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Impact of Age and Symptom Development on SARS-CoV-2 Transmission in Households With Children—Maryland, New York, and Utah, August 2020–October 2021

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Background. Households are common places for spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). We investigated factors associated with household transmission and acquisition of SARS-CoV-2.

Methods. Households with children age <18 years were enrolled into prospective, longitudinal cohorts and followed from August 2020 to August 2021 in Utah, September 2020 to August 2021 in New York City, and November 2020 to October 2021 in Maryland. Participants self-collected nasal swabs weekly and with onset of acute illness. Swabs were tested for SARS-CoV-2 using reverse transcription polymerase chain reaction. We assessed factors associated with SARS-CoV-2 acquisition using a multilevel logistic regression adjusted for household size and clustering and SARS-CoV-2 transmission using a logistic regression adjusted for household size.

Results. Among 2053 people (513 households) enrolled, 180 people (8.8%; in 76 households) tested positive for SARS-CoV-2. Compared with children age <12 years, the odds of acquiring infection were lower for adults age ≥18 years (adjusted odds ratio [aOR], 0.34; 95% CI, 0.14–0.87); however, this may reflect vaccination status, which protected against SARS-CoV-2 acquisition (aOR, 0.17; 95% CI, 0.03–0.91). The odds of onward transmission were similar between symptomatic and asymptomatic primary cases (aOR, 1.00; 95% CI, 0.35–2.93) and did not differ by age (12–17 years vs <12 years: aOR, 1.08; 95% CI, 0.20–5.62; ≥18 years vs <12 years: aOR, 1.70; 95% CI, 0.52–5.83).

Conclusions. Adults had lower odds of acquiring SARS-CoV-2 compared with children, but this association might be influenced by coronavirus disease 2019 (COVID-19) vaccination, which was primarily available for adults and protective against infection. In contrast, all ages, regardless of symptoms and COVID-19 vaccination, had similar odds of transmitting SARS-CoV-2. Our findings underscore the importance of SARS-CoV-2 mitigation measures for persons of all ages.

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

As of June 2022, >1 million people have died from infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in the United States [1]. Households are common places for SARS-CoV-2 to spread [2], and studies of households can be used to learn more about factors associated with virus transmission and susceptibility. Previous work has assessed the influence of personal characteristics, such as a person's age, symptom development, or coronavirus disease 2019 (COVID-19) vaccination status, on SARS-CoV-2 transmission and acquisition in the household [3–19]; however, most of these studies were limited by retrospective design [4, 7, 8, 11, 13, 17, 18] or use of data collected before the Delta wave [3–17].

We built upon previous work to investigate risk factors associated with transmission and acquisition of SARS-CoV-2 among children and adults in household-based, longitudinal cohorts in New York City, Utah, and Maryland [20, 21]. Following participants through the Alpha and Delta waves, we hypothesized that a person's age would not be associated with SARS-CoV-2 acquisition or transmission, COVID-19 vaccination status would protect against viral acquisition or transmission, and presence of symptoms would increase odds of transmission.

METHODS

Study Design

In response to the COVID-19 pandemic, the US Centers for Disease Control and Prevention (CDC) initiated 2 household-based, prospective cohort studies to estimate the incidence and within-household transmission of SARS-CoV-2: (i) the Coronavirus Household Evaluation and Respiratory Testing (C-HEaRT) study in New York City and Utah [20] and (ii) the SARS-CoV-2 Epidemiology And Response in Children (SEARCh) study in Maryland [21]. C-HEaRT recruited households with at least 1 child age <18 years from previously established cohorts and the broader community [22, 23]. SEARCh recruited households with at least 1 child age 0–4 years from pediatric primary care practices. Households were followed from enrollment until study end in C-HEaRT and for 8 months from enrollment in SEARCh. Study enrollment and follow-up occurred from August 2020 to August 2021 in Utah, September 2020 to August 2021 in New York City, and November 2020 to October 2021 in Maryland.

At enrollment, serum specimens were collected, and participants completed online surveys describing demographic characteristics, history of COVID-19 testing and infection, and household features. Throughout follow-up, participants completed a weekly survey, online or via text, about symptoms experienced in the preceding week and, if symptoms were experienced, mitigation measures they took like isolating and wearing a mask. SARS-CoV-2 vaccination information was collected through medical record abstraction of immunization records and self-reported on follow-up surveys. Specific questionnaires used are available in the Supplementary Data. Participants self-collected nasal swabs weekly and additional swabs with onset of acute illness with COVID-19-like symptoms; parents collected nasal swabs for young children at these same time points instead of the children self-swabbing.

Swabs were tested for SARS-CoV-2 using reverse transcription polymerase chain reaction (RT-PCR; Quidel Lyra SARS-CoV-2 Assay [24] or ThermoFisher TaqPath COVID-19 Combo Kit [25]) at Marshfield Clinic Research Institute in Wisconsin [20]. The CDC conducted viral whole-genome sequencing [26, 27] on an individual's first nasal swab specimen with a cycle threshold value ≤30 for the SARS-CoV-2 nucleocapsid target using the IDT xGen SARS-CoV-2 library prep kit [28]. Libraries were sequenced using 2×150 base pair Illumina Chemistry on a MiSeq or NovaSeq instrument. Demultiplexed data were down-sampled to 1 million reads per sample, primers were trimmed with BBDuk (BBMap, version 38.87) [29], and a single consensus genome for each sample was generated with Iterative Refinement Meta-Assembler (IRMA), version 1.0.2, using the default CoV configuration [30]. We performed clade assignments using Nextclade, version 1.13.2 [31], and assigned lineages using Pangolin, version 3.1.20 (pangoLEARN 1.2.123, Scorpio 0.3.16) [32].

