

Adverse Outcomes Associated with SARS-CoV-2 variant B.1.351 Infection in Vaccinated  
Residents of a Long Term Care Home, Ontario, Canada

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Dear Editor

We read with interest the description of an outbreak due to SARS-CoV-2 variant B.1.351 (501Y.V2) in a nursing home in France (1). Below we describe an outbreak due to the same variant in a long term care home (LTCH) in Canada. In this home, 138 of 139 residents were fully vaccinated with BNT162b2, with doses received between January 9<sup>th</sup> and March 18<sup>th</sup>, 2021. Of 243 staff, 204 (84%) had received at least one dose of an mRNA vaccine (122 fully vaccinated, and 82 with second dose delayed as part of Canada's vaccination strategy). Because of on-going community SARS-CoV-2 transmission, measures to prevent outbreaks for all Ontario LTCHs include daily symptom screening for staff and residents, visitor restriction to single caregivers, droplet-contact precautions for residents with symptoms compatible with COVID-19, and bi-weekly screening of staff with using either PCR or rapid antigen testing (Panbio®). All positive antigen tests were confirmed by PCR. All specimens yielding SARS-CoV-2 by PCR were screened for mutations at S-gene positions A23063T (aa:N501Y) and G23012A (aa:E484K) by PCR at Public Health Ontario Laboratory.

Available samples underwent whole genome sequencing (WGS) using an ARTICV3 Illumina protocol (<https://www.protocols.io/view/sars-cov-2-illumina-miseq-protocol-v-2-bs98nh9w>) with bioinformatics analysis, including lineage prediction and quality control of results using ncov-tools. (2-4)

In the second week of April, an unvaccinated staff member was diagnosed with COVID-19, subsequently demonstrated to be due to SARS-CoV-2 variant B.1.351. Outbreak control measures instituted included droplet-contact precautions for all residents, cohorting positive residents, enhanced cleaning, screening of staff and residents by PCR every three days.

Over the next 3 weeks, 4 staff members (2 fully vaccinated, 1 single dose, one unvaccinated) and 9 fully vaccinated residents developed COVID-19 due to variant B.1.351. Two unvaccinated staff members had infections due to other variants (one B.1.1.7, and one B.1.617.2) and 3 (1 fully vaccinated, 2 single dose) had positive tests with concentrations too low to identify lineage. Of the 9 residents infected with B.1.351, 1 was asymptomatic, 1 had symptoms without fever or other indicators of severity, 3 had a febrile cough illness which did not progress, and 4 developed hypoxemia. Of these latter 4, 2 required hospitalization, and 3 (including both hospitalized patients) died. Two of 4 staff were asymptomatic; 2 (1 unvaccinated, 1 single dose) had mild symptoms. Genomic analysis revealed that all B.1.351 genomes were highly related ( $\leq 2$  single nucleotide polymorphisms between sequences).

This outbreak confirms the observation of Bailly *et al.* that B.1.351 outbreaks associated with significant resident morbidity and mortality may occur in LTCHs with recent vaccination and high vaccination rates. Such outbreaks may be an on-going risk if this variant is circulating in the surrounding community, although very high vaccination rates such as those in this home may mitigate outbreak size and severity. In addition to on-going surveillance screening and testing, and work to optimize infection prevention practice, other interventions such as vaccines specifically against variants, and requirements for staff to be vaccinated, may need to be considered if LTCH residents are to be optimally protected.

**Potential Conflicts:**

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