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Authors

Donnelly, Marisa
Chuey, Meagan
Soto, Raymond
et al.

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Household Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Alpha Variant—United States, 2021

Marisa A. P. Donnelly,[1,2,3,a] Meagan R. Chuey,[1,2,4,a] Raymond Soto,[1,2,a] Noah G. Schwartz,[1,2] Victoria T. Chu,[1,2] Stacey L. Konkle,[1,2] Sadia Sleweon,[1] Jasmine Ruffin,[1] Dana L. Haberling,[1] Sarah Anne J. Guagliardo,[1] Robyn A. Stoddard,[1] Raydel D. Anderson,[1] Clint N. Morgan,[1] Rebecca Rossetti,[1] David W. McCormick,[1,2] Reed Magleby,[1,2] Sarah W. Sheldon,[1] Elizabeth A. Dietrich,[1] Anna Uehara,[1] Adam C. Retchless,[1] Suxiang Tong,[1] Jennifer M. Folster,[1] Jan Drobeniuc,[4] Marla E. Petway,[1] Brett Austin,[4] Sarah Stous,[4] Eric McDonald,[4] Seema Jain,[3] Meghan M. Hudziec,[5] Ginger Stringer,[5] Bernadette A. Albanese,[6] Sarah E. Totten,[5] J. Erin Staples,[1] Marie E. Killerby,[1] Laura Hughes,[1] Almea Matanock,[1] Mark Beatty,[4] Jacqueline E. Tate,[1] Hannah L. Kirking,[1] and Christopher H. Hsu[1]; for the COVID-19 Household Transmission Team[b]

[1]CDC COVID-19 Response, Centers for Disease Control and Prevention, Atlanta, Georgia, USA; [2]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, Georgia, USA; [3]California Department of Public Health, Richmond, California, USA; [4]County of San Diego Health and Human Services, San Diego, California, USA; [5]Colorado Department of Public Health and Environment, Denver, Colorado, USA; and [6]Tri-County Health Department, Westminster, Colorado, USA

Background. In Spring 2021, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) B.1.1.7 (Alpha) became the predominant variant in the United States. Research suggests that Alpha has increased transmissibility compared with non-Alpha lineages. We estimated household secondary infection risk (SIR), assessed characteristics associated with transmission, and compared symptoms of persons with Alpha and non-Alpha infections.

Methods. We followed households with SARS-CoV-2 infection for 2 weeks in San Diego County and metropolitan Denver, January to April 2021. We collected epidemiologic information and biospecimens for serology, reverse transcription–polymerase chain reaction (RT-PCR), and whole-genome sequencing. We stratified SIR and symptoms by lineage and identified characteristics associated with transmission using generalized estimating equations.

Results. We investigated 127 households with 322 household contacts; 72 households (56.7%) had member(s) with secondary infections. SIRs were not significantly higher for Alpha (61.0% [95% confidence interval, 52.4–69.0%]) than non-Alpha (55.6% [44.7–65.9%], $P = .49$). In households with Alpha, persons who identified as Asian or Hispanic/Latino had significantly higher SIRs than those who identified as White ($P = .01$ and .03, respectively). Close contact (eg, kissing, hugging) with primary cases was associated with increased transmission for all lineages. Persons with Alpha infection were more likely to report constitutional symptoms than persons with non-Alpha (86.9% vs 76.8%, $P = .05$).

Conclusions. Household SIRs were similar for Alpha and non-Alpha. Comparable SIRs may be due to saturation of transmission risk in households due to extensive close contact, or true lack of difference in transmission rates. Avoiding close contact within households may reduce SARS-CoV-2 transmission for all lineages among household members.

Keywords. SARS-CoV-2; COVID-19; Alpha; household; transmission.

In December 2020, the Alpha lineage of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus (a variant of concern [VOC], also known as B.1.1.7) was first detected in California and Colorado. By late April 2021, Alpha became the predominant circulating lineage in all regions of the United States [1]. Surveillance and modeling suggested that Alpha had increased transmissibility in community settings compared with non-Alpha lineages circulating at that time [2–4]. Understanding transmission dynamics for SARS-CoV-2 variants and factors that influence transmission is critical to informing prevention measures and lowering infection risk. Estimates of SARS-CoV-2 secondary infection risk (SIR) in households range from 22% to 63%, but the SIR of Alpha in households in the United States has not been measured [5–10]. Despite the decreasing circulation rate of Alpha and dominance of Delta and Omicron, understanding household transmission of SARS-CoV-2 VOCs may inform future SARS-CoV-2 preventive measures. Here we estimate the household SIR, describe characteristics associated with transmission and infection, and compare symptom profiles of persons infected with Alpha and non-Alpha lineage viruses.

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[a]M. A. P. D., M. R. C., and R. S. contributed equally.

[b]COVID-19 Household Transmission Team members are listed in the Notes.

Correspondence: M. A.P. Donnelly, Centers for Disease Control and Prevention, 850 Marina Bay Parkway, Richmond, CA, USA (marisa.donnelly@cdph.ca.gov).

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METHODS

Household Enrollment

The US Centers for Disease Control and Prevention (CDC) partnered with state and local public health departments in San Diego County, California, and metropolitan Denver (Adams, Arapahoe, and Douglas Counties), Colorado, to recruit households. Households were enrolled from 27 January–1 April 2021, in San Diego, and 22 March–16 April 2021, in metropolitan Denver. Public health agencies reported the first person in a household with a positive SARS-CoV-2 reverse transcription–polymerase chain reaction (RT-PCR) specimen (index case) to the CDC investigation team.

The CDC investigators contacted select households to evaluate eligibility and identify the likely household primary case, defined as the person within the household who had the earliest illness onset. Full details on household selection are in the Supplementary Appendix. Illness onset was defined as symptom onset date or, if asymptomatic, collection date of initial positive SARS-CoV-2 RT-PCR test. Infectious period was defined as 2 days before through 10 days after the illness onset date [11].

Households were eligible if the index case had an illness onset 10 or fewer days prior to enrollment, was not currently hospitalized, had at least 1 household contact, and was not living in a congregate setting. A household contact was defined as a person who spent 1 or more night in the household during the index case's infectious period. All household members who met inclusion criteria were eligible for participation.

