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RESEARCH ARTICLE

Behaviors Associated With Household Transmission of SARS-CoV-2 in California and Colorado, January 2021—April 2021

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Introduction: Mitigation behaviors are key to preventing SARS-CoV-2 transmission. We identified the behaviors associated with secondary transmission from confirmed SARS-CoV-2 primary cases to household contacts and described the characteristics associated with reporting these behaviors.

Methods: Households with confirmed SARS-CoV-2 infections were recruited in California and Colorado from January to April 2021. Self-reported behaviors and demographics were collected through interviews. We investigated behaviors associated with transmission and individual and household characteristics associated with behaviors using univariable and multivariable logistic regression with generalized estimating equations to account for household clustering.

Results: Among household contacts of primary cases, 43.3% (133 of 307) became infected with SARS-CoV-2. When an adjusted analysis was conducted, household contacts who slept in the same bedroom with the primary case (AOR=2.19; 95% CI=1.25, 3.84) and ate food prepared by the primary case (AOR=1.98; 95% CI=1.02, 3.87) had increased odds of SARS-CoV-2 infection. Household contacts in homes ≤2,000 square feet had increased odds of sleeping in the same bedroom as the primary case compared with those in homes >2,000 square feet (AOR=3.97; 95% CI=1.73, 9.10). Parents, siblings, and other relationships (extended family, friends, or roommates) of the primary case had decreased odds of eating food prepared by the primary case compared with partners.

Conclusions: Sleeping in the same bedroom as the primary case and eating food prepared by the primary case were associated with secondary transmission. Household dimension and relationship to the primary case were associated with these behaviors. Our findings encourage

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innovative means to promote adherence to mitigation measures that reduce household transmission.

INTRODUCTION

In early 2021, the U.S. saw a steady decline of coronavirus disease 2019 (COVID-19) cases, followed by a resurgence in July 2021 because of the Delta variant and in December 2021 from the Omicron variant.[1,2] Transmission has been reported in numerous settings, including prisons[3,4] and schools,[5,6] yet household contact remains a major source of transmission of COVID-19.[7] The Centers for Disease Control and Prevention (CDC) recommends mitigation measures to reduce household transmission risk when caring for and interacting with persons with COVID-19 at home. These measures include, when possible, avoiding physical contact with the infected person, limiting shared activities and items, wearing a mask, and practicing appropriate hand hygiene.[8] Household contacts of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) cases are also encouraged to self-monitor their health status, wear a mask when around others for 10 full days at home and in public, and undergo testing for SARS-CoV-2 at least 5 full days after last exposure regardless of vaccination status, while unvaccinated household contacts are also encouraged to quarantine.[9] If household contacts develop symptoms, they should get tested immediately and isolate.[9]

In December 2020, COVID-19 vaccines became available in the U.S. with priority given to individuals who were immunocompromised, elderly, or considered high risk for exposure (e.g., healthcare workers).[10] Individual uptake of mitigation behaviors has changed throughout the pandemic, and adherence to the recommended mitigation behaviors against SARS-CoV-2 transmission has been influenced by complex factors, posing unique challenges at the individual, household, and community levels.[11−15] For example, the U.S. COVID-19 Trends and Impact Survey found greater adherence to mitigation behaviors when a high number of COVID-19 cases were reported and less adherence when COVID-19 cases were low.[14] In addition, guidance on mitigation behaviors have changed in relation to the waves of reported cases within the U.S., which likely impacted adherence to these measures over time. Several studies on SARS-CoV-2 transmission in households have examined the impact of specific factors (e.g., demographics and mitigation behaviors) on secondary infection risk in the U.S. and globally.[16−21] However, there is limited research focusing on predicting factors among household members engaging in mitigation behaviors.

Investigating behaviors that increase or mitigate the risks of SARS-CoV-2 transmission in households may provide insight into important and effective public health interventions in affected households. In this article, we (1) identify the self-reported behaviors associated with household secondary transmission of SARS-CoV-2 and (2) describe the characteristics associated with engaging in these specific behaviors.

