



Transmissibility of SARS-CoV-2 Variants as a Secondary Attack in Thai Households: a Retrospective Study

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ABSTRACT

Objective: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spreads through person-to-person contact via small droplet particles, especially in poorly ventilated indoor settings such as households, estimating at 16.6% of secondary attack rate. This study aimed to explore the secondary attack rate in Thai households during the new SARS-CoV-2 variant outbreak.

Methods: We obtained a retrospective study of exposed members in households among 30 sets of patients with reverse transcriptase-polymerase chain reaction (RT-PCR) confirmed SARS-CoV-2 infection (index cases) at Chulabhorn Hospital, Bangkok, Thailand, from May 1 to June 30, 2021. Characteristic of index cases and households were extracted from medical records and analyzed.

Results: The 30 index cases were associated with 157 exposed household close contacts. Seventy-six were RT-PCR confirmed SARS-CoV-2 infections within 14 days after being exposed from an index case, with a secondary attack rate of 48%. However, there was no difference between secondary attack rates among the age of contact, household size, or SARS-CoV-2 variants.

Conclusion: Our data show high transmissibility of SARS-CoV-2, which was notably exaggerated compared to previous studies. Therefore, developing preventive strategies such as post-exposure prophylaxis (PEP) in close contact with SARS-CoV-2 infection would be a novel supplement to the current standard of care.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection, declared a public health emergency of international concern since February 2020 by the World Health Organization (WHO), has caused global impacts in all aspects of life. The incidence of coronavirus disease 2019 (COVID-19) cases has drastically increased, reaching over 187 million cases with over 4 million deaths by July 2021 (World Health Organization, 2021). We acknowledged thus far that SARS-CoV-2 spreading travels via small droplet particles by person-to-person contact, especially in poorly ventilated indoor settings (Meyerowitz et al., 2021). Therefore, it has brought us down to the spot where most fundamental human activities take place, household. In this report, we analyzed the infectivity rate of household contacts, as defined as individuals sharing the same residential address to the primary RT-PCR confirmed SARS-CoV-2 infection-individual (index case) in the household during the outbreak of new variants of SARS-CoV-2.

From previous studies published early in the pandemic, the global secondary infection rate of SARS-CoV-2 in household settings was estimated at 16.6% (Madewell et al., 2020). These ranges in number portray the divergence in regulations set among countries such as government control measures, national surveillance, heterogeneity in culture, or sample size restriction in some studies. Interestingly, the new variants of SARS-CoV-2 have been defined, thus provoking significant challenges to infection control measures. The novel forms of coronaviruses concerned (Variant of Concern: VOC) are becoming more transmissible, less susceptible to treatments and vaccines, and more aggressive in COVID-19 severity (Walensky et al., 2021).

We obtained a retrospective study of exposed members in households among 30 sets of patients with RT-PCR confirmed SARS-CoV-2 infection (index cases) at Chulabhorn Hospital, Bangkok, Thailand, from May 1 to June 30, 2021, in which Alpha (B.1.1.7) and Delta (B.1.617.2) variants

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Table 1
Clinical characteristic of index cases with SARS-CoV-2 infection (N=30)

Characteristics	Total (%)
Age, year (median, range)	41 (18-66)
Age ≥ 60 year	5 (17)
Male gender	11 (37)
Comorbid conditions ^a	11 (37)
COVID-19 vaccination ^b	
Unvaccinated	25 (83)
Incomplete vaccination	2 (7)
Complete vaccination	3 (10)
WHO clinical progression scale at presentation	
Asymptomatic	12 (40)
Symptomatic, mild	18 (60)
Household size, number of members	
<5	4 (13)
≥5	26 (87)
Household size (median, range)	5 (3-17)
SARS-CoV-2 Variants	
B.1.1.7 (Alpha)	7 (23)
B.1.617.2 (Delta)	7 (23)
Unknown	14 (54)

Abbreviation: WHO, World Health Organization

^a Comorbid conditions included type 2 diabetes mellitus, hypertension, dyslipidemia, heart diseases, obesity and chronic kidney disease.

