COG-UK summary for SAGE report to DfE on SARS-CoV-2 in educational settings

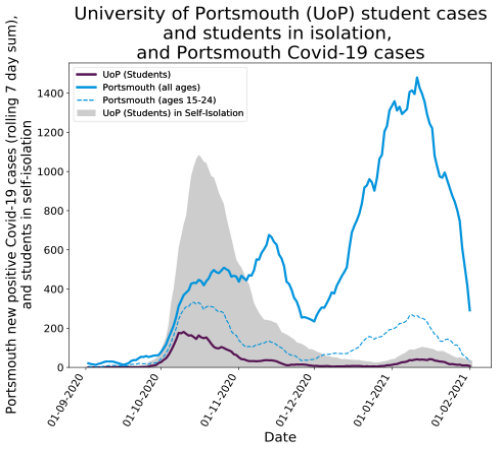
8th February 2021

Multiple academic and public health partners within the COVID-19 Genomics UK (COG-UK) consortium are sequencing SARS-CoV-2 positive samples from university testing programmes (asymptomatic and symptomatic), and as part of the public health outbreak response, to generate genomic insights into transmission among students and staff at their institution. As part of this effort, an interim report on the genomic epidemiology of SARS-CoV-2 at the University of Cambridge was submitted to SAGE on the 10th of December.

This summary briefly describes some of the broad level insights that can be taken from studies undertaken by COG-UK members at the University of Cambridge (UoC), the University of Portsmouth (UoP), and Public Health Scotland in collaboration with MRC-University of Glasgow (UoG) Centre for Virus Research who provided the sequencing. These broad level insights should be viewed as preliminary; detailed reports will be prepared in due course.

- *Rates of infection among student populations, how these have changed over time and what may have influenced changes (including closures and restrictions).*

At UoC and UoP, a similar pattern of positive cases among students could be discerned in the testing data, with prevalence increasing in the early weeks of term during October, followed by a decline towards the end of November. Occasional spikes in cases can be observed, which may be associated with gatherings of students. Based on testing data from UoP and the surrounding area, infection rates among students were lower than in the surrounding community (See figure). Similarly, cases associated with UoG initially rose in late September, involving off-campus student residential halls, in the week immediately following Freshers' week but the outbreak was rapidly curtailed following intervention measures. Overall, the pattern suggests that infection control measures, increased testing, use of remote learning, and self-isolation by students were successful in reducing prevalence in student communities.



*includes both symptomatic and asymptomatic cases.

- *Evidence of transmission between communities and students, students and staff and among students.*

Genome sequence data indicates that there were multiple SARS-CoV-2 variants introduced in mid-late September into UoG, and early October into UoC and UoP. While some formed clusters with a limited number of cases (which generally were not detected again after early weeks of the term), others seeded larger clusters consisting of cases from multiple halls of residence/colleges. The association of multiple distinct virus variants with one outbreak suggests multiple introductions into the residential halls, likely through shared common source(s) linked to social activity, and/or sporadic

introductions with origins from the local community and/or non-term-time domicile locations. However, the relatively low number of distinct viruses, compared to overall sequenced case numbers, suggests significant subsequent student-student transmission occurred. Residential halls and colleges present similar scenarios for shared households and facilities that may enable transmission of SARS-CoV-2. Potential asymptomatic transmission among students within halls of residence was observed. However, the likelihood of transmission events to and/or from the local community is likely to differ depending on the accommodation and social context of the student population and incidence in the local community. There was some evidence of potential acquisition of infection from, and onward transmission to, the local community in the case of off-campus residential halls, although further epidemiological and phylogenetic study is needed to understand these putative links.

- *Settings and factors associated with risk of transmission e.g., halls of residence compared to private accommodation, student migration and how this influences transmission/risk.*

There was no clear evidence for a difference in transmission among students living in halls of residence versus private accommodation, although the outbreak at UoG was centred around off-campus university residential halls.

Several important limitations should be considered when interpreting these findings:

- Infection risks associated with student social activities, or involving residential halls, cannot be directly quantified as the total numbers of infected and uninfected students were not known and some cases were probably asymptomatic and not tested.
- Interpretation of direct student-to-student transmission events is limited by lack of information on how cases are linked to individual households/flats within residential halls, lack of additional contact tracing information to further define contacts, chains of transmission and links to social events, and the low levels of variation in SARS-CoV-2 genomes making it difficult to conclusively define direct transmission events.
- The interpretation of the relative frequency and importance of separate introductions into halls, versus subsequent student-student transmission, is limited by the partial coverage of cases for sequencing and assumes that the sequenced cases represent a random selection of the overall cases.
- Interpretation of transmission events between students and the local community is limited by lack of knowledge of the non-term-time locations of students, their recent travel histories, and the likelihood that genomic surveillance will miss variants circulating in the community at a low level. The background context of circulating viruses is also complicated by the presence and numbers of SARS-CoV-2 lineage detections over time and across locations being biased by the targeted sampling of outbreaks and varying surveillance coverage.
- Further epidemiological and phylogenetic work is needed to further investigate the likely source of introductions from across the UK and abroad.