Abstract

South Africa has experienced multiple waves of infections by the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2), which causes coronavirus disease 2019 (COVID-19). Healthcare workers (HCWs) are at an increased risk of SARS-CoV-2 infections as a result of multiple exposures to infected individuals and contaminated work environments. HCWs may also contribute to nosocomial transmission of SARS-CoV-2 in hospital environments, including between themselves and patients.

We conducted surveillance for SARS-CoV-2 infections in HCW at Chris Hani Baragwanath Academic Hospital (CHBAH). The HCWs were tested weekly, irrespective of symptomatology, for SARS-CoV-2 infections using a nucleic acid amplification test (NAAT). Testing for SARS-CoV-2 was undertaken over three wave periods spanning from April 2020 to September 2021. Furthermore, the HCWs were encouraged to come forth for testing at any time if they displayed symptoms of a respiratory illness or were in close contact with a confirmed case of COVID-19. The NAAT reactive samples were sequenced to characterise the molecular epidemiology of positive cases and better understand virus transmission between HCWs at CHBAH. We defined HCW-HCW transmission if HCWs tested positive for SARS-CoV-2 within 3 to 10 days of one another, worked in the same or related departments and if HCW sequences were isogenic. However, we could not exclude that the infections could be due to potential viral transmission from patients to HCWs or that the HCW contracted the virus elsewhere.

Overall, 193 (35.2% of 549) HCWs had a reactive SARS-CoV-2 NAAT during the study. Of the 193 samples from HCW in which SARS-CoV-2 was detected, 85.0% (N=164/193) were successfully sequenced. We identified nine putative transmission clusters among HCWs using phylogenetic characterisation and single nucleotide polymorphism (SNP) analysis, including four clusters in the first and third waves and one cluster in the second wave of SARS-CoV-2 infections. Twenty-five percent of infections among the HCW (N=41/164) were part of these clusters of infections based on phylogenetic analysis. However, based on the HCW-HCW transmission definitions, only 11 (26.8% of 41) of the infections were associated with probable transmission between HCW.

We report modest transmission of SARS-CoV-2 infections between HCWs in our setting based on phylogenetic sequencing. The early detection of SARS-CoV-2 infection due to the active surveillance, could have led to a lower risk of SARS-CoV-2 infections among HCWs as those who were infected were identified timeously and went into isolation thereafter. The use of genomic sequencing enabled us to quantify the role of transmission between HCWs, in the overall burden of SARS-CoV-2 infections that affected this population.