Household Visits

The CDC investigators visited households at enrollment (day 0 [D0]) and at closeout (day 14 [D14]). At D0 and D14, enrolled household members ("participants") had blood collected for serology and nasopharyngeal (NP) swabs collected for RT-PCR. At D0 and D14, participants completed individual questionnaires assessing demographics, medical history including SARS-CoV-2 vaccination history, SARS-CoV-2 exposures, and symptoms. Each household completed a questionnaire assessing household physical characteristics and preventive behaviors at D0. Participants were asked to complete daily symptom diaries during the 2-week follow-up. If a participant developed new symptoms, they contacted the investigation team, and an interim visit was conducted where an NP swab was collected from all household participants (Supplementary Appendix).

Laboratory Testing

RT-PCR testing of NP swabs for SARS-CoV-2 was performed by the Colorado Department of Public Health and Environment (CDPHE) Laboratory using the TaqPath COVID-19 Combo Kit (ThermoFisher Scientific) and the San Diego County Public Health Laboratories (SD PHL) using the New Coronavirus Nucleic Acid Detection Kit (PerkinElmer). Serum was tested for the presence of SARS-CoV-2–specific antibodies at CDC using the VITROS Immunodiagnostic Products Anti-SARS-CoV-2 IgG Reagent Pack (Ortho-Clinical Diagnostics) or xMAP SARS-CoV-2 Multi-Antigen IgG Assay (Luminex) or at the SD PHL using the Alinity i SARS-CoV-2 IgG test (Abbott).

Nasopharyngeal specimens with an RT-PCR cycle threshold (Ct) value of less than 35 were selected for whole-genome sequencing (WGS). For San Diego specimens, sequencing was performed at the CDC as previously described [12]. Sequencing for Colorado specimens was performed locally at the CDPHE as previously described [13].

Household Case Classification

Primary and secondary case classifications were assigned post-investigation using available biospecimen and epidemiological data. Primary cases were defined as individuals in the household with a positive RT-PCR result and the earliest illness onset. The primary patient differed from the index patient if we confirmed SARS-CoV-2 infection in a person with an illness-onset date that was earlier than that of the index patient. Secondary cases were nonprimary household contacts who had a positive RT-PCR for SARS-CoV-2 or seroconverted during the investigation period without history of vaccination or previous infection less than 90 days prior to enrollment. Households were classified by the lineage of the primary case or, if sequencing results were unavailable for the primary case, lineage was assigned based on available household secondary case lineage. Households were excluded from analysis if the primary case could not be determined because multiple persons in a household had illness onset within 24 hours of each other (ie, co–primary infections), if the primary case had an illness onset more than 10 days prior to enrollment, or if all household contacts were lost to follow-up or withdrew.

Analysis

The RT-PCR Ct values for the N gene were plotted against the number of days between illness onset and NP swab collection date. The Phylogenetic Assignment of Named Global Outbreak Lineages (PANGOLIN) was used to assign SARS-CoV-2 lineages to sequenced genomes [14] (Supplementary Appendix). Demographic and household characteristics of primary cases and household contacts were described and compared by virus lineage (Alpha or non-Alpha). Phylogenetic relations between SARS-CoV-2 sequences within households were inferred using maximum likelihood analyses implemented in TreeTime using the Nextstrain pipeline [15].

Secondary Infection Risk

Secondary infection risks were calculated by dividing the number of secondary cases by the total number of household contacts. SIRs were calculated for all enrolled households ("overall SIR") and stratified by lineage group, individual and household characteristics, and vaccination status or history of

previous SARS-CoV-2 infection. Vaccination status definitions are provided in the Supplementary Appendix. Households where no sequencing data were obtained from any member were included in overall SIR estimations but excluded from lineage-specific SIR estimations. Serial intervals for secondary transmission were estimated as the median number of days between illness onset of the primary case and illness onset of secondary cases. Pearson's chi-square tests, Fisher's exact tests, and Wilson score intervals with 2-sided *P* values and 95% confidence intervals (CIs) were used to assess differences in proportions.

Risk Factor Analysis

To identify risk factors for secondary infection, we modeled the relationship between characteristics and individual odds of infection of household contacts by calculating adjusted odds ratios (ORs) using generalized estimating equations (GEEs) [16]. We built 2 models for each characteristic (1 for Alpha and 1 for non-Alpha) and adjusted ORs for age, sex, history of previous infection, and vaccination status of household contacts. An exchangeable correlation structure was used in GEE models to account for within-household correlation. Because characteristics of interest were selected a priori, and to minimize type II error, we did not adjust *P* values for multiple comparisons. Characteristics of primary cases, household contacts, and households were examined as potential risk factors for infection of household contacts. Symptom profiles of primary and secondary cases were described and stratified by household lineage group (Supplementary Appendix). For analyses involving race and ethnicity, we used 5 groups: persons who identified as Hispanic/Latino, White, Black, Asian, and "Other," which included anything other than previously stated. All modeling was conducted using the *geepack* package in R version 4.0.3 [17–19].

Ethical Considerations

This activity was reviewed by the CDC and was conducted consistent with applicable federal law and CDC policy [CDC ethics policy: see, eg, 45 CFR part 46, 21 CFR part 56; 42 USC §241(d); 5 USC §552a; 44 USC §3501 et seq].

RESULTS

Participant Characteristics and SARS-CoV-2 Lineage

We enrolled 127 households with 127 primary cases and 322 household contacts who met the inclusion criteria (Figure 1). Median time interval from primary case symptom onset to initial household visit for enrollment was 6 days (range, 2–10 days) (Supplementary Figure 1). Of the 322 household contacts, 146 became secondary cases, resulting in 273 primary and secondary cases (Table 1). One household contact never had a positive NP swab and did not give a D0 serology specimen but had a positive D14 serology specimen with new symptom onset consistent with SARS-CoV-2 within the investigation period and was therefore considered a secondary case.

