



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.



ELSEVIER

Contents lists available at ScienceDirect

International Journal of Infectious Diseases

journal homepage: www.elsevier.com/locate/ijid

Review

The role of children in household transmission of COVID-19: a systematic review and meta-analysis

Feifan Chen, Yan Tian[#], Lixin Zhang[#], Yuan Shi^{*}

Department of Neonatology, Ministry of Education Key Laboratory of Child Development and Disorders, National Clinical Research Center for Child Health and Disorders, China International Science and Technology Cooperation Base of Child Development and Critical Disorders, Chongqing Key Laboratory of Pediatrics, Children's Hospital of Chongqing Medical University, Chongqing, 400014, China

ARTICLE INFO

Article history:

Received 5 April 2022

Revised 3 May 2022

Accepted 7 May 2022

Keywords:

COVID-19

SARS-CoV-2

Household transmission

Child

ABSTRACT

Objectives: To explore household transmissibility of SARS-CoV-2 in children in new-variants dominating periods.

Methods: Through retrieval in PubMed and Embase, studies were included in two parts: meta-analysis of the household secondary attack rate (SAR) and case analysis of household pediatric infections.

Results: A total of 95 articles were included: 48 for meta-analysis and 47 for case analysis. Pediatric COVID-19 only comprised a minority of the household transmission. The total pooled household SAR of child index cases and contacts were 0.20 (95% confidence interval [CI]: 0.15–0.26) and 0.24 (95% CI: 0.18–0.30). Lower household transmissibility was reported in both child index cases and contacts than in adults (relative risk [RR] = 0.64, 95% CI: 0.50–0.81; RR = 0.74, 95% CI: 0.64–0.85). Younger children were as susceptible as the older children (RR = 0.89, 95% CI: 0.72–1.10). Through subgroup analyses of different variants and periods, increased household SAR was observed in children (Wild: 0.20; Alpha: 0.42; Delta: 0.35; Omicron: 0.56), and no significant difference was found in household SAR between children and adults when new variants dominated.

Conclusion: Although children were found not to be dominant in the household transmission, their transmissibility of SARS-CoV-2 appeared to be on the rise as new variants emerged.

© 2022 The Authors. Published by Elsevier Ltd on behalf of International Society for Infectious Diseases. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>)

Introduction

As of April 29, 2022, there have been 510.2 million confirmed COVID-19 cases and 6.2 million confirmed deaths worldwide, and individuals around the world are still experiencing the aftermath of the fourth wave of the pandemic, which was caused by the Omicron variant of SARS-CoV-2 (WHO COVID-19 Dashboard Data, 2022).

For outbreak control, breaking the chain of virus transmission is generally considered to be one of the most effective strategies besides vaccination. Previous studies have suggested that the household is potentially the highest-risk exposure setting of SARS-CoV-2 transmission, which may have led to a steep escalation of COVID-19 cases even after the policy of national lockdowns and extreme social distancing norms in many countries (Chakrabarti et al.,

2020; Coccia, 2020; Lewis et al., 2021). Children often play an important role in the transmission of some respiratory infectious diseases, such as influenza and measles (García-Salido, 2020; Viner et al., 2020; Yang, 2020). However, for SARS-CoV-2, it remains controversial (García-Salido, 2020; Goldstein et al., 2021; Lau et al., 2020; Lee and Raszka, 2020). Pediatric infections only comprise a small proportion of the total reported cases and children are usually reported with a lower infection rate and a milder clinical course compared with adult cases (Dong et al., 2020; Hoang et al., 2020; Irfan et al., 2021a; Ye et al., 2020). However, children may represent an essential chain of viral transmission and be responsible for the continuous spread of the virus on account of children frequently being asymptomatic carriers (de Souza et al., 2020; Irfan et al., 2021b). With the emergence of some new virus variants, such as Delta and Omicron, increased transmissibility of SARS-CoV-2 in children has been reported by many studies (Chun et al., 2022; Cloete et al., 2022; Elliott et al., 2022; Marks et al., 2022; Thelwall et al., 2022). What is worse is that although vaccinations for adults are ongoing, there is still a vacuum in children, especially for those younger than 12 years

^{*} Corresponding author: Yuan Shi, Children's Hospital of Chongqing Medical University, Chongqing 400014, China, Mob: 00862363635678.

E-mail address: shiyuan@hospital.cqmu.edu.cn (Y. Shi).

[#] Yan Tian and Lixin Zhang have contributed equally to this work (listed as co-second authors).

(Walter et al., 2022), which also may be an important reason for the viral transmission (Li et al., 2022).

Because an understanding of the role of children in the household transmission of SARS-CoV-2 is still evolving, further analysis is necessary. This study aimed to (1) assess the prevalence of pediatric COVID-19 in family clusters, (2) estimate the household secondary attack rate (SAR) of children in different periods and variants, and (3) compare the transmissibility of SARS-CoV-2 in different age groups and explore its potential determinants.

Methods

This systematic review and meta-analysis were conducted following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines, and the protocol was registered on PROSPERO (CRD42022313960).

Definition

A household transmission cluster was defined as a group of ≥ 2 confirmed COVID-19 cases in cohabiting individuals where the diagnosis of cases occurred within 2 weeks of each other. The index case, the primary case, was defined as the first person in the household to be infected with SARS-CoV-2. Household contacts were defined as family members or close relatives who had unprotected contact with the index case but did not necessarily live together. The transmissibility of SARS-CoV-2 was empirically estimated by the SAR. The household SAR was defined as the number of household secondary cases divided by the total household contacts. Children were individuals aged < 18 years. Notably, for studies dividing the age groups by 10 years, individuals aged 10–19 years were included in the child group.

Search strategy and eligibility criteria

A systematic retrieval was performed on two databases (PubMed and Embase) from inception to April 20, 2022, using the key search terms: COVID-19, SARS-CoV-2, family characteristics, household transmission, and so on (details in Table S1), with no restriction on the language, date, study type, or place of publication. Nonprimary documents and modeling studies were excluded.

Depending on the study type and provided data, studies were included in two parts: case analyses of household pediatric infections and meta-analysis on the household SAR. Case analyses mainly included case reports focusing on individual household transmission of SARS-CoV-2. The personal information of index cases, household contacts, family relationships, and the disease progression of COVID-19 cases must be provided. Although the SAR meta-analysis mainly included descriptive studies that had reported the household SARS-CoV-2 SAR in different age groups, at least two of the following were required: household contacts, household secondary cases, and SAR. Studies with insufficient data or possible duplicate cases were excluded.

Data extraction and quality assessment

Two authors (Tian and Zhang) independently extracted the following information from each of the included study: author, country, study type, study period, case definitions, testing protocol, contact tracing methods, demographic characteristic, COVID-19 data (exposures, index cases, household contacts, secondary infection cases, SAR), potential factors, and so on. Disagreements were resolved through consultation with the third author (Chen). To critically appraise the methodologic quality of included studies, the JBI critical appraisal checklist was applied (JBI, 2020). Each included study was scored independently by two authors (Tian and Zhang)

and was given an average point. Studies were ranked as high quality if they were scored ≥ 10 , medium if they were scored 7–9, and low if they were scored < 7 .

Data analysis

All analyses were performed using R 4.1.2 software. The SAR and its relative risk (RR) were calculated for each study. SARs were pooled with a random intercept logistic regression model after a Freeman-Tukey double arcsine transformation, and RRs were pooled using a random-effects model with Der Simonian and Laird weights. The within-study variation was estimated with the 95% confidence interval (CI), and the Higgin and Thompsons I^2 was used to assess heterogeneity between studies. Subgroup analyses were conducted to explore the source of heterogeneity. Publication bias was detected using the funnel plot and Egger test. $P < 0.05$ was considered statistically significant in all tests.

