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The impact of household physical distancing and its timing on the transmission of SARS-CoV-2: Insights from a household transmission evaluation study

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ABSTRACT

Background Studies on SARS-CoV-2 household transmission often assume random mixing, overlooking detailed contact patterns and the timing of physical distancing.

Methods To address this, we examined interactions within 280 households, including 280 index cases and 544 members, enrolled from April 2020 to April 2021 in Nashville, Tennessee, and central Wisconsin. Eligible households were enrolled within 7 days of index case symptom onset if at least one member was initially asymptomatic. Participants were monitored for 14 days, with symptoms and respiratory specimens collected daily, and contact data retrospectively assessed at three time points: the day before index case symptom onset, the day before enrollment, and 14 days post-enrollment. We fitted Exponential Random Graph Models to the contact pattern to identify drivers of household contact. We used the fitted household models to inform a two-level mixing model to account for community infection risk, and we calibrated it to the infection data. We then used the calibrated model to study different implementation of physical distancing.

Results Contact patterns showed a significant reduction in physical interactions after infection awareness, particularly avoidance of index cases, with a 77% reduction in contact density (95% CI [65%-84%], $p < 0.001$). Simulations from the two-level mixing model indicated that initiating contact reductions at symptom onset could lower secondary infections by over 25% in households of 4-5 members.

Conclusions These results demonstrate how behavior changes following infection awareness reduce transmission. Implementing physical distancing earlier, at symptom onset, could further limit secondary infections and enhance household transmission control.

1. Introduction

The rapid spread of the COVID-19 pandemic forced countries worldwide to take strong mitigation measures to prevent COVID-19-related morbidity and mortality and the collapse of healthcare systems. From this perspective, particular importance was placed on the isolation of infected individuals and quarantine of their close contacts. As households were identified as hot spots for disease transmission (World Health Organization, 2020), particular attention was devoted to the detail of SARS-CoV-2 transmission in households (Grijalva et al., 2020; Shen et al., 2020; Wu et al., 2020; Cerami et al., 2021; McLean et al., 2022). Most of these studies focused on epidemiological quantities such as the secondary attack rate, but did not consider the rich dynamics of household interactions, characterized by age specific heterogeneity (Layan et al., 2024). Although public health agencies, including the World Health Organization (WHO) and the Centers for Disease Control and Prevention (CDC), recommended that infected individuals should self-isolate (World Health Organization, 2022; Centers for Disease Control and Prevention, 2023) (and, concurrent to that,

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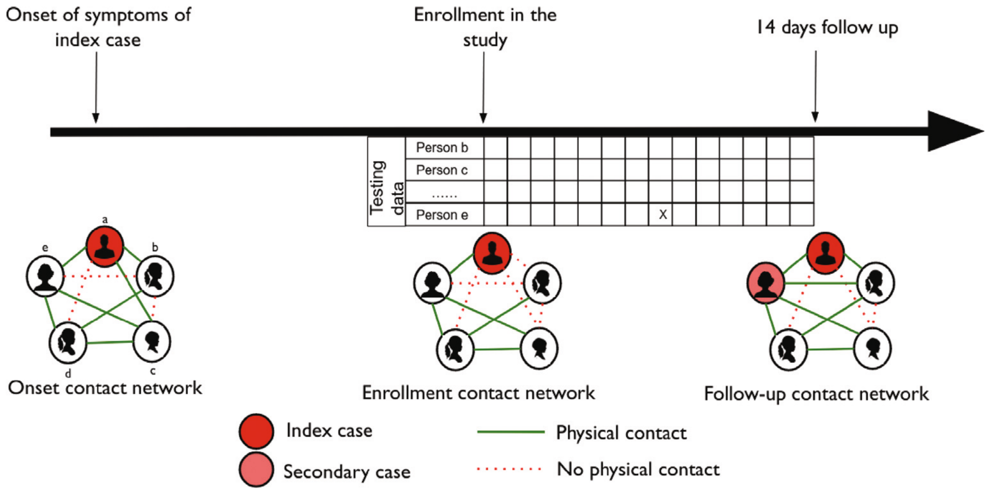

