

CLINICAL STUDY

Secondary attack rate of COVID-19 in shared households in Slovakia

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ABSTRACT

OBJECTIVE: The objective of this study was to estimate the secondary attack rate in unvaccinated members of households of two regions in the Slovak Republic for the period November 2020 – April 2021.

INTRODUCTION: SARS-CoV-2 infection poses a high risk of transmission in close-contact indoor settings, such as households. The household transmissibility of SARS-CoV-2 varies widely across countries.

METHODS: We included 278 households for SARS-CoV-2 transmission analysis. We calculated the secondary attack rate (SAR). We assessed sex, level of disease severity and means of isolation during infection of index cases as determinants of disease transmissibility

RESULTS: The secondary attack rate in 278 households was estimated at 63.7% (95%CI: 58.2–66.7%).

The SARs were different by sex (60.2% in females, 67.5% in males). The highest SAR was observed in the households of asymptomatic cases (77.8%), followed by moderate severity (66.5%), hospital admissions (63.2%) and mild disease (58.2%).

CONCLUSION: We found a high household secondary attack rate in two regions of Slovakia in the period when Alpha variant (B.1.1.7) of SARS-CoV-2 was dominant in the country. The results highlight the importance of monitoring transmission dynamics (Tab. 1, Fig. 1, Ref. 12). Text in PDF www.elis.sk

KEY WORDS: COVID-19, secondary attack rate, Slovak Republic, households.

Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), causing the disease COVID-19, has spread rapidly across the globe since the first cases were detected in the end of 2019 in Wuhan, China (1).

SARS-CoV-2 poses a high risk of transmission in close-contact indoor settings, such as households. The contact exposure in households is usually repeated and more intense than in other environments. This leads to a high risk of infection (2).

Basic indicator of transmission is the secondary attack rate (SAR), expressed as the number of new infections among contacts after exposure to an index case, divided by the total number of household contacts.

The household transmissibility of SARS-CoV-2 differs between individual variants. The meta-analysis of 135 studies found the secondary attack rates highest for the Omicron variant (42.7%), followed by the Alpha (36.4%) and Delta (29.7%) variants (3).

COVID-19 transmission and thus also the household SAR is to a large extent affected by governmental public health measures aiming to limit exposure to SARS-CoV-2 in public places (4).

The Slovak Republic, a country in Central Europe, applied strict measures to tackle the COVID-19 pandemic in 2020 and 2021, such as isolation, quarantine, school and business closures, universal lockdown and frequent testing (5). However, these did not prevent the rise of COVID-19 infections and related high mortality (6).

The objective of this study was to estimate the secondary attack rate in unvaccinated members of households of two regions in the Slovak Republic for the period November 2020–April 2021. This was the time period when Alpha variant (B.1.1.7) of SARS-CoV-2 became and remained dominant in the country.

Methods

We have conducted a study of SARS-CoV-2 transmission in households of two out of eight administrative regions of Slovakia: Bratislava and Trnava.

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Study population

The participants were recruited on a voluntary basis. Our study population included all members of households with at least one member testing positive for COVID-19 by RT-PCR test between November 2020 until March 2021. We included only households with at least two members.

We have tested 1007 study participants for SARS CoV-2 spike (S) protein antibodies, compiled epidemiologic data: date of positive RT-PCR/antigen COVID-19 test, presence and severity of symptoms.

We identified 278 households eligible for SARS-CoV-2 transmission analysis. In each household we identified the index case as the first member who tested positive for COVID-19. We have used the following definition of a household in the analysis: individuals living at the same address at the time of index case COVID-19 RT-PCR positivity, regardless of relationship.

All other members who tested RT-PCR/rapid antigen test positive for SARS-CoV-2 infection within seven days after the index case and/or COVID-19 was confirmed by SARS CoV-2 S antibody serological test within two months after the positivity of the index case were considered secondary cases. All study participants were unvaccinated against COVID-19 at the time of the study.

We calculated the secondary attack rate (SAR) after the COVID-19 positivity of the index case as follows:

(Number of household members with a positive RT-PCR/rapid antigen test within seven days after the index case and/or SARS CoV-2 S antibodies present within two months after the positivity of the index case, divided by the number of household members) x 100. Index case was excluded from both the numerator as well as denominator. We have calculated SAR with 95% confidence interval (CI).