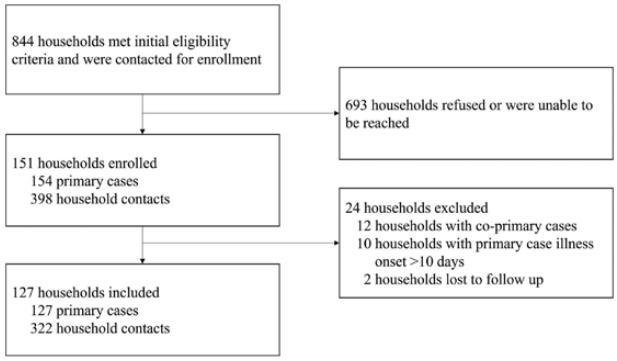

Figure 1. Household recruitment, enrollment, and exclusion. Enrollment of households for the investigation began with individuals being reported to public health with a positive SARS-CoV-2 RT-PCR test. Initial eligibility criteria for households included a positive SARS-CoV-2 test ≤10 days prior to contact for the first reported case in a household (index case). After enrollment was complete, 151 households agreed to the investigation. Following completion of the investigation, 24 households were excluded from analyses. Of excluded households, 12 households had co–primary cases, 10 households had a primary case with an illness onset date >10 days, and 2 households were lost to follow-up. Abbreviations: RT-PCR, reverse transcription–polymerase chain reaction; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

Two primary cases (1.6%) and 1 secondary case (0.7%) reported previous SARS-CoV-2 infections (Table 1). Eight primary cases (6.3%) were partially or fully vaccinated (Supplementary Table 1). Forty-seven household contacts (14.6%) were partially or fully vaccinated (Table 1). Fewer secondary cases were partially or fully vaccinated compared with uninfected contacts (9 [6.2%] vs 38 [21.6%]) (Table 1).

Overall, 104 (81.9%) households had a lineage assigned from primary case samples, 6 (4.7%) from secondary case samples, and 17 (13.4%) had no lineage assigned (Supplementary Tables 2 and 3). We identified no households with multiple lineages of SARS-CoV-2 among household members. Within households, sequenced viral isolates had a range of 0 to 5 single nucleotide polymorphisms (SNPs), while 132 (67%) of 197 comparisons had no SNPs (Supplementary Figure 2). Reference viral genomes from sequenced samples are provided in Supplementary Table 4. No significant differences were seen in the distribution of Ct values over time from illness onset between Alpha and non-Alpha lineages (Supplementary Figure 3). Household characteristics were comparable between Alpha and non-Alpha households and both groups had a median of 4 people per household (range, 2–10) (Supplementary Table 5).

Symptoms and Clinical Course of Illness

Most primary and secondary cases reported symptoms associated with their illness, regardless of lineage (254, 93.0%). Overall, Alpha cases were more likely to report constitutional symptoms than were non-Alpha cases (86.9% vs 76.8%, $P = .05$) (Table 2). Children (<18 years) with Alpha infections were more likely to report constitutional (78.0% vs 53.1%, $P = .018$) and lower respiratory symptoms (69.5% vs 46.9%, $P = .04$) than

Table 1. Demographic and Clinical Characteristics of Enrolled Primary Cases, Secondary Cases, and Uninfected Household Contacts

		Household Contacts, n (%)			
	Primary Cases (N = 127), n (%)	Total Household Contacts (N = 322)	Secondary Cases (n = 146)	Uninfected Contacts (n = 176)	Fisher's Exact Test *P* Values
Age (years)					
<5	6 (4.7)	18 (5.6)	9 (6.2)	9 (5.1)	.13
5–11	8 (6.3)	46 (14.3)	25 (17.1)	21 (11.9)	
12–17	22 (17.3)	57 (17.7)	27 (18.5)	30 (17.0)	
18–49	69 (54.3)	148 (46.0)	69 (47.3)	79 (44.9)	
50–64	19 (15.0)	36 (11.2)	13 (8.9)	23 (13.1)	
≥65	3 (2.4)	17 (5.3)	3 (2.1)	14 (8.0)	
Sex					
Female	63 (49.6)	168 (52.2)	76 (52.1)	92 (52.3)	1
Male	64 (50.4)	154 (47.8)	70 (47.9)	84 (47.7)	
Race/ethnicity					
Hispanic or Latino	30 (23.6)	71 (22.1)	42 (28.8)	29 (16.5)	.02[a]
Non-Hispanic White	75 (59.1)	185 (57.5)	76 (52.1)	109 (61.9)	
Black	3 (2.4)	13 (4.0)	6 (4.1)	7 (4.0)	
Asian	6 (4.7)	28 (8.7)	12 (8.2)	16 (9.1)	
Native Hawaiian or Pacific Islander	1 (0.8)	4 (1.2)	2 (1.4)	2 (1.1)	
American Indian or Alaska Native	0 (0.0)	4 (1.2)	4 (2.7)	0 (0.0)	
Multiracial/Other	12 (9.4)	16 (5.0)	4 (2.7)	12 (6.8)	
Unknown[b]	0 (0)	1 (0.3)	0 (0)	1 (0.6)	
Medical conditions					
Chronic lung disease	11 (8.7)	38 (11.8)	17 (11.6)	21 (11.9)	1
Cardiovascular disease	7 (5.5)	13 (4.0)	4 (2.7)	9 (5.1)	.40
Diabetes mellitus	5 (3.9)	14 (4.3)	7 (4.8)	7 (4.0)	.79
Chronic renal disease	2 (1.6)	3 (0.9)	3 (2.1)	0 (0.0)	.09
Chronic liver disease	0 (0.0)	3 (0.9)	0 (0.0)	3 (1.7)	.25
Any immunocompromising condition	8 (6.3)	7 (2.2)	2 (1.4)	5 (2.8)	.46
Hypertension	10 (7.9)	32 (9.9)	10 (6.8)	22 (12.5)	.10
Hyperlipidemia	4 (3.1)	13 (4.0)	6 (4.1)	7 (4.0)	1
Hypothyroid disease	5 (3.9)	11 (3.4)	5 (3.4)	6 (3.4)	1
Any other chronic disease	18 (14.2)	42 (13.0)	19 (13.0)	23 (13.1)	1
No medical conditions	82 (64.6)	200 (62.1)	95 (65.1)	105 (59.7)	.36
Smoking status[c]					
Current daily smoker	7 (5.5)	10 (3.1)	5 (3.4)	5 (2.8)	.37
Current some-days smoker	0 (0.0)	4 (1.2)	0 (0.0)	4 (2.3)	
Former smoker	18 (14.2)	23 (7.1)	10 (6.8)	13 (7.4)	
Never smoker	101 (79.5)	267 (82.9)	122 (83.6)	145 (82.4)	
Unknown	1 (0.8)	18 (5.6)	9 (6.2)	9 (5.1)	
Pregnant	2 (1.6)	1 (0.3)	0 (0.0)	1 (0.6)	1
Previous SARS-CoV-2 infection[d]					
Yes	2 (1.6)	7 (2.2)	1 (0.7)	6 (3.4)	.13
Participant's vaccination status[e]					
Not vaccinated	108 (85.0)	257 (79.8)	129 (88.4)	128 (72.7)	.001[a]
Recently vaccinated	11 (8.7)	18 (5.6)	8 (5.5)	10 (5.7)	
Partially vaccinated	5 (3.9)	21 (6.5)	3 (2.1)	18 (10.2)	
Fully vaccinated	3 (2.4)	26 (8.1)	6 (4.1)	20 (11.4)	
Genomic lineage					
B.1.1.7 (Alpha)	64 (50.4)	80 (24.8)	80 (54.8)	0 (0)	…
B.1.427	11 (8.7)	13 (4.0)	13 (8.9)	0 (0)	
B.1.429	5 (3.9)	5 (1.6)	5 (3.4)	0 (0)	
P.1	3 (2.4)	8 (2.5)	8 (5.5)	0 (0)	
Other	23 (18.1)	18 (5.6)	18 (12.3)	0 (0)	
Not able to be sequenced	21 (16.5)	21 (6.5)	21 (14.4)	0 (0)	