Acquisition of SARS-CoV-2

To assess household acquisition of SARS-CoV-2, the analysis was restricted to households with ≥1 RT-PCR-confirmed SARS-CoV-2 infection among enrolled household members. Participants with a positive test were classified as having a primary, secondary, or tertiary household infection. Primary cases were defined as participants with the first symptom onset or positive SARS-CoV-2 test, whichever occurred earlier, in the households. Co-primary cases were participants who had symptom onset or a positive test <2 days after the household's initial SARS-CoV-2 infection [33]. Participants who were secondary cases had a positive SARS-CoV-2 test ≥2 days after the household's first detected infection, and tertiary cases tested positive >2 days after a household's initial secondary infection date [33]. Tertiary cases were excluded from estimation of the crude secondary infection risk (SIR). Primary or co-primary cases were excluded from the acquisition analysis.

We then evaluated the association between household member characteristics and the odds of SARS-CoV-2 acquisition among people who were a secondary case or later using multilevel logistic regressions controlling for household size (households with <5 or ≥5 people) and clustering (household-level random intercept). The household size categorization threshold was chosen based on the median household size (5) of the participants in the analysis set. Models did not adjust for COVID-19 vaccination status because not all members were eligible for vaccination. Household member characteristics assessed included (i) study site (New York, Utah, or Maryland); (ii) age group (<12, 12–17, and ≥18 years); (iii) gender; (iv) presence of ≥1 high-risk medical condition; (v) vaccination status, defined as primary COVID-19 vaccination series receipt (1 dose of a vector-based vaccine or 2 doses of an mRNA vaccine) ≥14 days before the household was affected by SARS-CoV-2; and (vi) having a prior SARS-CoV-2 infection. A participant had a prior SARS-CoV-2 infection if at enrollment they self-reported a previous SARS-CoV-2 infection diagnosis or had SARS-CoV-2 antibodies present in enrollment serology based on results from the Roche Elecsys Anti-SARS-CoV-2 Assay (Maryland) [34] and Luminex xMAP-SARS-CoV-2 Multiantigen Assay (New York and Utah) [35].

Further analyses investigated how COVID-19 vaccination status impacted the relationship between a participant's age and the likelihood of SARS-CoV-2 acquisition. A multilevel logistic regression model adjusted for household size, and clustering was repeated using a composite variable of each participant's age group and COVID-19 vaccination status before household infection: (i) unvaccinated children (<12 years); (ii) unvaccinated adolescents (12–17 years); (iii) vaccinated adolescents; (iv) unvaccinated adults (≥18 years); and (v) vaccinated adults.

Transmission of SARS-CoV-2

Next, we evaluated the association between households' primary SARS-CoV-2 case characteristics and the odds of transmitting SARS-CoV-2 to ≥1 household member. Often, several household members acquired the infection at the same time, resulting in co-primary cases and challenging identification of which primary case was the source of infection for others in the household. To remove the influence of this uncertainty, we excluded households with co-primary cases from the transmission analysis. We supplemented the analysis by repeating it using a previously published probabilistic transmission trees approach that accounted for co-primary cases [36], with methods presented in the Supplementary Data.

Across the remaining primary cases, we assessed primary case characteristics related to SARS-CoV-2 transmission to ≥1 other nonprimary case household member. Characteristics assessed included (i) study site; (ii) age group; (iii) gender; (iv) presence of ≥1 high-risk medical condition; (v) receipt of primary COVID-19 vaccination series; (vi) prior SARS-CoV-2 infection; (vii) and symptomatic status, (viii) lineage (Delta [defined as B.1.617.2 and AY lineages] or other variant), and (ix) mitigation measures taken during the current SARS-CoV-2 infection. These associations were evaluated using a logistic regression model adjusted for household size; no household-level clustering was considered as models included only 1 individual per household. A sensitivity analysis assessed the association of (i) symptomatic status and (ii) SARS-CoV-2 lineage and odds of transmitting SARS-CoV-2 to a household member, additionally adjusting for the primary case's age. Additional sensitivity analyses were conducted to assess the association of primary case characteristics with onward transmission by (i) using the proportion of susceptible household contacts who were infected by the primary case as the main outcome in an adjusted Poisson regression; (ii) estimating an adjusted risk ratio of transmission using a log-risk regression model; and (iii) re-calculating the adjusted odds ratio of transmission across mitigation measures on a subset of symptomatic primary cases.

All analyses were conducted using the packages "tidyverse" and "lme4" in R, version 4.0.4 [37–39].