Results

As shown in the flow diagram in Figure S1, a total of 1632 records were identified through the data search and 236 articles were retrieved for full-text assessment. Finally, 95 articles were included in our analysis: 48 articles for household SAR meta-analysis and 47 articles for case analysis. Studies included in the SAR meta-analysis are listed in Table 1, of 48 studies, 26 were of high quality and 22 were of medium quality according to the quality assessment in Table S2, and the full details of family clusters included in case analyses are shown in Table S3. All included studies reported household COVID-19 from 18 countries and regions with a total of 1,153,693 participants (834,613 adults and 319,080 children).

Case analyses of household pediatric COVID-19

In the case analysis of pediatric COVID-19, 47 articles were included, identifying 78 household transmission clusters. As shown in Table 2, only 10.3% (8/78) familial clusters were identified with a pediatric index case. These pediatric index cases only led to 7.7% (16/207) of all secondary cases compared with the 92.3% of secondary cases caused by the adult index cases. Child contacts were identified as 29.8% (84/282) of all household contacts and reported in 60.3% (47/78) familial clusters. The child secondary infections only accounted for 30% (62/207) of all secondary infections compared with the 70% as adults.

Meta-analyses on household SAR of SARS-COV-2

Household SAR of child contacts

Secondary infections of the pediatric household contacts were identified in 41 studies, and the pooled SAR was 0.24 (95% CI: 0.18–0.30, $I^2 = 100\%$) (Figure 1). Publication bias was reported upon examination of a funnel plot (Egger test, $P = 0.021$) (Figure S2).

Subgroup analyses on household SAR of child contacts were performed on research periods and SARS-CoV-2 variants, as provided in Table 3. In different research periods, 31 studies were carried out between 2019 and February 2021, and the SAR was estimated at 0.18 (95% CI: 0.13–0.25, $I^2 = 99\%$). A total of 9 studies were conducted between February and November 2021, and the SAR was 0.39 (95% CI: 0.30–0.48, $I^2 = 97\%$). The SAR of two studies between November 2021 and 2022 was 0.51 (95% CI: 0.47–0.54, $I^2 = 0\%$). Significant difference in SAR was reported in different groups of research period ($P < 0.01$). For different SARS-CoV-2 variants, the SAR of Wild type in 33 included studies was 0.20 (95% CI: 0.14–0.26, $I^2 = 99\%$). The SAR of the Alpha variant in the three included studies was 0.42 (95% CI: 0.23–0.62, $I^2 = 94\%$). The Delta variant was investigated in five studies, and the SAR was 0.35 (95%

Table 1
Studies included in meta-analysis of household SAR.

Author (year)	Country	Study type	Cluster size	Public lockdown	Diagnostic method	Follow-up (days)	Quality
Afonso et al. (2022)	Brazil	Cross-sectional and analytical study	NA	Yes	RT-PCR	14	Medium
Baker et al. (2022)	United States	Retrospective study	183	NA	RT-PCR	NA	High
Bhatt et al. (2022)	Canada	Prospective study	180	NA	RT-PCR	14	High
Bi et al. (2021)	Switzerland	Cross-sectional population serosurvey	2267	Yes	Serological test	NA	High
Bi et al. (2020)	China	Retrospective cohort study	NA	Yes	RT-PCR	14	High
Calvani et al. (2021)	Italy	Case-control study	NA	NA	RT-PCR	NA	Medium
Cerami et al. (2021)	United States	Prospective study	100	NA	RT-PCR	28	High
Chaw et al. (2020)	Malaysia	Retrospective study	28	NA	RT-PCR	14	Medium
de Gier et al. (2021)	The Netherlands	Retrospective study	NA	NA	RT-PCR	10	Medium
Donnelly et al. (2022)	United States	Prospective study	127	NA	RT-PCR	14	High
Dupraz et al. (2021)	Switzerland	Cross-sectional epidemiological study	NA	Yes	Serological test	14	Medium
Galow et al. (2021)	Germany	Seroprevalence study	106	NA	Serological test	NA	Medium
Harris et al. (2021)	England	Retrospective study	NA	NA	RT-PCR	14	High
Hu et al. (2021)	China	Retrospective cohort study	NA	Yes	RT-PCR	14	High
Hua et al. (2020)	China	Retrospective cohort, multicenter study	314	Yes	RT-PCR	NA	Medium
Jalali et al. (2022)	Norway	Cohort study	NA	NA	RT-PCR	10	High
Jing et al. (2020)	China	Retrospective cohort study	195	Yes	RT-PCR	14	High
Kim et al. (2021)	South Korea	Retrospective observational study	NA	NA	RT-PCR	NA	Medium
Koureas et al. (2021)	Greece	Retrospective cohort study	40	Yes	RT-PCR	NA	Medium
Kuba et al. (2021)	Japan	Cohort study	NA	Yes	RT-PCR	14	Medium
Lewis et al. (2021)	United States		58	Yes	RT-PCR	14	High
Li et al. (2021)	China	Retrospective cohort study	24985	Yes	RT-PCR	≥22	High
Li et al. (2020)	China	Retrospective study	105	NA	RT-PCR	14	Medium
Liu et al. (2021)	United States	Prospective study	15	NA	RT-PCR	14	High
Lopez Bernal et al. (2022)	England	Prospective case-ascertained study	329	NA	RT-PCR	14	High
Lyngse et al. (2022)	Denmark	Retrospective study	24693	NA	RT-PCR	14	High
McLean et al. (2022)	United States	Prospective case-ascertained study	302	NA	RT-PCR	14	High
Metlay et al. (2021)	United States	Retrospective cohort study	NA	NA	RT-PCR	NA	Medium
Miller et al. (2021)	England	Prospective cohort study	NA	NA	RT-PCR	NA	Medium
Miyahara et al. (2021)	Japan	Cohort study	87	Yes	RT-PCR	14	Medium
Musa et al. (2021)	Bosnia and Herzegovina	Prospective observational study	360	NA	RT-PCR	28	High
Ng et al., 2022a	Malaysia	Retrospective observational study	185	Yes	RT-PCR	14	Medium
Ng et al., 2022b	Singapore	Retrospective cohort study	NA	Yes	RT-PCR	14	High
Ogata et al. (2021)	Japan	Cross-sectional study	183	Yes	RT-PCR	NA	Medium
Ogata et al. (2022)	Japan	Observational study	580	NA	RT-PCR	NA	High
Park et al. (2020)	South Korea	Cohort study	NA	NA	RT-PCR	14	Medium
Reukers et al. (2022)	The Netherlands	Prospective cohort study	55	NA	RT-PCR	NA	High
Rosenberg et al. (2020)	United States	Retrospective study	155	Yes	RT-PCR	NA	High
Song et al. (2022)	South Korea	Prospective study	25	NA	NA	NA	High
Soriano-Arandes et al. (2021)	Spain	Prospective, observational study	1108	Yes	RT-PCR	NA	Medium
Stich et al. (2021)	Germany	Multicenter, cross-sectional study	405	NA	Serological test	NA	High
Tanaka et al. (2021)	Japan	Cross-sectional study	NA	NA	RT-PCR	14	Medium
Waltenburg et al. (2022)	United States	Prospective study	127	NA	RT-PCR	14	High
Wang et al. (2020a)	China	Retrospective cohort study	124	NA	RT-PCR	14	High
Wang et al., (2020b)	China	Retrospective case series	85	Yes	RT-PCR	14	High
Wu et al. (2020)	China	Prospective observational study	35	NA	RT-PCR	NA	Medium
Yousaf et al. (2021)	United States	Prospective cohort study	NA	NA	RT-PCR	14	High
Yung et al. (2020)	Singapore	Prospective study	137	NA	RT-PCR	14	Medium

NA, not applicable; RT-PCR, reverse transcription polymerase chain reaction; SAR, secondary attack rate.