Table 1. Continued

	Primary Cases (N = 127), n (%)	Household Contacts, n (%)			Fisher's Exact Test *P* Values
		Total Household Contacts (N = 322)	Secondary Cases (n = 146)	Uninfected Contacts (n = 176)	
Enrollment site					
San Diego County, CA	58 (45.7)	130 (40.4)	67 (45.9)	63 (35.8)	.07
Metropolitan Denver, CO	69 (54.3)	192 (59.6)	79 (54.1)	113 (64.2)	

P values are from Fisher's exact tests and compare differences between distributions of secondary cases and uninfected contacts. Abbreviations: RT-PCR, reverse transcription–polymerase chain reaction; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

[a]*P* values ≤.05 indicate statistical significance.

[b]One uninfected household contact was missing race and ethnicity data.

[c]One primary case, 9 secondary cases, and 9 uninfected household contacts were missing data on smoking history.

[d]Previous SARS-CoV-2 infection defined as a previous positive RT-PCR or rapid test result prior to enrollment and at least 2 weeks before symptom onset in the primary case.

[e]Vaccination status for all household participants determined at the point of illness onset of primary case. Not vaccinated included individuals who had no history of ever receiving a SARS-CoV-2 vaccine. The recently vaccinated group includes only individuals who were vaccinated within the 2 weeks prior to the illness onset date of the household primary case, regardless of the type of vaccine. The partially vaccinated group includes individuals who were vaccinated at least 2 weeks prior to the illness onset date of the primary case but were not yet 2 weeks past the second dose of a 2-dose vaccine, or 2 weeks past the first dose of a 1-dose vaccine. The fully vaccinated group includes individuals who were at least 2 weeks past the second dose of a 2-dose vaccine, or 2 weeks past the first dose of a single-dose vaccine on the illness onset date of the primary case.

were children with non-Alpha infections (Table 2). Healthcare-seeking behavior was similar for Alpha and non-Alpha cases (17.5% vs 12.6%, $P = .37$) (Table 2); no participants died.

Secondary Infection Risk

Seventy-two households (56.7%) had at least 1 secondary case of SARS-CoV-2. The SIR for all household contacts (vaccinated and unvaccinated) was 45.3% (95% CI: 39.8–51.0%) (Supplementary Figure 4). The overall SIR for the unvaccinated group with no previous SARS-CoV-2 infection was 52.3% (95% CI: 46.1–58.4%) (Figure 2A). The SIR for the unvaccinated group with no previous SARS-CoV-2 infection with Alpha was 61.0% (95% CI: 52.4–69.0%), which was slightly higher but not significantly different from the unvaccinated group with no previous SARS-CoV-2 infection with the non-Alpha group (SIR, 55.6%; 95% CI: 44.7–65.9%) (Figure 2A, Supplementary Table 7). The highest SIRs observed for any subgroup were among persons who were Asian, with 91.7% (95% CI: 59.8–99.6%) of household contacts becoming infected in Alpha households and 0% (95% CI: 0–94.5%) in non-Alpha households (Figure 2D). For Alpha households, persons who identified as Asian or Hispanic/Latino had significantly higher SIRs than persons who identified as White (*P* values = .01 and .03, respectively) (Figure 2D).

There were no significant differences in SIRs between households with a child primary case compared with an adult primary case (Figure 2B). Household contacts who were partially (14.3%; 95% CI: 3.8–37.4%) or fully (23.1%; 95% CI: 9.8–44.1%) vaccinated or reported a previous infection (16.7%; 95% CI: .9–63.5%) had a lower overall SIR than household contacts who were unvaccinated and had no previous infection (52.3%; 95% CI: 46.1–58.4%) (Supplementary Figure 4). Sample sizes were too small to calculate SIRs for specific vaccine types (ie, Pfizer, Moderna, and Johnson & Johnson). The SIRs were not significantly different between Alpha and non-Alpha household contacts when stratifying by primary case symptom profiles (Supplementary Figure 5). The median interval between illness onset of symptomatic primary cases and symptomatic secondary cases was 3 days for Alpha (range, 0–23 days) and 4 days for non-Alpha (range, 0–20 days) (Supplementary Figure 6).

Risk Factors for Transmission

Sharing a bed was significantly associated with increased odds of secondary infection in both lineage groups. Intimate physical touch, sharing objects, sharing a bedroom, sharing a bathroom, riding in a car without a mask, and eating food prepared by the primary case were associated with a significantly increased odds of Alpha infection, while other, nonintimate direct contact was associated with a significantly increased odds of non-Alpha infection (Table 3, Supplementary Table 6). Contacts who reported using ventilation (air conditioners, fans, etc) had a significantly reduced odds of Alpha infection (OR, .35; 95% CI: .13–.95). Parents of child primary cases had a significantly reduced odds of Alpha infection relative to spouses of adult primary cases (OR, .31; 95% CI: .1–.91). Identifying as Black was a significant risk factor for Alpha infection (OR, 3.79; 95% CI: 1.18–12.13) and identifying as "Other" race/ethnicity was a significant protective factor for non-Alpha infection (OR, .36; 95% CI: .14–.88).

