was mitigated by matching on local geography and property type. Furthermore, the vaccination status of household contacts, which would impact onward transmission in this setting, was unknown. Therefore, further studies that include household size as a denominator and all individuals' 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 cases occurring in other residential settings that are 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 from this study to such settings.

As the Delta variant is identified in other countries, these transmissibility findings will be relevant to other industrialised countries and will be important in considering mitigation in public health responses. Similar approaches have been used to characterise the transmissibility of the Alpha variant when this initially emerged, and similar observations followed in other countries.

Overall, we found increased household transmission of COVID-19 associated with the Delta compared to the Alpha variant. Our study shows that households are important settings for the transmission of the Delta variant and with household settings being an important factor in wider community spread, it is vital to maintain policies to prevent transmission of COVID-19 in these settings.

With the results of this analysis suggesting increased transmissibility of this variant and the Delta variant now having been detected in many countries worldwide, the understanding of the transmissibility of this variant is important for informing public health policies internationally to control the COVID-19 pandemic.

Table 1. Characteristics of genomically sequenced confirmed SARS-CoV-2 cases and controls, in England 18 March to 17 May 2021

	Controls		Cases			
	Count	Percent	Count	Percent	χ^2	p-value
Total	**7,530**		**3,765**			
VARIANT						
Delta (B.1.617.2)	351	4.66	220	5.84	7.3	0.007
Alpha (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 15 March 2021	2402	31.90	1201	31.90	N/A	N/A
w/c 29 March 2021	2,048	27.20	1,024	27.20		
w/c 12 April 2021	1,206	16.02	603	16.02		
w/c 26 April 2021	1,312	17.42	656	8.71		
w/c 10 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						
Under 10	379	5.03	300	7.97	97	<0.001
10 to 19	1,782	23.67	892	23.69		
20 to 29	1,597	21.21	591	15.70		
30 to 39	1,582	21.01	869	23.08		
40 to 49	1,075	14.28	616	16.36		

	Controls		Cases			
	Count	**Percent**	**Count**	**Percent**	**χ^2**	**p-value**
50 to 59	698	9.27	336	8.92		
60 to 69	287	3.81	119	3.16		
Over 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. Univariate and multivariate conditional logistic regression of odds of household transmission in genomically sequenced confirmed SARS-CoV-2 cases, in England 18 March to 17 May 2021

	Household Transmission			
	OR (95% CI)	P value	adjusted OR (95% CI)	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	-	1.00	-
Sex				
Female	1.00	-	1.00	-
Male	0.99(0.91-1.07)	0.769	0.97(0.89-1.05)	0.415
Age group				
Under 10	1.46(1.23-1.74)	<0.001	1.46(1.23-1.75)	<0.001
10 to 19	0.92(0.82-1.03)		0.92(0.81-1.04)	
20 to 29	0.67(0.59-0.76)		0.67(0.59-0.76)	
30 to 39	1.00		1.00	
40 to 49	1.05(0.92-1.2)		1.05(0.92-1.19)	
50 to 59	0.88(0.75-1.03)		0.9(0.76-1.06)	
60 to 69	0.76(0.61-0.96)		0.79(0.62-1.01)	
Over 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				
Unvaccinated	1.00	0.010	1.00	0.012
<21 days post dose 1	0.99(0.85-1.16)		1.01(0.85-1.2)	
>=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)	
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 Table 1. Characteristics of excluded index cases and included index genomically sequenced confirmed SARS-CoV-2 cases, in England 18 March to 17 May 2021

	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						
Under 10	1291	5.72	679	6.01	166.7	<0.001
10 to 19	4471	19.82	2,674	23.67		
20 to 29	4607	20.43	2,188	19.37		
30 to 39	4901	21.73	2,451	21.70		
40 to 49	3349	14.85	1,691	14.97		
50 to 59	2185	9.69	1,034	9.15		
60 to 69	985	4.37	406	3.59		
Over 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		

	Exclusions		Inclusions			
	Count	**Percent**	**Count**	**Percent**	**χ^2**	**p-value**
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		
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		
Vaccination status						
Unknown	2109	9.35	920	8.15	70.4	<0.001
Unvaccinated	15,375	68.17	8,027	71.07		
<21 days post dose 1	1,382	6.13	779	6.90		
>=21 days post dose 1	3,425	15.19	1499	13.27		
>=14 days post dose 2	264	1.17	70	0.62		

Supplementary Table 2. Univariate and multivariate logistic regression of odds of household transmission in unmatched genomically sequenced confirmed SARS-CoV-2 cases, in England 18 March to 17 May 2021

