






ORIGINAL ARTICLE

Risk factors associated with household transmission of SARS-CoV-2 in Negeri Sembilan, Malaysia

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Aim: Households are a significant venue for the transmission of SARS-CoV-2. We conducted a study to characterise the transmission dynamics and identify risk factors for household transmission of SARS-CoV-2 in Negeri Sembilan, Malaysia.

Methods: This retrospective observational study included 185 families of paediatric COVID-19 cases from 1 February 2020 to 31 December 2020. We identified the index case for each household and gathered the socio-demographic, epidemiological investigation results and risk factors for household transmission from medical case records. The secondary attack rate was calculated, and logistic regression analyses were used to identify risk factors associated with secondary household transmission of SARS-CoV-2.

Results: Of the 848 household contacts, 466 acquired secondary infections, resulting in a secondary attack rate of 55%. The median age of the secondary cases was 12 years. Female household contacts and household contacts who slept in the same room with the index case were significantly associated with increased risk for COVID-19. Other independent risk factors associated with higher transmission risk in the household included an index case who was symptomatic, a household index case aged greater than 18 years and a male household index case.

Conclusions: High rates of household transmission of COVID-19 were found, indicating households were a major setting of transmission of SARS-CoV-2. Our data provide insight into the risk factors for household transmission of SARS-CoV-2 in Malaysia.

Key words: COVID-19; household; risk factor; SARS-CoV-2; secondary infection; transmission.

What is already known on this topic

- 1 Households are major transmission venues for COVID-19.
- 2 Majority of the index case in the household are adults.

What this paper adds

- 1 A high secondary attack rate of SARS-CoV-2 in the household was observed in the state of Negeri Sembilan, Malaysia, particularly when the index case was an adult male.
- 2 The secondary attack rate was significantly lower in households with paediatric index cases.
- 3 Household contacts who slept in the same room with the index case were at greater risk for secondary infection.

Transmission of SARS-CoV-2 can occur in various settings such as households, workplaces, health-care facilities, schools and social settings including religious events.¹ The household setting plays an essential role in disease transmission, where frequent and prolonged contact between family members occur.

The secondary attack rate (SAR) among household contacts varies widely from published literature, ranging from 11.2 to 62.3%.^{2–4} However, published data on household transmission of

SARS-CoV-2 in Southeast Asian countries remained scarce.⁵ We conducted a study on household transmission of SARS-CoV-2 in the state of Negeri Sembilan, Malaysia, to determine the transmission dynamics and identify risk factors for transmission in a household setting. This is the first study published from Malaysia that specifically studied SAR of COVID-19 among household contacts and is one of the largest COVID-19 household studies published from Asia outside China and South Korea.

Methods

The study was conducted from 1 February 2020 to 31 December 2020, when Malaysia implemented strict containment strategies. During the study period, schools remained closed for most of the year.⁶ As part of the public health response, early identification

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via contact tracing, vigorous testing and mandatory patient isolation were carried out. All cases with laboratory-confirmed SARS-CoV-2 infection were placed in isolation in three designated hospitals across the state and close contacts placed on strict quarantine for 14 days from the last exposure.

The study was conducted among the 185 households of paediatric COVID-19 cases in the state during the study period. We identified the index case for each household. We assessed the household transmission by estimating the SAR for household contacts and identified factors influencing secondary household transmission of SARS-CoV-2.

Confirmed cases were defined as individuals who had a positive result of real-time reverse transcription polymerase chain reaction (RT-PCR) assay from a combined nasopharyngeal and oropharyngeal swab. The index case was defined as the most likely source based on history and investigations. The first laboratory-confirmed case in the household was identified as the index case. When multiple family members were detected on the same day, the first family member who became symptomatic was regarded as the index case. Household contact was defined as all persons living in the same household of the index patient at diagnosis, regardless of duration or proximity of contact. Secondary cases were defined when the household contacts were tested positive by RT-PCR within 14 days from the last point of exposure. Non-cases were defined as those released from quarantine with a negative RT-PCR, while SAR was defined as the proportion of infected household contacts (excluding the index patient) among the total household contacts.

