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Competitive exclusion of two viral strains of COVID-19☆

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ABSTRACT

The pandemic COVID-19 has caused severe losses in public health and economy. One of the most difficult problems in prevention of the disease spread is the emergence of new variants. In this paper, a mathematical model is formulated, which captures the main feature of COVID-19 spread with two viral strains. It is shown by analytical method that the model exhibits the competitive exclusion principle, where one viral strain with the larger basic reproduction number is dominant and the viral strain with the smaller reproduction number is excluded. The results are important for the deployment of prevention policy of COVID-19.

1. Introduction

COVID-19 has caused severe losses in public health and economy. One of the most difficult problems in prevention of COVID-19 is the emergence of new variants. These strains of COVID-19 virus show the different levels of transmission ability and responses to vaccines (Ge & Wang, 2022). Then the key issue is how the original strain competes with a new strain for the shared susceptible population. From a longer time scale for prevention of the disease, it is important to know whether two strains coexist or one strain is dominant, because this information directs the deployment of medical resources.

Mathematical researches are powerful to reveal the evolutionary outcomes for strain competitions. Previous studies indicate that the competitive exclusion of viral strains holds for a variety of mathematical models for generic diseases (see (Bremermann & Thieme, 1989; Castillo-Chavez et al., 1999; Chen et al. 2015; Dang et al., 2017; Iggidr et al., 2006; Wang & Chen, 1997) and the references cited therein). However, there are also models that exhibit the coexistence of different strains due to heterogeneity in time and space (see (Lou & Salako, 2022; Matcheva, 2009) and the references cited therein).

A mathematical model is studied in this paper, which captures the main features of COVID-19 spread with two viral strains. Similar models are investigated in (de León et al., 2022; Massard et al., 2022), where the basic reproduction numbers are estimated from the data, and its sensitivity in the parameters are analyzed. The objective of the present paper is to show analytically that the model exhibits the competitive exclusion principle. That is, one viral strain with the larger basic reproduction number is dominant and the viral strain with the smaller reproduction number is excluded.

The organization of this paper is as follows. In the next section, we formulate the mathematical model. Section 3 presents the mathematical analysis of the model to show the competitive exclusion holds. The paper ends with brief discussions.

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2. Mathematical model

The population is divided into the 5 groups: susceptible, exposed, asymptomatic, symptomatic and recovered. Let S(t) and R(t) be the numbers of susceptible individuals at time t respectively, and $E_i(t)$ be the number of the exposed individuals infected by strain i ($i = 1, 2$) at time t. The asymptomatic individuals and symptomatic individuals at time t, who are transited from E_i, are denoted by $A_i(t)$ and $I_i(t)$ respectively. The flowchart of disease transmission and progression is shown Fig. 1.

The mathematical model is described by

$$\begin{aligned}
\frac{dS}{dt} &= \lambda - \mu S - \beta_1(I_1 + \delta_1 A_1)S - \beta_2(I_2 + \delta_2 A_2)S,\\
\frac{dE_1}{dt} &= \beta_1(I_1 + \delta_1 A_1)S - (\mu + \alpha_1)E_1,\\
\frac{dA_1}{dt} &= p_1\alpha_1 E_1 - (\mu + \gamma_1)A_1,\\
\frac{dI_1}{dt} &= (1 - p_1)\alpha_1 E_1 - (\mu + \gamma_1)I_1,\\
\frac{dE_2}{dt} &= \beta_2(I_2 + \delta_2 A_2)S - (\mu + \alpha_2)E_2,\\
\frac{dA_2}{dt} &= p_2\alpha_2 E_2 - (\mu + \gamma_2)A_2,\\
\frac{dI_2}{dt} &= (1 - p_2)\alpha_2 E_2 - (\mu + \gamma_2)I_2,\\
\frac{dR}{dt} &= \gamma_1(A_1 + I_1) + \gamma_2(A_2 + I_2) - \mu R,
\end{aligned} \tag{2.1}$$

where λ is the recruitment rate of the population, μ is the natural death rate of the population, β_i is the valid disease transmission coefficient by strain i, δ_i is the reduction coefficient of disease transmission coefficient for asymptomatic individuals, α_i is the transition rate from the exposed class to infectious class with the probability p_i being in asymptomatic class, and γ_i is the recovery rate.