METHODS

Study Sample

Details of household and individual enrollment for this investigation have been previously published. Briefly, a SARS-CoV-2 household transmission investigation was conducted from January to April 2021 at 2 sites: San Diego County, CA and metropolitan Denver, CO. These sites were chosen because the public health departments (HDs) and testing laboratories at these sites had established protocols for identifying household SARS-CoV-2 cases quickly during the increase in SARS-CoV-2 variant circulation when this investigation occurred and because there was an agreement between these HDs to collaborate on data collection with the CDC. Individuals positive for SARS-CoV-2 by reverse transcription-polymerase chain reaction (RT-PCR) were identified through community testing by the local HD at each site. Select households with an RT-PCR-confirmed case of SARS-CoV-2 were contacted to determine enrollment eligibility. Full details of household selection are reported elsewhere.[22] Household eligibility included having a nonhospitalized case with illness onset ≤10 days before enrollment and at least 1 household contact. *Illness onset date* was defined as the symptom onset date or, if asymptomatic, the date of the first positive SARS-CoV-2 RT-PCR test. A *household contact* was defined as a person who spent at least 1 night in the household during the infectious period (2 days before and 10 days after illness onset) of the primary case. A *primary case* was defined as the RT-PCR−positive individual in the household with the earliest illness onset.

Each household was followed for 15 days (Days 0 to 14). On Day 0 (date of first home visit), trained interviewers collected data on demographic information and self-reported behaviors from all household contacts. On Days 0 and 14, all household members had specimens collected, including nasopharyngeal swabs and blood serum. All nasopharyngeal swabs were tested for SARS-CoV-2 by RT-PCR (TaqPath COVID-19 Combo Kit or PerkinElmer New coronavirus nucleic-acid Detection Kit), and serum was tested for SARS-CoV-2−specific antibodies (using anti−SARS-CoV-2 IgG Reagent Pack, xMAP SARS-CoV-2 Multi-Antigen IgG Assay, or Alinity SARS-CoV-2 IgG test). Symptom diaries were completed daily by all household members during enrollment. Parents/guardians completed symptom diaries for children unable to complete the form. On Day 14, trained interviewers conducted a closeout questionnaire. Additional specimens were collected from all household members during interim visits prompted by the onset of a new symptom identified by a household member. Household contacts who withdrew or were lost to follow-up were excluded. Households with multiple primary cases or where the primary case was not the first confirmed case reported in the household were also excluded.

Adults provided written consent, and minors aged >7 years provided assent and parental consent. Parental consent was obtained for minors aged <7 years. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy (CDC ethics policy: see 45 C.F.R part 46 and 21 C.F.R. part 56 and 42 U.S.C. §241(d), 5 U.S.C. §552a, and 44 U.S.C. §3,501. Et Seq).

Measures

Secondary transmission. Secondary transmission was documented when household contacts tested positive for SARS-CoV-2 by RT-PCR or seroconverted during the investigation period. In these instances of transmission, the contact was considered a secondary case.

Behavioral practices. Household contacts were asked behavioral questions on their interaction with the primary case regarding mask use, physical contact, and shared activities (Appendix Table 1). The questions began with *Since the [date of illness onset of the primary case] up to and including today, how often did you... [behavior]* and included 4 response levels on a Likert scale (1=never, 2=some of the time, 3=most of the time, and 4=always). For analysis, responses were recategorized with *Never* recoded as *No* and the remaining 3 responses recoded as *Yes*.

Individual characteristics. Demographic information (age, sex, race or ethnicity, education level, vaccination status, and relationship to the primary case) was collected on Day 0. For analysis, race or ethnicity was combined into non-Hispanic White, Hispanic or Latino, and other (combination of the remaining non-Hispanic races reported) owing to limited sample size. For analysis, education was combined into 4 levels, including no degree; high-school degree; associate's, technical or bachelor's degree; and advanced degree. The COVID-19 vaccines available at the time of the investigation included the 2-dose messenger RNA (mRNA) vaccines, Pfizer-BioNTech[23] and Moderna,[24] and the single-dose viral vector vaccine, Johnson & Johnson's Janssen.[25] COVID-19 vaccination status for household contacts was determined on the basis of the date of the primary case's illness onset. Household contacts with a single dose of any COVID-19 vaccine ≤14 days from the date of the primary case's illness onset or ≤14 days from the second dose of an mRNA vaccine were categorized as partially vaccinated. Household contacts who received either the second dose of an mRNA vaccine or a single dose of a viral vector vaccine >14 days from the primary case's illness onset were categorized as fully vaccinated. For analysis, relationship to the primary case was stratified into 5 categories: son/daughter, parent, partner, sibling, and other (combination of extended family, roommates, and friends).

Household characteristics. The presence of children was a binary variable on the basis of having at least 1 household member aged <18 years enrolled in the investigation. We analyzed household dimension as a marker of the physical environment of the household. Household dimension was dichotomized at 2,000 square feet (ft^2) to represent the largest proportion of single-family houses in 2020 (1,800−2,399 ft^2) as estimated by the U.S. Census Bureau.[26]

Statistical Analysis

Characteristics of household contacts were stratified by case status. Logistic regression models were constructed to investigate (1) the association between case status (i.e., secondary transmission) and self-reported behaviors and (2) the associations between self-reported behaviors and individual/household characteristics. Generalized estimating equations[27] were used with an exchangeable working correlation and binomial distribution to account for clustering of household contacts.