DISCUSSION

The findings of this investigation suggest that household SIRs of Alpha compared with non-Alpha are not significantly different. These findings are in contrast to published literature reporting higher transmissibility of Alpha than wild-type lineages [3]. Consistent with previous reports, our results showed no difference in SIRs between child and adult primary cases [20]. A recent meta-analysis of household transmission estimated an overall SIR of 19% for all SARS-CoV-2

Table 2. COVID-19 Symptoms and Clinical Course in Primary and Secondary Cases in Alpha and Non-Alpha Households, Overall and Stratified by Child (<18 Years) and Adult (≥18 Years) Cases

	Alpha Households, n (%)			Non-Alpha Households, n (%)				
	Total Cases (N = 160), Adults (n = 101), Children (n = 59)	Primary Cases (N = 68), Adults (n = 47), Children (n = 21)	Secondary Cases (N = 92), Adults (n = 54), Children (n = 38)	Total Cases (N = 95), Adults (n = 63), Children (n = 32)	Primary Cases (N = 42), Adults (n = 32), Children (n = 10)	Secondary Cases (N = 53), Adults (n = 31), Children (n = 22)	Total Fisher's Exact Test *P* Value[a]	Secondary Fisher's Exact Test *P* Value[b]
Symptoms during illness[c]								
Asymptomatic	11 (6.9)	2 (2.9)	9 (9.8)	3 (3.2)	0 (0)	3 (5.7)	.26	.54
Adults (≥18)	3 (3)	0 (0)	3 (5.6)	1 (1.6)	0 (0)	1 (3.2)	1	1
Children (<18)	8 (13.6)	2 (9.5)	6 (15.8)	2 (6.2)	0 (0)	2 (9.1)	.48	.7
Constitutional (objective or subjective fever, chills, myalgia, fatigue)	139 (86.9)	64 (94.1)	75 (81.5)	73 (76.8)	33 (78.6)	40 (75.5)	.05[d]	.40
Adults (≥18)	93 (92.1)	46 (97.9)	47 (87)	56 (88.9)	28 (87.5)	28 (90.3)	.58	.74
Children (<18)	46 (78)	18 (85.7)	28 (73.7)	17 (53.1)	5 (50)	12 (54.5)	.018[d]	.16
Upper respiratory (rhinorrhea, nasal congestion, sore throat)	139 (86.9)	60 (88.2)	79 (85.9)	82 (86.3)	39 (92.9)	43 (81.1)	1	.48
Adults (≥18)	93 (92.1)	43 (91.5)	50 (92.6)	57 (90.5)	30 (93.8)	27 (87.1)	.78	.46
Children (<18)	46 (78)	17 (81)	29 (76.3)	25 (78.1)	9 (90)	16 (72.7)	1	0.77
Lower respiratory (cough, shortness of breath)	124 (77.5)	58 (85.3)	66 (71.7)	67 (70.5)	32 (76.2)	35 (66)	.23	.57
Adults (≥18)	83 (82.2)	43 (91.5)	40 (74.1)	52 (82.5)	26 (81.2)	26 (83.9)	1	.42
Children (<18)	41 (69.5)	15 (71.4)	26 (68.4)	15(46.9)	6 (60)	9 (40.9)	.04[d]	.06
Neurologic (headache, loss of taste and/or smell)	130 (81.2)	63 (92.6)	67 (72.8)	76 (80)	36 (85.7)	40 (75.5)	.87	.85
Adults (≥18)	92 (91.1)	46 (97.9)	46 (85.2)	59 (93.7)	30 (93.8)	29 (93.5)	.77	.31
Children (<18)	38 (64.4)	17 (81)	21 (55.3)	17 (53.1)	6 (60)	11 (50)	.37	.79
Gastrointestinal (nausea/vomiting, diarrhea, abdominal pain)	76 (47.5)	42 (61.8)	34 (37.0)	38 (40)	16 (38.1)	22 (41.5)	.30	.60
Adults (≥18)	53 (52.5)	29 (61.7)	24 (44.4)	32 (50.8)	13 (40.6)	19 (61.3)	.87	.18
Children (<18)	23 (39)	13 (61.9)	10 (26.3)	6 (18.8)	3 (30)	3 (13.6)	.06	.34
Clinical course								
Patient sought clinical care	28 (17.5)	15 (22.1)	13 (14.1)	12 (12.6)	7 (16.7)	5 (9.4)	.37	.60
Adults (≥18)	23 (22.8)	11 (23.4)	12 (22.2)	9 (14.3)	6 (18.8)	3 (9.7)	.23	.24
Children (<18)	5 (8.5)	4 (19)	1 (2.6)	3 (9.4)	1 (10)	2 (9.1)	1	.55
Hospitalized[e]	5 (3.1)	2 (2.9)	3 (3.3)	1 (1.1)	1 (2.4)	0 (0)	.42	.30
Adults (≥18)	5 (5)	2 (4.3)	3 (5.6)	1 (1.6)	1 (3.1)	0 (0)	.41	.3
Children (<18)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	…	…
Died	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	…	…
Adults (≥18)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	…	…

Table 2. Continued

	Alpha Households, n (%)			Non-Alpha Households, n (%)				
	Total Cases (N = 160), Adults (n = 101), Children (n = 59)	Primary Cases (N = 68), Adults (n = 47), Children (n = 21)	Secondary Cases (N = 92), Adults (n = 54), Children (n = 38)	Total Cases (N = 95), Adults (n = 63), Children (n = 32)	Primary Cases (N = 42), Adults (n = 32), Children (n = 10)	Secondary Cases (N = 53), Adults (n = 31), Children (n = 22)	Total Fisher's Exact Test *P* Value[a]	Secondary Fisher's Exact Test *P* Value[b]
Children (<18)	0 (0)	0(0)	0 (0)	0 (0)	0 (0)	0 (0)	…	…

Households without sequencing (n = 17) were omitted from this table. Abbreviation: COVID-19, coronavirus disease 2019.

[a]Comparing Alpha Household Total proportions with Non-Alpha Household Total proportions.

