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Epidemic Data Analysis of Three Variants of COVID-19 Spread in Indonesia

Inna Syafarina[1], Taufiq Wirahman[1,2], Syam Budi Iryanto[1], Arnida L. Latifah[1]

[1] Research Center for Informatics, National Research and Innovation Agency (BRIN),
Jl. Raya Bogor KM.47 Cibinong, Indonesia
[2] Applied Informatics Laboratory, Department of Systems Science, Graduate School of Informatics,
Kyoto University, Yoshida-honmachi, Sakyo-ku, Kyoto, 606-8501, Japan

Email:inna.syafarina@brin.go.id

Abstract

Three variants of COVID-19 had been found in Indonesia. A control strategy may rely on the transmission rate of the variant. This study aims to investigate how the variants spread in Indonesia by computing a basic and effective reproduction number on the national and province scale. The basic reproduction number shows the indicator of initial transmission rate of alpha variant computed by an exponential growth rate model. The effective reproduction number describes the dynamic of the transmission rate estimated based on a Bayesian approach. This study revealed that each variant shows different characteristics. The alpha variant of COVID-19 in Indonesia was mainly initiated from big cities, then it spread to all provinces quickly because the control strategies were not established well at the beginning. A rapid increase of the effective reproduction number about July 2021 showed a novel delta variant, but it could be managed quite well by a large number of testing and stronger restrictions. Before the end of 2021, a novel variant omicron was also shown by the steeper change of the effective reproduction number. Thus, the variant spread rate can be estimated by how steep the effective reproduction number change is.

Keywords: *effective reproductive number, COVID-19, exponential, Bayesian, infectious disease*

1. Introduction

At the time this paper is writing, the world is suffering from a global pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-COV-2) with the number of confirmed cases 318,648,834 infected and 5,518,343 death globally as of January 14th, 2022 [1]. Coronavirus disease 2019 (COVID-19) has spread worldwide and affected 222 countries [2] and was stated as Public Health Emergency of International Concern per February 1st, 2020 by the World Health Organization (WHO) [3]. The transmission is easily spread through droplets (by sneezing/coughing/ speaking) from infected people [2]. Indonesia announced the first case of COVID-19 from Depok city, West Java Province. There were two confirmed cases on March 2nd, 2020. By February 14th, 2022, COVID-19 has spread to 34 provinces in Indonesia with 4,844,279 confirmed cases, 145,321 deaths, and 4,232,101 recoveries [4]. Several attempts to reduce COVID-19 cases in Indonesia have been conducted, such as reducing mobility (work from home), applying social distancing in large scale population [5], wearing a mask, washing hands, and increasing immunity by consuming healthy food and a healthy lifestyle [6].

To measure the transmission of COVID-19, many studies used a reproduction number of the coronavirus as an indicator of the disease's ability to spread in both the early phase and the real-time [7–16]. A basic reproduction number (R_0) is an indicator whether a disease will become an outbreak or not [9]. It represents the average number of new susceptible people become infected at the beginning of the outbreak. However, it only represents the early phase transmission before any interventions are applied. In the period of interventions, an effective reproduction number (R_t) is more reliable to represent COVID-19 outbreaks in real-time [11]. R_t is the average of the infectious produced during an infectious period from a single infected individual as a function of time [17]. These two numbers can be compared only to see the speed of the disease spread during the beginning of the outbreak and the recent time. Both R_0 and R_t have a threshold value of 1. When the value of R_0 or R_t is higher than 1, the one infected person is able to transmit the disease to more than one susceptible person. Meanwhile, when the value of R_0 or R_t is less than 1, the disease is under controlled or not transmitted to other people [18]. Therefore, R_t is a preliminary indicator to estimate whether the disease will keep increasing or decreasing in the recent time. In order to see the time-varying condition of the pandemic in Indonesia, we analyze the early measure R_0 and the effective reproduction number in all provinces of Indonesia.

