THE BEST OF THE WEEK (17 apr – 23 apr 2023)

Dan-Yu Lin et al.

Durability of Bivalent Boosters against Omicron Subvariants

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Abstract

On September 1, 2022, the Moderna and Pfizer–BioNTech bivalent vaccines against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) containing equal amounts of spike messenger RNA from the ancestral and omicron BA.4–BA.5 subvariants replaced their monovalent counterparts as booster doses for persons who are 12 years of age or older in the United States. We previously reported surveillance data from North Carolina on the effectiveness of these two bivalent boosters against coronavirus disease 2019 (Covid-19) during the first 3 months after deployment (September 1 to December 8, 2022); the BA.4–BA.5 subvariants were predominant during the first 2.5 months of this period.1 Here, we present two additional months of data that were obtained during a period when the omicron BQ.1–BQ.1.1 and XBB–XBB.1.5 subvariants had become predominant to show the durability of protection conferred by these two bivalent boosters against a wider range of clinical outcomes than were included in our previous report.We considered four outcome measures: infection, severe infection resulting in hospitalization, severe infection resulting in hospitalization or death, and severe infection resulting in death. We fit the Cox regression model with a time-varying hazard ratio for severe infection and fit the proportional-rates model with a time-varying rate ratio for recurrent infection for each additional booster dose that was received (i.e., first booster vs. primary vaccination, second booster vs. first booster, or third booster vs. second booster); all measures were adjusted for the baseline characteristics shown in Table S1. We estimated the booster effectiveness on a particular day as 1 minus the hazard ratio or rate ratio on that day multiplied by 100%. The two types of bivalent boosters were associated with an additional reduction in the incidence of omicron infection among participants who had previously been vaccinated or boosted. Although the two bivalent vaccines were designed to target the BA.4–BA.5 subvariants, they were also associated with a lower risk of infection or severe infection with the BQ.1–BQ.1.1 and XBB–XBB.1.5 subvariants. The effectiveness was higher against hospitalization and death than against infection and waned gradually from its peak over time.

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Risk factors and vectors for SARS-CoV-2 household transmission: a prospective, longitudinal cohort study

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Abstract

Despite circumstantial evidence for aerosol and fomite spread of SARS-CoV-2, empirical data linking either pathway with transmission are scarce. Here we aimed to assess whether the presence of SARS-CoV-2 on frequently-touched surfaces and residents' hands was a predictor of SARS-CoV-2 household transmission.

Methods

In this longitudinal cohort study, during the pre-alpha (September to December, 2020) and alpha (B.1.1.7; December, 2020, to April, 2021) SARS-CoV-2 variant waves, we prospectively recruited contacts from households exposed to newly diagnosed COVID-19 primary cases, in London, UK. To maximally capture transmission events, contacts were recruited regardless of symptom status and serially tested for SARS-CoV-2 infection by RT-PCR on upper respiratory tract (URT) samples and, in a subcohort, by serial serology. Contacts' hands, primary cases' hands, and frequently-touched surface-samples from communal areas were tested for SARS-CoV-2 RNA. SARS-CoV-2 URT isolates from 25 primary case-contact pairs underwent whole-genome sequencing (WGS)

Findings

From Aug 1, 2020, until March 31, 2021, 620 contacts of PCR-confirmed SARS-CoV-2-infected primary cases were recruited. 414 household contacts (from 279 households) with available serial URT PCR results were analysed in the full household contacts' cohort, and of those, 134 contacts with available longitudinal serology data and not vaccinated pre-enrolment were analysed in the serology subcohort. Household infection rate was 28·4% (95% CI 20·8–37·5) for pre-alpha-exposed contacts and 51·8% (42·5–61·0) for alpha-exposed contacts (p=0·0047). Primary cases' URT RNA viral load did not correlate with transmission, but was associated with detection of SARS-CoV-2 RNA on their hands (p=0·031). SARS-CoV-2 detected on primary cases' hands, in turn, predicted contacts' risk of infection (adjusted relative risk [aRR]=1·70 [95% CI 1·24–2·31]), as did SARS-CoV-2 RNA presence on household surfaces (aRR=1·66 [1·09–2·55]) and contacts' hands (aRR=2·06 [1·57–2·69]). In six

contacts with an initial negative URT PCR result, hand-swab (n=3) and household surface-swab (n=3) PCR positivity preceded URT PCR positivity. WGS corroborated household transmission.

Interpretation

Presence of SARS-CoV-2 RNA on primary cases' and contacts' hands and on frequently-touched household surfaces associates with transmission, identifying these as potential vectors for spread in households.