

1 Infection-induced immunity is associated with protection against SARS-CoV-2 infection, but not
2 decreased infectivity during household transmission

3
4 Aaron M Frutos MPH¹, Guillermina Kuan MD^{2,4}, Roger Lopez MPH^{3,4}, Sergio Ojeda MD⁴,
5 Abigail Shotwell MPH¹, Nery Sanchez MD⁴, Saira Saborio MS^{3,4}, Miguel Plazaola MD⁴, Carlos
6 Barilla BA⁴, Eben Kenah ScD⁵, Angel Balmaseda MD^{3,4}, Aubree Gordon PhD, MPH^{1*}

7
8 ¹ Department of Epidemiology, School of Public Health, University of Michigan, Ann Arbor,
9 MI, USA

10 ² Health Center Sócrates Flores Vivas, Ministry of Health, Managua, Nicaragua

11 ³ Laboratorio Nacional de Virología, Centro Nacional de Diagnóstico y Referencia, Ministry of
12 Health, Managua, Nicaragua.

13 ⁴ Sustainable Sciences Institute, Managua, Nicaragua.

14 ⁵ Biostatistics Division, College of Public Health, The Ohio State University, Columbus, OH,
15 USA

16
17 **Keywords:** COVID-19, secondary attack rate, transmission, SARS-CoV-2, cohort study

18
19 **Running title:** SARS-CoV-2 household transmission

20
21 *Corresponding author

22 5622 SPH I School of Public Health

23 1415 Washington Heights

24 Ann Arbor, MI 48109-2029

25 Telephone: 734-763-3580

26 E-mail: gordonal@umich.edu (AG)

27

28 **Article summary:** Infection-induced immunity protects against SARS-CoV-2 infection for
29 adolescents and adults; however, there was no protection in children. Prior immunity in an
30 infected individual did not impact the probability they will spread SARS-CoV-2 in a household
31 setting.

32

33 **Background**

34 Understanding the impact of infection-induced immunity on SARS-CoV-2 transmission will
35 provide insight into the transition of SARS-CoV-2 to endemicity. Here we estimate the effects of
36 prior infection induced immunity and children on SARS-CoV-2 transmission in households.

37

38 **Methods**

39 We conducted a household cohort study between March 2020-June 2022 in Managua, Nicaragua
40 where when one household member tests positive for SARS-CoV-2, household members are
41 closely monitored for SARS-CoV-2 infection. Using a pairwise survival model, we estimate the
42 association of infection period, age, symptoms, and infection-induced immunity with secondary
43 attack risk.

44

45 **Results**

46 Overall transmission occurred in 72.4% of households, 42% of household contacts were infected
47 and the secondary attack risk was 13.0% (95% CI: 11.7, 14.6). Prior immunity did not impact the
48 probability of transmitting SARS-CoV-2. However, participants with pre-existing infection-
49 induced immunity were half as likely to be infected compared to naïve individuals (RR 0.53,
50 95% CI: 0.39, 0.72), but this reduction was not observed in children. Likewise, symptomatic
51 infected individuals were more likely to transmit (RR 24.4, 95% CI: 7.8, 76.1); however,
52 symptom presentation was not associated with infectivity of young children. Young children
53 were less likely to transmit SARS-CoV-2 than adults. During the omicron era, infection-induced
54 immunity remained protective against infection.

55

56 **Conclusions**

57 Infection-induced immunity is associated with protection against infection for adults and
58 adolescents. While young children are less infectious, prior infection and asymptomatic
59 presentation did not reduce their infectivity as was seen in adults. As SARS-CoV-2 transitions to
60 endemicity, children may become more important in transmission dynamics.

61

62 **Introduction**

63 As SARS-CoV-2 transitions from a pandemic phase to endemicity, more individuals will have
64 infection-induced immunity and children will increasingly represent the greatest proportion of
65 primary infections. [1] Thus, understanding the impact of infection-induced immunity on
66 transmission and contribution of children to SARS-CoV-2 transmission is essential to
67 understanding how this transition will occur.