Case notification was performed for every confirmed case of COVID-19, followed by contact tracing by the public health team. The household contacts were placed on strict quarantine at home or at a designated facility for 14 days. RT-PCR testing was required for all close contacts at the beginning of isolation and, if negative, repeated a day before the release (or earlier if the

household contacts develop symptoms compatible with COVID-19). Once they were identified positive for SARS-CoV-2, they would be transferred to the designated hospital for isolation and treatment. Release from quarantine was based on the absence of symptoms and negative RT-PCR results at the end of the quarantine period. The household contact RT-PCR results, socio-demographic characteristics and risk factors for household transmission were extracted from medical records using a standardised case record form. SAR was calculated and the two-sided 95% confidence interval (CI) for proportion was generated using the data obtained.

Continuous variables were expressed as median and interquartile range (IQR), and categorical variables as frequencies and percentages (%). Non-parametric two-tailed Mann-Whitney *U* tests were used to compare continuous variables, and categorical variables were compared with χ^2 test. Logistic regression analyses were used to identify risk factors associated with secondary household transmission. Factors with potential influence on the risk of transmission included characteristics of the index case (age, sex and symptoms manifestation) and characteristics of the household contacts (household size, age, sex, relationship with the index case and sleeping in the same room with the index case). With regard to age, we used 18 years as a cut off for logistic regression analysis to illustrate the extent of children as index patients. To determine the effect size of transmission rates in real-life scenarios, we subsequently dichotomised the age variable for ease of analysis and logical interpretations. The analysis was conducted using SPSS version 26.0 (IBM, Armonk, New York, United States) and a *P* value of <0.05 was considered statistically significant.

The study was registered with the National Medical Research Register (NMRR-20-2924-57631) and approved by the Medical Research and Ethics Committee, Ministry of Health, Malaysia (KKM/NIHSEC/P21-72(4)).

Table 1 Baseline characteristics of index patients and their household contacts

| Characteristics | Index patient (<i>n</i> = 185) | Secondary cases (<i>n</i> = 466) | Non-cases (<i>n</i> = 382) | <i>P</i> value [†] |
|---------------------------------|------------------------------------|--------------------------------------|--------------------------------|-----------------------------|
| Median age, IQR | 36 (26–42) | 12 (6–33) | 18 (8–35) | <0.001 |
| Age group (years), <i>n</i> (%) | | | | 0.002 |
| <12 | 36 (19.5) | 241 (51.7) | 145 (38.0) | |
| 13–17 | 3 (1.6) | 35 (7.5) | 42 (11.0) | |
| 18–30 | 26 (14.0) | 61 (13.1) | 64 (16.7) | |
| 31–50 | 105 (56.8) | 100 (21.5) | 102 (26.7) | |
| >50 | 15 (8.1) | 29 (6.2) | 29 (7.6) | |
| Gender, <i>n</i> (%) | | | | 0.002 |
| Male | 125 (67.6) | 185 (39.7) | 193 (50.5) | |
| Female | 60 (32.4) | 281 (60.3) | 189 (49.5) | |
| Race, <i>n</i> (%) | | | | — [‡] |
| Malay | 166 (89.7) | 421 (90.3) | 324 (84.8) | |
| Chinese | 4 (2.2) | 7 (1.5) | 8 (2.1) | |
| Indian | 14 (7.6) | 36 (7.7) | 43 (11.3) | |
| Others | 1 (0.5) | 2 (0.4) | 7 (1.8) | |

[†] *P* value indicated differences between secondary cases and non-cases.

[‡] Conditions for Pearson's χ^2 test not met due to two cells (25%) had expected counts <5.

IQR, interquartile range.

