Mathematical Biosciences and Engineering

http://www.aimspress.com/journal/mbe

MBE, 20(9): 16114–16130.
DOI: 10.3934/mbe.2023719
Received: 27 May 2023
Revised: 11 July 2023
Accepted: 18 July 2023
Published: 8 August 2023

Research article

Synergistic effects of vaccination and virus testing on the transmission of an infectious disease

Lili Han[1], **Mingfeng He**[1,2], **Xiao He** [3,*] **and Qiuhui Pan**[1,2]

[1] School of Mathematical Sciences, Dalian University of Technology, Dalian 116024, China
[2] School of Innovation and Entrepreneurship, Dalian University of Technology, Dalian 116024, China
[3] Department of Mathematics, Dalian Minzu University, Dalian 116600, China

* **Correspondence:** Email: xiaohemath@163.com; Tel: +8618940935263.

Abstract: Under the background that asymptomatic virus carriers have infectivity for an infectious disease, we establish a difference equations model with vaccination and virus testing in this paper. Assuming that the vaccine is 100% effective for susceptible people but cannot stop the infectivity of asymptomatic virus carriers, we study how to combine vaccination and virus testing at the beginning of an epidemic to effectively block the spread of infectious disease in different population sizes. By considering the daily processing capacity of the vaccine and daily proportion of testing, the corresponding numerical simulation results are obtained. It is shown that when vaccine availability and virus testing capacity are insufficient, a reasonable combination of the above two measures can slow down or even block the spread of infectious disease. Single virus testing or vaccination can also block the spread of infectious disease, but this requires a lot of manpower, material and financial resources. When the daily proportion of virus testing is fixed, the ratio of the minimum daily processing capacity of vaccines used to block the spread of infectious disease to the corresponding population size is rather stable. It demonstrates that effective protective measures of the same infectious disease in countries and regions with different population sizes can be used as a reference. These results also provide a certain reference for decision makers on how to coordinate vaccines and virus testing resources to curb the spread of such an infectious disease in a certain population size.

Keywords: difference equations model; population size; synergistic effects; vaccination; virus testing

1. Introduction

Infectious diseases have always been the main cause of death from diseases all over the world and they bring enormous suffering to millions of families. Due to the absence of effective specific drug

therapies or vaccines for many infectious diseases, no country is safe and can afford to ignore their threat when they strike. Therefore, how to prevent the outbreaks of infectious diseases has become a challenging topic in public health. To address this challenge, medical researchers are continuously working to develop a variety of targeted vaccines and antibiotics [1, 2]. Meanwhile, mathematicians and epidemiologists have built various epidemic models to study the dynamic behavior of infectious disease transmission [3–5].

As is known, when an infectious disease breaks out, personal response also has a significant impact on its spread. During the outbreak of SARS in 2003, many people spontaneously wore masks and some schools were temporarily closed to avoid further development of the epidemic [6]. With the rapid development of medical technology, vaccination has become the most effective public health intervention to prevent the spread of infectious disease, reduce the incidence rate and mortality, and mitigate its secondary consequences [7]. Chao et al. [8] established a mathematical model of cholera transmission and evaluated the effects of different vaccination strategies. Their results showed that in the case of limited vaccine quantities, vaccines are most effective when concentrated in high-risk areas. Li et al. [9] established an SIS epidemic ODE model with a constant vaccination rate, and they concluded that it was necessary to evaluate the efficacy of vaccines to prevent and control the spread of infectious diseases. Moneim [10] studied the spread of some infectious diseases in children by establishing a model with a non-constant vaccination rate. The results indicated that inoculating with appropriate doses of the vaccine before the peak of severe infection could prevent a new wave of the epidemic. Li and Li [11] studied the dynamic behavior of infectious diseases for a complex network and obtained that incomplete vaccination would seriously hinder the prevention and control of infectious diseases. Tang et al. [12] constructed a COVID-19 dynamics model by taking into account the epidemiological characteristics of individuals, public health interventions, population vaccine immunity and strain variation. Their conclusion showed that mass vaccination is effective only if the vaccine efficacy is sufficiently strong. Some studies also considered the impact of vaccination on the spread of infectious disease [13–15], as well as the impact of quarantine on the prevention and control of infectious disease [16–18].

Based on the time series data of cumulative cases in Ontario, Canada, Tang et al. [19] established an ODE model and concluded that it is necessary to strengthen social distancing, personal protection, contact tracing and the intensity of quarantine to avoid the rebound of the epidemic. Feng et al. [20] constructed a COVID-19 epidemic model with media coverage and quarantine, which showed that people still needed to wear masks, avoid contact, reduce outings and take corresponding quarantine measures to mitigate the spread of the virus. Villela [21] established an infectious disease model with imperfect detection (false positive and false negative in the detection results). By considering the specificity and sensitivity of the detection, the corresponding results suggested that the epidemic would not break out at a high detection rate. Moore et al. [22] and Steyn et al. [23] explored the corresponding models and concluded that it is impossible for countries to implement vaccination alone to achieve herd immunity, so other public health measures need to be coordinated to achieve this goal. Foy et al. [24] established an extended SEIR model with a social contact matrix and age structure, and they concluded that the optimal vaccine distribution strategy is determined by the characteristics of the vaccine, the intensity of non-pharmaceutical interventions and targeted specific goals. Rella et al. [25] built a modified SIR model by considering the emergence of vaccine resistant strains and various risk factors, and they concluded that when most people get vaccinated, reducing the intensity

of non-pharmaceutical interventions would lead to a significant increase in drug-resistant strains.

Notably, for such infectious diseases, due to the infectivity of the virus during its incubation period, asymptomatic virus carriers who have not been tested in time may be vaccinated, which pose unprecedented challenges to epidemic prevention and control. In addition, the speeds of vaccination and virus testing will be greatly limited due to the production capacity and limited staffing. Therefore, based on the premise that the vaccine is 100% effective for susceptible people but has no effect on the infectivity of asymptomatic virus carriers, we study how to match the daily processing capacity of vaccines with a daily proportion of testing when an epidemic begins, in order to effectively block the spread of infectious disease in different population sizes.

The article is organized as follows. In Section 2, a difference equation model with vaccination and virus testing is proposed. We use the next generation matrix method to obtain the basic and effective reproduction numbers corresponding to the transmission dynamics model, as well as give the mathematical analysis of the model in Section 3. The main numerical simulation results are in Section 4. Section 5 summarizes the main conclusions.

2. Model

In order to establish the difference equation model describing the spread of such an epidemic, we have divided the population into five categories, namely, susceptible (S); asymptomatic virus carriers (E): people who are asymptomatic but infectious in the latent period; vaccinated asymptomatic virus carriers (E_v); symptomatic infected (I): people who have been infected and have symptoms but have not yet been quarantined; and removed (R): containing the vaccinated susceptible, quarantined and isolated, recovered, dead. In order to make our mathematical model more realistic and easy to understand, we have the following assumptions.

1) There is no injection of susceptible people in any part of the process, the population is evenly mixed and the contact rate for people outside of the hospital is the same.

2) The probability of infection in the susceptible population has nothing to do with age or gender. We only consider contact infection and ignore the immunity losses, the possibility of vaccine breakthrough infections and reinfection in the short term.

3) Considering the full and reasonable utilization of epidemic prevention resources and the synergy between prevention and control measures, it is assumed that the vaccinated individuals will no longer be tested.