[b]Comparing Alpha Household Secondary cases proportions with Non-Alpha Household Secondary cases proportions.

[c]Symptoms were recorded at the beginning of the investigation at day 0 and throughout the 14 days of follow up during the investigation via self-recorded daily symptom diaries.

[d]*P* values ≤.05 indicate statistical significance.

[e]One participant was hospitalized for <24 hours, 2 participants for 1 day, 1 participant for 2 days, 1 participant for 4 days, and 1 participant for 7 days.

lineages and 24.5% for Alpha [21]. The household Alpha and non-Alpha SIRs we observed were higher than these estimations, possibly due to our longitudinal study design (where participants were tested at multiple time points regardless of symptoms) that may have captured more transmission than other investigations. Additionally, serologic testing detected a likely seroconversion of a case who may have had a short PCR-positivity window. A median SNP difference of 0 between infections within the same household further suggests that our investigation detected SARS-CoV-2 transmission occurring within households, rather than from multiple outside introductions.

While Alpha may have characteristics that make it intrinsically more transmissible than some SARS-CoV-2 variants, relative differences in transmissibility were not detected in our investigation. Unlike community settings, which may provide more limited exposure to SARS-CoV-2, household contacts likely experience repeated transmission opportunities during the infectious period due to shared living spaces and repeated interactions, potentially resulting in higher infection odds [22]. Quarantine guidelines may also result in household contacts having continued exposure to someone with SARS-CoV-2 if they quarantine within the same household. Overall closer exposure may result in saturation of transmission despite the virus lineage, resulting in comparable SIRs between Alpha and non-Alpha lineages. While we did not observe significant differences in household SIRs between lineage groups, even small differences in SIRs in community settings may explain the rapid expansion of Alpha. Additionally, factors not captured in this investigation (eg, changes in community mitigation, susceptible populations, or population drivers of infection, such as school outbreaks) likely contributed to the rapid spread of Alpha locally and globally [23]. As persons from some racial and ethnic minority communities or economically disadvantaged households are more likely to live in crowded housing, mitigation strategies such as providing culturally appropriate sponsored quarantine locations is important for health equity [24].

Even with high household transmission risk, specific behaviors were associated with increased SARS-CoV-2 infection odds, suggesting that avoidance of these behaviors may decrease infection risk among household contacts. Consistent with other literature, we found that increased direct and indirect contact with infected household members (eg, hugging, sharing a bedroom) was associated with increased infection odds after adjusting for age, sex, and vaccination status [25, 26]. This suggests that mitigation measures such as isolation and social distancing should be maintained by infected persons even if preventive measures, such as vaccination, are taken by household contacts. Contact with primary patient fomites (eg, sharing utensils) significantly increased Alpha infection risk. While limited viable SARS-CoV-2 has been cultured from environmental samples previously, differences in lineage-specific viability of

