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Risk of Airborne Transmission During Home Isolation: A Modeling Study

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Objective: The worldwide pandemic of SARS-CoV-2 and its B.1.1.529 variant, Omicron, remain a threat to health. In Japan, self-isolation in a room at home has been recommended in some prefectures to reduce the burden on hospitals. With the aim of preventing the infection of family members in other rooms, this study quantified the risk of infection by airborne transmission to mask-wearing, non-infected members of the household.

Methods: A mathematical modeling approach was used to estimate the risk of airborne infection.

Results: For pre-SARS-CoV-2 variants of concern (VOC), the risk of infection of non-mask-wearing family members had an LN distribution with GM of 0.11, GD of 5.38, and median of 0.11; whereas that of mask-wearing members had an LN distribution with GM of 0.05, GD of 5.46, and median of 0.05. For Delta variant, the risk of infection of non-mask-wearing family members had an LN distribution with GM of 0.39, GD of 76.30, and median of 0.40, and that of mask-wearing members had an LN distribution with GM of 0.18, GD of 76.30, and median of 0.18. The difference of these medians was 0.22, which suggests that family members wearing masks is effective for preventing infection, even for highly infectious variants.

Key words: SARS-CoV-2, home isolation, household infection, airborne transmission, mathematical model

INTRODUCTION

Japan has suffered six waves of outbreak of SARS-CoV-2, between mid-January 2020 and early March 2022, and the Ministry of Health, Labour and Welfare's (MHLW) pandemic advisory board announced on 18 February 2022 that the sixth wave of infection in Japan was considered to have passed its peak [1]. During late 2020, the emergence of variants that posed an increased risk to global public health prompted the characterization of specific variants of concern (VOCs). The Delta VOC (B.1.617.2) was the dominant strain during the fifth wave in the summer of 2021, whereas the Omicron VOC (B.1.1.529) was the dominant strain in the 6th wave, from December 2021 [2]. On 5 January 2022, the MHLW of Japan notified local governments that if local medical systems became strained, people infected with Omicron could isolate at home instead of being hospitalized [3]. It has been reported that at the end of January 2022, more than 70,000 residents of Tokyo infected with Omicron were self-isolating at home [4].

Regarding the routes of transmission of SARS-CoV-2, early in the pandemic the emphasis was on direct-contact and indirect-contact modes of transmission [5], and the long-range airborne route has only recently been recognized as a modality of transmission [6–9].

The purpose of this study was to estimate the risk of infection of other family members from a self-isolating member with COVID-19, using the model developed by Buonanno *et al.* [10, 11] and Rothamer *et al.* [12]. It is well known that face masks are effective barriers to transmission when family members have contact with an infected case, but few studies have investigated the infection route via air leakage from an isolation room [13]. Therefore, this study quantified the risk of infection to family members from another self-isolating member infected with a COVID-19 variant, based on data that are currently available.

MATERIALS AND METHODS

Model framework

The Wells–Riley equation (Riley, Murphy, and Riley [14]) predicts the probability of infection P of a susceptible individual who inhales an infectious quantum dose, Dq, during an infectious period as follows:

$$P = 1 - \exp(-Dq).$$

A single infectious quantum is related to the number of bioaerosol particles containing numerous viable virus copies that are inhaled and cause disease in 63% of exposed susceptible subjects. Thus, the probability of infection is expressed as follows:

$$P = 1 - \exp(-1) = 63.2\%.$$

The quanta emission rate (ERq, quanta/h) of a SARS-CoV-2 infected subject is expressed as

$$ERq = c_v \cdot c_i \cdot IR \cdot Vd = c_v \cdot \frac{1}{c_{RNA} \cdot c_{PFU}} \cdot IR \cdot Vd, \qquad (1)$$

where c_v is the viral load in the sputum (RNA copies/mL), c_i is a conversion factor (quanta/RNA copies) defined as the ratio between one infectious quantum and the infectious dose (RNA copies), IR is the inha-

