Journal of Infection xxx (xxxx) xxx

Contents lists available at ScienceDirect

Journal of Infection

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

Commentary

Transmission of SARS-CoV-2 by children and young people in households and schools: A meta-analysis of population-based and contact-tracing studies

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ARTICLE INFO

Article history:
Accepted 18 December 2021
Available online xxx

SUMMARY

Background: The role of children and young people (CYP) in transmission of SARS-CoV-2 in household and educational settings remains unclear. We undertook a systematic review and meta-analysis of contact-tracing and population-based studies at low risk of bias.

Methods: We searched 4 electronic databases on 28 July 2021 for contact-tracing studies and population-based studies informative about transmission of SARS-CoV-2 from 0 to 19 year olds in household or educational settings. We excluded studies at high risk of bias, including from under-ascertainment of asymptomatic infections. We undertook multilevel random effects meta-analyses of secondary attack rates (SAR: contact-tracing studies) and school infection prevalence, and used meta-regression to examine the impact of community SARS-CoV-2 incidence on school infection prevalence.

Findings: 4529 abstracts were reviewed, resulting in 37 included studies (16 contact-tracing; 19 population studies; 2 mixed studies). The pooled relative transmissibility of CYP compared with adults was 0.92 (0.68, 1.26) in adjusted household studies. The pooled SAR from CYP was lower ($p = 0.002$) in school studies 0.7% (0.2, 2.7) than household studies (7.6% (3.6, 15.9) . There was no difference in SAR from CYP to child or adult contacts. School population studies showed some evidence of clustering in classes within schools. School infection prevalence was associated with contemporary community 14-day incidence (OR 1.003 (1.001, 1.004), $p<0.001$).

Interpretation: We found no difference in transmission of SARS-CoV-2 from CYP compared with adults within household settings. SAR were markedly lower in school compared with household settings, suggesting that household transmission is more important than school transmission in this pandemic. School infection prevalence was associated with community infection incidence, supporting hypotheses that school infections broadly reflect community infections. These findings are important for guiding policy decisions on shielding, vaccination school and operations during the pandemic.

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https://doi.org/10.1016/j.jinf.2021.12.026

Background

The role of children and young people (CYP) in transmission of SARS-CoV-2 remains unclear, in both households and child-specific settings, such as schools and nurseries.[1] Observations of low incidence of symptomatic infection in CYP early in the pandemic led to assumptions that they played a very limited role in infection or transmission. This view has been challenged by the recognition that high proportions of asymptomatic infections in CYP led to low ascertainment of infections in this age-group,[1] particularly when testing capacity was limited. Findings from some large contact-tracing studies (contact-tracing studies)[2] have suggested CYP do play an important role in household transmission. In educational settings, whilst outbreaks have been reported in day-care nurseries,[3] schools[4-6] and school-like residential camps,[7,8] a number of population-based school studies have found evidence of limited transmission especially between children.[9,10] It remains unclear the extent to which cases and outbreaks in schools reflect transmission in schools or the wider community.

Epidemiological studies that can provide useful information about transmission with the lowest risk of bias include contact-tracing studies with active follow-up and testing of all contacts regardless of symptoms and population-based studies which test all members of the population regardless of symptoms. Population-based studies are informative about prevalence across age-groups and risk factors for infection, and may provide information about clustering or timing of infection within a setting (e.g. households or schools). Studies have shown that children under 10–12 years have lower susceptibility to SARS-CoV-2 infection than adults, although the risk in teenagers appears to be closer to young adults.[11] However CYP also tend to have the highest social mixing rates across society, including during the pandemic,[12] and transmission is a complex interaction of viral properties, susceptibility, social mixing and population age structures. For these reasons, studies of incidence of symptomatic infection in CYP provide a weak basis for inference around children's role in transmission.[11]

Over 18 months into the COVID-19 pandemic, there are only now sufficient data to allow meta-analysis of relevant data only including studies at low risk of bias. Existing systematic reviews are now outdated, including only data from early in the pandemic,[13-18] and are critically biased by their inclusion of studies which systematically under-ascertained asymptomatic infections in CYP. A large literature has since been published, including several population-based studies of CYP within schools.[9,10] Many of these date from late 2020 or early 2021 when schools had extensive mitigation measures in place that are hypothesized to reduce transmission within schools, as does reducing attendance during periods of hybrid in-person and online learning, yet data on the effects of such measures are lacking.[19,20]

We undertook a systematic review and meta-analysis of high quality epidemiological studies published during the first 18 months of the pandemic (Jan 2020- July 2021) to answer the following questions: (a) To what extent do CYP under 20 years of age transmit SARS-CoV-2 to other CYP and to adults in household and child-specific (e.g. educational) settings?; (b) how does transmission differ between household and educational settings?; and (c) is community infection incidence associated with prevalence of or transmission of infection within educational settings?

Methods

The search was undertaken using a protocol registered with Prospero registry (CRD42021222276).

Search strategy

We searched four electronic databases (PubMed; medRxiv; COVID-19 Living Evidence database; Europe PMC) to 28 July 2021. The search terms for PubMed were ("COVID-19" [Text Word] OR "2019-nCoV" [Text Word] OR "SARS-CoV-2" [Text Word]) AND ("child*" [All Fields] OR "infant*" [All Fields]) AND ("disease transmission, infectious" [MeSH Terms] OR "epidemiology" [MeSH Terms] OR "schools" [MeSH Terms]) with terms for other databases shown in Appendix Table 1.

We defined children and young people as being < 20 years of age, but note that different studies used different age-ranges across childhood. We did not limit studies by date or language. The reference lists of identified relevant reviews were checked for additional likely studies. Studies were also identified through other systematic reviews and the professional networks of the authors.

Eligibility

We searched for contact-tracing studies and community incidence studies to answer questions a) and b), and school incidence or prevalence studies to answer question c). We included published or unpublished reports of studies of SARS-CoV-2 infection of the following types:

a. Contact-tracing studies informative about transmission from primary or index cases aged 0–19 years separately to adult index cases and which identified and tested all contacts regardless of symptoms
b. Population-based studies that were either:
   i. longitudinal incidence studies in any setting which reported or modelled transmission chains between 0 and 19 year olds and others
   ii. studies of prevalence or incidence in 0–19 year olds in child-specific settings (e.g. day-care, nurseries or schools) using either longitudinal or cross-sectional designs

We only included studies which identified SARS-CoV-2 infection through RT-PCR on oral or nasal samples or through established serological methods. We did not include studies which used less well validated methods such as rapid antigen tests, stool samples[21] or wastewater methods.

We excluded studies of transmission from single individuals or within single institutions; modeling studies that did not provide observational data; studies of vertical transmission; systematic reviews; studies only of school staff; and biological studies of transmission dynamics such as viral load, viral shedding or aerosolization. We excluded ecological level studies of the impact of school opening or closing on community transmission as this has been examined in a separate review.[22]

We excluded studies judged to be at critical risk of bias relating to inadequate ascertainment of asymptomatic infections in CYP. We, therefore, excluded:

1. contact-tracing studies which only tested symptomatic contacts, tested low proportions of recruited contacts or provided insufficient information to judge completeness of contact testing.
2. population studies where infection was identified only by testing of symptomatic individuals or recruitment from clinical settings
3. non-representative population studies due to limited sampling of the target population e.g. where testing was only performed in low proportions of participants

Study selection

Titles and abstracts of identified studies were reviewed for potential eligibility by one researcher (RV). Those potentially eligible

Table 1
Study characteristics.

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Blaisdell et al.	PubMed	USA	June-August 2020	NS	Population	Contact-tracing	Four residential summer school camps for children and staff. Mixture of outdoor and indoor activities. Approximately 75% of usual enrolment.	1022 attendees from 41 US states (642 children, 380 staff); 1006 tested (98%). Attended from 44 to 62 days. 3 primary cases and 41 contacts (30 children, 11 staff)	7–18y	RT-PCR (swab site not stated) before arrival, on arrival and at 4 and 9 days	3 attendees (0.3%) (2 staff, 1 child) tested positive after arrival and their cohorts (n = 41 contacts) isolated for 8–14d, being released after 2 negative tests. No secondary cases in contacts in 30 contacts of child primary and 11 contacts of the 2 adult primary cases.
Varma et al.	Professional	USA	Period 1 9 Oct-20 Nov; Period 2: 6–18 Dec 2020	NS	A) Population and B) Infection	A) Surveillance & B) Contact tracing	A) Surveillance: Routine testing of a random sample CYP attending public schools in New York City; 12 Oct-20 Nov: 26% of CYP attended 1–3 days per week with remainder learning online; all schools closed 19Nov-6 Dec and only elementary schools reopened in Dec; B) Routine public health data from city database and contact-tracing. Contacts quarantined for 14 days.	A) Surveiillance in schools: 10–20% of each school selected: Period 1: n = 60,783 CYP (41% of eligible consent), Period 2: n = 34,556 CYP (61% of eligible consented); B) Contact-tracing: 2231 cases (child & adult) linked with schools and their 36,423 school-based contacts identified across entire period.	5–14y	RT-PCR (NP swab): A) Monthly testing for all schools with some schools moving to weekly in November and all primary schools weekly in Dec. B) RT-PCR testing of contacts of identified cases. Proportion of contacts identified and tested not stated - mean 16.2 contacts per case tested	A) Surveillance: Prevalence: Period 1 12Oct-20Nov: 0–4y 0.45% (1/223) 5–14y 0.28%(148/52,050) 15–24y 0.28%(24/8600); Period 2: 7–18Dec: 0–4y 1.61%(1/62) 5–14y 0.77%(257/33,330) 15–24y 0.69%(8/1164). B) Contact tracing: 191/36,423 = 0.5% contacts tested positive. Of these 132 cases (69%) had information to allow assessment of transmission: 67 (51%) staff-to-staff, 36 (27%) from staff-to-student, 18 (14%) student-to-staff, and 11 (8%) from student-to-student
Park et al.	Handsearch	South Korea	20 Jan-27 Mar 2020	NS	Infection	Contact-tracing	Households. National Korea Centers for Disease Control contact-tracing database used. High quality testing, tracing and isolation system.	10,962 index cases (29 (0.5%) aged 0–9y, 124 (2.2%) 10–19y) and 10,592 HH contacts (57 for 0–9y index; 231 for 10–19y index). Data on HH contacts only used, as all HH contacts routinely tested while other contacts tested if symptomatic.	0–19y	RT-PCR (swab site not stated)	SAR for 0–9y index: 5.3%(1.3, 13.7; 3/57). SAR for 10–19y index: 18.6%(14.0, 24.0; 43/231). Compared with 10.5% (889/8440) in 20–59 year olds.
Schoeps et al.	medRxiv	Germany	17 Aug-16 Dec 2020	NS	Infection	Contact-tracing	K-12 schools in 1 state (Rhineland-Palatinate): FTF. Data from school reopening in August 2020 through to lockdown on 16 Dec 2020	Population: 1492 schools, 406,607 schoolchildren & 144,245 children < 6 years in day-care. 784 index cases notified; information on contacts available on 441 index cases (346 students, 91 staff, 20 unknown) with 14,591 contacts of whom 13,005 were tested contacts.	3–18y	Public health notification of PCR+cases (NP swab) linked to educational institutions; all close contacts offered PCR testing routinely - 89% of contacts (87% of child contacts) were PCR-tested (13,005 contacts).	When restricted to PCR-tested contacts (441 index cases & 13,005 contacts), overall SAR was 1•51 (1•30–1•73); SAR from children 99/10,716=0.92(0.75–1.12). These 99 secondary cases occurred in 53 clusters of 3 cases or more; SAR from teachers 91/2858=3.18(2.57–3.90); transmission from teacher index was greater than from child index IRR 4.4 p<0.001; calculated each teacher index resulted in 0.5 secondary cases, whereas there was only 1 teacher secondary for 25 child indexes.