Fig. 1. Schematic representation of the study design. Individuals with a positive SARS-CoV-2 (RT-PCR) test result (index case) enrolled in the study, together with their household members who agreed to participate. The participants reported their household contacts at three time points: the day before the symptom onset of the index case, the day before the enrollment, and after a two weeks of follow-up. Specimens from household members were collected daily and throughout the study period and tested for SARS-CoV-2, to identify secondary infections in the household.

household members of infected individuals should follow prevention measures) few studies have assessed changes in household contact network following the introduction of SARS-CoV-2 infections in households. Information on household contact networks can be used to understand the occurrence of infections (Wallinga et al., 2006; Sun et al., 2023) and to reconstruct infection trees and inform models of disease transmission (Goeyvaerts et al., 2018; Keeling and Eames, 2005) that could, in turn, be used to evaluate the impact of intervention strategies (Cencetti et al., 2021). In this study, we sought to characterize household contact patterns and how those evolved at three time points: before the onset of the first symptom in the household, at study enrollment after the household became aware of a positive clinical test, and two weeks after enrollment. We then used these data-informed contact networks in an individual-based stochastic model of COVID-19 to assess the impact of self-induced physical distancing on the risk of secondary infections under different scenarios.

2. Methods

2.1. Study design and household contact data

The Influenza Household Transmission Evaluation Study for COVID-19 (FluTES-C) was a case-ascertained household transmission study conducted from April 2020 through April 2021 by Vanderbilt University Medical Center (VUMC) and Marshfield Clinic Research Institute (MCRI) (Grijalva et al., 2020). The methods have been previously described (Grijalva et al., 2020; McLean et al., 2022). In brief, the study prospectively identified individuals with a positive SARS-CoV-2 reverse transcription-polymerase chain reaction (RT-PCR) test results from outpatient medical clinics, consented and enrolled individuals who were the first identified infected household members (index cases) in a household, together with their household members who agreed to participate in the study. As the study was an observational study, no specific recommendation about preventive measures were provided to the participants at enrollment. At enrollment, the study collected sociodemographic information and data on household characteristics. After enrollment, daily follow-up continued for 14 days. During each day of follow-up, participants reported symptoms and self-collected a respiratory specimen, regardless of the presence of symptoms (Grijalva et al., 2020; McLean et al., 2022). The interactions between household members in terms of time spent in the same room and physical contacts were recorded at three time points: the day before the onset of symptoms in the index case (referred to as “onset”, the day before the enrollment (“enrollment”) and after the two-week follow-up period post enrollment ended (“follow-up”).The list of symptoms used to define symptoms onset included: cough, sore throat, runny nose, nasal congestion, fatigue/feeling run down, wheezing and trouble breathing/shortness of breath. Fig. 1 shows a schematic summary of the study design and timing of contacts assessments. We constructed the household contact network for the three time points considering only physical contacts, as we assumed these are a better proxy for an infection event than, for example, conversational interactions with other individuals (Goeyvaerts et al., 2018). A physical contact was defined as an interaction between household members that involved skin-to-skin contact e.g., hugging, kissing, touching. We assumed reciprocity of contacts, considering a contact between two participants to happen if either of the two reported a physical contact. Figure S1 presents a selection diagram for participants and the corresponding households.

2.2. Inference of household contact network

Exponential Random Graph Models (ERGM) (Robins et al., 2007) are statistical models used to describe the probability of observing a specific network structure among nodes. In this work, we used ERGM to estimate the probability of physical contact between household members based on individual features (e.g., age) and household characteristics (e.g., size).

Our model includes terms for edges (physical contact, e.g., a and b in Fig. 1), 2-stars (two individuals in contact with a third person but not with each other, e.g., e and b in Fig. 1), and triangles (three individuals all in contact, e.g., a, c, and e in Fig. 1) (Robins et al., 2007; Krivitsky et al., 2023; Anon, 2012). Within this modeling approach, a positive 2-star parameter would indicate a tendency for two household members that do not have a physical contact with each other to both have physical contact with a third individual. In contrast, a negative parameter suggests avoidance of such configurations. Analogously, a positive triangle parameter would suggest triadic closure, where individuals in contact with a third person are likely to contact each other.