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Table Values of parameters used in the simulation

	Distribution	Mean	SD or Range	Unit	Source
$\log_{10} c_v$ for non-VOC	normal	7.0	0.71	RNA copies/mL	[11]
$\log_{10} c_v$ for Delta	normal	4.1	[6.3 8.8]	RNA copies/mL	[15]
c_{RNA}	normal	1.3×10^2	1.3×10^2	RNA copies/PFU	[19]
c_{PFU}	normal	2.1×10^2	2.1×10^1	PFU/quanta	[18]
Vd	normal	2×10^{-3}	5×10^{-4}	mL/m^3	[11, 16]

	Point value	Unit			
IR	0.54	m^3/h			[11, 17]
λ	1.98	/h			Appendix
Vr	10	m^3			The present study
t_d	24	h			The present study
$\eta_{f,Minh}$	0.545				Appendix
$\eta_{f,Mexh}$	0.545				Appendix

lation rate (m^3/h), and Vd is the droplet volume concentration expelled by the infectious person (mL/m^3). In addition, c_{PFU} is the quanta-to-plaque forming unit (PFU) conversion parameter (PFU/quanta), and c_{RNA} is the number of infectious virus particles (RNA copies) needed to initiate the infection (RNA copies/PFU).

Under the condition that ERq is small (i.e. $ERq \leq 0.2$) and assuming a steady-state value of quanta in the room, the probability of infection P is approximated as [12]

$$P \approx \frac{ERq}{\lambda\,\mathrm{Vr}} t_d (1 - \eta_{f,Minh})(1 - \eta_{f,Mexh}), \tag{2}$$

where λ is the loss rate, including the mechanism for particle removal and a loss term for virus inactivation; Vr is the room volume shared by the family members; t_d is the duration of exposure; and $1 - \eta_{\mathrm{f,\ Minh}}$ and $1 - \eta_{\mathrm{f,\ Mexh}}$ represent mask penetration values for inhalation by susceptible individuals and for exhalation by the infector, respectively.

The overall risk of infection was calculated using the Monte Carlo simulation with probability distributions for the input parameters, with a total of 10,000 simulations conducted. All analyses were performed using Microsoft Excel 2010 (Microsoft Corp., Redmond, WA) and Crystal Ball™, software (Oracle Corp., Redwood Shores, CA). The Anderson–Darling statistic was used as a test of fit for the distributions.

Parameters

Regarding the value of c_v for the non-VOC ancestral strain, log-transformed c_v had a normal distribution with mean of 7.0 and standard deviation (SD) of 0.71 $\log_{10}$ (RNA copies/mL) [11], and log-transformed c_v for the Delta strain had a normal distribution with median of 7.83 and range from 6.3 to 8.8 $\log_{10}$ (RNA copies/mL) [15].

The value of Vd had a normal distribution with mean 2×10^{-3} and SD 5×10^{-4} mL/m^3 for oral breathing [11, 16], and the value of IR was 0.54 m^3/h for the scenario that the activity level of the susceptible subject was either sitting or standing [11, 17]. The value of c_{PFU} had a normal distribution with mean 2.1×10^2 PFU/quanta and SD equal to 2.1×10^1 PFU/quanta [18], and the value of c_{RNA} with mean 1.3×10^2 RNA copies/PFU and SD equal to 1.3×10^1 RNA copies/PFU according to the results of Fears *et al.* [19]. The values of these parameters are summarized in Table and parts of the values are explained in the Appendix.

Simulation scenarios

In this study, the estimated risk of infection for one day was calculated for the condition of one infector isolated in a room of volume 5 m^3, and other family members in a nearby room of volume 10 m^3. It was assumed that there was leakage of air between the two rooms.