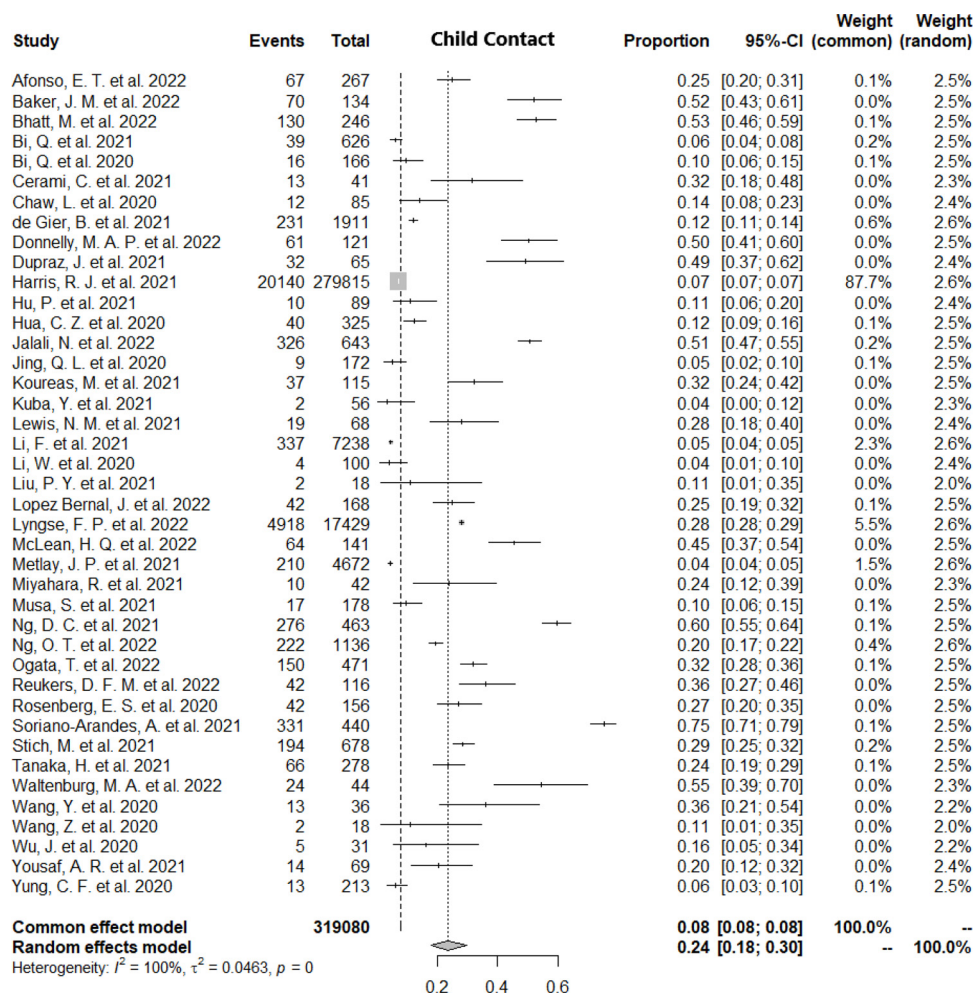


Figure 1. Pooled household SAR of child contacts. CI, confidence interval; SAR, secondary attack rate.

Table 2
Case analyses of household pediatric COVID-19 infections.

Characteristics	Cluster (n = 78), %	Secondary cases (n = 207), %
Child as the index case	8 (10.3)	16 (7.7)
Adult as the index case	70 (89.7)	191 (92.3)
Child as the contacts	47 (60.3)	62 (30.0)
Adult as the contacts	77 (98.7)	145 (70.0)

COVID-19, coronavirus disease.

Table 3
Subgroup analyses on household SAR of child contacts.

Subgroups	No. of studies	SAR (95% CI)	I ²	P-value
Research period				<0.01
2019-Feb, 2021	31	0.18 (0.13–0.25)	99%	
Feb–Nov, 2021	9	0.39 (0.30–0.48)	97%	
Nov, 2021–2022	2	0.51 (0.47–0.54)	0%	
SARS-CoV-2 variant				<0.01
Wild type	33	0.20 (0.14–0.26)	99%	
Alpha	3	0.42 (0.23–0.62)	94%	
Delta	5	0.35 (0.25–0.45)	98%	
Omicron	2	0.56 (0.51–0.61)	20%	

CI, confidence interval; SAR, secondary attack rate; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

CI: 0.25–0.45, I² = 98%). The SAR of the Omicron variant in two studies was 0.56 (95% CI: 0.51–0.61, I² = 20%). A significant difference in SAR was also reported among different variants (P < 0.01).

In the analyses on household SAR of child contacts in different age groups, children younger than 10 years were found to be less susceptible than children older than 10 years (RR = 0.74, 95% CI: 0.56–0.97, I² = 0%). However, no significant difference was shown between children younger and older than 12 years (RR = 1.12, 95% CI: 0.90–1.39, I² = 77%). In the combined analysis on the previous two cases, the younger child contacts were not significantly associated with a lower SAR than the older ones (RR = 1.01, 95% CI: 0.84–1.21, I² = 66%) (Figure 2).

Household SAR of adult contacts

The SAR of adult household contacts was estimated at 0.32 (95% CI: 0.27–0.37, I² = 99%) on the basis of 41 included studies (Figure S3). Publication bias was also reported in the funnel plot of Figure S4 (Egger test, P < 0.01). In the analysis on adult household contacts of different age groups, the old adults were significantly associated with a higher SAR than young adults (>60 vs <60 years: RR = 1.45, 95% CI: 1.24–1.70, I² = 52%; >65 vs <65 years: RR = 1.24, 95% CI: 1.02–1.50, I² = 55%). The same trend was also found in the combined analysis (the old adults vs the young adults: RR = 1.35, 95% CI: 1.19–1.54, I² = 77%) (Figure S5).

Household SAR comparison between child and adult contacts

In the household SAR comparison between child and adult contacts in 37 studies, children were demonstrated to be less likely to be infected with SARS-COV-2 than adults when exposed to

