Prevalence of SARS-CoV-2 infections among Swedish healthcare workers on duty in December 2023

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SARS-CoV-2 continues to spread and the emergence of new variants within the Omicron lineage has introduced additional complexity to the SARS-CoV-2 viral phylogeny.[1] New variants have demonstrated unprecedented potential for rapid viral transmissibility and evasion of infection- and vaccine-induced immune responses,[2] thereby reducing efficacy of monovalent and bivalent booster doses delivering only the wildtype or the wildtype and BA.1/BA.5 spike proteins.[3] Updated monovalent vaccines targeting the XBB.1.5 spike variant have therefore recently replaced these vaccines in many countries. We[4] and others[5] have demonstrated that the monovalent XBB.1.5-adapted booster substantially enhances both binding and neutralizing antibody responses against a spectrum of variants suggesting a cross-protection against severe disease. However, vaccine-induced protection against infection has to date been limited, and current Swedish recommendations for this booster are restricted to people with certain medical conditions, immunocompromised and individuals over 65 years of age.

To assess the current prevalence of SARS-CoV-2 infections and the associated viral variants among healthcare workers (HCW) on duty, we conducted a point prevalence screening at Danderyd Hospital, Stockholm, Sweden, 4–15 December, 2023. Participants were recruited through the established and ongoing COMMUNITY HCW cohort study, where the participants are followed every four months since April 2020.[6–8] The current prevalence study encompassed self-administered naso-oropharyngeal/saliva swab sampling followed by RT-PCR for detection of SARS-CoV-2 infection in conjunction with the regular cohort follow-up in December 2023 (Supplementary Page 2 and Fig. S1). HCW who were unwell at home were not included. Prior to participation, all participants provided written informed consent, and the study was approved by the Swedish Ethical Review Authority (dnr 2020–01653).

A total of 635 participants opted to be included in the PCR screening study, of which 4 PCR analyses were invalid due to lack of signal in the internal control gene and were hence excluded from analyses. The RT-PCR screening thus included 631 HCW who were tested during their working hours in the hospital. The median age was 55 years (range 24–76 years), and the majority (88%) were women who had received three or four vaccine doses, and had at least one previously registered SARS-CoV-2 infection (Table S1 for demographics and prior immunizations). In total, 45 HCW out of 631 (7.1% [95% confidence interval (CI): 5.4–9.4%) tested positive for SARS-CoV-2 during the two week period (Fig. 1A and Table S2), with median cycle threshold value of 33.6 (Fig. 1B). Strikingly, almost half the participants 22/45 (49%) were asymptomatic and 23/45 (51%) reported only mild symptoms (Table S2). Notably, those who reported mild symptoms were well enough to attend work at the hospital. Whole genome sequencing revealed a variety of variants, dominated by JN.1 sublineages (Fig. 1C and Table S2). Four out of the 45 HCW testing positive had received the monovalent XBB.1.5-adapted booster (Table S2).

Taken together, our findings demonstrate a high prevalence of SARS-CoV-2 infection among HCW on duty in the hospital December 4–15, 2023, potentially escalating the transmission of SARS-CoV-2. Although an XBB.1.5 booster dose is unlikely to prevent infections, these findings indicate a high societal spread, emphasizing the importance of continued XBB.1.5 monovalent booster doses to vulnerable populations at risk of severe disease.

Contributors

KA, OB, UM, NGN, SH, JK, MÅ, KB, JJA, and CT conceived and designed the study. KA, OB, NGN, AR, DU, and FCN collected and analyzed the data. All authors interpreted the data.

KA wrote the first draft of the manuscript. All authors revised and edited the manuscript.