Clearly, the last equation of the model (2.1) can be decoupled from the system. Henceforth, we consider only the following model:

$$\begin{aligned}
\frac{dS}{dt} &= \lambda - \mu S - \beta_1(I_1 + \delta_1 A_1)S - \beta_2(I_2 + \delta_2 A_2)S,\\
\frac{dE_1}{dt} &= \beta_1(I_1 + \delta_1 A_1)S - (\mu + \alpha_1)E_1,\\
\frac{dA_1}{dt} &= p_1\alpha_1 E_1 - (\mu + \gamma_1)A_1,\\
\frac{dI_1}{dt} &= (1 - p_1)\alpha_1 E_1 - (\mu + \gamma_1)I_1,\\
\frac{dE_2}{dt} &= \beta_2(I_2 + \delta_2 A_2)S - (\mu + \alpha_2)E_2,\\
\frac{dA_2}{dt} &= p_2\alpha_2 E_2 - (\mu + \gamma_2)A_2,\\
\frac{dI_2}{dt} &= (1 - p_2)\alpha_2 E_2 - (\mu + \gamma_2)I_2.
\end{aligned} \tag{2.2}$$

3. Mathematical analysis

Let us start from the subsystem of the first strain:

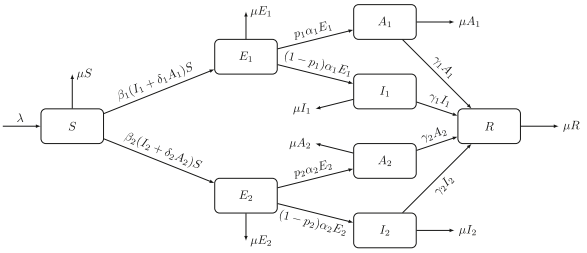

Fig. 1. The transmission and progression of COVID-19 disease.

$$\begin{aligned}
\frac{dS}{dt} &= \lambda - \mu S - \beta_1(I_1 + \delta_1 A_1)S,\\
\frac{dE_1}{dt} &= \beta_1(I_1 + \delta_1 A_1)S - (\mu + \alpha_1)E_1,\\
\frac{dA_1}{dt} &= p_1\alpha_1 E_1 - (\mu + \gamma_1)A_1,\\
\frac{dI_1}{dt} &= (1-p_1)\alpha_1 E_1 - (\mu + \gamma_1)I_1.
\end{aligned} \tag{3.1}$$

The disease-free equilibrium is $E_0^1 = (\lambda/\mu, 0, 0, 0)$. Set

$$F_1 = \begin{pmatrix} 0 & \beta_1\delta\lambda/\mu & \beta_1\lambda/\mu \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad V_1 = \begin{pmatrix} \mu+\alpha & 0 & 0 \\ -p_1\alpha_1 & \mu+\gamma_1 & 0 \\ -(1-p_1)\alpha_1 & 0 & \mu+\gamma_1 \end{pmatrix}.$$

By (van den Driessche & Watmough, 2002), the basic reproduction number of the first strain is

$$R_0^1 = \frac{\beta_1\,\lambda\,\alpha_1\,(\delta_1\,p_1 + 1 - p_1)}{\mu\,(\mu+\gamma_1)(\mu+\alpha_1)}.$$

Similarly, the basic reproduction number of the second strain is

$$R_0^2 = \frac{\beta_2\,\lambda\,\alpha_2\,(\delta_2\,p_2 + 1 - p_2)}{\mu(\mu+\gamma_2)(\mu+\alpha_2)}.$$

Theorem 3.1. *The disease-free equilibrium E_0^1 of* (3.1) *is globally stable if $R_0^1 < 1$.*

