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Review

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



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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.

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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.,

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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

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(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.

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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 < 0.05was 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 metaanalysis 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%

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 (2021)	China	Retrospective cohort multicenter study	314	Yes	RT-PCR	NA	Medium
lalali et al (2022)	Norway	Cohort study	NA	NA	RT-PCR	10	High
ling et al. (2022)	China	Retrospective cohort study	195	Ves	RT-PCR	14	High
Kim et al. (2020)	South Korea	Retrospective observational study	NA	NA	RT-PCR	NA	Medium
Kourses et al. (2021)		Retrospective cohort study	40	Voc	RT_DCR	NΔ	Medium
Kuba at al. (2021)	Japan	Cohort study	40 NA	Voc	DT DCD	14	Modium
$E_{\text{AUDA et al.}}(2021)$	Japan United States	conort study	59	Voc	DT DCD	14	Ligh
Li et al. (2021)	China	Potrospoctivo cohort study	24095	Voc	DT DCD	1 4 \	Ligh
Li et al. (2021)	China	Retrospective conort study	105	NA	DT DCD	222	Madium
Li et al. (2020)	United States	Prospective study	105	NA	RI-PCR DT DCD	14	Uich
Liu et al. (2021)		Prospective study	15	NA	RI-PCR	14	High
Lopez Bernai et al. (2022)	England	Prospective case-ascertained study	329	NA	KI-PCK	14	High
Lyngse et al. (2022)	Denmark	Retrospective study	24693	NA	RI-PCR	14	High
McLean et al. (2022)	United States	Prospective case-ascertained study	302	NA	RI-PCR	14	High
Metlay et al. (2021)	United States	Retrospective cohort study	NA	NA	RI-PCR	NA	Medium
Miller et al. (2021)	England	Prospective cohort study	NA	NA	RI-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)	Snain	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)	lanan	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. (2020_2)	China	Retrospective cohort study	127	NA	RT-PCR	14	High
Wang et al. $(2020a)$	China	Retrospective case series	85	Vec	RT-PCR	14	High
W_{11} et al. (2020)	China	Prospective observational study	35	NΔ	RT_DCR	NΔ	Medium
Volume f at al. (2020)	United States	Prospective cohort study	NA NA	NA	DT DCD	1/	Ligh
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.