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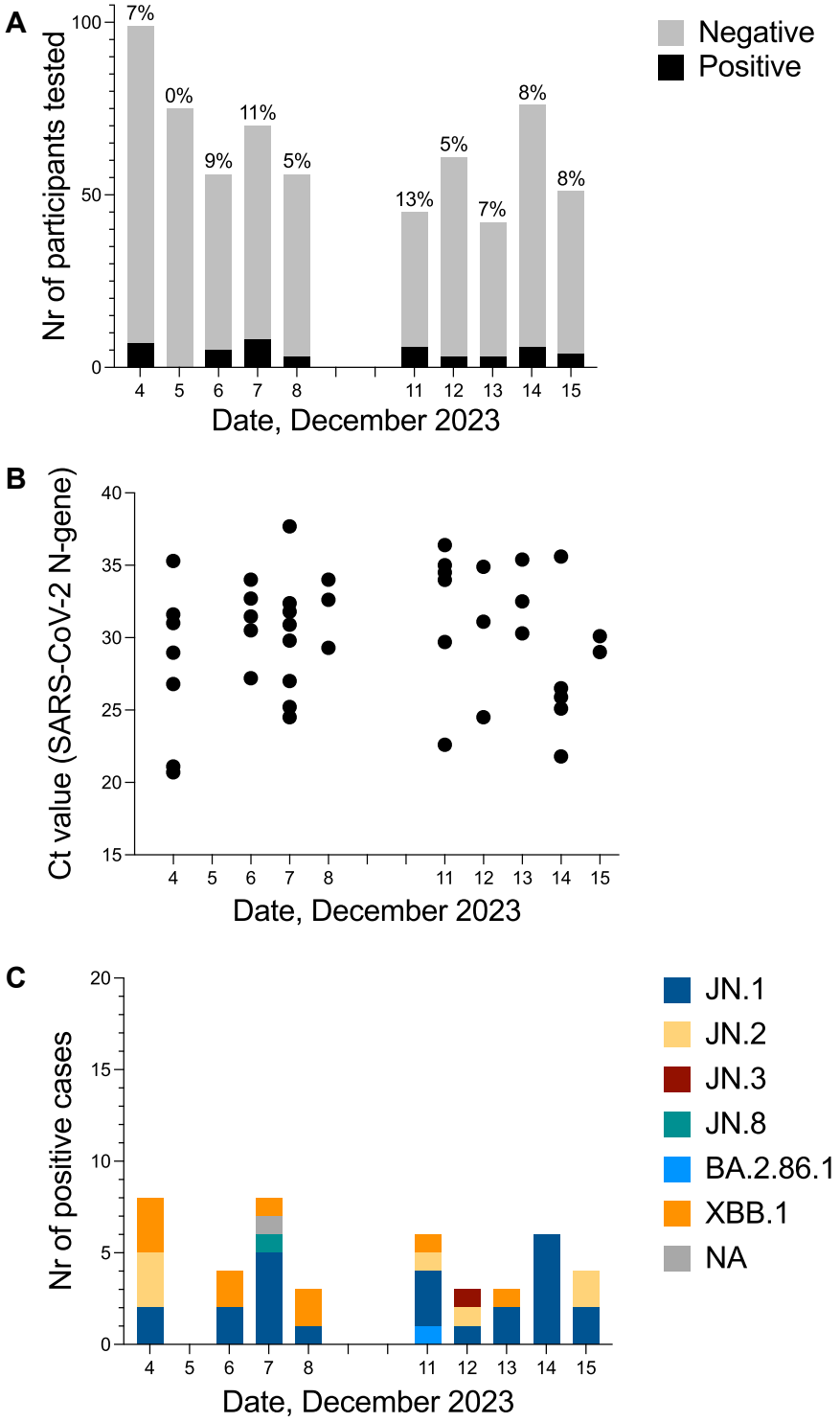

Fig. 1: **Prevalence, viral load, and viral variants among Swedish healthcare workers on duty in December 2023.** A) Percentage positive per day during December 4–15, 2023. Bars show total number of tested participants per day; grey = negative; black = positive. Numbers above bar depict percent positive. B) Individual Ct-values (SARS CoV-2 N-gene) for each positive sample as an indication of viral load. C) Viral variant identification by whole genome sequencing in each positive sample December 4–15, 2023. Bars show total number of diagnosed infections per day, and their individual variants JN.1, JN.2, JN.3, JN.8, BA.2.86.1 and XBB.1. Ct; Cyclic threshold, NA; Not available.

All authors reviewed and approved the final version of the manuscript.

Data sharing statement

Data sharing is regulated by the General Data Protection Regulation 2016/679, the Swedish Law on Biobanking and approved ethical permits. The data material in this study comprises personally identifiable and sensitive information that cannot be shared.

Declaration of interests

All authors declare no competing interests.

Appendix A. Supplementary data

Supplementary data related to this article can be found at https://doi.org/10.1016/j.lanepe.2024.100872.

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