4) The vaccine is 100% effective for susceptible people, but has no effect on the infectivity of asymptomatic virus carriers [26, 27].

5) Daily vaccination and testing are carried out successively. Because the susceptible and asymptomatic virus carriers are identical in appearance, they are both likely to be vaccinated and tested. Let the daily processing capacity of vaccines for the susceptible and the asymptomatic virus carriers be q_1 and q_2, respectively. After vaccination, the vaccinated susceptible individuals will transfer to R and the asymptomatic virus carriers who are vaccinated will transfer to E_v. The aim of this paper is to consider the synergies of vaccination and testing, so only the remaining S and E after vaccination were tested. Let the daily proportion of testing be γ. After testing, S is

directly returned to the compartment S. E is isolated for treatment, and thus transfers to R. I is not involved in the testing.

6) Since the virus carriers in the incubation period are contagious for this infectious disease, the infection source belongs to E, E_v and I. The probability of transmission per contact between I and the susceptible group is denoted by β. The ratio of infection rate for the latent individuals (E or E_v) to the infection rate for I is η ($0 < \eta < 1$) [28,29]. The infected individual S transfers to E.

7) The incubation period of this infectious disease is denoted by $\frac{1}{\alpha}$. After onset, both E and E_v transfer to I. I may be treated in isolation, undergo self-recovery or die. Either way, I will eventually move to the compartment R at the rate of v.

The transformation relationships for various populations are shown in Figure 1.

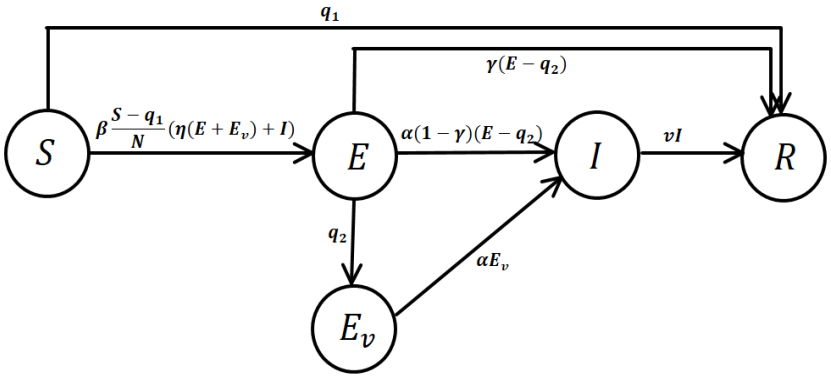

Figure 1. Diagram of transformation relationships for various compartments.

Based on Figure 1, we develop a difference equation model, as shown below.

$$\begin{cases} S(t+1) = S(t) - q_1 - \beta\dfrac{\eta(E(t)+E_v(t))+I(t)}{N}(S(t)-q_1), \\ E(t+1) = \beta\dfrac{\eta(E(t)+E_v(t))+I(t)}{N}(S(t)-q_1) + (1-\gamma)(1-\alpha)(E(t)-q_1), \\ E_v(t+1) = E_v(t) + q_2 - \alpha E_v(t), \\ I(t+1) = I(t) + \alpha(1-\gamma)(E(t)-q_2) + \alpha E_v(t) - vI(t), \\ R(t+1) = R(t) + q_1 + \gamma(E(t)-q_2) + vI(t). \end{cases} \tag{2.1}$$

The initial values of (2.1) are

$$S(0) = S^0,\ E(0) = E^0,\ E_v(0) = E_v^0,\ I(0) = I^0,\ R(0) = R^0. \tag{2.2}$$

Limited by vaccine production capacity and vaccination efficiency, the daily processing capacity of a vaccine is restricted to Q. So the daily processing capacity of a vaccine for the susceptible group is q_1=min$\{\frac{S(t)Q}{S(t)+E(t)}, S(t)\}$, and the daily processing capacity of a vaccine for the asymptomatic virus carriers is q_2=min$\{\frac{E(t)Q}{S(t)+E(t)}, E(t)\}$.

The values of the parameters in (2.1) are summarized in Table 1, quoted and estimated based on the epidemic data of SARS-CoV-2 infection.

Table 1. Descriptions, range or estimated values and the sources of parameters.

Parameters	Descriptions	Range or Estimated values	Sources
β	The probability of being infected when S contacts with I	0.6	[30]
η	The ratio of the infection rate for the latent to the infection rate for I	0.4	[28,29]
$\frac{1}{\alpha}$	The incubation period of the infectious disease	4	[31,32]
γ	The daily proportion of testing	$[0,1]$	Variable
v	Removal rate of I	0.3	Estimated
Q	The daily vaccine processing capacity	$[0,N]$	Variable
q_1	The daily processing capacity of vaccine for the susceptible group		
q_2	The daily processing capacity of vaccine for the asymptomatic virus carriers		
N	Population size		Variable

3. Model analysis

Based on q_1, q_2, model (2.1) can be divided to two stages. The first stage is the period when $0 \le Q < S(t) + E(t)$, and the second stage is the period when $Q \ge S(t) + E(t)$.

1) In the first stage, i.e., when $0 \le Q < S(t) + E(t)$, the equivalent differential equations of (2.1) are

$$\begin{cases} \dot{S} = -S\dfrac{Q}{S+E} - \beta S\dfrac{\eta(E+E_v)+I}{N}(1-\dfrac{Q}{S+E}), \\ \dot{E} = \beta S\dfrac{\eta(E+E_v)+I}{N}(1-\dfrac{Q}{S+E}) - (\alpha+\gamma-\alpha\gamma)E(1-\dfrac{Q}{S+E}) - E\dfrac{Q}{S+E}, \\ \dot{E}_v = E\dfrac{Q}{S+E} - \alpha E_v, \\ \dot{I} = \alpha(1-\gamma)E(1-\dfrac{Q}{S+E}) + \alpha E_v - vI, \\ \dot{R} = S\dfrac{Q}{S+E} + \gamma E(1-\dfrac{Q}{S+E}) + vI. \end{cases} \tag{3.1}$$

The corresponding initial values are the same as (2.2).

2) In the second stage, i.e., when $Q \ge S(t) + E(t)$, the corresponding difference equations of (2.1) are

$$\begin{cases} S(t+1) = 0, \\ E(t+1) = 0, \\ E_v(t+1) = E_v(t) + E(t) - \alpha E_v(t), \\ I(t+1) = I(t) + \alpha E_v(t) - vI(t), \\ R(t+1) = R(t) + S(t) + vI(t). \end{cases} \tag{3.2}$$

3.1. Boundedness and positivity of solutions

Suppose that the initial datum of model (3.1) satisfies

$$S^0 > 0,\ E^0, E_v^0, I^0, R^0 \ge 0,\ S^0 + E^0 + E_v^0 + I^0 + R^0 = N(0). \tag{3.3}$$

Let

$$\Omega = \Big\{(S(t), E(t), E_v(t), I(t), R(t)) \in \mathbb{R}_+^5 : N(t) = S(t) + E(t) + E_v(t) + I(t) + R(t) \equiv N(0),\ S(t) + E(t) > 0\Big\}.$$

The existence and uniqueness of the solution of (3.1) could be obtained via a procedure similar to that of Theorem 1 in [33], so we omit the details. Now, we give the boundedness and positivity of the solution of (3.1).

