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Short Communication

Impact of SARS-CoV-2 Alpha variant (B.1.1.7) on prisons, England

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ABSTRACT

Objectives: Prisons are high-risk settings for infectious disease outbreaks because of their highly dynamic and crowded nature. During late 2020, prisons in England observed a surge in COVID-19 infection. This study describes the emergence of the Alpha variant in prisons during this period.

Methods: Alpha and non-Alpha variant COVID-19 cases were identified in prisoners in England using address-matched laboratory notifications and genomic information from COG-UK.

Results: Of 14,094 COVID-19-positive prisoner cases between 1 October 2020 and 28 March 2021, 11.5% (n = 1621) had sequencing results. Of these, 1082 (66.7%) were identified as the Alpha variant. Twenty-nine (2.7%) Alpha cases required hospitalisation compared with only five (1.0%; $P = 0.02$) non-Alpha cases. A total of 14 outbreaks were identified with the median attack rate higher for Alpha (17.9%, interquartile range [IQR] 3.2%–32.2%; $P = 0.11$) than non-Alpha outbreaks (3.5%, IQR 2.0%–10.2%).

Conclusion: Higher attack rates and increased likelihood of hospitalisations were observed for Alpha cases compared with non-Alpha. This suggests a key contribution to the rise in cases, hospitalisations and outbreaks in prisons in the second wave. With prisons prone to COVID-19 outbreaks and the potential to act as reservoirs for variants of concern, sequencing of prison-associated cases alongside whole-institution vaccination should be prioritised.

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Introduction

In November 2020, a rise in SARS-CoV-2 infections was observed in the United Kingdom despite lockdown measures, coinciding with the emergence of a new SARS-CoV-2 variant, Alpha (B.1.1.7), first identified in Southeast England. Surveillance and modelling data indicated that this variant had greater transmissibility compared with non-Alpha cases,^{1,2} leading to widespread concern and immediate foreign travel restrictions.

During late 2020, prisons in England observed a rise in COVID-19 outbreaks as well as increased case and age-standardised mortality rates compared with community settings.³ To protect residents and staff, the Ministry of Justice implemented measures across the prison estate, which included restricting regimes to

implement social distancing, stopping all visits, limiting movement of prisoners between facilities and compartmentalising prisons to isolate symptomatic prisoners, shield the vulnerable and quarantine new entrants.⁴ Reception testing of prisoners and mass testing of prison residents during outbreaks were also introduced during the second wave of the pandemic in England.

Given the increased risk of SARS-CoV-2 transmission and illness due to both the prison environment and the susceptibility of the population, understanding the introduction of variants into such institutional settings is a public health priority.

The aim of this study was to describe the impact of the emergence of the Alpha variant on prison-associated cases and outbreaks of COVID-19.

Methods

Data sources

As a statutory requirement, positive SARS-CoV-2 tests are notified to the national Second Generation Surveillance System,

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capturing both laboratory and point-of-care tests. Records for cases among prisoners were identified between 1 October 2020 and 28 March 2021 using an address-matching process described elsewhere.⁵ Alpha and non-Alpha variant cases were identified from the national COG-UK consortium database. As no other variants of concern (VOC) or variant under investigation (VUI) were identified within this cohort, non-Alpha refers to non-VOC/VUI samples identified in this study. Hospitalisation data were obtained by linkage to national admission and accident and emergency data.⁶

Definitions

Outbreaks in prisons were defined as ≥ 2 cases within a 14-day rolling window (by specimen date) residing at the same prison. Outbreaks were classified as Alpha or non-Alpha according to sequencing results available. Outbreaks still ongoing at the end of the study period were excluded, as were outbreaks containing mixed sequencing results. Outbreaks with at least one sequenced case were included regardless of the order of sequenced and non-sequenced cases. Analyses were conducted on all cases within the outbreaks regardless of whether sequenced. Attack rates were defined as the number of cases among prisoners in the outbreak (numerator) divided by the population of prisoners in that specific facility (denominator) derived from the February 2021 Prison Population Bulletin.⁷ Attack rates were only calculated on the first outbreak in prisons where multiple outbreaks were identified.