Univariable analysis was initially performed to determine which behavior variables were associated with secondary transmission. Behavior variables from univariable analysis with a p-value <0.25 were initially included in the multivariable analysis, followed by the removal of behaviors with the highest p-value until only behavior variables with a p-value <0.05 remained in the model. Potential confounders (age, sex, race or ethnicity, and vaccination status) were assessed after selection of behaviors by individual addition to the final multivariable model. Confounders were included in the final multivariable model if they either changed the estimated odds ratios by >10% or decreased the quasi-likelihood under the independence model criterion indicating improved model fit.

To determine the household and individual characteristics associated with behaviors impacting secondary transmission, we modeled the behaviors associated with case status in the final multivariable model. Model selection was also performed using the same p-value criterion as described earlier to select household and individual characteristics for inclusion in the final multivariable analysis.

Demographic reference groups (except age) were based on lower trend of SARS-CoV-2 infection[28] or greater social advantages.[29] A 2-sided $p<0.05$ was considered statistically significant. Records with missing data were excluded from analysis and noted in the results. Data analysis was performed using SAS software, version 9.4 (SAS Institute, Cary, NC).

RESULTS

Of the 122 households with 122 primary cases, a total of 307 household contacts were included in the analysis (Figure 1). Ages ranged from 1 month to 83 years, with a median age of 31 years (Table 1). Most household contacts were female (53.1%; 163 of 307) and non-Hispanic White (58.6%; 180 of 307). Among household contacts, 43.3% (133 of 307) became infected with SARS-CoV-2. Of the secondary cases, 4.5% (6 of 133) and 6.8% (9 of 133) were fully vaccinated and partially vaccinated, respectively, compared with 10.9% (19 of 174) and 16.1% (28 of 174) among noncases. There were 33.8% (45 of 133) secondary cases who were sons or daughters

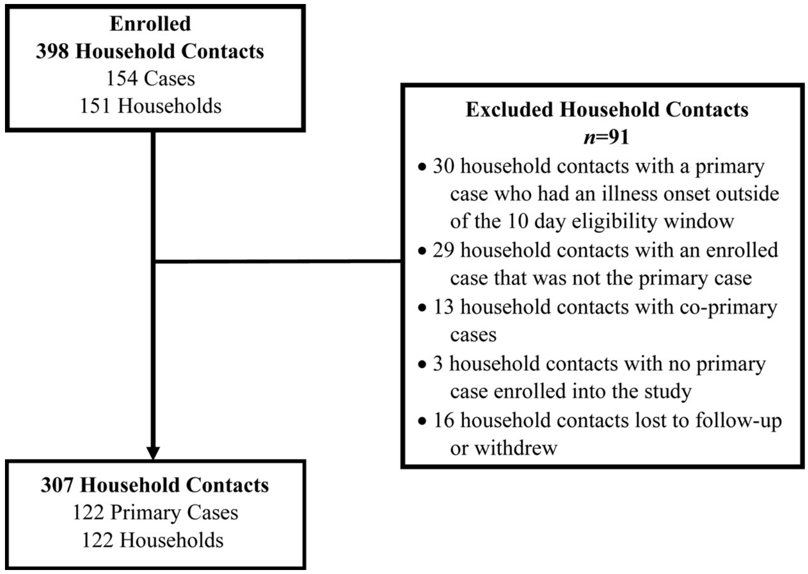

Figure 1. Household contact exclusion criteria and sample size.

of the primary case, and 32.8% (57 of 174) of noncases were the parent of the primary case. A greater proportion of secondary cases lived in homes ≤2,000 ft^2 (51.9%; 69 of 133), whereas more noncases lived in homes >2,000 ft^2 (59.8%; 104 of 174).

Among self-reported behaviors, 50% (66 of 133) of secondary cases used a mask in the same room as the primary case compared with 62% (107 of 173) of noncases (Figure 2). A total of 56% (74 of 133) of secondary cases and 40% (70 of 174) of noncases had direct physical contact, whereas 55% (73 of 132) of secondary cases and 41% (71 of 174) of noncases ate at the same table with the primary case. In addition, 36% (48 of 133) of secondary cases and 19% (33 of 174) of noncases slept in the same bedroom as the primary case.

