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Research article

Mathematical modeling to study the interactions of two risk populations in COVID-19 spread in Thailand

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Abstract: The use of vaccines has always been controversial. Individuals in society may have different opinions about the benefits of vaccines. As a result, some people decide to get vaccinated, while others decide otherwise. The conflicting opinions about vaccinations have a significant impact on the spread of a disease and the dynamics of an epidemic. This study proposes a mathematical model of COVID-19 to understand the interactions of two populations: the low risk population and the high risk population, with two preventive measures. Unvaccinated individuals with chronic diseases are classified as high risk population while the rest are a low risk population. Preventive measures used by low risk group include vaccination (pharmaceutical way), while for the high risk population they include wearing masks, social distancing and regular hand washing (non-pharmaceutical ways). The susceptible and infected sub-populations in both the low risk and the high risk groups were studied in detail through calculations of the effective reproduction number, model analysis, and numerical simulations. Our results show that the introduction of vaccination in the low risk population will significantly reduce infections in both subgroups.

Keywords: COVID-19 disease; effective reproduction number; mathematical model; preventive measures; risk population; vaccination
Mathematics Subject Classification: 34A34, 65L20, 65L80, 93A30

1. Introduction

After more than a year of continuing to impose different travel restrictions to combat the COVID-19 pandemic, Thailand has lifted its pre-arrival and arrival testing requirements for

international visitors [1]. For several months only few locally transmitted COVID-19 cases have been reported due to strict quarantine rules for arrivals. As of June 17, 2022, more than 30,000 deaths and over 4 million COVID-19 cases have been recorded, with an average of 2,000 COVID-19 cases per day [2]. Vaccination is an essential tool for primary prevention and the major way for the long-term management strategy of the COVID-19 outbreak [3]. As of June 22, 2022, 66.3 percent of the world's population has been vaccinated against COVID-19 with at least one dose of vaccine. Globally, 12 billion doses have been administered with 6.33 million people vaccinated each day. Only 17.8 percent of people in low-income countries have received at least one dose [4]. In Thailand, about 81 percent of the population have received at least one vaccine dose; 73 percent have received two vaccine doses; and a third dose have been received by 36 percent of the population [5]. The geographic distribution of vaccine coverage in Thailand shows that people who live in Bangkok have been vaccinated with at least one dose, while people living in provinces of the metropolitan area have also received the first dose of vaccination. However, there was significantly less vaccination coverage for people in areas far from Bangkok [6]. The use of vaccines has always been controversial. A large proportion of the population in many countries remains reluctant to get the COVID-19 vaccination [7] because it is believed that the vaccination side effects may be worse than the disease itself. Others cite their religious and political beliefs as reasons [8]. People in a society may have different opinions about the benefits of vaccines and may convince relatives or friends not to get a vaccination [9]. At the inception of COVID-19, individuals from different countries worldwide were skeptical about the COVID-19 shots. The governments of these countries came up with different techniques and mediums to enforce the vaccinations. These include fines (Greece), lockdowns of unvaccinated (Austria), refusal of entry into bars and restaurants (Finland and Lithuania), travel and entry bans (all countries), compulsory vaccination of employees (Hungary), voucher gifts (Slovakia), and self-payment of medical bills (Singapore) [10]. The attitudes towards vaccines have clear consequences on the spread of diseases and their transformation into epidemics [9]. At the time of writing this article, at least 218 countries and territories have administered more than 12 billion doses of a COVID-19 vaccine. Furthermore, several different vaccines have been developed at record speed, in large part due to years of research on related viruses and billions of dollars in investment. Therefore, to measure the progress of different countries is a challenge because many countries are using two-dose vaccines. These inconsistent data make it difficult to determine the total or partial number of people vaccinated [11]. Tourism is a huge driver of the Thai economy earning about 20% of its gross domestic product (GDP). In 2019, Thailand was the 8th largest tourist destination in the world, with China being an important market. It has also welcomed 40 million visitors, with the top three spending categories for inbound visitors being accommodation (28%), shopping (24%), and food and beverage (21%). Unfortunately, the pandemic and related restrictions have affected Thai tourism. This is due to the decline in international travel, with passengers on international flights to Thailand down 95 percent in September 2021 compared to the previous year [12]. Recently, Thailand's Centre of COVID-19 Situation Administration (CCSA) has approved the cancellation of Thailand Pass registration and US$ 10,000 health insurance requirements for foreign tourists visiting Thailand, effective July 1, 2022 [13]. Currently, 32.9% of the world's population has not been vaccinated [14]. Thailand remains one of the most popular tourist destinations in the world. Thus, it is expected that many individuals (vaccinated and unvaccinated) worldwide will look to travel here, especially since most governments and airlines are less strict with travel requirements. Inspired by

this situation, this study was done through modeling and simulation techniques in order to understand the interactions that will occur between individuals who are considered low risk (people who have received two or more doses of the vaccine) and individuals at a high risk (people who have not been vaccinated, have underlying diseases, and those under 5 years of age) in Thailand by considering Bangkok and Phuket as case studies. Bangkok is included because that it is the capital city of Thailand. In addition, from January to June 2021, Bangkok generated the highest amount of tourist revenue namely slightly over 41 billion baht (1, 154, 216, 830 USD). Besides Bangkok, Phuket is also a popular tourist destination for foreigners [15].

This paper is organized as follows. In Section 2, we generate a new model with some assumptions which address the COVID-19 situation in Thailand, by presenting a diagram for describing a system of differential equations. In Section 3, we present the model dynamsics and analysis including to compute the effective reproduction number. Results are discussed in Section 4. Finally, we summarize and conclude our work with recommendations in Section 5.