The basic reproduction number is about 2.68 in Mainland China [7], 3.10 in Italy [7], 3.25-3.4 in China [9], 6-10 in Southeast Asia [10]. The study of [11] and [12] used a SEIR model to estimate the basic reproduction number of Indonesia and derived R_0 are 7.97 and 2.9685, respectively. Nevertheless, there is still no literature estimating the basic reproduction number of COVID-19 across 34 provinces in Indonesia. Several recent studies also calculated the effective reproduction number of the COVID-19 pandemic to monitor the disease spreading over the world [14–16, 19, 20]. A study of [20] estimated the effective reproduction number by applying a renewal equation with a mean time serial interval of four days and resulted in 3.98 for Mainland China before a lockdown. The effective reproduction number of COVID-19 transmission in South Korea is 1.5 using a discretized probability distribution of the generation interval [13]. Meanwhile, [14] calculated R_t in the first 10-days using serial interval proposed by [21] and derived the median of R_t is 2.90 in Spain, 2.83 in Italy, 3.95 in Ecuador, 3.67 in Panama, 2.91 in Brazil, 2.67 in Chile, 2.67 in Columbia, 2.36 in Peru, and 2.42 in Mexico. As of July 21st 2020, the mean value of R_t in Bangladesh is 1.32 [16]. The R_t values in these countries are still relatively high because the studies computed R_t only in the early time of the pandemic, as if the basic reproduction number.

In this study, we calculate the basic reproduction number by an exponential growth rate model. Meanwhile, the effective reproduction number during almost two years in the period 2 March 2020 to 10 January 2022 is calculated by implementing the Bayesian approach proposed by [22] that was applied for the pandemic of H5N1 influenza. This method has a simple computational structure and allows an efficient estimation with available sparse data that is often found in the province cases, especially in the early time when there was still few laboratories for COVID-19 testing available.

The dynamic value of the reproduction number relies on the number of the confirmed cases every day. Nevertheless, there must be many factors that are related to the increasing and decreasing of the reproduction number. Therefore, we also try to investigate whether the number of testing and the interventions are factors related to the reproduction number of COVID-19 in Indonesia.

2. Material and Methods

2.1. Data

The datasets used in this study are the official confirmed COVID-19 new cases and obtained from the Ministry of Health of Indonesia [4]. We used the data in the period 2 March 2020 to 10 January 2022. Due to a limited testing capability in the earliest phase, the calculation of R_0 is based on various initial time intervals from 25 up to 39 days in which the data seems to be more reliable, see Table 1. The values of R_0 are computed as an ensemble mean of all duration in the various early phases (25, 30, 35, and 39 days). We chose these duration because we considered the interventions' time and the time delay of the reported cases which may take up to two weeks. The daily data of the number of testing is retrieved from [23], while the timeline interventions (i.e. social restriction and public holidays) are obtained from media.

Table 1. Number of days to compute R_0.

Ensemble member	Duration since first case (days)
1	25
2	30
3	35
4	39

There has been three variants of COVID-19 detected in Indonesia. The first cases of of COVID-19 is detected on March 2020 in Depok city. Delta variant is detected in India for the first time, on October 2020. This variant has 30-100% higher transmission rate than previous variants. Children and adult under 50 are three times more at risk of being infected with this variant [24]. In Indonesia, delta variant is detected for the first time in Jakarta since the beginning of May 2021. The latest variant of COVID-19 is omicron which found first time in Bostwana (November 11, 2021) and the next three days in South Africa [25]. Omicron variant spread in Indonesia for the first time on late November 2021 carried by an Indonesian came back from Nigeria [26]. Omicron variant has a higher growth rate than the delta variant and doubling time two to three days [27].

2.2. Exponential growth rate

Most epidemics grow approximately exponentially during the initial phase of the epidemic [9], [28], [29]. This is also based on the SIR (Susceptible – Infected – Recovered) model [30] that is formulated as follows:

$$\frac{\delta S}{\delta t} = -\frac{\beta S I}{N} \tag{1}$$

$$\frac{\delta I}{\delta t} = \frac{\beta S I}{N} - \sigma I \tag{2}$$

$$\frac{\delta R}{\delta t} = \sigma I \tag{3}$$

where $S + I + R = N$ in which N is a fixed total population, β is a transmission rate, and σ is a recovery rate. At the initial time when there is no disease, $(S = N, I = 0, R = 0)$, then we have:

$$\frac{\delta I}{\delta t} = (\beta - \sigma) I \tag{4}$$

which results in an exponential growth (EG) for the infected population with a positive growth rate $r = \beta - \sigma$. Instead of finding the best fit for the parameters β and σ, the exponential growth (EG) model tries to find the best fit for the parameter r. The model parameter fitting uses Bayesian Ridge regression instead of linear to resolve the insufficient data in the early time. The fitness between the model and the data is measured by a coefficient determination (R^2). The basic reproduction number is defined as the ratio between the transmission rate and the recovery rate and then using a parametric approach of σ that is assumed to be independent with r, we have:

$$R_0 = \frac{\beta}{\sigma} = \frac{r}{\sigma} + 1 \tag{5}$$

where $\frac{1}{\sigma}$ is the incubation (serial) time. From the previous studies, the serial time of COVID-19 is in the range of 2.1-11.1 days and can be up to 14 days [21, 31, 32]. In this study, we use 7 days serial time to compute the basic reproduction number, so $R_0 = 7r + 1$.

2.3. Bayesian approach

We calculate the effective reproduction number (R_t) using a Bayesian approach as implemented by [22]. Given a time series of new cases, we approximate the probability of the reproduction number at a time t. The probability model for an observed data ΔI with an unknown parameter R_t is assumed as $P(\Delta I \mid R_t)$, where $P(R_t)$ is a prior distribution and R_t is randomly distributed [33]. Then, the posterior probability of R_t can be computed as follows:

$$\begin{aligned} P(R_t \mid \Delta I) &= \frac{(P(\Delta I \mid R_t) \cdot P(R_t)}{P(\Delta I)} \\ &= \frac{P(\Delta I \mid R_t) \cdot P(R_t)}{\int P(\Delta I \mid R_t) \cdot P(\Delta I) dR_t} \end{aligned} \tag{6}$$

in which $\Delta I = I(t+1) - I(t)$ is the number of new cases in a day and $I(t)$ is the number of cases at time t. The probability $P(R_t)$ is estimated by a Gaussian probability with a mean at R_{t-1} and a standard deviation σ. In this paper, we assumed that the changes of the R_t is not so large approximately 0.1 at most, so $P(R_t) = N(R_{t-1}, 0.1)$. Meanwhile, the number of cases is generated according to a Poisson distribution, so that for a given an expected case λ, we have:

$$P(I \mid \lambda) = \frac{(\lambda^I e^{-\lambda})}{I!} \tag{7}$$

To compute $P(I \mid R_t)$ we need to have a relation between λ and R_t. It can be derived from the equation of the infected cases in the SIR model:

$$\frac{\delta I}{\delta t} = \beta \frac{SI}{N} - \sigma I = \sigma \left(R_0 \frac{S}{N} - 1 \right) \tag{8}$$

By integrating (2) in a day interval, we obtain the relation between λ and R_t:

$$\lambda = I(t-1) \tag{9}$$

Here, we assume a serial interval of 7 days [9]. Then the effective reproduction number can be estimated by iteration of the probability equation (1) and we take R_t from the mean of its probability distribution.

3. Results

3.1. Basic reproduction number

The estimated basic reproduction number of COVID-19 in Indonesia computed by the EG model is shown in Figure 1, while R_0 for each province is shown in Figure 2. It shows that the EG model describes the early transmission in the first 39 days since COVID-19 found in Indonesia on March 2^{nd}

2020. The ensemble mean value of R_0 in the first 25, 30, 35, and 39 days for the national case is 3.014 with $R^2 = 0.941$.

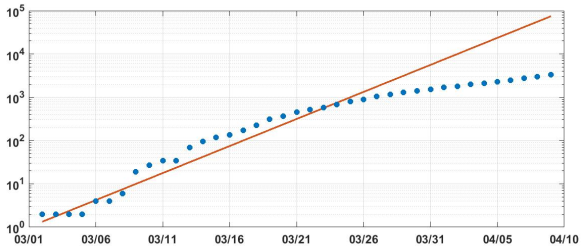

Figure 1. The cumulative number of infected people (dotted) and the estimated exponential growth model (solid) in the first 39 days of the pandemic in Indonesia

The estimated R_0 of 34 provinces over Indonesia is described in Figure 2. It shows the values of R_0 in the 34 provinces are in the range 1.135–3.014, while the mean value is 2.026. It is in line with previous studies that most of R_t is above 2 before applying some interventions. The highest R_0 is obtained when we use the data of the national scale. Over the provinces, the highest R_0 is in East Java (JAWA TIMUR) and the lowest R_0 is in Riau. The fitness between the model and data sets are in the range 0.45 – 0.97, with R^2 mean is 0.857. The lowest R^2 occurs in Aceh and Riau representing a lower correlation between the model and the dataset that may be caused by insufficient and delayed reported data in these regions.