RESULTS

Study Population

Of 2244 people (548 households) contacted to participate in the cohorts, 2053 participants (513 households) enrolled in the longitudinal study across 3 states: 508 (24.7%) in New York, 852 (41.5%) in Utah, and 693 (33.8%) in Maryland (Figure 1; Supplementary Table 1). Participants were enrolled if they consented to the study and completed an individual enrollment questionnaire. From August 2020 to October 2021, 180 people (8.8%; 76 households) tested positive for SARS-CoV-2. Infections were observed throughout the period of observation, but some clustered in time corresponding to increased community circulation (Figure 2) [1]. Most households with infections were in Utah (53.9%). Our analysis focused on each household's first cluster of infections, so we excluded 3 SARS-CoV-2 infections that occurred in participants ≥3 months after their households were initially affected. After excluding these infections, the analysis included 357 people, 177 with SARS-CoV-2, in 76 households with ≥1 member who tested positive for SARS-CoV-2 (Table 1).
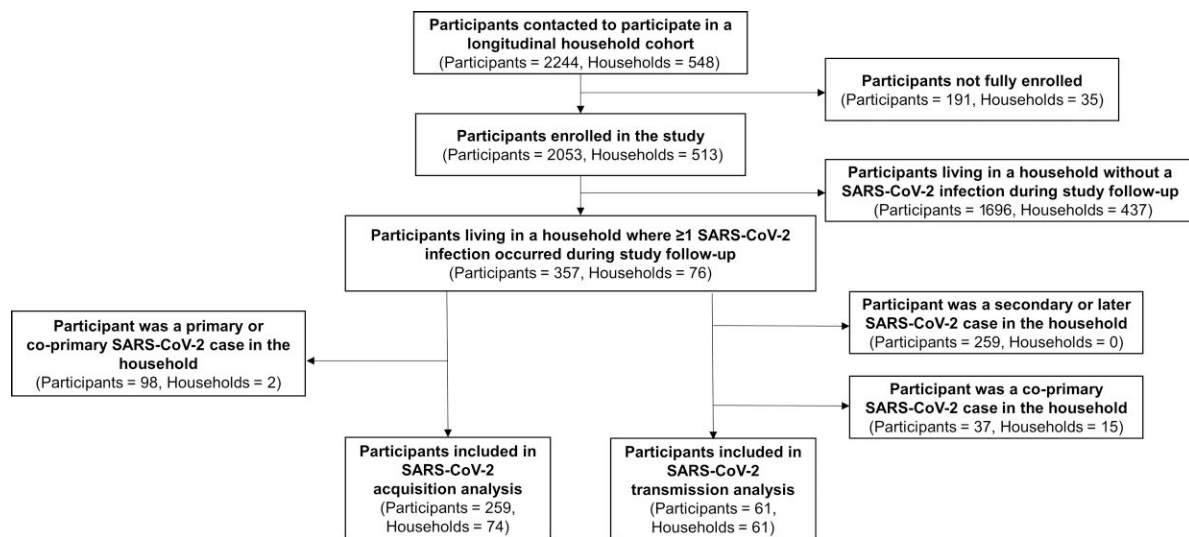
Figure 1. Participants included in analysis data set. This chart depicts how many participants were contacted, fully enrolled in the study, and included in the final analysis data set. Only participants living in a household with at least 1 SARS-CoV-2 infection during study follow-up were included in the analysis data set. Additional criteria were enforced for the acquisition and transmission analyses. Abbreviation: SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.
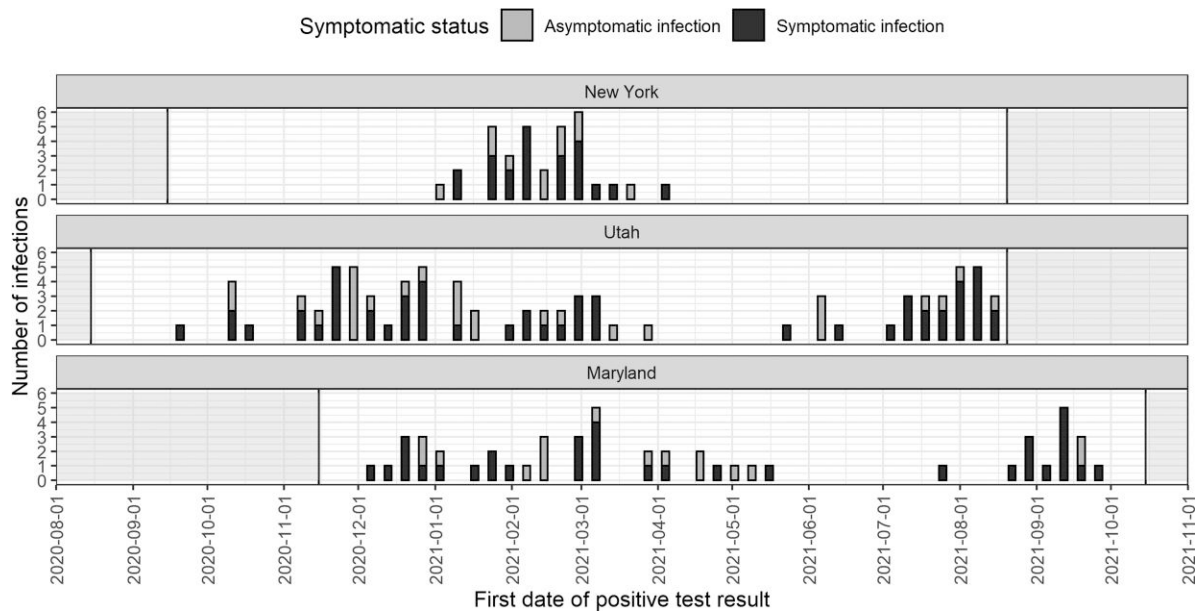
Figure 2. Distribution of SARS-CoV-2 cases over time across longitudinal household cohorts. The distribution of SARS-CoV-2 cases over time is shown stratified by the 3 cohort sites: New York, Utah, and Maryland. Asymptomatic infections are indicated by the gray bars and symptomatic infections by the black bars. The period of follow-up for each study site is indicated by the white area. Abbreviation: SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