						Weight	Weight
Study	Events	Total	Child Contact	Proportion	95%-CI	(common)	(random)
Afonso, E. T. et al. 2022	67	267	 	0.25	[0.20; 0.31]	0.1%	2.5%
Baker, J. M. et al. 2022	70	134	· · · · · · · · · · · · · · · · · · ·	0.52	[0.43; 0.61]	0.0%	2.5%
3hatt, M. et al. 2022	130	246		0.53	[0.46: 0.59]	0.1%	2.5%
Bi, Q. et al. 2021	39	626	+	0.06	[0.04; 0.08]	0.2%	2.5%
Bi, Q. et al. 2020	16	166		0.10	[0.06; 0.15]	0.1%	2.5%
Cerami, C. et al. 2021	13	41		0.32	[0.18; 0.48]	0.0%	2.3%
Chaw, L. et al. 2020	12	85		0.14	[0.08; 0.23]	0.0%	2.4%
de Gier, B. et al. 2021	231	1911	+	0.12	[0.11; 0.14]	0.6%	2.6%
Donnelly, M. A. P. et al. 2022	61	121		0.50	[0.41; 0.60]	0.0%	2.5%
Dupraz, J. et al. 2021	32	65	<u> </u>	0.49	[0.37; 0.62]	0.0%	2.4%
Harris, R. J. et al. 2021	20140	279815		0.07	[0.07; 0.07]	87.7%	2.6%
Hu, P. et al. 2021	10	89		0.11	[0.06; 0.20]	0.0%	2.4%
Hua, C. Z. et al. 2020	40	325		0.12	[0.09; 0.16]	0.1%	2.5%
Jalali, N. et al. 2022	326	643		0.51	[0.47; 0.55]	0.2%	2.5%
Jing, Q. L. et al. 2020	9	172	-++	0.05	[0.02; 0.10]	0.1%	2.5%
Koureas, M. et al. 2021	37	115		0.32	[0.24; 0.42]	0.0%	2.5%
Kuba, Y. et al. 2021	2	56		0.04	[0.00; 0.12]	0.0%	2.3%
_ewis, N. M. et al. 2021	19	68		0.28	[0.18; 0.40]	0.0%	2.4%
_i, F. et al. 2021	337	7238	•	0.05	[0.04; 0.05]	2.3%	2.6%
_i, W. et al. 2020	4	100		0.04	[0.01; 0.10]	0.0%	2.4%
Liu, P. Y. et al. 2021	2	18		0.11	[0.01; 0.35]	0.0%	2.0%
opez Bernal, J. et al. 2022	42	168		0.25	[0.19; 0.32]	0.1%	2.5%
_yngse, F. P. et al. 2022	4918	17429	•	0.28	[0.28; 0.29]	5.5%	2.6%
VicLean, H. Q. et al. 2022	64	141		0.45	[0.37; 0.54]	0.0%	2.5%
Vietlay, J. P. et al. 2021	210	4672	+	0.04	[0.04; 0.05]	1.5%	2.6%
vilyanara, R. et al. 2021	10	42		0.24	[0.12; 0.39]	0.0%	2.3%
VIUSA, S. et al. 2021	17	1/8		0.10	[0.06; 0.15]	0.1%	2.5%
Ng, D. C. et al. 2021	276	403		0.60	[0.55; 0.64]	0.1%	2.5%
Ng, U. T. et al. 2022	150	1130		0.20	[0.17, 0.22]	0.4%	2.0%
Jgala, T. et al. 2022	150	4/1		0.32	[0.28, 0.30]	0.1%	2.5%
Reukers, D. F. M. et al. 2022	42	110		0.30	[0.27, 0.40]	0.0%	2.0%
Rosenberg, E. S. et al. 2020	42	100		0.27	[0.20, 0.35]	0.0%	2.5%
Stich M of al 2021	104	679		0.75	[0.71, 0.79]	0.1%	2.0%
Fanaka H otal 2021	194	279		0.29	[0.25, 0.52]	0.2%	2.0%
Maltonburg M A ot al 2022	24	210		0.24	[0.19, 0.29]	0.1%	2.3%
Mana V ot al 2020	13	36		0.36	[0.33, 0.70]	0.0%	2.0%
Mang, 7. et al. 2020	2	18		0.30	[0.21, 0.34]	0.0%	2.2/0
Mu L of al 2020	2 5	31		0.11	[0.01, 0.33]	0.0%	2.0 /0
ousaf Δ R otal 2021	14	69		0.10	[0.03, 0.34]	0.0%	2.2%
lung C E ot al 2020	13	213		0.20	[0.12, 0.32]	0.0%	2.4 /0
rung, 0. P. et al. 2020	15	215		0.00	[0.03, 0.10]	0.170	2.370
Common effect model		319080		0.08	[0.08; 0.08]	100.0%	
$\frac{1}{2}$	462 n = 0			0.24	[0.18; 0.30]		100.0%
t = 100%, t = 0.0	403, p – t	'	02 04 06				
			0.2 0.4 0.0				

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, $I^2 = 98\%$). The SAR of the Omicron variant in two studies was 0.56 (95% CI: 0.51–0.61, $I^2 = 20\%$). 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, $I^2 = 0\%$). However, no significant difference was shown between children younger and older than 12 years (RR = 1.12, 95% CI: 0.90–1.39, $I^2 = 77\%$). 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, $I^2 = 66\%$) (Figure 2).

Household SAR of adult contacts

The SAR of adult household contacts was estimated at 0.32 (95% CI: 0.27–0.37, $I^2 = 99\%$) 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, $I^2 = 52\%$; >65 vs <65 years: RR = 1.24, 95% CI: 1.02–1.50, $I^2 = 55\%$). 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, $I^2 = 77\%$) (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