Yamanaka [13] investigated the local cumulative dose [LCD] of quanta [quanta·h/m^3] in two rooms of volumes 5 m^3 and 10 m^3. He assumed that the infector was isolated in a room of volume 5 m^3, and that each room had natural airflow ventilation of 30 m^3/h between the room and outside, and airflow of 30 m^3/h between the two rooms. As he also reported LCD ratio of 1:2 between two rooms; isolation room and common room, in the present calculations $1/2 \cdot ERq$ was used instead of ERq in equation (2).

RESULTS AND DISCUSSION

In this study, the risks of infection were compared between mask-wearing and non-mask-wearing susceptible family members in the home, and risks of infection were calculated for cases of infection with the pre-VOC and Delta variant strains.

In the case of infection with pre-VOC, the estimated value of the quanta emission rate ERq of the infector had a log-normal (LN) distribution with geometric mean (GM) of 0.39, geometric deviation (GD) of 5.41, and the median value was 0.40. The risk of infection in non-mask-wearing family members had an LN distribution with GM of 0.11, GD of 5.38, and median of 0.11, and the risk in mask-wearing family members had an LN distribution with GM of 0.05, GD of 5.46, and median of 0.05. The difference in median values between these groups was 0.11 - 0.05 = 0.06.

In the case of infection with Delta, the estimated value of the quanta emission rate ERq of the infector had an LN distribution with GM of 1.42, GD of 76.30, and median of 1.44. The risk of infection in non-mask-wearing family members had an LN distribution with GM of 0.39, GD of 76.30, and median of 0.40, and the risk in mask-wearing family members had an LN distribution with GM of 0.18, GD of 76.30, and median of 0.18. The difference between the medians was 0.40 - 0.18 = 0.22.

The median of the estimated value of the quanta emission rate ERq was higher for Delta than for pre-VOC, which indicates higher infectiousness. These results demonstrate that family members wearing masks is effective for preventing infection, even for a variant that is highly infectious.

Transmission within households is an important feature of SARS-CoV-2 infection, as has been observed in several previous studies [20–23]. The household secondary attack rate (SAR) was greater than that for infection by other contacts (OR = 10.72, 95%CI: 5.70–20.17) [20]. Wang *et al.* [21] reported that the close-contact infection rate was 38% for households with 1 contact, 50% for households with 2 contacts, and 31% for households with 3 contacts. Madewell *et al.* [22] showed that increases in household SAR were more frequently caused by symptomatic index cases (18.0%) than asymptomatic index cases (0.7%), by adult contacts (28.3%) than child contacts (16.8%), by spouses (37.8%) than other family contacts (17.8%), and in households with 1 contact (41.5%) than in households with 3 or more contacts (22.8%). The higher SAR associated with symptomatic index cases and households with 1 contact suggest the importance of the airborne infection route.

Wong *et al.* [24] reported intra-hotel transmission in a designated quarantine hotel and showed that infectious aerosols that leaked from guest rooms to corridors could be inhaled by guests in neighboring rooms when the doors were opened. Laumbach *et al.* [25] reported the first naturalistic observations of household air contamination with SARS-CoV-2 RNA by air sampling in an isolation room and a common room. They identified SARS-CoV-2 RNA in rooms (including a common room) other than the isolation room, and suggested that this is the most reasonable explanation for the high household attack rates. The risk of infection by airflow leakage between two rooms also existed in the present study, and the present results showed that other family members wearing masks reduced the risk of infection.

This study had some limitations. First, the mode of transmission for SARS-CoV-2 was limited to airborne infection, and valid parameters for estimating the risk of Omicron infection were not available. Second, vaccine-induced immunity was not considered in the model. Third, the actual airflow and environments are different from the values of parameters used in the present study.

New SARS-CoV-2 variants that are more highly infectious will result in a larger numbers of people isolating at home, and it will become increasingly important to prevent infection within the household. The importance of family members wearing masks will also be emphasized. Further studies are needed to gather stronger evidence for preventing household transmission of SARS-CoV-2 infection.

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AUTHORS' CONTRIBUTIONS

The author was solely responsible for conceptualizing, calculating the model, and writing this paper.