Among 177 people with SARS-CoV-2, 81 (45.8%) were children age <12 years, 18 (10.2%) were adolescents age 12–17 years, and 78 (44.1%) were adults age ≥18 years (Supplementary Table 2). During their infection, from the first week of SARS-CoV-2 detection to the last week of detection preceding 2 negative or missed weekly swabs, 120 (67.8%) people reported symptoms. Thirty-two (18.1%) people infected during follow-up had evidence of prior SARS-CoV-2 infection, from self-report or serologic testing, and 16 (9.0%) people infected had received the primary vaccination series. Supplementary Table 3 further describes vaccination information in the cohort, including brand and age eligibility. Across the 177 SARS-CoV-2 infections, 61 (34.5%) were classified as single primary cases, 37 (20.9%) as co-primary cases, 61 (34.5%) as secondary cases, and 18 (10.2%) as tertiary cases. The crude SIR among household members excluding tertiary cases was 23.6% (95% CI, 0.19–0.29; SIR range by site, 22.4%–29.4%).

Risk Factors for Acquisition of SARS-CoV-2

Excluding participants who were primary or co-primary SARS-CoV-2 cases in their households, the association between household member characteristics and SARS-CoV-2 acquisition was assessed among 259 participants in 74 households (Table 2). There was no association with odds of infection in Utah (adjusted odds ratio [aOR], 0.30; 95% CI, 0.03–2.72) and Maryland (aOR, 0.35; 95% CI, 0.03–3.74) compared with New York. Compared with children age <12 years, adults (aOR, 0.34; 95% CI, 0.14–0.87) were less likely to acquire

SARS-CoV-2 from a household member; however, no association was found between children age <12 years and adolescents age 12–17 years and acquisition of SARS-CoV-2 (aOR, 0.33; 95% CI, 0.07–1.45), possibly due to limited sample size. Participants who received the primary COVID-19 vaccination series before household SARS-CoV-2 introduction had significantly lower odds of SARS-CoV-2 infection (aOR, 0.17; 95% CI, 0.03–0.91). When unvaccinated adults were compared with unvaccinated children age <12 years, there was no longer an association with odds of acquiring SARS-CoV-2 (aOR, 0.51; 95% CI, 0.18–1.45); vaccinated adults compared with unvaccinated children age <12 years had significantly lower odds of infection (aOR, 0.10; 95% CI, 0.01–0.65). Prior SARS-CoV-2 infection was not associated with odds of SARS-CoV-2 reacquisition (aOR, 0.82; 95% CI, 0.20–3.36); this pattern was also observed when prior infection was defined only based on presence of SARS-CoV-2 antibodies at enrollment (aOR, 2.27; 95% CI, 0.45–11.46).

Risk Factors for Transmission of SARS-CoV-2

After excluding households with co-primary cases (Supplementary Table 4), risk factors for SARS-CoV-2 transmission from infected primary cases to their household members were assessed. Across 61 households with single primary cases, 32 (52.5%) did not transmit SARS-CoV-2 to another enrolled household member, whereas 29 (47.5%) did. Of the 29 households with onward transmission, 13 (44.8%) experienced transmission to only 1 other person in the household, and 5 (17.2%) had all

Table 1. Characteristics of Participants Living in a Household With a SARS-CoV-2-Positive Participant

	C-HEaRT		SEARCh	Total
	New York No. (%)	Utah No. (%)	Maryland No. (%)	No. (%)
Total households	13	41	22	76
Total participants	52	211	94	357
Age groups				
<12 y	17 (32.7)	95 (45.0)	45 (47.9)	157 (44.0)
12–17 y	7 (13.5)	31 (14.7)	5 (5.3)	43 (12.0)
≥18 y	28 (53.8)	85 (40.3)	44 (46.8)	157 (44.0)
Gender				
Male	28 (53.8)	99 (46.9)	46 (48.9)	173 (48.5)
Female	23 (44.2)	112 (53.1)	48 (51.1)	183 (51.3)
Nonbinary/third gender	1 (1.9)	0 (0.0)	0 (0.0)	1 (0.3)
Race/ethnicity				
White, non-Hispanic	6 (11.5)	191 (90.5)	73 (77.7)	270 (75.6)
Black, non-Hispanic	2 (3.8)	1 (0.5)	2 (2.1)	5 (1.4)
Asian, non-Hispanic	0 (0.0)	0 (0.0)	3 (3.2)	3 (0.8)
Other, non-Hispanic	0 (0.0)	1 (0.5)	0 (0.0)	1 (0.3)
Multiracial, non-Hispanic	3 (5.8)	4 (1.9)	14 (14.9)	21 (5.9)
Hispanic	41 (78.8)	13 (6.2)	2 (2.1)	56 (15.7)
Unknown	0 (0.0)	1 (0.5)	0 (0.0)	1 (0.3)
High-risk medical condition[a]				
No	35 (67.3)	149 (70.6)	61 (64.9)	245 (68.6)
Yes	17 (32.7)	62 (29.4)	33 (35.1)	112 (31.4)
Primary vaccination series before household infection				
No	52 (100.0)	180 (85.3)	82 (87.2)	314 (88.0)
Yes	0 (0.0)	31 (14.7)	12 (12.8)	43 (12.0)
Previous SARS-CoV-2 infection[b]				
No	36 (69.2)	187 (88.6)	66 (70.2)	289 (81.0)
Yes	16 (30.8)	24 (11.4)	27 (28.7)	67 (18.8)
Unknown	0 (0.0)	0 (0.0)	1 (1.1)	1 (0.3)
SARS-CoV-2 infection during study follow-up[c]				
No	19 (36.5)	118 (55.9)	43 (45.7)	180 (50.4)
Yes	33 (63.5)	93 (44.1)	51 (54.3)	177 (49.6)

Abbreviations: C-HEaRT, Coronavirus Household Evaluation and Respiratory Testing study; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; SEARCh, SARS-CoV-2 Epidemiology And Response in Children study.

