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## Research Brief

# Infection trends in home health care, 2013–2018

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Infections are a frequent cause of hospital (re)admissions for older adults receiving home health care (HHC), and the Joint Commission has identified infection prevention and control in HHC as a national patient safety goal.[1] HHC patients who are immunocompromised or recovering from surgical procedures are particularly susceptible to infections.[2] Many sepsis survivors are discharged from the hospital to HHC and have high rates of readmission for recurrent infections and related complications.[2–4]

Reported prevalence of infections in HHC has varied from 5% to 80%, depending on the patient population.[5] Using data from the Outcome and Assessment Information Set (OASIS), the standardized assessment tool mandated for all Medicare-certified HHC agencies, Shang et al[6] found that 17% of unplanned hospitalizations in HHC were due to 4 types of infection: (1) respiratory infection, (2) urinary tract infection (UTI), (3) wound site (skin or soft-tissue) infection, and (4) intravenous (IV) catheter-related. OASIS assessments are completed by clinicians at least twice during a HHC episode, including upon admission and for any change in health status that leads to inpatient transfer, discharge from HHC, death, or 60-day recertification if none of these events have occurred. However, this study likely underestimated the prevalence of infections leading to hospitalization because the data were limited to infections reported in OASIS.[6]

In this study, we used 2013–2018 OASIS assessment data linked to Medicare inpatient data to estimate trends in the prevalence of infection in hospital transfers among HHC patients and subsequent 30-day mortality.

## Methods

We identified a random sample of 1,481 Medicare-certified HHC agencies stratified by US Census region (Northeast, South, Midwest, or West), ownership (nonprofit, for-profit, or government), and rural or urban location. We obtained OASIS assessment data for all Medicare beneficiaries who received HHC services from these agencies between 2013 and 2018 (n = 2,258,105). We identified 60-day HHC episodes (n = 5,203,696). HHC episodes with a hospital transfer (all causes) were linked to corresponding inpatient records in the Medicare Provider Analysis and Review file (MedPAR).

We estimated the percentage of all hospital transfers with (1) infection present on admission (POA) and (2) infection as the primary cause. We also estimated 30-day mortality following hospital transfer with infection as the primary cause. Bacterial or suspected bacterial infections were identified using *International Classification of Diseases, Ninth Revision* (ICD-9) and ICD-10 codes in MedPAR (see the Appendix online). We classified infections by site: respiratory, UTI, skin and soft tissue, IV catheter-related (including peripheral and central IVs), and all (including other or unspecified infection site). We also identified sepsis diagnoses. Hospital transfers could be associated with >1 infection classification. We classified all transfers for which infection was POA in any of the 25 diagnosis codes as transfers with infection POA. We further classified hospital transfers with infection as the primary cause if infection was indicated (1) as the principal diagnosis and POA or (2) as the admitting diagnosis and POA. For transfers with infection as the primary cause, we identified 30-day mortality following the hospital admission date based on the patient date of death (if applicable) in the Master Beneficiary Summary File. Analyses were limited to hospital transfers reported in OASIS with a corresponding MedPAR record (85% match rate). All models were adjusted for clustering of observations within HHC agencies. This study was approved by the Columbia University and RAND institutional review boards.

## Results

From 2013 through 2018, the percentage of 60-day HHC episodes with 1 or more hospital transfers (all causes) varied from ˜15% to 16%. Table 1 reports the outcomes of interest from 2013 to 2018, overall and by infection site.

Nearly half of all hospital transfers among HHC patients had an infection POA, ranging from 45.00% in 2013 to 47.32% in 2018. Approximately 15% of hospital transfers had respiratory infections POA and ˜20% had UTIs POA. The percentage of transfers with sepsis POA increased from 9.00% in 2013 to 13.58% in 2018 ($P < .001$).

Infection was the primary cause for >25% of all hospital transfers among HHC patients, ranging from 25.86% of transfers in 2013 to 27.57% in 2018. Sepsis was the most frequent infection-related cause of hospital transfer, followed by respiratory infection and UTI. Notably, hospital transfers caused by sepsis increased from 7.51% of transfers in 2013 to 11.49% in 2018, while the percentage of transfers caused by other infection types decreased ($P < .001$ for all).

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**Table 1.** The Burden of Infection in Hospital Transfers in Home Health Care, 2013–2018

| Outcome | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 |
|---|---|---|---|---|---|---|
| **Hospital transfers with infection present on admission, %** | | | | | | |
| Any infection | 45.00 | 45.76 | 46.49 | 45.89 | 47.20 | 47.32 |
| Sepsis | 9.00 | 10.15 | 11.51 | 12.24 | 13.13 | 13.58 |
| Respiratory | 14.70 | 14.84 | 15.63 | 15.09 | 15.81 | 15.07 |
| UTI | 19.88 | 20.57 | 20.76 | 20.25 | 19.50 | 18.62 |
| Skin or soft tissue | 7.41 | 7.48 | 7.31 | 7.36 | 7.44 | 7.77 |
| IV catheter | 0.52 | 0.47 | 0.38 | 0.22 | 0.24 | 0.23 |
| **Hospital transfers with infection as the primary cause, %** | | | | | | |
| Any infection | 25.86 | 26.59 | 27.09 | 26.43 | 27.29 | 27.57 |
| Sepsis | 7.51 | 8.55 | 9.67 | 10.32 | 11.11 | 11.49 |
| Respiratory | 7.12 | 6.92 | 6.87 | 6.39 | 6.23 | 5.85 |
| UTI | 5.90 | 6.27 | 6.23 | 5.81 | 4.87 | 4.79 |
| Skin or soft tissue | 3.13 | 3.11 | 3.03 | 2.98 | 2.93 | 2.98 |
| IV catheter | 0.41 | 0.38 | 0.30 | 0.17 | 0.20 | 0.20 |
| **30-day mortality following hospital transfer with infection as the primary cause, %** | | | | | | |
| Any infection | 14.14 | 14.22 | 14.40 | 14.67 | 14.58 | 14.98 |
| Sepsis | 26.51 | 24.79 | 24.39 | 23.83 | 23.14 | 23.79 |
| Respiratory | 14.90 | 15.00 | 14.11 | 14.15 | 13.96 | 14.10 |
| UTI | 7.46 | 7.98 | 7.63 | 7.34 | 7.05 | 6.75 |
| Skin or soft tissue | 5.56 | 5.59 | 5.02 | 4.87 | 4.86 | 5.04 |
| IV catheter | 7.38 | 11.82 | 12.42 | 9.68 | 14.33 | 15.19 |