We assessed sex and number of household members as the demographic determinants of disease transmissibility and conta-

Tab. 1. Demographic characteristics of index cases included in the study, characteristics of their disease, household, and transmission patterns.

Characteristic	Females n=136 (19%)	Males n=142 (51%)	Total n=278	P
Age, mean (SD)	43.3 (12.7)	42.7 (11.7)	43 (12.1)	0.686
Disease severity n (%)				
<i>Not Sick</i>	1 (1%)	1 (1%)	2 (1%)	0.042
<i>Asymptomatic</i>	1 (1%)	5 (4%)	6 (2%)	
<i>Mild</i>	69 (51%)	48 (34%)	117 (42%)	
<i>Moderate</i>	62 (46%)	81 (57%)	143 (52%)	
<i>Hospitalized</i>	3 (2%)	6 (4%)	9 (3%)	
Number of persons in household n (%)				
2	42 (31%)	58 (41%)	100 (36%)	0.213
3	33 (24%)	39 (28%)	72 (26%)	
4	42 (31%)	34 (24%)	76 (27%)	
5	12 (9%)	6 (4%)	18 (7%)	
6	6 (4%)	3 (2%)	9 (3%)	
7	1 (1%)	2 (1%)	3 (1%)	
Level of isolation during infection n (%)				
<i>Own Bathroom and Bedroom</i>	10 (8%)	8 (6%)	18 (7%)	0.112
<i>Shared Bathroom – Own Bedroom</i>	28 (21%)	47 (35%)	75 (28%)	
<i>Shared Bathroom and Bedroom</i>	93 (72%)	81 (60%)	174 (65%)	
Number of exposed in household n (%)				
1	42 (31%)	59 (42%)	101 (36%)	0.089
2	35 (26%)	40 (28%)	75 (27%)	
3	40 (29%)	32 (23%)	72 (26%)	
4	13 (10%)	6 (4%)	19 (7%)	
5	6 (4%)	3 (2%)	9 (3%)	
6	0	2 (1%)	2 (1%)	
Number of infected in household n (%)				
0	30 (22%)	24 (17%)	54 (19%)	0.591
1	57 (42%)	68 (48%)	125 (45%)	
2	29 (21%)	32 (23%)	61 (22%)	
3	10 (7%)	13 (9%)	23 (8%)	
4	6 (4%)	3 (2%)	9 (3%)	
5	4 (3%)	3 (1%)	6 (2%)	
Number of infected/household, Mean (95%CI)				
	1.4 (1.2–1.6)	1.4 (1.2–1.6)	1.4 (1.2–1.6)	0.82
Secondary Attack Rate (%), 95%CI)				
	60.2 (54.5–65.6)	67.5 (61.7–72.8)	63.7 (58.2–66.7)	0.84

giosity of COVID-19 index cases during their incubation period. Among factors that might have contributed to or prevent the transmission we assessed their level of disease severity and the extent of their isolation during infection.

We tested the difference between the proportions by Chi-square test. Statistical significance level was 0.05. Data analyses were performed by Stata Statistical Software: Release 18. College Station, TX: StataCorp LLC.

Detection of SARS-CoV-2 antibodies

We detected the anti-SARS-CoV-2 S antibodies by the electrochemiluminescence (ECLIA) method, using Roche Elecsys Anti SARS CoV-2 S kit on Cobas e411 automatic analyser. The test is based on a modified double-antigen sandwich immunoassay using recombinant S protein and is used for the specific detection of total SARS-CoV-2 S antibodies, including IgM and IgG.

Results

Overall, 1007 subjects were initially tested and interviewed, of which 641 were eligible to be included in the study and in 278 cases data on the number of exposed and number of infected persons in the households were available, making it possible to obtain SAR. Of the 278 index cases 142 (51%) were male. The mean age was 43 years (SD=12.2).

Table 1 presents the characteristics of the subjects, their households, and the patterns of transmission of the disease in their households. Both sex groups had similar age distributions (mean age of 42.7 in females and 43 in males), which combined with the almost equal split by sex suggests a very homogenous cohort of subjects regarding their basic demographic characteristics.