Study Ex	vents To	<10 otal Ev	; vents To	>10 otal	Risk Ratio	RR	95%-CI	Weight (common)	Weight (random)
Afonso, E. T. et al. 2022 Bi, Q. et al. 2021	18 8	94 167	49 31	173 459		0.68 0.71	[0.42; 1.09] [0.33; 1.51]	36.2% 17.4%	31.9% 12.7%
Bi, Q. et al. 2020	10	109	6 15	57		0.87	0.33; 2.28]	8.3%	7.9%
Kuba, Y. et al. 2021	0	17	2	39 —		0.45	0.02; 8.92]	1.6%	0.8%
Miller, E. et al. 2021	7	40	11	40		0.64	0.27; 1.47]	11.5%	10.3%
Yung, C. F. et al. 2020	1	152	6	61		0.47	0.16; 1.34]	9.0%	6.6%
Common effect model Random effects model Heterogeneity: $l^2 = 0\%$, $\tau^2 = 0$	p = 0.74	6 12	1	861		0.74 [0.78 [0.56; 0.97] 0.59; 1.02]	100.0% 	 100.0%
	, F				0.1 0.5 1 2 10				
Study	Events	<12 Total	Events	>12 Total	Risk Ratio	RR	95%-CI	(common)	(random)
Dhaff Markal 0000	40	54			h:	0.00	10, 45, 0, 401	4 500	5.00
Cerami, C. et al. 2022	18	51 27	5 5	14 14		0.99	[0.45; 2.19]	1.5%	5.0%
Donnelly, M. A. P. et al. 2022	34	64	27	57		1.12	[0.78; 1.60]	5.5%	10.8%
Koureas, M. et al. 2021	27	85	10	30		0.95	[0.53; 1.73]	2.9%	7.1%
LI, F. et al. 2021 McLean H. O. et al. 2022	196	4975	141	2263		0.63	[0.51; 0.78]	37.6%	13.3%
Musa S et al 2021	13	113	4	65	<u>[</u>	- 1.03	[0.71, 1.40]	1.0%	3.2%
Ng, D. C. et al. 2021	241	386	35	77	<u>i</u>	1.37	[1.06; 1.78]	11.3%	12.6%
Ng, O. T. et al. 2022	173	757	49	379		1.77	[1.32; 2.37]	12.7%	11.9%
Reukers, D. F. M. et al. 2022	21	46	21	70	<u> </u>	1.52	[0.94; 2.45]	3.2%	8.8%
Stich, M. et al. 2021	126	434	68	244		1.04	[0.81; 1.34]	16.9%	12.7%
Common effect model Random effects model		7012		3280		1.04 1.12	[0.93; 1.15] [0.90; 1.39]	100.0% 	 100.0%
Heterogeneity: $I^2 = 77\%$, $\tau^2 = 0$).0798, p <	< 0.01				5			
					0.2 0.3 1 2	0			Weight
	younge	r child	older	child				Weight	_
Study	Events	r child Total	older Events	child Total	Risk Ratio	RR	95%-CI	Weight (common)	(random)
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022	Events	r child Total 94	older Events	Total	Risk Ratio	RR 0.68	95%-CI [0.42; 1.09]	Weight (common) 5.6%	(random)
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi O. et al. 2021	Events 18 18	94 51 167	older Events 49 5 31	Child Total 173 14 459	Risk Ratio	RR 0.68 0.99 0.71	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51]	Weight (common) 5.6% 1.3% 2.7%	(random) 6.5% 3.6% 3.9%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020	Events 18 18 8 10	94 51 167 109	older Events 49 5 31 6	child Total 173 14 459 57	Risk Ratio	RR 0.68 0.99 0.71 0.87	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28]	Weight (common) 5.6% 1.3% 2.7% 1.3%	(random) 6.5% 3.6% 3.9% 2.8%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021	18 18 18 18 10 8	94 51 167 109 27	older Events 49 5 31 6 5	child Total 173 14 459 57 14	Risk Ratio	RR 0.68 0.99 0.71 0.87 0.83	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1%	(random) 6.5% 3.6% 3.9% 2.8% 3.0%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022	2 344	94 51 167 109 27 64	older Events 49 5 31 6 5 27	child Total 173 14 459 57 14 57	Risk Ratio	RR 0.68 0.99 0.71 0.87 0.83 1.12	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 8.0%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Kauraca M. et al. 2021	2 34 2 27 2 27 2 27 2 27 2 27 2 27 2 27 2 2	r child Total 94 51 167 109 27 64 33	older Events 49 5 31 6 5 27 15	child Total 173 14 459 57 14 57 32	Risk Ratio	RR 0.68 0.99 0.71 0.87 0.83 1.12 1.10	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.67; 1.80]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 