2. Model formulation

Recently, Asempapa et al. [16] formulated a COVID-19 mathematical model in low- and high-risk populations with pharmaceutical and non-pharmaceutical measures. Brazil and South Africa were the subjects of case studies. In their study, the non-pharmaceutical interventions considered for the low risk population included wearing masks, social distancing, and regular hand washing. On the other hand, the high risk individuals must comply with additional precautions such as telework, and avoiding social gatherings or public places to reduce the spread of infection. Their study also classified people with chronic diseases and the elderly as high risk individuals while the rest are classified as low risk. One research gap in their study was that the effects of vaccination were not considered in either low- or high-risk groups. By using the enormous amount of data available in the studies mentioned above, we have created a model to understand the interactions that will occur between two different population groups in Thailand. The model will be divided into eight compartments, namely high risk susceptible (S_H), low risk susceptible (S_L), high risk exposed (E_H), low risk exposed (E_L), high risk infected (I_H), low risk infected (I_L), quarantined (Q), and recovered (R). In addition, the interventions were considered by Asempapa et al. [16], so our study focuses on vaccination in the low risk compartments.

The assumptions relating to the model are as follows:

- We assumed that the high risk susceptible class becomes exposed after interacting with the high risk infected, low risk infected, or those who are quarantined.
- Similarly, low risk susceptible population becomes exposed after interacting with the high risk infected, low risk infected, or those who are quarantined.
- High risk individuals considered in this study are individuals with underlying chronic diseases and the elderly (ages 60 and above) who have not been vaccinated.
- In low risk infection, we assumed that individuals are fully vaccinated. Thus, deaths can only arise naturally and not due to COVID-19 infection. However, in high risk infection compartment, death can occur naturally and due to COVID-19.

- We assumed that individuals both in the high risk and low risk class first move to quarantine. If they recover, then they move to the recovery compartment. Otherwise, they move to either the high risk infected class or low risk infected class, respectively.
- Also, reinfection in this model is not considered as a result of the current nature of COVID-19.

A diagram of the model based on above assumptions is illustrated in Figure 1.

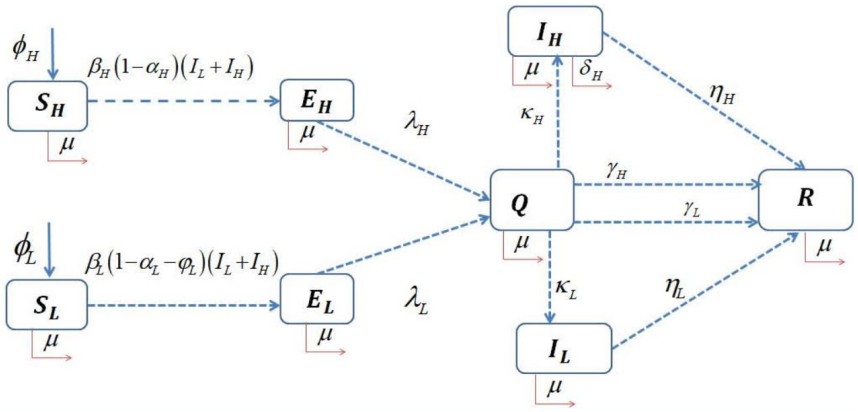

Figure 1. The dynamics of transitions between compartments of the model.

Furthermore, the mathematical representation and variable descriptions of the dynamics in Figure 1 are given in (2.1) and Table 1, respectively.

$$\begin{aligned}
\frac{dS_L}{dt} &= \phi_L - \beta_L(1-\alpha_L-\varphi_L)(I_L+I_H)S_L - \mu S_L,\\
\frac{dS_H}{dt} &= \phi_H - \beta_H(1-\alpha_H)(I_L+I_H)S_H - \mu S_H,\\
\frac{dE_L}{dt} &= \beta_L(1-\alpha_L-\varphi_L)(I_L+I_H)S_L - (\lambda_L+\mu)E_L,\\
\frac{dE_H}{dt} &= \beta_H(1-\alpha_H)(I_L+I_H)S_H - (\lambda_H+\mu)E_H,\\
\frac{dQ}{dt} &= \lambda_L E_L + \lambda_H E_H - (\gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu)Q,\\
\frac{dI_L}{dt} &= \kappa_L Q - (\eta_L+\mu)I_L,\\
\frac{dI_H}{dt} &= \kappa_H Q - (\eta_H+\delta_H+\mu)I_H,\\
\frac{dR}{dt} &= \eta_H I_H + \eta_L I_L + \gamma_L Q + \gamma_H Q - \mu R.
\end{aligned} \tag{2.1}$$

Table 1. Descriptions of variables and parameters in the model formulation.

Variable/Parameter	Description
S_L	susceptible compartment for low risk individuals
E_L	exposed compartment for low risk individuals
I_L	infected compartment for low risk individuals
S_H	susceptible compartment for high risk individuals
E_H	exposed compartment for high risk individuals
I_H	infected compartment for high risk individuals
Q	quarantine compartment
R	recovered compartment
ϕ_L	recruitment to the low risk susceptible class
ϕ_H	recruitment to the high risk susceptible class
β_L	effective contact rate of low risk individuals
β_H	effective contact rate of high risk individuals
α_L	the use of non-pharmaceutical intervention (face masks) used by low risk individuals
α_H	the use of non-pharmaceutical intervention (face masks) by high risk to reduce the transmission
φ_L	the use of pharmaceutical intervention (vaccination) used by the low risk individuals to reduce the transmission spread
λ_H	rate of progression by individuals in the high risk exposed compartment to the quarantine compartment
λ_L	rate of progression by individuals in the low risk exposed compartment to the quarantine compartment
κ_H	rate of progression by individuals in the high risk exposed compartment to the infected compartment
κ_L	rate of progression by individuals in the low risk exposed compartment to the infected compartment
η_H	rate of progression by individuals in the high risk infected compartment to the recovered compartment
η_L	rate of progression by individuals in the low risk infected compartment to the recovered compartment
δ_H	COVID-19 mortality rate for individuals in the high risk infected compartment
γ_L	recovery rate for low risk individuals in the quarantine compartment
γ_H	recovery rate for high risk individuals in the quarantine compartment
μ	natural death rate for individuals in all compartments