68
69 Prior transmission studies show that vaccination reduces the likelihood of transmission, [2, 3]
70 and infection-induced immunity is associated with shorter shedding duration and lower viral
71 load;[4] however, the effect of infection-induced immunity on SARS-CoV-2 transmission has
72 not been well established.[5] Given the high infectivity of SARS-CoV-2 and its emerging
73 variants, many children have already been infected worldwide.[6-9]. Further, as of June 2022,
74 SARS-CoV-2 vaccine availability and uptake has been limited for children globally.[10]

75
76 Questions persist about the contribution of children to SARS-CoV-2 transmission. Evidence on
77 the contribution of children to transmission generally shows that children have a lower risk of
78 SARS-CoV-2 transmission when infected compared to adults [11-13] while other work,
79 particularly after the emergence of SARS-CoV-2 variants, finds that children have similar or
80 increased risk of transmission.[14, 15]

81
82 We present results from an ongoing, community-based, household transmission study located in
83 Managua, Nicaragua from June 2020-June 2022. We evaluate the effect of prior infection-

84 induced immunity on transmission as well as the contribution of children to SARS-CoV-2
85 household transmission.

86

87 **Methods**

88 This study was approved by institutional review boards at the Nicaraguan Ministry of Health and
89 the University of Michigan. Adults and parents/guardians of children provided written informed
90 consent and children six years or older provided verbal assent.

91

92 Participants included in this analysis are members of the ongoing Household Influenza Cohort
93 Study (HICS) which began in 2017. HICS is a community-based prospective household cohort
94 study located in District II of Managua, Nicaragua. In June 2020, the study was expanded to
95 include a transmission sub-study of SARS-CoV-2. Participants attend the Health Center Sócrates
96 Flores Vivas at the first signs of a fever or respiratory illness. A respiratory sample is collected
97 and tested for influenza and SARS-CoV-2 via reverse-transcription polymerase chain reaction
98 (PCR).

99

100 When a participant tests positive for SARS-CoV-2, household members are invited to participate
101 in the SARS-CoV-2 transmission sub-study. A separate consent was collected for the sub-study.
102 Study staff visit the home up to six times to collect respiratory samples (days 0, 3, 7, 14, 21, and
103 30) and conduct a final follow-up visit 45-60 days later. Daily symptom data is collected by staff
104 during each visit. [16]

105

106 Blood samples were collected twice per year and risk factor surveys were collected annually. All
107 blood samples collected from 2020-2021 were tested for SARS-CoV-2 IgG antibody to the spike
108 receptor binding domain via an enzyme-linked immunosorbent assay (ELISA) following a
109 protocol adapted from Mount Sinai.[17]

110
111 Prior SARS-CoV-2 infection-induced immunity included both PCR and serologically confirmed
112 infections. We categorize SARS-CoV-2 infections into three periods: March 2020- February
113 2021 (pre-variant era), March 2021- December 2021 (pre-omicron variants, predominantly
114 gamma and delta), and January 2022- June 2022 (omicron variant).

115
116 SARS-CoV-2 vaccinations in the cohort began in 2021. Most vaccinated participants received
117 their first vaccine beginning in September of 2021. A variety of vaccines have been used, with
118 AstraZeneca, Abdala, and the Soberana 02 being the three most common vaccines administered.
119 Participants are considered fully vaccinated 14 days after the final dose. We compared age at
120 enrollment, sex, SARS CoV-2 vaccination, and presence of SARS-CoV-2 antibodies before
121 January 1, 2022, between participants who did and did not participate in intensive monitoring
122 using a chi-square and Fisher-exact tests. Using these tests, we also compared infection period,
123 sex, age, bedroom- and bed-sharing, prior infections, vaccination, and index case symptoms
124 between households that did and did not have transmission (an observed SAR-CoV-2 infection
125 among household members) and (except for symptoms) between PCR- and PCR+ household
126 contacts.

127

128 To estimate the household secondary attack risk (SAR) and rate ratios (RR), we used pairwise
129 survival models which estimate failure time based on contact intervals between infectious and
130 susceptible contacts. These models can account simultaneously for within-household
131 transmission and the risk of infection from outside the household. The SAR from these models
132 can be interpreted as the probability of transmission from one infected household member to one
133 susceptible. [18, 19]

134

135 We assumed an incubation period of six days, a latency period of three, and a 10-day duration of
136 infectiousness; [20-22] therefore, participants were considered infectious three days before to
137 seven days following infection. Participants were considered symptomatic during their infectious
138 period if they reported symptoms within seven days following the infection date.