8.0% 6.3%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Koureas, M. et al. 2021	2000 Events 18 18 18 10 8 10 8 34 17 27 0	r child Total 94 51 167 109 27 64 33 85 17	older Events 49 5 31 6 5 27 15 10 2	child Total 173 14 459 57 14 57 32 30 30	Risk Ratio	RR 0.68 0.99 0.71 0.87 0.83 1.12 1.10 0.95 0.45	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.67; 1.80] [0.65; 1.73] [0.02; 8.92]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5% 2.4% 0.3%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 6.3% 6.3% 0.4%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Koureas, M. et al. 2021 Li, F. et al. 2021	youngel Events 18 18 10 8 34 10 8 34 17 27 0 196	r child Total 94 51 167 109 27 64 33 85 17 4975	older Events 49 5 31 6 5 27 15 10 2 2 141	child Total 173 14 459 57 14 57 32 30 39 2263	Risk Ratio	RR 0.68 0.99 0.71 0.87 0.83 1.12 1.10 0.95 0.45 0.63	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.67; 1.80] [0.53; 1.73] [0.02; 8.92] [0.51]: 0.78]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5% 2.4% 0.3% 31.7%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 6.3% 6.3% 5.2% 0.4% 10.0%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Koureas, M. et al. 2021 Li, F. et al. 2021 McLean, H. Q. et al. 2022	2000 Events 18 18 10 8 10 8 10 8 10 10 8 2 34 17 27 0 196 34 34 34 34 34 34 34 34 34 34	r child Total 94 51 167 109 27 64 33 85 17 4975 74	older Events 49 5 31 6 5 27 15 10 2 2 141 30	child Total 173 14 459 57 14 57 32 30 39 2263 67	Risk Ratio	RR 0.68 0.99 0.71 0.87 0.83 1.12 1.10 0.95 0.45 0.63 1.03	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.67; 1.80] [0.53; 1.73] [0.02; 8.92] [0.51; 0.78] [0.71; 1.48]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5% 2.4% 0.3% 31.7% 5.2%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 8.0% 6.3% 5.2% 0.4% 10.0% 8.0%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Koureas, M. et al. 2021 Kuba, Y. et al. 2021 Li, F. et al. 2021 McLean, H. Q. et al. 2022 Miller, E. et al. 2021	2 34 17 27 0 196 34 17 27 0 196 34 7 7	r child Total 94 51 167 109 27 64 33 85 17 4975 74 40	older Events 49 5 31 6 5 27 15 10 2 141 30 11	child Total 173 14 459 57 14 57 32 30 39 2263 67 40	Risk Ratio	RR 0.68 0.99 0.71 0.87 0.83 1.12 1.10 0.95 0.45 0.63 1.03 0.64	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.67; 1.80] [0.53; 1.73] [0.02; 8.92] [0.51; 0.78] [0.71; 1.48] [0.27; 1.47]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5% 0.3% 31.7% 5.2% 1.8%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 8.0% 6.3% 5.2% 0.4% 10.0% 8.0% 3.4%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Koureas, M. et al. 2021 Kuba, Y. et al. 2021 Li, F. et al. 2021 McLean, H. Q. et al. 2022 Miller, E. et al. 2021 Musa, S. et al. 2021	2 34 18 18 18 18 18 18 18 18 18 18 18 10 8 34 17 27 0 196 34 7 13	r child Total 94 51 167 109 27 64 33 85 17 4975 74 40 113 202	older Events 49 5 31 6 5 27 15 10 2 2 141 30 11 4 4 2	child Total 173 14 459 57 14 57 32 30 39 2263 67 40 67 7 2263	Risk Ratio	RR 0.68 0.99 0.71 0.83 1.12 1.10 0.95 0.45 0.63 1.03 0.64 1.83	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.67; 1.80] [0.57; 1.73] [0.02; 8.92] [0.51; 0.78] [0.71; 1.48] [0.27; 1.47] [0.64; 5.50]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5% 0.3% 31.7% 5.2% 1.8% 0.8%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 8.0% 6.3% 5.2% 0.4% 10.0% 8.0% 3.4% 