We modeled whether a physical contact occurred in the household. Covariates included household characteristics (logarithm of household size as linear and quadratic terms), individual attributes (e.g., index case status, self-reported immuno-compromising condition, and age–index case interaction), and pairwise features (e.g., both individuals’ age classes). For 2-stars and triangles, we considered only household size’s linear and quadratic effects. Age-specific mixing parameters were included to estimate physical contact levels in households, categorizing individuals into *children* (0–17), *younger adults* (18–34), and *older adults* (35–64). Parameters for individuals aged 65+ were excluded due to insufficient data , as elderly individuals were only present in households of size two.

We modeled household contact networks at three time points and selected models using the Akaike Information Criterion (Akaike, 1998) (AIC). For the best-fit models, we also explored whether the study site (VUMC or MCRI) would be a relevant covariate for the probability of a physical contact. Model fitting was performed using the "ergm.multi" R package (Krivitsky, 2022), part of the 'statnet' suite (Handcock et al., 2019), which enables joint model fitting across multiple networks and provides Goodness of Fit (GOF) diagnostics (Krivitsky et al., 2023).

2.3. Epidemic modeling

We first computed and described the cumulative infection rates among household members as the proportion of the total number of household members (excluding the index case) with laboratory-confirmed infections. We then modeled the spread of SARS-CoV-2 infections in households via an individual-based, two-level mixing SEIR (Susceptible–Exposed–Infected–Recovered) model (Ball et al., 1997). The two-level mixing model assumes that at each simulation step (a day), household individuals can acquire the infection either from one infected household member with whom they reported a contact (with probability β_{hh}) or from the community (with a probability β_c). It allows therefore to model separately these two levels of mixing: the community mixing and the within household mixing. . We calibrated the transmission parameters β_{hh} and β_c by fitting the model to the observed epidemic data using a Bayesian Markov Chain Monte Carlo (MCMC) approach, assuming uniform priors and running 5 chains of 100,000 iterations. Posterior distributions were summarized, and 95% credible intervals were obtained using equally tailed intervals (ETIs). Convergence was ensured using Gelman–Rubin diagnostic and effective sample sizes. We implemented the algorithm using the BayesianTools R package.We assumed that at the beginning of the simulation, i.e. the reported date for the start of symptoms, participants interacted according to the contact data reported for the day prior to the index case's onset of symptom. When participants became aware that one positive case was present in the household (i.e., usually at study enrollment) we assumed that they changed their contact behavior and we therefore used the contact data reported at enrollment. We used the empirical (i.e. collected) contact networks for the fitting procedure, and used ERGM generated samples of network for simulating the different scenarios. Sensitivity analyses were performed varying the assumed duration of infectiousness and allowing the community transmission parameter to vary over time. More details on the model and on the fitting procedure can be found in the Supporting Information.

2.4. Definition of scenarios

To evaluate the impact of changing contact patterns, we used the best-fit parameters to simulate the epidemic for three scenarios. In all scenarios, we generated household contact networks from the best-fit models of the contact data. The first scenario is the *Physical distancing after test results*. This is analogous to the fitting scheme, with participants changing their contact behavior after knowing the presence of a positive case in the household. We therefore generated household contact network from the best fit of the *onset* network up to the date when one positive case was reported in the household; after this date, we generated household contact network from the best fit of the *enrollment* network. In the *no physical distancing* scenario, individuals do not change their contact behavior over the course of modeled time and household contact patterns were derived from the ERGM based on surveys conducted on the day before index symptom onset. In the *Physical distancing after symptoms* scenario, we derived the household contact network from the ERGM of the enrollment network only and applied those contact patterns for the entirety of the simulation; this implied that all participants changed contact patterns as soon as there was an individual with symptoms in the household. In all scenarios, we used the contact network at enrollment to model physical distancing. However, this contact network may be affected by two, competing effects: the necessity to implement physical distancing with respect to the index case and the potential need to take care of the index case. We limited the scenario analysis to the households that reported contacts both at onset and enrollment and simulated each scenario

