Latino Household Transmission of SARS-CoV-2

Diego A. Martinez, PhD[1], Eili Y. Klein, PhD[1], Cassandra Parent[2], Diana Prieto, PhD[3], Benjamin F. Bigelow, BS[4], Ronald E. Saxton, MSPH[4], Kathleen R. Page[4]

[1] Department of Emergency Medicine, Johns Hopkins University School of Medicine, Baltimore, MD

[2] Department of Biomedical Engineering, Johns Hopkins University Whiting School of Engineering, Baltimore, MD

[3] School of Industrial Engineering, Pontificia Universidad Católica de Valparaíso, Chile

[4] Department of Medicine, Johns Hopkins University School of Medicine, Baltimore, MD

Corresponding: Diego A. Martinez, PhD

Department of Emergency Medicine, Johns Hopkins University School of Medicine, Baltimore, MD

5801 Smith Ave, Davis Bldg Ste 220, Baltimore MD 21209

dmart101@jhmi.edu

Abstract

We assessed temporal changes in the household secondary attack rate of SARS-CoV-2 and identified risk factors for transmission in vulnerable Latino households of Baltimore, Maryland. The household SAR was 45.8%, and it appeared to increase as the alpha variant spread, highlighting the magnified risk of spread in unvaccinated populations.

Keywords: COVID-19; SARS-CoV-2; disparity; household; transmission

Introduction

The coronavirus disease 2019 (COVID-19) pandemic has disproportionately affected Latinos in the US with increased infection, hospitalization, and mortality rates.[1] Greater housing density is one of the primary hypotheses suggested for this disparity.[2] However, limited data exist on household transmission rates among Latinos in the US, and none since the emergence of the alpha variant (B.1.1.7).[3,4] Latinos of Baltimore, in particular, are the fastest-growing ethnic group and account for 5.5% of the population. They also are more likely to be foreign-born and undocumented and to have a lower income, lower educational attainment, lower insurance coverage, and lower English proficiency when compared with the general Latino population of the US.[5,6] Recent studies have shown a high prevalence of COVID-19 in this community.[7,8] We assessed temporal changes in the household secondary attack rate (SAR) and identified risk factors for transmission in vulnerable Latino households of Baltimore, Maryland.

Methods

Samples and patient characteristics were collected at free, community-based Latino testing events in Baltimore, Maryland, between June 11, 2020, and May 20, 2021. Patients and their household members were encouraged to return to the same care centers for testing, and active case follow-up was used to ascertain subsequent diagnoses in a household. Samples were tested using the reverse transcriptase-polymerase chain reaction (RT-PCR) test for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Primary and secondary household cases were identified as a positive SARS-CoV-2 RT-PCR test, with secondary cases testing positive within 14 days after exposure to a primary case. Ambiguities in a household primary case were resolved through random imputation. That is, if two or more individuals in a household tested positive at the same time, where any infectee who could have been infected by multiple individuals was randomly assigned one as their actual infector. The at-risk cohort was identified as all individuals living in the address of a primary case. The SAR was calculated as the percentage of at-risk individuals who were later confirmed to have SARS-CoV-2 infection. 2018 CDC US social vulnerability index data at the census tract-level was linked to the household address of every patient.

Segmented regression analysis was used to estimate changes in SAR over time. ANOVA was used to compare trends in SAR and testing volume over time. Mixed-effects logistic regression modeling was used to calculate the adjusted infection risk, accounting for clustering of exposed subjects within households. All analyses were performed with R version 4.0.2. The Johns Hopkins Institutional Review Board approved this study.

Results

A total of 277 primary COVID-19 cases were identified and linked to 638 additional at-risk individuals. At-risk individuals consisted of 594 (93.1%) Latinos who resided in 2-9 people households. Their mean (SD) age was 29.8 (18.3), and 50 (7.8%) were 60+ years old. Among them, 292 patients were subsequently diagnosed with COVID-19, resulting in an overall household SAR of 45.8%. The average time to diagnosis from the date of the primary case was 1.98 days.

The spread of B.1.1.7, which first appeared in Maryland in January 2021, significantly changed the SAR rate over time (slope) from basically flat (0.2%) to increasing at 2.3% per week (*P* < .001; Figure 1A). Fluctuations in testing volume overtime did not correlate with SAR (*P* = .298; Figure 1B).

Independent factors significantly associated with higher household transmission risk included residing in neighborhoods of higher socioeconomic vulnerability (adjusted odds ratio (adj. OR) for those living in the poorest areas, 1.87; 95% confidence interval (CI), 0.94-3.71; *P* = .0741) and denser housing (adj. OR for those living in 4-people households, 2.06; 95% CI, 0.99-4.29; *P* = .0525).