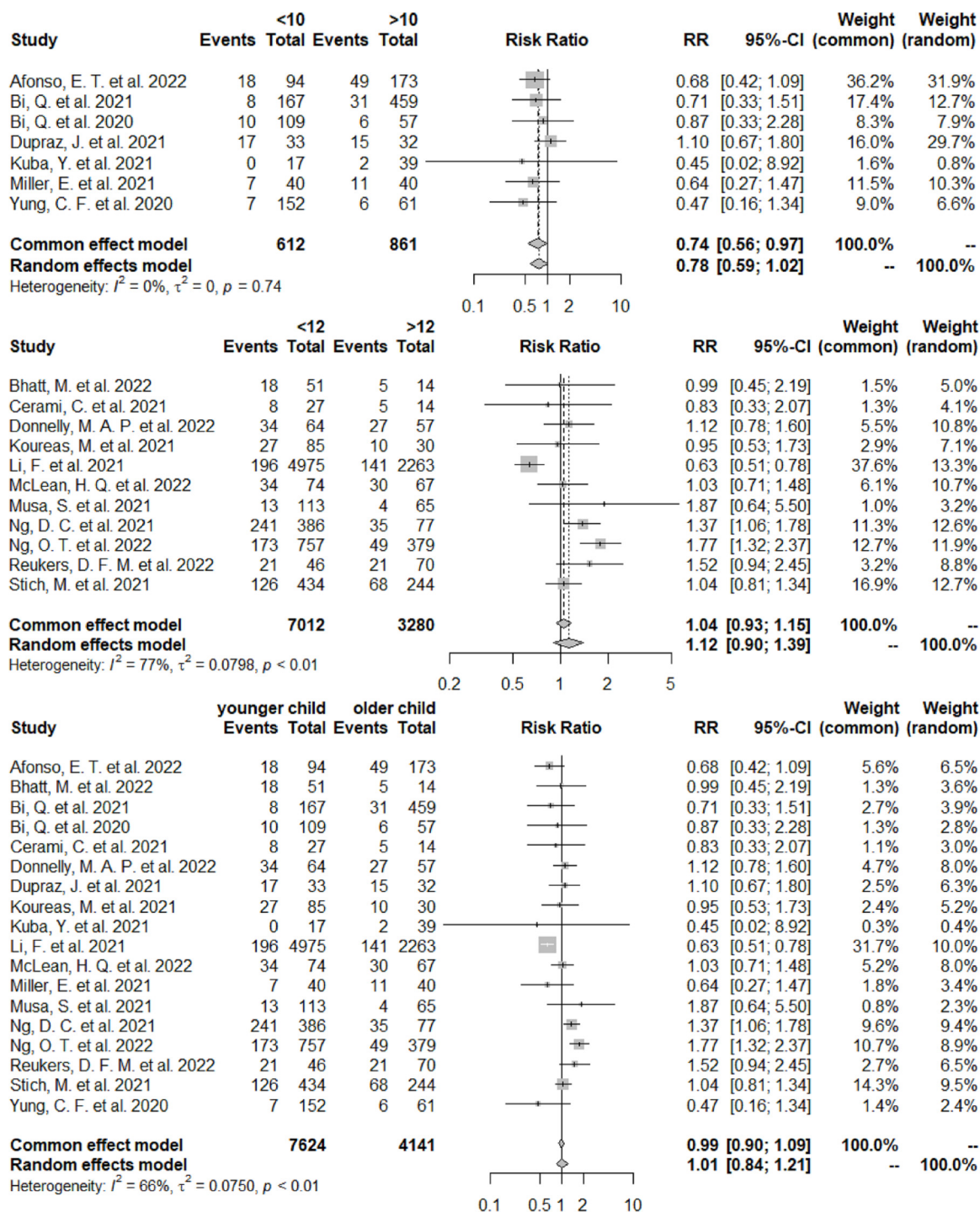


Figure 2. Subgroup analyses on household SAR of child contacts in different age groups. CI, confidence interval; RR, risk ratio; SAR, secondary attack rate.

household index cases (RR = 0.74, 95% CI: 0.64–0.85, $I^2 = 97\%$) (Figure 3). No obvious publication bias was found in the funnel plot of Figure S6 (Egger test, $P = 0.31$).

Subgroup analyses of the comparison were performed on research periods and SARS-CoV-2 variants, as detailed in Table 4. In different research periods, 27 studies were carried out between 2019 and February 2021, in which lower transmissibility was reported in child contacts than adult contacts (RR = 0.62, 95% CI: 0.52–0.75, $I^2 = 95\%$). For nine studies between February and November 2021 and two studies between November 2021 and 2022, no significant difference in SAR was found between child and

adult contacts (RR = 0.98, 95% CI: 0.86–1.12, $I^2 = 80\%$; RR = 1.09, 95% CI: 0.89–1.34, $I^2 = 73\%$). A significant difference in RR was reported in different groups of research period ($P < 0.01$). For different SARS-CoV-2 variants, children were significantly associated with a lower SAR than adult contacts in 29 studies of the Wild type variant (RR = 0.65, 95% CI: 0.55–0.77, $I^2 = 95\%$). However, no significant difference in SAR was observed between child and adult contacts in studies of other variants (Alpha: RR = 1.04, 95% CI: 0.76–1.42, $I^2 = 76\%$; Delta: RR = 0.99, 95% CI: 0.82–1.19, $I^2 = 88\%$; Omicron: RR = 1.09, 95% CI: 0.88–1.35, $I^2 = 74\%$). Significant difference in RR was also reported in different variants ($P < 0.01$).

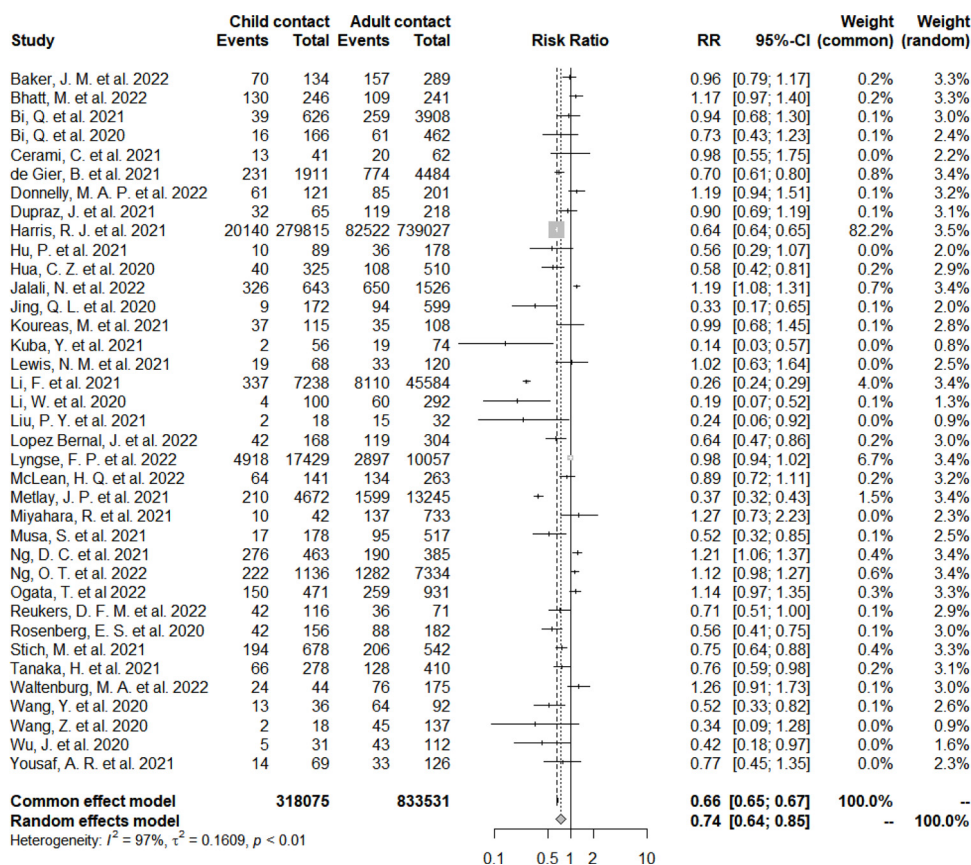


Figure 3. Household SAR comparison between child and adult contacts. CI, confidence interval; RR, risk ratio; SAR, secondary attack rate.

Table 4
Subgroup analyses of household SAR comparison between child and adult contacts.

Subgroups	No. of studies	RR (95% CI)	I^2	P-value
Research period				<0.01
2019–June, 2020	27	0.62 (0.52–0.75)	95%	<0.01
February–November, 2021	9	0.98 (0.86–1.12)	80%	>0.05
November, 2021–2022	2	1.09 (0.89–1.34)	73%	>0.05
SARS-CoV-2 variant				<0.01
Wild type	29	0.65 (0.55–0.77)	95%	<0.01
Alpha	3	1.04 (0.76–1.42)	76%	>0.05
Delta	5	0.99 (0.82–1.19)	88%	>0.05
Omicron	2	1.09 (0.88–1.35)	74%	>0.05

CI, confidence interval; RR, relative risk; SAR, secondary attack rate; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

Household SAR of child and adult index cases

A total of 18 studies reported the respective SAR of child and adult index cases in familial clusters. The estimated SAR of the child index case was 0.20 (95% CI: 0.15–0.26, $I^2 = 100\%$). For the adult index cases, it was 0.36 (95% CI: 0.27–0.46, $I^2 = 100\%$). Compared with the adult index cases, the child index cases were significantly associated with a lower possibility to transmit SARS-CoV-2 to their family members (RR = 0.64, 95% CI: 0.50–0.81, $I^2 = 96\%$) (Figure 4).