On univariable analysis, household contacts aged between 18 and 49 years had increased odds of SARS-CoV-2 infection compared with those aged ≥50 years (OR=2.13; 95% CI=1.07, 4.24) (Table 2). Household contacts who used the same bathroom as the primary case had increased odds of SARS-CoV-2 infection compared with those who did not use the same bathroom (OR=2.15; 95% CI=1.31, 3.54). Household contacts who slept in the same bed as the primary case had increased odds of SARS-CoV-2 infection compared with those who did not sleep in the same bed (OR=2.03; 95% CI=1.19, 3.45). Household contacts who traveled in the same vehicle as the primary case with masks off also had increased odds of infection (OR=1.68; 95% CI=1.09, 2.57).

After multivariable model selection, the behaviors—slept in the same bedroom and ate food prepared by the primary case—remained in the model along with vaccination status as confounders. During adjusted analysis, household contacts who slept in the same bedroom as the primary case had increased odds of SARS-CoV-2 infection (AOR=2.19; 95% CI=1.25, 3.84). After adjusting, household contacts who ate food prepared by the primary case had increased odds of SARS-CoV-2 infection (AOR=1.98; 95% CI=1.02, 3.87).

On univariable analysis, household contacts with no high-school degree had decreased odds of having slept in the same bedroom as the primary case compared with those with an advanced degree (OR=0.35; 95% CI=0.17, 0.75) (Table 3). Household contacts with children in the home had decreased odds of having slept in the same bedroom as the primary case compared with those with no children in the home (OR=0.47; 95% CI=0.25, 0.88). After model selection, the final multivariable analysis included the following characteristics: age, race or ethnicity, relationship to the primary case, and household dimension. During adjusted analysis, household contacts who lived in homes ≤2,000 ft^2 had increased odds of having slept in the same bedroom as the primary case compared with household contacts who lived in homes >2,000 ft^2 (AOR=3.97; 95% CI=1.73, 9.10). All relationships to the primary case had significantly lower odds of having slept in the same bedroom as the primary case compared with the partner of the primary case. Household contacts aged <50 years had increased odds of having slept in the same bedroom as the primary case compared with household contacts aged ≥50 years. Hispanic or Latino household contacts had decreased odds of having slept in the same bedroom as the primary case

Table 1. Demographics and Characteristics of Household Contacts in California and Colorado, January 2021—April 2021

Characteristics	Total N=307, *n* (%)	Secondary cases *n*=133, *n* (%)	Noncases *n*=174, *n* (%)
Age (years)			
<18	115 (37.5)	56 (42.1)	59 (33.9)
18–49	142 (46.3)	63 (47.4)	79 (45.4)
≥50	50 (16.3)	14 (10.5)	36 (20.7)
Median (range)	31 (0–83)	22 (1–83)	33 (0–83)
Sex			
Female	163 (53.1)	72 (54.1)	91 (52.3)
Male	144 (46.9)	61 (45.9)	83 (47.7)
Race/ethnicity			
White, NH	180 (58.6)	72 (54.1)	108 (62.1)
Hispanic or Latino	63 (20.5)	35 (26.3)	28 (16.1)
Asian, NH	28 (9.1)	12 (9.0)	16 (9.2)
Multi-racial, NH	16 (5.2)	4 (3.0)	12 (6.9)
Black, NH	12 (3.9)	5 (3.8)	7 (4.0)
Native Hawaiian or Pacific Islander, NH	4 (1.3)	2 (1.5)	2 (1.1)
American Indian or Alaska Native, NH	3 (1.0)	3 (2.3)	0 (0)
Unknown	1 (0.3)	0 (0)	1 (0.6)
Education			
No degree[a]	121 (39.4)	59 (44.4)	62 (35.6)
High-school degree	70 (22.8)	35 (26.3)	35 (20.1)
Technical, associate, or bachelor's degree	81 (26.4)	27 (20.3)	54 (31.0)
Advanced degree	34 (11.1)	12 (9.0)	22 (12.6)
Unknown	1 (0.3)	0 (0)	1 (0.6)
Vaccination status			
Fully	25 (8.1)	6 (4.5)	19 (10.9)
Partially	37 (12.1)	9 (6.8)	28 (16.1)
Unvaccinated	245 (79.8)	118 (88.7)	127 (73.0)
Relationship to primary case			
Son/daughter	88 (28.7)	45 (33.8)	43 (24.7)
Parent	81 (26.4)	24 (18.1)	57 (32.8)
Partner[b]	60 (19.5)	31 (23.3)	29 (16.7)
Sibling	46 (15.0)	20 (15.0)	26 (14.9)
Other[c]	32 (10.4)	13 (9.8)	19 (10.9)
Children in the home			
With children	233 (75.9)	107 (80.5)	126 (72.4)
No children	74 (24.1)	26 (19.5)	48 (27.6)
Household dimension			
≤2,000 ft^2	132 (43.0)	69 (51.9)	63 (36.2)
>2,000 ft^2	159 (51.8)	55 (41.4)	104 (59.8)
Missing	16 (5.2)	9 (6.8)	7 (4.0)