139 SAS version 9.4 (SAS Institute Inc.) and R version 4.1.1 with the transtat package were used to
140 conduct the analysis.[18, 23] The models included infection period, number of household
141 members, age, sex, presence of symptoms, cough, rhinorrhea, prior SARS-CoV-2 infection,
142 SARS-CoV-2 vaccination, and bed- and bedroom- sharing. We also include an interaction term
143 for age with presence of symptoms, cough, rhinorrhea, and prior SARS-CoV-2 infection.

144

145 To evaluate if the household SARs were different when considering only households infected
146 with the omicron variant, we reran the univariate models for household activation for 2020/2021
147 and 2022. For sensitivity analyses, we adjusted the assumed incubation, latency, and infectious
148 periods. We also reran the univariate models including only households where all household
149 members consented to participate in the household activation and serial swabbing.

150

151 **Results**

152 From March 2020-June 2022, there were 2,398 active participants in the cohort with 84 new/re-
153 enrollees, 251 withdrawn, and 23 deaths (Supplemental Figure 1). Within the SARS-CoV-2
154 transmission sub-study, a total of 209 households (48% of all cohort houses) were activated
155 (some multiple times) with 297 total activations and 1,189 household contacts that consented to
156 intensive monitoring and 258 that declined participation or were not present. Participants in
157 activated households that did not participate in intensive monitoring were generally working-age
158 adults and male. They also had lower cohort participation, were more likely to have missed
159 cohort blood collections since the start of the pandemic and were less likely to have reported
160 vaccination or have documented SARS-CoV-2 antibodies (Table 1, Supplemental Figure 2). In
161 addition to the 297 primary cases, 494 household contacts (42%) were infected.

162
163 Over half of household activations (n=164, 55%) occurred from March 2021-December 2021, a
164 period when multiple variants circulated, and delta predominated.[24] Additionally, there were
165 29 (10%) participating households in March 2020-February 2021 and 104 (35%) households in
166 January 2022- June 2022. Overall, transmission occurred in 72.4% of households (Figure 1).
167 There were a greater proportion of primary cases that were 20-64 years old in households that
168 had transmission compared to those where no transmission occurred (52% vs 37%) although the
169 overall age group distribution was not significantly different (p-value: 0.0531). There were no
170 differences in sex, bedroom- and bed- sharing, number of prior SARS-CoV-2 infections, SARS-
171 CoV-2 vaccinations, or symptoms between primary cases of households with and without
172 transmission (Supplemental Table 1, 2).

173

174 The overall estimated household SAR was 13.0% (95% CI: 11.7%, 14.6%). The estimated
175 household SAR was smaller for larger households (8.3% compared to 15.4% for households with
176 10+ and 2-5 members respectively). Children (ages 5-10), and adults and adolescents (ages 11+)
177 were much more likely to infect others compared to young children (ages 0-4) (RR of 4.20 (95%
178 CI 1.55, 11.35) and 6.64 (95% CI: 2.59, 16.99) respectively). In absolute terms, the difference in
179 the secondary attack rates between young children, and adults and adolescents was 11.9% (SAR
180 of 3.2% vs 15.1%). However, there was no difference in the risk of being infected by age.
181 Symptomatic infectious individuals were 24.37 times (95% CI: 7.80, 76.14) more likely to
182 transmit the virus compared to asymptomatic individuals, with an absolute difference in the
183 probability of transmission of 15.6% (SAR of 16.7% vs 1.1%). Prior SARS-CoV-2 infection was
184 associated with protection against infection (RR=0.53, 95% CI: 0.39, 0.72) (Figure 2).

185
186 For infected young children, we observed no difference by symptom status in the risk of
187 transmitting the virus. For both infectious children and adults and adolescents, the probability of
188 transmission was lower for asymptomatic compared to symptomatic presentation (14.5% vs
189 1.1% and 19.3% vs 0.4%). We note that prior infection was not associated with the probability of
190 transmission in all age groups. Prior infection was only associated with protection against
191 infection for adults and adolescents (Figure 3). Thus, while individuals that were previously
192 infected were less likely to be reinfected, when reinfected they were just as likely to transmit.

193
194 Consistent with the pre-Omicron era results, during the omicron variant era, the risk of
195 transmission was higher for symptomatic individuals (RR= 14.77, 95% CI: 3.12, 70.03) and did
196 not vary by vaccination, and bed- or bedroom-sharing; additionally, risk of infection did not vary

197 by age. Prior infection was still associated with protection against infection (RR=0.25, 95% CI:
198 0.11, 0.56). However, the risk of transmission did not vary by age as it did in the overall results.
199 The risk of transmission was lower for males compared to females (RR= 0.30, 95% CI:
200 0.15,0.61) (Supplemental Figure 3, 4).