	Household Transmission			
	Univariate OR (95% CI)	**Univariate P value**	**Multivariate OR (95% CI)**	**Multivariate P value**
VARIANT				
B.1.617.2	1.53(1.4-1.67)	<0.001	1.61(1.44-1.8)	<0.001
B.1.1.7	1.00	base	1.00	base
Sex				
Female	1.00	base	1.00	base
Male	1.01(0.96-1.07)	0.70	0.99(0.94-1.05)	0.73
Age group				
Under 10	1.43(1.28-1.6)	<0.001	1.36(1.21-1.52)	<0.001
10 to 19	0.93(0.86-1)		0.88(0.81-0.96)	
20 to 29	0.64(0.58-0.69)		0.64(0.59-0.7)	
30 to 39	1.00		1.00	
40 to 49	1.15(1.05-1.25)		1.14(1.04-1.24)	
50 to 59	0.87(0.78-0.97)		0.88(0.79-0.99)	
60 to 69	0.74(0.64-0.87)		0.75(0.64-0.88)	
Over 70	0.64(0.49-0.82)		0.68(0.52-0.89)	
Ethnicity				
Mixed	0.91(0.76-1.1)	<0.001	0.91(0.75-1.1)	<0.001
Asian	1.36(1.26-1.47)		1.32(1.22-1.43)	
Black	0.75(0.63-0.9)		0.82(0.68-0.98)	
White	1.00		1.00	
Other	1.19(1.04-1.37)		1.26(1.09-1.46)	
IMD quintile				
1-most deprived	0.98(0.9-1.06)	0.039	1(0.92-1.09)	0.564
2	1.04(0.95-1.13)		1.06(0.97-1.16)	
3	1.00		1.00	
4	1.07(0.98-1.18)		1.05(0.95-1.15)	
5-least deprived	1.1(1-1.21)		1.04(0.94-1.15)	

	Household Transmission			
	Univariate OR (95% CI)	**Univariate P value**	**Multivariate OR (95% CI)**	**Multivariate P value**
Vaccination status				
Unknown	0.86(0.77-0.95)	0.004	0.85(0.77-0.94)	0.014
Unvaccinated	1.00		1.00	
<21 days post dose 1	1.02(0.92-1.14)		1.01(0.9-1.13)	
>=21 days post dose 1	0.91(0.85-0.99)		0.94(0.86-1.03)	
>=14 days post dose 2	0.8(0.58-1.1)		0.77(0.55-1.08)	
PHE Centre				
East Midlands	1.00	<0.001	1.00	<0.001
East of England	1.13(1.01-1.27)		1.11(0.99-1.25)	
London	0.83(0.73-0.94)		0.91(0.79-1.04)	
North East	0.85(0.75-0.97)		0.89(0.79-1.02)	
North West	0.88(0.8-0.96)		0.84(0.76-0.92)	
South East	1.01(0.88-1.17)		1.05(0.91-1.21)	
South West	1.04(0.83-1.3)		1.11(0.88-1.39)	
West Midlands	0.91(0.81-1.02)		0.93(0.83-1.04)	
Yorkshire and Humber	0.85(0.78-0.93)		0.89(0.81-0.98)	
Household Type				
Terraced	0.91(0.85-0.99)	<0.001	0.92(0.85-1)	<0.001
Semi-detached	0.93(0.86-1)		0.95(0.88-1.03)	
Detached	1.00		1.00	
Flat	0.56(0.5-0.63)		0.58(0.51-0.65)	
Specimen date (2-week period)				
w/c 15 March 2021	1.00	<0.001	1.00	0.008
w/c 29 March 2021	0.89(0.83-0.96)		0.91(0.84-0.98)	
w/c 12 April 2021	0.87(0.8-0.94)		0.9(0.82-0.97)	
w/c 26 April 2021	0.99(0.91-1.07)		0.94(0.87-1.02)	
w/c 10 May 2021	1.03(0.94-1.13)		0.85(0.76-0.94)	

Supplementary Table 3. Univariate and multivariate conditional logistic regression of odds of household transmission in genomically sequenced confirmed SARS-CoV-2 cases including travellers and non-travellers, in England 18 March to 17 May 2021

	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				
Under 10	1.41(1.19-1.67)	<0.001	1.4(1.18-1.66)	<0.001
10 to 19	0.95(0.84-1.06)		0.94(0.84-1.06)	
20 to 29	0.7(0.62-0.79)		0.69(0.61-0.78)	
30 to 39	1.00		1.00	
40 to 49	1.05(0.92-1.19)		1.05(0.93-1.2)	
50 to 59	0.86(0.74-1)		0.89(0.75-1.05)	
60 to 69	0.72(0.57-0.9)		0.76(0.6-0.97)	
Over 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	
Other	1.4(1.14-1.73)		1.39(1.12-1.73)	

	Household transmission			
	Univariate OR (95% CI)	**Univariate P value**	**Multivariate OR (95% CI)**	**Multivariate P value**
IMD quintile				
1-most deprived	1.09(0.96-1.23)		1.05(0.93-1.19)	
2	1.08(0.94-1.23)		1.06(0.93-1.21)	
3	1.00	0.748	1.00	0.894
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)		0.99(0.83-1.17)	
>=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)	0.019	0.92(0.8-1.06)	0.108
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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