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Original Research

Socio-demographic heterogeneity in the prevalence of COVID-19 during lockdown is associated with ethnicity and household size: Results from an observational cohort study

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ABSTRACT

Background: Accumulating evidence indicates that COVID-19 causes adverse outcomes in ethnic minority groups. However, little is known about the impact of ethnicity and household size on acquiring infection with SARS-CoV-2.

Methods: We undertook a retrospective cohort study, in Leicester (UK), of all individuals assessed for COVID-19 with polymerase chain reaction (PCR) testing at University Hospitals of Leicester NHS Trust between 1st March and 28th April 2020. We used logistic regression to identify sociodemographic, clinical and temporal factors associated with SARS-CoV-2 PCR positivity before/after lockdown.

Findings: 971/4051 (24.0%) patients with suspected COVID-19 were found to be PCR positive for SARS-CoV-2. PCR positivity was more common amongst individuals from ethnic minortiy backgrounds than their White counterparts (White 20.0%, South Asian 37.5%, Black 36.1%, Other 32.2%; $p<0.001$ for all ethnic minority groups vs White). After adjustment, compared to White ethnicity, South Asian (aOR 2.44 95%CI 2.01, 2.97), Black (aOR 2.56 95%CI 1.71, 3.84) and Other (aOR 2.53 95%CI 1.74, 3.70) ethnicities were more likely to test positive, as were those with a larger estimated household size (aOR 1.06 95%CI 1.02, 1.11). We saw increasing proportions of positive tests in the three weeks post-lockdown amongst the ethnic minority , but not the White, cohort. Estimated household size was associated with PCR positivity after, but not before, lockdown (aOR 1.10 95%CI 1.03, 1.16).

Interpretation: In individuals presenting with suspected COVID-19, those from ethnic minority communities and larger households had an increased likelihood of SARS-CoV-2 PCR positivity. Pandemic control measures may have more rapid impact on slowing viral transmission amongst those of White ethnicity compared to ethnic minority groups, Research is urgently required to understand the mechanisms underlying these dis-

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parities and whether public health interventions have differential effects on individuals from ethnic minority groups.
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Research in context

Evidence before this study

We searched MEDLINE and EMBASE on 15th May 2020, for articles including the search terms ("COVID-19", "novel coronavirus", "2019-ncov", "ncov", "novel betacov", "novel betacoronavirus") AND ("ethnicity"). Of 207 papers identified, we found 17 published studies of patients with COVID-19 which reported data on ethnicity; 1 reported an increased risk of acquiring SARS-CoV-2 in Black compared to White patients and 5 reported no association between ethnicity and clinical outcomes. Increasing numbers of articles from the UK and USA, in the grey literature as well as in preprint, suggest that individuals from ethnic minority communities are at increased risk of infection from SARS-CoV-2 and adverse clinical outcomes including hospitalization, ITU admission and mortality. However, little is known about the impact of demographics, including ethnicity, and clinical factors on acquiring infection with SARS-CoV-2 or whether pandemic control measures differ in their effectiveness according to ethnicity.

Added value of this study

We found that individuals from all ethnic minority groups are at higher likelihood of testing positive for SARS-CoV-2. We also found an association with PCR positivity and estimated household size and to suggest that the effect of lockdown measures on slowing viral transmission may be lessened for those in larger households. We show a trend in increasing proportions of individuals from ethnic minority groups testing positive in the three weeks after lockdown that is not evident in the White cohort.

Implications of all the available evidence

Evidence is accumulating that individuals from ethnic minority groups are disproportionately affected by COVID-19 both in terms of acquisition of infection and adverse outcome. Household size may be an important factor related to transmission of infection post-lockdown. Taken together these findings have implications on how COVID-19 public health messages are designed and implemented for individuals from ethnic minority groups.

1. Introduction

Coronavirus disease 2019 (COVID-19), a novel viral respiratory infection caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), has spread rapidly across the globe since first appearing in China in December 2019 [1]. As the pandemic has spread to parts of the world with more ethnically diverse populations, including the United Kingdom (UK) and United States of America (US), reports have emerged that COVID-19 results in disproportionately serious adverse outcomes, including intensive care admission and mortality, in individuals from ethnic minority communities [2–6]. Reasons underlying this increased risk remain uncertain but are likely to be multifactorial and driven by a combination of social, cultural, economic and comorbidity factors and are currently subject to a UK governmental inquiry[7].