Hospitalisation was defined as an admission to hospital within 14 days following a positive COVID-19 test. Associated deaths were defined as deaths in cases occurring up to 60 days following the earliest positive specimen date or where COVID-19 was stated on their death certificate.

Analysis

Alpha and non-Alpha cases were compared using the Mann–Whitney U and Chi-squared tests as appropriate. The distribution of attack rates was compared using Kruskal–Wallis tests.

Results

We identified 14,094 SARS-CoV-2 cases among those residing in prisons during the study period, with every prison in England ($n = 112$) identified as having ≥ 1 confirmed case. Of these cases, 11.5% ($n = 1621$) were sequenced with 79.5% of all prisons ($n = 89$) having at least one sequenced case. Sequenced cases were broadly reflective of prison cases during the study period in terms of sex, age, ethnicity and prison type (Supplementary Table 1). A smaller proportion of Alpha cases were female (0.7 vs 6.7%; $P < 0.001$) or of White ethnicity (55.9 vs 75.3%, $P < 0.001$) compared with non-Alpha variants (Supplementary Table 1). Most Alpha cases (55.2%) were in male category C trainer prisons, whereas most non-Alpha cases were in local prisons.

The majority of sequenced cases ($n = 1,082$, 66.7%) were Alpha (Fig. 1), accounting for 0.74% of all sequenced Alpha variant cases in England ($n = 146,479$). Of the 1621 sequenced cases associated with prisons, 2.7% ($n = 29$) of Alpha cases required hospitalisation compared with only 0.9% ($n = 5$) of non-Alpha cases ($P = 0.02$); however, there were no significant differences observed regarding mortality, likely because of the small number of deaths observed.

Prison outbreaks

There were 74 prison outbreaks included in the analysis, of which 33 were Alpha outbreaks and 41 non-Alpha outbreaks, involving 1803 and 1756 number of prisoners, respectively. The majority (27; 81.8%) of Alpha outbreaks started between December 2020 and January 2021.

The median size of Alpha outbreaks (24; interquartile range [IQR] 6–63) was slightly greater than non-Alpha outbreaks (18; IQR 9–63), but the median outbreak duration was greater in non-Alpha outbreaks (31 days; IQR 17–46) compared with Alpha variant outbreaks (22 days; IQR 14–51); however, these differences were not statistically significant ($P > 0.05$).

Attack rates were just over five times higher in Alpha only outbreaks compared with non-Alpha only, 17.9% (IQR 3.2%–32.2%)