Lemma 3.1. *Let $X(t) = (S(t), E(t), E_v(t), I(t), R(t))$ be a solution of (3.1). Then it is non-negative and bounded. Besides, under condition (3.3), the feasible biological region given by Ω is positively invariant.*

Proof. Since $0 \le Q < S(t) + E(t)$, $0 \le \dfrac{Q}{S(t)+E(t)} < 1$. Then we have

$$0 < 1 - \frac{Q}{S(t)+E(t)} \le 1. \tag{3.4}$$

From the first equation of (3.1), we know that

$$\frac{dS}{S} = \Big(- \frac{Q}{S+E} - \beta \frac{\eta(E+E_v)+I}{N}\Big(1 - \frac{Q}{S+E}\Big)\Big)dt.$$

So,

$$S(t) = S(0)\exp\Big(- \int_0^t \Big(\frac{Q}{S(r)+E(r)} + \beta \frac{\eta(E(r)+E_v(r))+I(r)}{N}(1 - \frac{Q}{S(r)+E(r)})\Big)dr\Big).$$

Therefore, $\forall\ t > 0$; we have

$$S(t) > 0. \tag{3.5}$$

1) For the case $E^0 > 0$, $E_v^0 \ge 0$ and $I^0 \ge 0$, assume that there exists $t_1 > 0$ such that $E(t) > 0$ for $t < t_1$ and $E(t_1) = 0$. It follows from (3.5) and the third equation of (3.1) with some simple calculations that

$$E_v(t) = e^{-\alpha t}\Big(\int_0^t e^{\alpha s} \frac{E(s)Q}{S(s)+E(s)} ds + E_v^0\Big) > 0,\ \forall\ 0 < t \le t_1. \tag{3.6}$$

It follows from (3.5), (3.6) and the fourth equation of (3.1) that

$$I(t) = e^{-\nu t}\Big(\int_0^t e^{\nu s}\Big(\alpha(1-\gamma)(1 - \frac{Q}{S+E})E + \alpha E_v\Big)ds + I^0\Big) > 0,\ \forall\ 0 < t \le t_1. \tag{3.7}$$

From the second equation of (3.1) and (3.4), we know that

$$\begin{aligned} \dot{E} + (\alpha + \gamma - \alpha\gamma)E &= \beta S \frac{\eta(E+E_v)+I}{N}\Big(1 - \frac{Q}{S+E}\Big) - (1-\alpha)(1-\gamma)E\frac{Q}{S+E} \\ &> \beta S \frac{\eta(E+E_v)+I}{N}\Big(1 - \frac{Q}{S+E}\Big) - (1-\alpha)(1-\gamma)E. \end{aligned}$$

And thus,

$$\dot{E} + E > \beta S \frac{\eta(E+E_v)+I}{N}\Big(1 - \frac{Q}{S+E}\Big),$$

which implies that

$$(e^t E)' > e^t \beta S \frac{\eta(E + E_v) + I}{N}\Big(1 - \frac{Q}{S + E}\Big) > 0, \ \forall\, 0 < t \le t_1. \tag{3.8}$$

Then $E(t_1) > e^{-t_1} E^0 > 0$, which is in contradiction with $E(t_1) = 0$. Finally, we have

$$E(t) > 0 \ \text{ for } t > 0. \tag{3.9}$$

From (3.6) and (3.7), it is easy to check that

$$E_v(t), \ I(t) > 0 \ \text{ for } t > 0. \tag{3.10}$$

From (3.5), (3.9), (3.10) and the fifth equation of (3.1), we arrive at

$$R(t) = R^0 + \int_0^t \Big(\frac{S\,Q}{S + E} + \gamma E\Big(1 - \frac{Q}{S + E}\Big) + vI\Big)dr > 0, \ \forall\, t > 0. \tag{3.11}$$

2) For the case $E^0 = 0, \ E_v^0 > 0$ and $I^0 \ge 0$ or $E^0 = 0, \ E_v^0 \ge 0$ and $I^0 > 0$, $\eta(E^0 + E_v^0) + I^0 > 0$. Assume that there exists $t_1 > 0$ such that $\eta(E(t_1)+E_v(t_1))+I(t_1) = 0$, and $\eta(E(t)+E_v(t))+I(t) > 0$ for $t < t_1$. Using (3.8) again to have that $E(t) > E(0)e^{-t} = 0$ for all $0 < t \le t_1$, which together with (3.6) and (3.7) also implies that $E_v(t), I(t) > 0$. This is in contradiction with $\eta(E(t_1) + E_v(t_1)) + I(t_1) = 0$. So, we obtain that $\eta(E(t) + E_v(t)) + I(t) > 0$ for all $t > 0$. Thus, $E(t) > 0$ by (3.8), $E_v(t) > 0$ by (3.6), $I(t) > 0$ by (3.7), and $R(t) > 0$ by (3.11), respectively.

3) For the case $E^0 = 0, \ E_v^0 = 0$ and $I^0 = 0$, the solution of (3.1) is $(S^0 - Qt, 0, 0, 0, R^0 + Qt)$.

To sum up, the solution of (3.1) is non-negative.

Adding all of the equations of (3.1) to have that $\dfrac{dN(t)}{dt} = 0$, which means that the conservation law is true in the system. Then, $0 \le S(t), E(t), E_v(t), I(t), R(t) \le N(t) = N(0)$ due to their own respective positivity. And thus, the solution of (3.1) is bounded. In addition, the feasible biological region given by Ω is positively invariant. □

The initial datum of (3.2) comprises the values of $S(t), E(t), E_v(t), I(t), R(t)$ at the end of the first stage. By Lemma (3.1), these values are non-negative. We add all of the equations of (3.2) to obtain $S(t+1)+E(t+1)+E_v(t+1)+I(t+1)+R(t+1) = S(t)+E(t)+E_v(t)+I(t)+R(t) \equiv N(0)$. Thus, the solution of (3.2) is also non-negative and bounded. Now we know that the solution of (2.1) is non-negative and bounded.

3.2. Basic reproduction number and control reproduction number

The study of infectious diseases cannot be separated from the discussion on the basic reproduction number without any measures and the control reproduction number with preventing and controlling measures. The basic reproduction number $\mathscr{R}_0$ is one of the core indicators in infectious disease research, as it represents the number of people infected by a single virus carrier in a completely susceptible population during the infection period without any intervention. Usually, if $\mathscr{R}_0 > 1$, the infectious disease will spread. Otherwise, the infectious disease will die out. Based on the

transmission characteristics of infectious diseases, a differential equation model is established, and the spectral radius of the next generation matrix at the disease-free equilibrium (DFE) is obtained to get the basic reproduction number $\mathscr{R}_0$ [34, 35]. The control reproduction number $\mathscr{R}_c$ is used to characterize the effectiveness of the disease control measures. The method of solving $\mathscr{R}_c$ is given in [35].