The distribution of disease severity identified among the index cases differed significantly by sex. A shift towards more severe cases is observed in the male group compared to females (57% of moderate in males vs 46% of moderate cases in females and 4% vs 2% rate of hospital admission). Overall, 94% of the cases were of mild or moderate severity.

Most of the subjects lived in a household with one other person (n=100, 36%). Male subjects tended to live with fewer household members than women – 31% of males lived in a household with 3 or more other persons vs 45% of women. Overall, the majority (91%) of the subjects lived in households of 4 or less persons.

The level of isolation between the members of the household was in most cases limited, as 93% of all households had shared bathrooms and bedrooms. The distribution

was slightly different between the subjects by sex, with more females living in households with shared bathroom and bedroom (72% vs 60% in males).

On average, 1.4 persons were infected in the household without any significant differences between the sex of the subject. In about 19% of households, no transmission of the infection was recorded. The infection was transmitted to one or two members of the household in most cases (67% overall, 71% in male subjects and 63% in females).

Overall the secondary attack rate in the households of 278 subjects included in the study was estimated at 63.7% (95%CI: 58.2%–66.7%). The SARs were different between the households of the subjects by sex, but the difference was not statistically significant (60.2% in females, 67.5% in males).

Figure 1 presents the estimated SARs in the households by the index case disease severity (Panel A) and by the level of isolation between the members of the household (Panel B). Regarding the disease severity of index cases, the highest SAR was observed in the households of asymptomatic cases (77.8%), followed by moderate severity (66.5%), hospital admissions (63.2%) and mild disease (58.2%). No statistically significant differences were found. When compared by the level of isolation, the highest estimated SAR was in households with own bathrooms and bedrooms of index cases (78.3%), whereas the lowest SAR was observed in

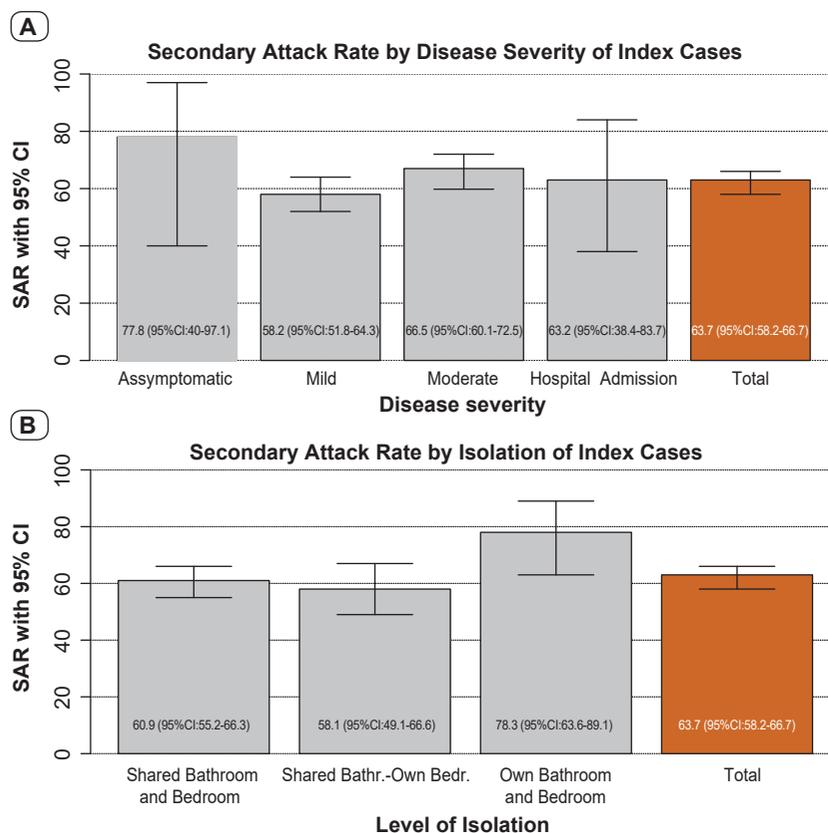


Fig. 1. Secondary attack rates of SARS-Cov-2 infections in households of the subjects included in the study, stratified by disease severity (Panel A) and by the level of isolation (Panel B) of the index cases.

households with shared bathroom and own bedroom (58.1%) – the differences were not statistically significant (Fig. 1).