Proof. Choose $\varepsilon > 0$ small enough such that

$$R_0^1(\varepsilon) = \frac{\beta_1\,(\lambda+\varepsilon)\,\alpha_1\,(\delta_1\,p_1 + 1 - p_1)}{\mu\,(\mu+\gamma_1)(\mu+\alpha_1)} < 1, \tag{3.2}$$

which is possible because of $R_0^1 < 1$. From the first equation of (3.1), we see that a nonnegative solution of (3.1) satisfies

$$S(t) < \frac{\lambda+\varepsilon}{\mu}, \quad \text{for large } t.$$

As a result, we get

$$\begin{aligned}
\frac{dE_1}{dt} &\le \beta_1(I_1 + \delta_1 A_1)\frac{\lambda+\varepsilon}{\mu} - (\mu+\alpha_1)E_1,\\
\frac{dA_1}{dt} &= p_1\alpha_1 E_1 - (\mu+\gamma_1)A_1,\\
\frac{dI_1}{dt} &= (1-p_1)\alpha_1 E_1 - (\mu+\gamma_1)I_1
\end{aligned} \tag{3.3}$$

for large t. Since $R_0^1(\varepsilon) < 1$, the zero solution of the linear comparison system

$$\begin{aligned} \frac{dE_1}{dt} &= \beta_1(I_1 + \delta_1 A_1)\frac{\lambda+\varepsilon}{\mu} - (\mu+\alpha_1)E_1, \\ \frac{dA_1}{dt} &= p_1\alpha_1 E_1 - (\mu+\gamma_1)A_1, \\ \frac{dI_1}{dt} &= (1-p_1)\alpha_1 E_1 - (\mu+\gamma_1)I_1 \end{aligned} \tag{3.4}$$

is asymptotically stable. It follows from (3.3) that the nonnegative solution of (3.1) satisfies (E(t), A(t), I(t)) → (0, 0, 0) as t → ∞. Then it is easy to see S(t) → λ/μ as t → ∞. This means that the disease-free equilibrium E_0^1 of (3.1) is globally attractive. Since R_0^1 implies E_0^1 is asymptotically stable, we conclude the global stability of E_0^1 when $R_0^1 < 1$. □

We show now that (3.1) admits a unique endemic equilibrium $(S_1^*, E_1^*, A_1^*, I_1^*)$ if $R_0^1 > 1$. Indeed, the endemic equilibrium solves

$$\begin{aligned} \lambda - \mu S_1^* - \beta_1(I_1^* + \delta_1 A_1^*)S_1^* &= 0, \\ \beta_1(I_1^* + \delta_1 A_1^*)S_1^* - (\mu+\alpha_1)E_1^* &= 0, \\ p_1\alpha_1 E_1^* - (\mu+\gamma_1)A_1^* &= 0, \\ (1-p_1)\alpha_1 E_1^* - (\mu+\gamma_1)I_1^* &= 0. \end{aligned} \tag{3.5}$$

Direct calculations yield

$$E_1^* = \frac{\lambda}{\mu+\alpha_1}\left(1 - \frac{1}{R_0^1}\right), \quad I_1^* = \frac{(1-p_1)\alpha_1}{\mu+\gamma_1}E_1^*, \quad A_1^* = \frac{p_1\alpha_1}{\mu+\gamma_1}E_1^*, \quad S_1^* = -\frac{\mu+\alpha_1}{\mu}E_1^* + \frac{\lambda}{\mu}.$$

Then simple computation leads to

$$S_1^* = \frac{(\mu+\alpha_1)(\mu+\gamma_1)}{(\delta_1 p_1 - p_1 + 1)\beta_1 \alpha_1}. \tag{3.6}$$

Consequently, we conclude the existence and uniqueness of endemic equilibrium in (3.1) when $R_0^1 > 1$. The next theorem states that this endemic equilibrium is globally stable.