[a]High-risk medical conditions included were asthma, chronic lung disease, active tuberculosis, chronic bronchitis, cystic fibrosis, chronic obstructive pulmonary disease, obstructive sleep apnea, chronic metabolic disease, diabetes, thyroid problems, blood disorders, hypertension, cardiovascular disease, bladder disease, liver disease, immunocompromised condition, leukemia, cancer, long-term steroid treatment, organ transplant, neurologic condition, or autoimmune condition.

[b]Defined using self-reported prior SARS-CoV-2 infection or antibodies detected in serology at enrollment.

[c]Three people in the Utah cohort had SARS-CoV-2 infection during follow-up 3 months or more after their households' initial SARS-CoV-2 introduction. Households were censored from the analysis after their initial SARS-CoV-2 introduction, so these 3 infections were excluded from the analysis and not presented here.

enrolled members infected (range of household size, 2–7 people) (Figure 3).

No demographic characteristics of people infected with SARS-CoV-2 were found to significantly modify their odds of transmitting the virus to at least 1 other household member (Table 3). The odds that the primary case transmitted SARS-CoV-2 to a household member were not significantly different across study sites (Utah vs New York: aOR, 0.44; 95% CI, 0.07–2.27; Maryland vs New York: aOR, 0.41; 95% CI, 0.07–2.11). Compared with children age <12 years, adolescents (aOR, 1.08; 95% CI, 0.20–5.62) and adults (aOR, 1.70; 95% CI, 0.52–5.83) had overall similar odds of transmitting SARS-CoV-2 to other household members.

There was no association between the odds of SARS-CoV-2 transmission from participants who completed the primary COVID-19 vaccination series vs those who were unvaccinated (aOR, 0.44; 95% CI, 0.06–2.57). Compared with those without prior infection, people with prior SARS-CoV-2 infection (aOR, 0.96; 95% CI, 0.24–3.65) had similar odds of SARS-CoV-2 transmission to another household member; results were similar when prior infection was defined only based on presence of SARS-CoV-2 antibodies at enrollment (aOR, 1.61; 95% CI, 0.37–7.58). When we cast the outcome as the proportion of susceptible household members who became infected, we found that adult primary cases transmitted within the household at a significantly greater rate than

Table 2. Odds of SARS-CoV-2 Acquisition After Household Introduction Across Household Member Characteristics

	No. of Susceptible Participants After Household Introduction[a] No. (%)	No. of SARS-CoV-2 Infections No. (% of Row Total)	Odds of Infection After Household Introduction Adjusted for Household Size and Clustering aOR (95% CI)[b]
Total participants	259	79 (30.5)	…
Total households	74	37 (50.0)	…
Study site			
C-HEaRT: New York	34 (13.1)	15 (44.1)	Ref
C-HEaRT: Utah	161 (62.2)	43 (26.7)	0.30 (0.03–2.72)
SEARCh: Maryland	64 (24.7)	21 (32.8)	0.35 (0.03–3.74)
Age group			
<12 y	123 (47.5)	47 (38.2)	Ref
12–17 y	32 (12.4)	7 (21.9)	0.33 (0.07–1.45)
≥18 y	104 (40.2)	25 (24.0)	0.34 (0.14–0.87)
Gender, No. (%)[c]			
Male	122 (47.3)	40 (32.8)	Ref
Female	136 (52.7)	39 (28.7)	1.00 (0.43–2.34)
High-risk medical condition[d]			
No	182 (70.3)	56 (30.8)	Ref
Yes	77 (29.7)	23 (29.9)	1.46 (0.54–3.97)
Primary vaccination series before household infection			
No	228 (88.0)	75 (32.9)	Ref
Yes	31 (12.0)	4 (12.9)	0.17 (0.03–0.91)
Previous SARS-CoV-2 infection[e,f]			
No	212 (82.2)	68 (32.1)	Ref
Yes	46 (17.8)	11 (23.9)	0.82 (0.20–3.36)

Abbreviations: aOR, adjusted odds ratio; C-HEaRT, Coronavirus Household Evaluation and Respiratory Testing study; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; SEARCh, SARS-CoV-2 Epidemiology And Response in Children study.

[a]Primary and co-primary cases are excluded.

[b]Results from a multilevel logistic regression model adjusted for household size and clustering.

[c]Nonbinary/third gender was excluded from this association due to data sparsity (n = 1 observation).

[d]High-risk medical conditions included were asthma, chronic lung disease, active tuberculosis, chronic bronchitis, cystic fibrosis, chronic obstructive pulmonary disease, obstructive sleep apnea, chronic metabolic disease, diabetes, thyroid problems, blood disorders, hypertension, cardiovascular disease, bladder disease, liver disease, immunocompromised condition, leukemia, cancer, long-term steroid treatment, organ transplant, neurologic condition, or autoimmune condition.

[e]Defined using self-reported prior SARS-CoV-2 infection or antibodies detected in serology at enrollment.