201
202 To examine the effect of our assumptions on our estimates, we varied the incubation, latency,
203 and infectious parameters (Supplemental Figure 5). Overall, there were minor differences in the
204 estimated SARs; however, our main findings held. To examine the effect of non-participation,
205 we reran models limiting to households where all members participated. The overall SAR was
206 slightly higher, but there were no differences in the direction of the association age, infection-
207 induced immunity, or any other variable (Supplemental Figure 6).

208

209 **Discussion**

210 We estimated the household SARS-CoV-2 SAR for a large community-based prospective cohort
211 study in Managua, Nicaragua; to our knowledge, this is the first study that compares the
212 association between infection-induced immunity and household SAR. We observed a decreased
213 risk of infection for adults and adolescents who had a prior SARS-CoV-2 infection, but this was
214 not observed among children. While estimated household SARs were much lower when the
215 infectious contact was asymptomatic, this was not observed among young children. These results
216 suggest distinct immune responses to natural SARS-CoV-2 infection between younger and older
217 participants that may impact transmission dynamics.[25, 26]

218

219 Although we expected infection-induced immunity to be associated with a lower probability of
220 transmission because of the association with decreased shedding duration and viral load,[4] this
221 did not occur. When infected, individuals with and without infection-induced immunity had the
222 same probability of transmission. However, these results are not inconsistent; decreased
223 shedding duration may have little impact on household transmission of SARS-CoV-2 where
224 household members have repeated close contact with each other early in illness. Outside of the
225 household, decreased shedding and viral load likely leads to decrease in transmission as contact
226 with others is likely shorter and less frequent.

227

228 During the period of the spread of the omicron variant, the results were similar to the overall
229 findings, albeit with generally higher probability of transmission. Infection-induced immunity
230 was still associated with protection against infection. Surprisingly, risk of transmission did not
231 vary by age. These differences may suggest changing SARS-CoV-2 dynamics due to the
232 omicron variant. [15, 27]

233

234 While a reduction in SARS-CoV-2 transmission for pre or asymptomatic compared to
235 symptomatic infectious individuals has been previously noted [14, 28] and SARS-CoV-2
236 transmission from children compared to adults is less common [28, 29], we show that the
237 presence of symptoms in young children is not associated with infectiousness. Thus, the
238 increased likelihood of asymptomatic presentation of children infected with SARS-CoV-2 does
239 not account for the differences in infectiousness between adults and children.[29]

240

241 The overall estimated household SAR of 13.0% is comparable with estimates from studies in
242 China that also used a statistical transmission model with similar parameters (10.4% and 12.4%
243 for incubation period of 5 days and a 13-day infectious period).[14, 30] However, studies that
244 used estimates from primarily binomial models before and after the emergence of the omicron
245 variant estimated a higher household SAR across settings; [2, 28, 31] while many factors may
246 explain this difference, the use of binomial models rather than statistical transmission models
247 likely bias the estimated SAR upwards. A prior study showed that these biased estimates cannot
248 be interpreted as the probability of transmission, and instead statistical transmission models
249 should be used.[18]

250

251 Our study has several strengths and limitations. Strengths include close monitoring of
252 participants inside of an ongoing cohort, which allows us to know infection histories prior to
253 SARS-CoV-2 entering the household as well as detect mild and asymptomatic infections. Our
254 study is also large and spans both pre-variant and variant eras. One limitation of our study is that
255 although PCR testing occurred frequently during monitoring, it is possible that SARS-CoV-2
256 infections were missed and thus we may underestimate the household SAR. Second, not all
257 household members participated in intensive monitoring and those that declined or were not
258 available for intensive monitoring were different from those that did participate; although the
259 proportion with detectable SARS-CoV-2 antibodies was lower among those did not participate in
260 activation, they on average had fewer blood samples collected. The exclusion of these
261 participants likely leads to an underestimation of the household SAR; however, when analyzing
262 only households where all participants consented to intensive monitoring, the probability of
263 transmission was only slightly larger. Statistical power was also limited in our analysis of the