To date the focus has been on the clinical outcomes of COVID-19 in different ethnic groups. However, emerging evidence seems to suggest that demographic factors including ethnicity may impact upon risk of acquiring infection with SARS-CoV-2 (defined by a positive polymerase chain reaction (PCR) assay for SARS-CoV-2 on nasopharyngeal sampling). A recent UK study has demonstrated male gender, Black ethnicity, urban living and deprivation to be associated with PCR positivity in a primary care setting. However, those from ethnic minority backgrounds comprised less than 10% of the total cohort [8]. A UK Biobank study, which included data on hospital attenders, found that risk of infection was higher in those of Black and South Asian ethnicity and also demonstrated that socioeconomic deprivation and lower educational level may also increase risk [9]. Previous work in China from specialised clinics found conflicting results for age and sex predicting PCR positivity [10] and a recent meta-analysis suggested 56% of PCR positive patients were male [11] but did not present data on ethnicity.

These emerging data underpin an urgent need to confirm an association between ethnicity and the probability of SARS-CoV-2 PCR in individuals presenting to hospital for clinical assessment for suspected COVID-19 and to discuss the underlying mechanisms driving such an association. Additionally, little is known about whether the social distancing and lockdown measures, implemented by most governments across the world in response to increases in COVID-19 case numbers, vary in efficacy in different ethnic and socioeconomic groups. Understanding any such association is highly relevant to the design of effective health policies worldwide, as it would have a significant impact on the clinical assessment and management of suspected COVID-19 and allow for targeted public health interventions aimed at specific ethnic minority groups in advance of future pandemic waves.

We therefore undertook an observational cohort study of patients admitted to the University Hospitals of Leicester NHS Trust, which provides secondary healthcare to a catchment population of over 1 million people in one of the most ethnically diverse regions of the UK. Our objectives were firstly to investigate the factors associated with prevalent COVID-19 among hospital attenders, and secondly to establish whether temporal changes in the proportion of positive test results before and after institution of lockdown measures differ by ethnicity.

2. Methods

2.1. Study design and study centre

This retrospective cohort study was undertaken in Leicester (UK), one of the most ethnically diverse cities in the UK with an estimated population of 354,000, of whom 141,000 are foreign born [12]. University Hospitals of Leicester (UHL) NHS Trust is the only hospital trust serving the populations of Leicester city, Leicestershire and Rutland (combined population: 1053,486 mid-2018 estimate) and sees the vast majority of patients presenting with COVID-19 in these areas.

2.2. Study population

We included all patients seeking attention at UHL NHS Trust, one of the largest trusts in the UK, between 1st March 2020 and 28th

April 2020 with suspected COVID-19. The decision to take nasopharyngeal samples for SARS-CoV-2 PCR testing was based on Public Health England guidelines at the time, which advised that any patient with a cough of recent onset, fever or evidence of pneumonia should undergo testing[13]. Individuals who developed these symptoms and were swabbed whilst admitted to hospital for other reasons were also included in the analysis.

2.3. Clinical and virological assessment of patients

Patients were assessed using a combination of the National Early Warning Score[14] (NEWS) or Paediatric Early Warning Score (PEWS)[15], nationally adopted tools for the assessment of acute severity of illness, and assessment by a member of the clinical team. All patients meeting the criteria for SARS-CoV-2 testing had a nasopharyngeal viral swab collected and sent for PCR testing in the Virology Department in the Department of Clinical Microbiology at University Hospitals of Leicester NHS Trust.

2.4. SARS-CoV-2 testing

Identification of SARS-CoV-2 was achieved through a real-time reverse transcription PCR assay using primers targeted at regions of the viral genome. The assay had a turnaround time of around one day at the time of the review, so all clinical decisions and record keeping were made without knowledge of the result.

2.5. Data collection

We extracted data from the hospital electronic record concerning; age, gender, ethnicity (self-assigned and categorised as White, South Asian, Black and Other – Supplementary Table 1), result of the SARS-CoV-2 PCR assay and the date the nasopharyngeal swab was received in the laboratory, postcode and comorbidities inclusive of diabetes, hypertension, cardiovascular disease, cerebrovascular disease and respiratory disease (see Supplementary Table 2). We used postcode to derive decile of Index of Multiple Deprivation (IMD) by use of an online tool provided by the UK government[16]. IMD is the official measure of relative deprivation for small areas of England and combines information on 7 domains (income, employment, education, health, crime, barriers to housing/services and living environment), these areas are ranked from 1 – 32,844 and can be divided into deciles. Higher deciles indicate less deprivation. In order to estimate household size, which we used as a proxy measure for the number of people living in one household, we divided the number of people living in a postcode area by the number of occupied residences in that area using 2011 census data [17]. We also collated data on the NEWS or PEWS (hereafter referred to as Early Warning Score, EWS) as appropriate and acute kidney injury (AKI) status at time of presentation as markers of disease severity. AKI data was based on laboratory analysis of renal function and an automated flag on the patient's electronic record.

2.6. Data analysis

Continuous demographic information was summarised as median and interquartile range (IQR), categorical as count (%). Levels of missing data were assessed for all recorded variables. Individual ethnic minority groups were compared to White individuals using Wilcoxon rank-sum test for non-parametric data and chi-square statistic for categorical variables. We computed the overall, and ethnic group stratified, prevalence of SARS-CoV-2 PCR positivity.