2.3%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Koureas, M. et al. 2021 Kuba, Y. et al. 2021 Li, F. et al. 2021 McLean, H. Q. et al. 2022 Miller, E. et al. 2021 Musa, S. et al. 2021 Ng, D. C. et al. 2022	younge Events 18 18 18 18 18 18 18 18 18 18 18 18 18 18 10 8 10 172 0 196 34 7 13 241 172	r child Total 94 51 167 109 27 64 33 85 17 4975 74 40 113 386 757	older Events 49 5 31 6 5 27 15 10 2 2 141 30 11 4 35 40	child Total 173 14 459 57 14 57 32 30 39 2263 67 40 65 77 370	Risk Ratio	RR 0.68 0.99 0.71 0.83 1.12 1.10 0.95 0.45 0.63 1.03 0.64 1.87 1.37	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.57; 1.80] [0.53; 1.73] [0.02; 8.92] [0.51; 0.78] [0.71; 1.48] [0.27; 1.47] [0.64; 5.50] [1.06; 1.78] [1.32; 2.37]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5% 0.3% 31.7% 5.2% 1.8% 0.8% 9.6%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 8.0% 6.3% 5.2% 0.4% 10.0% 8.0% 3.4% 2.3% 9.4% 8.0%
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Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Kuba, Y. et al. 2021 Kuba, Y. et al. 2021 McLean, H. Q. et al. 2022 Miller, E. et al. 2021 Musa, S. et al. 2021 Ng, D. C. et al. 2022 Reukers, D. F. M. et al. 2022 Stich, M. et al. 2021 Yung, C. F. et al. 2020	younge Events 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 10 17 17 173 241 173 21 126 7	r child Total 94 51 167 109 27 64 33 85 17 4975 74 40 113 386 757 46 434 152	older Events 49 5 31 6 5 27 10 2 141 30 2 141 30 11 4 35 49 21 68 6	child Total 173 14 459 57 14 57 30 39 2263 67 40 65 77 379 70 244 61	Risk Ratio	RR 0.68 0.99 0.71 0.83 1.12 1.10 0.95 0.45 0.63 1.03 0.64 1.03 0.64 1.37 1.37 1.37 1.52 1.04 0.47	95%-Cl [0.42; 1.09] [0.33; 1.51] [0.33; 2.28] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.67; 1.80] [0.53; 1.73] [0.27; 1.48] [0.27; 1.47] [0.64; 5.50] [1.06; 1.78] [1.32; 2.37] [0.94; 2.45] [0.81; 1.34] [0.16; 1.34]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5% 2.4% 0.3% 31.7% 5.2% 1.8% 9.6% 9.6% 9.6% 10.7% 2.7% 14.3% 1.4%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 6.3% 5.2% 0.4% 10.0% 8.0% 3.4% 2.3% 9.4% 8.9% 6.5% 9.5% 2.4%
Study Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Bi, Q. et al. 2021 Bi, Q. et al. 2020 Cerami, C. et al. 2021 Donnelly, M. A. P. et al. 2022 Dupraz, J. et al. 2021 Koureas, M. et al. 2021 Kuba, Y. et al. 2021 Li, F. et al. 2021 McLean, H. Q. et al. 2022 Miller, E. et al. 2021 Musa, S. et al. 2021 Ng, D. C. et al. 2022 Reukers, D. F. M. et al. 2022 Stich, M. et al. 2021 Yung, C. F. et al. 2020 Common effect model Bandom effect model	younge Events 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 10 8 34 17 0 196 34 7 13 211 126 7	Child 94 51 167 109 27 64 33 855 17 4975 74 40 113 386 757 46 434 152 7624	older Events 49 5 31 6 5 27 15 15 10 2 141 30 11 4 35 49 21 68 6	child Total 173 14 459 57 14 57 32 30 39 2263 67 40 65 77 379 70 244 61 4141	Risk Ratio	RR 0.68 0.99 0.71 0.87 0.83 1.12 1.10 0.95 0.45 0.63 1.03 0.64 1.87 1.37 1.77 1.52 1.04 0.47	95%-Cl [0.42; 1.09] [0.45; 2.19] [0.33; 1.51] [0.33; 2.28] [0.33; 2.07] [0.78; 1.60] [0.53; 1.73] [0.53; 1.73] [0.51; 0.78] [0.51; 0.78] [0.71; 1.48] [0.27; 1.47] [0.64; 5.50] [1.06; 1.78] [1.32; 2.37] [0.94; 2.45] [0.81; 1.34] [0.16; 1.34] [0.90; 1.09]	Weight (common) 5.6% 1.3% 2.7% 1.3% 1.1% 4.7% 2.5% 2.4% 0.3% 31.7% 5.2% 1.8% 0.8% 9.6% 10.7% 2.7% 14.3% 1.4% 100.0%	(random) 6.5% 3.6% 3.9% 2.8% 3.0% 8.0% 6.3% 5.2% 0.4% 10.0% 8.0% 3.4% 2.3% 9.4% 8.9% 6.5% 9.5% 2.4%