Note: Some categories are not equal 100% owing to rounding.
[a]Children aged <18 years are included in the no degree category.
[b]Partner includes husband, wife, partner, boyfriend, girlfriend, and fiancé.
[c]Other relationships to the primary case include extended family, friends, and roommates.
ft^2, square feet; NH, Non-Hispanic.

compared with non-Hispanic White household contacts (AOR=0.23; 95% CI=0.06, 0.92).

Through univariable analysis, parents, siblings, and other relationships (extended family, friends, or roommates) of the primary case had decreased odds of having eaten food prepared by the primary case compared with partners (Table 3). After model selection, the final multivariable analysis included relationship to the

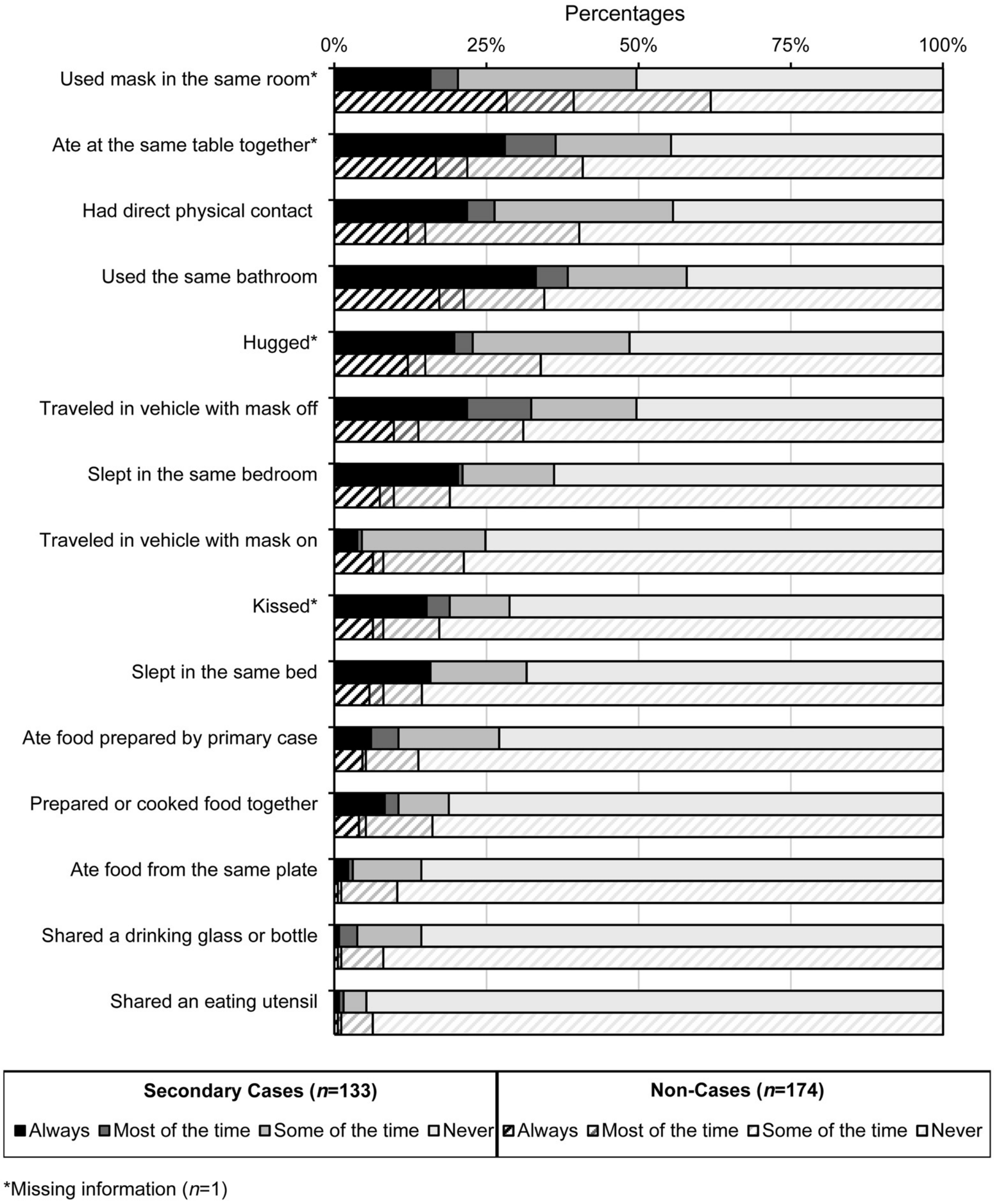

Figure 2. Self-reported behaviors of household contacts during interactions with primary case (N=307).