Discussion

We characterised the transmissibility of SARS-CoV-2 within households and the associated risk factors in two administrative regions of Slovakia in the period November 2020 – April 2021. Our study showed the household secondary attack rate (SAR) of 63.7%. The SAR was higher in households with male (67.5%) than female index cases (60.2%).

Our findings are much higher than the estimated household SAR of 18.9% presented by the systematic review and meta-analysis of 87 studies that were published in the period October 2020 – June 2021 (3). Majority of the included studies concerned the transmission of the original SARS-CoV-2 virus identified first in Wuhan, China in December 2019. An updated systematic review and meta-analysis estimated household SAR of 36.4% for Alpha variant of the SARS-CoV-2 virus (7). The SAR estimated by the individual studies from this review varies from as low as 25% to as high as 50%. The factors behind the highly varying SAR in the published studies (8, 9) are mainly different inclusion criteria (such as all spectrum of disease severity versus symptomatic contacts only), methods of detection of SARS-CoV-2 infection (e.g. any viral presence test or RT-PCR test positivity only), social aspects such as household crowding and public health measures implemented by individual countries.

In studies where the contacts were tested more frequently or with combination of serological and RT-PCR/antigen testing larger SARs tend to be generated (10). This is the case of our study design.

Social factor behind our high estimate of SAR is the effect of the public health measures imposed by the government and implemented in the Slovak Republic in the study period. Mandated isolation and quarantine of persons with COVID-19 infection and their contacts, school and business closures increased the proportion of people that stayed at home and thus led to the increase of household transmission.

Our SAR of 63.7% was irrespective of the symptoms in the index case. In asymptomatic index cases, the SAR was even higher, 77.8%. Across several published studies higher transmission is consistently reported from symptomatic or presymptomatic cases (11).

In our study the SAR was higher for households where the index case had their own bathroom and bedroom – 78.3% as opposed to 60.9% for households with shared both bathroom and bedroom and 58.1% for households with shared bathroom and own bedroom. The change of behaviour of household members once informed about the SARS-CoV-2 infection, that led to reduced physical contact with the infected, person is a possible explanation of this phenomenon (12).

While before the COVID-19 vaccination rollout secondary attack rate was measured to assess the SARS-CoV-2 transmissibility, later studies monitored household SAR to estimate vaccine effectiveness (3).

Our study has several limitations. As our study sample is not representative, households with higher COVID-19 risk may be

over- or underrepresented. For the identification of SARS-CoV-2 infection in household members of the index case we used two criteria – positivity of RT-PCR/rapid antigen test within seven days after the index case and/or SARS CoV-2 S antibodies present within two months after the positivity of the index case. Rapid antigen detection tests were of high sensitivity and specificity, however false positivity cannot be ruled out. Majority (94%) of the household contacts reporting positivity of RT-PCR/rapid antigen test underwent serological analysis to establish the presence of anti-SARS-CoV-2 S antibodies. We excluded the households with members that were aware of other than index case exposure from the analysis. However, the presence of anti-SARS-CoV-2 S antibodies without the record of RT-PCR/rapid antigen test may signal infection acquired from another source than the index case. To reduce such cases, detailed epidemiologic information was collected, a maximum of two month window since the positivity of index case was observed and household contact with history of COVID-19 infection acquired before the study period were excluded from the analysis.

Conclusion

We found a high household secondary attack rate of 63.7% in two regions of Slovakia for the period of November 2020 – March 2021 when Alpha variant (B.1.1.7) of SARS-CoV-2 was dominant in the country. While other published secondary attack rates may be underestimated, our high estimate may be driven also by public health measures implemented at the time of the study.

Understanding of the extent, nature, and determinants of transmission in households is important for public health response to disease spreading dynamics.