Unadjusted associations of SARS-CoV-2 PCR positivity with age, gender, ethnicity, EWS at presentation, decile of IMD, estimated household size and number and type of comorbidities were assessed using logistic regression. We reported associations as unadjusted odds ratios (OR) and 95% confidence intervals (CIs). We then calculated the adjusted odds ratios (aORs) for PCR positivity by adjusting for factors which had a priori biological plausibility in determining PCR status including: age, gender, ethnicity, EWS at presentation, decile of IMD, estimated household size and comorbidities.

We computed the proportions of positive and negative swabs (together with exact 95% CIs) stratified by ethnicity on a weekly basis from the start of our study time-period; these were compared using chi-squared tests. We evaluated interactions between ethnicity and lockdown and household size and lockdown using multivariable logistic regression. In the model, lockdown is a binary variable, the value of which depends on whether an individual's swab was received before or after 30th March 2020 (one week after UK governmental lockdown on 23rd March 2020). We selected this threshold date to account for the lag time between implementing pandemic control measures and observation of the effects of these measures on hospital attendances.

Multiple imputation was used to replace missing data in all models fitted, the multiple imputation model included all variables bar those being imputed. Rubin's Rule was used to combine the parameter estimates and standard errors from 10 imputations into a single set of results [18].

All analyses were conducted using STATA (StataCorp. 2017. Stata Statistical Software: Release 15. College Station, TX: StataCorp LLC.). Figures were plotted using Microsoft Excel (version 16.16.18, 2018). p values <0.05 were considered statistically significant.

2.7. Ethical approval

We consulted the NHS Health Research Authority decision aid to ascertain whether ethical approval was required. It was deemed that approval was not required, as this work represents a service evaluation/surveillance, which utilises data collected as part of the routine delivery of a clinical service. In addition, we confirmed approval from our Caldicott Guardian to undertake this work as an audit (UHL10579).

2.8. Role of funding

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

3. Results

3.1. Attendance and sampling

Over the study period, 4051 patients were evaluated for suspected COVID-19 with a nasopharyngeal sample obtained for SARS-CoV-2 PCR testing.

3.2. Description of cohort

Overall 2072/4051 (51.2%) of the cohort were male; median age was 64 (IQR 45 – 78) and 24.3% were from ethnic minority backgrounds. 2318/4051 (57.2%) had no comorbidities, 688 (17.0%) had 1 comorbidity and 1045 (25.8%) had $\geq$2 comorbidities. 1667 (41.2%). Median (IQR) IMD was 6 (3 – 8) . Median estimated household size was 2.5 (2.1 – 3.0). Missing data were only present for three of the variables of interest, EWS on admission (n = 68), household size (n = 24) and IMD (n = 4). Description of the cohort, stratified by PCR positivity status, is in Table 1.

Table 2 shows demographic characteristics of the cohort by ethnic group. We found that South Asian and Black individuals were significantly younger than the White cohort (57 vs 68, $p<0.0001$; 50.5 vs 68, $p<0.0001$ respectively). South Asian patients were significantly

Table 1
Demographic characteristics of cohort by SARS-CoV-2 PCR status.

Variable	Total (n = 4051)	PCR Positive (n = 971)	PCR Negative (n = 3080)
Age (years), median (IQR)	64 (45 – 78)	65 (51 – 78)	64 (42 – 79)
Gender, n(%)			
Female	1979 (48.9%)	433 (44.6%)	1546 (50.2%)
Male	2072 (51.2%)	538 (55.4%)	1534 (49.8%)
Ethnicity, n(%)			
White Caucasian	3067 (75.7%)	612 (63.0%)	2455 (79.7%)
South Asian	710 (17.5%)	266 (27.4%)	444 (14.4%)
Black	122 (3.0%)	44 (4.5%)	78 (2.5%)
Other	152 (2.75%)	49 (5.1%)	103 (3.3%)
Index of Multiple Deprivation Decile, n(%)			
1 (most deprived)	443 (10.9%)	93 (9.6%)	350 (11.4%)
2	326 (8.1%)	93 (9.6%)	233 (7.6%)
3	483 (11.9%)	142 (14.6%)	341 (11.1%)
4	415 (10.2%)	117 (12.1%)	298 (9.7%)
5	324 (8.0%)	58 (6.0%)	266 (8.6%)
6	368 (9.1%)	94 (9.7%)	274 (8.9%)
7	405 (10.0%)	90 (9.3%)	315 (10.2%)
8	454 (11.2%)	98 (10.1%)	356 (11.6%)
9	418 (10.3%)	100 (10.3%)	318 (10.3%)
10 (least deprived)	411 (10.2%)	85 (8.8%)	326 (10.6%)
Missing	4 (0.1%)	1 (0.1%)	3 (0.1%)
Estimated household size, median (IQR)	2.5 (2.1 – 3.0)	2.6 (2.3 – 3.3)	2.5 (2.1 – 2.9)
Missing, n(%)	24 (0.6%)	6 (0.6%)	18 (0.6%)
Number of comorbidities, n(%)			
0	2318 (57.2%)	482 (49.6%)	1836 (59.6%)
1	688 (17.0%)	199 (20.5%)	489 (15.9%)
≥2	1045 (25.8%)	290 (29.9%)	755 (24.5%)
Type of comorbidity, n(%)			
Hypertension	963 (23.8%)	277 (28.5%)	686 (22.2%)
Diabetes	495 (12.2%)	167 (17.2%)	328 (10.7%)
Other cardiovascular	415 (10.2%)	104 (10.7%)	311 (10.1%)
Cerebrovascular	180 (4.4%)	52 (5.4%)	128 (4.2%)
Respiratory	556 (13.7%)	133 (13.7%)	423 (13.7%)
AKI on admission, n(%)	508 (12.5%)	172 (17.7%)	336 (10.9%)
EWS on admission, median (IQR)	2 (0 – 3)	2 (1 – 4)	1 (0 – 3)
Missing, n(%)	68 (1.7%)	20 (2.1%)	48 (1.6%)