3. Model dynamics and analysis

In this section, we will present details relating to dynamics and analysis of the formulated model.

3.1. Model dynamics

The dynamics of the model are carried out by examining if it exists in an invariant region.

3.1.1. Invariant region

In this section, the COVID-19 model given in (2.1) will be analyzed in a suitable feasible region to show that it is biologically relevant (mathematically well-posed and meaningful biologically) when all the variables and parameters in the model are non-negative for all time $t \geq 0$.

Lemma 3.1. *The region* $\Omega = \{(S_L, S_H, E_L, E_H, Q, I_L, I_H, R) \in \mathcal{R}_+^8 \leq \frac{\phi_L+\phi_H}{\mu}\}$ *is positively-invariant for Model (2.1) with non-negative initial conditions in* $\mathcal{R}_+^8$.

Proof. If $(S_L, S_H, E_L, E_H, Q, I_L, I_H, R) \in \mathcal{R}_+^8$ denote any solutions of Model (2.1), then the addition of all the model equations yield:

$$\frac{dN}{dt} = \phi_L + \phi_H - \mu N - \delta_H I_H \leq \phi_L + \phi_H - \mu N.$$

Since $(S_L, S_H, E_L, E_H, Q, I_L, I_H, R)$ are all non-negative, then $N(0) \geq 0$. Using integration, this becomes

$$N(t) \leq N(0)e^{-\mu t} + \frac{\phi_L + \phi_H}{\mu}(1 - e^{-\mu t}).$$

Thus, if $N(t) \leq \frac{\phi_L+\phi_H}{\mu}$, then $N(0) \leq \frac{\phi_L+\phi_H}{\mu}$. Hence, it follows from [17] that Ω is positively invariant and initial conditions in Ω will remain in Ω for all time $t > 0$. □

3.2. Model analysis

The details relating to the analysis of the Model (2.1) are presented in this section. We begin with computing all the equilibrium points of Model (2.1) by setting all derivatives of each compartment to zero. This is represented by

$$\frac{dS_L}{dt} = \frac{dS_H}{dt} = \frac{dE_L}{dt} = \frac{dE_H}{dt} = \frac{dI_L}{dt} = \frac{dI_H}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = 0. \tag{3.1}$$

We can find several equilibrium points from Eq (3.1), but in epidemiology, we focus on two equilibrium points: the COVID-19 free equilibrium and the COVID-19 endemic equilibrium.

3.2.1. The COVID-19 free equilibrium point

The COVID-19 free equilibrium point is that there are no COVID-19 infections within the two populations (low risk and high risk) considered in this study. This implies that $I_L = I_H = 0$. Thus, we denote the COVID-19 free equilibrium point as Ω_0 which is

$$\Omega_0 = (S_L^*, E_L^*, I_L^*, S_H^*, E_H^*, I_H^*, Q^*, R^*) = (\frac{\phi_L}{\mu}, 0, 0, \frac{\phi_H}{\mu}, 0, 0, 0, 0),$$

where $\frac{\phi_L}{\mu}$ denotes the initial size of the low risk individuals in the susceptible compartment, and $\frac{\phi_H}{\mu}$ represents the initial size of the high risk individuals in the susceptible compartment.

3.2.2. The effective reproduction number

One of the widely repeated terms during the outbreak of COVID-19 pandemic is the basic reproduction number (BRN). It denotes the average number of secondary infections that arise from a single infected individual. It is often denoted by R_0. It is also regarded as a central concept in epidemiology, which indicates infection risk with respect to epidemic spread [16]. If $R_0 > 1$, then the infected number of individuals is expected to rise. However, if $R_0 < 1$, transmissions are expected to reduce or die out. In this study, we redefine the BRN as effective reproduction number (ERN) denoted as R_{HL}. Here, R_{HL} denotes the number of secondary cases of COVID-19 infection arising from one individual infected with COVID-19 in the presence of different pharmaceutical and non-pharmaceutical interventions. Using the next-generation matrix approach [18], the computation of R_{HL} of Model (2.1) is given from Eq (3.2) to Eq (3.6).

$$\frac{d}{dt}\begin{bmatrix} E_L \\ I_L \\ E_H \\ I_H \\ Q \end{bmatrix} = \begin{bmatrix} \beta_L(1-\alpha_L-\varphi_L)(I_L+I_H)S_L \\ 0 \\ \beta_H(1-\alpha_H)(I_L+I_H)S_H \\ 0 \\ 0 \end{bmatrix} - \begin{bmatrix} (\lambda_L+\mu)E_L \\ (\eta_L+\mu)I_L-\kappa_L Q \\ (\lambda_H+\mu)E_H \\ (\eta_H+\delta_H+\mu)I_H-\kappa_H Q \\ (\gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu)Q-\lambda_L E_L-\lambda_H E_H \end{bmatrix}. \tag{3.2}$$