3. Results

3.1. Study population

In total 302 households were included in the study between April of 2020 and April of 2021, resulting in 879 individuals, 438 (49.8%) from the Marshfield Clinic Research Institute site and 441 (50.2%) from the Vanderbilt University Medical Center site (Table 1). The median age of the participants was 32 years (95% CI [3:70]) with 5% of individuals aged ≥65 years. The majority of index cases were adults (81%; 32% aged 18–34 years and 49% aged 35–64 years). The median household size was 3 (Interquartile range [2:4]), with the majority of participants (332, 37.8%) living in a household of size 2 and ~50% of participants living in households of size 3, 4 and 5 (18.1%, 19.6% and 16.5%, respectively). A small number of participants (17, 1.9%) reported immuno-compromising conditions and only 34 participants (3.9%) received one or more doses of COVID-19 vaccine. After excluding 55 participants who did not report contact with household members at any time (Figure S1), the onset network included 269 households with 800 individuals (with 750 physical contacts among household members), the enrollment network included 200 households with 638 individuals and 530 physical contacts among household members) and the follow-up network included 239 households with 715 individuals (670 physical contacts among household members). Included households were similar to overall enrolled households in terms of household size and age of the household members (see Table S1). The median time between the index case's symptom onset and enrollment was 3 days (95% CI: [1:7] days (See Figure S8), with 0.16% of participants enrolling on the same day of the symptom onset of the index case. The mean risk of infection among household members (excluding index case) was 0.38 (95% CI [0:0.8]). Most of the infected household members (113 cases, 35.2% of the total) were aged 35–64 years, with children being the second most common age class (109 cases, 34% of the total).

The aggregated, average probability of physical contact with another household member was significantly greater at symptom onset than at enrollment for people in households of size 4 ($P < 0.05$, two-sample Kolmogorov–Smirnov test) (Figure S2). In 3-person households and households of 5 people or more, there was a similar trend, though not statistically significant. Households of size two, instead, did not show any change in the probability of a physical contact between the three time points and in particular were always complete networks (i.e. with the one potential physical contact being realized).

3.2. Contact network inference

Model selection for contact networks considered household size, participant age, whether the participant was the index case, self-reported immuno-compromising conditions, and the presence of a child in the household. The selected models, based on the lowest AIC, included covariates for household size, participant age, and whether the participant was the index case. Interaction effects of age and being an index case were selected only for networks at enrollment, although with no significance. We also included 2-stars and triangles to model interactions involving three participants. The selected models for the three time points include linear and quadratic effects of household size

Table 1
Sample compositions of household study participants, April 2020–May 2021.

Category	Group	Index cases (N = 302)	Infected household members(N = 321)	Uninfected household members(N = 256)	Total (N = 879)
Age (years)	0–17	43 (14.24%)	109 (33.96%)	94 (36.72%)	246 (27.99%)
	18–34	97 (32.12%)	79 (24.61%)	49 (19.14%)	225 (25.60%)
	35–65	147 (48.68%)	113 (35.20%)	104 (40.62%)	364 (41.41%)
	65+	15 (4.97%)	20 (6.23%)	9 (3.52%)	44 (5.01%)
Household size	2	166 (54.97%)	108 (33.64%)	58 (22.66%)	332 (37.77%)
	3	53 (17.55%)	56 (17.45%)	50 (19.53%)	159 (18.09%)
	4	43 (14.24%)	73 (22.74%)	56 (21.88%)	172 (19.57%)
	5	29 (9.60%)	59 (18.38%)	57 (22.27%)	145 (16.50%)
	6	6 (1.99%)	19 (5.92%)	11 (4.30%)	36 (4.10%)
	7	5 (1.66%)	6 (1.87%)	24 (9.38%)	35 (3.98%)
Immuno-compromised individuals	Refused to answer	76 (25.17%)	90 (28.04%)	90 (35.16%)	256 (29.12%)
	No	219 (72.52%)	231 (71.96%)	156 (60.94%)	606 (68.94%)
	Yes	7 (2.32%)	0	10 (3.91%)	17 (1.93%)
Site	Marshfield Clinic Research Institute (WI)	137 (45.36%)	157 (48.91%)	144 (56.25%)	438 (49.83%)
	Vanderbilt University Medical Center (TN)	165 (54.64%)	164 (51.09%)	112 (43.75%)	441 (50.17%)
Vaccinated (any dose)	Refused to answer	225 (74.50%)	245 (76.32%)	182 (71.09%)	652 (74.18%)
	No	70 (23.18%)	70 (21.81%)	53 (20.70%)	193 (21.96%)
	Yes	7 (2.32%)	6 (1.87%)	21 (8.20%)	34 (3.87%)

on edges and 2-stars. Different results are observed for triangles, with the best-fit model for onset and enrollment networks only including a linear term, whereas the best-fit models for follow-up included a linear and a quadratic effect. Additional results on model selection can be found in the SI section 1.3.2, with a summary of all the tested models reported in Table S2.