Footnote: 'Other cardiovascular' comprises; pacemaker in situ, congenital cardiac failure, congestive heart failure, ischaemic heart disease, mitral valve disorder, left heart failure. 'Respiratory' comprises; chronic bronchitis, chronic obstructive lung disease, asthma, pulmonary emphysema. 'Cerebrovascular' comprises; cerebral haemorrhage, cerebral infarction, cerebrovascular accident, cerebrovascular disease, hemiplegia, subarachnoid haemorrhage.

more likely to have diabetes mellitus than those in the White cohort (19.0% vs 10.8%, $p<0.001$).

When compared to the White cohort, South Asian and Black individuals were more likely to live in a deprived area (median IMD 6 vs 4, $p<0.001$ and 6 vs 3, $p<0.001$ respectively). Those from ethnic minority groups had significantly greater estimated household sizes than those of White ethnicity (2.4 vs 2.9, $p<0.0001$). When we compared other ethnic groups to their White counterparts, the greatest difference in estimated household size was found between the White and South Asian cohort (2.4 vs 3.1, $p<0.0001$).

3.3. Prevalence of SARS-COV-2 in patients presenting for clinical assessment

971/4051 (24.0%) of patients were found to be PCR positive for SARS-CoV-2. PCR positivity was significantly more common amongst individuals from ethnic minority backgrounds than their White counterparts (White 20.0%, South Asian 37.5%, Black 36.1%, Other 32.2%; $p<0.001$ for all ethnic minority groups vs White).

3.4. Demographic factors associated with PCR positivity

Table 3 outlines the results of the unadjusted and adjusted logistic regression model. After adjustment, older age, male gender, ethnic minority groups, as well as estimated household size were associated with PCR positivity. South Asian, Black and Other ethnicities all had around a 2.5 increased odds of being PCR positive compared to White individuals. For each person increase in estimated household size the odds of being PCR positive increased by 6%.

3.5. Severity markers associated with PCR positivity

After adjustment, having AKI was associated with a 43% increased odds of PCR positivity and for each unit increase in admission EWS the odds of PCR positivity increased by 14% (Table 3).

3.6. Temporal changes in SARS-COV-2 PCR positivity stratified by ethnicity

Fig. 1 illustrates the weekly temporal changes in SARS-COV-2 PCR positivity stratified by ethnicity. The proportion of positive tests in the ethnic minority cohort was significantly higher than that in the White cohort in each week from the week commencing 16th March onwards. The proportion of individuals from ethnic minority groups testing positive continued to rise in the three weeks after UK lockdown on 23rd March 2020, peaking at 50.9% of tested patients in this cohort. By contrast, proportions of positive tests in the White cohort remain consistent, between 24 – 26%.

Belonging to a minority ehtnic group was associated with PCR positivity both before and after the 30th March 2020 (aOR 2.70 95% CI 1.86, 3.91 and aOR 2.45 95% CI 1.98, 3.02, see Supplementary Table 3). The interaction between ethnicity and lockdown was not significant (p = 0.37). However, a significant interaction between estimated

Table 2
Demographic, comorbidity and physiological characteristics of cohort by ethnicity.