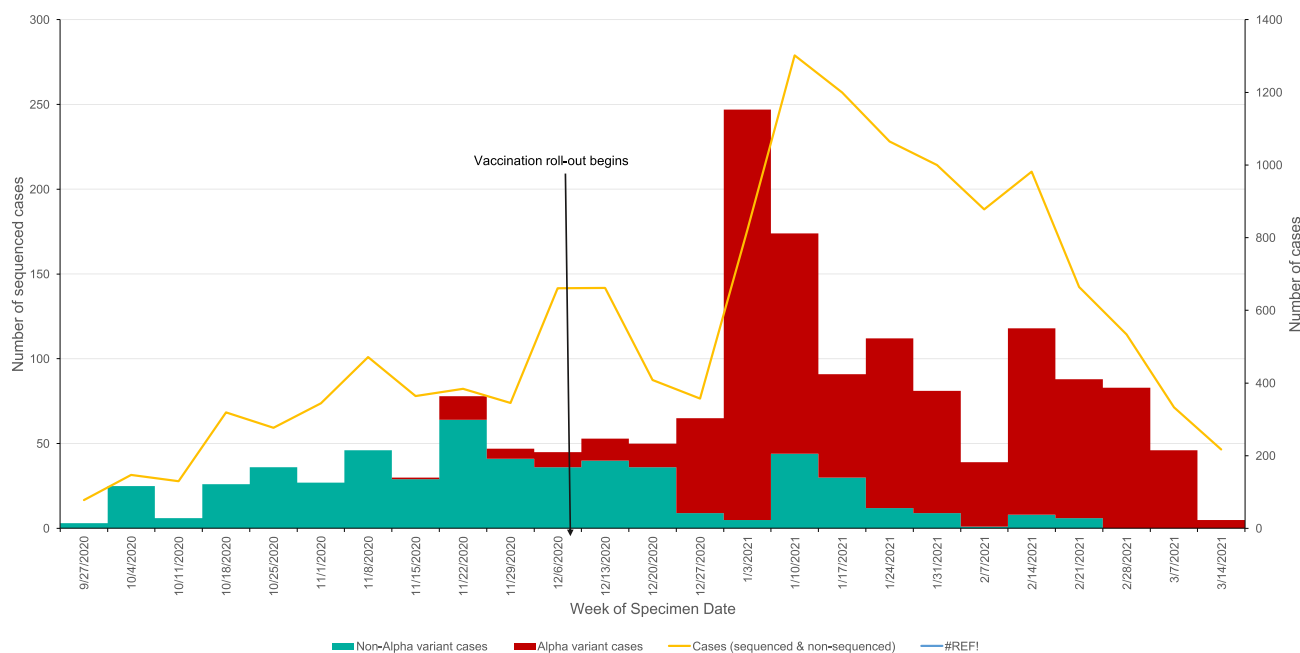


Fig. 1. Weekly number of COVID-19-positive prisoners ($n = 14,094$) and sequencing results ($n = 1621$), England.

and 3.5% (IQR 2.0%–10.2%) respectively; however, there was only weak evidence for a difference ($P = 0.11$).

Discussion

This study is the first nationwide assessment of the impact of the Alpha variant in prisons, benefiting from a robust enrichment process of residential property assignment and genomic sequencing results.

We identified Alpha as the predominant variant in prisons during England's second pandemic wave, reflecting the COVID-19 trend nationally. Prisons are not isolated from society, and ingress of infection from staff, visitors and new receptions remains an ongoing threat.⁸ In its assessment of emerging threats during the pandemic, the Scientific Advisory Group for Emergencies (SAGE) in England has cited prisons as a particular infection hazard to the community, given the risk that these establishments can become 'reservoirs and amplifiers of infection, including variants of concern'.⁹ This risk is not limited to SARS-CoV-2, and a recent systematic review has identified examples of the public health risk of prison outbreaks, including the release of prisoners exposed to TB into the community.¹⁰ Among sequenced cases, there was some evidence for greater hospitalisations in Alpha cases when compared with non-Alpha cases, consistent with findings in the wider population.⁵ Attack rates were five times higher in Alpha variant outbreaks compared with non-Alpha only outbreaks, which suggest increased transmissibility of the Alpha variant, in line with other published findings¹ and its contribution to the rise in cases in prisons in the second wave. However, with the majority of Alpha outbreaks in December and January, this finding may also be reflective of greater indoor mixing during the winter months, higher community incidence and change in testing regimes.⁴

Limitations of this study include low sequencing coverage over the study period, hence the need to assume that non-sequenced cases within an outbreak were of the same variant as the sequenced cases and, second, the crude assessment of hospitalisations, potentially limiting generalizability. Furthermore, we were unable to discern whether there were multiple introductions of Alpha into the prison rather than a continuous outbreak using our data set.

Prisons are prone to infectious disease outbreaks because of their highly dynamic and crowded nature and the vulnerability of residents. These factors can lead to prisons acting as potential reservoirs for VOC; therefore, alongside early whole-institution vaccination, prioritisation of prison-associated cases for sequencing is important. This would allow for early identification of VOC, improve understanding of transmission dynamics and changing epidemiology, thus informing disease control measures to prevent further spread of COVID-19 in prisons and the wider community.

Author statements

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involved in notification of all COVID-19 samples as well as whole genome sequencing of these samples.

Ethical approval

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

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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/privacy reasons.

Authors' contributions

A.V., T.L. and D.C. were the principal investigators, and A.V. led the writing of this report. T.L., D.C. and A.V. made significant contributions to conception of the study design. All authors contributed to the interpretation of results and critical review.

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.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.puhe.2021.12.018>.

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