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Hu et al.	medRxiv then published	China (Hunan)	13 Jan-2 April 2020	NS	Infection	Contact-tracing	Households in Hunan province	1178 index cases (61 aged 0–14y) and 15,648 close contacts (1706 aged 0–14y): 471 secondary cases	Children & adults: child age <15y	Hunan Province CDC dataset: all contacts quarantined for 14 days and tested regardless of symptoms	Age-related transmission could be examined in 461 index cases (25 0–14y). Unadjusted OR for secondary infection from 0 to 14yo 0.33(0.04, 2.83) compared with 15–64yo, however small numbers of index children (25/461=5%). In adjusted general linear models, this association was again not significant (0.28(0.04, 2.04).
Dattner et al.	medrxiv then published	Israel	17 Mar-3 May 2020	NS	Population	Contact-tracing	637 HH in Bnei Brak, Israel where all HH members were tested. Note 51% of population <20y.	3353 (1809 adults and 1544 children 0–19y)	0–19y	RT-PCR (site not stated) all HH contacts; Serology IgG in 130/637HH	Joint PCR & serology transmission mode: Relative susceptibility of <20y compared with adults was 43% (31%, 55%) and relative transmissibility/infectivity 63%(37,88). Positive PCR: excluding index cases, 44% of adults were infected compared to 25% of the children. Serology positive: <20y= 34% (141/417), adults= 48% (137/288)
Yoon et al.	medrxiv then published	South Korea	20 May-31 July 2020	NS	Infection	Contact-tracing	National school surveillance data from test-trace system. Schools resumed FTF learning in 4 steps from 20 May (Year 12 only) through to 8 June. Efficient test-trace system with testing of all contacts	44 index children and >13,100 contacts attending 38 schools/EYS: 6 EYS(4-5y), 17 primary school(7-12y), 6 middle school (13-15y) and 15 high school (16-18y). Contacts: 875 YES, 3374 primary, 1525 middle and 6255 high school. All contacts tested;% contacts participating not stated however tested mean 297 contacts per index	4–18y	RT-PCR (swab, siting not stated)	SAR (children and adults) from child index cases: total 1/13,100: EYS 0%(0/875), primary 0.03% (1/3374), middle and high 0% (0/7780). Identified source for 29/44 child index cases: 79%(23) infected by family members.
Li et al.	medrxiv then published	China (Wuhan)	2 Dec 2019–18 Apr 2020	NS	Infection	Contact-tracing	Retrospective regional data from Wuhan Center for Disease Control and Prevention system.	29,578 primary cases in 29,405 HH and 57,581 HH contacts. Test data were available for 48,962 contacts (85%; data missing for remainder & unclear if tested or not; all HH contacts tested after 2 Feb but not before). For HH with a single primary case, there were 24,985 index cases (327 were <20y (1.3%)) and 52,822 contacts. Note that non-tested contacts were assumed to be negative	0–19y	RT-PCR (swab site not stated)	SAR for primary cases <20y 5.8%(4.3, 7.7; 46/793). Unconditional GEE models suggested lower transmissibility for <20y (OR 0•66 (0•48–0•90) compared with >=60y) whereas conditional chain-binomial models suggested higher infectivity for <20y (OR 1•58 (1.28,1.95) compared with >=60y

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Laxminarayan et al.	medrxiv then published	India	5 Mar-June 2020	NS	Infection	Contact-tracing	Community and HH CTS of state national surveillance-identified positive cases in Andhra Pradesh and Tamil Nadu	Index cases 6063 <18y + 78,866 adults; contacts 57,415 <18y + 507,476 adults. All recruited contacts tested. 20% of reported cases included and 19% of traced contacts participated	<18y	RT-PCR (site not stated). All contacts were quarantined for 14 days and PCR-tested at least once during quarantine.	SAR= 7.2% (4110/57,415) from 0 to 17y and 7.4%(37,479/507,476) for 18 plus.
Larosa et al.	Professional	Italy	1 Sep-15 Oct 2020	NS	Infection	Contact-tracing	Schools and early years settings in Reggio Emilia province after reopening of schools. Schools reopened 15 Sep, very largely FTF although some large schools operated 50% hybrid teaching if classrooms don't allow distancing	48 index cases (43 children, 5 staff) identified in 41 classes of 36 schools; 1198/1200 contacts tested (99.8%; 994 children, 204 staff)	0–19y	RT-PCR - swab, site not stated. Cases identified through routine public health systems. Included all cases noted to have connection with schools in 48H before symptoms/test. Contacts tested once each.	38 secondary cases in 9 clusters amongst children (SAR = 3.8%, 38/994) and no secondary cases amongst teachers. Overall school SAR from child+adult index cases 3.2% (38/1198). No secondary cases amongst children in early years settings. SAR from children only calculable for primary schools (only child index cases $n = 14$): 0.4%(1/266)
Macartney et al.	Professional	Australia	4 July - 18 Dec 2020: Term3 (4 July-25 Sep), Term 4 (26 Sep-18 Dec).	WT; no VOC detected	Infection	Contact-tracing	State-wide surveillance of cases identified attending schools in New South Wales while infectious. Schools fully open FTF; 88% attendance Term 3 and 4.	RT-PCR. Term 3: 39 primary cases (32 students, 7 staff) and 3641 contacts: 95% of contacts tested. Term 4: 10 primary cases (9 students, 1 staff) and 1098 contacts (99% contacts tested)	3–18y	RT-PCR (Np swab). Note serology also conducted on small numbers - not reported here.	TERM 3: 33 secondary cases (28 stent, 5 staff) - SAR=0.9% (33/3641). EYS: 6 primary cases (2 children, 4 staff): overall SAR 1.7% (13/754); SAR from 2 child primary cases: SAR to children 0% (0/58), SAR to adults 0% (0/11) Primary schools:13 primary cases (11 children, 2 staff) in 12 schools: SAR from child primary: SAR to children 0.3% (2/643) SAR to adults 0% (0/76) Secondary schools: 20 primary cases (19 student, 1 staff): overall SAR 1.1%(27/2466) - 19 student primary in 16 schools: SAR to students 1.27%(26/2045), SAR to adults 0.4% (1/226). TERM 4: 13 secondary cases (12 student, 1 staff) occurred in 4 settings (2 primary, 2 EYS) - overall SAR 1.2% (13/1098). EYS: 4 primary child cases (no adult) resulted in 4 secondary cases (3 children, 1 adult). SAR from child index: child 0.8% (3/393) adult 1.3% (1/79) Primary: 3 primary cases (2 children, 1 staff) in 3 schools: 9 secondary children, 0 secondary staff cases. SAR from child index: child 0.4% (1/269) adult 0% (0/33) Secondary: 3 primary children in 3 schools: 0 secondary cases in 199 student and 43 staff contacts.

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Kim et al.	PubMed	South Korea	20 Jan-6-Apr 2020	NS	Infection	Contact-tracing	HH contact-tracing study of all confirmed cases ≤18 years in South Korea	First 107 index cases ≤18y identified nationally and their 248 HH members (defined as close contacts; mean 4.3 per child)	<18y	RT-PCR (site not stated) of all contacts (100%); quarantined for 14D	41/248 (16.5%) were positive but 40 of these were assessed to likely have the same initial exposure as the child therefore removed from total contact number. O 1 definite secondary case was identified from index<19y – SAR = 1/208=0.48 (reported in paper as 0.4 using total contact number)
Verberk et al	medRxiv; data obtained from authors	Netherlands & Belgium	Apr-December 2020	WT; recruitment before VOC circulating	Infection	Contact-tracing	HH in Utrecht or Antwerp recruited through a positive index case in HH with 2 or more members. Households approached after positive PCR test in one member; not designed to be representative of broader population	272 Households recruited. Interim data in the preprint provided on first 117 HH. Data provided by authors on 39 index cases aged 0–18y and their 131 HH contacts.	0–18y	RT-PCR (nasopharyngeal) and serology IgG of all HH members at baseline (median Day 5 after index diagnosis) and repeated if symptomatic or for all participants at D21. Secondary infection defined as PCR or seropositive	Preprint findings: overall SAR 27.9% (95%-CI: 22.7–33.8%); SAR highest from parent to child (36.1%) and lowest from child to parent (15.7%). Data supplied by authors: infections from 39 index children: SAR for 0–11y 4.3% (2/47) and 12–18y 17.9% (15/84)
Brandal et al.	PubMed	Norway	28 Aug-11 Nov 2020	NS	Infection	Contact-tracing	Primary schools in 2 counties with highest prevalence	13 child index cases identified during period; 292 contacts (234 child; 58 adults). Contact participation was 73% child & 78% adult.	5–13y	RT-PCR on saliva: Cases were PCR+ & attended school within 48 h of sample/symptom; 2 saliva RT-PCR for all contacts: immediate and at 10 days of isolation	All child index cases except 1 had HH members who tested positive before child. SAR from child index cases = 0.9%(2/234) for children and 1.7% (1/58) for adults
Reukers et al.	medRxiv then published	Netherlands	Mar-May 2020	NS	Infection	Contact-tracing	Households in Utrecht region: all HH with a positive adult and <18 h in HH were contacted to recruit entire HH; studied within 24 hrs of recruitment;% of eligible indexes not stated	55 HH: 242 participants (55 adult index cases, 187 contacts (70 children 1-11y, 46 adolescents 12-17y). Entire households participated.	1–17y	RT-PCR (NP and oral swabs) and serology for entire HH 3 times - on Days 1, 14–21 and 28–42. Participation rate for contacts not stated but implied to be 100%	In 1/55 HH the primary case was an adolescent and not the index adult. No secondary cases in 17HH and 100% secondary infections in 11 HH. Overall SAR 43%(33,53): lower risk of infection for 1–11yo compared with adults in adjusted models. Adjusted SAR 1–11y 35%(24,46), 12–18y 41%(27,56) and 18yplus 51%(39,63). Transmission/susceptibility model: susceptibility compared to adults: 1–11y 0.67(0.40,1.1) 12–17y 0.93(0.51, 1.7). Transmissibility compared with adults: 1–11y 0.73(0.04, 2.6) 12–17y 2.7(0.98,5.6)
Lyngse et al.	medRxiv	Denmark	25 Aug 2020–10 Feb 2021	NS	Infection/ Population	Contact-tracing	Danish population register linked with national testing database, including all contact-tracing data. Reconstructed HH and identified transmission chains using time data. 73% of national primary cases included.	66,311 primary cases (36,388 aged 0-19y) and 213,576 HH contacts (148,724 aged 0–19y). 89% of HH contacts tested	<20y	RT-PCR (swab site not stated)	SAR from primary aged 0–5y 22%(3313/14,306), 5–10y 39%(5960/15,263), 10–15y 43%(8908/20,596) 15–20y 51% (12,440/24,197) compared with 52.3% (72,761/139,177) aged 20y plus. Adjusted OR for transmission from index aged 0–5y 1.11(1.03,1.19), 5–10y 0.95(0.90, 1.0), 10–15y 0.82(0.78,0.85), 15–20y 0.70(0.67,0.72) compared with 30–35yo.