The DFE of model (3.1) in the absence of any control measures, i.e., $Q = 0$ and $\gamma = 0$, is $P_0 = (N, 0, 0, 0, 0)$. Recalling that infected compartments contain E, E_v and I, we define $X = (E, E_v, I)^T$. Let the non-negative matrix $\mathscr{F}$ be the number of new infections in infected compartments per unit time, and let the non-singular M-matrix $\mathscr{V}$ be the number of transitions from infected compartments to other compartments per unit time. Then for model (3.1) without any measures,

$$\mathscr{F}(X) = \begin{bmatrix} \beta\frac{S}{N}(\eta(E + E_v) + I) \\ 0 \\ 0 \end{bmatrix}, \quad \mathscr{V}(X) = \begin{bmatrix} \alpha E \\ \alpha E_v \\ -\alpha(E + E_v) + vI \end{bmatrix}.$$

Let F and V be the Jacobian matrices of $\mathscr{F}$ and $\mathscr{V}$ at P_0, respectively. We have

$$F = \begin{bmatrix} \beta\eta & \beta\eta & \beta \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} \alpha & 0 & 0 \\ 0 & \alpha & 0 \\ -\alpha & -\alpha & v \end{bmatrix}.$$

Therefore, the basic reproduction number of our model is

$$\mathscr{R}_0 = \rho(FV^{-1}) = \beta\left(\frac{\eta}{\alpha} + \frac{1}{v}\right), \tag{3.12}$$

where $\rho(FV^{-1})$ is the spectral radius of the next generation matrix FV^{-1}.

$\mathscr{R}_c$ refers to the number of people that an infected person can infect during the infection period when taking control measures [35]. It is well known that the outbreaks can be prevented if $\mathscr{R}_c$ is below the threshold of 1. Otherwise, the greater the value of $\mathscr{R}_c$, the greater the exponential growth rate of the outbreak. The outbreaks cannot be prevented. To obtain the control reproduction number $\mathscr{R}_c$, the non-negative matrix $\mathscr{F}'$ and the non-singular M-matrix $\mathscr{V}'$ are

$$\mathscr{F}'(X) = \begin{bmatrix} \beta S(1 - \frac{Q}{S+E})\frac{\eta(E+E_v)+I}{N} \\ 0 \\ 0 \end{bmatrix}, \quad \mathscr{V}'(X) = \begin{bmatrix} (\alpha + \gamma - \alpha\gamma)E(1 - \frac{Q}{S+E}) + \frac{EQ}{S+E} \\ \alpha E_v - \frac{EQ}{S+E} \\ -\alpha(1-\gamma)E(1 - \frac{Q}{S+E}) - \alpha E_v + vI \end{bmatrix}.$$

When $Q = 0$, the DFE of model (3.1) is also P_0. Similar to $\mathscr{R}_0$, we have

$$\mathscr{R}_c = \beta\left(\frac{\eta}{\alpha + \gamma - \alpha\gamma} + \frac{\alpha(1-\gamma)}{v(\alpha + \gamma - \alpha\gamma)}\right).$$

4. Results and discussion

According to the method of [30] and the actual epidemic data of Wuhan [36], we chose $\beta = 0.6$. We also applied $\eta = 0.4$ according to [28, 29] and set $\frac{1}{\alpha} = 4$ according to [31, 32]. The initial values of the numerical simulations are

$$S(0) = N,\ E(0) = 1,\ E_v(0) = 0,\ I(0) = 0,\ R(0) = 0.$$

In the absence of any measures, we have that $\mathscr{R}_0 = 2.96 > 1$ according to (3.12). Since preventive measures can reduce the reproduction number, the implementation of prevention and control measures is particularly important. To achieve this goal, we can use $\mathscr{R}_c \leq 1$ to obtain the intensity of the implementation measures.

Let $\mathscr{R}_c \leq 1$. We have

$$\gamma \geq \frac{-\alpha + \beta\eta + \frac{\beta\alpha}{v}}{1 - \alpha + \frac{\beta\alpha}{v}} = 0.392. \tag{4.1}$$

Therefore, as long as the daily proportion of testing satisfies (4.1), only virus testing measures can block the spread of such infectious diseases.

The minimum value of daily processing capacity of the vaccine and the minimum daily testing proportion required to prevent the spread of infectious disease are denoted by Q_{min} and γ_{min}, respectively.

Normally, at the beginning of an infectious disease, vaccine production capacity and staffing are both insufficient. The speed of vaccination and virus testing cannot keep up with demand. Under the assumption that the ratio of the population size N to the daily processing capacity of vaccine Q is 400, we investigated the changes in the peak values of asymptomatic virus carriers E, asymptomatic virus carriers who have been vaccinated E_v, symptomatic individuals I and the duration of the epidemic with the daily proportion of testing γ. The numerical results are shown in Figure 2.

From Figure 2(a)–(c), it can be seen that as γ increases, the peak values of E, E_v and I decrease. The peak values of E, E_v and I increase gradually with the increase of N. According to Figure 2(d), with the increase of γ, the duration of the epidemic gradually increases, and then rapidly decreases, until it reaches 0. The larger the value of N, the longer the duration of the epidemic and the larger the peak of the duration of the epidemic, but the corresponding proportion of daily testing is smaller. When $\gamma > 0.26$ and $N = 2\times10^6,\ 4\times10^6,\ 8\times10^6,\ 1.6\times10^7$, respectively, the duration of the epidemic is the same. Assume that $\frac{Q}{N} = \frac{1}{400}$. If $\gamma = 0$, vaccination is ineffective in stopping the spread of infectious disease. But if $\gamma \geq 0.33$, a combination of the daily proportion of testing and the daily processing capacity of the vaccine can effectively block the spread of infectious disease. This requires a more reasonable vaccine distribution strategy and high speeds of vaccination and virus testing. Besides, as shown in Figure 2, for different values of N, when $\frac{Q}{N}$ is the same, there exists almost the same γ_{min}.