3.2. Effective reproduction number

We compute the effective reproduction number in both national and province cases. For each province, some sparse data in the early time is neglected in the computation. The effective reproduction number in the national case is shown in the time series plot in Figure 3. At the beginning of the contagion of COVID-19, the national case had the mean value of $R_t = 2.76$ and then it decreased rapidly until the end of April. This value is computed approximately when the interventions, social restriction, work/study/pray at home, were applied. This dynamic value of R_t describes the fluctuation of the spread and also the uncertainty of the metric shown by the confidence interval. In the beginning, the uncertainty of the spread metric was quite wide, then it started to be smaller in the second year of the pandemic. However, it started to grow a bit approximately at the end of the year 2021. Significant jumps were occurred during the novel of the new variant (delta), see Figure 3 the first box from the left. The second box presented a high jump caused by a novel omicron variant and related to the relaxing restriction and year-end holidays. By seeing the steep changes of effective reproduction number, it shows the new variant of COVID-19 spread.

Figure 4 presents the result of the effective reproduction number of 34 provinces. It shows that the starting time of the estimated R_t of each province is different, but it does not precisely represent the starting time of the contagion of COVID-19. Over 34 provinces, the value of R_t started in the range 1.4 - 5.8. In the beginning, the lowest R_t occurred in Kepulauan Bangka Belitung, while the highest transmission occurred in Sumatera Utara with a big city Medan. Almost two years all provinces still show a fluctuating value of R_t until July 2021 when Indonesia hit by tremendous amount of COVID-19 cases caused by delta variant. During delta variant spread (mid of July 2021), R_t significantly increase and the value is between 1 and 2. This can be seen from Figure 4, R_t reach 2 or more in almost all provinces in Indonesia. After the delta variant spread, the number of R_t decrease constantly up to less than 1 showing that the transmission approximately controllable. The R_t value is drastically reduce due to the government applied level 3 and 4 of Enforcement of Community Activity Restrictions (ECAR/PPKM) in all provinces due to the high explosion of delta variant of COVID-19. The highest peak of new confirmed cases during delta variant spread is up to 44,721 on July 18, 2021 for the national cases. Afterward, during the omicron variant spread (beginning of December 2021) and at the same time a year-end holidays, only two provinces shows an increase $R_t > 1$ in the capital city of Jakarta and Riau Island Province.

4. Discussions

This paper examined the transmission of COVID-19 in Indonesia by measuring the basic and effective reproduction number over 34 provinces in Indonesia. Based on EG model, the R_0 value of national cases is 3.014. It agrees quite well with the study of [12] that used another method, namely SEIR model. The value is also fairly the same as the basic reproduction number of COVID-19 in China [9] and Italy [8]. The beginning of the pandemic in Indonesia started from the Capital City of Jakarta and Jawa Barat with R_0=2.2 and R_0=2.35, respectively. The R_0 value for Jakarta is lower compared to the study of [34] and [35] that used other methods and probably different periods.

The COVID-19 cases in Indonesia spread over the whole provinces with the value of R_t mostly