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Telle et al.	medRxiv then published	Norway	1 March 2020–1 Jan 2021	NS	Infection/ Population	Contact-tracing	Norwegian Population Registry linked with all national COVID testing databases including test and trace. Included all HH with children <20y and a single identifiable index case. 3 million of the Norwegian population of 5.4million were tested during study period.	7548 single index cases (1498 <=16y; 200<7y, 517 7-12y, 781 13-16y) and their HH, including 26,991 individuals (14,808 <20y and 12,184 adults). Testing of contacts within 14D varied with index age: 92% 0-6y, 88% 7-12y, 87% 13-16y and 60-70% for 17 plus.	0–16y (17–19y not reported as contact testing <85%)	RT-PCR (swab site not stated) of all contacts regardless of symptoms (after April 2020)	SAR within 14d: SAR was highest from 0 to 6y and from parents to both children and adults. SAR from children: index 0–6y 23%(18,30) to children and 29%(24–34) to parents; index 7–12y 12%(10,15) to children and 21%(19,24) to parents; index 13–16y 15%(13,18) to children and 18%(16,21) to parents. SAR from parents: 24%(23,25) to children and 38%(36,40) to other parents.
Hoehl et al.	Handsearch for R1; medRxiv (Shenk et al.) for R2&3	Germany	R1: 18 Jun-10 Sep 2020 R2: 18 Jan-Feb 11 2021 R3: 17 May-June 11 2021,	R1: NS R2: WT dominant, alpha emerging R3: alpha dominant	Population	Surveillance	SAFE KiDS study Rounds 1-3. Representative sample of 50 daycare centres (R1), 47 centres (R2) and 46 centres (R3) in state of Hesse (1% of facilities in Hesse). 30 individuals (children and staff) per facility invited for weekly home testing. R1 was low community incidence with wild type virus; R2 was high incidence, R3 was moderate incidence	R1: 1235 participants from 50 centres (859 children; 376 staff). Total of 13,273 swabs tested (56% oral). Median 6 samples per child and 7 per staff member. R2: 47 centres with 577 children and 334 staff providing 1 or more swabs. R3: 46 centres with 756 children and 226 staff providing 1 or more swabs	3 months to 8y	RT-PCR weekly (buccal and anal swabs from each participant weekly). Buccal only R3. Only buccal data included here	R1: 2 positive from 2 staff members (2/376). No positive swabs from children (0/9057 swabs in 859 children). R2: 2 positive in children (2/577) and 0 staff (0/334). All S-gene positive i.e. unlikely to be alpha variant R3: 0 children or staff positive
Kriemler et al	medRxiv then published	Switzerland	1–11 Dec 2020	NS	Population	Surveillance	14 invited primary and secondary schools from high prevalence areas of Zurich: a subset of the 55 schools participating in Ulyte et al.	641/1299 (49%) of invited children participated, from 67 classes	6–16y	RT-PCR oral swab: participants tested twice 1 week apart.	positive RT-PCR in 1 child = 0.2%(0,1.1); no evidence of clustering in classes
Theuring et al.	medRxiv	Germany	2–16 Nov 2020	NS	Population	Surveillance	24 randomly selected schools in Berlin as per Hommes et al. 1 class from each school and their HH members. FTF teaching till 16 Dec	*N* = 1119 (352 students (177 primary, 175 secondary), 142 staff and 625 HH members). Mean 65% eligible children participated	8–18y	RT-PCR - oral and NP combined swabs- on all participants (98.6% students, 100% staff and 99.5% HH). Serology on dried blood spots. Participants in 8 classes with positive cases were retested after 1 week.	Prevalence: 2.7%(1.2, 5.0) in students (6/177 primary, 3/175 secondary) and 0.7%(0.0, 3.9) in staff (1/142); 8/24 classes had 1 or 2 cases, with none >2. HH prevalence: 2.3(1.3, 3.8) = 14 cases in 9 HH. 3/9 HH had positive students in the study but origin of infection unclear. Seropositivity in 2.0%(0.8, 4.1) students and 1.4%(0.6, 2.7) of staff; 8 classes with a positive test were retested after 1 week (after variable quarantine): 1 student and 1 staff were positive but judged not to be school related.
Thielecke et al.	medRxiv then published	Germany	28 Sep-2 Oct 2020	NS	Population	Surveillance	12 randomly selected kindergartens from >2700 in Berlin. FTF	*N* = 720: 155 children, 78 staff, 487 HH members.% of eligible participating not stated.	1–6y	RT-PCR (combined oral and NP swabs) and serology IgG on dried blood spots	None of 701 PCR samples was positive; no children, nil HH and 1 staff were seropositive .

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Hoch et al.	medRxiv then published	Germany	Time 1: 15 Jun-26 July; Time 2: 7 Sep-1 Nov 2020	NS	Population	Surveillance	Sentinel surveillance in 5 randomly selected primary schools & 6 kindergartens in Munich over two 6-week periods. FTF	3169 total swabs over 12 weeks: overall 2149 children (1065 Wks1–6; 1084 wks 7–12), 1020 staff. $N = 527$ serology samples from staff.% of eligible recruited not stated	1–11y	Weekly RT-PCR (oral swab) testing on 20 randomly selected children and 5 staff from each institution each week. Serology IgG on staff only	Time 1: All swabs and serology negative. Time 2: 2 positive PCR from 1 primary school (1 child; 1 teacher), all serology negative
Lubke et al.	medRxiv	Germany	10 June –7 July 2020	NS	Population	Surveillance	Representative sample of 115 daycare facilities in Dusseldorf, North Rhine-Westphalia. Representative across social deprivation in the city. 115 facilities selected from 314 respondents of 364 invited. Schooling resumed 8 June. Routine twice weekly testing of participating children and staff.	115 daycare facilities with 5210 participants (3955 children, 1255 staff). Participation by children was 60% of total attending children. 94.6% provided at least 1 sample.	2–6y	RT-PCR (saliva) - twice weekly for 4 weeks.	Prevalence: children 0.03% (1/3955), staff 0% 0/1255
Espenhain et al.	medRxiv	Denmark	3 rounds: R1 May 2020; R2 August 2020; R3 Oct - Dec 2020, with two subrounds defined as October and December 2020	NS	Population	Surveillance	Nationally representative community survey, linked with national COVID-19 testing database and routine health administrative data.	R1: 2512 (48% participation), nil 12–17y; R2: 7015 (39%) of whom 1492 aged 12–17y(31% participation); R3: 18,161 (26%) participants of whom 5631 aged 12–17y (20% participation). 1244 families had a child and at least one parent tested.	12–17y	Serology IgG	Seroprevalence: August 12–17y 0.9%(0.2, 2.0), 18–39y 2.8%(2.2, 3.6); October 12–17y 2.8%(1.6,4.5) 18/39y 3.3%(2.6,4.1); December 12–17y 6.4%(3.8,10) 18–39y 5.2%(4.0, 6.6). Of families with at least 1 child and 1 parent tested, 6.4%(79/1244) had at least 1 seropositive family member: 21/79 families had both child and parent(s) positive, 19 families only child positive and 39 families only parent(s) positive.
Doron et al.	medRxiv	USA	16 Sept –31 Dec 2020. Three periods Baseline Week 1 (mid Sept); Period 2 week 6–13 (1 Oct to 20 Nov) and Period 3 Weeks 15–18 (7–31 Dec 2020).	NS	Population	Surveillance	Massachusetts educational settings through Wellesley schools: early-years to Grade 12 in 10 schools (7 primary schools, 1 preschool and 1 middle (G6–8)and 1 high schools (G9–12)). Baseline screening offered to all staff and students in week 1. Subsequent weekly screening offered to all staff and to students from middle and high schools from start of hybrid learning in week 6.	921 eligible staff (10 schools) and 2403 eligible students: depending on week, participation 58–77% students and 73–83% staff	11–18y	RT-PCR (saliva): Baseline then weekly RT-PCR (pooled, then confirmatory)	126 positive cases amongst enrolled students and staff: 37 identified through screening program and 89 identified through outside tests (e.g. public health system). Including all cases: Week 1 baseline: students positive 0.03% (1/3596); staff 0.01% (2/1005); Weeks 6–13: students: 1.7% (42/2403) staff 2.6% (24/921); Wk 15–18: student 1.8% (43/2403) staff 1.2% (11/921) . Concluded in-school clusters and therefore transmission was rare