	White Caucasian	South Asian	Black	Other
Total	3067 (75.7%)	710 (17.5%)	122 (3.0%)	152 (3.8%)
Age (years), median (IQR)	68 (49 – 80)	57 (39 – 70)*	50.5 (37 – 64)*	37.5 (23 – 56)*
Gender, n(%)				
Female	1516 (49.4%)	331 (46.6%)	62 (50.8%)	70 (46.1%)
Male	1551 (50.6%)	379 (53.4%)	60 (49.2%)	82 (54.0%)
Index of Multiple Deprivation Decile, n(%)				
1 (most deprived)	337 (11.0%)	58 (8.2%)	34 (27.9%)	14 (9.2%)
2	199 (6.5%)	90 (12.7%)	18 (14.8%)	19 (12.5%)
3	287 (9.4%)	146 (20.6%)	19 (15.6%)	31 (20.4%)
4	247 (8.1%)	128 (18.0%)	16 (13.1%)	24 (15.8%)
5	242 (7.9%)	61 (8.6%)	9 (7.4%)	12 (7.9%)
6	269 (8.8%)	72 (10.1%)	10 (8.2%)	17 (11.2%)
7	337 (11.0%)	53 (7.5%)	6 (4.9%)	9 (5.9%)
8	413 (13.5%)	32 (4.5%)	1 (0.8%)	8 (5.3%)
9	373 (12.2%)	36 (5.1%)	5 (4.1%)	4 (2.6%)
10 (least deprived)	362 (11.8%)	33 (4.7%)	3 (2.5%)	13 (8.6%)
missing	1 (0.03%)	1 (0.1%)	1 (0.8%)	1 (0.7%)
Estimated household size, median (IQR)	2.4 (2.1 – 2.8)	3.1 (2.6 – 3.6)*	2.5 (2.00 – 3.00)	2.7 (2.3 – 3.1)*
Number of comorbidities, n(%)				
0	1704 (55.6%)	421 (59.3%)	77 (63.1%)	116 (76.3%)*
1	533 (17.4%)	114 (16.1%)	20 (16.4%)	21 (13.8%)
≥2	830 (27.1%)	175 (24.7%)	25 (20.5%)	15 (9.9%)*
Type of comorbidity, n(%)				
Hypertension	760 (24.8%)	165 (23.2%)	25 (20.5%)	13 (8.6%)*
Diabetes	330 (10.8%)	135 (19.0%)*	20 (16.4%)	10 (6.6%)
Other cardiovascular	339 (11.1%)	66 (9.3%)	5 (4.1%)*	5 (3.3%)*
Cerebrovascular	151 (4.9%)	22 (3.1%)*	4 (3.3%)	3 (2.0%)
Respiratory	469 (15.3%)	65 (9.2%)*	8 (6.6%)*	14 (9.2%)*
AKI on admission, n(%)	387 (12.6%)	93 (13.1%)	17 (13.9%)	11 (7.2%)*
EWS on admission, median (IQR)	2 (0 – 3)	2 (0 – 4)	2 (1 – 4)	1 (0 – 3)

Footnote: 'Other cardiovascular' comprises; pacemaker in situ, congenital cardiac failure, congestive heart failure, ischaemic heart disease, mitral valve disorder and left heart failure. 'Respiratory' comprises; chronic bronchitis, chronic obstructive lung disease, asthma and pulmonary emphysema. 'Cerebrovascular' comprises; cerebral haemorrhage, cerebral infarction, cerebrovascular accident, cerebrovascular disease, hemiplegia and subarachnoid haemorrhage.

* chi2 (for proportions) or Wilcoxon rank-sum (for continuous, non-parametric variables), $p<0.05$ as compared to White cohort.

household size, lockdown and PCR positivity was found (aOR 1.21 95% CI 1.03. 1.43, $p = 0.019$).

4. Discussion

In this observational study of an ethnically diverse population during the peak period of COVID-19 admissions to hospital, we identified significant independent associations of Black, South Asian and other ethnic minority groups and higher estimated household size, in addition to older age and male gender, with nasopharyngeal SARS-CoV-2 PCR positivity. We also found a possible association between the institution of pandemic control measures and an increasing proportion of positive tests amongst individuals from minority ethnic groups in the three weeks following lockdown and demonstrated that the association of estimated household size with PCR positivity was present post-lockdown but not before.