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

0.512

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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, I² = 74%). Significant difference in RR was also reported in different variants (P < 0.01).

Study	Child Events	contact Total	Adult Events	contact Total	Risk Ratio	RR	95%-CI	Weight (common)	Weight (random)
Baker, J. M. et al. 2022	70	134	157	289	<u> +</u>	0.96	[0.79: 1.17]	0.2%	3.3%
Bhatt, M. et al. 2022	130	246	109	241	<u>∦</u> +-	1.17	[0.97: 1.40]	0.2%	3.3%
Bi, Q. et al. 2021	39	626	259	3908	<u> </u>	0.94	[0.68; 1.30]	0.1%	3.0%
Bi, Q. et al. 2020	16	166	61	462	_ <u>+</u> +-	0.73	[0.43; 1.23]	0.1%	2.4%
Cerami, C. et al. 2021	13	41	20	62		0.98	[0.55; 1.75]	0.0%	2.2%
de Gier, B. et al. 2021	231	1911	774	4484	8	0.70	[0.61; 0.80]	0.8%	3.4%
Donnelly, M. A. P. et al. 2022	61	121	85	201		1.19	[0.94; 1.51]	0.1%	3.2%
Dupraz, J. et al. 2021	32	65	119	218	÷+-	0.90	[0.69; 1.19]	0.1%	3.1%
Harris, R. J. et al. 2021	20140	279815	82522	739027		0.64	[0.64; 0.65]	82.2%	3.5%
Hu, P. et al. 2021	10	89	36	178		0.56	[0.29; 1.07]	0.0%	2.0%
Hua, C. Z. et al. 2020	40	325	108	510		0.58	[0.42; 0.81]	0.2%	2.9%
Jalali, N. et al. 2022	326	643	650	1526	1 +	1.19	[1.08; 1.31]	0.7%	3.4%
Jing, Q. L. et al. 2020	9	172	94	599		0.33	[0.17; 0.65]	0.1%	2.0%
Koureas, M. et al. 2021	37	115	35	108	<u>+</u>	0.99	[0.68; 1.45]	0.1%	2.8%
Kuba, Y. et al. 2021	2	56	19	74		0.14	[0.03; 0.57]	0.0%	0.8%
Lewis, N. M. et al. 2021	19	68	33	120	÷+	1.02	[0.63; 1.64]	0.0%	2.5%
Li, F. et al. 2021	337	7238	8110	45584	+	0.26	[0.24; 0.29]	4.0%	3.4%
Li, W. et al. 2020	4	100	60	292		0.19	[0.07; 0.52]	0.1%	1.3%
Liu, P. Y. et al. 2021	2	18	15	32		0.24	[0.06; 0.92]	0.0%	0.9%
Lopez Bernal, J. et al. 2022	42	168	119	304		0.64	[0.47; 0.86]	0.2%	3.0%
Lyngse, F. P. et al. 2022	4918	17429	2897	10057	持 中	0.98	[0.94; 1.02]	6.7%	3.4%
McLean, H. Q. et al. 2022	64	141	134	263	1 th	0.89	[0.72; 1.11]	0.2%	3.2%
Metlay, J. P. et al. 2021	210	4672	1599	13245	+	0.37	[0.32; 0.43]	1.5%	3.4%
Miyahara, R. et al. 2021	10	42	137	733	<u> </u>	1.27	[0.73; 2.23]	0.0%	2.3%
Musa, S. et al. 2021	17	178	95	517		0.52	[0.32; 0.85]	0.1%	2.5%
Ng, D. C. et al. 2021	276	463	190	385	1 +	1.21	[1.06; 1.37]	0.4%	3.4%
Ng, O. T. et al. 2022	222	1136	1282	7334		1.12	[0.98; 1.27]	0.6%	3.4%
Ogata, T. et al 2022	150	4/1	259	931	11	1.14	[0.97; 1.35]	0.3%	3.3%
Reukers, D. F. M. et al. 2022	42	116	36	/1		0.71	[0.51; 1.00]	0.1%	2.9%
Rosenberg, E. S. et al. 2020	42	156	88	182		0.56	[0.41; 0.75]	0.1%	3.0%
Stich, M. et al. 2021	194	678	206	542	<u>†</u>	0.75	[0.64; 0.88]	0.4%	3.3%
Tanaka, H. et al. 2021	66	2/8	128	410		0.76	[0.59; 0.98]	0.2%	3.1%
Wattenburg, M. A. et al. 2022	24	44	76	1/5	1 1	1.26	[0.91; 1.73]	0.1%	3.0%
wang, Y. et al. 2020	13	30	64	92		0.52	[0.33; 0.82]	0.1%	2.6%
Wang, Z. et al. 2020	2	18	45	137		0.34	[0.09; 1.28]	0.0%	0.9%
vvu, J. et al. 2020	5	31	43	112		0.42	[0.18; 0.97]	0.0%	1.6%
Yousat, A. R. et al. 2021	14	69	33	126		0.77	[0.45; 1.35]	0.0%	2.3%
Common effect model		318075		833531		0.66	[0.65; 0.67]	100.0%	-
Random effects model					×	0.74	[0.64; 0.85]		100.0%
Heterogeneity: $I^2 = 97\%$, $\tau^2 = 0$.1609, <i>p</i> <	< 0.01			01 051 2 10				