APPENDIX

(1) λ is the loss rate, including the mechanism for particle removal and a loss term for virus inactivation. In this study, it was assumed that natural ventilation was 1.00/h (one air change per hour), particle settling loss rate was 0.35/h [26], and a loss term for virus inactivation was 0.63/h [12]. In total, λ, was 1.00 + 0.35 + 0.63 = 1.98/h.

(2) In this study, the mask that the infector and susceptible subjects wore was assumed to have similar effective filtration efficiency with the mask composed of three layers of spunbond polypropylene designed by the UW-Madison emergency operations committee. Thus, the mask was assumed to have 54.5% effective filtration efficiency through inhalation and exhalation [12] and the values of $\eta_{f,Minh}$ and $\eta_{f,Mexh}$ were both 0.545.

REFERENCES

1) The Japan Times. February 17, 2022. https://www.japantimes.co.jp/news/2022/02/17/national/sixth-wave-past-peak/.
2) NIID. Current Situation of Infection, from December 22, 2021 to March 2, 2022. https://www.niid.go.jp/niid/en/2019-ncov-e/.
3) Nippon Communications Foundation News. Japan to Allow Omicron Carriers to Isolate at Home. https://www.nippon.com/en/news/yjj2022010501086/.
4) NHK WEB. https://www3.nhk.or.jp/news/html/20220131/k10013459761000.html (in Japanese).
5) WHO. Modes of transmission of virus causing COVID-19: implications for IPC precaution recommendations. https://www.who.int/news-room/commentaries/detail/modes-of-transmission-of-virus-causing-covid-19-implications-for-ipc-precaution-recommendations.
6) Zhang R, Li Y, Zhang AL, Wang Y, Molina MJ. Identifying airborne transmission as the dominant route for the spread of COVID-19. Proc Natl Acad Sci. 2020; 117(26): 14857–14863.
7) Klompas M, Baker MA, Rhee C. Airborne Transmission of SARS-CoV-2: Theoretical Considerations and Available Evidence. JAMA. 2020; doi: 10.1001/jama.2020.12458.
8) Noorimotlagh Z, Jaafarzadeh N, Martínez SS, Mirzaee SA. A systematic review of possible airborne transmission of the COVID-19 virus (SARS-CoV-2) in the indoor air environment. Environ Res. 2021; 193: 110612.
9) Shen J, Kong M, Dong B, Birnkrant MJ and Zhang J. Airborne transmission of SARS-CoV-2 in indoor environments: A comprehensive review, Science and Technology for the Built Environment, 2021; 27: 10, 1331–1367.
10) Buonanno G, Stabile L, Morawska L. Estimation of airborne viral emission: Quanta emission rate of SARS-CoV-2 for infection risk assessment. Environ Int. 2020; 141: 105794. doi: 10.1016/j.envint.2020.105794.
11) Buonanno G, Morawska L, Stabile L. Quantitative assessment of the risk of airborne transmission of SARS-CoV-2 infection: Prospective and retrospective applications. Environ Int. 2020; 145: 106112.
12) Rothamer DA, Sanders S, Reindl D, Bertram TH. Strategies to minimize SARS-CoV-2 transmission in classroom settings: combined impacts of ventilation and mask effective filtration efficiency. Science and Technology for the Built Environment, 2021; 27: 9, 1181–1203.
13) Yamanaka T. Natural ventilation and prediction of infection risk. Journal of the Society of Heating, Air-Conditioning and

Sanitary Engineers of Japan. 2021; 95: 11–17 (in Japanese).

14) Riley EC, Murphy G, Riley RL. Airborne spread of measles in a suburban elementary school. Am J Epidemiol. 1978; 107(5): 421–32.