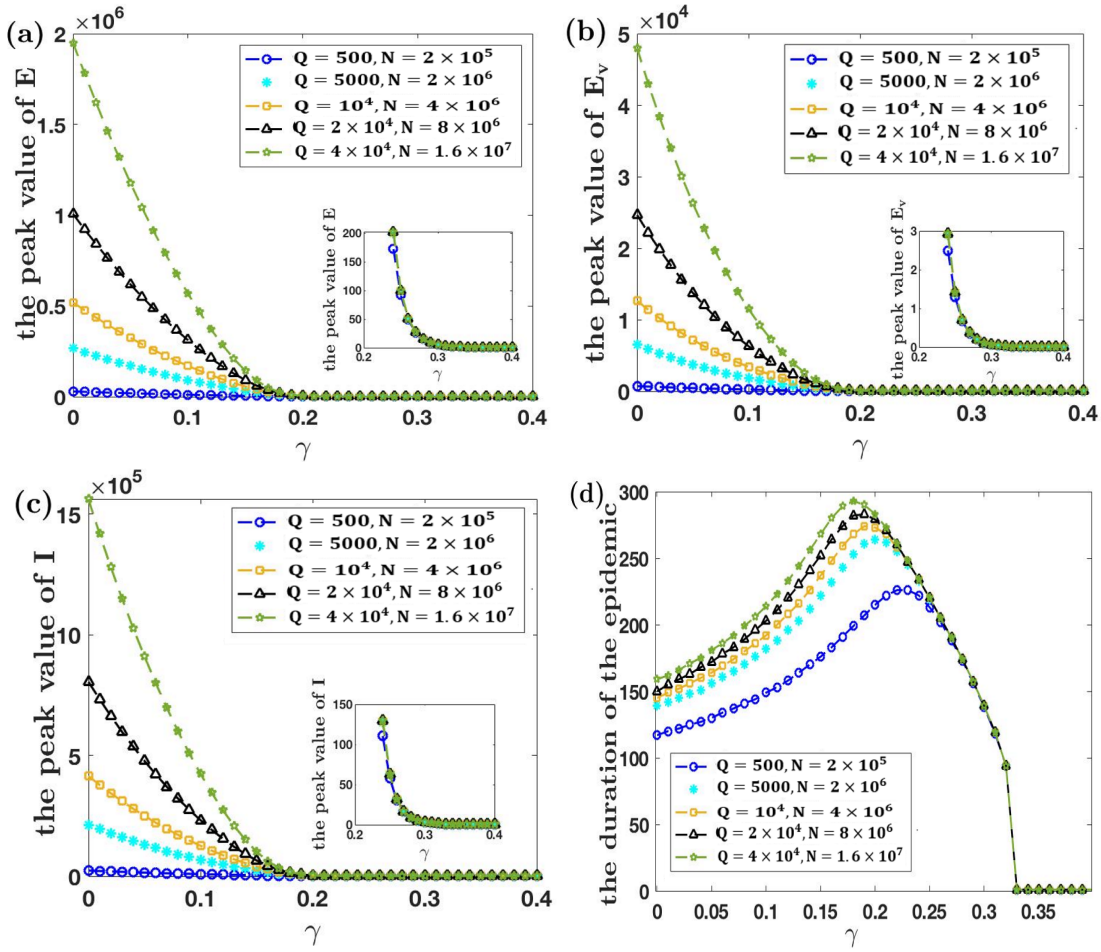

Figure 2. When $\frac{Q}{N} = \frac{1}{400}$, the changes of peak values of E, E_v, I and the duration of the epidemic with γ .

In the process of the transmission of an infectious disease, vaccine supplies will gradually increase. Next, we consider the cases $N = 4\times10^6$ and $Q = 0,\ 10^4,\ 1.5\times10^4,\ 2\times10^4,\ 2.5\times10^4,\ 5\times10^4,\ 10^5,\ 4\times10^5$, respectively. The changes of the peak values of E, E_v and I and the duration of the epidemic with γ are shown in Figure 3.

From Figure 3(a)–(c), as γ increases, the peak values of E, E_v and I decrease. The larger the value of Q, the smaller the peak values of E, E_v and I. When $Q = 2\times10^4,\ 2.5\times10^4,\ 5\times10^4,\ 10^5$, respectively, the peak value of E_v decreases with the increase of Q. There exists γ^{**} such that when $\gamma < \gamma^{**}$, the peak value of E_v is higher for $Q = 1.5\times10^4$ than that for $Q = 10^4$. But when $\gamma > \gamma^{**}$, the peak value of E_v is smaller for $Q = 1.5\times10^4$ than that for $Q = 10^4$. Therefore, the peak value of E_v is non-monotonic with respect to Q. When $Q = 4\times10^5$ and $\gamma = 0$, since the peak of infection source is 0, the infectious disease does not spread. When $\gamma = 0.4$, the spread of infectious disease can be prevented by even testing alone. These results indicate that a single prevention and control measure can prevent the spread of infectious disease, but it requires a higher vaccine production capacity and higher speeds of vaccination and virus testing.

As shown in Figure 3(d), in the case of $Q = 0$, the duration of the epidemic increases slowly first and then rapidly. This resulted in a prolonged epidemic with a low incidence of the disease. When $\gamma = 0.4$,

the duration of the epidemic is 0, and the epidemic dies out. When $Q = 10^4,\ 1.5\times10^4,\ 2\times10^4,\ 2.5\times10^4$, respectively, the duration of the epidemic increases first and then decreases to 0 with the increase of γ. The smaller the value of Q, the larger the peak of the duration of the epidemic and the value of γ corresponding to the peak. Before the peak, the smaller the value of Q, the shorter the duration of the epidemic. But after the peak, the lager the value of Q, the shorter the duration of the epidemic. When $Q = 5\times10^4,\ 10^5$, the duration of the epidemic decreases slowly first and then rapidly to decreases 0. When vaccination and virus testing are combined, with the increase of Q, γ_{min} decreases.

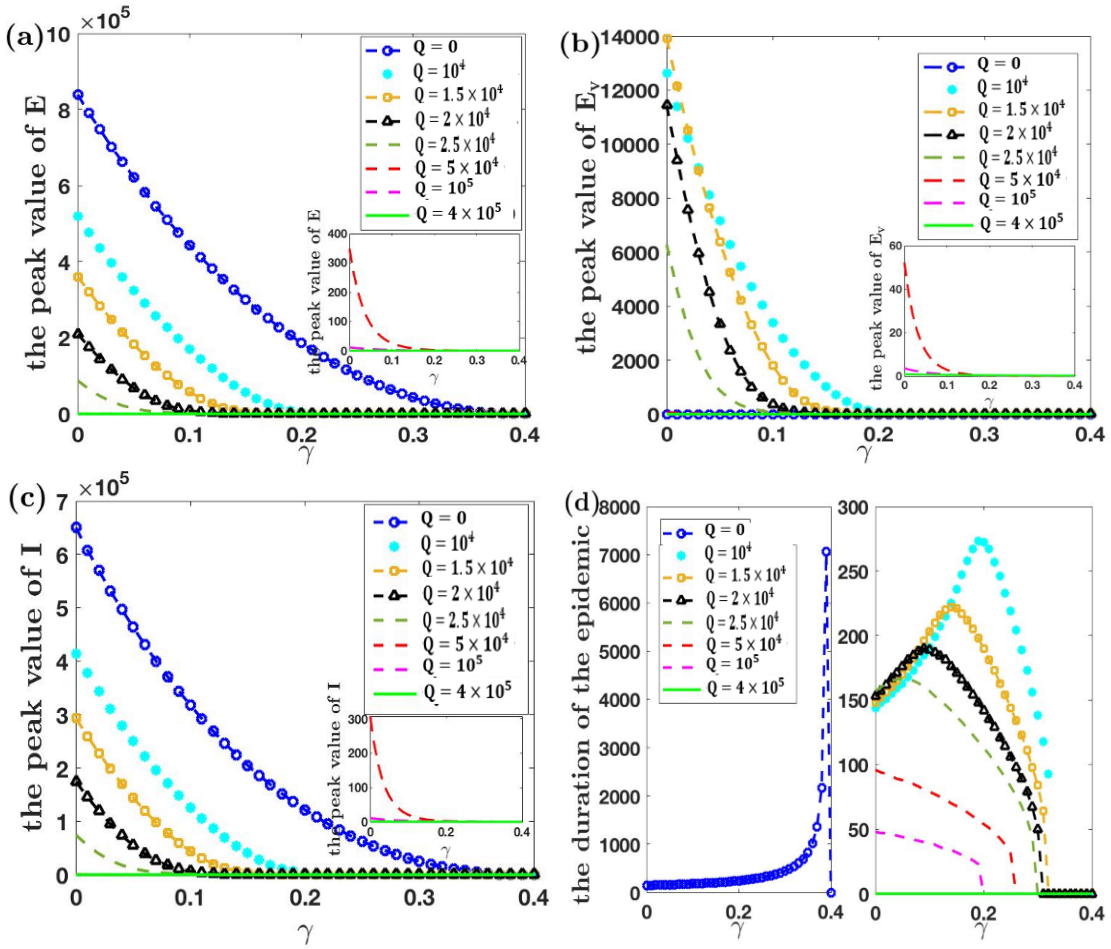

Figure 3. Given $N = 4\times10^6$ and $Q = 0,\ 10^4,\ 1.5\times10^4,\ 2\times10^4,\ 2.5\times10^4,\ 5\times10^4,\ 10^5,\ 4\times10^5$, respectively, we show the changes of peak values of E, E_v, I and the duration of the epidemic with γ.