primary case and education. During adjusted analysis, parents, siblings, and other relationships (extended family, friends, or roommates) had decreased odds of having eaten food prepared by the primary case compared with partners. Household contacts with a technical, associate, or bachelor's degree had decreased odds of having eaten food prepared by the primary case compared with those with an advanced degree (AOR=0.44; 95% CI=0.23, 0.82).

DISCUSSION

This investigation examined the behaviors of individuals living with a person with SARS-CoV-2 infection (primary case). Household SARS-CoV-2 secondary transmission has been documented in multiple studies,[7,17,19,30,31] therefore underscoring the importance of addressing effective mitigation in this setting.

Sleeping in the same bedroom with the primary case significantly increased secondary transmission to household contacts in this investigation. In particular, the relationship to the primary case was found to be a significant characteristic of sleeping in the same bedroom. Among all the relationships assessed, partners of the primary case were most likely to sleep in the same bedroom as the primary case compared with other relationships in a household. This finding is similar to that reported in a

Table 2. Association of Secondary Transmission With Self-Reported Behaviors or Demographic Characteristics Among Household Contacts (N=307)

Behaviors or Characteristics	2° Cases[a] *n*	Noncases *n*	Univariable analysis		Multivariable analysis	
			OR (95% CI)	*p*-value	AOR (95% CI)	*p*-value
Slept in the same bedroom	48	33	2.29 (1.34, 3.92)	**<0.01**	2.19 (1.25, 3.84)	**0.01**
Ate food prepared by primary case	36	24	2.55 (1.31, 4.98)	**0.01**	1.98 (1.02, 3.87)	**0.04**
Vaccination status						
Fully	6	19	0.58 (0.26, 1.28)	0.18	0.61 (0.24, 1.52)	0.29
Partially	9	28	0.45 (0.17, 1.19)	0.11	0.43 (0.16, 1.21)	0.11
Unvaccinated	118	127	ref		ref	
Age, years						
<18	56	59	2.06 (0.95, 4.49)	0.07		
18−49	63	79	2.13 (1.07, 4.24)	**0.03**		
≥50	14	36	ref			
Sex						
Female	72	91	1.05 (0.70, 1.58)	0.81		
Male	61	83	ref			
Race/ethnicity[b]						
Hispanic/Latino	35	28	1.49 (0.70, 3.16)	0.30		
All other NH races	26	37	0.82 (0.37, 1.80)	0.62		
NH White	72	108	ref			
Used mask in the same room[b]	66	107	0.68 (0.45, 1.04)	0.07		
Ate at the same table together[b]	73	71	1.49 (0.84, 2.65)	0.17		
Had direct physical contact	74	70	1.47 (0.96, 2.25)	0.08		
Used the same bathroom	77	60	2.15 (1.31, 3.54)	**<0.01**		
Hugged[b]	64	59	1.54 (0.99, 2.40)	0.06		
Traveled in vehicle with mask off	66	54	1.68 (1.09, 2.57)	**0.02**		
Traveled in vehicle with mask on	33	37	0.98 (0.60, 1.59)	0.92		
Kissed[b]	38	30	1.28 (0.77, 2.13)	0.34		
Slept in the same bed	42	25	2.03 (1.19, 3.45)	**0.01**		
Prepared food or cooked together	25	28	1.32 (0.68, 2.56)	0.41		
Ate food from the same plate	19	18	1.53 (0.68, 3.41)	0.30		
Shared a drinking glass or bottle	19	14	1.62 (0.85, 3.08)	0.15		
Shared an eating utensil	7	11	1.04 (0.31, 3.47)	0.95		

Note: Boldface indicates statistical significance ($p<0.05$).
Logistic regression models were estimated using GEEs with a binary distribution and exchangeable working correlation to account for household clustering. The multivariable GEE analysis includes behaviors chosen by a detailed selection method adjusting for vaccination status identified as confounders.
[a]Secondary cases.
[b]Missing information (n=1).
GEE, generalized estimating equation; NH, Non-Hispanic.