264 period of omicron spread. We also note that these results are from a community where most were
265 infected with SARS-CoV-2 prior to the availability of SARS-CoV-2 vaccines. [24] Although
266 adults in other settings may have been vaccinated before their first SARS-CoV-2 infection, most
267 children have not been. [6-9] However, both infection then vaccination and vaccination then
268 infection produces broad, hybrid immunity to SARS-CoV-2 with no observed differences by
269 sequence. [32-35]

270
271 Our study highlights the differences in SARS-CoV-2 transmission between children and
272 adolescents and adults which may impact transmission dynamics and the transition to
273 endemicity. Infection-induced immunity is associated with protection against infection, even in
274 the omicron variant era, but previously infected individuals were just as likely to transmit as
275 those that had not been previously infected. At the beginning of the SARS-CoV-2 pandemic, it
276 was established that the contribution of children to SARS-CoV-2 transmission was minor [13].
277 The absence of protection against infection from infection-induced immunity among children
278 and the changing transmission dynamics from emerging SARS-CoV-2 variants suggests that
279 children may already have more meaningful contributions to SARS-CoV-2 transmission; this
280 contribution may further increase as new children are born without immunity to SARS-CoV-2
281 and increasingly represent the greatest proportion of primary cases. [1]

282

283 **Contributions**

284 AMF and AG contributed to the conceptualization of the manuscript. GK, RL, SO, NS, SS, MP,
285 CB, and AB contributed to the investigation for the manuscript. AMF conducted the statistical
286 analysis in consultation with EK. AS was responsible for data curation. AMF and AG wrote the

287 original draft of the manuscript and all co-authors contributed to the review and editing of the
288 manuscript. AF, AS, GK, AB, and AG had access to data and verify its authenticity.

289

290

291 **Declaration of interests**

292 AG serves on an RSV vaccine scientific advisory board for Janssen Pharmaceuticals and has
293 served on a COVID-19 scientific advisory board for Gilead Sciences. All other authors have no
294 interests to declare.

295

296 **Funding**

297 This work was supported by the National Institute of Allergy and Infectious Diseases at the
298 National Institutes of Health through awards given to AG (R01 AI120997,
299 HHSN272201400006C, and 75N93021C00016).

300

301 **References**

302

- 303 1. Lavine JS, Bjornstad ON, Antia R. Immunological characteristics govern the transition of COVID-
304 19 to endemicity. *Science* **2021**; 371(6530): 741-5.
- 305 2. Madewell ZJ, Yang Y, Longini IM, Jr., Halloran ME, Dean NE. Household Secondary Attack Rates
306 of SARS-CoV-2 by Variant and Vaccination Status: An Updated Systematic Review and Meta-
307 analysis. *JAMA Netw Open* **2022**; 5(4): e229317.
- 308 3. Jung J, Kim JY, Park H, et al. Transmission and Infectious SARS-CoV-2 Shedding Kinetics in
309 Vaccinated and Unvaccinated Individuals. *JAMA Netw Open* **2022**; 5(5): e2213606.
- 310 4. Maier HE, Plazaola M, Lopez R, et al. SARS-CoV-2 infection-induced immunity and the duration
311 of viral shedding: results from a Nicaraguan household cohort study. *medRxiv* **2022**:
312 2022.06.17.22276565.
- 313 5. Tan ST, Kwan AT, Rodriguez-Barraquer I, et al. Infectiousness of SARS-CoV-2 breakthrough
314 infections and reinfections during the Omicron wave. *medRxiv* **2022**: 2022.08.08.22278547.
- 315 6. Kubale J, Balmaseda A, Frutos AM, et al. Association of SARS-CoV-2 Seropositivity and
316 Symptomatic Reinfection in Children in Nicaragua. *JAMA Netw Open* **2022**; 5(6): e2218794.