In the above, matrix F and matrix V of the transition terms are given by

$$F = \begin{bmatrix} 0 & \beta_L(1-\alpha_L-\varphi_L)S_L^* & 0 & \beta_L(1-\alpha_L-\varphi_L)S_L^* & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & \beta_H(1-\alpha_H)S_H^* & 0 & \beta_H(1-\alpha_H)S_H^* & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}, \tag{3.3}$$

and

$$V = \begin{bmatrix} \lambda_L+\mu & 0 & 0 & 0 & 0 \\ 0 & \eta_L+\mu & 0 & 0 & -\kappa_L \\ 0 & 0 & \lambda_H+\mu & 0 & 0 \\ 0 & 0 & 0 & \eta_H+\delta_H+\mu & -\kappa_H \\ -\lambda_L & 0 & -\lambda_H & 0 & \gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu \end{bmatrix}. \tag{3.4}$$

The effective reproduction number obtained from the Model (2.1) is defined as the spectral radius of the product FV^{-1} which is given below

$$\mathcal{R}_{HL} = \mathcal{R}_L + \mathcal{R}_H, \tag{3.5}$$

where

$$\mathcal{R}_L = \frac{\lambda_L\phi_L\kappa_L\beta_L(1-\alpha_L-\varphi_L)}{\mu(\lambda_L+\mu)(\eta_L+\mu)(\gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu)} \text{ and}$$
$$\mathcal{R}_H = \frac{\lambda_H\phi_H\kappa_H\beta_L(1-\alpha_H)}{\mu(\lambda_H+\mu)(\eta_H+\delta_H+\mu)(\gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu)}.$$

As earlier stated in Section 3.2, R_{HL} denotes the number of secondary cases of COVID-19 infection arising from one individual infected with COVID-19 in the presence of different pharmaceutical and non-pharmaceutical interventions. In this study, to achieve a low infection rate, then

$$R_{HL} = \frac{\lambda_L \phi_L \kappa_L \beta_L (1-\alpha_L-\varphi_L)}{K_1} + \frac{\lambda_H \phi_H \kappa_H \beta_L (1-\alpha_H)}{K_2} < 1$$

where $K_1 = \mu(\lambda_L+\mu)(\eta_L+\mu)(\gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu)$ and $K_2 = \mu(\lambda_H+\mu)(\eta_H+\delta_H+\mu)(\gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu)$. Note that the optimal R_{HL} will be computed in the numerical simulation section.

3.2.3. The COVID-19 endemic equilibrium point

Here, we investigate the existence of endemic equilibrium point in Model (2.1) whenever $R_{HL} > 1$. Suppose we denote $\Omega^0 = (S_L^{**}, S_H^{**}, E_L^{**}, E_H^{**}, Q^{**}, I_L^{**}, I_H^{**}, R^{**})$ as the endemic equilibrium point of Model (2.1), then Ω^0 can be computed by setting the derivatives of each compartments in Model (2.1) to zero as shown below:

$$\begin{aligned}
\phi_L - \beta_L(1-\alpha_L-\varphi_L)(I_L^{**}+I_H^{**})S_L^{**} - \mu S_L^{**} &= 0,\\
\phi_H - \beta_H(1-\alpha_H)(I_L^{**}+I_H^{**})S_H^{**} - \mu S_H^{**} &= 0,\\
\beta_L(1-\alpha_L-\varphi_L)(I_L^{**}+I_H^{**})S_L^{**} - (\lambda_L+\mu)E_L^{**} &= 0,\\
\beta_H(1-\alpha_H)(I_L^{**}+I_H^{**})S_H^{**} - (\lambda_H+\mu)E_H^{**} &= 0,\\
\lambda_L E_L^{**} + \lambda_H E_H^{**} - (\gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu)Q^{**} &= 0,\\
\kappa_L Q^{**} - (\eta_L+\mu)I_L^{**} &= 0,\\
\kappa_H Q^{**} - (\eta_H+\delta_H+\mu)I_H^{**} &= 0,\\
\eta_H I_H^{**} + \eta_L I_L^{**} + \gamma_L Q^{**} + \gamma_H Q^{**} - \mu R^{**} &= 0.
\end{aligned} \tag{3.6}$$

Simplify Eq (3.6) by calculating $S_L^{**}, S_H^{**}, E_L^{**}, E_H^{**}, Q^{**}, I_L^{**}, I_H^{**}$ and R^{**} to obtain

$$\begin{aligned}
S_L^{**} &= \frac{\phi_L}{\beta_L(1-\alpha_L-\varphi_L)(I_L^{**}+I_H^{**})-\mu},\\
S_H^{**} &= \frac{\phi_H}{\beta_H(1-\alpha_H)(I_L^{**}+I_H^{**})-\mu},\\
E_L^{**} &= \frac{\phi_L(1-\alpha_L-\varphi_L)(I_L^{**}+I_H^{**})}{(\lambda_L+\mu)(1-\alpha_L-\varphi_L)-\mu},\\
E_H^{**} &= \frac{\phi_H(1-\alpha_H)(I_L^{**}+I_H^{**})}{(\lambda_H+\mu)(1-\alpha_H)},\\
Q^{**} &= \frac{\lambda_L E_L^{**} + \lambda_H E_H^{**}}{\gamma_L+\gamma_H+\kappa_L+\kappa_H+\mu},\\
I_L^{**} &= \frac{\kappa_L Q^{**}}{\eta_L+\mu},\\
I_H^{**} &= \frac{\kappa_H Q^{**}}{\eta_H+\delta_H+\mu},\\
R^{**} &= \frac{\eta_H I_H^{**} + \eta_L I_L^{**} + \gamma_L Q^{**} + \gamma_H Q^{**}}{\mu}.
\end{aligned} \tag{3.7}$$