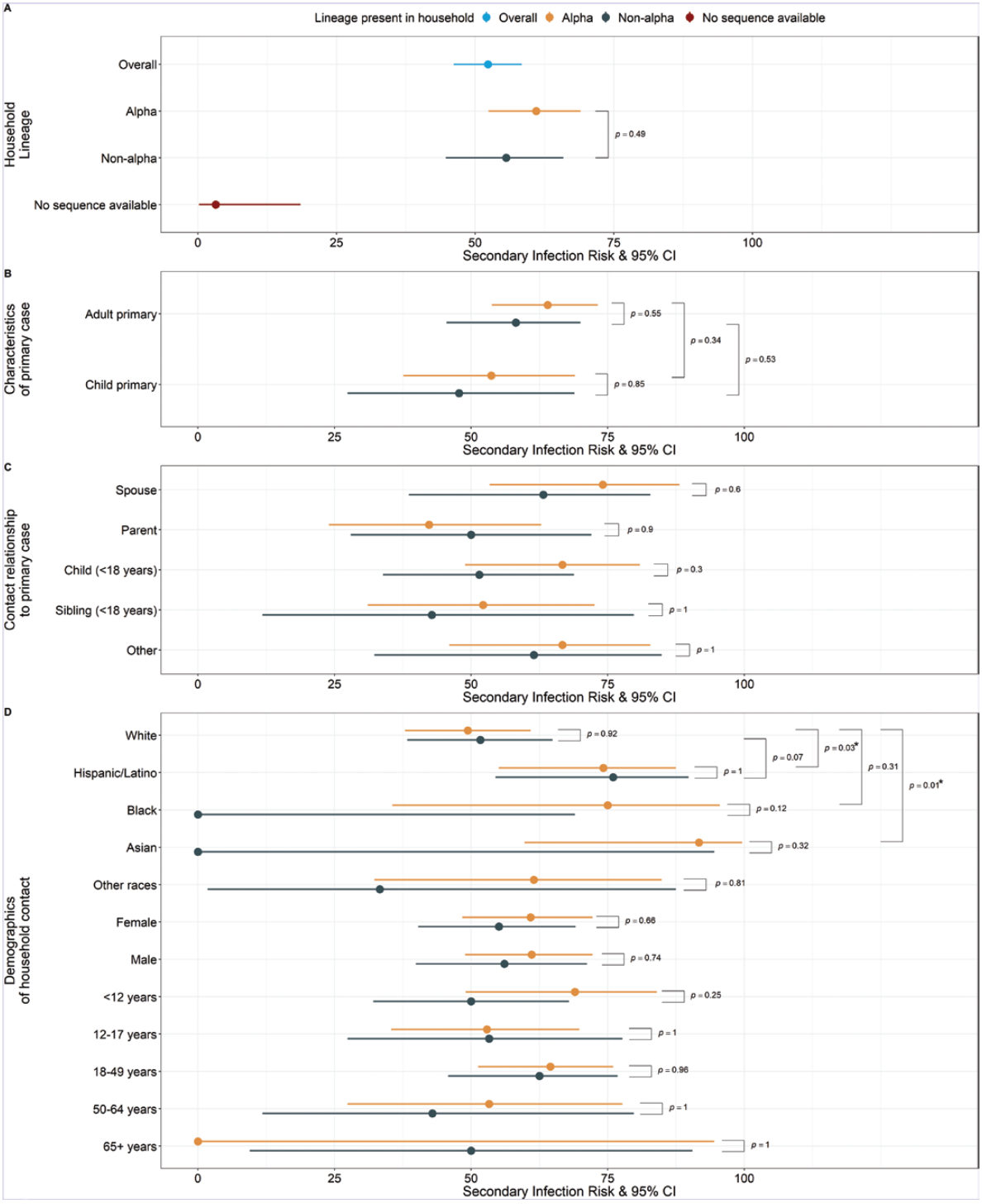

Figure 2. *A*, SIRs and 95% CIs in unvaccinated household contacts without history of previous SARS-CoV-2 infection, stratified by household lineage group. The overall group is a combination of households with Alpha infections, non-Alpha infections, and infections of unknown lineage. There was no significant difference found between unstratified SIRs in households with only Alpha infections and households with only non-Alpha infections ($P = .49$). *B*, SIRs and 95% CIs for subgroups of household contacts stratified by characteristics of household primary cases. There were no significant differences in SIRs between Alpha and non-Alpha household lineage groups within adult ($P = .55$) or child ($P = .85$) categories and there were no significant differences in SIRs for child versus adult primary cases within the Alpha lineage group ($P = .34$) and the non-Alpha lineage group ($P = .53$). *C*, SIRs and 95% CIs for subgroups of household contacts stratified by the relationship of household contacts to the primary case. There were no significant differences in SIRs between Alpha and non-Alpha household lineage groups within any relationship category (see Supplementary Figure 4) and there were no significant differences between relationship categories within lineage groups (see Supplementary Figure 4). The other category for relationship to primary case includes extended family, work colleagues, and significant others. *D*, SIRs and 95% CIs for subgroups of household contacts stratified by demographic characteristics of household contacts. When comparing SIRs within the same lineage group across demographic characteristics, the Hispanic/Latino and Asian race/ethnicity categories both had significantly higher SIRs than the White race/ethnicity categories for Alpha infections (Hispanic/Latino $P = .03$, Asian $P = .01$). Corresponding values for Figure 2 can be found in Supplementary Table 7. Abbreviations: CI, confidence interval; SIR, secondary infection risk.

Table 3. Odds Ratios of Infection and 95% Confidence Intervals of Potential Risk Factors for SARS-CoV-2 Infection in Household Contacts

Variable	Alpha Households			Non-Alpha Households		
	Alpha OR (95% CI)	No. of Secondary Cases = 92, No. of Noncases = 83		Non-Alpha OR (95% CI)	No. of Secondary Cases = 53, No. of Noncases = 51	
		No. of Alpha Secondary Cases With Risk Factor	Alpha *P* Value		No. of Non-Alpha Secondary Cases With Risk Factor	Non-Alpha *P* Value
Primary case demographics, clinical characteristics, and behaviors						
Primary case vaccination status						
Not vaccinated (ref)	…	91	…	…	53	…
Partially vaccinated	1.62 (.82, 3.18)	1	.16	0 (0, 0)	0	<.001[a]
Fully vaccinated[b]	…[c]	0	…	0 (0, 0)	0	<.001[a]
Primary case mask wearing indoors						
Yes	.47 (.19, 1.13)	53[e]	.09	.37 (.11, 1.24)	31	.11
Contact demographics, clinical characteristics, and behaviors						
Contact relationship to primary case						
Spouse (ref)	…	20[e]	…	…	13[e]	…
Child <18 years	.64 (.29, 1.38)	24[e]	.25	.94 (.4, 2.19)	17[e]	.89
Parent	.31 (.1, .91)	15[e]	.03[a]	.42 (.1, 1.77)	9[e]	.24
Child sibling <18 years	.37 (.12, 1.19)	12[e]	.1	.51 (.1, 2.51)	4[e]	.41
Other[d]	.51 (.17, 1.56)	20[e]	.24	.56 (.11, 2.69)	8[e]	.47
Contact race and ethnicity						
White (ref)	…	43 (46.7%)	…	…	33 (62.3%)	…
Hispanic/Latino	1.84 (.68, 5.01)	23 (25%)	.23	1.67 (.49, 5.72)	19 (35.8%)	.42
Black	3.79 (1.18, 12.13)	6 (6.5%)	.02[a]	…[c]	0 (0%)	…
Asian	2.29 (.7, 7.46)	12 (13.0)	.17	…[c]	0 (0%)	…
All other races and ethnicities	.99 (.32, 3.12)	8 (8.7%)	.99	.36 (.14, .88)	1 (1.9%)	.03[a]
Contact vaccination status						
Not vaccinated (ref)	…	86	…	…	50	…
Partially vaccinated	.11 (.01, 1.19)	1	.07	.86 (.08, 9.02)	2	.90
Fully vaccinated	.34 (.14, .85)	5	.02[a]	1.5 (.08, 29.43)	1	.79
Contact interactions/behaviors						
Intimate physical touch (kissing, hugging, sharing same bed)	2.61 (1.42, 4.79)	48[e]	<.001[a]	2.11 (.9, 4.98)	24[e]	.09
Other direct physical contact with the primary case	1.36 (.75, 2.46)	49[f]	.31	2.24 (1.06, 4.74)	25[g]	.04[a]
Indirect contact with primary patient fomites (eg, sharing utensils, plates, cups, other objects)	3.42 (1.06, 11.04)	21[e]	.04[a]	1.28 (.39, 4.18)	11[e]	.69
Shared bedroom	3.33 (1.43, 7.74)	33[e]	.01[a]	2.5 (.81, 7.69)	14[e]	.11
Shared bed	2.48 (1.11, 5.58)	29[f]	.03[a]	3.29 (1.02, 10.59)	13[g]	.05[a]
Shared bathroom	2.79 (1.46, 5.35)	54[e]	<.001[a]	2.27 (.9, 5.71)	28[e]	.08
Ate food that was prepared by primary case	3.62 (1.43, 9.13)	22[e]	.01[a]	1.87 (.49, 7.16)	12[e]	.36
Rode in a car with primary case without a mask	3.12 (1.79, 5.42)	45[e]	<.001[a]	1.85 (.89, 3.84)	22[e]	.1
Household characteristics						
Used any ventilation system during illness period	.35 (.13, .95)	58[e]	.04[a]	.95 (.29, 3.15)	39	.94

The middle columns of the table depict models investigating relationships between variables of interest and odds of Alpha infection in household contacts, adjusted for age, sex, history of previous SARS-CoV-2 infection, and vaccination status at the time of illness onset of primary case. The right-side columns of the table depict models investigating relationships between variables of interest and odds of non-Alpha infection in household contacts, adjusted for age, sex, history of previous SARS-CoV-2 infection, and vaccination status at the time of illness onset of primary case. Individual generalized estimating equation models were built for each variable and lineage group. Variables presented in this table are only those that were statistically significant. Only households where SARS-CoV-2 lineage could be determined are included. All variables examined are in Supplementary Table 6. Abbreviations: CI, confidence interval; OR, odds ratio; ref, reference; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

[a] *P* values ≤.05 indicate statistical significance.