[f]One observation was missing and excluded from this association.

children age <12 years (adjusted rate ratio [aRR], 1.97; 95% CI, 1.07–3.91) (Supplementary Table 5), as did primary cases with a high-risk medical condition (aRR, 2.69; 95% CI, 1.51–4.68).

People with symptomatic compared with asymptomatic infections (aOR, 1.00; 95% CI, 0.35–2.93) had comparable odds of SARS-CoV-2 transmission, which was also reflected in the crude frequencies of asymptomatic (47.6%) and symptomatic (47.5%) primary cases who transmitted SARS-CoV-2 in their households (Table 3). No association with odds of transmission was seen among people experiencing chills (aOR, 2.25; 95% CI, 0.32–19.53), cough (aOR, 1.36; 95% CI, 0.39–4.84), diarrhea (aOR, 1.22; 95% CI, 0.14–11.06), headache (aOR, 1.22; 95% CI, 0.36–4.22), or loss of taste or smell (aOR, 2.42; 95% CI, 0.43–18.63) during the course of their illness; however, data were underpowered to detect associations across many specific symptoms. A sensitivity analysis of odds of transmission by a person's symptomatic status adjusted for age in addition to household size produced a similar point estimate (symptomatic

vs asymptomatic: aOR, 0.71; 95% CI, 0.19–2.47), but a higher proportion of primary case adults (85.3%) reported symptoms than adolescents (60.0%) or children (29.4%) (Supplementary Table 6). Participants infected with the Delta variant (23.1%) compared with another lineage (76.9%) of SARS-CoV-2 were not associated with odds of SARS-CoV-2 transmission to another household member (aOR, 1.23; 95% CI, 0.27–5.88); results remained similar when also adjusting for age (aOR, 1.46; 95% CI, 0.28–8.74).

The only mitigation measure significantly associated with reduced odds of SARS-CoV-2 transmission was staying in a separate room from other household members (aOR, 0.17; 95% CI, 0.02–0.97) (Table 3). Among a subset of only symptomatic primary cases, mitigation measure results were the same (Supplementary Table 7). Across demographic and infection risk factors, results were similar using the proportion of susceptible household contacts who were infected as an alternative measure of transmission (Supplementary Table 5), log-risk regression to estimate an adjusted risk ratio of transmission
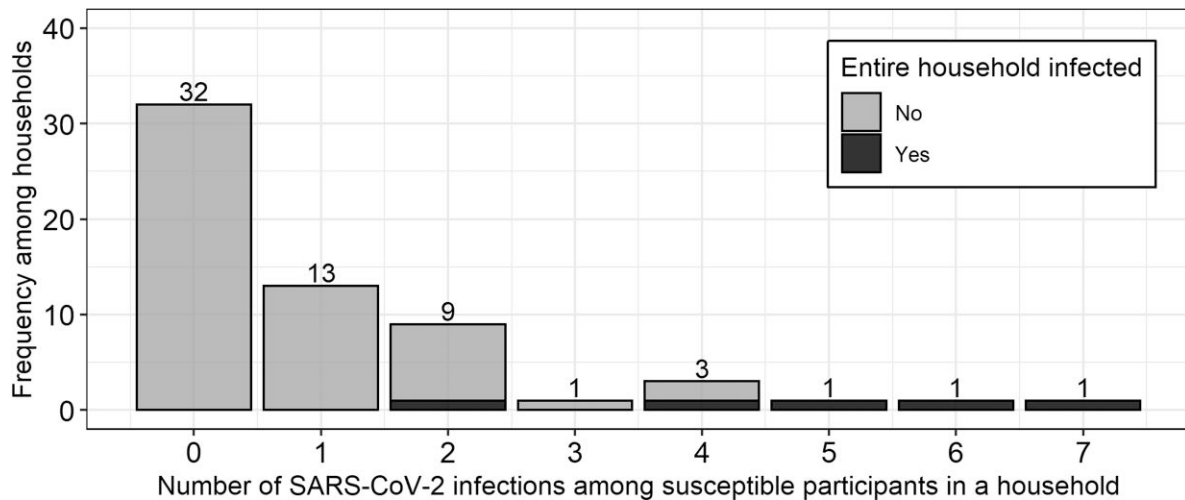
Figure 3. Distribution of number of susceptible people who acquired SARS-CoV-2 in their households from the primary case among households with only 1 primary case. The distribution of SARS-CoV-2 infections susceptible people acquired in their households is displayed. Households with co-primary cases were excluded. Abbreviation: SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

(Supplementary Table 8), and a probabilistic modeling approach (Supplementary Results, Supplementary Tables 9–11).

DISCUSSION

Within large, multisite prospective cohorts of households with children who were under active symptom surveillance and tested weekly, we found that 1 in 4 households experienced onward spread of SARS-CoV-2 among household contacts. We examined factors associated with odds of acquiring or transmitting SARS-CoV-2 in the household and observed that individuals of all ages and symptomatic status had similar odds of transmitting SARS-CoV-2. Fully vaccinated individuals had reduced odds of SARS-CoV-2 infection. Adults also had lower odds of infection, possibly due to higher rates of COVID-19 vaccination. Infected individuals who stayed in a separate room had lower odds of transmitting SARS-CoV-2 to another household member. These findings underscore the importance of COVID-19 vaccination and following recommendations to prevent infection and control transmission within the household regardless of the age or symptoms of the primary case [40].