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
ONS SIS	Professional	UK	Round 1: 3–19 Nov 2020; Round 2: 2–10 Dec 2020; (Round 3 not undertaken due to school closures) Round 4: 15–31 March 2021; Round 5: 5–21 May 2021	R1: NS R2: alpha emerging R4: alpha dominant R5: delta dominant by late May	Population	Surveillance	Oversampling of schools in high prevalence areas of England.	Round 1: 105 schools (63 secondary, 42 primary) in 14 local authorities (64% high prevalence, 36% low prevalence); $n = 9662$ (students: primary 2137 secondary 3099; staff primary 1068 secondary 3054) - participation 17% students 51% staff. Round 2: 121 schools (41 primary, 80 secondary) in 15 local authorities: $n = 5114$ staff, 7089 pupils. Participation 15% students 40% staff. Note: 7751(4429 students 3322 staff) participated in both rounds. Round 4: 137 schools in 15 local authorities: data reported on 7156 secondary students and 2645 staff (17% of eligible students; 29% staff). Round 5: 57 primary and 85 secondary schools: 4207 primary and 8297 secondary students & 1348 primary and 2637 secondary staff (estimated response rate 25% primary & 17% secondary students)	4–19y	RT-PCR (NP swab); serology IgG on all participating students and staff in participating schools	Round 1: PCR+ child: primary school 0.89%(0.54, 1.39) secondary 1.48%(1.10, 1.98), PCR+ staff: primary 0.75%(0.32, 1.47) secondary 1.47%(1.08, 1.97). Higher proportions of students and staff tested positive in higher prevalence areas: students low prevalence: primary 0%(0, 0.7) secondary 1.12%(0.62, 1.19), high prevalence: primary 1.18%(0.71, 1.83) secondary 1.73%(1.18, 2.43). No infections identified in 47/105 schools, 29 had 1 positive case and 28% had 2–5 cases. Round 2 PCR+: child primary 0.94%(0.44,1.76) secondary 1.22%(0.60, 2.2), staff primary 0.99%(0.37, 2.12) 1.64%(1.1, 2.33). No positive cases in 46% of primary and 37% of secondary. Seropositivity data from Round 1: positive students primary 7.7%(5.9, 9.8) secondary 11.0%(8.8, 13.5). Seropositivity in Round 2: primary 9.05% (7.33, 11.0), secondary 13.45% (11.67, 15.4) Round 4: PCR+ 0.34%(0.16, 0.63) of secondary students (primary too low to be reported) and 0.19% (0.04, 0.58) of staff. Round 5: PCR+ 0.65% (0.27, 1.29) primary and 0.05% (0.01, 0.18) secondary students.
House et al.	Professional	UK	26 Apr 2020–15 Feb2021 R1: 26 Ap-1 Sep 2020:; R2: 1 Sep-15 Nov 2020; R3: 15 Nov 2020–1 Jan 2021; R4: 1 Jan-15 Feb 2021	R1: WT R2: WT R3: alpha emerging R4: alpha dominant	Population	Surveillance	National longitudinal HH population surveillance study (ONS COVID-19 Infection Survey): weekly testing of a nationally representative set of households in England. Analyses limited to HH <7 persons. R1: schools closed, low prevalence R2: high prevalence, schools open R3: high prevalence, schools mainly open R4: schools closed, high prevalence	Total across rounds 371,420 individuals (29,793 <12y, 20,091 12–16y) in 181,710 HH: 19,548 positive cases of which 7151 were consistent with B.1.1.7 variant. Numbers of participants increased across tranches (T1 89,624; T2 293,570; T3 315,187; T4 329,532). Longitudinal attrition <5%. Initially 20,000 HH approached in April 2020 and 51% of approached HH participated. An additional 5000 HH per week have been approached since mid 2020 however 14% of approached HH have agreed to participate since July 2020. Approx 90% of eligible individuals in participating HH are tested.	2–16y	RT-PCR weekly (NP and oral swab)	Bayesian transmission probability models estimated susceptible-infectious transmission probabilities including infectivity and external force of infection by age, based upon first case within each HH. Found relative transmissibility not significantly different to adults for 2–11y for each tranche, with 12–16y having significantly lower transmissibility in T3 (RR 0.7) but not in other tranches. The relative external exposure compared with adults was significantly higher for 2–11y for T3 (RR 1.4) and for 12–16y for T2 and T3 (RR 1.64 and 2.35 respectively).

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Villani et al	PubMed	Italy	21 Sep-4 Dec 2020, in 3 periods: 21 Sep-12 Oct; 19 Oct-13 Nov; 16 Nov-4 Dec	NS	Population	Surveillance	Schools: 2 K12 schools in Rome	1083 students and 168 staff: 96.5–100% student participation by age	3–18y	RT-PCR: oral swabs: 3 monthly samples all participants	13 positive students & 3 staff across 3 rounds (3431 samples). Positive Round 1: 1/1099, Round 2: 12/1075; Round 3: 3/1257. Using the participant N of students as swab number for each round, prevalence in children was R1: 1/1083, R2: 9/1083 and R3: 3/1083 (swab numbers for students not given). Only 2 classrooms had >=1 positive (2 students; 1 with student and staff member). Note 2 +students were siblings. Prevalence of 0.1, 1.1 and 0.2% was lower than background for age
Hommes et al.	medRxiv then published	Germany	11–19 Jun 2020	NS	Population	Surveillance	24 randomly selected schools in Berlin; FTF teaching reopened 28 April but 15% of teaching virtual in primary and 50% in secondaries.	n = 535: 192 primary and 192 secondary students and 150 school staff.65% of students participated	8–18y	RT-PCR- oral and NP combined swabs- plus dried blood spot serology on all participants	1 positive case identified in 16yo: prevalence 0.5% for secondary and no teachers. Positive IgG in 7 students (1.8%) and no teachers: 3 clustered in one secondary class.
Kirsten et al.	medRxiv (as Armann et al.) then published as Kirsten et al.	Germany	Time 1 25 May-30 June 2020; Time 2: 15 Sep-13 Oct 2020	NS	Population	Surveillance	13 secondary schools in eastern Saxony. School recruitment not stated. Schools reopened FTF 18 May and then late August after summer break	T1: 1538 students (76% participation) & 507 teachers; T2: 1334 students (87% of T1) & 445 teachers	12–19y	Serology IgG	Seroprevalence T1: 12 positive (11 students, 1 teacher) = 0.6%; T2: 12 positive (11 students, 1 teacher). Positives in 7/13 schools, with maximum of 4 in any school.
Ulyte et al.	R1 & 2: medrxiv then published R3: medrxiv	Switzerland	R1: 16 Jun-9 July 2020 R2: 26 Oct-19 Nov 2020 R3: 15 Mar - 16 April 2021	R1 & 2: NS R3: alpha dominant	Population	Surveillance	Ciao Corona study (3 rounds): Primary and secondary schools in Zurich; 55 randomly selected schools (55/156 invited), 275 classes; FTF learning at all rounds	R1 n = 2603; R2 n = 2552. R3: n = 2487, including 250 newly enrolled children. Retention was 84% from R1-R2 and 88% from R2-R3.	6–16y	Serology IgG	R1 seropositive = 74/2496. R2 seropositive = 173/2503. Modelled seroprevalence R1 2.4%(1.4,3.6); R2 new seropositive 4.5%(3.2, 6.0); positive R1&2 7.8%(6.2, 9.5). No clear age differences across schools. Clustering of >=3 cases slightly higher than expected from chance R3: Raw data: 447 positive out of 2483 tests: modelled seroprevalence 16.4% (12.1, 19.5). Clustering of >=3 cases slightly higher than expected from chance

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Willeit et al.	medRxiv then published	Austria	Time 1: 28 Sep-22 Oct 2020; Time 2: 10–16 Nov 2020	NS	Population	Surveillance	Random sample of 6% of all Austrian primary & secondary schools =250. 60 students per school invited (across all classes). Random sample of teachers. Fully FTF. Note schools closed 16 Nov due to national lockdown	T1: 10,156 samples from 243 schools participating (97.2% of schools; no data on% children participating) n = 8934 students & 1222 teachers; T2: 3745 samples from 88 schools (reduced due to lockdown). Median 40 children and 6 teachers per school. N = 3295 students & 450 teachers	6–16y	RT-PCR (gargle specimens)	T1: prevalence students 0.4%(0.3, 0.5) teachers 0.6%(0.3, 1.3); 0 cases in 209/243 schools, 1 in 28 schools and 2 in 6 schools. T2: children 1.5%(1.1, 2.0) teachers 0.4%(0.1, 1.8). 0 cases in 52/88 schools, 1 in 23, 2 in 10 and 3 cases in 4 schools. No significant difference in prevalence in primary versus secondary. in regression analyses, social deprivation and community prevalence predicted school prevalence. 100% increase in community prevalence increased odds of school prevalence by 66% (OR 1.66(1.39,1.99)
Ladhani et al. sKIDSs	Professional	UK	June-Dec 2020: RT-PCR June-July. Serology round 1 June, round 2 July, round 3 Nov-Dec 2020;	R1: WT R2: WT dominant, alpha emerging	Population	Surveillance	English primary schools (across all regions) and early years settings after reopening of schools June 2020 (SKIDS study (Rounds 1 & 2)). Schools all FTF. Note alpha variant predominant for Round 4.	RT-PCR: Round 1: 11 966 participants (6727 students, 4628 staff, and 611 with unknown staff or student status) in 131 schools had 40 501 swabs taken: . Serology: 45 schools (816 students, 209 staff) recruited. 95% participant recruitment.	4–12y	RT-PCR (NP swab) and Serology IgG	Round 1: RT-PCR: 1 student and 5 staff positive during 4 weeks: estimated incidence rate/wk student 4•1 (0•1–22•8), staff: 12•5(1•5–45•0) per 100 000. Seropositive: Round 1: children 11•2%(7•9,15•1) staff 15.2%(11.9,18.9). Seropositivity was not clustered (in model after adjustment) by school for children but was for staff. Seropositivity was not associated with school attendance during lockdown (children or staff). Round 2: 74% participation: children 10.4% staff 13.1% - only 5 seroconversions (staff & children) between rounds. Round 3: 54.2% participation for children: 8.6% of children and 11.2% of staff.
Jordan et al.	Professional	Spain	29- Jun - 31 July 2020	NS	Population	Surveillance (prospective) with contact-tracing	Children and staff in 22 summer schools in Barcelona over 2–5 weeks. Attended 40 h/week. Note additional data on children identified through symptom-based screening (Recruitment Pathway 2) not included here.	5240 samples from 1905 participants in 22 camps (45% of recruited camps) 1509 children and 396 adults; 9 child and 3 adult primary cases identified through screening. 89 close contacts of the 9 child cases identified and tested. 90% of contacts participated.	3–15y	RT-PCR saliva samples. Prospective weekly testing of all children; contacts tested at 0,7,14 days. nd serology IgG: all children at time 0; contacts at 0 and 5 weeks.	PCR+: 12 /5240 over 5 weeks (5/580 nasopharyngeal validation tests were positive): 9/1509 children = 0.6%. SAR from 9 child index = 1.1% (1/89). SAR from adult index was 1.6% (1/63)

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Table 1 (*continued*)