Theorem 3.2. *Let $R_0^1 > 1$. Then system* (3.1) *has a unique endemic equilibrium which is globally stable.*

Proof. It is sufficient to prove that $(S_1^*, E_1^*, A_1^*, I_1^*)$ is globally stable when $R_0^1 > 1$. Define a Lyapunov function by

$$\begin{aligned} V_1 = {} & S - S_1^* - S_1^* \ln\frac{S}{S_1^*} + E_1 - E_1^* - E_1^* \ln\frac{E_1}{E_1^*} \\ & + \frac{\beta_1 S_1^*}{\mu+\gamma_1}\left[I_1 + \delta_1 A_1 - (I_1^* + \delta_1 A_1^*) - (I_1^* + \delta_1 A_1^*)\ln\frac{I_1 + \delta A_1}{I_1^* + \delta A_1^*}\right]. \end{aligned}$$

Calculating the derivative of V along the solution of model (3.1), we get

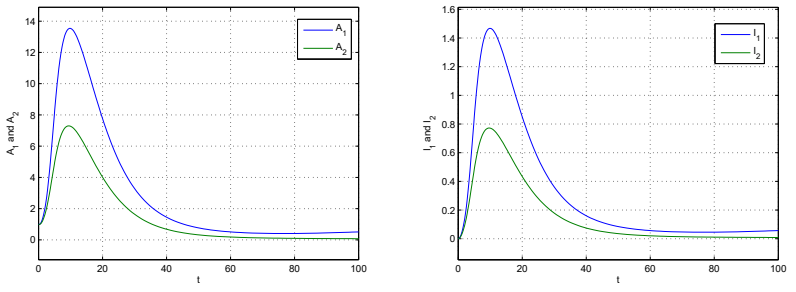

Fig. 2. The first strain is dominant and the second strain is excluded, where $R_0^1 = 7.5238, R_0^2 = 5.4286$.

$$\begin{aligned}\frac{dV_1}{dt} = & \lambda - \mu S - \frac{S_1^*}{S}\lambda + \mu S_1^* + \beta_1 S_1^*(I_1 + \delta_1 A_1) \\ & -(\mu+\alpha_1)E_1 - \frac{E_1^*}{E_1}\beta_1 S(I_1 + \delta_1 A_1) + (\mu+\alpha_1)E_1^* \\ & + \frac{\beta_1 S_1^*}{\mu+\gamma_1}\{(1-p_1+\delta_1 p_1)\alpha_1 E_1 - (\mu+\gamma_1)(I_1+\delta A_1) \\ & - \frac{I_1^* + \delta_1 A_1^*}{I_1+\delta_1 A_1}(1-p_1+\delta_1 p_1)\alpha_1 E_1 + (I_1^* + \delta_1 A_1^*)(\mu+\gamma_1)\Big\}.\end{aligned}$$

Using (3.6), it follows from $\lambda = \mu S_1^* + (\mu+\alpha_1)E_1^*$ and $\beta_1 S_1^*(I_1^* + \delta_1 A_1^*) = (\mu+\alpha_1)E_1^*$ that

$$\begin{aligned}\frac{dV_1}{dt} = & \mu S_1^*\left(2 - \frac{S}{S_1^*} - \frac{S_1^*}{S}\right) + 2(\mu+\alpha_1)E_1^* \\ & - \frac{S_1^*}{S}(\mu+\alpha_1)E_1^* - \frac{E_1^*}{E_1}\beta_1 S(I_1+\delta_1 A_1) \\ & - \frac{(\mu+\alpha_1)E_1^*}{(I_1+\delta_1 A_1)(\mu+\gamma_1)}(1-p_1+\delta_1 p_1)\alpha_1 E_1 + (\mu+\alpha_1)E_1^*.\end{aligned}$$

As a result, we get

$$\begin{aligned}\frac{dV_1}{dt} = & \mu S_1^*\left(2 - \frac{S}{S_1^*} - \frac{S_1^*}{S}\right) \\ & + (\mu+\alpha_1)E_1^*\left\{3 - \frac{S_1^*}{S} - \frac{\beta_1 S(I_1+\delta_1 A_1)}{E_1(\mu+\alpha_1)} - \frac{(1-p_1+\delta_1 p_1)\alpha_1 E_1}{(I_1+\delta_1 A_1)(\mu+\gamma_1)}\right\}.\end{aligned}$$