3.3. Stability analysis

As described in the model formulation, the Model (2.1) was formulated based on two COVID-19 risk conditions: low and high risks. In order to attain a mathematical tractability, the Model (2.1) will be divided into two-sub models as follows: the first sub-model is

$$\begin{aligned}
\frac{dS_L}{dt} &= \phi_L - \beta_L(1-\alpha_L-\varphi_L)I_L S_L - \mu S_L,\\
\frac{dE_L}{dt} &= \beta_L(1-\alpha_L-\varphi_L)I_L S_L - (\lambda_L+\mu)E_L,\\
\frac{dQ}{dt} &= \lambda_L E_L - (\gamma_L+\kappa_L+\mu)Q,\\
\frac{dI_L}{dt} &= \kappa_L Q - (\eta_L+\mu)I_L,\\
\frac{dR}{dt} &= \eta_L I_L + \gamma_L Q - \mu R,
\end{aligned} \tag{3.8}$$

and the second one is

$$\begin{aligned}
\frac{dS_H}{dt} &= \phi_H - \beta_H(1-\alpha_H)I_H S_H - \mu S_H,\\
\frac{dE_H}{dt} &= \beta_H(1-\alpha_H)I_H S_H - (\lambda_H+\mu)E_H,\\
\frac{dQ}{dt} &= \lambda_H E_H - (\gamma_H+\kappa_H+\mu)Q,\\
\frac{dI_H}{dt} &= \kappa_H Q - (\eta_H+\delta_H+\mu)I_H,\\
\frac{dR}{dt} &= \eta_H I_H + \gamma_H Q - \mu R.
\end{aligned} \tag{3.9}$$

where Eq (3.8) is low risk sub-model and Eq (3.9) is high risk sub-model, respectively. Since the long time behaviour of individuals to COVID-19 is of upmost importance, therefore, the stability analysis will only consider the global stability case. In addition, only the high risk sub-model will be analyzed.

3.4. Global stability analysis of the COVID-19 free equilibrium point (high risk)

The global stability analysis of Model (3.9) at the COVID-19 free equilibrium point is shown by the following theorem.

Theorem 3.2. *For the Model* (3.9)*, if* $\mathcal{R}_H < 1$*, then the global asymptotic stability holds for the COVID-19 free equilibrium point when* $S_H = S_H^*$ *and if* $\mathcal{R}_H > 1$*, the the COVID-19 free equilibrium point is unstable.*

Proof. To show the global stability at the COVID-19 free equilibrium point, the following Lyapunov function is considered

$$U(S_H, E_H, I_H, Q, R) = \frac{1}{3}[(S_H - S_H^*) + (E_H - E_H^*) + (I_H - I_H^*) + (Q - Q^*) + (R - R^*)]^3. \tag{3.10}$$

Equation (3.10) is greater than zero at the COVID-19 free equilibrium point and equal to zero if we set $S_H = S_H^* = \frac{\phi_H}{\mu}, E_H = E_H^* = 0, I_H = I_H^* = 0, Q = Q^* = 0, R = R^* = 0$.

Differentiating (3.10), we obtain

$$\frac{dU}{dt}(S_H,\ 0,\ 0,\ 0,\ 0) = (S_H - S_H^*)^2 \times \frac{dS_H}{dt}. \tag{3.11}$$

The simplification of (3.11) yields

$$\frac{dU}{dt}(S_H,\ 0,\ 0,\ 0,\ 0) = -(S_H - S_H^*)^2 \times (\mu S_H - \phi_H). \tag{3.12}$$

Thus $\frac{dU}{dt}(S_H,\ 0,\ 0,\ 0,\ 0) < 0$ which is globally asymptotic stability for the COVID-19 free equilibrium point is satisfied if and only if $S_H > \frac{\phi_H}{\mu}$. □

3.5. Global stability analysis of the COVID-19 endemic equilibrium point (high risk)

The global asymptotic stability of the high risk sub-model will be discussed in this subsection using the Lyapunov's direct method and following from the study of De León (2009) [19].

Theorem 3.3. *If $\mathcal{R}_H > 1$, then the COVID-19 endemic equilibrium point of the high risk sub-model denoted as EE is globally asymptotically stable in the interior of region $\Omega_H = \{(S_H, E_H, Q, I_H, R) \in \mathcal{R}_+^5 \leq \frac{\phi_H}{\mu}\}$.*

Proof. Suppose $W : \{(S_H, E_H, Q, I_H, R) \in \Omega_H : S_H, E_H, Q, I_H, R > 0\} \to \mathbb{R}$. Constructing a common quadratic function using the high risk sub-model, we obtain:

$$W(S_H, E_H, Q, I_H, R) = \frac{1}{2}[(S_H - S_H^{**}) + (E_H - E_H^{**}) + (Q - Q^{**}) + (I_H - I_H^{**}) + (R - R^{**})]^2. \tag{3.13}$$

W is C^1 on the interior of Ω_H where EE is the global minimum of W on Ω_H, and $W(S_H^{**}, E_H^{**}, Q^{**}, I_H^{**}, R^{**}) = 0$. Differentiating W along the solutions of high risk sub-Model (3.9), we obtain

$$\begin{aligned}\frac{\partial W}{\partial t} &= [(S_H - S_H^{**}) + (E_H - E_H^{**}) + (Q - Q^{**}) + (I_H - I_H^{**}) + (R - R^{**})] \\ &\quad \times \frac{d}{dt}(S_H + E_H + Q + I_H + R),\end{aligned}$$

where

$$\frac{d}{dt}(S_H + E_H + Q + I_H + R) = \phi_H - \mu(S_H + E_H + Q + I_H + R) - \delta_H I_H.$$