- 317 7. Madhi SA, Kwatra G, Myers JE, et al. Population Immunity and Covid-19 Severity with Omicron
318 Variant in South Africa. *N Engl J Med* **2022**; 386(14): 1314-26.
- 319 8. Almudarra S, Kamel S, Saleh E, et al. High seroprevalence of SARS-CoV-2 among high-density
320 communities in Saudi Arabia. *Infection* **2022**; 50(3): 643-9.
- 321 9. Boehme KW, Kennedy JL, Snowden J, et al. Pediatric SARS-CoV-2 Seroprevalence in Arkansas
322 Over the First Year of the COVID-19 Pandemic. *J Pediatric Infect Dis Soc* **2022**.
- 323 10. Interim statement on COVID-19 vaccination for children and adolescents. World Health
324 Organization, **2021**.
- 325 11. Dattner I, Goldberg Y, Katriel G, et al. The role of children in the spread of COVID-19: Using
326 household data from Bnei Brak, Israel, to estimate the relative susceptibility and infectivity of
327 children. *PLoS Comput Biol* **2021**; 17(2): e1008559.
- 328 12. Kim J, Choe YJ, Lee J, et al. Role of children in household transmission of COVID-19. *Arch Dis*
329 *Child* **2021**; 106(7): 709-11.
- 330 13. Zhu Y, Bloxham CJ, Hulme KD, et al. A Meta-analysis on the Role of Children in Severe Acute
331 Respiratory Syndrome Coronavirus 2 in Household Transmission Clusters. *Clin Infect Dis* **2021**;
332 72(12): e1146-e53.
- 333 14. Li F, Li YY, Liu MJ, et al. Household transmission of SARS-CoV-2 and risk factors for susceptibility
334 and infectivity in Wuhan: a retrospective observational study. *Lancet Infect Dis* **2021**; 21(5): 617-
335 28.
- 336 15. Zhu Y, Xia Y, Pickering J, Bowen AC, Short KR. The Role of Children in SARS-CoV-2 Variant of
337 Concerns Transmission within Households: A Meta-analysis. *medRxiv* **2022**:
338 2022.07.21.22277914.
- 339 16. Maier HE, Kuan G, Saborio S, et al. Clinical spectrum of SARS-CoV-2 infection and protection
340 from symptomatic re-infection. *Clin Infect Dis* **2021**.
- 341 17. Stadlbauer D, Amanat F, Chromikova V, et al. SARS-CoV-2 Seroconversion in Humans: A Detailed
342 Protocol for a Serological Assay, Antigen Production, and Test Setup. *Current Protocols in*
343 *Microbiology* **2020**; 57(1): e100.
- 344 18. Sharker Y, Kenah E. Estimating and interpreting secondary attack risk: Binomial considered
345 biased. *PLoS Comput Biol* **2021**; 17(1): e1008601.
- 346 19. Kenah E. Handbook of infectious disease data analysis. In: Held Lee, Hens Nee, O'Neill PDee,
347 Wallinga Jee. Chapman & Hall/CRC handbooks of modern statistical methods: CRC Press,
348 **2020**:221-42.
- 349 20. Ending Isolation and Precautions for People with COVID-19: Interim Guidance. Available at:
350 <https://www.cdc.gov/coronavirus/2019-ncov/hcp/duration-isolation.html>. Accessed 5/6/2022.
- 351 21. Xin H, Li Y, Wu P, et al. Estimating the Latent Period of Coronavirus Disease 2019 (COVID-19).
352 *Clin Infect Dis* **2022**; 74(9): 1678-81.
- 353 22. Zhao S, Tang B, Musa SS, et al. Estimating the generation interval and inferring the latent period
354 of COVID-19 from the contact tracing data. *Epidemics* **2021**; 36: 100482.
- 355 23. Kenah E, Yang Y. transtat: Statistical Methods for Infectious Disease Transmission. Available at:
356 <https://github.com/ekenah/transtat>.
- 357 24. Maier HE, Balmaseda A, Saborio S, et al. Protection Associated with Previous SARS-CoV-2
358 Infection in Nicaragua. *N Engl J Med* **2022**; 387(6): 568-70.
- 359 25. Khan T, Rahman M, Ali FA, et al. Distinct antibody repertoires against endemic human
360 coronaviruses in children and adults. *JCI Insight* **2021**; 6(4).
- 361 26. Di Chiara C, Cantarutti A, Costenaro P, et al. Long-term Immune Response to SARS-CoV-2
362 Infection Among Children and Adults After Mild Infection. *JAMA Netw Open* **2022**; 5(7):
363 e2221616.