Authors	Source	Site	Dates	Virus/ variant	Case identification	Study type	Setting and exposure	N	Age of CYP	Testing	Findings
Fontanet et al.	medRxiv then published	France	28–30 April 2020	NS	Population	Surveillance	6 French primary schools in a city that had previously experienced an outbreak in the local high-school. Data included here from the primary schools; the single high school data not included as this was a single institution outbreak and data were not population-based	510 children (49% of eligible/invited) and 42 teachers (82% of invited) provided samples. Also 641 parents of children and 119 other HH members provided samples.	6–11y	Serology IgG	Seropositivity in 8.8%(45/510) of primary school children, 7.1(3/42)% of teachers, 11.9%(76/641) of parents and 11.8%(14/119) other HH members. Seroprevalence did not vary significantly by age. Note 61% of parents of an infected pupil were seropositive compared with 6.9% of parents of non-infected parents), suggesting transmission occurred primarily within households. 44% of seropositive children <12y were asymptomatic.
Ladhani et al. sKIDSsPLUS	medRxiv	UK	R1: 22 Sep-17 Oct 2020 R2: 3–17 Dec 2020 R3: 23 Mar-21 April 2021	R1: WT R2: WT dominant, alpha emerging R3: alpha dominant, delta emerging	Population	Surveillance	sKIDsPLUS study of 18 secondary schools purposively recruited across England, aligned with sKIDs study of primary schools also included here. Round 4 - undertaken immediately after schools reopened after lengthy lockdown (1 Jan to 7 March 2021). Schools all FTF. Note alpha variant predominant for Round 4.	R1: 893 students, 861 staff R2: 893 students, 873 staff R3: 1094 students and 792 staff.	11–18y	RT-PCR (NP swab) and Serology IgG. Data provided for various assays - the Abbott assay data were used consistently across R1–3 and therefore used here.	PCR data only provided for Round 3: Positive in 0.18% (2/1094) children and 0/792 staff. Clustering was not significant ($p = 0.1$) for school infections in Round 3. Serology data provided for Rounds 1–3: Serology data provided for Rounds 1–3: R1: seropositive student 12.8% (114/893) staff 9.2% (79/861); R2: 13.1% student (117/893) 13.4% staff (117/873); Round 3: students 22.1% (227/1029), staff 19.5% (150/771).
Lachassinne et al.	Professional	France	4 Jun-3 July 2020	NS	Population	Surveillance	Early years setting: recruited children and staff who attended daycare during national lockdown (15 Mar-9 May 2020) as parents were essential workers; recruited from 22 early years settings in Paris region. All children invited to participate and recruitment ceased once planned N achieved. Also studied parental serology.	Recruited the first 327 children agreed to participate, along with 197 daycare staff i.e. 100% of recruited were tested.	0.5–4y	RT-PCR nasal swabs. Stool samples also collected but data not examined here. Serology Ig & IgM.	Seropositivity in 4.3% (14/327) children and 17.7% (4/197) staff. The 14 seropositive children came from 13 daycare centres - i.e. no evidence of clustering of infection. 55% (6/11) of seropositive children had a seropositive parent compared with 14% (22/149) of seronegative children. PCR - 0/197 nasal swabs were positive. Found no evidence of transmission within daycare centres in this high risk group. Concluded most children were infected from household contacts.

Oral = oropharyngeal.
NP= nasopharyngeal.
R=Round.
Brackets () show 95% CI.
Variant: NS = not stated; likely original or wild-type virus. VOC = variant of concern. WT = wild type (original) virus.

Table 2
Moderators of prevalence and seroprevalence in school studies.

Age	PCR prevalence Odds ratios (95% CI)	p	Seroprevalence Odds ratios (95% CI)	p
0–19 years (reference)	1	–	1	–
Early years ≤7 years	0.245 (0.030, 2.000)	0.189	–	–
Children 5–12 years	0.649 (0.207, 2.034)	0.458	1.567 (0.228, 10.773)	0.648
Adolescents 12–19 years	1.433 (0.429, 4.787)	0.559	1.185 (0.178, 7.877)	0.860
Community SARS-CoV-2 14 day incidence per 100,000 population (continuous)				
Contemporary with study	1.003 (1.001, 1.004)	<0.001	1.001 (0.999, 1.003)	0.307
Month previous to study	1.003 (1.001, 1.006)	0.008	1.005 (1.000, 1.007)	0.038
Two months previous to study	1.001 (0.997, 1.005)	0.591	1.005 (1.002, 1.008)	0.003
School attendance (% in face-to-face learning)	1.001 (0.982, 1.021)	0.908	1.020 (0.977, 1.066)	0.375
PCR source				
Swab (nasopharyngeal or oropharyngeal)	1		–	
Saliva or gargle	1.54 (0.49, 4.84)	0.456	–	

were retrieved in full-text and reviewed independently by 2 researchers (RV and CW or OM) for eligibility and quality.

Outcomes and data extraction

Outcomes of interest were:

1. From contact-tracing studies: secondary attack rates (SAR) by age of index cases (<18–20 years compared adults) in contact-tracing studies. SAR by age of contact, SAR from adult index cases and effect estimates for adjusted transmission models from CYP were also extracted where data allowed.
2. From population-based studies:
   a. School studies: prevalence or seroprevalence of SARS-CoV-2 infection and presence of clustering (frequency of occurrence of >2 cases) of infection within settings. We also extracted data on school attendance (see below under meta-regression)
   b. Longitudinal incidence studies: effect estimates for transmission models from CYP aged 0–19 years.

Data from each study were extracted to a spreadsheet and checked for accuracy by four reviewers (RV, JC, CW and JW). Source of data in each study are shown in Appendix Table 2. We approached authors for further data where necessary.

Quality and bias evaluation

Methodological quality was independently assessed by two authors (RV and CW) using a score adapted from previously published quality assessment tools[23-26] for prevalence, cohort and case-control studies (see Appendix for details and Appendix Tables 3 and 4). Only studies of high and medium quality at low risk of bias were included in these analyses.

Data synthesis and analysis

Studies were included in random effects meta-analyses and meta-regressions using a multilevel framework. This accounted for many studies collecting multiple rounds of data collection over time or for studies providing data for CYP age-groups (e.g. primary or secondary students). Analyses used the *metafor* package in R, using log-transformed proportions.

For contact-tracing studies, meta-analyses were undertaken of secondary attack rate (SAR) from index children grouped by setting, age of index child and age of contact. Meta-analysis comparing SAR from child index cases with SAR from adult index cases was undertaken first using raw SAR data and then using estimates of relative transmissibility from adjusted transmission models where data were provided.

For school population-based studies, we first undertook separate meta-analyses of studies providing prevalence and seroprevalence data grouped by age-group. We then used meta-regression to examine associations of school prevalence with:

1. Community 14-day incidence of SARS-CoV-2 across the study period and for the one and two months prior (see Appendix Table 5 for data and sources).
2. School attendance (% face-to-face) in each study (Appendix Table 6). Attendance was measured at the measurement-round level as this varied within a study over time.

We also undertook a post-hoc analysis to examine whether the use of nasopharyngeal or oral swab compared with saliva or gargle sample influenced estimates.

Role of the funding source

No funding obtained for these analyses.

Ethics

Ethics permission not required for these secondary analyses of published data.

Results

The PRISMA flow diagram is shown in Fig. 1. Titles and abstracts of 4511 articles were reviewed from electronic databases. Two additional studies were identified through searching citation lists and 16 through professional networks. 336 were assessed in full-text and 89 articles were judged potentially eligible. 45 studies (46 articles) were excluded as being at critical risk of bias (see Appendix Table 7). Characteristics of the 37 included studies (described in 43 articles, some of which describe later rounds of a study) are shown in Table 1.

Sixteen studies were contact-tracing studies (6 school;[27-33] 10 household[2,34-42]), 2 provided both contact-tracing and population data (both school studies[43,44]) and 19 were population studies (17 in educational settings;[9,10,45-59] 2 were national community surveillance surveys[60,61]).

Twenty-four studies were high quality (13 population; 10 contact-tracing and 1 study providing both data) and 13 studies were medium quality (6 population, 6 contact-tracing and 1 study providing both data). Of the 43 articles reporting the 37 studies, 26 (60%) were published, 11 (26%) were preprints and 6 (14%) were government or university reports.

Eight studies were from Germany, 4 from the UK, 3 from South Korea and the USA, 2 each from China, France, Switzerland, Denmark, Italy and Norway, one included data from both the Nether-

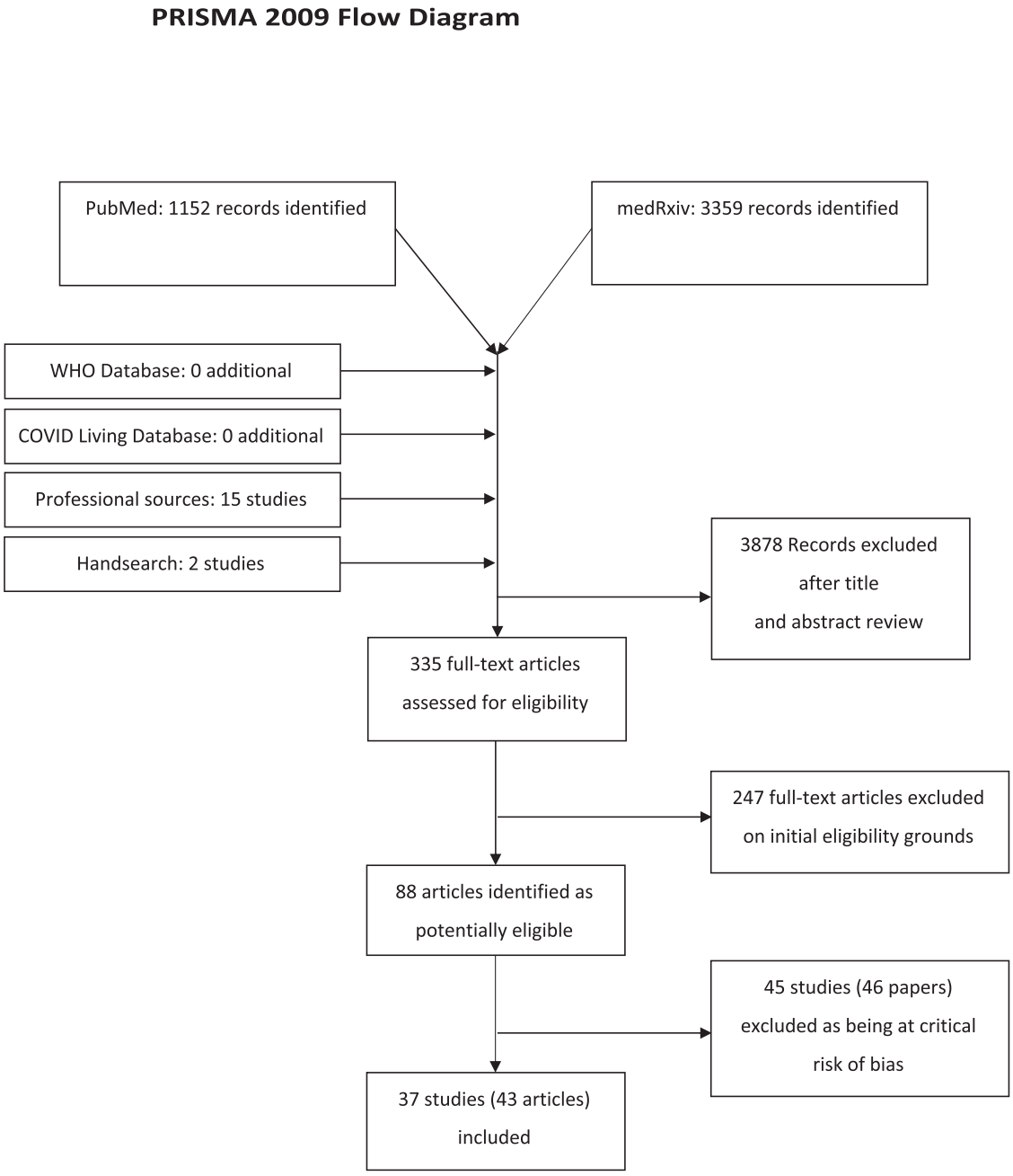

Fig. 1. FLOW diagram.

lands and Belgium, and 1 study each from Netherlands, Austria, Israel, India, Spain, and Australia.