Potential determinants of the household SAR

Potential determinants of the household transmission of SARS-COV-2 were identified on the basis of prespecified characteristics

and studies with sufficient data (Table S4). Symptomatic index cases were associated with a higher SAR than asymptomatic index cases (RR = 2.68, 95% CI: 1.39–3.58, $I^2 = 94\%$). In different family relationships, the spouse relationship-to-index case was reported to have a significantly higher SAR than other relationships (RR = 1.78, 95% CI: 1.25–2.53, $I^2 = 91\%$), whereas the same trend was not shown in the parent-child relationship (RR = 0.84, 95% CI: 0.59–1.19, $I^2 = 87\%$). Household contacts with comorbidities were at a higher risk for secondary infections than those without comorbidities (RR = 1.98, 95% CI: 1.52–2.59, $I^2 = 63\%$). In terms of sex, the female contacts were observed to be slightly more susceptible than the male contacts (RR = 1.08, 95% CI: 1.01–1.16, $I^2 = 42\%$). Another important factor was the household size: a larger household size might be associated with a lower SAR (>4 vs <4 members: RR = 0.69, 95% CI: 0.55–0.85, $I^2 = 94\%$; >6 vs <6 members: RR = 0.69, 95% CI: 0.50–0.95, $I^2 = 90\%$).

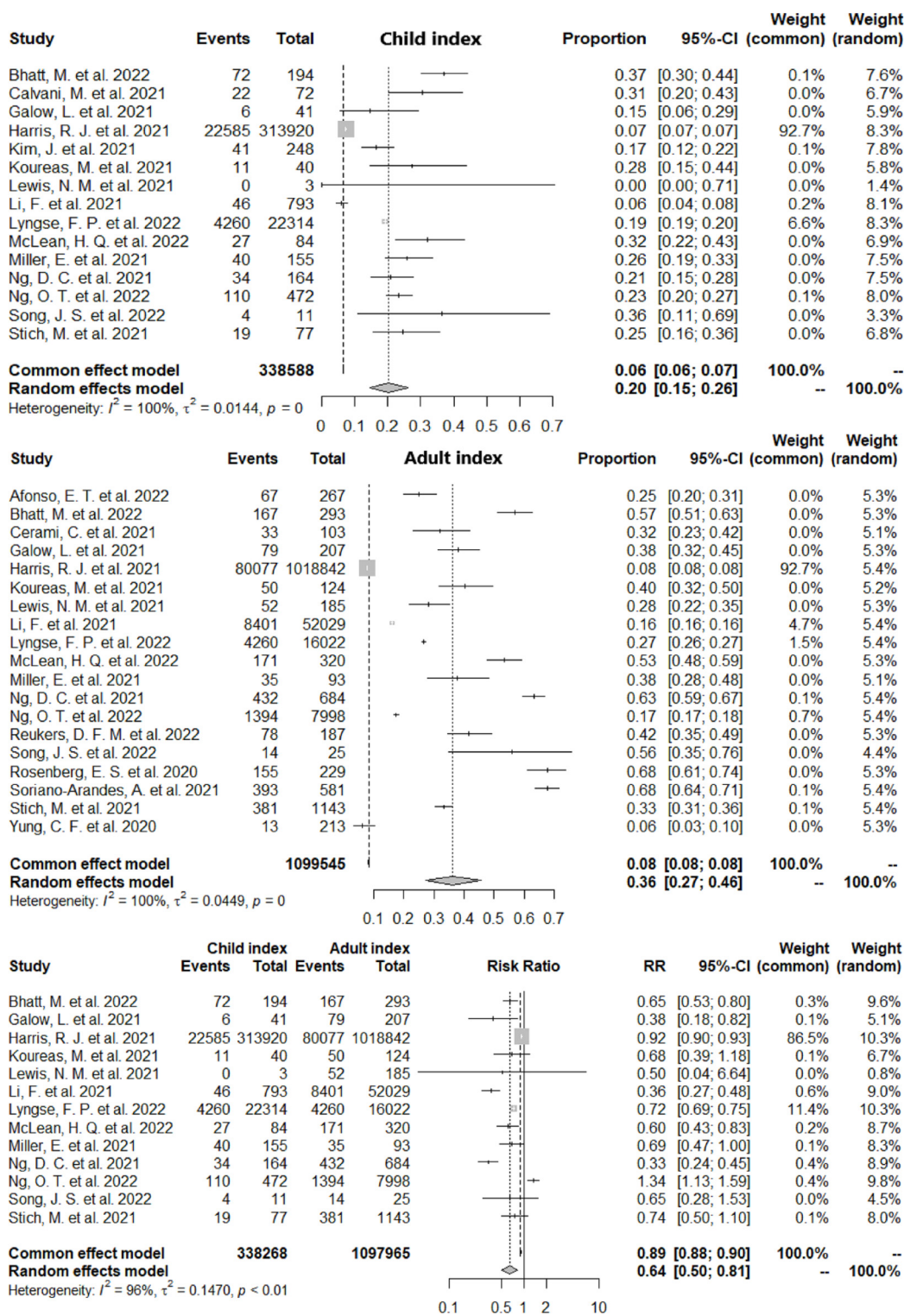


Figure 4. Comparison on household SAR between child and adult index cases. CI, confidence interval; RR, risk ratio; SAR, secondary attack rate.

Discussion

Analyses of the household transmission of SARS-COV-2 will certainly facilitate a better understanding of the transmission chain and contribute to the epidemic control. Many studies have been conducted on household SAR of SARS-COV-2 (Fung et al., 2021; Koh et al., 2020; Li et al., 2021; Madewell et al., 2020; Shah et al., 2020; Thompson et al., 2021), but only a minority focused on the

child group. Irfan et al. (2021) and Zhu et al. (2021) performed meta-analyses on the role of children in household transmission in the early periods of the epidemic, but the results were still unclear because of the limited number of included studies and pediatric index cases. On the basis of previous research, more articles were included in our study. With more timely articles, more comprehensive analyses were conducted. Other than the total pooled household SAR of child contacts and index cases, subgroup analy-

ses were also performed in different SARS-CoV-2 variants and different periods, as well as the transmissibility comparison between child and adult contacts. To the best of our knowledge, almost no previous meta-analyses have been conducted on the pediatric household transmission of different SARS-CoV-2 variants.

Our results show that both the child index cases and secondary cases only comprised a small proportion of the household transmission in case analyses, which suggested that children were unlikely to be the main source of SARS-CoV-2 in familial clusters. In the total unclassified results of SAR meta-analyses, lower household transmissibility was demonstrated in both pediatric index cases and contacts than in adults. This was consistent with these previous meta-analyses (Grijalva et al., 2020; Madewell et al., 2021, 2020; Zhu et al., 2021). These findings imply that children are less vulnerable to SARS-CoV-2 than adults. Similar to what previous data have shown, the older adults also had a higher SAR than the young adults. Contrary to the analysis by Zhu et al. (2021), a significant difference was found between children younger than and older than 10 years in our analyses, and a recent population-based cohort study also suggested a higher transmissibility of SARS-CoV-2 in younger children than older children (Paul et al., 2021). However, this difference still lacked statistical power because of the limited included studies and relatively little advantage, and negative results were also noted in our comprehensive analyses. Therefore, future studies are still required.

Notably, some new findings were found in the subgroup analyses on household SAR of different periods and SARS-CoV-2 variants. In the early period of the pandemic (the Wild type mainly dominated during 2019–2020), a relatively low household SAR was observed in children (10–30%), and child contacts usually had lower transmissibility than adults. However, with the emergence of some new variants (Alpha and Delta) in the beginning of 2021, household SAR in children seemed to increase (30–40%). Consistent with our results, many epidemiologic studies have pointed out that children and adolescents had become more susceptible to these new variants (Allen et al., 2022; Chun et al., 2022; Li et al., 2022; Ng et al., 2021; Paul et al., 2021). At the end of 2021, the Omicron variant emerged with the highest transmissibility so far: household SAR in both children and adults seemed to be more than 50%. Plenty of recent research also reported that the rapid increase in infections and hospitalizations was caused by the Omicron variant (Baker et al., 2022; Cloete et al., 2022; Elliott et al., 2022; Marks et al., 2022). Additionally, no significant difference was found in household SAR comparison between children and adults with new variants in our analyses, which also supported the increased vulnerability in children. This was in line with the result of a newly published meta-analysis conducted by Viner et al. (2022). Some research attributed the increased transmissibility to immune escape and reduced effectiveness of vaccination (Meng et al., 2022; Mlcochova et al., 2021; Planas et al., 2021). However, data have proven the protective effect of vaccination even in new variant periods (Fowlkes et al., 2022; Harris et al., 2021; Prunas et al., 2022). Limited by insufficient data, the subgroup analysis on vaccination status was not conducted and the number of articles included in variants analyses was also few. Therefore, original studies that include more virologic data and information on the vaccination status of the participants are still necessary for more convincing results.