364 27. Chen F, Tian Y, Zhang L, Shi Y. The role of children in household transmission of COVID-19: a
365 systematic review and meta-analysis. *Int J Infect Dis* **2022**; 122: 266-75.
366 28. Madewell ZJ, Yang Y, Longini IM, Jr., Halloran ME, Dean NE. Household Transmission of SARS-
367 CoV-2: A Systematic Review and Meta-analysis. *JAMA Netw Open* **2020**; 3(12): e2031756.
368 29. Silverberg SL, Zhang BY, Li SNJ, et al. Child transmission of SARS-CoV-2: a systematic review and
369 meta-analysis. *BMC Pediatr* **2022**; 22(1): 172.
370 30. Jing QL, Liu MJ, Zhang ZB, et al. Household secondary attack rate of COVID-19 and associated
371 determinants in Guangzhou, China: a retrospective cohort study. *Lancet Infect Dis* **2020**; 20(10):
372 1141-50.
373 31. Jorgensen SB, Nygard K, Kacelnik O, Telle K. Secondary Attack Rates for Omicron and Delta
374 Variants of SARS-CoV-2 in Norwegian Households. *JAMA* **2022**; 327(16): 1610-1.
375 32. Suryawanshi R, Ott M. SARS-CoV-2 hybrid immunity: silver bullet or silver lining? *Nat Rev*
376 *Immunol* **2022**; 22(10): 591-2.
377 33. Hall V, Foulkes S, Insalata F, et al. Protection against SARS-CoV-2 after Covid-19 Vaccination and
378 Previous Infection. *N Engl J Med* **2022**; 386(13): 1207-20.
379 34. Wang Z, Muecksch F, Schaefer-Babajew D, et al. Naturally enhanced neutralizing breadth against
380 SARS-CoV-2 one year after infection. *Nature* **2021**; 595(7867): 426-31.
381 35. Goldberg Y, Mandel M, Bar-On YM, et al. Protection and Waning of Natural and Hybrid
382 Immunity to SARS-CoV-2. *N Engl J Med* **2022**; 386(23): 2201-12.

383

384

385 **Table 1- Demographics of participants eligible for SARS-CoV-2 intensive monitoring in**
386 **Managua Nicaragua, March 2020-June 2022**

	Participants (n=960)	Declined/not present for activation enrollment (n=224)	p-value*
Age at enrollment (%)			0.0001
0-4	224 (23)	32 (14)	
5-10	197 (21)	29 (13)	
11-19	133 (14)	50 (22)	
20-64	378 (39)	110 (49)	
65+	28 (3)	3 (1)	
Female (%)	602 (63)	104 (46)	<.0001
SARS-CoV-2 vaccination (%)†			0.0007
Full	284 (30)	53 (23)	
Partial	368 (38)	69 (31)	
Unvaccinated	52 (5)	5 (2)	
No reported vaccination	256 (27)	97 (43)	
SARS-CoV-2 antibodies (%)†			<.0001

	Yes	870 (91)	173 (77)	
	No	87 (9)	47 (21)	
	Missing	3 (0)	4 (2)	
Blood samples collected				<.0001
	0	3 (0)	4 (2)	
	1	13 (1)	10 (5)	
	2	24 (3)	35 (16)	
	3	127 (13)	74 (33)	
	4	793 (83)	101 (45)	

*from chi-square or Fisher's exact test

†before Jan 1, 2022

387

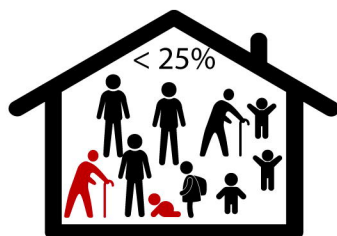
388 **Figure 1- Proportion of activated households with SARS-CoV-2 transmission**

389 **Figure 2. Estimated secondary attack risk and rate ratios**

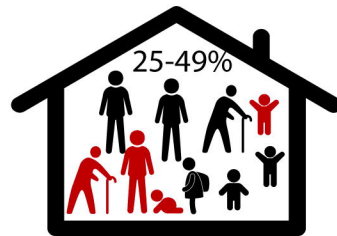
390 **Figure 3. Secondary attack risk stratified by age**