When the efficacy and immunization coverage rate for vaccines among the population are high enough, the infectious disease will not spread even if other intervention measures are reduced. However, before forming a high-level immunity barrier, if only one intervention measure is implemented, the manpower, material and financial resources required for epidemic prevention and control will be great. Therefore, two or more protective measures should be combined to achieve effective epidemic prevention and control. For a γ that is fixed, we study the changes of Q_{min} for different values of N to prevent the spread of infectious disease. The results are shown in Figure 4.

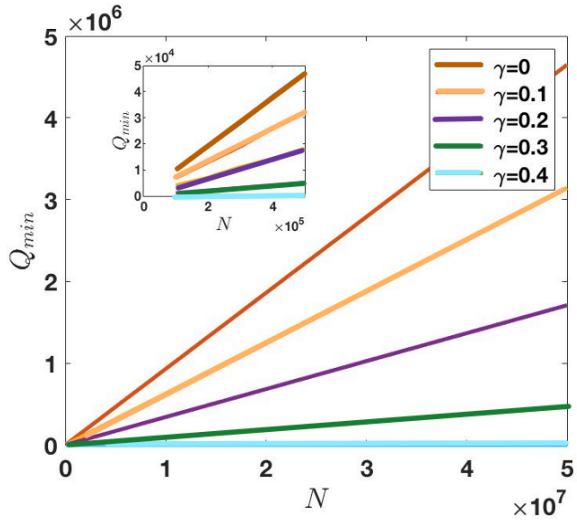

Figure 4. Given $\gamma = 0,\ 0.1,\ 0.2,\ 0.3,\ 0.4$ and $N \in [10^5, 5 \times 10^7]$, we show the changes of Q_{min}.

As seen from Figure 4, when $\gamma = 0,\ 0.1,\ 0.2,\ 0.3$, with the increase of N, Q_{min} increases. When N is fixed, with the increase of γ, Q_{min} gradually reduces. When $\gamma = 0.4$, the spread of an infectious disease can be prevented without vaccination. This means that the increase of γ can effectively prevent the spread of the infectious disease and greatly alleviate the pressure of vaccination. Hence, when the infectious disease begins to transmit, an appropriate daily proportion of testing can make it disappear. Meanwhile, if the required daily proportion of testing cannot be achieved, the transmission of the infectious disease can also be effectively prevented by coupling it with an appropriate daily vaccination.

Due to the limited vaccine production capacity and daily vaccination rate, it is difficult to achieve population-wide vaccination in a short time. The virus testing is particular important. Now we discuss the correlations between N and γ_{min}, which are shown in Figure 5.

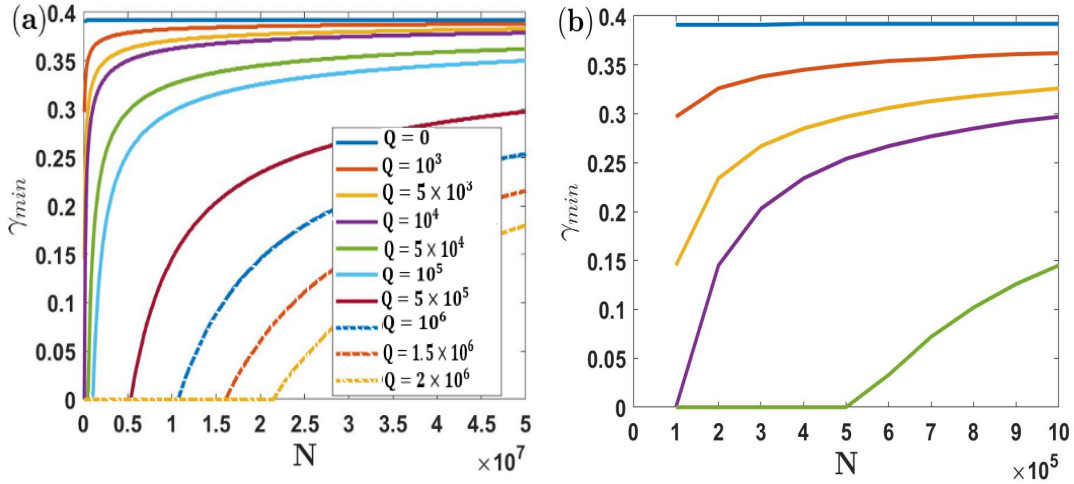

Figure 5. The changes of γ_{min} with N. (a) $Q = 0,\ 10^3,\ 5 \times 10^3,\ 10^4,\ 5 \times 10^4,\ 10^5,\ 5 \times 10^5,\ 10^6,\ 1.5 \times 10^6,\ 2 \times 10^6$, respectively, $N \in [10^5,\ 5 \times 10^7]$; (b) $Q = 0,\ 10^3,\ 5 \times 10^3,\ 10^4,\ 5 \times 10^4$, respectively, $N \in [10^5,\ 10^6]$.

As shown in Figure 5(a), when $Q = 0$ and $\gamma_{min} = 0.392$, the infectious disease cannot spread, which is consistent with (4.1). When $Q = 10^3$, 5×10^3, 10^4, respectively, with the increase of N, γ_{min} increases rapidly, and then slowly increases until it becomes stable. When $Q = 5 \times 10^4$, 10^5, 5×10^5, respectively, γ_{min} stays at 0 first, increases rapidly and then slowly. When 10^6, 1.5×10^6, 2×10^6, respectively, γ_{min} stays at 0 first, and then increases slowly. When $Q \geq 10^4$, $\gamma = 0$ and the infectious disease is effectively curbed, the corresponding maximum population sizes are 10^5, 5×10^5, 10^6, 5.4×10^6,1.08×10^7, 1.62×10^7, 2.16×10^7, respectively. This implies that when $\frac{Q}{N} \geq 9.3\%$, vaccination alone can prevent the spread of the infectious disease. It can be seen that when 10^3, 5×10^3, 10^4, 5×10^4, 10^5, respectively, the minimum daily proportion of testing γ_{min} required to prevent the spread of infectious disease needs a higher proportion of growth when the population size increases slightly.

In general, if a case is found in an area, the area will immediately fall into a state of alert. First, the movement path of the case will be tracked and investigated; then, the closely contacted people will be tested and isolated and the corresponding areas will be subject to blockade and control at the same time. In this way, the prevention and control of the infectious disease can be carried out within a certain population size. When N is fixed, how can we couple γ with Q to effectively curb the spread of infectious disease? We applied $N = 10^6$, 5×10^6, 10^7, 1.5×10^7, 2×10^7, 2.5×10^7, 3×10^7, 3.5×10^7, 4×10^7, 4.5×10^7, 5×10^7, respectively. The correlations between γ and $\frac{Q_{min}}{N}$ to block the spread of infectious disease are shown in Figure 6.