In our study, people of all ages acquired and transmitted SARS-CoV-2 within their households, but the odds of viral acquisition were lower in adults. Other studies had variable results concerning the association between age and SARS-CoV-2 infection, with some studies finding that young children had lower infection rates than adults [7, 8, 11, 14, 17] and others no clear association [12, 15]. Meta-analyses have described comparable SARS-CoV-2 transmission by all age groups (as we found) [2] but higher SARS-CoV-2 secondary acquisition in adults [2, 41], which differs from our results. We observed roughly 70% lower odds of household acquisition of

SARS-CoV-2 among adults compared with children age <12 years, but the apparent protective effect of age on SARS-CoV-2 acquisition may be related to vaccination status, as adults had earlier access to COVID-19 vaccination during the study period than children or adolescents. When we compared SARS-CoV-2 acquisition in unvaccinated adults with unvaccinated children, the protective association with age was greatly reduced and no longer significant, suggesting that vaccination status played a role in the association between age and SARS-CoV-2 infection; however, results were limited by small sample size. Additional larger studies may be able to better disentangle the effect of age and COVID-19 vaccination on risk of household SARS-CoV-2 acquisition.

COVID-19 vaccination was associated with reduced odds of SARS-CoV-2 infection, but there was not a significant reduction in the likelihood of vaccinated individuals transmitting the virus. Previous results from data collected early in COVID-19 vaccine availability suggested that vaccination lessened the likelihood of transmission to household members [42]. Other work found that this protective effect was reduced but still present with the emergence of the Delta variant [43]. Similar to our findings, recent household cohort studies restricting analyses to Delta variant circulation indicated that COVID-19 vaccination reduced household SARS-CoV-2 acquisition but was not significantly protective against transmission [18, 19]. Because the effect of COVID-19 vaccination at preventing household transmission may differ with new SARS-CoV-2 variants, it is important to follow recommendations to mitigate transmission in the household even when the primary case has been vaccinated.

Table 3.   Odds of SARS-CoV-2 Transmission to a Household Member Across Characteristics of Primary Cases

	No. of Primary Cases[a] No. (%)	No. of Primary Cases who Transmitted SARS-CoV-2 No. (% of Row Total)	Odds of Transmission to a Household Member Adjusted for Household Size aOR (95% CI)[b]
Characteristics of participants			
Total households	61	29 (47.5)	...
Study site			
C-HEaRT: New York	9 (14.8)	6 (66.7)	Ref
C-HEaRT: Utah	34 (55.7)	15 (44.1)	0.44 (0.07–2.27)
SEARCh: Maryland	18 (29.5)	8 (44.4)	0.41 (0.07–2.11)
Age group			
<12 y	17 (27.9)	7 (41.2)	Ref
12–17 y	10 (16.4)	4 (40.0)	1.08 (0.20–5.62)
≥18 y	34 (55.7)	18 (52.9)	1.70 (0.52–5.83)
Gender[c]			
Male	30 (49.2)	17 (56.7)	Ref
Female	31 (50.8)	12 (38.7)	0.45 (0.15–1.25)
High-risk medical condition[d]			
No	39 (63.9)	17 (43.6)	Ref
Yes	22 (36.1)	12 (54.5)	1.61 (0.56–4.75)
Primary vaccination series before household infection			
No	55 (90.2)	27 (49.1)	Ref
Yes	6 (9.8)	2 (33.3)	0.44 (0.06–2.57)
Previous SARS-CoV-2 infection[e]			
No	50 (82.0)	24 (48.0)	Ref
Yes	11 (18.0)	5 (45.5)	0.96 (0.24–3.65)
SARS-CoV-2 infection characteristics			
Symptomatic status			
Asymptomatic infection	21 (34.4)	10 (47.6)	Ref
Symptomatic infection	40 (65.6)	19 (47.5)	1.00 (0.35–2.93)
Presence of specific symptoms[f]			
Shortness of breath	6 (9.8)	3 (50.0)	1.05 (0.18–6.19)
Chills	5 (8.2)	3 (60.0)	2.25 (0.32–19.53)
Cough	13 (21.3)	7 (53.8)	1.36 (0.39–4.84)
Nausea	3 (4.9)	1 (33.3)	...
Vomiting	0 (0.0)	0 (0.0)	...
Diarrhea	4 (6.6)	2 (50.0)	1.22 (0.14–11.06)
Fatigue	10 (16.4)	5 (50.0)	1.18 (0.29–4.79)
Fever	12 (19.7)	5 (41.7)	0.77 (0.20–2.77)
Headache	14 (23.0)	7 (50.0)	1.22 (0.36–4.22)
Body aches	12 (19.7)	5 (41.7)	0.77 (0.20–2.77)
Joint pain	5 (8.2)	4 (80.0)	...
Abdominal pain	3 (4.9)	1 (33.3)	...
Chest pain	2 (3.3)	1 (50.0)	...
Nasal congestion	20 (32.8)	10 (50.0)	1.16 (0.39–3.44)
Sore throat	14 (23.0)	7 (50.0)	1.14 (0.34–3.85)
Loss of taste or smell	6 (9.8)	4 (66.7)	2.42 (0.43–18.63)
Conjunctivitis	1 (1.6)	0 (0.0)	...
SARS-CoV-2 lineage			
Other lineage	30 (49.2)	15 (50.0)	Ref
Delta lineage	9 (14.8)	5 (55.6)	1.23 (0.27–5.88)
Unknown	22 (36.1)	9 (40.9)	...
Mitigation measures[g]			
Used own bathroom			
No	17 (27.9)	10 (58.8)	Ref
Yes	9 (14.8)	3 (33.3)	0.35 (0.06–1.81)
Unknown	35 (57.4)	16 (45.7)	...
Did not receive care from another member			
No	14 (23.0)	5 (35.7)	Ref