[b] There were no primary cases with Alpha infections who were fully vaccinated, and there was no secondary transmission in households where the primary case had a non-Alpha infection and was fully vaccinated.

[c] Odds ratios could not be estimated due to small sample sizes.

[d] Other category for relationship to primary case includes extended family, work colleagues, and significant others.

[e] Some household contacts did not have complete data for all survey questions: a) there was 1 household with 1 household contact where the primary case did not answer this question, b) 1 household secondary case was missing data for this question, and c) 2 household secondary cases were missing data.

fomites may impact transmission risk [27]. We found that both the use of ventilation systems within homes and full vaccination reduced Alpha infection odds among household contacts. Even with presymptomatic transmission, which likely predated the implementation of prevention measures once a household member became symptomatic, specific behaviors altered secondary transmission risk.

These findings are subject to limitations. First, our investigation excluded hospitalized cases due to limitations in follow-up. This may have biased our sample toward recruiting fewer persons who experienced severe symptoms or had underlying health conditions. Second, our sample was not random nor representative of all persons and households in San Diego and metropolitan Denver. Third, our sample size may limit our ability to identify significant findings, particularly in smaller demographic subgroups. Fourth, our analysis compared Alpha with non-Alpha lineages, collapsing other VOCs with wild-type SARS-CoV-2 into a comparison group. As non-Alpha VOCs may have increased transmission compared with wild-type, our sample may not have been large enough to detect smaller effect sizes [28, 29]. Fifth, there was potential for misclassification of the household primary case due to self-report of symptom onset date and timing of SARS-CoV-2 testing. Last, our analysis does not distinguish between secondary and tertiary cases, which may bias our SIR higher than an estimation of direct transmission lines from 1 infected person. However, our SIR calculations accomplished the overall goal of estimating how many people in a household became infected when SARS-CoV-2 was introduced.

In conclusion, SARS-CoV-2 household transmission risk is over 50% in both Alpha and non-Alpha lineages. These findings may inform public health response to VOCs broadly, as a deeper understanding of household transmission across lineages may impact transmission mitigation. With the recent emergence of Delta and Omicron variants (B.1.617.2 and B.1.1.529), which are more transmissible, our findings may guide implementation of prevention practices within homes [30, 31]. Behaviors such as avoiding close contact or wearing a mask while riding in cars with someone who is ill may reduce SARS-CoV-2 transmission risk regardless of lineage. For persons unable to avoid close contact, other transmission-prevention strategies such as SARS-CoV-2 vaccination and mask wearing may reduce infection risk within households. As the coronavirus disease 2019 (COVID-19) pandemic continues, newer highly transmissible variants may develop, underscoring a continued need for mitigation factors such as these in communities and within households regardless of circulating SARS-CoV-2 variants.

Supplementary Data

Supplementary materials are available at *Clinical Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

Notes

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COVID-19 Household Transmission Team. Centers for Disease Control and Prevention COVID-19 Response: Apophia Namageyo-Funa, Byron F. Robinson, Monique A. Foster, Lorraine N. Alexander, Michelle O'Hegarty, Tarah S. Somers, Horacio Ruisenor Escudero, Yessica Gomez, Winston E. Abara, Elizabeth Garza, Ben W. Humrighouse, Benjamin P. Monroe, Melissa Arons, Blake Cherney, Ayan K. Chakrabarti, Melissa J. Whaley, Jeni Vuong, Laird J. Ruth, Kristine Lindell, Joaudimir Castro Georgi, Susanna N. Visser, Maggie Silver, Grace E. Marx, Rebecca J. Chancey, Paul Mead, Michelle A. Waltenburg, Jennifer Lehman, Anna Drexler, Jamie Pawloski, Janae Stovall, Karen L. Boroughs, Aaron C. Brault, Sabrina Weis-Torres, Lili Punkova, Tao Lily Jia, Peter Browning, Shanna Bolcen, Panagiotis Maniatis, So Hee Park, Kimberly M. Moss, Briana Zellner, Kristina Ortiz, Ying Tao, Yan Li, Anna Kelleher, Han Jia Justin NG, Jing Zhang, Brian Lynch, Peter W. Cook, Clinton R. Paden, Krista Queen, Magdalena Medrzycki, Shannon Rogers, Phili Wong, Shilpi Jain, Alexandra Tejada, John Michael Metz, Ebenezer David, Xiaoling Tang, Nhien T. Wynn, Rebekah Tiller, Senthilkumar K. Sakthivel, Srinivasan Velusamy, Brett Whitaker. Centers for Disease Control and Prevention Epidemic Intelligence Service: Ian W. Pray, Perrine Marcenac, Caroline Q. Pratt, Rachael L. Ticho Zacks, Anna R. Yousaf, Hannah E. Segaloff, Farrell A. Tobolowsky, Melanie J. Firestone, Emily N. Schmitt-Matzen, Talya Shragai. Centers for Disease Control and Prevention Laboratory Leadership Service: Stephen P. LaVoie, Kaitlin F. Mitchell. County of San Diego Health and Human Services: Maria I. Dionicio Bernabe, Graciela Zuniga-Groot, Anna Liza M. Manlutac. Colorado Department of Public Health and Environment: Christopher Grano, Heather Baily, Alexis Burakoff, Lindsey Martin Webb. Colorado State Public Health Laboratory: Tara M. Stitzlein, Kimberly Huynh-Templeman, Shaun Dunyak, Nicholas J. Pysnack, Christopher Delmonico, Wyatt Giddmore, Hannah M. Fortune, Hunter Olsen, Evelyn Alvarez, Cassandra N. Bundalian, Hannah Collins, Aleigha M. Ricci, Tia Ling, Janet C. McAllister.

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