Since the arithmetical mean is great than or equal to the geometric mean, it follows from (3.6) that

$$\frac{dV_1}{dt} \le 0.$$

Furthermore, we let

$$D_1 := \left\{(S, E_1, A_1, I_1) \in \text{int } R_+^4 : \frac{dV_1}{dt} = 0\right\}.$$

Since $R_0^1 > 1$, by similar arguments to those in (Wang & Chen, 1997; Wang & Zhao, 2004) we see that the positive solutions of (3.1) are permanent. As a result, the positive solutions of (3.1) approach the maximal compact invariant set in D_1, which lies in the interior of R_+^4, as $t \to \infty$. To locate such a set, we see from $\frac{dV_1}{dt} = 0$ that $S = S_1^*$ and $E_1(\mu+\alpha_1) = \beta_1 S_1^*(I_1 + \delta_1 A_1)$. It follows from the second equation that $E_1(t)$ is a constant. Similarly, one can deduce that $I_1(t) + \delta_1 A_1(t)$ is a constant. Hence,

$$\begin{aligned}\lambda - \mu S_1^* - \beta_1(I_1+\delta_1 A_1)S_1^* &= 0, \\ \beta_1(I_1+\delta_1 A_1)S_1^* - (\mu+\alpha_1)E_1 &= 0, \\ (1-p_1+\delta_1 p_1)\alpha_1 E_1^* - (\mu+\gamma_1)(I_1+\delta_1 A_1) &= 0.\end{aligned}$$

It follows that

$$E_1 = E_1^*, \quad I_1 + \delta_1 A_1 = \frac{(1-p_1+\delta_1 p_1)\alpha_1}{\mu+\gamma_1} = I_1^* + \delta_1 A_1^*.$$

Consequently, the last two equations of (3.1) imply that $A_1 = A_1^*, I_1 = I_1^*$ in the maximal compact invariant set in D_1. Therefore, the maximal compact invariant set in D_1 is

$$\{(S, E_1, A_1, I_1) : S = S_1^*, E_1 = E_1^*, A_1 = A_1^*, I_1 = I_1^*\}.$$

The Lyapunov-LaSalle theorem (Hale & Verduyn Lunel, 1993) implies that all positive solutions of (3.1) approach the maximal invariant set in D_1 and the endemic equilibrium $(S_1^*, E_1^*, A_1^*, I_1^*)$ is globally stable. This completes the proof. □

Let us consider the subsystem of the second strain:

$$\begin{aligned} \frac{dS}{dt} &= \lambda - \mu S - \beta_1(I_2 + \delta_1 A_2)S, \\ \frac{dE_2}{dt} &= \beta_2(I_2 + \delta_2 A_2)S - (\mu + \alpha_2)E_2, \\ \frac{dA_2}{dt} &= p_2\alpha_2 E_2 - (\mu + \gamma_2)A_2, \\ \frac{dI_2}{dt} &= (1 - p_2)\alpha_2 E_2 - (\mu + \gamma_2)I_2. \end{aligned} \tag{3.7}$$

Similarly, the disease-free equilibrium is globally stable if $R_0^2 < 1$ and an endemic equilibrium $(S_2^*, E_2^*, A_2^*, I_2^*)$ is globally stable if $R_0^2 > 1$, where

$$E_2^* = \frac{\lambda}{\mu + \alpha_2}\left(1 - \frac{1}{R_0^2}\right), \quad I_2^* = \frac{(1 - p_2)\alpha_2}{\mu + \gamma_2}E_2^*, \quad A_2^* = \frac{p_2\alpha_2}{\mu + \gamma_2}E_2^*,$$

and

$$S_2^* = \frac{(\mu + \alpha_2)(\mu + \gamma_2)}{(\delta_2 p_2 - p_2 + 1)\beta_2 \alpha_2}. \tag{3.8}$$

The evolution outcomes of the disease driven by two virus strains are described by the following theorems.