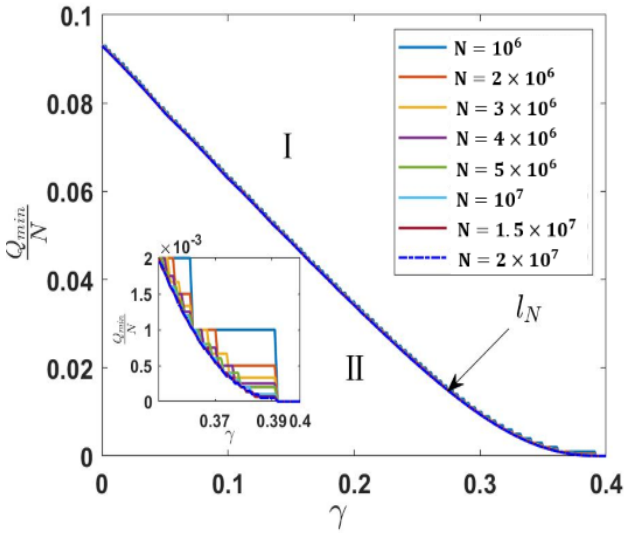

Figure 6. Given $N = 100$, 200, 300, 400, 500, 1000, 1500, 2000 million, respectively, we show the correlation between γ and $\frac{Q_{min}}{N}$.

From Figure 6, when $N = 10^6$, 2×10^6, 3×10^6, 4×10^6, 5×10^6, 10^7, 1.5×10^7, 2×10^7 respectively, the ratios of Q_{min} to N gradually decrease to 0 with the increase of γ. When γ is fixed, $\frac{Q_{min}}{N}$ basically remains the same to prevent the spread of the infectious disease. As long as $\frac{Q}{N} \geq 9.3\%$, the spread of the infectious disease can be curbed even without testing. When $\gamma \geq 39.2\%$, the spread of the infectious disease can also be prevented in a certain population size even without vaccination. Therefore, under the condition that the vaccine is fully effective and the intensity of testing is the same, when the rate of

Q to N belongs to area I or curve l_N, the spread of the infectious disease can be curbed. When the rate of Q to N belongs to area II, the spread of the infectious disease cannot be blocked. Thus, an effective combination of daily testing and vaccination can stop the spread of an infectious disease within a given population size.

5. Conclusions

In this paper, we have explored an SEE_vIR dynamics model to study the effects of daily vaccination and virus testing in the susceptible population and asymptomatic virus carriers on the transmission of an infectious disease in different population sizes. Under the assumption that vaccination is completely effective for susceptible individuals but could not change the infectivity of asymptomatic virus carriers, the simulation results show that when the ratio of population size to the daily processing capacity of vaccine is 400, the peaks of asymptomatic virus carriers, asymptomatic virus carriers who have vaccinated and the symptomatic gradually decrease with the increase of the daily proportion of testing. When the daily proportion of testing is no less than 0.33, the epidemic can be completely controlled. When the population size is fixed, the ratio of the minimum daily vaccine processing capacity required to prevent the spread of infectious disease to the corresponding population size gradually decreases to 0 with the increase of the daily proportion of testing. When $\gamma = 0$ (no testing), as long as $\frac{Q}{N} \geq 9.3\%$, the infectious disease cannot spread. When $\gamma \geq 39.2\%$, the infectious disease cannot transmit even without vaccination. When the daily proportion of testing is fixed ($\gamma < 0.392$), the ratios of the minimum daily vaccine processing capacity required to prevent the spread of infectious disease to the corresponding population size are basically the same. It indicates that effective epidemic prevention and control measures and strategies can learn from each other when the same infectious disease spreads in different countries and regions.

Here, we have assumed that the vaccine is completely effective and population-wide vaccination will occur, without considering factors such as the environment and vaccine effectiveness. In the future, more factors will be incorporated into our model to study the impact of protective measures on the epidemic in a more realistic way.

Use of AI tools declaration

The authors declare that they have not used artificial intelligence tools in the creation of this article.

Acknowledgments

This research was supported in part by the National Natural Science Foundation of China (12226328, 12226329, 12071058 and 11701067) and Natural Science Foundation of Liaoning (2019-ZD-0180).

Conflict of interest

The authors declare that there is no conflict of interest.

References

1. L. Kim, L. McGee, S. Tomczyk, B. Beall, Biological and epidemiological features of antibiotic-resistant streptococcus pneumoniae in pre- and post-conjugate vaccine eras: a united state perspective, *Clin. Microbiol. Rev.*, **29** (2016), 525–552. https://doi.org/10.1128/CMR.00058-15
2. S. K. Saha, B. Hossain, M. Islam, Md Hasanuzzaman, S. Saha, M. Hasan, et al., Epidemiology of invasive pneumococcal disease in Bangladeshi children before introduction of pneumococcal conjugate vaccine, *Pediatr. Infect. Dis. J.*, **35** (2016), 655–661. https://doi.org/10.1097/INF.0000000000001037
3. H. W. Hethcote, Three basic epidemiological models, *Appl. Math. Ecol.*, **18** (1989), 119–144. https://doi.org/10.1007/978-3-642-61317-3_5
4. H. W. Hethcote, The mathematics of infectious diseases, *SIAM Rev.*, **42** (2000), 599–653. https://doi.org/10.1137/S0036144500371907
5. H. W. Hethcote, P. Van den Driessche, Some epidemiological models with nonlinear Incidence, *Journal of Mathematical Biology*, **29** (1991), 271–287. https://doi.org/10.1007/BF00160539
6. J. T. F. Lau, X. L. Yang, E. L. Pang, H. Y. Tsui, E. Wong, Y. K. Wing, SARS-Related perceptions in Hong Kong, *Emerg. Infect. Dis.*, **11** (2005), 417–424. https://doi.org/10.3201/eid1103.040675
7. L. A. Grohskopf, L. Z. Sokolow, K. R. Broder, E. B. Walter, A. M. Fry, D. B. Jernigan, Prevention and control of seasonal influenza with vaccines: recommendations of the advisory committee on immunization Practices-United States, 2018-19 Influenza Season, *MMWR Recomm. Rep.*, **68** (2019), 1–20. http://dx.doi.org/10.15585/mmwr.rr6803a1
8. D. L. Chao, M. E. Halloran, I. M. Longini, Vaccination strategies for epidemic cholera in Haiti with implications for the developing world, *Proc. Natl. Acad. Sci. U. S. A.*, **108** (2011), 7081–7085. https://doi.org/10.1073/pnas.1102149108
9. J. Q. Li, Z. E. Ma, Y. C. Zhou, Global analysis of SIS epidemic model with a simple vaccination and multiple endemic equilibria, *Acta Math. Sci.*, **26** (2006), 83–93. https://doi.org/10.1016/S0252-9602(06)60029-5
10. I. A. Moneim, An SEIR model with infectious latent and a periodic vaccination strategy, *Math. Model. Anal.*, **26** (2021), 236–252. https://doi.org/10.3846/mma.2021.12945
11. C. L. Li, C. H. Li, Dynamics of an epidemic model with imperfect vaccinations on complex networks, *J. Phys. A Math. Theor.*, **53** (2020), 464001. https://doi.org/10.1088/1751-8121/abb9ee
12. B. Tang, X. Zhang, Q. Li, N. L. Bragazzi, D. Golemi-Kotra, J. Wu , The minimal COVID-19 vaccination coverage and efficacy to compensate for potential increase of transmission contacts, and increased transmission probability of the emerging strains, *BMC Public Health*, **22** (2022), 1258. https://doi.org/10.1186/s12889-022-13429-w
13. Q. Q. Cui, Q. Zhang, Z. P. Qiu, X. Yang, Transmission dynamics of an epidemic model with vaccination, treatment and isolation, *Bull. Malaysian Math. Sci. Soc.*, **42** (2019), 885–896. https://doi.org/10.1007/s40840-017-0519-3
14. D. P. Gao, N. J. Huang, S. M. Kang, C. Zhang, Global stability analysis of an SVEIR epidemic model with general incidence rate, *Bound. Value Probl.*, **2018** (2018), 42. https://doi.org/10.1186/s13661-018-0961-7