Results from network modeling are shown in Table S3, which shows the best-fit estimates for all model covariates. From these, the probability for a physical contact to happen can be computed considering all the relevant covariates (e.g. age of individuals involved, household size, etc.). Covariates that have a significant effect on the probability of a physical contact were similar when considering the three time points, with the exception of being an index case. More specifically, being an index case reduced the odds of a physical contact at enrollment (when household members are aware of the positive test result of the index case) but was not significant at the other two time points. Also, no significant interaction with the age of the index case was found, suggesting that reductions in contact after test results were known did not differ by age. The household networks at all three time points also suggested that the probability of contact depended on the age of the two individuals involved. The models estimated that the age-specific probability of physical contact between participants was similar across time, with the exception of interactions between two older adults, which had a lower probability at enrollment compared with onset (Figure S3). However, no formal statistical testing of this difference was pursued, as the selected model for the three time points differed in terms of covariates. The effect of household size on edges, 2-stars, and triangles is summarized in Figure S5. Increasing household size was associated with lower odds of a physical contact and higher (lower) odds of forming a 2-stars (triangle). In particular, the formation of a triangle presented a strong dependence on household size, being very likely in households of size three (odds in favor of 100 or more) and not so favored in households of size 7 (odds in favor approaching 1). No significant dependence on the study site (VUMC or MCRI) was observed.

3.3. Epidemic modeling and impact of physical distancing

We estimated the best-fit parameter values for the daily probability to acquire infection from an infectious household member upon physical contact (β_{hh}) and from the community (β_c) to be 0.120 (95% CI [0.052:0.193] and 0.0113 (95% CI [0.0005:0.0348] , respectively. Goodness of fit showed a good agreement between epidemic data and simulation, with the exception of households of size two and seven (Figure S7). However, given that all households of size two in our sample are complete networks (i.e. with the one potential physical contact being realized) we could expect some lack of fit from the ERGM network model, with the corresponding misalignment of epidemic results for households of size two. Goodness of fit was difficult to assess for very large households (e.g. seven household members) because there were very few such observations.

Fig. 2 shows the probability of a secondary infection among household members who were not the index case for the three scenarios considered, by household size. Among these, the *physical distancing after test* scenario was the reference scenario, as it corresponded to the actual data collection, with participants implementing physical distancing after a positive case was reported in the household. The *no physical distancing* scenario was not significantly different from the *physical distancing after test* scenario. When comparing the *physical distancing after test* scenario with the *physical distancing after symptoms* scenario statistically significant differences in the secondary infections in the household were observed for household sizes of 3, 4, and 5 and above, with an average reduction of 16%, 25% and 26%, respectively, in the mean number of secondary cases.

Because of the age-specific contact patterns of household interactions and the age distribution of the index cases the reduction in the probability of acquiring a secondary infection was age-specific (Fig. 3). In particular, the reduction in the probability of secondary infections when implementing physical distancing after symptoms (with respect to implementing physical distancing after test) was statistically significant only for children (0–17 years of age) and older adults (35–64 years of age) with an average reduction of 23% (95% CI [3%–37%], $P< 0.001$, t-test) and 30% (95% CI [2%–38%], $P< 0.001$, t-test) , respectively.

In our epidemic model we assumed a constant infectivity over time in the course of a person's infection. We tested the impact of this assumption by including a time-varying infectivity profile (Puhach et al., 2022) in the model (see section 1.6 in the Supporting Information) . Results in terms of the reduction of secondary infection when implementing physical distancing after symptoms with respect to implementing physical distancing after positive tests were similar (Figure S13), although the model resulted in a worse fit to the epidemic data. We also assessed the impact of our assumption of constant community transmission (see section 1.5 of the Supporting Information). Using the number of reported cases in the state of the study sites as a proxy for community transmission we repeated our analysis. Again, the model with time-varying community transmission provided a worse fit to the epidemic data and provided a smaller reduction in the number of secondary infections when implementing physical distancing after symptoms compared with implementing physical distancing after positive test (Figure S12).