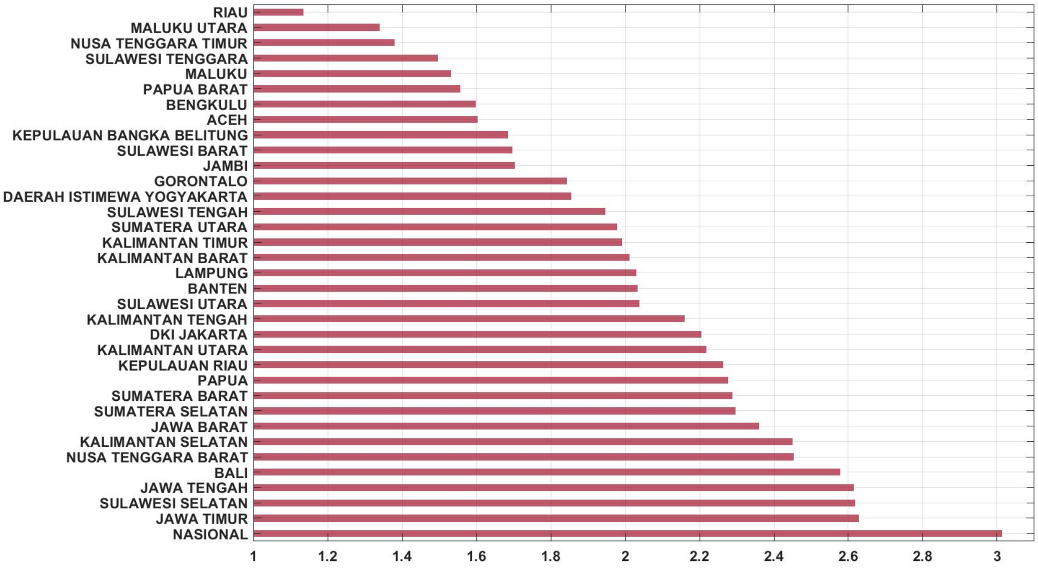

Figure 2. The estimated basic reproduction number (R_0) over 34 provinces in Indonesia

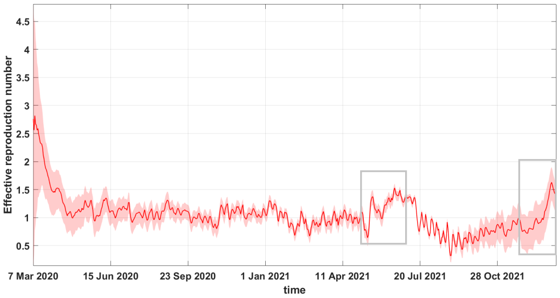

Figure 3. The effective reproduction number R_t over the national case in Indonesia. The shadow represents the 95% confidence interval. The grey box area shows a considerable increasing trend of R_t

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larger than 2 at the beginning of the pandemic. All provinces in Java Island (Jawa Tengah, Jawa Timur, Jawa Barat, DKI Jakarta, Daerah Istimewa Yogyakarta, Banten), Sulawesi Selatan, Bali, and Sumatera Utara started the transmission earlier, see Figure 4. It shows that COVID-19 spread more quickly through big cities where most human activities are centered.

Even though the COVID-19 pandemic in Indonesia started in Depok city, Jawa Barat, the highest R_0 is larger than 2.6 and occurred in Jawa Timur, Sulawesi Selatan, and Jawa Tengah. This shows that at the initial time, COVID-19 spread in these provinces are faster than the other provinces. This also indicates that the mitigation to prevent the transmission of COVID-19 to enter these provinces is still less effective. According to the effective reproduction number, the COVID-19 cases in Indonesia spread strongly in the early pandemic. It reduced significantly after the government suggested protocols such as wearing a mask, washing hands, and social distancing, and also applied a social restriction [5]. However, the long reduction only lasted until the end of April. The implemented control system seems still less optimal as the virus is still spreading shown by the value of R_t that is mostly larger than 1 and never continuously decreased to below zero until the second year of the pandemic. In Indonesia's case, it began to decrease into $R_t < 2$ on March 22^{nd} after the government of Indonesia conducted a regulation to work and study from home. The formal social restriction in Jakarta started on March 16^{th}. This agrees with the study of [36] that applying lockdown in the Capital City of Jakarta affects the other provinces. Unfortunately, in more than a year the effective reproduction number in Indonesia still fluctuated around 1, even increasing up to more than 2 during the delta variant spread in the second year of the pandemic. The interventions conducted by the government may reduce the COVID-19 transmission, but it still cannot stop the virus from spreading. This is also stated by the study of [34] that based on their estimated effective reproductive number in the Capital city of Jakarta, Large Scale Social Restriction (LSSR) is effective to control the