Thus, (3.5) becomes:

$$\begin{aligned}\frac{\partial W}{\partial t} &= [(S_H - S_H^{**}) + (E_H - E_H^{**}) + (Q - Q^{**}) + (I_H - I_H^{**}) + (R - R^{**})] \\ &\quad \times (\phi_H - \mu(S_H + E_H + Q + I_H + R) - \delta_H I_H).\end{aligned} \tag{3.14}$$

Using $\phi_H = \mu(S_H^{**} + E_H^{**} + Q^{**} + I_H^{**} + R^{**}) - \delta_H I_H^{**}$, (3.14) becomes:

$$\begin{aligned}\frac{\partial W}{\partial t} &= [(S_H - S_H^{**}) + (E_H - E_H^{**}) + (Q - Q^{**}) + (I_H - I_H^{**}) + (R - R^{**})] \\ &\times \quad (\mu(S_H^{**} + E_H^{**} + Q^{**} + I_H^{**} + R^{**}) - \mu(S_H + E_H + Q + I_H + R) - \delta_H I_H^{**} - \delta_H I_H).\end{aligned} \tag{3.15}$$

From (3.15) we obtain:

$$\begin{aligned}\frac{\partial W}{\partial t} &= [(S_H - S_H^{**}) + (E_H - E_H^{**}) + (Q - Q^{**}) + (I_H - I_H^{**}) + (R - R^{**})] \\ &\times \Big(- \mu[(S_H - S_H^{**}) + (E_H - E_H^{**}) + (Q - Q^{**}) + (I_H - I_H^{**}) + (R - R^{**})] - \delta_H(I_H - I_H^{**})\Big).\end{aligned} \tag{3.16}$$

Let $A_1 = S_H - S_H^{**}, A_2 = E_H - E_H^{**}, A_3 = Q - Q^{**}, A_4 = I_H - I_H^{**}$ $A_5 = R - R^{**}$, and $A_6 = A_1 + A_2 + A_3 + A_4 + A_5$. Thus, (3.16) becomes

$$\frac{\partial W}{\partial t} = A_6(-\mu A_6 - \delta_H A_4). \tag{3.17}$$

From (3.17), we obtain

$$\frac{\partial W}{\partial t} = -(\mu A_6^2 + \delta_H A_4 A_6). \tag{3.18}$$

Hence

$$\frac{\partial W}{\partial t} = -(\mu A_6^2 + \delta_H A_4 A_6) \leq 0. \tag{3.19}$$

Also, $\frac{\partial W}{\partial t} = 0$ if $S_H = S_H^{**}, E_H = E_H^{**}, Q = Q^{**}$, $I_H = I_H^{**}$ and $R = R^{**}$ in (3.16). Hence, the largest compact invariant set in $\{(S_H, E_H, Q, I_H, R) \in \Omega_H : \frac{\partial W}{\partial t} = 0\}$ is the singleton EE, where EE is the COVID-19 endemic equilibrium point. Therefore by Lasalle's invariance principle, EE is globally asymptotically stable in the interior of Ω_H. □

4. Numerical simulations

The numerical simulations carried out in this study are presented in this section. The simulation largely focused on the effect of vaccination in the two populations. As stated earlier in the Introduction and Model formulation sections, an important assumption guiding the model is that only non-pharmaceutical intervention (wearing face masks) was employed by individuals in the high risk population. However, in addition to the non-pharmaceutical intervention, individuals in the low risk population have also employed pharmaceutical intervention (vaccination). To get a proper understanding of the effect and importance of vaccination used by individuals in the low risk compartment, a comparison of the infected population in the two groups was conducted by considering four scenarios as presented in Table 2.

Table 2. Scenarios for considering in numerical simulations.

Scenarios	Low risk population	High risk population
Scenario 1	wearing masks	wearing masks
Scenario 2	wearing masks and taking one vaccine dose	wearing masks
Scenario 3	wearing masks and taking two vaccine doses	wearing masks
Scenario 4	wearing masks and taking two vaccine doses with booster shot	wearing masks

The parameter values used for the numerical simulation and their respective source are provided in Table 3.

Table 3. The parameter values used in numerical simulations.

Parameter	Value	Source
ϕ_L	assumed	–
ϕ_H	assumed	–
β_L	assumed	–
β_H	assumed	–
$\alpha_L = \alpha_H$	$1/10$ day$^-1$	[20]-[21]
φ_L	$0.51 - 0.95$ day$^-1$	[22]
$\lambda_L = \lambda_H$	$1/7$ day$^-1$	[23]-[24]
$\kappa_L = \kappa_H$	$1/6$ day$^-1$	[25]
$\eta_L = \eta_H$	$1/14$ day$^-1$	[23]-[24]
δ_H	0.015 day$^-1$	[26]
γ_H	$1/10$ day$^-1$	[20]-[21]
γ_L	0.05 day$^-1$	[20]-[21]
μ	3.625×10^{-5} day$^-1$	[27]

4.1. Dynamics of the four scenarios relating to vaccination

Since the approval of COVID-19 vaccines, Thailand has administered and combined different vaccines (Sinovac, AstraZeneca, Pfizer, and Moderna). The vaccine most administered is Astra Zeneca [28]. For the simulation relating to the dynamics of the four scenarios, three parameters, φ_L (use of vaccination), α_L (effect of face mask in low risk population) and α_H (effect of face mask in high risk population) were of utmost importance. For scenario 1, $\varphi_L = 0$. For Scenarios 2–4, respectively, $\varphi_L = 0.51, 0.879$ and 0.95. The values mentioned induce the expected decrease in infections as a result of one vaccine dose, two vaccine doses, and the combination of two vaccine doses with a booster dose, respectively. Plots obtained from the simulations are presented in Figures 2–5.