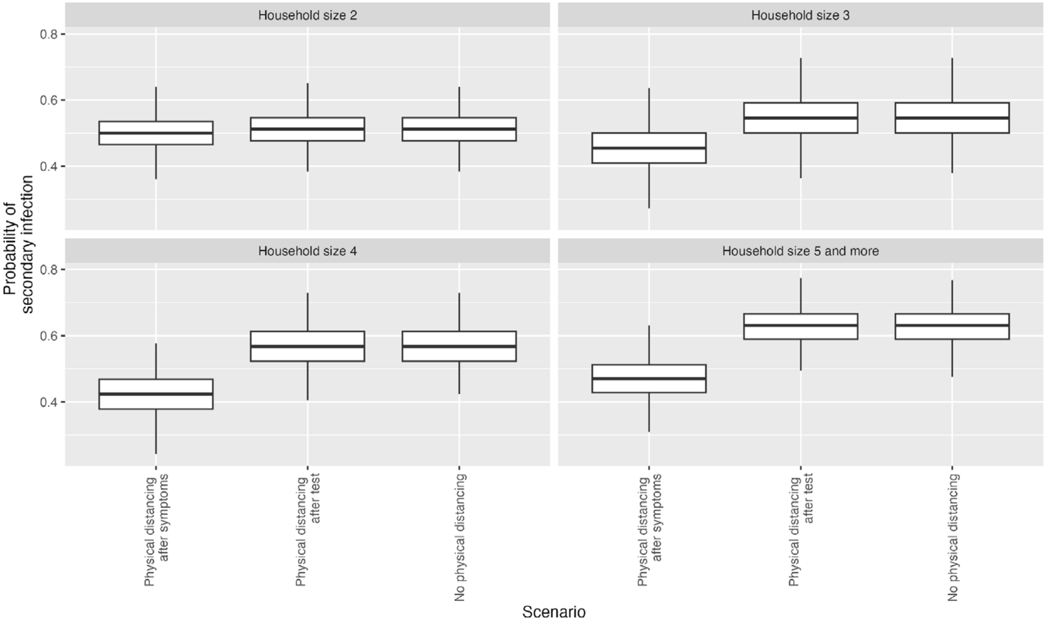

Fig. 2. Probability of secondary infections for the three scenarios, stratified by household size. The solid line marks the median value, with the box marking the 25th–75th percentile and whiskers marking the 95% confidence interval.

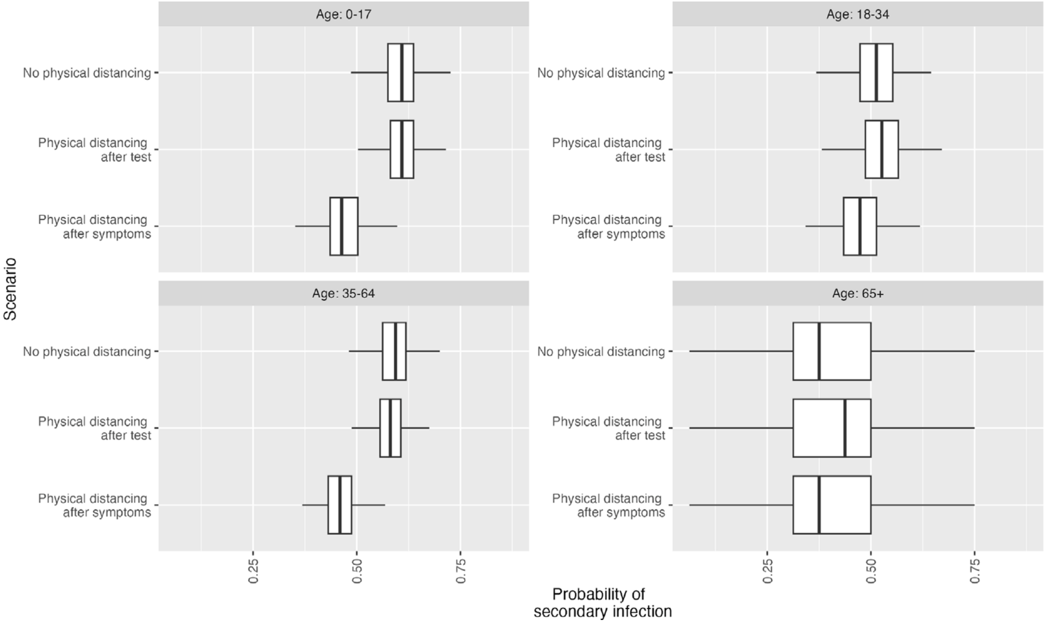

Fig. 3. Probability of secondary infections after follow-up for the three scenarios, stratified by age category of the contact. Solid line marks the median value, with the box marking the 25th–75th percentile and whiskers marking the 95% confidence interval.