study in Brunei, which focused on transmission in different settings.[32] The nature of the relationship between parent−child, married couples, and roommate is such that shared activities (e.g., sleeping in the same bed or bedroom) are commonplace.[33,34]

Eating food prepared by the primary case also significantly increased secondary transmission among household contacts in this investigation. It is worth noting that restaurant closures and stay-at-home policies during the pandemic resulted in shifts to food preparation in the home.[35,36] There is no evidence that SARS-CoV-2 is spread through food, but rather transmission may occur when a household member gathers with family.[37] Eating food prepared by the primary case may therefore reflect the risk of the primary case not isolating. Parents, siblings, and others related to the primary case were noted as less likely to eat food prepared by the primary case. It is possible that they prepared the meals for the primary case. Although we found an association between education level and eating food prepared by the primary case, there was no observable trend. Within the education levels, factors such as risk perception, attitude toward the behavior, and knowledge about the behavior as it relates to COVID-19 may have played a role in the reported finding but were not accounted for in our analysis.

Table 3. Association of Each Self-Reported Behavior With Individual or Household Characteristics Among Household Contacts (N=307)

Characteristics	Slept in the same bedroom				Ate food prepared by the primary case			
	Univariable analysis		Multivariable analysis		Univariable analysis		Multivariable Analysis	
	OR (95% CI)	*p*-value	AOR (95% CI)	*p*-value	OR (95% CI)	*p*-value	AOR (95% CI)	*p*-value
Age, years								
<18	1.11 (0.44, 2.83)	0.82	18.42 (3.90, 86.94)	**<0.01**	1.11 (0.61, 2.00)	0.74		
18–49	2.71 (1.18, 6.24)	**0.02**	2.69 (1.11, 6.48)	**0.03**	1.17 (0.62, 2.20)	0.63		
≥50	ref		ref		ref			
Race/ethnicity[a]								
Hispanic/Latino	0.55 (0.26, 1.20)	0.13	0.23 (0.06, 0.92)	**0.04**	0.89 (0.34, 2.31)	0.81		
All other NH races	1.01 (0.43, 2.39)	0.97	0.92 (0.28, 3.04)	0.89	0.65 (0.37, 1.15)	0.14		
NH White	ref		ref		ref			
Relationship to primary case								
Partner	ref		ref		ref		ref	
Son/daughter	0.09 (0.04, 0.21)	**<0.01**	0.01 (<0.01, 0.04)	**<0.01**	0.89 (0.58, 1.38)	0.60	1.24 (0.71, 2.16)	0.46
Parent	0.10 (0.04, 0.24)	**<0.01**	0.08 (0.03, 0.23)	**<0.01**	0.29 (0.12, 0.71)	**0.01**	0.31 (0.13, 0.75)	**0.01**
Sibling	0.13 (0.05, 0.33)	**<0.01**	0.02 (<0.01, 0.07)	**<0.01**	0.17 (0.06, 0.47)	**<0.01**	0.23 (0.07, 0.77)	**0.02**
Other	0.04 (0.01, 0.17)	**<0.01**	0.03 (0.01, 0.13)	**<0.01**	0.18 (0.06, 0.59)	**<0.01**	0.21 (0.06, 0.69)	**0.01**
Household dimension[b]								
≤2,000 ft^2	2.17 (1.14, 4.13)	**0.02**	3.97 (1.73, 9.10)	**<0.01**	1.92 (0.85, 4.33)	0.12		
>2,000 ft^2	ref		ref		ref			
Sex								
Female	1.16 (0.72, 1.86)	0.53			0.78 (0.56, 1.10)	0.16		
Male	ref				ref			
Education[a]								
No degree	0.35 (0.17, 0.75)	**0.01**			0.61 (0.37, 1.00)	0.05	0.45 (0.21, 0.98)	**0.04**
High-school degree	0.80 (0.34, 1.89)	0.60			0.77 (0.40, 1.46)	0.42	0.68 (0.33, 1.42)	0.31
Technical, associate, or bachelor's degree	0.61 (0.29, 1.30)	0.20			0.46 (0.27, 0.79)	**<0.01**	0.44 (0.23, 0.82)	**0.01**
Advanced degree	ref				ref		ref	
Vaccination status								
Fully	0.62 (0.23, 1.68)	0.35			0.66 (0.29, 1.55)	0.34		
Partially	1.19 (0.55, 2.57)	0.65			0.67 (0.37, 1.20)	0.18		
Unvaccinated	ref				ref			
Children in the home								
With children	0.47 (0.25, 0.88)	**0.02**			0.55 (0.25, 1.20)	0.13		
No children	ref				ref			

Note: Boldface indicates statistical significance ($p<0.05$).
Logistic regression models were estimated using GEE with a binary distribution and exchangeable working correlation to account for household clustering. The multivariable GEE analysis includes characteristics chosen by a detailed selection method.
[a]Missing information (n=1).
[b]Household dimension not provided (n=16).
ft^2, square feet; GEE, generalized estimating equation; NH, Non-Hispanic.