Table 2 Risk factors associated with secondary household transmissions of SARS-CoV-2

| Risk factors | Household cases (n = 466) | Total contacts (n = 848) | SAR, % (95% CI) | cOR (95% CI) | aOR (95% CI) |
|---|------------------------------|-----------------------------|--------------------|----------------------------|-----------------------------|
| Age of household contacts (years) | | | | | |
| <18 | 276 | 463 | 59.6 (55.1–64.1) | 1.5 (1.2–2.0) [†] | 1.4 (0.9–2.0) |
| ≥18 | 190 | 385 | 49.4 (44.1–54.4) | 1.0 | 1.0 |
| Sex of household contacts | | | | | |
| Male | 185 | 378 | 48.9 (43.8–53.9) | 1.0 | 1.0 |
| Female | 281 | 470 | 59.8 (55.3–64.2) | 1.7 (1.2–2.0) [†] | 1.6 (1.1–2.1) [†] |
| Household size (persons) | | | | | |
| <3 | 32 | 44 | 72.7 (59.5–85.9) | 2.3 (1.2–4.5) [†] | 1.2 (0.5–2.7) |
| ≥3 | 434 | 804 | 54.0 (50.6–57.4) | 1.0 | 1.0 |
| Relationship with household contacts | | | | | |
| Spousal | 94 | 128 | 73.4 (65.7–81.1) | 2.6 (1.7–3.9) [†] | 1.1 (0.7–2.0) |
| Non-spousal | 372 | 720 | 51.7 (48.0–55.4) | 1.0 | 1.0 |
| Sleeping in the same room with the index case | | | | | |
| Yes | 249 | 378 | 65.9 (61.1–70.6) | 2.3 (1.7–3.0) [†] | 2.9 (2.0–4.2) [†] |
| No | 217 | 470 | 46.2 (41.7–50.7) | 1.0 | 1.0 |
| Age of the index case | | | | | |
| <18 | 34 | 164 | 20.7 (14.5–26.9) | 1.0 | 1.0 |
| ≥18 | 432 | 684 | 63.2 (59.6–66.8) | 6.5 (4.3–9.8) [†] | 7.0 (4.4–11.3) [†] |
| Sex of the index case | | | | | |
| Male | 335 | 556 | 60.3 (56.2–64.4) | 1.8 (1.4–2.5) [†] | 1.6 (1.2–2.3) [†] |
| Female | 131 | 292 | 44.9 (39.2–50.6) | 1.0 | 1.0 |
| Manifestation of the index case | | | | | |
| Asymptomatic | 93 | 217 | 42.9 (36.3–49.5) | 1.0 | 1.0 |
| Symptomatic | 373 | 631 | 59.1 (55.3–62.9) | 1.9 (1.4–2.6) [†] | 1.5 (1.1–2.2) [†] |

[†] Statistical significance ($P < 0.05$). Total model accounted for 25.7% of the variance.

aOR, adjusted odds ratio; CI, confidence interval; cOR, crude odds ratio; SAR, secondary attack rate.

Results

The study included 185 index patients. The median age of the index patient was 36 years (IQR 26–42 years) and 125 (67.6%) were males. The age of the index case was non-normally distributed with 105 (56.8%) aged between 31 and 50 years. Thirty-six (19.5%) index patients were aged <12 years. Among the index patients, 166 (89.7%) were Malays, 14 (7.6%) were Indians and 4 (2.2%) were Chinese.

A total of 848 household contacts from the 185 family clusters were included in this study. The median household size was 5 (IQR 4–7). Of the 848 household contacts, 466 acquired secondary infections, resulting in a SAR of 55% (95% CI 51.5–58.2%). Two hundred and eighty-one (60.3%) were females. The median age of the secondary cases was 12 years (IQR 6–33), with 241 (51.7%) below 12 years of age (Table 1). Among these 241 children, 94.6% (228/241) were secondary to an adult index case and 1.7% (4/241) were infected by a sibling who was below 12 years of age. When the household index was below 12 years, the SAR was 13.4% (95% CI 7.9–18.9%).

Female household contacts (adjusted odds ratio (aOR) 1.6; 95% CI 1.1–2.1) and household contacts who slept in the same room with the index case (aOR 2.9; 95% CI 2.0–4.2) were significantly associated with increased risk for COVID-19 (Table 2). Other independent risk factors that were

significantly associated with higher transmission risk in the household included an index case who was symptomatic (aOR 1.5; 95% CI 1.1–2.2), household index aged greater than 18 years (aOR 7.0; 95% CI 4.4–11.3) and a male household index (aOR 1.6; 95% CI 1.2–2.3). The total transmission model in the regression analysis was statistically significant and accounted for 26% of the variance.