4. Discussion

Household transmission has been shown to contribute substantially to the spread of COVID-19 (Wu et al., 2020; Shen et al., 2020). Therefore, efficient physical distancing measures in households are regarded as crucial to interrupt chains of transmission and to reduce disease spread. However, quantifying the impact of physical distancing measures requires detailed information on household contact patterns together with systematic sequential testing of the household members, which is usually not available. Using data from a case-ascertained household transmission study, we found that households in the US, early during the COVID-19 pandemic, reduced self-reported physical contact with the index case , even though no specific recommendation about preventive measures were provided.

Through additional modeling, we found that reducing physical contact when the index case started having symptoms may substantially reduce the risk of infection in other household members. As estimated from our model, the probability of acquiring infection from an infected household member with whom a physical contact is established is ∼ 12% per day, much higher than the probability of acquiring infections from the community, estimated as ∼ 1% per day, marking the intimate nature of physical contacts in household and their higher spreading potential with respect to contacts outside the household. However, this comparison stands only when there is a positive case inside the household, and the overall impact of community transmission could be larger, especially over longer periods of time with no positive case in the household. This also relates with infections between households being better described via a density-dependent mass action principle, while infections in the community being better described via a frequency-dependent mass action principle (Wilson and Worcester, 1945).

Our results showed reduced physical contact after a positive test result, with index cases less likely than other household members to establish new contacts during symptom development, as signaled by the statistical significance for the term for being an index case in the model for the enrollment network. However, this effect was absent in two-person households, likely due to caregiving roles. In fact, the reduced contact with the index case measured at enrollment may be influenced by two opposite effects: physical distancing and increased need of taking care. Contact formation depended also on factors like household size and age-specific patterns. In particular, our analysis has found that household interactions among older adults (from 35 to 65 years of age) are reduced when an individual reported a positive test. This marks a stronger tendency of this age group, compared with other (typically, younger) age groups, to implement physical distancing. Additionally, physical contact was more likely if both individuals had contact with a third member.

In a situation when households are not aware of positive cases, our findings align with prior studies (Krivitsky et al., 2023; Ozella et al., 2018) that observed strong role-specific interactions between household members, contrasting random mixing (Goeyvaerts et al., 2018). Households with positive cases showed reduced contact with the index case and among non-index members, potentially disrupting transmission chains.

We observed that almost half of the index cases were in the older adults age group (35–64), followed by younger adults and, less commonly, children. This is consistent with the time of the study, during which several kids were likely not attending school and thus may be less likely to introduce infections into the households (Tan, 2021).

Secondary infections were instead more likely in older adults and children (with respect to younger adults and elderly), with comparable probabilities. This situation is consistent with the specific structure of household interactions, that present high age-group homophily together with inter-generational mixing. Observing the age-specific interactions, it is expected that index cases in the older adults age group (aged 35–64) would generate most of the secondary infections in the same age group and, to a weaker extent, in children. For index cases in the younger adults age group (aged 18–34) it is instead expected to have more infections in the children age class than in the same age class. Therefore, the high fraction of secondary infections in children may be due to the high interactions that these have with their parents, either in the younger or in the older adults age group. A study conducted in French households in 2020 (Novelli et al., 2024) already observed age-specific within household transmission, however could not disentangle the contribution due to contact patterns. Although age-dependent effects in transmission both in terms of infectivity and susceptibility are widely known (Davies et al., 2020) our findings highlight the crucial role of household contact patterns in shaping the dynamics of COVID-19.

