Supplementary Online Content

Meuris C, Kremer C, Geerinck A, et al. Transmission of SARS-CoV-2 after COVID-19 screening and mitigation measures for primary school children attending school in Liège, Belgium. JAMA Netw Open. 2021;4(10):e2128757.
doi:10.1001/jamanetworkopen.2021.28757

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This supplementary material has been provided by the authors to give readers additional information about their work.

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eMethods.

Mitigation measures implemented at school
The standards implemented in the school in September were hand hygiene and facial mask wearing for adults (allowing breaks within the classroom, when seated at their desk). Mask wearing and social distance between children was never implemented within the classroom nor during the breaks. From 16 November, children had to eat inside the classroom and adults could take off their mask only outside while respecting 1.5m of distance.

During the course of the study, national guidelines recommended testing children over 6 years of age if a major symptom (cough, dysgeusia, anosmia or dyspnea) or two minor symptoms (including fever, diarrhea, rhinitis, myalgia, headache) were present. Testing for asymptomatic contacts was interrupted between October 21 and November 22 because of a lack of testing capacity. According to the national guidelines, classroom contacts between children or children and adults were classified as low risk contacts. Testing was not recommended in case of only one positive case within a classroom. Class closure and 10 days quarantine occurred if more than two cases were detected within a classroom.

SARS-CoV-2 sequencing
RNA was extracted from throat washing (300µl) via a Maxwell 48 device using the Maxwell RSC Viral TNA kit (Promega) with a viral inactivation step using Proteinase K, following the manufacturer’s instructions. RNA was eluted in 50µL of RNAse free water. 3.3 µl of the eluted RNA was combined with 1.2 µl of SuperScript IV VILOTM Master Mix and 1.5 µl of H2O to carry out Reverse Transcription. This was incubated at 25°C for 10 min, 50°C for 10 min and 85°C for 5 min. PCR was carried out using Q5® High-Fidelity DNA Polymerase (NEB) and primers to obtain 1,200 bp amplicons as described by Freed and colleagues. PCR conditions followed the recommendations in the sequencing protocol of the ARTIC Network. We multiplexed the samples following the manufacturer's recommendations using the Oxford Nanopore Native Barcoding Expansion kits 1-12, 13-24, and 96 in conjunction with Ligation Sequencing Kit 109 (Oxford Nanopore). We carried out sequencing on a Minion using R9.4.1 flow cells.

Adjusted likelihood
Suppose there is a transmission chain \( j \rightarrow m \rightarrow i \), of which we only observe cases \( i \) and \( j \). Denote \( X \) the estimate of the generation time that we would obtain without accounting for the unobserved case. This is then in reality the sum of two generation times, i.e. \( X = X_1 + X_2 \), with \( X_1 \) the generation time between \( j \) and \( m \), and \( X_2 \) the generation time between \( m \) and \( i \). Assuming \( X_1 \) and \( X_2 \) are independent, and follow the same distribution \( \text{Gamma}(\alpha_\kappa, \beta) \), then the convolution \( X \sim \text{Gamma}(\Sigma \alpha_\kappa, \beta) \). Let \( \kappa_i \) be the
number of generations between case $i$ and $j$. In addition, if $\pi$ is the probability of observation, the probability of missing $\kappa_i - 1$ cases before observing case $i$ is

$$p(\kappa_i \mid \pi) = \text{NB}(1 \mid \kappa_i - 1, \pi).$$

Adapting the likelihood from Ganyani et al. to account for these unobserved intermediate cases, we obtain

$$L(\theta, v(i)_{\text{miss}} \mid z_i, v(i)_{\text{obs}}, \pi, \kappa_i) = \prod_{i=2}^{n} \left( \left[ \frac{1}{J} \sum_{j=1}^{J} f^{\kappa_i}(z_i - y_j \mid \theta) \right] p(\kappa_i \mid \pi) \right)$$

where $f^{\kappa_i}(.)$ is the convolution of $\kappa$, i.i.d. Gamma distributions, i.e. $X \sim \text{Gamma}(\sum_{k=1}^{K_i} \alpha_k, \beta)$.

**MCMC algorithm**

The algorithm consists of two steps that are repeated until convergence: 1) update the transmission tree and corresponding values for $\kappa$ based on the current parameter values, and 2) update the parameter values based on the currently accepted transmission tree and $\kappa$. For computational reasons, 10 000 possible trees were sampled before running the MCMC, and during step 1 above one of these trees was randomly selected (for details see below). We assume that both the generation interval and the incubation period follow a Gamma distribution. The incubation period distribution was fixed with a mean of 5.2 and standard deviation of 2.8 days. Minimally informative uniform priors were used for the parameters of the generation interval distribution, which were updated using a random-walk Metropolis-Hastings algorithm with a uniform proposal distribution. The posterior distribution was evaluated using 3 000 000 iterations of which the first 1 000 000 were discarded as burn-in. Thinning was applied by taking every 200th iteration. Posterior point estimates of the mean and standard deviation of the generation interval distribution are given by the 50th percentiles of the converged MCMC chain. Credible intervals (CrI) are given by the 2.5th and 97.5th percentiles. From all accepted trees, we visualize the most likely transmission tree (i.e. the one that is most often accepted by the MCMC algorithm). These analyses were performed using R software version 3.6.1.