References

1. Masood N, Malik SS, Raja MN, Mubarak S, Yu C. Unraveling the Epidemiology, Geographical Distribution, and Genomic Evolution of Potentially Lethal Coronaviruses (SARS, MERS, and SARS CoV-2). *Front Cell Infect Microbiol* 2020; 10: 499.
2. Koh WC, Naing L, Rosledzana MA, et al. What do we know about SARS-CoV-2 transmission? A systematic review and meta-analysis of the secondary attack rate, serial interval, and asymptomatic infection. *PLoS One* 2020; 15: e0240205.
3. Madewell ZJ, Yang Y, Longini Jr IM, H alloran ME, Dean NE. Household Secondary Attack Rates of SARS-CoV-2 by Variant and Vaccination Status An Updated Systematic Review and Meta-analysis *JAMA Network Open* 2022; 5 (4): e229317.
4. Talic S, Shah S, Wild H, Gasevic D, Maharaj A, Ademi Z, Li X, Xu W, Mesa-Eguiaaray I, Rostron J, Theodoratou E, Zhang X, Motee A, Liew D, Ilic D. Effectiveness of public health measures in reducing the incidence of COVID-19, SARS-CoV-2 transmission, and COVID-19 mortality: systematic review and meta-analysis. *BMJ* 2021; 375: e068302.
5. Kovanic M, Steuer M. Fighting against COVID-19: With or without politics? *Soc Sci Med* 2023; 337: 116297.
6. Rajan S, McKee M, Hernández-Quevedo C, Karanikolos M, Richardson E, Webb E, Cylus J. What have European countries done to prevent the spread of COVID-19? Lessons from the COVID-19 Health system response monitor. *Health Policy* 2022; 126 (5): 355–361.

7. Madewell ZJ, Yang Y, Longini Jr IM, Halloran ME, Dean NE. Factors Associated With Household Transmission of SARS-CoV-2 An Updated Systematic Review and Meta-analysis. *JAMA Network Open* 2021; 4 (8): e2122240.
8. Cohen C, Kleynhans J, von Gottberg A, McMorrow ML, Wolter N, Bhiman JN, Moyes J, du Plessis M, Carrim M, Buys A, Martinson NA, Kahn K, Tollman S, Lebina L, Wafawanaka F, du Toit JD, Gómez-Olivé FX, Dawood FS, Mkhencele T, Sun K, Viboud C, Tempia S; PHIRST-C Group. SARS-CoV-2 incidence, transmission, and reinfection in a rural and an urban setting: results of the PHIRST-C cohort study, South Africa, 2020–21. *Lancet Infect Dis* 2022; 22 (6): 821–834.
9. Watanapokasin N, Siripongboonsitti T, Ungtrakul T, Muadchimkaew M, Wongpatcharawarakul S, Auewarakul C, Mahanonda N. Transmissibility of SARS-CoV-2 Variants as a Secondary Attack in Thai Households: a Retrospective Study. *IJID Reg* 2021; 1: 1–2.
10. Fung HF, Martinez L, Alarid-Escudero F, Salomon JA, Studdert DM, Andrews JR, Goldhaber-Fiebert JD; Stanford-CIDE Coronavirus Simulation Model (SC-COSMO) Modeling Group. The Household Secondary Attack Rate of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2): A Rapid Review. *Clin Infect Dis* 2021; 73 (Suppl 2): S138–S145.
11. Buitrago-Garcia D, Ipekci AM, Heron L, Imeri H, Araujo-Chaveron L, Arevalo-Rodriguez I, Ciapponi A, Cevik M, Hauser A, Alam MI, Meili K, Meyerowitz EA, Prajapati N, Qiu X, Richterman A, Robles-Rodriguez WG, Thapa S, Zhelyazkov I, Salanti G, Low N. Occurrence and transmission potential of asymptomatic and presymptomatic SARS-CoV-2 infections: Update of a living systematic review and meta-analysis. *PLoS Med* 2022; 19 (5): e1003987.
12. Sun K, Loria V, Aparicio A, Porras C, Vanegas JC, Zúñiga M, Morera M, Avila C, Abdelnour A, Gail MH, Pfeiffer R, Cohen JI, Burbelo PD, Abed MA, Viboud C, Hildesheim A, Herrero R, Prevots DR; RESPIRA Study Group. Behavioral factors and SARS-CoV-2 transmission heterogeneity within a household cohort in Costa Rica. *Commun Med (Lond)* 2023; 3 (1): 102.

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