Thirty-one studies (84%) were undertaken before November 2020 and involved the wild-type virus, although only 2 explicitly reported this; 6 (16%) studies included rounds with the alpha variant emerging (1) or dominant (5), with 2 (5%) also including rounds in which the delta variant was emerging.

Contact-tracing studies (household and school)

Eighteen studies provided data on secondary infection or attack rates (SAR) from child index cases, including five large regional[2,31,32,35,37] and five national[34,38,41,62,63] studies. Fifteen (8 household;[2,34,35,37-39,41,63] 7 school[27-33,44]) provided sufficient data to include in meta-analyses of secondary attack rates.

Forest plots of SAR from child index cases to all-age contacts are shown in Fig. 2 separately by setting. The pooled estimates of SAR were 7.6% (3.6, 15.9) for household studies (panel A), significantly higher than the pooled estimate for school studies of 0.7% (0.2, 2.7) (panel B) (difference QM (df=1) = 9.325, $p = 0.0023$).

Transmission from child index cases by age of contacts could be assessed in 4 school studies and 1 household study (Appendix Fig. 1). Pooled SAR to child contacts was not different to that to adult contacts ($p = 0.45$).

Odds of being a secondary case (of any age) from a child index compared with an adult index case were calculated from 11 rounds of data (6 household, 5 school; see Fig. 3). Across all studies, pooled risk of transmission was lower from child index cases than adults (OR 0.49 (0.25, 0.98); in sub-group analyses the OR was 0.27 (0.06,1.28) for school studies and 0.72 (0.45, 1.16) for household studies, all with high heterogeneity.

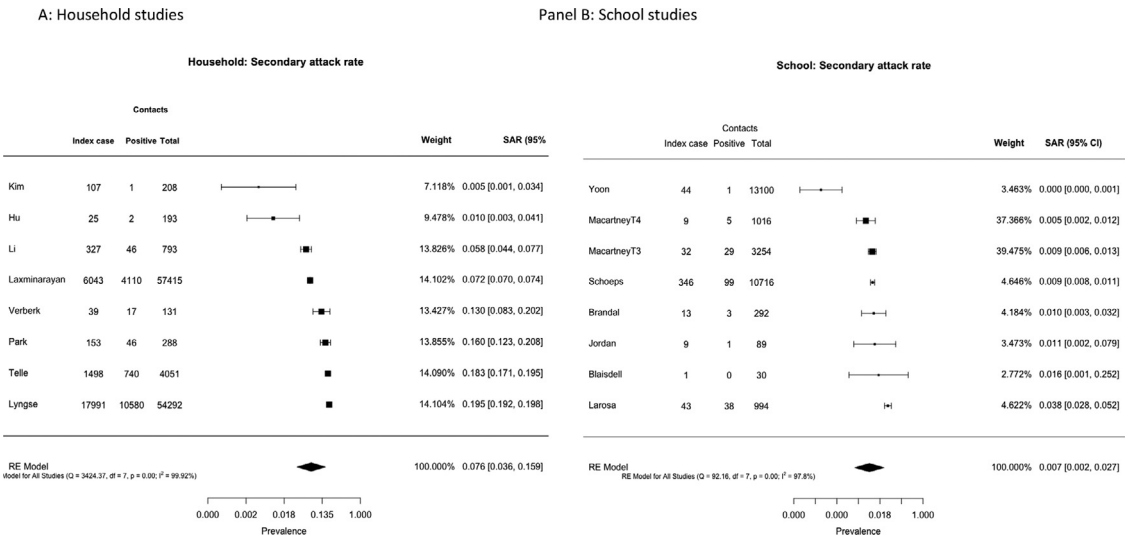

Fig. 2. Secondary attack rates from child index cases to all contacts for (A) household studies and (B) school contact-tracing studies.

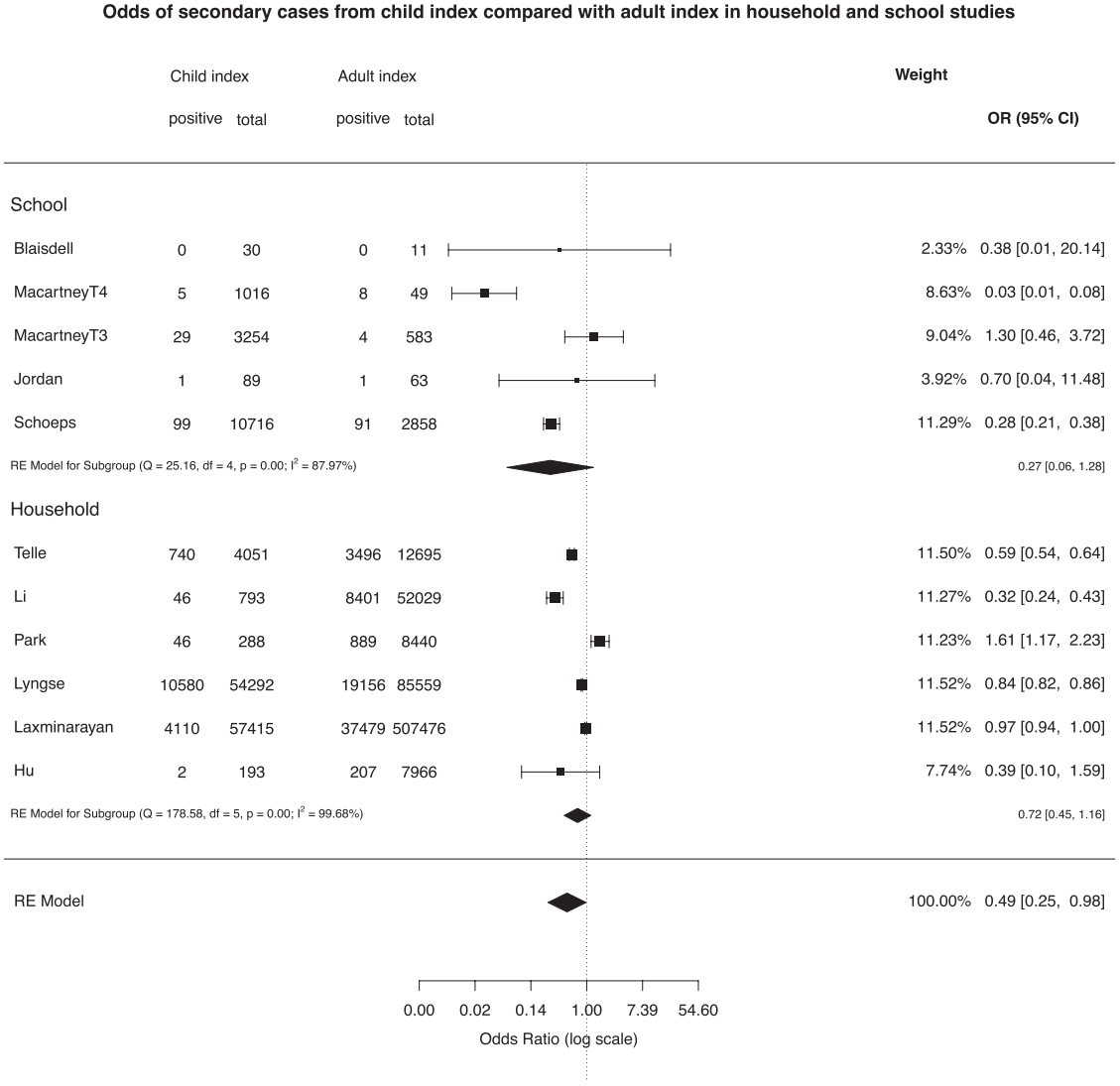

Fig. 3. Odds of being a secondary case from child compared with adult index cases.

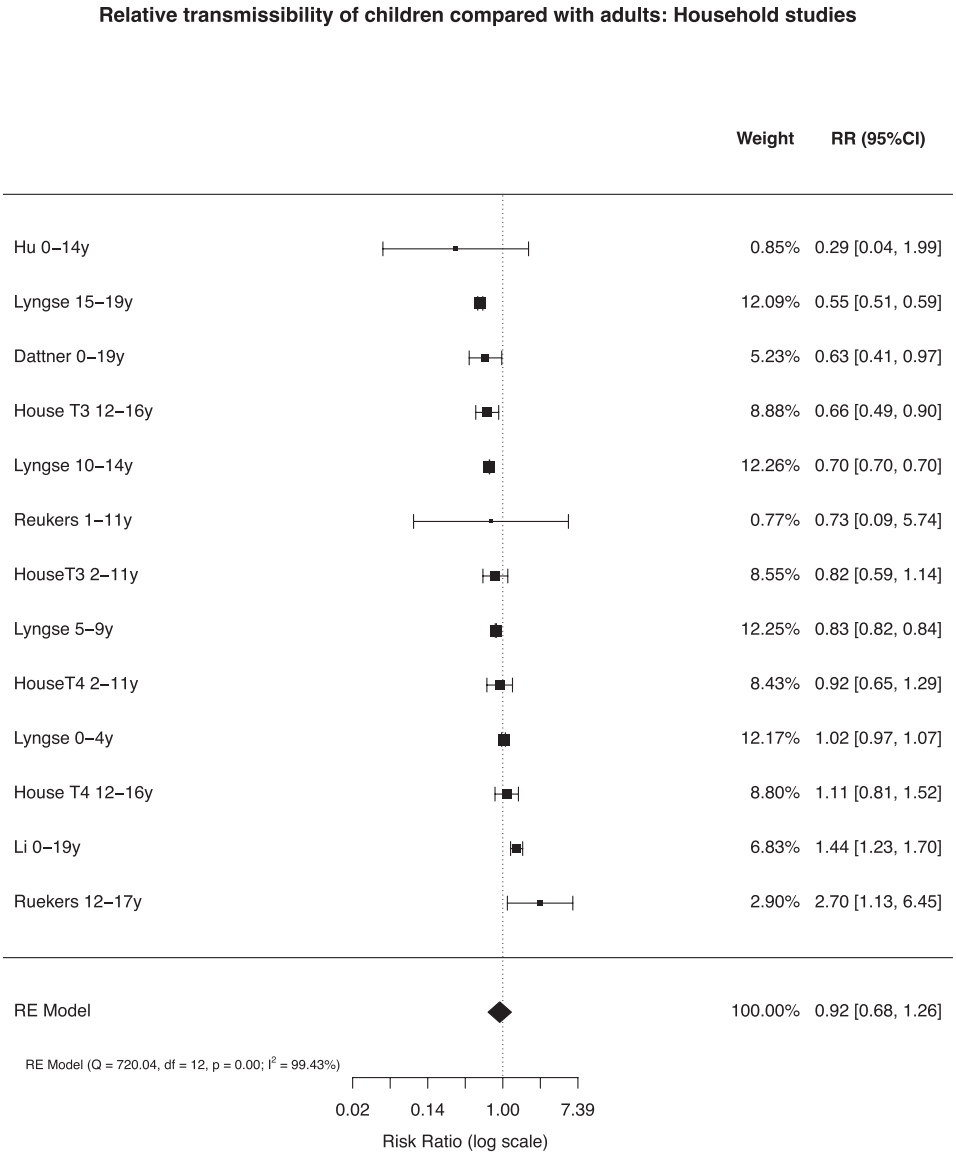

Fig. 4. Relative transmissibility of children and adolescents compared with adults in adjusted household models
Note: Analysis includes the last two periods from House et al. and estimates by age from other studies.