Our finding that patients from ethnic minority groups were twice as likely to be PCR positive at the time of presentation to hospital as the White ethnic group adds significant weight to the emerging data suggesting that ethnic minority groups have a disproportionate risk of acquiring infection. Our findings are in-line with a recent study using UK Biobank data, which suggested an increased risk of testing positive amongst Black and South Asian hospital attenders[9] and a smaller, primary care based study in the UK with a less ethnically diverse cohort, which found Black, but not Asian, ethnicity to be associated with PCR positivity[8]. These findings are not unique to COVID-19 as a similar observation was made during the 2009 H1N1 influenza pandemic, with individuals from Asian and Black ethnic groups presenting to hospital being more likely to be PCR positive for influenza [19]. The reasons underlying these findings in relation to COVID-19 are likely to be multifaceted [4]. It is possible that individuals from ethnic minority groups are more susceptible to acquiring the infection, which is likely to be driven by different exposure risk profiles determined by varying sociodemographic characteristics, including intergenerational living with larger household sizes [20]. We controlled for a proxy measure of household size in our analysis and still demonstrated a strong association between Black, South Asian and Other ethnicities and PCR positivity implying the influence of factors on which we did not have data, for example, differing occupational roles leading to higher exposure [20]. Other possibilities for ethnic differences in PCR positivity include presentation at different points in the course of the illness through differing health-seeking behaviour, but this may be less likely for patients admitted to hospital. Variations in testing resulting in White patients being more likely to be tested than those from ethnic minority groups, and thereby reducing the prevalence in this cohort also seems less likely in the context of a pandemic where testing was driven by a nationally directed protocol based on specific clinical features [13]. A further consideration is that those from ethnic minority groups may have a higher viral load at the time of swabbing resulting in a lower likelihood of a false negative result. This may partly explain the accumulating evidence of adverse outcome with COVID-19 in ethnic minority groups both in the UK [2,21–23] and more recently from a study of New York City boroughs in the United States [6]. Others have found genetic associations with severe disease [24] and further work is required to determine if this translates to ethnic group and susceptibility to infection.

Regardless of the underlying reasons, if individuals from ethnic minority groups, as compared to those of White ethnicity, are more likely to acquire infection with SARS-CoV-2 and, as mounting evidence suggests, have an increased risk of adverse outcomes from COVID-19 [21,25], then policy-makers must begin to implement

Table 3
Unadjusted and adjusted analysis of factors associated with SARS-CoV-2 PCR positivity.

Variable	n positive / n total 971 / 4051 (23.9%)	OR (95% CI)	p value	aOR (95% CI)	p value
Age (years)	–	1.01 (1.01 – 1.01)	<0.001	1.01 (1.01 – 1.01)	<0.001
Gender					
Female	433 / 1979 (21.9%)	–	–	–	–
Male	538 / 2072 (26.0%)	1.25 (1.08 – 1.45)	0.002	1.21 (1.03 – 1.40)	0.016
Ethnicity					
White	612 / 3067 (20.0%)	–	–	–	–
South Asian	266 / 710 (37.5%)	2.40 (2.02 – 2.87)	<0.001	2.44 (2.01 – 2.97)	<0.001
Black	44 / 122 (36.1%)	2.26 (1.55 – 3.31)	<0.001	2.56 (1.71 – 3.84)	<0.001
Other	49 / 152 (32.2%)	1.91 (1.34 – 2.71)	<0.001	2.53 (1.74 – 3.70)	<0.001
IMD decile					
1 (most deprived)	92 / 443 (21.0%)	–	–	–	–
2	93 / 326 (28.5%)	1.50 (1.08 – 2.09)	0.03	1.33 (0.93 – 1.88)	0.12
3	142 / 483 (29.4%)	1.57 (1.16 – 2.12)	0.01	1.28 (0.93 – 1.76)	0.13
4	117 / 415 (28.2%)	1.48 (1.08 – 2.02)	0.01	1.30 (0.93 – 1.81)	0.12
5	58 / 324 (17.9%)	0.82 (0.57 – 1.18)	0.29	0.80 (0.55 – 1.17)	0.25
6	94 / 368 (25.5%)	1.29 (0.93 – 1.79)	0.13	1.23 (0.87 – 1.73)	0.24
7	90 / 405 (22.2%)	1.08 (0.78 – 1.49)	0.66	1.09 (0.77 – 1.54)	0.63
8	98 / 454 (21.6%)	1.04 (0.75 – 1.43)	0.82	1.18 (0.84 – 1.65)	0.34
9	100 / 418 (23.7%)	1.18 (0.86 – 1.63)	0.30	1.36 (0.97 – 1.91)	0.07
10 (least deprived)	85 / 411 (20.7%)	0.98 (0.71 – 1.37)	0.92	1.08 (0.76 – 1.53)	0.66
Estimated household size	–	1.10 (1.05 – 1.15)	<0.001	1.06 (1.02 – 1.11)	0.006
Number of comorbidities					
0	482 / 2318 (20.8%)	–	–	–	–
1	199 / 688 (28.9%)	1.55 (1.28 – 1.88)	<0.001	1.41 (1.11 – 1.79)	0.005
≥2	290 / 1045 (27.8%)	1.46 (1.24 – 1.73)	<0.001	1.23 (0.87 – 1.73)	0.24
Type of comorbidity					
Hypertension	277 / 963 (28.8%)	1.39 (1.18 – 1.64)	<0.001	0.96 (0.75 – 1.23)	0.75
Other cardiovascular	104 / 415 (25.1%)	1.07 (0.84 – 1.35)	0.57	0.74 (0.56 – 0.98)	0.04
Diabetes	167/495 (33.7%)	1.74 (1.42 – 2.13)	<0.001	1.23 (0.95 – 1.60)	0.11
Cerebrovascular	52/180 (28.9%)	1.30 (0.94 – 1.82)	0.12	1.05 (0.73 – 1.53)	0.78
Respiratory	133/556 (23.9%)	1.00 (0.81 – 1.23)	0.98	0.86 (0.67 – 1.11)	0.25
AKI on admission	172/508 (33.9%)	1.76 (1.44 – 2.15)	<0.001	1.43 (1.15 – 1.77)	0.001
EWS on admission	–	1.17 (1.14 – 1.20)	<0.001	1.14 (1.11 – 1.17)	<0.001