Interpretation of the results in the determinant assessment should be more conservative in consideration of the high heterogeneity. A higher SAR was observed in the symptomatic index cases than in asymptomatic. Extensive evidence has proved that mild or asymptomatic patients are less contagious than those with typical clinical symptoms (Cevik et al., 2021; Heald-Sargent et al., 2020; Luo et al., 2020). A larger household size might be associated with a lower SAR. One possible reason may be that large

families usually have a low average age and young people tend to be less susceptible. The spouse relationship emerged as a susceptible group in our result. Chaw et al. (2020) suggested that intimate relationships with frequent interaction and prolonged proximity in a closed environment were risk factors. However, negative outcome occurred in the parent-child relationship, which might result from the children's low vulnerability. Household contacts with comorbidities or female contacts were found to be more susceptible, which was also reported in many large population studies (Lyngse et al., 2022; Prunas et al., 2022).

There are several limitations of our systematic review and meta-analysis. First, because the articles included in case analyses were limited and relatively insufficient, larger data sets or more scientific methods are necessary for a more accurate prevalence assessment. In meta-analyses, some included studies were of the retrospective or cross-sectional type, and the information of index cases and contacts was mainly obtained from contact-tracing data sets. Therefore, the determination of the case status might be uncertain, especially the asymptomatic child index cases, which were often mistakenly identified as secondary cases, distorting transmission pathways. The epidemiologic information was self-reported and subject to recall bias and response bias. In addition, the SAR would be overestimated for not excluding infection resource outside the household and was also underestimated in studies in which only the symptomatic contacts were tested. Because of data insufficiency, many other potential determinants associated with the SAR were not investigated in detail, such as the incubation and infectious periods and public lockdown policy; subgroup analyses of child index cases were also not conducted. Last and most importantly, high unexplained heterogeneity in our analyses constituted an important obstacle when interpreting the results. This might be attributed to the great variation in the design of studies: different definitions of index cases and contacts, inconsistent testing protocols and follow-up time, sociodemographic factors, and so on. Many previous meta-analyses on SAR also ran into the same dilemma (Irfan et al., 2021; Madewell et al., 2020; Shah et al., 2020; Zhu et al., 2021). All of these implied a multitude of related factors and substantial differences among populations. Therefore, the generalizability of our results is limited; compared with the quantitative results, the qualitative conclusions might be more reliable.

Conclusion

Although children were demonstrated to be not dominant in the household transmission, their transmissibility of SARS-CoV-2 appeared to increase as new variants emerged. Given the potentially serious complications of pediatric COVID-19, vaccination research and implementation in children remain a must.

Potential competing interest

None.

Financial support

None.

Ethics approval

No ethics approval was required for this work.

Acknowledgment

The authors especially express their appreciation to Miss Mou for her kind help with data analysis (Jialing Mou, Ph.D., Institute

of Biochemistry and Cell Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences).

Author contributions

Concept and design: Yuan Shi and Feifan Chen. Retrieval, selection, and extraction: Feifan Chen, Yan Tian, and Lixin Zhang. Statistical analysis and interpretation: all authors. Drafting of the manuscript: Feifan Chen, Yan Tian, and Lixin Zhang. Critical revision: Yuan Shi and Feifan Chen. Supervision: Yuan Shi.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ijid.2022.05.016.