Convergence of the MCMC was assessed using trace plots. As can be seen in Figure S4, adequate convergence is reached for the mean generation interval in most scenarios. For scenario 2, discarding the first 4000 iterations seen in the plot results in similar estimates as the ones reported (4.88 (95%CrI 3.43 – 6.58)). Convergence of the variance parameters is suboptimal in scenarios 2 and 3, but we believe this does not affect our conclusions and this nuisance parameter was not of main interest.
Construction of possible transmission trees
Confirmed cases were linked based on available information on known contacts and viral sequences. Cases that reported a high-risk contact with someone outside of the study population were assumed to have been infected by those contacts and were set as index cases (i.e. not infected by someone from the study population). We assumed that children could have had contact with their household members, the teacher of their own class, and all other children in the school. Teachers were assumed to have had contact with each other, other school employees, children from their class, and with their own household members. Parents were assumed to only have had contact with other study participants if they were household members. Contact between two cases belonging to a different genetic cluster was excluded. Some cases may have no possible contacts based on the above assumptions, and hence were excluded from the analyses. Sensitivity analysis was performed assuming that, within the school, children only had contact with their teacher and children from their own class.

To speed up the MCMC, 10 000 unique possible transmission trees were sampled beforehand as follows:

1) Define possible infectors based on known contacts and sequencing information
2) Impute missing dates of symptom onset:
   a. Sample from from range \([ \min(t_{v(i)}) - 5 ; t_{i}^{lab} ]\) where \(t_{i}^{lab}\) is the time of positive test, and \(\min(t_{v(i)})\) is the earliest symptom onset time among contacts of case \(i\)
   b. If onset times are also missing for all contacts of a case, we set the lower bound of the range to the earlier onset time in the cluster -5 days
3) Constrain serial interval to \(\geq\) -5 days and consequently change the list of possible infectors
4) Make sure every cluster has an assigned index case to avoid cycles in the network
5) Sample a transmission tree based on the list of possible infectors (with equal probabilities) taking into account the above constraints
6) Repeat step 2-5 to obtain 10 000 sampled trees

Values for the number of generations (\(\kappa\)) between two observed cases were sampled as follows:

- \(\kappa = 1\) if observed serial interval shorter or equal to 5 days -> no intermediate case
- \(\kappa = 1\) or 2 if observed serial interval between 6 and 12 days -> one intermediate case if \(\kappa = 2\)
- \(\kappa = 2\) or 3 if observed serial interval longer than 12 days -> two intermediate cases if \(\kappa = 3\)
**eFigure 1. Kaplan-Meier Curves**

The survival plot below shows the incidence of positive tests over time for two groups in the sample, the children and all adults taken together. When accounting for clustering of individuals in households and classrooms, the time to positive test was not different between adults and children (p=0.14).

![Kaplan-Meier Curves](image)
eFigure 2. Most Likely Transmission Tree Under Scenario 3, Assuming an 80% Probability of Observation (as Compared With a 60% Probability of Observation Under the Baseline Scenario)
**eFigure 3.** Most Likely Transmission Tree Under Scenario 4, Assuming Children Only Had Contact With Their Own Classmates Instead of all Children in the School, and a 60% Probability of Observation
eFigure 4. Trace Plots to Assess MCMC Convergence (GI = generation interval).
Table S1. Distribution of children according to class groups

| Class group   | N  | %  | # Cases |
|---------------|----|----|---------|
| Kindergarten  | 1  | 1.6| 0       |
| 1A            | 4  | 6.3| 1       |
| 1B            | 4  | 6.3| 0       |
| 2A            | 6  | 9.5| 3       |
| 2B            | 2  | 3.2| 1       |
| 3A            | 5  | 7.9| 1       |
| 3B            | 9  | 14.3| 4       |
| 4A            | 4  | 6.3| 0       |
| 4B            | 7  | 11.1| 0      |
| 5A            | 7  | 11.1| 0      |
| 5B            | 3  | 4.8| 1       |
| 6A            | 4  | 6.3| 1       |
| 6B            | 2  | 3.2| 0       |
| 6C            | 4  | 6.3| 1       |
| Missing data  | 1  | 1.6| 0       |
**Table 2. Symptoms Experienced in Complete Sample**