Footnote: 'Other cardiovascular' comprises; pacemaker in situ, congenital cardiac failure, congestive heart failure, ischaemic heart disease, mitral valve disorder and left heart failure. 'Respiratory' comprises; chronic bronchitis, chronic obstructive lung disease, asthma and pulmonary emphysema. 'Cerebrovascular' comprises; cerebral haemorrhage, cerebral infarction, cerebrovascular accident, cerebrovascular disease, hemiplegia and subarachnoid haemorrhage.

public health measures including occupational risk profiling and shielding to protect these individuals.

Interestingly, our data indicate both that individuals from ethnic minority groups live in households with a higher number of residents and that an increasing number of residents per household is associated with testing positive for SARS-CoV-2. UK census data indicates that those of South Asian ethnicity live in households with a greater number of residents than those of White ethnicity [26] and it is likely that some of this effect can be attributed to an increased propensity for intergenerational living amongst those of Asian descent [27]. Previous studies have suggested increased population density aids transmission of viral respiratory tract infections [28] and this may explain the association between estimated household size and PCR positivity in the current study.

We demonstrated that AKI and a higher NEWS score at the time of presentation was associated with a positive PCR result. Although previous authors have shown that AKI is a marker of disease severity which results in poorer outcomes [29,30], our data raises the possibility that patients presenting with AKI or a higher NEWS score are more likely to have more aggressive disease with a higher viral load [31] and, therefore, a positive test result. These findings should be interpreted with caution as, given the observational nature of the study, we can only speculate on the temporal relationship between SARS-CoV-2 infection and AKI.

Other comorbidities, including hypertension and diabetes mellitus which have previously been shown to be common amongst those infected with SARS-CoV-2 and may have effects on outcome [21,32–34], were not found to be associated with PCR positivity in multivariable analysis.

In accordance with the published literature, we found that increasing age and male gender were associated with PCR positivity [8,27,35–38]. Epidemiological studies of Middle East respiratory syndrome coronavirus (MERS-CoV) have also demonstrated greater incidence amongst older males [39].

A previous study examining viral load dynamics in patients infected with SARS-CoV-2 has shown that being male and aged over 60 are both associated with a longer period of viral shedding [31]. This increased window for test positivity may partly explain why older men were more likely to test positive in the current study. A biological explanation for increased susceptibility to SARS-CoV-2 infection in men has been postulated to relate to the differential expression of an androgen regulated gene coding for a protein (TMPRSS2) which plays a role in the fusion of viral and host membranes in SARS-CoV infection [40]. Evidence for the role of androgens in SARS-CoV-2 infection has been demonstrated by a study observing that prostate cancer patients receiving androgen deprivation therapies are partially protected from COVID-19 [41].

There was a trend for increasing proportions of positive PCR tests in the three weeks after lockdown in ethnic minority groups but not for those of White ethnicity. To our knowledge this is the first time this effect has been described. This suggests that government imposed distancing measures have a more rapid impact on slowing viral transmission amongst individuals of White ethnicity as compared to those from ethnic minority groups. These findings should be interpreted with caution as, on regression analysis, we were unable to demonstrate a significant interaction between ethnicity and swab date before or after 30th March. The factors underlying a differential effect of lockdown measures on viral transmission in different ethnic