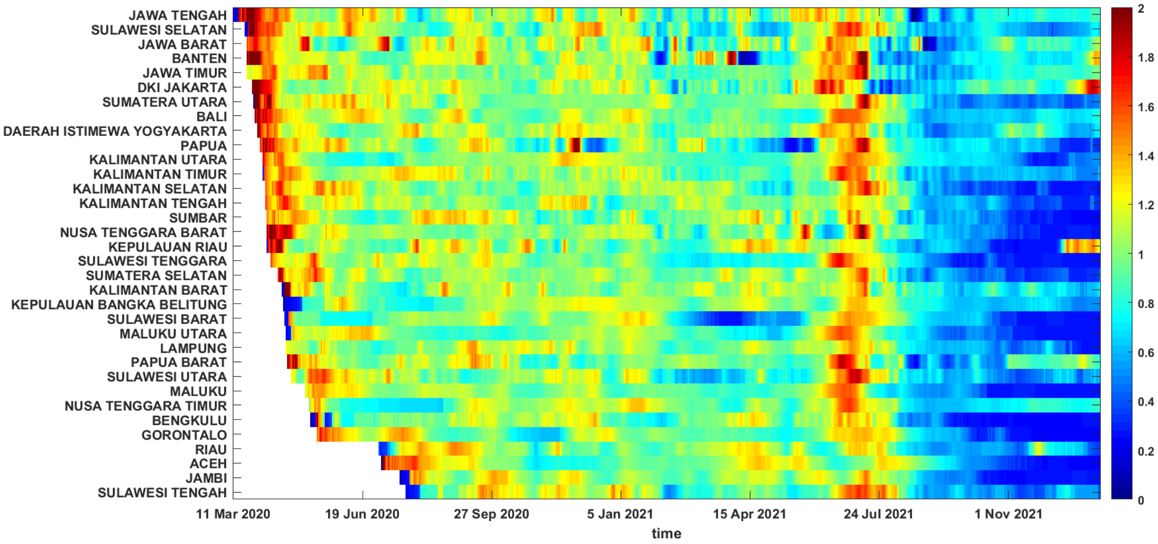

Figure 4. The effective reproduction number R_t over 34 provinces

spread of COVID-19 in Jakarta with $R_t < 1$, but it increases again when LSSR is relaxed or other interventions occurred such as a long weekend or big event holidays [5, 37]. For example, in May 2020 when there was Ramadhan and Eid Al Fitr days, the human activities and mobilities seemed to increase. This made the transmission of COVID-19 also increased approximately a month after the events.

Another strong intervention is a novel of delta variant that was faced by whole countries. A much more rapid spread of this variant forced the government to push the number of testing as one of control strategy, see the grey shaded in Figure 5. With the huge number of testing and tighter control restrictions (double mask, restricted travel, restricted public places), the spread were controlled quickly, much faster compared to the beginning of the pandemic. Afterward, the spread seemingly decrease continuously up to less than 1 in most provinces. However, the government should consider the strategies to control the transmission of the third novel of omicron variant that spread along with a relaxed restriction and year-end holidays that may worsen the situation.

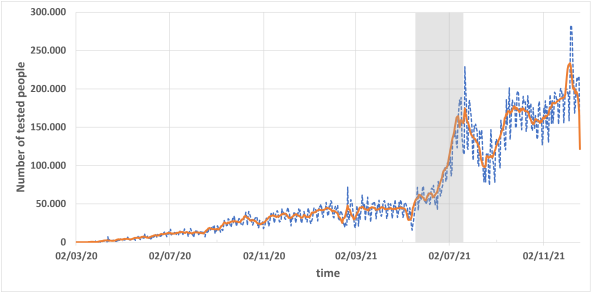

Figure 5. Daily number of tested people in Indonesia (dashed blue line) and the 7-days moving average (solid orange line)

5. Conclusion

This study estimated the transmission of COVID-19 in Indonesia from the period of alpha, delta, and omicron variants. We used an effective reproduction number computed by the Bayesian approach. As a result, the alpha variant spread mildly for more than a year until a novel delta variant. The steeper changes of the effective reproduction number of the delta and omicron variant show that they spread more rapidly. This study also observed that all variants were mainly coming from the big cities. Therefore, a tight control system and a large number of testing, especially in the big cities must be applied to prevent COVID-19 to spread over the whole region as these strategies could reduce the transmission efficiently.

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Author Contributions

Conceptualization: IS, ALL. Data and general support: SBI, TW. Methodology: IS, ALL. Writing – review & editing: IS, TW, SBI, ALL. Final writing: IS, ALL. All authors have read and agreed to the published version of the manuscript.

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