| Code | Symptoms         | Total (n=44) | Adults (n=31) | Children (n=13) | p-value |
|------|------------------|--------------|---------------|-----------------|---------|
|      | **Asymptomatic** |              |               |                 |         |
| 1    | Fever            | 10 (22.7%)   | 4 (12.9%)     | 6 (46.2%)       | 0.043   |
| 2    | Cough            | 8 (18.2%)    | 6 (19.4%)     | 2 (15.4%)       | 1.000   |
| 3    | Ageusia          | 11 (25.0%)   | 10 (31.3%)    | 1 (7.7%)        | 0.132   |
| 4    | Anosmia          | 18 (40.9%)   | 17 (54.8%)    | 1 (7.7%)        | 0.006   |
| 5    | Headaches        | 15 (34.1%)   | 14 (45.2%)    | 1 (7.7%)        | 0.034   |
| 6    | Myalgia          | 10 (22.7%)   | 10 (32.3%)    | 0 (0.0%)        | 0.021   |
| 7    | Diarrhea         | 4 (9.1%)     | 4 (12.9%)     | 0 (0.0%)        | 0.302   |
| 8    | Rhinorrhea       | 8 (18.2%)    | 7 (22.6%)     | 1 (7.7%)        | 0.402   |
| 10   | Asthenia         | 21 (47.7%)   | 20 (64.5%)    | 1 (7.7%)        | 0.001   |
| 11   | Anorexia         | 4 (9.1%)     | 4 (12.9%)     | 0 (0.0%)        | 0.302   |
| 12   | Chest pain       | 7 (15.9%)    | 7 (22.6%)     | 0 (0.0%)        | 0.086   |
| 13   | Heart palpitation| 1 (2.3%)     | 1 (3.2%)      | 0 (0.0%)        | 1.000   |
| 14   | Nausea           | 2 (4.5%)     | 1 (3.2%)      | 1 (7.7%)        | 0.508   |
| 15   | Dyspnea          | 5 (11.4%)    | 5 (16.1%)     | 0 (0.0%)        | 0.301   |
| 16   | Cutaneous rash   | 2 (4.5%)     | 1 (3.2%)      | 1 (7.7%)        | 0.508   |
| 17   | Abdominal pain   | 1 (2.3%)     | 1 (3.2%)      | 0 (0.0%)        | 1.000   |

Remark: Data missing for 1 participant, therefore % are calculated on a sample of 44/31/13. P-value from Fisher’s exact test. One participant can experience multiple symptoms.
### eTable 3. Duration of Symptoms

| Length (days) | n | %  |
|--------------|---|----|
| 0            | 10| 23.8 |
| 1            | 4 | 9.5  |
| 4            | 2 | 4.8  |
| 7            | 4 | 9.5  |
| 8            | 1 | 2.4  |
| 9            | 1 | 2.4  |
| 11           | 1 | 2.4  |
| 14           | 2 | 4.8  |
| 15           | 5 | 11.9 |
| 20           | 2 | 4.8  |
| 21           | 2 | 4.8  |
| 22           | 1 | 2.4  |
| 24           | 1 | 2.4  |
| 25           | 1 | 2.4  |
| 33           | 1 | 2.4  |
| 40           | 2 | 4.8  |
| 41           | 1 | 2.4  |
| 56           | 1 | 2.4  |
**Table 4. Duration of Positivity**

| Duration of positivity (in weeks) | Children (N=13) | Adults (N=32) |
|-----------------------------------|-----------------|---------------|
|                                   | N   | %   | N   | %   |
| 1                                 | 8   | 61.5 | 18  | 56.3 |
| 2                                 | 5   | 38.5 | 10  | 31.3 |
| 3                                 | 0   | 0.0  | 2   | 6.3  |
| 4                                 | 0   | 0.0  | 2   | 6.3  |
### eTable 5. Comparison of Cycle Thresholds Between Children and Adults

|                   | Children (n=13)                  | Adults (n=32)                  | P-value |
|-------------------|----------------------------------|--------------------------------|---------|
| Cycle threshold   | 29.80 (28.31-31.10)              | 29.00 (23.49-35.56)            | 0.51    |
Table 6. Complete Data Used for Outbreak Reconstruction

Link to SARS-CoV-2 sequences are available (see codes to access to sequences on GISAID (Global Initiative on Sharing Avian Influenza Data) platform https://www.gisaid.org/).
**Table 7. Posterior Point Estimates for the Parameters of the Generation and Serial Interval Distribution**

Table S7. Posterior point estimates for the parameters of the generation and serial interval distribution, and their 95% credible interval (CrI), under different scenarios. SD = standard deviation.

| Scenario       | Generation interval | Serial interval |
|----------------|---------------------|-----------------|
|                | Mean (95%CrI)       | SD (95%CrI)     | Mean (95%CrI) | SD (95%CrI) |
| Scenario 1 (baseline) | 4.67 (3.06 – 6.47)  | 2.49 (0.98 – 7.17) | 4.68 (-4.32 – 14.36) | 4.68 (4.08 – 8.19) |
| Scenario 2     | 4.82 (2.87 – 8.39)  | 3.37 (1.03 – 12.41) | 4.81 (-4.70 – 16.06) | 5.20 (4.09 – 13.03) |
| Scenario 3     | 4.61 (2.75 – 6.76)  | 3.53 (1.15 – 7.77) | 4.60 (-4.96 – 16.24) | 5.30 (4.12 – 8.72) |
| Scenario 4     | 4.74 (3.07 – 6.57)  | 2.88 (1.03 – 6.43) | 4.74 (-4.49 – 15.06) | 4.90 (4.09 – 7.56) |

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