References

- Afonso ET, Marques SM, Costa LDC, et al. Secondary household transmission of SARS-CoV-2 among children and adolescents: clinical and epidemiological aspects. *Pediatr Pulmonol* 2022;57:162–75.
- Allen H, Vusirikala A, Flannagan J, et al. Household transmission of COVID-19 cases associated with SARS-CoV-2 delta variant (B.1.617.2): national case-control study. *Lancet Reg Health Eur* 2022;12.
- Baker JM, Nakayama JY, O'Hegarty M, et al. SARS-CoV-2 B.1.1.529 (Omicron) variant transmission within households – four U.S. jurisdictions, November 2021–February 2022. *MMWR Morb Mortal Wkly Rep* 2022;71:341–6.
- Bhatt M, Plint AC, Tang K, et al. Household transmission of SARS-CoV-2 from unvaccinated asymptomatic and symptomatic household members with confirmed SARS-CoV-2 infection: an antibody-surveillance study. *CMAJ Open* 2022;10:E357–66.
- Bi Q, Lessler J, Eckerle I, et al. Insights into household transmission of SARS-CoV-2 from a population-based serological survey. *Nat Commun* 2021;12:3643.
- Bi Q, Wu Y, Mei S, et al. Epidemiology and transmission of COVID-19 in 391 cases and 1286 of their close contacts in Shenzhen, China: a retrospective cohort study. *Lancet Infect Dis* 2020;20:911–19.
- Calvani M, Cantello G, Cavani M, et al. Reasons for SARS-CoV-2 infection in children and their role in the transmission of infection according to age: a case-control study. *Ital J Pediatr* 2021;47:193.
- Cerami C, Popkin-Hall ZR, Rapp T, et al. Household transmission of SARS-CoV-2 in the United States: living density, viral load, and disproportionate impact on communities of color. [published online ahead of print, 2021 Aug 12]. *Clin Infect Dis* 2021:ciab701. doi:10.1093/cid/ciab701.
- Cevik M, Tate M, Lloyd O, Maraolo AE, Schafers J, Ho A. SARS-CoV-2, SARS-CoV, and MERS-CoV viral load dynamics, duration of viral shedding, and infectiousness: a systematic review and meta-analysis. *Lancet Microbe* 2021;2:e13–22.
- Chakrabarti SS, Kaur U, Banerjee A, et al. COVID-19 in India: are biological and environmental factors helping to stem the incidence and severity? *Aging Dis* 2020;11:480–8.
- Chaw L, Koh WC, Jamaludin SA, Naing L, Alikhan MF, Wong J. Analysis of SARS-CoV-2 transmission in different settings. *Brunei. Emerg Infect Dis* 2020;26:2598–606.
- Chun JY, Jeong H, Kim Y. Age-varying susceptibility to the delta variant (B.1.617.2) of SARS-CoV-2. *JAMA Netw Open* 2022;5.
- Cloete J, Kruger A, Masha M, et al. Paediatric hospitalisations due to COVID-19 during the first SARS-CoV-2 omicron (B.1.1.529) variant wave in South Africa: a multicentre observational study. *Lancet Child Adolesc Health* 2022;6:294–302.
- Coccia M. Factors determining the diffusion of COVID-19 and suggested strategy to prevent future accelerated viral infectivity similar to COVID. *Sci Total Environ* 2020;729.
- JBI. Critical appraisal tools – checklist for systematic reviews. <https://jbi.global/critical-appraisal-tools>, 2020 (accessed 14 February 2022).
- de Gier B, Andeweg S, Backer JA, et al. Vaccine effectiveness against SARS-CoV-2 transmission to household contacts during dominance of Delta variant (B.1.617.2), the Netherlands, August to September 2021. *Euro Surveill* 2021;26.
- de Souza TH, Nadal JA, Nogueira RJN, Pereira RM, Brandão MB. Clinical manifestations of children with COVID-19: a systematic review. *Pediatr Pulmonol* 2020;55:1892–9.
- Dong Y, Mo X, Hu Y, et al. Epidemiology of COVID-19 among children in China. *Pediatrics* 2020;145.
- Donnelly MAP, Chuey MR, Soto R, et al. Household transmission of SARS-CoV-2 Alpha variant - United States, 2021. [published online ahead of print, 2022 Feb 11]. *Clin Infect Dis* 2022:ciac125. doi:10.1093/cid/ciac125.
- Dupraz J, Butty A, Duperrex O, et al. Prevalence of SARS-CoV-2 in household members and other close contacts of COVID-19 cases: a serologic study in canton of Vaud, Switzerland. *Open Forum Infect Dis* 2021;8:ofab149.
- Elliott P, Bodinier B, Eales O, et al. Rapid increase in Omicron infections in England during December 2021: REACT-1 study. *Science* 2022;375:1406–11.
- Fowlkes AL, Yoon SK, Lutrick K, et al. Effectiveness of 2-dose BNT162b2 (Pfizer BioNTech) mRNA vaccine in preventing SARS-CoV-2 infection among children aged 5–11 years and adolescents aged 12–15 years—PROTECT cohort, July 2021–February 2022. *MMWR Morb Mortal Wkly Rep* 2022;71:422–8.
- Fung HF, Martinez L, Alarid-Escudero F, et al. The household secondary attack rate of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2): a rapid review. *Clin Infect Dis* 2021;73(Suppl 2):S138–SS45.
- Galow L, Haag L, Kahre E, et al. Lower household transmission rates of SARS-CoV-2 from children compared to adults. *J Infect* 2021;83:e34–6.
- García-Salido A. SARS-COV-2 children transmission: the evidence is that today we do not have enough evidence. *Acta Paediatr* 2020;109:1912.
- Goldstein E, Lipsitch M, Cevik M. On the effect of age on the transmission of SARS-CoV-2 in households, schools, and the community. *J Infect Dis* 2021;223:362–9.
- Grijalva CG, Rolfes MA, Zhu Y, et al. Transmission of SARS-CoV-2 infections in households – Tennessee and Wisconsin, April–September 2020. *MMWR Morb Mortal Wkly Rep* 2020;69:1631–4.
- Harris RJ, Hall JA, Zaidi A, Andrews NJ, Dunbar JK, Dabrera G. Effect of vaccination on household transmission of SARS-CoV-2 in England. *N Engl J Med* 2021;385:759–60.
- Heald-Sargent T, Muller WJ, Zheng X, Rippe J, Patel AB, Kociolek LK. Age-related differences in nasopharyngeal severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) levels in patients with mild to moderate coronavirus disease 2019 (COVID-19). *JAMA Pediatr* 2020;174:902–3.
- Hoang A, Chorath K, Moreira A, et al. COVID-19 in 7780 pediatric patients: a systematic review. *EclinicalMedicine* 2020;24.
- Hu P, Ma M, Jing Q, et al. Retrospective study identifies infection related risk factors in close contacts during COVID-19 epidemic. *Int J Infect Dis* 2021;103:395–401.
- Hua CZ, Miao ZP, Zheng JS, et al. Epidemiological features and viral shedding in children with SARS-CoV-2 infection. *J Med Virol* 2020;92:2804–12.
- Irfan O, Li J, Tang K, Wang Z, Bhutta ZA. Risk of infection and transmission of SARS-CoV-2 among children and adolescents in households, communities and educational settings: a systematic review and meta-analysis. *J Glob Health* 2021a;11:05013.
- Irfan O, Muttalib F, Tang K, Jiang L, Lassi ZS, Bhutta Z. Clinical characteristics, treatment and outcomes of paediatric COVID-19: a systematic review and meta-analysis. *Arch Dis Child* 2021b;106:440–8.
- Jalali N, Brustad HK, Frigessi A, et al. Increased household transmission and immune escape of the SARS-CoV-2 Omicron variant compared to the Delta variant: evidence from Norwegian contact tracing and vaccination data. *Research Square*. 18 February 2022. <https://www.researchsquare.com/article/rs-1370541/v1> (accessed 25 Apr 2022).
- Jing QL, Liu MJ, Zhang ZB, et al. Household secondary attack rate of COVID-19 and associated determinants in Guangzhou, China: a retrospective cohort study. *Lancet Infect Dis* 2020;20:1141–50.
- Kim J, Choe YJ, Lee J, et al. Role of children in household transmission of COVID-19. *Arch Dis Child* 2021;106:709–11.
- Koh WC, Naing L, Chaw L, et al. What do we know about SARS-CoV-2 transmission? A systematic review and meta-analysis of the secondary attack rate and associated risk factors. *PLoS One* 2020;15.
- Koureas M, Speletas M, Bogogiannidou Z, et al. Transmission dynamics of SARS-CoV-2 during an outbreak in a Roma community in Thessaly, Greece—control measures and lessons learned. *Int J Environ Res Public Health* 2021;18:2878.
- Kuba Y, Shingaki A, Nidaira M, et al. Characteristics of household transmission of COVID-19 during its outbreak in Okinawa, Japan from February to May 2020. *Jpn J Infect Dis* 2021;74:579–83.
- Lau MSY, Grenfell B, Thomas M, Bryan M, Nelson K, Lopman B. Characterizing superspreading events and age-specific infectiousness of SARS-CoV-2 transmission in Georgia, USA. *Proc Natl Acad Sci U S A* 2020;117:22430–5.
- Lee B, Raszka Jr WV. COVID-19 transmission and children: the child is not to blame. *Pediatrics* 2020;146.
- Lewis NM, Chu VT, Ye D, et al. Household transmission of severe acute respiratory syndrome coronavirus-2 in the United States. *Clin Infect Dis* 2021;73:1805–13.
- Li F, Li YY, Liu MJ, et al. Household transmission of SARS-CoV-2 and risk factors for susceptibility and infectivity in Wuhan: a retrospective observational study. *Lancet Infect Dis* 2021;21:617–28.
- Li H, Lin H, Chen X, et al. Unvaccinated children are an important link in the transmission of SARS-CoV-2 delta variant (B.1.617.2): comparative clinical evidence from a recent community surge. *Front Cell Infect Microbiol* 2022;12.
- Li W, Zhang B, Lu J, et al. Characteristics of household transmission of COVID-19. *Clin Infect Dis* 2020;71:1943–6.
- Liu PY, Gragnani CM, Timmerman J, et al. Pediatric household transmission of severe acute respiratory coronavirus-2 infection - Los Angeles County, December 2020 to February 2021. *Pediatr Infect Dis J* 2021;40:e379–81.
- Lopez Bernal J, Panagiotopoulos N, Byers C, et al. Transmission dynamics of COVID-19 in household and community settings in the United Kingdom, January to March 2020. *Euro Surveill* 2022;27.
- Luo L, Liu D, Liao X, et al. Contact settings and risk for transmission in 3410 close contacts of patients with COVID-19 in Guangzhou, China: a prospective cohort study. *Ann Intern Med* 2020;173:879–87.
- Lyngse FP, Mølbak K, Denwood M, et al. Effect of vaccination on household transmission of SARS-CoV-2 Delta VOC. *medRxiv*. 6 January 2022. <https://www.medrxiv.org/content/10.1101/2022.01.06.22268841v1.full.pdf>. (accessed 25 Apr 2022).
- Madewell ZJ, Yang Y, Longini Jr IM, Halloran ME, Dean NE. Factors associated with household transmission of SARS-CoV-2: an updated systematic review and meta-analysis. *JAMA Netw Open* 2021;4.
- Madewell ZJ, Yang Y, Longini Jr IM, Halloran ME, Dean NE. Household transmission of SARS-CoV-2: a systematic review and meta-analysis. *JAMA Netw Open* 2020;3.

