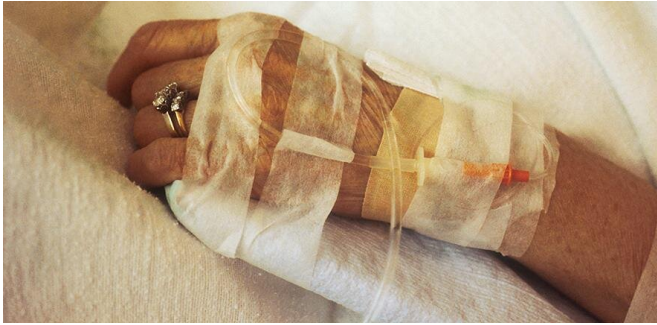


# Genomics study identifies routes of transmission of coronavirus in care homes

3 March 2021, by Craig Brierley



Credit: [National Cancer Institute](#)

Genomic surveillance—using information about genetic differences between virus samples—can help identify how SARS-CoV-2 spreads in care home settings, whose residents are at particular risk, according to new research published today.

Care homes are at high risk of experiencing outbreaks of COVID-19, the disease caused by SARS-CoV-2. Older people and those affected by heart disease, respiratory disease and type 2 diabetes—all of which increase with age—are at greatest risk of severe disease and even death, making the care home population especially vulnerable.

Care homes are known to be high-risk settings for infectious diseases, owing to a combination of the underlying vulnerability of residents who are often frail and elderly, the shared living environment with multiple communal spaces, and the high number of contacts between residents, staff and visitors in an enclosed space.

In research published today in *eLife*, a team led by scientists at the University of Cambridge and Wellcome Sanger Institute used a combination of genome sequencing and detailed epidemiological information to examine the impact of COVID-19 on

care homes and to look at how the virus spreads in these settings.

SARS-CoV-2 is an RNA virus and as such its genetic code is prone to errors each time it replicates. It is currently estimated that the virus mutates at a rate of 2.5 nucleotides (the A, C, G and U of its genetic code) per month. Reading—or 'sequencing'—the genetic code of the virus can provide valuable information on its biology and transmission. It allows researchers to create 'family trees'—known as phylogenetic trees—that show how samples relate to each other.

Scientists and clinicians in Cambridge have pioneered the use of genome sequencing and epidemiological information to trace outbreaks and transmission networks in hospitals and community-based healthcare settings, helping inform [infection control measures](#) and break the chains of transmission. Since March 2020, they have been applying this method to SARS-CoV-2 as part of the COVID-19 Genomics UK (COG-UK) Consortium.

In this new study, researchers analyzed samples collected from 6,600 patients between 26 February and 10 May 2020 and tested at the Public Health England (PHE) Laboratory in Cambridge. Out of all the cases, 1,167 (18%) were care home residents from 337 care homes, 193 of which were residential homes and 144 nursing homes, the majority in the East of England. The median age of care home residents was 86 years.

While the median number of cases per care home was two, the ten care homes with the largest number of cases accounted for 164 cases. There was a slight trend for nursing homes to have more cases per home than [residential homes](#), with a median of three cases.

Compared with non-care home residents admitted to hospital with COVID-19, hospitalized care home residents were less likely to be admitted to

intensive care units (less than 7% versus 21%) and more likely to die (47% versus 20%).

The researchers also explored links between care homes and hospitals. 68% of care home residents were admitted to hospital during the study period. 57% were admitted with COVID-19, 6% of cases had suspected hospital-acquired infection, and 33% were discharged from hospital within seven days of a positive test. These findings highlight the ample opportunities for SARS-CoV-2 transmission between hospital and care home settings.

When the researchers examined the viral sequences, they found that for several of the care homes with the highest number of cases, all of the cases clustered closely together on a phylogenetic tree with either identical genomes or just one base pair difference. This was consistent with a single outbreak spreading within the care home.

By contrast, for several other care homes, cases were distributed across the phylogenetic tree, with more widespread [genetic differences](#), suggesting that each of these cases was independent and not related to a shared transmission source.

"Older people, particularly those in care homes who may be frail, are at particular risk from COVID-19, so it's essential we do all that we can to protect them," said Dr. Estée Török, an Honorary Consultant at Addenbrooke's Hospital, Cambridge University Hospitals (CUH), and an Honorary Senior Visiting Fellow at the University of Cambridge.

"Preventing the introduction of new infections into care homes should be a key priority to limit outbreaks, alongside infection control efforts to limit transmission within care homes, including once an outbreak has been identified."

The team found two clusters that were linked to healthcare workers. One of these involved care home residents, a carer from that home and another from an unknown care home, paramedics and people living with them. The second involved several care home residents and acute medical staff at Cambridge University Hospitals NHS Foundation Trust who cared for at least one of the

residents. It was not possible to say where these clusters originated from and how the virus spread.

"Using this technique of 'genomic surveillance' can help institutions such as care homes and hospitals better understand the transmission networks that allow the spread of COVID-19," added Dr. William Hamilton from the University of Cambridge and CUH. "This can then inform infection control measures, helping ensure that these places are as safe as possible for residents, patients, staff and visitors."

The absolute number of diagnosed COVID-19 cases from care home residents declined more slowly in April than for non-[care home residents](#), increasing the proportion of cases from [care homes](#) and contributing to the slow rate of decline in total case numbers during April and early May 2020.

"Our data suggest that care home transmission was more resistant to lockdown measures than non-care home settings. This may reflect the underlying vulnerability of the care home population, and the infection control challenges of nursing multiple residents who may also share communal living spaces," said Gerry Tonkin-Hill from the Wellcome Sanger Institute.

The team found no new viral lineages from outside the UK, which may reflect the success of travel restrictions in limiting new viral introductions into the general population during the first epidemic wave and lockdown period.

**More information:** William L Hamilton et al. Genomic epidemiology of COVID-19 in care homes in the East of England, *eLife* (2021). [DOI: 10.7554/eLife.64618](#)

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