Discussion

At Latino testing events in Baltimore, the household SAR of SARS-CoV-2 was 45.8%, corresponding to some of the highest rates reported early in the COVID-19 pandemic.[3,4] The SAR appeared to increase in the Latino community as the alpha variant spread, consistent with its noted higher transmissibility.[9] The rising SAR, which occurred before vaccination was widespread, highlights the magnified risk of spread in unvaccinated populations; Latinos remain 30% less likely to be vaccinated against COVID-19 than non-Latino whites.[10]

While testing inclusion criteria were standardized across sites and over time, differential awareness of testing events, an inability to identify and test every potential household contact, and rule out common infections may contribute to bias in SAR estimation. That is, some of the coded secondary cases might have been exposed at the same time as the primary case, and not infected within the household. The high community transmission documented in Baltimore suggests that exposure to SARS-CoV-2 could have occurred elsewhere.[7,8]

Nonetheless, the highest risk for transmission remains in home contacts. We believe our community-led testing approach provided a unique opportunity for risk estimation of a vulnerable population and suggests that Latino household SARS-CoV-2 transmission is a major driver of COVID-19 disparities.

Article Information: Dr. Martinez had full access to the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

Concept and design: Martinez, Klein, Parent, Prieto, Page.

Acquisition, analysis, or interpretation of data: Martinez, Klein, Parent, Prieto, Saxton, Page.

Drafting of the manuscript: Martinez, Klein, Prieto, Page.

Critical revision of the manuscript for important intellectual content: All authors.

Statistical analysis: Martinez, Klein, Parent, Prieto.

Obtained funding: Martinez, Page.

Administrative, technical, or material support: Bigelow, Page.

Supervision: Klein, Page.

Conflict of Interest Disclosures: Martinez, Page, and Parent reported receiving grants from the National Institutes of Health (NIH RADx-UP R01 DA045556-04S1) (NIH funding to expand testing in underserved communities) and personal fees from the Johns Hopkins Health System during the conduct of the study. Klein reported receiving grants from the Centers for Disease Control and Prevention (5U01CK000536-03) during the conduct of the study. No other disclosures were reported.

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Figure 1. SARS-CoV-2 Secondary Attack Rate (SAR) Among 638 Exposed Household Members in Baltimore, Maryland, June 11, 2020, and May 20, 2021. Abbreviations: SARS-CoV-2, severe acute respiratory syndrome coronavirus 2. Panel A: Bi-weekly secondary attack rate as points, estimated linear trends (pre-B.1.1.7 in blue and post-B.1.1.7 in red) and 95% confidence intervals (light grey shading). Statistically significant differences (*P* < .001) during the pre and post emergence of B.1.1.7 were evaluated across time periods with segmented regression analysis, including generalized linear models with logit link and linear splines for changes in trend and level pre (blue dots) and post (red dots) the emergence of B.1.1.7 in January 2021. Panel B: Bi-weekly number of samples tested stratified by SARS-CoV-2 test result. Abbreviations: SAR, secondary attack rate; No., number.