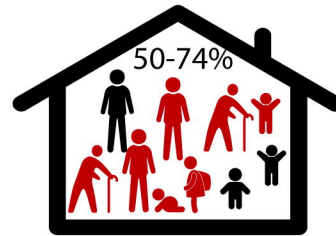
27.6%



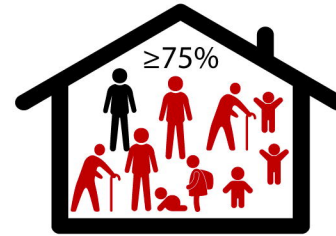
7.5%



16.3%

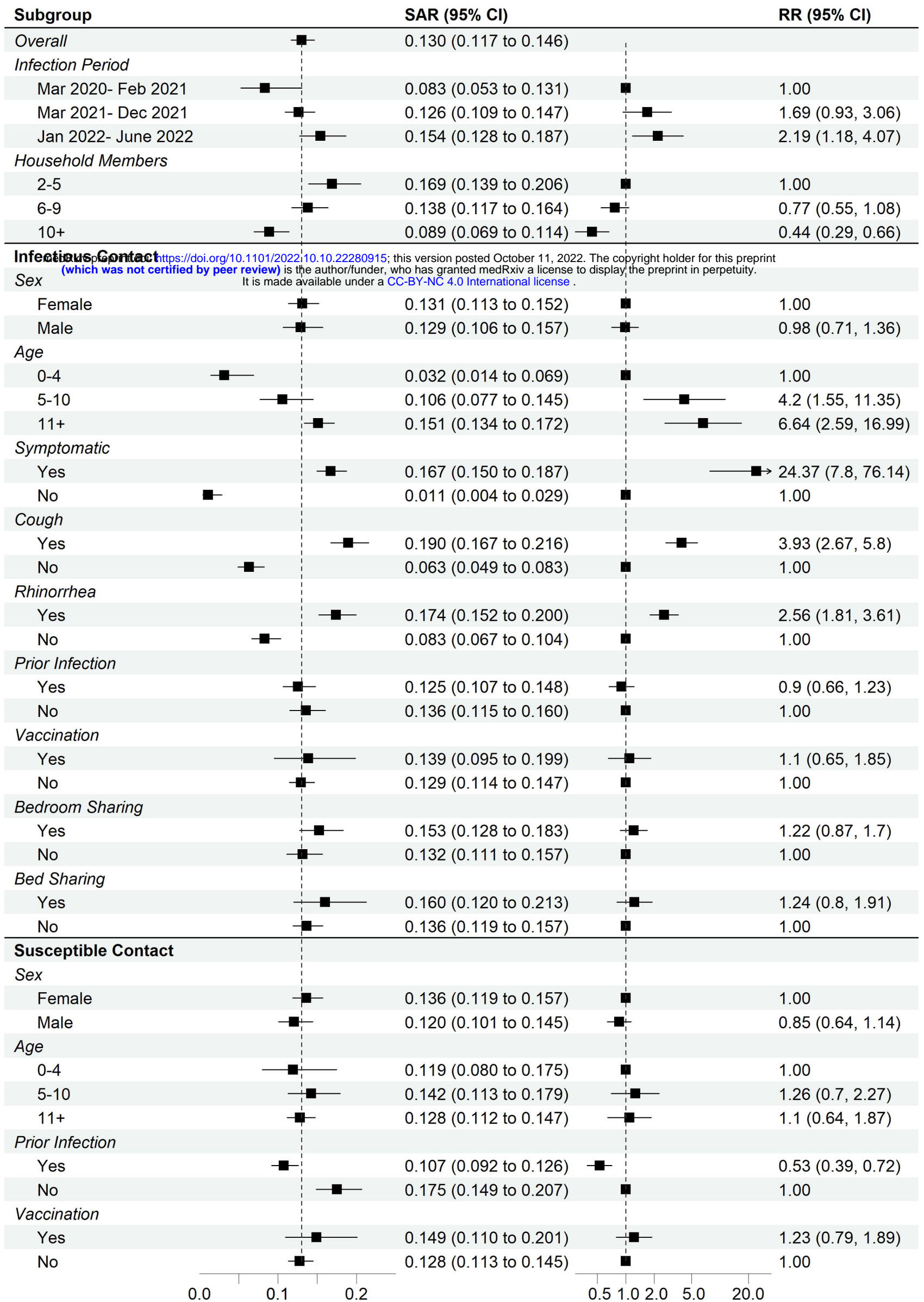


26.5%



22.1%

% of households:



Infectious Contact <https://doi.org/10.1101/2022.10.10.22280915>; this version posted October 11, 2022. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted medRxiv a license to display the preprint in perpetuity. It is made available under a [CC-BY-NC 4.0 International license](https://creativecommons.org/licenses/by-nc/4.0/).