Note. Hospital transfers may be associated with >1 infection classification (eg, sepsis may overlap with other infection classifications). Due to large sample sizes, all changes from 2013 to 2018 are statistically significant ($P < .001$). All confidence intervals are within ±0.008 percentage points for transfers with infection POA and transfers with infection as the primary cause and within ±0.05 percentage points for 30-day mortality following transfer with infection as the primary cause.

Overall, 30-day mortality following hospital transfer with infection as the primary cause ranged from 14.14% in 2013 to 14.98% in 2018. Mortality rates following hospital transfers caused by infection were highest for sepsis, ranging from 23.14% to 26.51%. In comparison, 30-day mortality following all-cause hospital transfer, excluding transfers with infection as the primary cause, ranged from 11.52% to 11.68% between 2013 and 2018.

## Discussion

Our findings demonstrate that infections are a persistent problem in HHC and a more frequent cause of hospital transfers in HHC than previously reported.[6] Our findings also emphasize the importance of infection prevention in HHC because infections occurring in HHC were associated with substantial 30-day mortality, particularly following transfers caused by sepsis. Many factors may play a role in the observed trends, including possible changes in coding practices following the transition from ICD-9 to ICD-10 in October 2015. The increasing trend in hospital transfers with sepsis as the primary cause may potentially indicate improvement in early recognition and treatment of sepsis in HHC and emergency departments, consistent with initiatives in New York, New Jersey, and Illinois.[7–10] Policies to promote best practices for infection prevention and control in the HHC setting are important for improving quality of care.

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**Conflicts of interest.** All authors report no conflicts of interest relevant to this article.

**Supplementary material.** To view supplementary material for this article, please visit https://doi.org/10.1017/ice.2021.248

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# Severe acute respiratory coronavirus virus 2 (SARS-CoV-2) infection in asymptomatic vaccinated healthcare workers

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection has caused >2.7 million deaths worldwide,[1] devasting health systems end economies worldwide. Since the first months of the pandemic, a rapid and massive effort has been performed by the scientific community to develop a safe and effective vaccine against SARS-CoV-2.[2] In Italy, the first population to receive the vaccine was healthcare workers (HCWs) who are principally exposed to SARS-CoV-2 infection during the management of coronavirus disease 2019 (COVID-19) patients.[3] Several doubts remain concerning the neutralizing properties of antibodies produced after vaccination.[4] Moreover, little is known about transient infections in vaccinated individuals who therefore could be potential carriers of the disease.[5] Finally, it is important to understand the actual efficacy of the approved vaccines against SARS-CoV-2 variants, which have led to enhanced virus transmissibility, morbidity, and mortality.[6,7]

Here, we report several asymptomatic and vaccinated HCWs who tested positive for SARS-CoV-2 during surveillance testing.

## Methods

### Samples

Approximately 500 nasopharyngeal swab specimens of HCWs and hospitalized patients were collected at the Hospital Ss. Annunziata of Chieti, Italy, and analyzed by the Laboratory of Molecular Genetics Test Diagnosis COVID-19 of the Center for Advanced Studies and Technology (CAST) at Gabriele d'Annunzio University of Chieti-Pescara, Italy.

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### RNA extraction and qRT-PCR

RNA was extracted from nasopharyngeal specimens, using the MagMAX Viral/Pathogen II Nucleic Acid Isolation Kit on the automated KingFisher processor (Thermo Fisher Scientific, Waltham, MA). The extracted RNA underwent real-time reverse transcription polymerase chain reaction (qRT-PCR) with 2 commercial kits: the TaqPath COVID-19 CE-IVD RT-PCR Kit assay (Thermo Fisher Scientific) and Allplex SARS-CoV-2 Variants I Assay (Seegene, Korea).

### Next-generation sequencing (NGS)

For whole viral genome sequencing, total RNA was reverse transcribed using Invitrogen SuperScript VILO cDNA Synthesis Kit (Thermo Fisher Scientific). cDNA libraries were prepared using the Ion AmpliSeq SARS-CoV-2 Research Panel (Thermo Fisher Scientific). Sequencing was performed on the Ion GeneStudio S5 System (Thermo Fisher Scientific). The consensus sequences were aligned with the Wuhan-Hu reference SARS-CoV-2 genome using the Torrent Suite platform (Thermo Fisher Scientific). For phylogenetic analysis the whole-genome sequences of the isolates were uploaded on Pangolin COVID-19 Lineage Assigner.[8]

## Results

From January to March 2021, we were informed that among those who tested positive for SARS-CoV-2, 7 were HCWs who had received the BNT162b2 vaccination (Table 1). All were contacted and gave informed consent for this study.

Of these 7 HCWs, 6 had received both doses of the vaccine and 1 had received only the first dose. HCWs 2, 4, and 5 received positive SARS-COV-2 results between 3 and 8 days after receiving the second dose. The remaining 3 cases (HCWs 3, 6, and 7) received positive results between 23 and 36 days after the administration of the second dose of vaccine.