The secondary infection rates found in this study are in line with studies conducted in the US during the first phase of the pandemic, roughly from 2020 to mid-2021 (McLean et al., 2022; Rosenberg et al., 2020; Lewis et al., 2021), although estimates of secondary infection rates are highly heterogeneous (Madewell et al., 2020, 2022; Layan et al., 2022). Previous work also highlighted an increase of secondary infection rates in individuals with immuno-compromising conditions (Lewis et al., 2021) and a reduction due to vaccination (Rolfes et al., 2024; Layan et al., 2022; Guo et al., 2024), which we did not observe. However, our sample has fairly limited representation of immuno-compromised or vaccinated individuals (the study was conducted early in the pandemic), with only 17 and 34 individuals included, respectively.

Simulations of an individual-based model showed reduced secondary infections when distancing began at symptom onset, with stronger effects in larger households. In two-person households, distancing was less effective, likely due to shared space and impossibility to isolate in a two-people house. No significant difference was measured when comparing the physical distancing after symptoms scenario with no physical distancing.

Our results were robust when considering a different community infectivity profile over time (Yan et al., 2021; Puhach et al., 2022), highlighting how household transmission can be disrupted by early physical distancing, regardless of the duration or trajectory of infectious shedding. When considering a time-varying probability of infection from the community we found a reduced impact of physical distancing. This is however to be expected, as household physical distancing can only reduce within-household risk of transmission: if community-mediated risk of transmission is large (e.g. during peak activity) household members are more likely to acquire infection from the community. Furthermore, as the median time between the onset of symptoms of the index case and the enrollment is 3 days, our results underscore how implementing household physical distancing just a few days sooner can significantly decrease the number of secondary infections in the household by as much as 25% .

Although this is one of the few studies that attempted to describe changes in household contact networks due to physical distancing because of a positive test, our work is affected by several limitations. First, index cases were defined as the first symptomatic individual, though concurrent infections cannot be ruled out. However, only in 25 participants additional infections have been detected on the same day or the day after the index case. We therefore expect the infection of a household member concurrently with the index case (e.g. co-primary cases) to be unlikely and with limited impact on our results. In addition to this, as household enrollment was conditioned on a COVID-19 positive case, we could not include in our study the situation of unnecessary physical distancing, i.e. physical distancing implemented on symptoms in the absence of COVID-19. As several pathogens may cause the symptoms we considered, the trade off between the benefit of early physical distancing vs the possibility of unnecessary physical distancing should be properly evaluated. Also, enrollment criteria excluded scenarios of unnecessary distancing (e.g., symptoms without COVID-19), which requires further evaluation. Self-induced distancing may be higher in tested households than in untested ones. Finally, since our study was conducted at two sites in the United States between April 2020 and May 2021 our findings may not be directly applicable to other settings or in a highly vaccinated population, where contact patterns may differ (Wambua et al., 2022, 2023) or different variants may be co-circulating.

5. Conclusions

We showed how the awareness of viral infection introduction into the household reduces physical contact with the index case and leads to an overall lower number of physical contacts in the household. If such self-induced physical distancing would be implemented when a household member first develops symptoms instead of after a positive test, the risk of infections among household members could be reduced by a considerable fraction.

CRediT authorship contribution statement

Pietro Coletti: Writing – review & editing, Writing – original draft, Methodology, Investigation, Formal analysis, Conceptualization. **Niel Hens:** Writing – review & editing, Conceptualization. **Christel Faes:** Writing – review & editing, Conceptualization. **Huong Q. McLean:** Writing – review & editing, Data curation. **Edward A. Belongia:** Writing – review & editing, Data curation. **Melissa Rolfes:** Writing – review & editing, Data curation. **Alexandra Mellis:** Writing – review & editing,

Data curation. **Carrie Reed:** Writing – review & editing, Data curation. **Jessica Biddle:** Writing – review & editing, Data curation. **Ahra Kim:** Writing – review & editing, Data curation. **Yuwei Zhu:** Writing – review & editing, Project administration, Data curation. **H. Keipp Talbot:** Writing – review & editing. **Carlos G. Grijalva:** Writing – review & editing, Funding acquisition, Conceptualization.

Declaration of competing interest

The authors declare no Conflict of Interest.

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Appendix A. Supplementary data

Supplementary material related to this article can be found online at https://doi.org/10.1016/j.epidem.2025.100868.

Data availability

Data will be made available on request.

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