15. G. P. Sahu, J. Dhar, Analysis of an SVEIS epidemic model with partial temporary immunity and saturation incidence rate, *Appl. Math. Model.*, **36** (2012), 908–923. https://doi.org/10.1016/j.apm.2011.07.044

16. J. Liu, K. Wang, Hopf bifurcation of a delayed SIQR epidemic model with constant input and nonlinear incidence rate, *Adv. Differ. Equations*, **2016** (2016), 168. https://doi.org/10.1186/s13662-016-0899-y

17. X. Y. Chen, J. D. Cao, J. H. Park, J. Qiu, Stability analysis and estimation of domain of attraction for the endemic equilibrium of an SEIQ epidemic model, *Nonlinear Dyn.*, **87** (2017), 975–985. https://doi.org/10.1007/s11071-016-3092-7

18. G. J. Lan, Z. W. Chen, C. J. Wei, S. Zhang, Stationary distribution of a stochastic SIQR epidemic model with saturated incidence and degenerate diffusion, *Phys. A Stat. Mech. Appl.*, **511** (2018), 61–77. https://doi.org/10.1016/j.physa.2018.07.041

19. B. Tang, F. Scarabel, N. L. Bragazzi, Z. McCarthy, M. Glazer, Y. Xiao, et al., De-Escalation by reversing the escalation with a stronger synergistic package of contact tracing, quarantine, isolation and personal protection: Feasibility of preventing a COVID-19 rebound in Ontario, Canada, as a case study, *Biol. Basel*, **9** (2022), 100. https://doi.org/10.3390/biology9050100

20. L. X. Feng, S. L. Jing, S. K. Hu, D. Wang, H. Huo, Modelling the effects of media coverage and quarantine on the COVID-19 infections in the UK, *Math. Biosci. Eng.*, **17** (2020), 3618–3636. https://doi.org/10.3934/mbe.2020204

21. D. A. M. Villela, Imperfect testing of individuals for infectious diseases: Mathematical model and analysis, *Commun. Nonliner Sci. Numerical Simul.*, **46** (2017), 153–160. https://doi.org/10.1016/j.cnsns.2016.10.010

22. S. Moore, E. M. Hill, M.J. Tildesley, L. Dyson, M. J. Keeling, Vaccination and non-pharmaceutical interventions for COVID-19: A mathematical modelling study, *Lancet Infect. Dis.*, **21** (2021), 793–802. https://doi.org/10.1016/S1473-3099(21)00143-2

23. N. Steyn, M. J. Plank, R. N. Binny, S. C. Hendy, A. Lustig, K. Ridings, A COVID-19 vaccination model for Aotearoa New Zealand, *Sci. Rep.*, **12** (2022), 2720. https://doi.org/10.1038/s41598-022-06707-5

24. B. H. Foy, B. Wahl, K. Mehta, A. Shet, G. I. Menon, C. Britto, Comparing COVID-19 vaccine allocation strategies in India: A mathematical modelling study, *Int. J. Infect. Dis.*, **103** (2021), 431–438. https://doi.org/10.1016/j.ijid.2020.12.075

25. S. A. Rella, Y. A. Kulikova, E. T. Dermitzakis, A. Shet, G. I. Menon, C. Britto, Rates of SARS-CoV-2 transmission and vaccination impact the fate of vaccine-resistant strains, *Sci. Rep.*, **11** (2021), 15729. https://doi.org/10.1038/s41598-021-95025-3

26. J. L. Wang, D. Wu, H. Q. Sun, Analysis of an SVIC model with age-dependent infection and asymptomatic carriers, *Appl. Anal.*, **97** (2018), 1467–1495. https://doi.org/10.1080/00036811.2017.1313409

27. S. Kurmi, U. Chouhan, A multicompartment mathematical model to study the dynamic behaviour of COVID-19 using vaccination as control parameter, *Nonlinear Dyn.*, **109** (2022), 2185–2201. https://doi.org/10.1007/s11071-022-07591-4

28. X. Wang, S. Y. Tang, Y. Chen, X. Feng, Y. Xiao, Z. Xu, When will be the resumption of work in Wuhan and its surrounding areas during COVID-19 epidemic ? A data-driven network modeling analysis, *Sci. Sinica Math.*, **50** (2020), 969–978. https://doi.org/10.1360/SSM-2020-0037

29. T. M. Chen, J. Rui, Q. P. Wang, Z. Zhao, J. Cui, L. Yin, A mathematical model for simulating the phase-based transmissibility of a novel coronavirus, *Infect. Dis. Poverty*, **9** (2020), 24. https://doi.org/10.1186/s40249-020-00640-3

30. Z. F. Yang, Z. Q. Zeng, K. Wang, S. Wong, W. Liang, M. Zanin, Modified SEIR and AI prediction of the epidemics trend of COVID-19 in China under public health interventions, *J. Thorac. Dis.*, **12** (2020), 165–174. https://doi.org/10.21037/jtd.2020.02.64

31. R. Pung, C. J. Chiew, B. E. Young, S. Chin, M. Chen, H. E. Clapham , Investigation of three clusters of COVID-19 in Singapore: implications for surveillance and response measures, *Lancet*, **395** (2020), 1039–1046. https://doi.org/10.1016/S0140-6736(20)30528-6

32. W. Guan, Z. Ni, Y. Hu, W. Liang, C. Ou, J. He, Clinical characteristics of coronavirus disease 2019 in China, *N. Engl. J. Med.*, **382** (2020), 1708–1720. https://doi.org/10.1056/NEJMoa2002032

33. L. L. Han, Q. H. Pan, B. L. Kang, M. F. He, Effects of masks on the transmission of infectious diseases, *Adv. Differ. Equations*, **2021** (2021), 169. https://doi.org/10.1186/s13662-021-03321-z

34. P. van den Driessche, Reproduction numbers of infectious disease models, *Infect. Dis. Model.*, **2** (2017), 288–303. https://doi.org/10.1016/j.idm.2017.06.002

35. P. van den Driessche, J. Watmough, Further notes on the basic reproduction number, in *Mathematical Epidemiology*, Springer-Verlag Berlin Heidelberg, **1945** (2008), 159–178. https://doi.org/10.1007/978-3-540-78911-6_6

36. *National Health Commission of the People's Republic of China: Home: daily Briefing (February 1 to March 18)(2020)*, 2020. Available from: http://en.nhc.gov.cn/DailyBriefing.html.

AIMS Press