- Marks KJ, Whitaker M, Agathis NT, et al. Hospitalization of infants and children aged 0–4 years with laboratory-confirmed COVID-19 - COVID-NET, 14 states, March 2020–February 2022. *MMWR Morb Mortal Wkly Rep* 2022;71:429–36.
- McLean HQ, Grijalva CG, Hanson KE, et al. Household transmission and clinical features of SARS-CoV-2 infections. *Pediatrics* 2022;149.
- Meng B, Abdullahi A, Ferreira IATM, et al. Altered TMPRSS2 usage by SARS-CoV-2 Omicron impacts infectivity and fusogenicity. *Nature* 2022;603:706–14.
- Metlay JP, Haas JS, Soltoff AE, Armstrong KA. Household transmission of SARS-CoV-2. *JAMA Netw Open* 2021;4.
- Miller E, Waight PA, Andrews NJ, et al. Transmission of SARS-CoV-2 in the household setting: a prospective cohort study in children and adults in England. *J Infect* 2021;83:483–9.
- Miyahara R, Tsuchiya N, Yasuda I, et al. Familial clusters of coronavirus disease in 10 prefectures, Japan, February–May 2020. *Emerg Infect Dis* 2021;27:915–19.
- Mlcochova P, Kemp SA, Dhar MS, et al. SARS-CoV-2 B.1.617.2 Delta variant replication and immune evasion. *Nature* 2021;599:114–19.
- Musa S, Kissling E, Valenciano M, et al. Household transmission of SARS-CoV-2: a prospective observational study in Bosnia and Herzegovina, August–December 2020. *Int J Infect Dis* 2021;112:352–61.
- Ng DC, Tan KK, Chin L, et al. Risk factors associated with household transmission of SARS-CoV-2 in Negeri Sembilan, Malaysia. *J Paediatr Child Health* 2022a;58:769–73.
- Ng OT, Koh V, Chiew CJ, et al. Impact of Delta variant and vaccination on SARS-CoV-2 secondary attack rate among household close contacts. *Lancet Reg Health West Pac* 2021;17.
- Ng OT, Koh V, Chiew CJ, et al. Impact of SARS-CoV-2 vaccination and paediatric age on Delta variant household transmission. [published online ahead of print, 2022 Mar 22]. *Clin Infect Dis* 2022b:ciac219. doi:10.1093/cid/ciac219.
- Ogata T, Irie F, Ogawa E, et al. Secondary attack rate among non-spousal household contacts of coronavirus disease 2019 in Tsuchiura, Japan, August 2020–February 2021. *Int J Environ Res Public Health* 2021;18:8921.
- Ogata T, Tanaka H, Nozawa Y, et al. Increased secondary attack rate among unvaccinated household contacts of coronavirus disease 2019 patients with Delta variant in Japan. *Int J Environ Res Public Health* 2022;19:3889.
- Park SY, Kim YM, Yi S, et al. Coronavirus disease outbreak in call center. *South Korea. Emerg Infect Dis* 2020;26:1666–70.
- Paul LA, Daneman N, Schwartz KL, et al. Association of age and pediatric household transmission of SARS-CoV-2 infection. *JAMA Pediatr* 2021;175:1151–8.
- Planas D, Veyer D, Baidaliuk A, et al. Reduced sensitivity of SARS-CoV-2 variant Delta to antibody neutralization. *Nature* 2021;596:276–80.
- Prunas O, Warren JL, Crawford FW, et al. Vaccination with BNT162b2 reduces transmission of SARS-CoV-2 to household contacts in Israel. *Science* 2022;375:1151–4.
- Reukers DFM, van Boven M, Meijer A, et al. High infection secondary attack rates of severe acute respiratory syndrome coronavirus 2 in Dutch households revealed by dense sampling. *Clin Infect Dis* 2022;74:52–8.
- Rosenberg ES, Dufort EM, Blog DS, et al. COVID-19 testing, epidemic features, hospital outcomes, and household prevalence, New York State–March 2020. *Clin Infect Dis* 2020;71:1953–9.
- Shah K, Saxena D, Mavalankar D. Secondary attack rate of COVID-19 in household contacts: a systematic review. *QJM* 2020;113:841–50.
- Song JS, Lee J, Kim M, et al. Serial intervals and household transmission of SARS-CoV-2 Omicron variant, South Korea, 2021. *Emerg Infect Dis* 2022;28:756–9.
- Soriano-Aranda A, Gatell A, Serrano P, et al. Household severe acute respiratory syndrome coronavirus 2 transmission and children: a network prospective study. *Clin Infect Dis* 2021;73:e1261–9.
- Stich M, Elling R, Renk H, et al. Transmission of severe acute respiratory syndrome coronavirus 2 in households with children, Southwest Germany, May–August 2020. *Emerg Infect Dis* 2021;27:3009–19.
- Tanaka H, Hirayama A, Nagai H, et al. Increased transmissibility of the SARS-CoV-2 alpha variant in a Japanese population. *Int J Environ Res Public Health* 2021;18:7752.
- Thelwall S, Aiano F, Harman K, Dabrera G, Ladhani SN. Risk of hospitalisation and death in children with SARS-CoV-2 delta (B.1.612.2) infection. *Lancet Child Adolesc Health* 2022;6:e16–17.
- Thompson HA, Mousa A, Dighe A, et al. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) setting-specific transmission rates: a systematic review and meta-analysis. *Clin Infect Dis* 2021;73:e754–64.
- Viner R, Waddington C, Mytton O, et al. Transmission of SARS-CoV-2 by children and young people in households and schools: a meta-analysis of population-based and contact-tracing studies. *J Infect* 2022;84:361–82.
- Viner RM, Russell SJ, Croker H, et al. School closure and management practices during coronavirus outbreaks including COVID-19: a rapid systematic review. *Lancet Child Adolesc Health* 2020;4:397–404.
- Waltenburg MA, Whaley MJ, Chancey RJ, et al. Household transmission and symptomatology of SARS-CoV-2 Alpha variant among children–California and Colorado, 2021. [published online ahead of print, 2022 Apr 18]. *J Pediatr* 2022 S0022-3476(22)00338-9. doi:10.1016/j.jpeds.2022.04.032.
- Walter EB, Talaat KR, Sabharwal C, et al. Evaluation of the BNT162b2 Covid-19 vaccine in children 5 to 11 years of age. *N Engl J Med* 2022;386:35–46.
- Wang Y, Tian H, Zhang L, et al. Reduction of secondary transmission of SARS-CoV-2 in households by face mask use, disinfection and social distancing: a cohort study in Beijing, China. *BMJ Glob Health* 2020a;5.
- Wang Z, Ma W, Zheng X, Wu G, Zhang R. Household transmission of SARS-CoV-2. *J Infect* 2020b;81:179–82.
- World Health Organization, WHO Coronavirus (COVID-19) Dashboard. <https://covid19.who.int/>, 2022 (accessed 29 April 2022).
- Wu J, Huang Y, Tu C, et al. Household transmission of SARS-CoV-2, Zhuhai, China, 2020. *Clin Infect Dis* 2020;71:2099–108.
- Yang W. Transmission dynamics of and insights from the 2018–2019 measles outbreak in New York City: a modeling study. *Sci Adv* 2020;6:eaz4037.
- Ye F, Xu S, Rong Z, et al. Delivery of infection from asymptomatic carriers of COVID-19 in a familial cluster. *Int J Infect Dis* 2020;94:133–8.
- Yousaf AR, Duca LM, Chu V, et al. A prospective cohort study in nonhospitalized household contacts with severe acute respiratory syndrome coronavirus 2 infection: symptom profiles and symptom change over time. *Clin Infect Dis* 2021;73:e1841–9.
- Yung CF, Kam KQ, Chong CY, et al. Household transmission of severe acute respiratory syndrome coronavirus 2 from adults to children. *J Pediatr* 2020;225:249–51.
- Zhu Y, Bloxham CJ, Hulme KD, et al. A meta-analysis on the role of children in severe acute respiratory syndrome coronavirus 2 in household transmission clusters. *Clin Infect Dis* 2021;72:e1146–53.