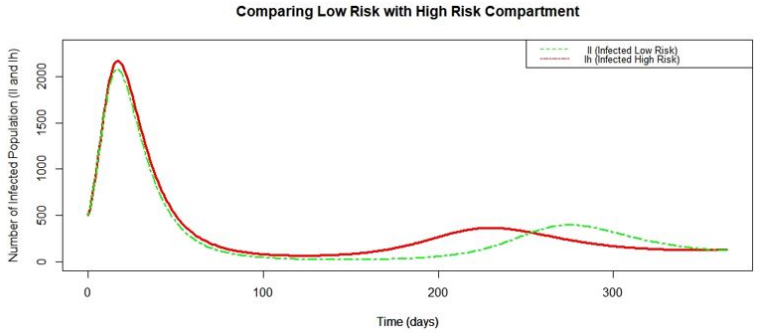

Figure 2. A graphical representation of Scenario 1: Only non-preventive measure (face mask) is considered by the two population.

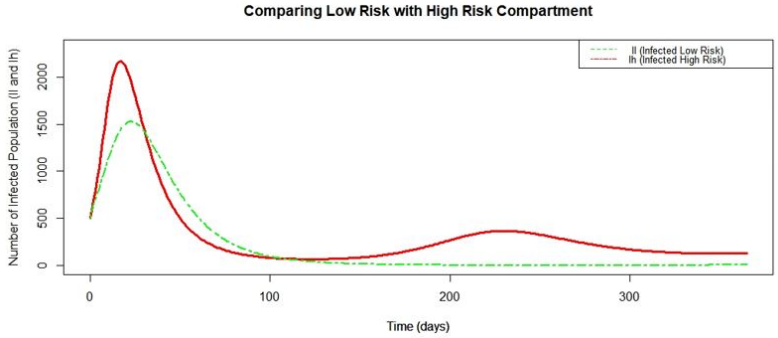

Figure 3. A graphical representation of Scenario 2: Use of face mask and one vaccine dose in the low risk population while only face mask is used by individuals in high risk population.

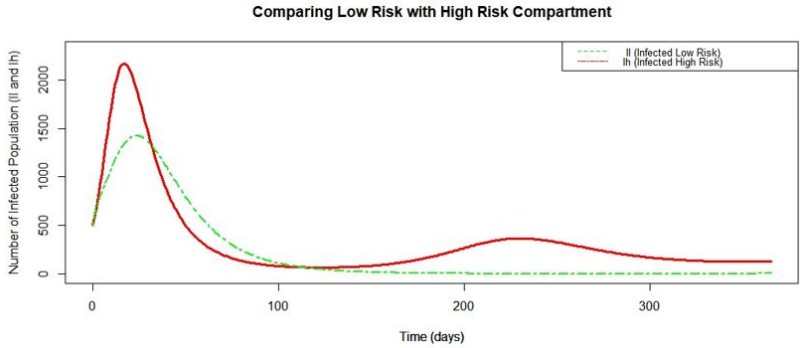

Figure 4. A graphical representation of Scenario 3: Use of face mask and two vaccine doses in the low risk population while only face mask is used by individuals in high risk population.

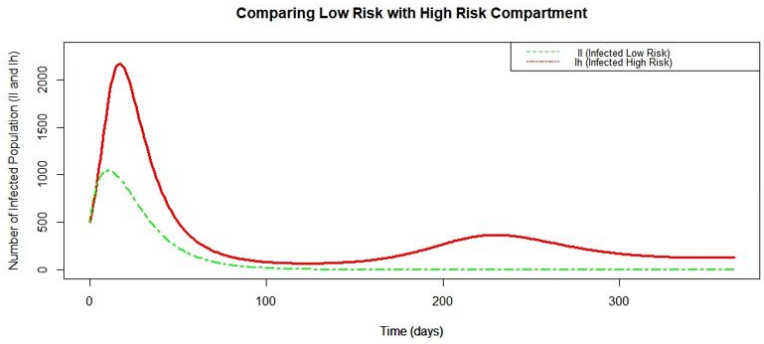

Figure 5. A graphical representation of Scenario 4: Use of face mask and two vaccine doses with booster shot in the low risk population while only face mask is used by individuals in high risk population.

In addition to the plots obtained for each scenario, the effective reproduction number, associated with each scenario is presented in Table 4.

Table 4. The effective reproduction number associated with each scenario.

Scenarios	Effective reproduction number (R_L)	Effective reproduction number (R_H)
Scenario 1	$R_L = 2.745 > 1$	$R_H = 3.369 > 1$
Scenario 2	$R_L = 1.345 > 1$	$R_H = 3.369 > 1$
Scenario 3	$R_L = 0.737 < 1$	$R_H = 3.369 > 1$
Scenario 4	$R_L = 0.485 < 1$	$R_H = 3.369 > 1$

As expected, the tabular results of the ERN associated with the four scenarios show that the vaccination plays a vital role in reducing the number of infections that can occur within the population.