Two studies could not be included in the meta-analyses. Varma et al. undertook a large school contact-tracing study from New York City[43] and reported that the overall school SAR from CYP and adults was 0.5%; of the 69% of secondary cases for which a source of infection could be identified, 51% were staff-to-staff, 27% staff-to-student, 14% student-to-staff, and 8% from student-to-student. Espenhain et al.[61] used data from 4 rounds of a Danish nationally representative community survey to examine transmission in 1244 households with resident adolescents. They reported that, in 73% of families with at least one seropositive family member, only the parent(s) or the child were seropositive, concluding that transmission between generations was uncommon.

Adjusted household transmission models

Six studies examined transmission from CYP to household members using adjusted transmission models accounting for a range of factors including individual exposure histories, potential tertiary transmission, poverty and the age-structure of populations. Two studies used nationally representative data from England[60] and Denmark,[41] and four were contact-tracing studies (from China,[35,37] Israel[36] and the Netherlands[40]).

House et al.[60] used longitudinal weekly PCR testing from a very large representative national sample of English household[64] to estimate susceptible-infectious transmission probabilities from models in four periods from April 2020 to February 2021 across low and high prevalence, schools being reopened and the emergence of the alpha (B.1.1.7) variant in late 2020. They found transmissibility did not differ by age. However they did observe that the risk of bringing infection into household (relative external exposure) was higher amongst 12–16y than for adults although these included periods of national lockdown for adults whilst all children continued to attend full-time schooling. A Dutch contact-tracing study similarly concluded there were no differences in transmissibility between children and adults,[40] whilst a large national Danish study[41] and an Israeli contact-tracing study[36] found lower relative transmissibility in children and young people compared to adults. Two contact-tracing studies from China found that, whilst in unadjusted analyses infected children generated fewer secondary cases than

Panel A. PCR

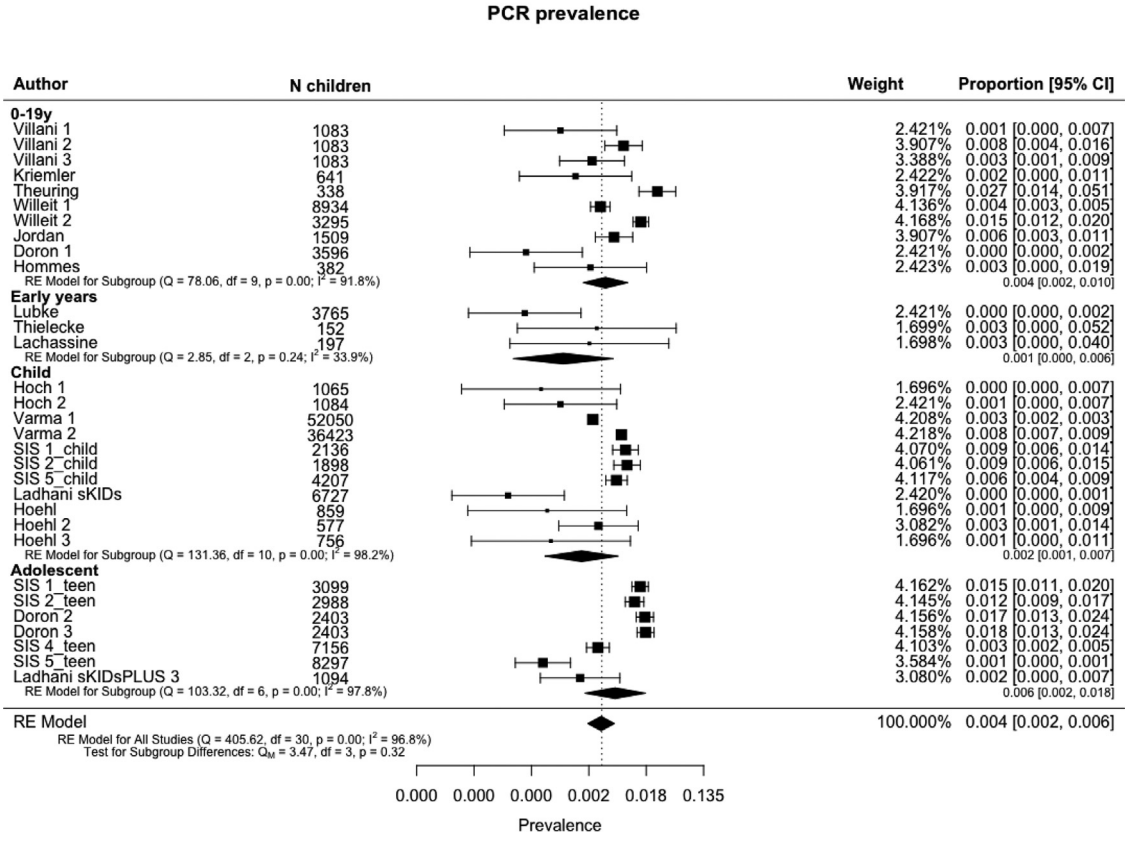

Fig. 5. . Prevalence and seroprevalence of SARS-CoV-2 infection in schools by age-group: (A) PCR prevalence and (B) Seroprevalence.

adults, adjusted models showed no difference,[35] or higher infectivity.[37]

Multilevel random-effects meta-analysis of relative transmissibility from CYP compared with adults included 13 estimates from 6 studies with total person-observations from 127,822

CYP and 1526,117 adults (Fig. 4). The pooled relative transmissibility from CYP was 0.92 (0.68, 1.26) compared with adults, with high heterogeneity (99.43%). Data did not allow sub-group analyses by age of child.

School prevalence studies

Infection prevalence in schools or nurseries was measured in 16 studies (31 rounds of observations; total 161,280 child-observations) and antibody prevalence was measured in 9 studies (20 rounds; 26,509 child-observations). Some provided data for single age-groups (e.g. early-years, primary or secondary students) while others provided cross age-group data. In the main analyses, we used overall estimates where they exist and estimates by age-group where the former were not provided.

Forest plots of PCR prevalence and seroprevalence by age are shown in Fig. 5. Meta-regression models are shown in Table 2. Pooled infection (PCR) prevalence across all studies was 0.4% (0.2, 0.6), not significantly different by age-group ($p = 0.32$). Prevalence was also associated with contemporary community 14-day incidence (OR 1.003 (1.001, 1.004), $p<0.001$) and prevalence in the month prior to the study (OR 1.003 (1.001, 1.006), $p = 0.008$) but not with 2 months prior. PCR prevalence was not associated with school attendance rate nor PCR source. Plot of predicted school prevalence by 14-day incidence is shown across age-groups in Fig. 6.

Pooled seroprevalence across all studies was 4.8% (2.4, 9.9), with no significant difference by age-group. Seroprevalence was associated with community incidence in the month and two months prior to the study, but not with contemporary incidence. Seroprevalence was not associated with school attendance.

No school studies fitted adjusted transmission models. Only two studies undertook a detailed analysis of clustering; Ulyte et al.[9,65] reported that clusters of ≥3 cases occurred in 7 of 129 classes in Round 2 and 24 of 119 in Round, more than the 4 and 17 classes expected by chance respectively. A very large school contact-tracing study by Schoeps et al.[28] reported that 83% of 784 school index cases led to no secondary cases. All other studies reported no evidence of clustering of infections (i.e. > 3–5 infections per class) within schools.[10,46,47,51-56,59,66,67] Other observations supporting limited transmission in schools were calculations showing that where direction of transmission was available, the majority appeared to be from adults to children[28,43,49,51,68] or that origins of transmission chains were outside schools;[47] and observations that virus prevalence in school children and teachers was lower than in the local community at the time despite higher levels of testing within schools.[43,52,53,67] Seroprevalence studies, however, reported similar antibody prevalence amongst students and teachers[54,67,68] or adults in the local community.[9,67,68]

The association of school prevalence with community infection rates was examined in two school studies, both of which reported positive associations.[43,56] Only one study examined associations of prevalence with social deprivation, reporting a positive association.[56]