15) Teyssou E, Delagrèverie H, Visseaux B, Lambert-Niclot S, Brichler S, Ferre V, Marot S, Jary A, Todesco E, Schnuriger A, Ghidaoui E, Abdi B, Akhavan S, Houhou-Fidouh N, Charpentier C, Morand-Joubert L, Boutolleau D, Descamps D, Calvez V, Marcelin AG, Soulie C. The Delta SARS-CoV-2 variant has a higher viral load than the Beta and the historical variants in nasopharyngeal samples from newly diagnosed COVID-19 patients. J Infect. 2021; 83(4): e1–e3.

16) Stadnytskyi V, Bax CE, Bax A, Anfinrud P. The airborne lifetime of small speech droplets and their potential importance in SARS-CoV-2 transmission. Proc Natl Acad Sci U S A. 2020; 117(22): 11875–11877.

17) Adams WC. Measurement of Breathing Rate and Volume in Routinely Performed Daily Activities. Final Report. Human Performance Laboratory, Physical Education Department, University of California, Davis. Human Performance Laboratory, Physical Education Department, University of California, Davis. Prepared for the California Air Resources Board, Contract No. A033–205, 1993.

18) Watanabe T, Bartrand TA, Weir MH, Omura T, Haas CN. Development of a dose-response model for SARS coronavirus. Risk Anal. 2010; 30(7): 1129–1138.

19) Fears AC, Klimstra WB, Duprex P, Hartman A, Weaver SC, Plante KC, Mirchandani D, Plante JA, Aguilar PV, Fernández D, Nalca A, Totura A, Dyer D, Kearney B, Lackemeyer M, Bohannon JK, Johnson R, Garry RF, Reed DS, Roy CJ. Comparative dynamic aerosol efficiencies of three emergent coronaviruses and the unusual persistence of SARS-CoV-2 in aerosol suspensions. medRxiv 2020.04.13.20063784. https://doi.org/10.1101/2020.04.13.20063784.

20) Lei H, Xu X, Xiao S, Wu X, Shu Y. Household transmission of COVID-19-a systematic review and meta-analysis. J Infect. 2020; 81(6): 979–997.

21) Wang Z, Ma W, Zheng X, Wu G, Zhang R. Household transmission of SARS-CoV-2. J Infect. 2020; 81(1): 179–182.

22) Madewell ZJ, Yang Y, Longini IM Jr, Halloran ME, Dean NE. Household Transmission of SARS-CoV-2: A Systematic Review and Meta-analysis. JAMA Netw Open. 2020; 3(12): e2031756.

23) Li W, Zhang B, Lu J, Liu S, Chang Z, Peng C, Liu X, Zhang P, Ling Y, Tao K, Chen J. Characteristics of Household Transmission of COVID-19. Clin Infect Dis. 2020; 71(8): 1943–1946.

24) Wong SC, Au AK, Chen H, Yuen LL, Li X, Lung DC, Chu AW, Ip JD, Chan WM, Tsoi HW, To KK, Yuen KY, Cheng VC. Transmission of Omicron (B.1.1.529) - SARS-CoV-2 Variant of Concern in a designated quarantine hotel for travelers: a challenge of elimination strategy of COVID-19. Lancet Reg Health West Pac. 2022; 18: 100360. doi: 10.1016/j.lanwpc.2021.100360.

25) Laumbach RJ, Mainelis G, Black KG, Myers NT, Ohman-Strickland P, Alimokhtari S, Hastings S, Legard A, de Resende A, Calderón L, Lu FT, Kipen HM. Presence of SARS-CoV-2 Aerosol in Residences of Adults with COVID-19. Ann Am Thorac Soc. 2022; 19(2): 338–341. doi: 10.1513/AnnalsATS.202107-847RL.

26) van Doremalen N, Bushmaker T, Morris DH, Holbrook MG, Gamble A, Williamson BN, Tamin A, Harcourt JL, Thornburg NJ, Gerber SI, Lloyd-Smith JO, de Wit E, Munster VJ. Aerosol and Surface Stability of SARS-CoV-2 as Compared with SARS-CoV-1. N Engl J Med. 2020; 382(16): 1564–1567. doi: 10.1056/NEJMc2004973.