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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

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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. © 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 (Garcia-Salido, 2020; Viner et al., 2020; Yang, 2020). However, for SARS-CoV-2, it remains controversial (Garcia-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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* Corresponding author: Yuan Shi, Children’s Hospital of Chongqing Medical University, Chongqing 400014, China, Mob: 0862363635678.
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 characteristics, COVID-19 data (exposure, 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 arc sine 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 I² 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, I² = 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, I² = 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, I² = 97%). The SAR of two studies between November 2021 and 2022 was 0.51 (95% CI: 0.47–0.54, I² = 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, I² = 99%). The SAR of the Alpha variant in the three included studies was 0.42 (95% CI: 0.23–0.62, I² = 94%). The Delta variant was investigated in five studies, and the SAR was 0.35 (95% CI: 0.24–0.47, I² = 89%).
| Author (year)          | Country          | Study type                           | Cluster size | Public lockdown | Diagnostic method       | Follow-up (days) | Quality |
|-----------------------|------------------|--------------------------------------|--------------|----------------|-------------------------|-----------------|---------|
| Alonso 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                  | 14              | 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  |
| Jalal et al. (2022)   | Norway           | Cohort study                         | NA           | NA             | RT-PCR                  | 10              | High    |
| Jing et al. (2020)    | China            | Retrospective cohort study           | 195          | NA             | RT-PCR                  | 14              | High    |
| Kim et al. (2021)     | South Korea      | Retrospective observational study     | NA           | NA             | RT-PCR                  | NA              | Medium  |
| Kourkas et al. (2021) | Greece           | Retrospective cohort study           | 40           | Yes            | RT-PCR                  | NA              | Medium  |
| Kubai et al. (2021)   | Japan            | Cohort study                         | NA           | Yes            | RT-PCR                  | 14              | Medium  |
| Lewis et al. (2021)   | United States    | Cohort study                         | 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)  | United States    | Retrospective 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          | Yes            | 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             | RT-PCR                  | NA              | High    |
| Soriano-Arandes et al. (2021) | Spain    | Prospective, observational study     | 1108         | Yes            | RT-PCR                  | NA              | Medium  |
| Stick 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. (2021a)   | China            | Retrospective cohort study           | 124          | NA             | RT-PCR                  | 14              | High    |
| Wang et al. (2021b)   | China            | Retrospective case series            | 85           | Yes            | RT-PCR                  | 14              | High    |
| Wu et al. (2020)      | China            | Prospective observational study      | 35           | NA             | RT-PCR                  | NA              | Medium  |
| Yousuf 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.
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 COVID-19, coronavirus disease.

| Characteristics | Cluster (n = 78), % | Secondary cases (n = 207), % |
|-----------------|-------------------|-----------------------------|
| Child as the index case | 8 (10.3) | 16 (7.7) |
| Adult as the index case | 79 (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.**
Figure 2. Subgroup analyses on household SAR of child contacts in different age groups. CI, confidence interval; RR, risk ratio; SAR, secondary attack rate.

Subgroup analyses on household SAR of child contacts in different age groups (RR = 0.74, 95% CI: 0.64–0.85, I² = 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, I² = 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, I² = 80%; RR = 1.09, 95% CI: 0.89–1.34, I² = 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, I² = 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, I² = 76%; Delta: RR = 0.99, 95% CI: 0.82–1.19, I² = 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).
**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, I² = 100%). For the adult index cases, it was 0.36 (95% CI: 0.27–0.46, I² = 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, I² = 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, I² = 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, I² = 91%), whereas the same trend was not shown in the parent-child relationship (RR = 0.84, 95% CI: 0.59–1.19, I² = 87%), Households contacts with comorbidities were at a higher risk for secondary infections than those without comorbidities (RR = 1.98, 95% CI: 1.52–2.59, I² = 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, I² = 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, I² = 94%; >6 vs <6 members: RR = 0.69, 95% CI: 0.50–0.95, I² = 90%).

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**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) | I² | P-value |
|-------------------------------|----------------|-------------|----|---------|
| **Research period**           |                |             |    |         |
| 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**        |                |             |    |         |
| 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.
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-

| Study | Events | Total | Child index | Proportion | 95%-CI (common) | Weight (common) | Weight (random) | 95%-CI (random) |
|-------|--------|-------|-------------|------------|----------------|----------------|----------------|----------------|
| Total | 122 22 | 266-275 |

| Study | Events | Total | Adult index | Proportion | 95%-CI (common) | Weight (common) | Weight (random) |
|-------|--------|-------|-------------|------------|----------------|----------------|----------------|
| Total | 122 22 | 266-275 |

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

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Ethics approval

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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.jid.2022.05.016.

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