Panel B. Seroprevalence

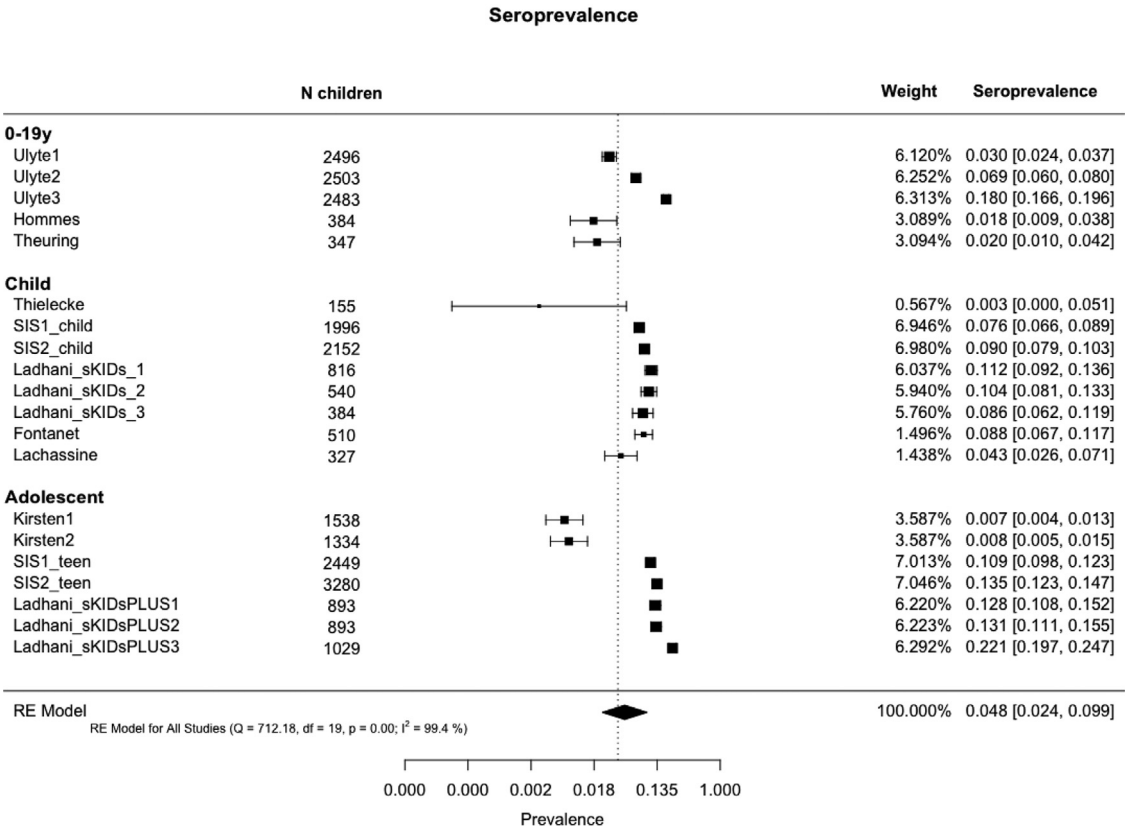

Fig. 5. Continued

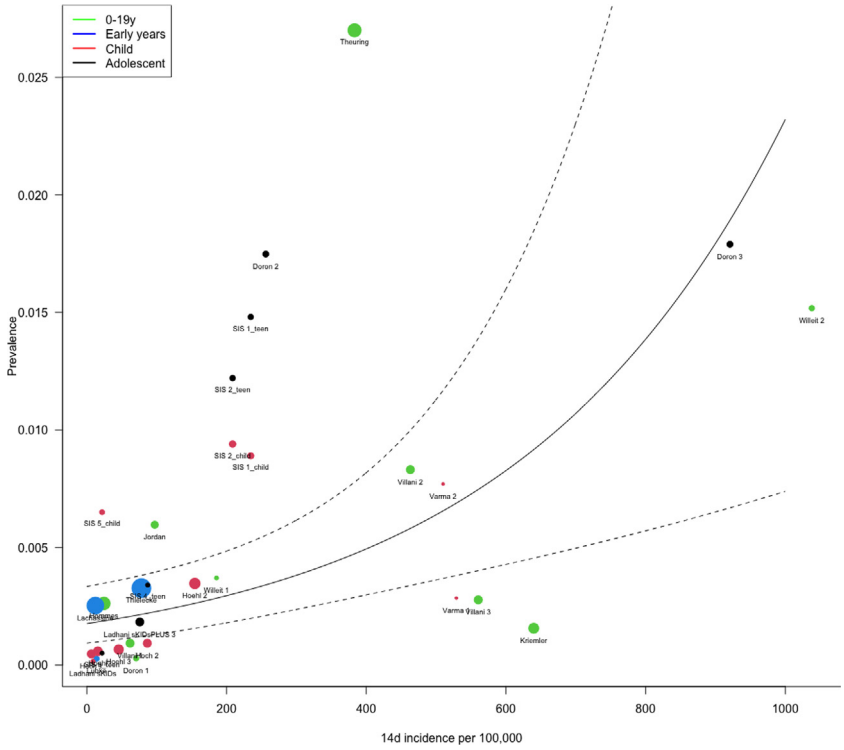

Fig. 6. Plot of predicted prevalence and 95% CI in school studies by community 14-day incidence of SARS-CoV-2 infections per 100,000.

Discussion

We report the first findings relating to SARS-CoV-2 transmission from CYP through meta-analysis of studies with low risk of bias. Meta-analysis of household studies which undertook adjusted transmission analyses showed no difference in relative transmissibility between CYP and adults (OR 0.92 (0.68, 1.26)), although meta-analysis of unadjusted secondary attack rates suggested that transmission from CYP was lower than from adults, although with wide confidence intervals. There are a number of sources of potential bias in the unadjusted analyses, including low numbers of child index cases as well as differential transmission from children across generations of spread within households, and it is likely that these analyses under-estimate relative transmissibility. These findings suggest that, within households, CYP play a role in transmission that is to similar but not higher than adults. The only study to examine external force of infection suggests CYP play a role in bringing infection into the house when schools are open, but this included periods when the country was in lockdown whilst schools remained fully open.[60]

We found a striking difference in transmission from CYP across different settings, with the pooled SAR from CYP index cases in household studies (7.6%) being 10-fold higher than in school studies (0.7%), despite a similar quantity and quality of evidence in both settings. We were unable to draw conclusions about transmissibility from CYP compared with adults in educational settings, due to wide confidence intervals and lack of studies reporting adjusted analyses. We found no evidence that transmission differed from CYP index cases to contacts of differing ages. Similar to our findings, other studies have concluded that household settings have higher transmission potential than other settings such as schools.[17,18] This disparity may reflect differences in the duration and intensity of social mixing within schools compared with households, with more prolonged, intense and intimate contacts between children and siblings or parents within households carrying a greater risk of transmission.[69] Our findings may also reflect the successful operation of NPI mitigations within schools in markedly reducing transmission.[70] This observation is supported by findings from some of the included school studies, including a lower prevalence in schools than in surrounding communities and the lack of notable clustering of infection within classrooms, even when local prevalence was high. Lack of clustering is supported by a number of studies not included in our review for quality reasons including a national study from Luxembourg.[71] There may, however, be systematic bias that might contribute to lower transmission in school compared with household studies. For example, CYP who are known to be infected or are contacts of positive cases are usually excluded from school but would be included within household studies. However, a substantial proportion of infected CYP are likely to be asymptomatic and, therefore, unlikely to be absent from school.[10] Biases related to relatively low numbers of CYP index cases, adequacy of contact-tracing and validity of PCR or serology testing in CYP apply equally to both school and household studies.

Our meta-regression findings that local community incidence was positively associated with school infection prevalence, as was incidence in the month prior, whereas seroprevalence was only associated with historical community incidence, show the interdependence of schools with their localities with respect to infection levels. Ismail et al.[72] reported the risk of an outbreak increased by 72% for every five cases per 100 000 population increase in community incidence, whilst Willeit et al.[56] reported that the odds of testing positive in schools were 1.64 (1.38, 1.96) for a two-fold higher community incidence. Our findings support the hypothesis that school infections predominantly reflect community infection levels, although our analysis could not attribute causality.

Our review included a number of studies undertaken when the prevalence of variants with higher transmissibility (e.g. alpha or B.1.1.7 variant) was rising or dominant, although most studies preceded this. No contact-tracing studies were included of transmission related to the delta variant although two school prevalence studies included data collection whilst delta infection was rising. Our findings therefore cannot be assumed to apply to periods when delta was predominant. However, whilst the delta variant has substantially higher overall transmissibility, and the prevalence of delta infection in children has been high at a time when adult populations had high vaccination coverage, there is no evidence of variant-specific differential transmission between children and adults. It is possible that the differential in transmission between school and household settings is lower for the higher transmissibility variants such as delta or omicron than reported here, although the higher transmissibility of the delta variant appears not to be setting-specific.

Limitations

Our data are subject to a number of limitations. Potential biases in school studies have been discussed above. RT-PCR studies may under-estimate infection in children compared with serology,[36] and different seroassays may provide differing results. Many of the included studies, however, combined findings from both PCR and serology,[10,31,32,39,40,44,47,48,54,67] or undertook repeated PCR measures[40,44,45,49-51,53,60] Importantly, though, these issues are likely to be similar across both contact-tracing and population studies and, therefore, would not alter the notable differences we found by setting.

Contact-tracing studies are open to bias due to missed testing of contacts, although we only included those who planned routine testing of all contacts and who achieved a high proportion of contacts tested. Low numbers of child index cases and their contacts in some studies may also be a source of bias. Population studies may be biased by higher participation by higher socioeconomic status groups and also as some studies specifically excluded those with recent contacts or symptoms.[50]

We conducted multi-level analyses accounting for the nesting of multiple rounds of data-collection within single studies. Some of the smaller meta-analyses, however, may have been overly influenced by studies with many rounds of testing. Meta-regression analyses are conducted at study rather than individual level and are, therefore, subject to ecological biases and cannot infer causality.

Our findings relate largely to the original/Wuhan virus and the alpha variant and it is unclear how generalisable they will be to the delta or other variants. Paucity of data meant we were unable to compare transmissibility from CYP between the Wuhan and alpha variants. Additionally all data precede widespread vaccination of adults and no studies included populations of teenagers who had been vaccinated. Our data were largely limited to high-income countries and there is an urgent need for similar studies from low-and-middle-income countries.

Conclusions and implications

We found no difference in transmission of SARS-CoV-2 from CYP compared with adults within household settings. Secondary attack rates were markedly lower in school compared with household settings and there was little clustering of infections within schools, suggesting that household transmission is more high risk than school transmission in this pandemic.

School infection prevalence was associated with community infection incidence in the month before and during the study, with seroprevalence associated with historical community infections,

supporting hypotheses that school infections broadly reflect community infections. These findings are important for guiding policy decisions on school operations during the pandemic. With appropriate mitigations, school infections can be limited and face-to-face learning is feasible, even at times of moderate to high community prevalence and in the presence of variants with higher transmissibility.

Our findings support a potential role for vaccination of CYP, if proven safe, in reducing transmission within households. Where countries go on to achieve very high levels of adult vaccination, this will focus transmission amongst the unvaccinated, increasing the relative importance of transmission amongst CYP.

Our findings largely relate to SARS-CoV-2 transmission from children before highly transmissible variants such as delta or omicron became predominant and this work needs replication once sufficient data are available from periods dominated by other variants. A number of other gaps in our knowledge remain about transmission from CYP, particularly relating to potential age-differences between younger and older children, and effectiveness of various NPIs, especially face masks, to reduce transmission in child-specific settings. Detailed population studies are required which link households and schools and use a combination of repeated PCR and serology testing to assess the risk of infection and direction of transmission across settings.

Contributions

RV and CB conceptualised the paper and led the writing of the manuscript,RV undertook the searches, contributed to data extraction and quality assessment and undertook the meta-analyses. . CW, OM, JC and JW contributed to eligibility assessment, data extraction and quality assessment. GMT and CB contributed to planning the analyses. All authors contributed to writing and editing of the manuscript.

Funding

No funding obtained.

Declaration of Competing Interests

All authors declare no competing interests.

Acknowledgments

We thank Kjetil Telle, Norwegian Institute of Public Health, and Marieke de Hoog, University Medical Center Utrecht, for providing additional data for their studies included here. We also thank Semina Michalopoulou and Zainab Dedat for checking the accuracy of data extraction.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.jinf.2021.12.026.

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