CDC has issued public health recommendations for prevention of household transmission of SARS-CoV-2[8]; however, adherence to these recommendations continues to be a challenge. The COVID-19 pandemic has disrupted lives globally, resulting in stressful situations that require social support.[38] There may therefore be practical challenges with restricting shared activities among household contacts that may increase exposure to the primary case. For example, a study in Nigeria reported overcrowding in small homes posing challenges to adhering to mitigation behaviors.[39] The investigation showed that household dimension was associated with sleeping in the same bedroom as the primary case. Households with small dimensions may encounter challenges of isolating cases if, for example, the number of people living in the household is large or if there is only 1 bedroom in the household, characteristics not examined in this investigation. Compounding these challenges, households may be frustrated and fatigued from efforts to follow the recommended mitigation practices[15,40] as the pandemic progresses beyond 2 years.

This investigation occurred during the initial phase of the SARS-CoV-2 vaccine introduction in early 2021. Thus, a small percentage of participants were partially vaccinated, and even fewer were fully vaccinated. The analysis showed that vaccination status was associated with nonsignificant decreased risks of secondary transmission; however, the number of vaccinated persons at that point in the pandemic was small, and statistical power was likely limited. Vaccines have been shown to be safe and efficacious in preventing serious morbidity and reducing the risk of mortality by SARS-CoV-2.[41–43] Mitigation should therefore complement effective preventive behaviors and vaccination.[44,45]

Engaging in healthy behavior can be complex, and different factors play a role in motivating individuals.[46] Although half of the household contacts who were secondary cases never used masks in the same room or had direct physical contact with the primary case, the findings showed no association with secondary transmission. This finding does not imply that these behaviors are not associated with secondary transmission. A potential reason could be that transmission may have occurred before household contacts and primary cases were aware of the infection and could have little to do with adherence to mitigation recommendations. Individuals not wearing masks may have done so at a distance from the primary case. Furthermore, when in direct physical contact with the primary case, household contacts may have engaged in effective hygiene practices—all of which are encouraged in CDC guidelines for preventing the spread of SARS-CoV-2.[8] In addition, the small sample size of the investigation may have limited power to detect multiple behaviors associated with transmission or interactions between behaviors.

The findings suggest the need to develop messaging that promotes adherence to effective mitigation measures for varying household settings, such as increasing air circulation by opening windows or using a fan, frequent hand washing, sleeping in a separate room, and, if not possible, wearing masks inside the home or isolating the primary case in another dwelling (makeshift isolation sites). This will be key as the pandemic continues to evolve with the possible emergence of new variants, the potential increase in the number of confirmed cases, and individuals choosing to recover in their homes.

Limitations

The findings from this investigation should be interpreted with the following limitations. First, the behaviors were self-reported, and individuals may have either provided socially desirable responses or been unable to recall their actual behaviors. Second, the investigation used a convenience sample, which limits the generalizability of the findings. Furthermore, because this investigation was conducted in early 2021 near the beginning of SARS-CoV-2 vaccine introductions, the findings are not generalizable to the current context in which vaccine-induced and natural immunity are higher. Third, owing to the eligibility criteria of illness onset ≤10 days before enrollment, we assumed that all secondary cases were infected by the primary case; we cannot rule out the possibility of tertiary (contact-to-contact) transmission. Fourth, our investigation did not consider the age of children in the household (specifically young children), a characteristic that may have played a role in the findings on sharing a bed with the primary case and eating food prepared by the primary case. Finally, we were unable to make inferences on race or ethnicity given the small sample size of our investigation.

CONCLUSIONS

We found that sleeping in the same bedroom as and eating food prepared by the primary case were significantly associated with secondary transmission. Household dimension and relationship to the primary case were associated with these behaviors. These characteristics describe the current mitigation efforts and limited options for mitigation behaviors of members within a household. Mitigation efforts should strongly emphasize feasible measures while recognizing challenges posed to individuals in households with a confirmed SARS-CoV-2 infection. Our findings underscore the importance of implementing innovative means to promote adherence to mitigation measures that reduce household transmission.

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SUPPLEMENTARY MATERIALS

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.focus.2022.100004.

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