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Title

Factors associated with transmission across three waves of SARS-COV-2 in a community-based study of households with children

Priority 1 (Research Category)

COVID-19

Presenters

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Abstract

Context: Household transmission of SARS-CoV-2 is a driver of the ongoing COVID-19 pandemic. Understanding factors that contribute to secondary infection rates (SIR) can define changing trends and inform public health policies. Objective: We analyzed data from a prospective, community-based, and laboratory-supported household transmission study to determine how SIR changed over 18 months and three waves of SARS-CoV-2 variants, and which household factors may have been associated with SIR. Study Design and Analysis: The OREGON CHild Absenteeism due to Respiratory Disease Study (ORCHARDS) is a longitudinal, laboratory-supported, school-based, ARI surveillance study designed to monitor respiratory virus activity in K-12 grade schools. Setting: Oregon School District, Dane County, Wisconsin, USA, between October 28, 2020, and May 16, 2022. Population Studied: Households with students who had ≥ 2 respiratory symptoms were eligible and opted to participate in ORCHARDS. Intervention/Instrument: All household members provided self-collected nasal specimens on days 0, 7, and 14 for SARS-CoV-2 detection using RT-PCR. Variant was ascertained through whole genome sequencing. We used logistic regression to investigate individual- and household-level characteristics associated with SARS-CoV-2 transmission. Outcome Measures: Estimated SIR for each variant. Results: Overall, 127 households comprising 572 individuals (48% female; 52% male; 77% >18 years) had at least one detection of SARS-CoV-2. The overall SIR was 47% and decreased over time (pre-Delta=72% [95%CI: 58%-83%]; Delta=51% [40%-63%]; and Omicron=41% [36%-47%]). Odds of household transmission were 63% lower during the Omicron period compared to the pre-Delta period (OR=0.36 [95%CI: 0.13-0.94] P=0.037). Greater household density (members/bedroom) was significantly associated with household transmission during the Omicron period (OR=6.8, [2.19-21.37] P=0.001). Index case age, illness severity, and individual symptoms were not significantly associated with household transmission. Eliminating households with discordant strains (n=13) of SARS-CoV-2 modestly reduced overall SIR (47 to 43%).

Conclusion: Greater household density was associated with higher risk of SARS-CoV-2 transmission, but the risk declined over time with subsequent variants. Interplay between variants, prior infection, and individual/household factors may identify modifiable factors (e.g., behavior, vaccination) to reduce future transmission risk.

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