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 was <4 members: RR = 0.69, 95% CI: 0.55–0.85, $l^2 = 94\%$; >6 vs <6 members: RR = 0.69, 95% CI: 0.50–0.95, $I^2 = 90\%$).

Study	Events	Total	Chile	d index	Proportion	95%-CI	Weight (common)	Weight (random)
Bhatt, M. et al. 2022 Calvani, M. et al. 2021 Galow, L. et al. 2021 Harris, R. J. et al. 2021 Kim, J. et al. 2021 Koureas, M. et al. 2021 Lewis, N. M. et al. 2021 Li, F. et al. 2021 Lyngse, F. P. et al. 2022 Miller, E. et al. 2022 Miller, E. et al. 2021 Ng, D. C. et al. 2022 Song, J. S. et al. 2022 Stich, M. et al. 2021	72 22 6 22585 3 41 11 0 46 4260 27 40 34 110 4 19	194 72 41 13920 248 40 3 793 - 22314 84 155 164 472 11 77			0.37 0.31 0.15 0.07 0.17 0.28 0.00 0.06 0.19 0.32 0.26 0.21 0.23 0.36 0.25	$ \begin{bmatrix} 0.30; 0.44] \\ 0.20; 0.43] \\ 0.06; 0.29] \\ 0.07; 0.07] \\ 0.12; 0.22] \\ 0.00; 0.71] \\ 0.00; 0.71] \\ 0.00; 0.71] \\ 0.04; 0.08] \\ 0.19; 0.20] \\ 0.19; 0.23] \\ 0.15; 0.28] \\ 0.20; 0.27] \\ 0.11; 0.69] \\ 0.16; 0.36] \\ 0.16; 0.36] $	0.1% 0.0% 0.7% 92.7% 0.0% 0.0% 0.2% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0%	7.6% 6.7% 5.9% 8.3% 7.8% 5.8% 1.4% 8.1% 8.3% 6.9% 7.5% 8.0% 3.3% 6.8%
Random effects model Heterogeneity: $I^2 = 100\%$, τ	2 ² = 0.0144,	p=0	+	3 04 05 06 07	0.00	[0.06; 0.07] [0.15; 0.26]		 100.0%
Study	Even	ts Total	A	dult index	Proportion	95%-CI	Weight (common)	Weight (random)
Afonso, E. T. et al. 2022 Bhatt, M. et al. 2022 Cerami, C. et al. 2021 Galow, L. et al. 2021 Harris, R. J. et al. 2021 Koureas, M. et al. 2021 Lewis, N. M. et al. 2021 Lyngse, F. P. et al. 2022 Miller, E. et al. 2022 Miller, E. et al. 2022 Miller, E. et al. 2022 Ng, D. C. et al. 2022 Reukers, D. F. M. et al. 2022 Song, J. S. et al. 2022 Rosenberg, E. S. et al. 2022 Soriano-Arandes, A. et al. 202 Stich, M. et al. 2020 Common effect model Ratom effect model Heterogeneity: $l^2 = 100\%$, τ^2	6 16 37 8007 5 5 840 426 43 139 22 7 1 0 5 2021 39 38 38 1 1 2021 39 38 1 1 2021 39 38 1 1 2021 39 38	37 267 33 103 39 207 70 1018842 50 124 52 185 51 52029 50 16022 60 16022 71 320 84 47998 86 187 14 25 55 229 33 581 31 1143 33 213 1099545 = 0			0.25 0.57 0.32 0.38 0.40 0.28 0.16 0.27 0.53 0.38 0.63 0.17 0.42 - 0.66 - 0.68 0.33 0.06 0.08 0.36 0.36	 [0.20; 0.31] [0.51; 0.63] [0.23; 0.42] [0.32; 0.45] [0.08; 0.03] [0.22; 0.50] [0.22; 0.35] [0.16; 0.16] [0.26; 0.27] [0.77; 0.18] [0.35; 0.76] [0.64; 0.71] [0.31; 0.36] [0.08; 0.08] [0.08; 0.08] [0.08; 0.08] [0.27; 0.46] 	0.0% 0.0% 92.7% 0.0% 4.7% 1.5% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0.0% 0	5.3% 5.3% 5.4% 5.2% 5.3% 5.4% 5.4% 5.4% 5.4% 5.4% 5.3% 4.4% 5.3% 5.4% 5.3% 5.4% 5.3%