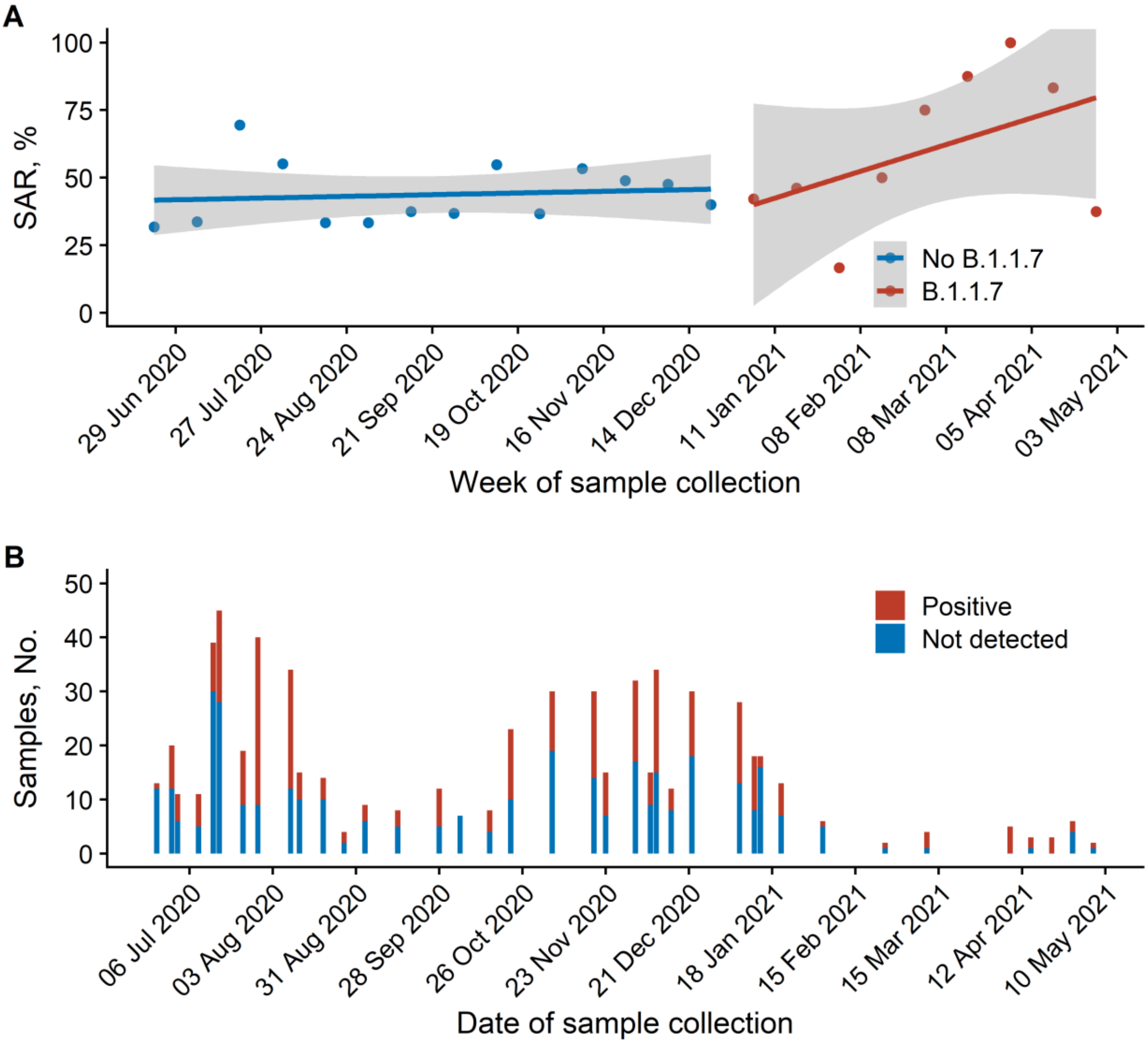
Table 1. COVID-19 Infection Risk Factors Among 638 Exposed Household Members in Baltimore, Maryland, June 11, 2020, and May 20, 2021.

Characteristic	N (%)	Adjusted OR[a] (95% CI)	*P* value
Age group			
≤18	212	1 (Reference)	
19-29	105	0.92 (0.49-1.74)	0.7778
30-49	232	1.04 (0.64-1.69)	0.8644
≥50	89	0.42 (0.20-0.87)	0.0206
Household size, members			
2-3	260	1 (Reference)	
4	116	2.06 (0.99-4.29)	0.0525
≥5	262	1.04 (0.57-1.89)	0.9018
Neighborhood socioeconomic status			
Least poor	151	1 (Reference)	
Poor	148	1.86 (0.84-4.11)	0.1252
Very Poor	112	2.90 (1.30-6.47)	0.0094
Poorest	227	1.87 (0.94-3.71)	0.0741

Abbreviations: SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; OR, odds ratio; CI, confidence interval.

[a] Results are from mixed-effects logistic regression adjusted for the exposed individual´s age, household size, and neighborhood socioeconomic status, with the household address as a crossed random effect (Variance 1.561, Std Dev 1.249).

Figure 1


A
SAR, %
100
75
50
25
0
No B.1.1.7
B.1.1.7
29 Jun 2020
27 Jul 2020
24 Aug 2020
21 Sep 2020
19 Oct 2020
16 Nov 2020
14 Dec 2020
11 Jan 2021
08 Feb 2021
08 Mar 2021
05 Apr 2021
03 May 2021
Week of sample collection
B
Samples, No.
50
40
30
20
10
0
Positive
Not detected
06 Jul 2020
03 Aug 2020
31 Aug 2020
28 Sep 2020
26 Oct 2020
23 Nov 2020
21 Dec 2020
18 Jan 2021
15 Feb 2021
15 Mar 2021
12 Apr 2021
10 May 2021
Date of sample collection