^b COVID-19 vaccination included Coronavac and ChAdOx1 nCoV-19 vaccine

Table 2
Independent risk factors for SARS-CoV-2 infection among 157 exposed household members

Characteristics	Secondary attack rate, n/N (%)	OR (95% CI)	P-value
Age of contacts, years			
<18	21/38 (55)	1 [Reference]	
18-59	34/83 (41)	0.56 (0.26-1.22)	0.14
≥60	21/36 (58)	1.33 (0.45-2.85)	0.79
Household size			
<5	4/11 (36)	1 [Reference]	
≥5	72/146 (49)	1.70 (0.48-6.07)	0.41
SARS-CoV-2 variants			
B.1.1.7 (Alpha)	17/35 (49)	1 [Reference]	
B.1.617.2 (Delta)	15/43 (35)	0.57 (0.23-1.41)	0.22
Unknown	44/79 (56)	1.33 (0.60-2.96)	0.48

Abbreviation: n, number of individuals with SARS-CoV-2 infection N, number of individuals exposed OR, Odds ratio CI, Confident interval

were the main variants during this outbreak. Index cases and household information were extracted from medical records and analyzed the secondary attack rate in the household within 14 days after exposure was the main primary objective.

The 30 index cases were associated with 157 exposed individual households. Among index cases, 11 were male with a median age of 41. Most were unvaccinated with asymptomatic or mild illness at presentation. Household size ranges from 3 to 17 members with a median of 5. The Alpha, Delta, and unknown SARS-CoV-2 variants were 23%, 23 %, and 54%, respectively (Table 1).

Among 157 exposed household contacts, 76 were RT-PCR confirmed SARS-CoV-2 infection within 14 days after being exposed from an index case, with a secondary attack rate of 48%. Of all the 76 secondary cases, 19 patients were reported SARS-CoV-2 infection at the first time screening, with 57 patients were subsequently confirmed at their second time nasopharyngeal specimen collection. The transmission rate in non-adults was high as 55%. However, There was no difference observed between secondary attack rates among the age of contact, household size, or SARS-CoV-2 variants (Table 2).

Our data show high transmissibility of SARS-CoV-2, which was notably more than the previous studies reported. It could be explained that most Thai cultures typically live in multigenerational houses with large household sizes and household crowding, especially in the capital city. Asymptomatic or mild symptomatic index cases of working age can easily transmit SARS-CoV-2 to vulnerable household groups, leading to high morbidity and death (Johansson et al., 2021). New variants of concerns of SARS-CoV2: Delta variants may also spread fast, especially where inadequate herd immunity such as low vaccination rates.

However, the study remained a few limitations because half of the SARS-CoV-2 variants in our study were unknown variants. The study was conducted in the short period of the outbreak resulting in small population size, and it was difficult to prove the statistical differences when comparing the Delta and Alpha variants. Our study could not demonstrate that patients in the unknown variant, which had more attack rate, might be more Delta variants than the Alpha variant. The false-negative rate of SARS-CoV-2 infection among exposed households during the initial day of exposure is very challenging. The surge of new case outbreak probably needed frequent re-testing in the exposed household population to reduce transmissions. The next-generation sequencing or whole-genome sequencing would be beneficial for transmissibility study and outbreak investigation.

Besides, in the low vaccination coverage, we are still in the pipeline for achieving herd immunity. Due to SARS-CoV-2 high transmission ability, infection control in the household over this pandemic has posed significant global challenges. Even though the preventive measures have already been established, it seems sensitively unmanageable when applied to household settings. Therefore, developing preventive strategies- post-exposure prophylaxis (PEP) in close contact with SARS-CoV-2 infection case exposure-would be a novel supplement to the current standard of care protocols, self-observation, home isolation, and home environment control.

Declaration of Competing Interest

All authors declare no conflict of interest

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Ethical approval

This study was approved by Human Research and Ethics Committee, Chulabhorn Research Institute

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