Table 3. Continued

	No. of Primary Cases[a] No. (%)	No. of Primary Cases who Transmitted SARS-CoV-2 No. (% of Row Total)	Odds of Transmission to a Household Member Adjusted for Household Size aOR (95% CI)[b]
Yes	13 (21.3)	8 (61.5)	3.00 (0.64–15.95)
Unknown	34 (55.7)	16 (47.1)	…
Avoided close contact			
No	20 (32.8)	11 (55.0)	Ref
Yes	7 (11.5)	2 (28.6)	0.33 (0.04–1.94)
Unknown	34 (55.7)	16 (47.1)	…
Wore mask			
No	18 (29.5)	9 (50.0)	Ref
Yes	9 (14.8)	4 (44.4)	0.81 (0.15–4.08)
Unknown	34 (55.7)	16 (47.1)	…
Avoided sharing drinks and utensils			
No	5 (8.2)	3 (60.0)	Ref
Yes	22 (36.1)	10 (45.5)	0.52 (0.06–3.87)
Unknown	34 (55.7)	16 (47.1)	…
Slept in alone in room			
No	14 (23.0)	7 (50.0)	Ref
Yes	13 (21.3)	6 (46.2)	0.85 (0.18–3.90)
Unknown	34 (55.7)	16 (47.1)	…
Stayed in separate room			
No	18 (29.5)	11 (61.1)	Ref
Yes	9 (14.8)	2 (22.2)	0.17 (0.02–0.97)
Unknown	34 (55.7)	16 (47.1)	…

Abbreviations: aOR, adjusted odds ratio; C-HEaRT, Coronavirus Household Evaluation and Respiratory Testing study; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; SEARCh, SARS-CoV-2 Epidemiology And Response in Children study.

[a]Households with co-primary cases were excluded.

[b]Results from a logistic regression model adjusted for household size.

[c]No primary cases identified as nonbinary/third gender.

[d]High-risk medical conditions included were asthma, chronic lung disease, active tuberculosis, chronic bronchitis, cystic fibrosis, chronic obstructive pulmonary disease, obstructive sleep apnea, chronic metabolic disease, diabetes, thyroid problems, blood disorders, hypertension, cardiovascular disease, bladder disease, liver disease, immunocompromised condition, leukemia, cancer, long-term steroid treatment, organ transplant, neurologic condition, or autoimmune condition.

[e]Defined using self-reported prior SARS-CoV-2 infection or antibodies detected in serology at enrollment.

[f]For specific symptoms listed, referent is absence of that symptom during illness with SARS-CoV-2. Adjusted odds ratios were not calculated for some specific symptoms due to sparse data.

[g]Those who did not report use of mitigation measures and those who responded as "unknown" about use of mitigation measures were categorized as "unknown" in the table and excluded from analyses.

A strength of our study, with weekly SARS-CoV-2 testing, was that primary cases in households were captured prospectively and irrespective of symptoms, enabling us to compare transmission risk from symptomatic and asymptomatic primary cases. We found no association between a person having an asymptomatic or symptomatic SARS-CoV-2 infection and odds of transmission to another household member. This aligns with previous work that found no effect of symptom development on transmissibility [11, 15]; however, 2 meta-analyses observed that symptomatic compared with asymptomatic infections were associated with increased transmission to household members [2, 41]. Due to the cross-sectional [16] or retrospective nature [4, 7, 8, 11, 13, 17] of many household cohorts, some studies may have underascertained asymptomatic infections, which could bias findings toward a positive association between the presence of symptoms during infection and transmission; our study design was less likely to be impacted by this bias.

Our study was subject to a few limitations. Due to use of a nonprobabilistic modeling approach, households with multiple primary (co-primary) cases were excluded from the transmission analysis, decreasing our sample size and power to detect small effects. Our approach assumed that all household members were infected from the household's primary case, possibly misclassifying some infections as stemming from the household rather than the community. Because transmission results were generally similar in sensitivity analyses using a probabilistic approach that included households with co-primary cases and accounted for community transmission and because SARS-CoV-2 sequences were similar within households, we anticipate that these limitations had minimal effect on study findings. Comparison of mitigation measures associated with the odds of SARS-CoV-2 transmission were limited by the large number of unknown observations (range, 55.7% to 57.4% depending on the questionnaire item). Finally, this analysis was likely underpowered to detect differences in susceptibility while

accounting for COVID-19 vaccination across age groups; to mitigate this, a sensitivity analysis assessed how odds of acquisition changed in vaccinated adults, unvaccinated adults, and unvaccinated children and found that vaccination played a role in the association between age and acquisition.

In summary, we found that in a household setting people of all ages transmit and acquire SARS-CoV-2, those with asymptomatic infection were as likely to transmit SARS-CoV-2 as those with symptomatic infection, and those who had completed a primary COVID-19 vaccine series were less likely to be infected. To reduce the likelihood of ongoing transmission, households with a SARS-CoV-2-infected member should follow recommended prevention measures [40], irrespective of the presence or absence of symptoms, COVID-19 vaccination status, or age of the affected household member. To reduce transmission potential, nonpharmaceutical interventions could be adopted by all age-eligible household members when possible, including children with asymptomatic infection and caregivers of those children. Future studies could investigate how these associations change with the emergence of new SARS-CoV-2 variants or vaccine approval for younger children.

Supplementary Data

Supplementary materials are available at *Open Forum 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.

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