4.2. Optimal effective reproduction number

In order to obtain the optimal ERN number when the two populations (R_L and R_H) are combined, we consider the application of Scenario 4 in two different cases. We recall that Scenario 4 is when the preventive measure for the low risk population is by "face masks, two vaccine doses and a booster vaccine shot". In case 1, we assume that individuals in the low risk population believe that since they have taken 3 vaccine shots, then there is no need to use face mask. For the high risk population, we assume that 50% of the population were constantly using face masks. In case 2, we assume that half of the low risk populations (50%) irrespective of their vaccine status continues to use face masks. In case 2, 90% of the high risk population used face masks. These assumptions are made based on the fact that so many countries worldwide are beginning to drop or lessen their mask mandates. The simulations of both cases were implemented using the values in Table 3 and the resulting graphical plots are presented in Figures 6 and 7, respectively.

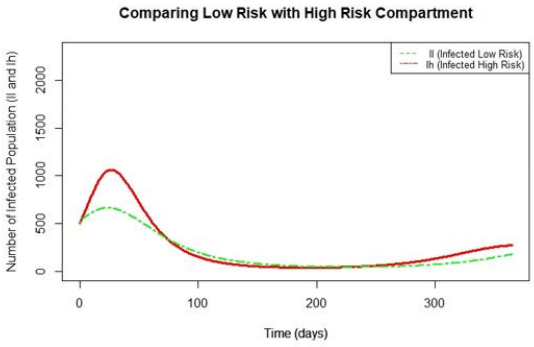

Figure 6. The graphical representation of Scenario 4, Case 1: No use of face mask and two vaccine doses in the low risk population while 50% use of face masks by individuals in high risk population.

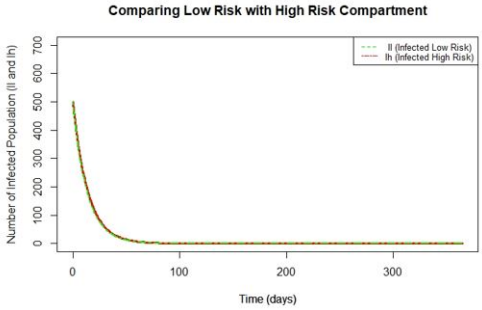

Figure 7. The graphical representation of Scenario 4, Case 2: 50% use of face mask and two vaccine doses in the low risk population while 90% use of face masks by individuals in high risk population.

The plot in Figure 6 indicates that even though everyone in the low risk population has received 3 vaccine shot doses, there are still infections arising in the population with ERN as $R_{HL} = 0.985 < 1$. However, these infections will likely not lead to hospitalizations. There is no vaccine that provides a 100% protection for any disease. This does not imply that the COVID-19 vaccines are not effective, it simply indicates that not everyone who received the vaccines in the low risk population has 100 percent protection. In Figure 7, the plot shows that there are fewer infections which will arise compared to Figure 6 with ERN as $R_{HL} = 0.275 < 1$. The reason for fewer infections is the fact that even though mask mandate has been dropped, half of the population are not just ready yet to stop wearing masks because they feel safer and secured when they use masks.

4.3. Introduction of vaccination in the high risk compartment

To examine the effects for introducing vaccination into a high risk population, different vaccination intakes were tested. Our assumption for this simulation is that vaccination replaces face mask (α_H). Thus $\varphi_L = \alpha_H$. As earlier defined in the Table 1, φ_L denotes the use of vaccination and the values for different vaccination intake is provided in Section 4.1. For this simulation, the first, second and third vaccination intakes, respectively, were used together with other parameter values in Table 3 for the simulation. The obtained result from the simulation is presented in Figure 8.

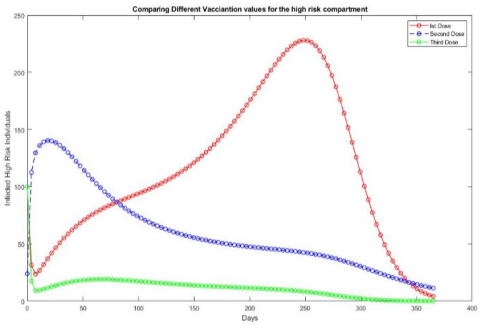

Figure 8. Assessing the effects of introducing vaccine in the high risk population. Three vaccine doses were considered where $\alpha_H = 0.51, 0.879$ and 0.95 for the first, second, and third doses, respectively.

Overall, three doses of vaccine intakes will result into less infected individual compared to two and one doses, respectively. The obtained result also reaffirms the idea that getting two or more vaccination doses contributes favourable in reducing the number of COVID-19 cases and deaths. Lastly, though this study has mostly shown the benefits of vaccination, according to the New York times (2022) [29] only 70.3% of the global population have received at least one dose as of October 10, 2022. Thus, there is still a need for the Thai government to continuously monitor the number of cases to build a strong system of prevention and control in Thailand to keep the tourism sector working.

5. Conclusions and recommendations

In this study, we formulate a model to understand the interactions that exists within two populations: low risk and high risk populations and the preventive measures adopted by the respective populations. The formulated model was modified from Asempapa et al. [16] by adding vaccination as a preventive measure for the low risk population. The results have shown that vaccination is vital in reducing COVID-19 pandemic in Thailand. The Thai government has recently intensified efforts to achieve herd immunity through an efficient vaccination program. Initial shortage of vaccine supply together with a lack of vaccine options have slowed down this process. However, this has been improved. Thailand has opened its borders to foreign tourists on the 1st of July, 2022. Thus, it is important for individuals in Thailand to complete their full immunization to achieve herd immunity for COVID-19. Attaining herd immunity will go a long way in protecting individuals classified as having high risk and other individuals who are susceptible or vulnerable to the infection.

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Conflict of interest

There are no conflicts of interest as declared by the authors.

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