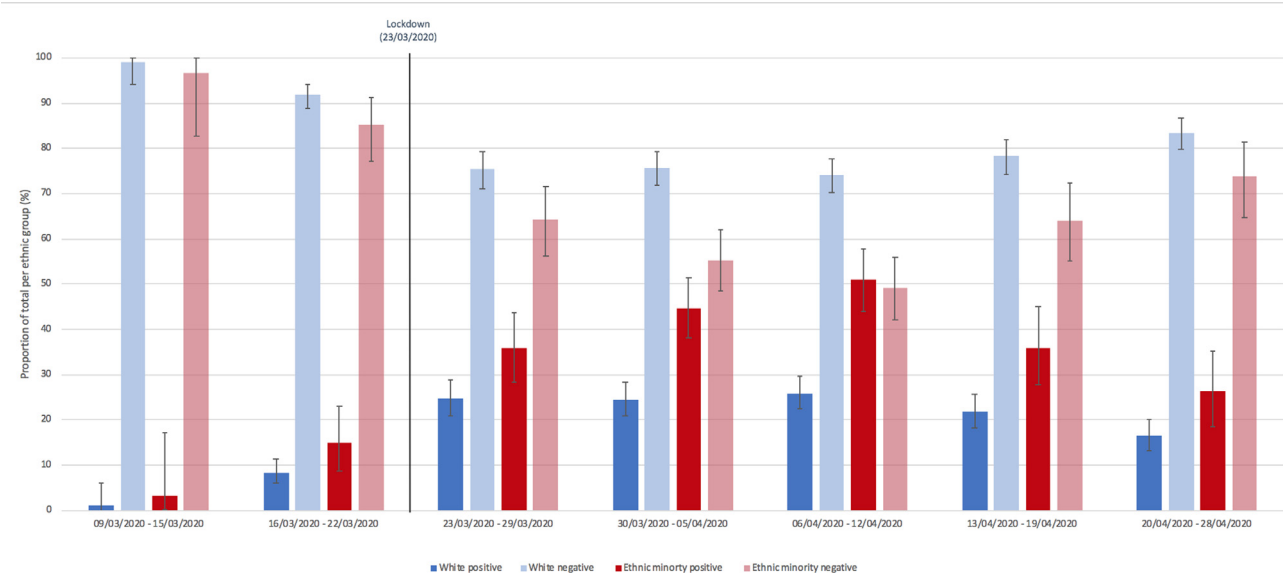

Fig. 1. Temporal change in proportions of positive and negative swabs in each week over the timecourse of the study, stratified by ethnicity. Proportions of positive and negative tests per week of the study if total number of tests in that week exceeds 50. This excludes 1st March 2020 – 8th March 2020 (n = 22). Final week includes 27th and 28th April and represents a 9 day period.

groups would likely be multidimensional. Linguistic and cultural barriers may prevent timely access to information, leading to a lack of understanding of the importance of pandemic control measures [4,19]. Occupational roles are likely to be an important consideration. Individuals from ethnic minority groups are overrepresented in professions that require close contact with others leading to higher occupational exposure to SARS-CoV-2 [42], and are also more likely to work in 'low-skilled' positions that cannot be performed from home [43] and may experience more pressure to work during lockdown elevating their risk of infection further. Additionally, these individuals are more likely to live in densely populated areas making social distancing more difficult [44,45]. Indeed, our analysis suggests that household size is not significantly associated with prevalent infection pre-lockdown but becomes so afterward and that the interaction between lockdown and household size is associated with PCR positivity. This could indicate that pandemic control measures may have less efficacy in controlling viral transmission amongst those living in larger households, or that the effects are delayed amongst those in larger households due to the increased risk of residual cross-infection after these measures are employed. Given the potential public health implications, these associations should be urgently investigated to determine if any small effects noted in this study are genuine.

Our study had limitations. Although the data is reported from a single centre, the number of patients in our cohort was large. Our overall prevalence of 24% swab positivity at the time of presentation was comparable with national UK data, reporting 20–30% swab positive rates [46]. Our method of estimating household size is based on census data from 2011. Population densities in the postcode regions included in the study may have changed since 2011 and this has the potential to give rise to results that may differ from an analysis carried out with current population data. However, it should be noted that this is the most up-to-date census in the UK and average household size in the UK in 2017 was 2.4 [47] which is line with our data. A slightly higher average household size might be expected in Leicester given the ethnic diversity of the local population, for reasons discussed above. Future prospective studies should aim to collect individual level data on household size to confirm the association with risk of infection with SARS-CoV-2. We only included information that was routinely entered into the electronic patient record and therefore did not have information on certain clinical features, BMI, occupational status and educational level which would be important in future prospective studies. We categorised individuals into South Asian and Other ethnicity (the latter included those of Chinese ethnicity) as this gave more granularity but we acknowledge the difficulties, and potential inaccuracies, in defining ethnicity. Although our findings are based on those seeking hospital attention, rather than the general population, the findings provide key, novel, information to policy makers.

In summary, in individuals presenting with suspected COVID-19 infection, persons from ethnic minority communities and those living in larger households had an increased likelihood of SARS-CoV-2 PCR positivity. We saw an increase in the proportion of ethnic minority individuals testing positive for SARS-CoV-2 in the weeks following lockdown, an effect that was not seen in the White cohort. Research is urgently required to better understand the mechanisms underlying these disparities and whether current public health interventions have differential and suboptimal effects in slowing viral transmission amongst individuals from ethnic minority groups.

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Data sharing statement

The patient cohort was extracted under Caldicott Guardian approval for a specific purpose and as part of our undertaking with them we are not to further routinely share this data. The data is held in an institutional repository and interested parties, with appropriate approvals, can apply for data access through the Corresponding author. Reasonable requests will be assessed on a case-by-case basis in discussion with the Caldicott Guardian.

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Declaration of Competing Interest

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Supplementary materials

Supplementary material associated with this article can be found in the online version at doi:10.1016/j.eclinm.2020.100466.

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