Discussion

Our study showed substantial transmission of SARS-CoV-2 in the household setting. There was considerable heterogeneity in the household SAR estimates from previous studies.^{2,4,7} The household SAR in our population was higher than the SAR estimated by two meta-analyses (17%).^{8,9} Several factors could contribute to our higher SAR, including the methodology to identify or define secondary cases and social and behavioural differences among our households. In our study, all household contacts were placed on strict home quarantine after the index case was identified and were tested at least twice before being released from quarantine, regardless of symptoms. Studies with less intensive testing would have underestimated the number of asymptomatic cases.⁷

In our study, 67.6% of the index cases were males. The gender discrepancy between the index cases was likely due to men being the breadwinner for most families and at higher risk of being infected from sources outside their homes. Notably, the majority of the index cases were adults, which was compatible with observations elsewhere.^{2,10} This was not unexpected as children had limited interactions outside their homes as schools remained closed for most of the study period, providing an attractive study design to assess household transmission as infected children were likely secondary household cases rather than acquired from the community.

The SAR was significantly lower in households with an index case below 18 years of age, and notably much lower when the household index case was below 12 years of age. This suggests that children are less likely to be drivers of the pandemic, in agreement with previous reports.^{3,11,12} Considering young children were less likely to be vectors for SARS-CoV-2 transmission within household settings, schools can be opened safely with adequate mitigation measures in place. The prolonged interruption in education due to school closures deprives children of real-life interactions essential for their full development.¹³ Outbreaks in schools were also reported to be uncommon, particularly when precautions were taken to reduce transmission.^{14–16}

We observed that household contacts of a male index case had increased odds of secondary infection, which was described in a previous household study in the USA.² The reason for this is unclear but could be related to gender differences in behaviour, with female index cases more likely to embrace preventive measures such as physical distancing, mask-wearing and hand hygiene.¹⁷ The household SAR from symptomatic index cases that were significantly higher than those from asymptomatic index cases was compatible with other studies.^{18–20}

We observed no significant differences in SAR across age categories of household contacts, in contrast with other published reports.^{20,21} However, we observed that household contacts who slept in the same room with the index case were at higher risk for secondary infection. This behavioural factor probably led to a longer exposure period to the infectious index patient, resulting in an increased risk of secondary transmission.

The findings are subject to several limitations. First, our study assumed that household transmission was responsible for all secondary infections among household contacts. This may oversimplify the chain of transmission because infections acquired from the community or tertiary infection within the household could occur. Second, we considered the household member who first became symptomatic as the index patient when multiple household members were detected concurrently. This discounts the possibility of two individuals in a household being infected simultaneously from a common exposure, with one being incorrectly identified as the sole index case of the household due to earlier symptom onset. Third, genomic sequencing for variants were not performed for the cases in this study. However, the local B.1.524 lineages were identified as the predominant circulating variants in the country during the study period.²² Lastly, the lack of serological investigations were a limitation. Household cases that were solely identified by RT-PCR may have underestimated the SAR,²³ as those who have recovered or those with short-lived viral shedding would not have been detected as cases. The household SAR could be potentially higher than what was recorded if

serological investigations were routinely carried out for all household contacts.

Conclusions

In conclusion, households were a major setting of transmission of SARS-CoV-2 in Negeri Sembilan. Our study further provides insights into the secondary infection rates and risk factors for household transmission. The risk of secondary household transmission was high when the index case was an adult above 18 years of age, and the SAR was low when the household index was a child below 12 years of age. This suggests that young children do not play a significant role in driving COVID-19 transmission. We also observed increased SAR with household contacts sleeping in the same room as the index case. Thus, household contacts can adopt precautionary measures accordingly to reduce the risk of secondary transmission.

The household SAR could evolve with the emergence of new variants of SARS-CoV-2 with higher transmissibility. Nevertheless, the findings of this study reinforce the dynamics of infection in children and can support public health interventions. As the rollout of COVID-19 vaccinations offers hope to drive down transmission, global vaccine equity is essential to hasten recovery from the pandemic.

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The Arctic Sea by Maria Park (age 10) from Operation Art 2021