Study E	Child ind vents To	dex Ad otal Events	ult index Total	Risk Ratio	R	R 95%-C	Weight I (common)	Weight (random)
Bhatt, M. et al. 2022 Galow, L. et al. 2021 Harris, R. J. et al. 2021 Koureas, M. et al. 2021 Lewis, N. M. et al. 2021 Lyngse, F. P. et al. 2022 McLean, H. Q. et al. 2022 Miller, E. et al. 2021 Ng, D. C. et al. 2021 Ng, O. T. et al. 2022 Song, J. S. et al. 2022 Stich, M. et al. 2021	72 6 22585 3139 11 0 46 7 4260 223 27 40 7 34 7 110 4 19	194 167 41 79 920 80077 40 50 3 52 793 8401 814 4260 84 171 155 35 164 432 472 1394 11 14 77 381	293 207 1018842 124 185 52029 16022 320 93 684 7998 25 1143		0.6 0.3 0.9 0.6 0.5 0.3 0.7 0.6 0.6 0.6 0.3 1.3 0.6 0.7	55 [0.53], 0.80 88 [0.18], 0.82 12 [0.90], 0.93 88 [0.39], 1.18 50 [0.04], 6.64 60 [0.27], 0.48 72 [0.69], 0.75 50 [0.47], 1.03 50 [0.47], 1.03 50 [0.47], 1.03 50 [0.28], 1.53 55 [0.28], 1.53 54 [1.13], 1.59 55 [0.28], 1.53 54 [0.50], 1.10] 0.3%] 0.1%] 86.5%] 0.1%] 0.6%] 0.6%] 0.1%] 0.2%] 0.4%] 0.4%] 0.4%] 0.4%] 0.4%] 0.1%	9.6% 5.1% 10.3% 6.7% 9.0% 10.3% 8.7% 8.9% 9.8% 4.5% 8.0%
Common effect model Random effects model Heterogeneity: I^2 = 96%, τ^2 =	3382 0.1470, <i>p</i> < 0	2 68).01	1097965	0.1 0.5 1 2	0.8 0.6	89 [0.88; 0.90 64 [0.50; 0.81] 100.0%]	 100.0%

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 analyses 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 contacttracing 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.

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Ethics approval

No ethics approval was required for this work.

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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, Cantiello 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 ÅL, 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 (B1.617.2): 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– 918.
- 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-Arandes 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 symptomology 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:eaaz4037.
- 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.