Theorem 3.3. *Let $R_0^1 < 1$. Then the disease of first strain dies out. That is, any positive solution of* (2.2) *satisfies*

$$(E_1(t), A_1(t), I_1(t)) \to (0, 0, 0) \text{ as } t \to \infty.$$

If $R_0^2 < 1$, then the disease of second strain dies out. That is, any positive solution of (2.2) *satisfies*

$$(E_2(t), A_2(t), I_2(t)) \to (0, 0, 0) \text{ as } t \to \infty.$$

proof. The proofs are omitted because they are the minor modifications to the proof of Theorem 3.1. □

Theorem 3.4. *Let $R_0^1 > R_0^2 > 1$. Then the first strain is dominant and the second strain is excluded. That is, any positive solution of* (2.2) *satisfies*

$$(S(t), E_1(t), A_1(t), I_1(t), E_2(t), A_2(t), I_2(t)) \to (S_1^*, E_1^*, A_1^*, I_1^*, 0, 0, 0) \text{ as } t \to \infty.$$

Proof. First, we note that the strain reproduction numbers can be rewritten as

$$R_0^1 = \frac{\lambda}{\mu S_1^*}, \quad R_0^2 = \frac{\lambda}{\mu S_2^*}.$$

Thus, $R_0^1 > R_0^2 > 1$ imply

$$S_1^* < S_2^*. \tag{3.9}$$

Set

$$x_1 = \frac{\beta_2 S_2^* \delta_2}{\mu + \gamma_2}, \quad x_2 = \frac{\beta_2 S_2^*}{\mu + \gamma_2}. \tag{3.10}$$

It follows from (3.8) that

$$p_2x_1 + (1-p_2)x_2 = \frac{\beta_2 S_2^*(1-p_2+p_2\delta_2)}{\mu+\gamma_2} = \frac{\mu+\alpha_2}{\alpha_2}. \tag{3.11}$$

Now, let us consider the Lyapunov function:

$$\begin{aligned} V = & S - S_1^* - S_1^* \ln\frac{S}{S_1^*} + E_1 - E_1^* - E_1^* \ln\frac{E_1}{E_1^*} \\ & + \frac{\beta_1 S_1^*}{\mu+\gamma_1}\left[I_1 + \delta_1 A_1 - (I_1^* + \delta_1 A_1^*) - (I_1^* + \delta_1 A_1^*)\ln\frac{I_1+\delta A_1}{I_1^* + \delta A_1^*}\right] \\ & + E_2 + x_1 A_2 + x_2 I_2. \end{aligned}$$

Calculating the derivative of V along the solution of (2.2), we obtain

$$\begin{aligned} \frac{dV}{dt} = & \lambda - \mu S - \frac{S_1^*}{S}\lambda + \mu S_1^* + \beta_1 S_1^*(I_1 + \delta_1 A_1) + \beta_2 S_1^*(I_2 + \delta_2 A_2) \\ & - (\mu+\alpha_1)E_1 - \frac{E_1^*}{E_1}\beta_1 S(I_1 + \delta_1 A_1) + (\mu+\alpha_1)E_1^* \\ & + \frac{\beta_1 S_1^*}{\mu+\gamma_1}\{(1-p_1+\delta_1 p_1)\alpha_1 E_1 - (\mu+\gamma_1)(I_1+\delta A_1) \\ & - \frac{I_1^* + \delta_1 A_1^*}{I_1 + \delta_1 A_1}(1-p_1+\delta_1 p_1)\alpha_1 E_1 + (I_1^* + \delta_1 A_1^*)(\mu+\gamma_1)\Big\} \\ & - (\mu+\alpha_2)E_2 + x_1 p_2 \alpha_2 E_2 - x_1(\mu+\gamma_2)A_2 + x_2(1-p_2)\alpha_2 E_2 - x_2(\mu+\gamma_2)I_2. \end{aligned}$$

Using (3.10) and (3.11), we simplify it into

$$\begin{aligned} \frac{dV}{dt} = & \lambda - \mu S - \frac{S_1^*}{S}\lambda + \mu S_1^* + \beta_1 S_1^*(I_1 + \delta_1 A_1) + \beta_2 (S_1^* - S_2^*)(I_2 + \delta_2 A_2) \\ & - (\mu+\alpha_1)E_1 - \frac{E_1^*}{E_1}\beta_1 S(I_1 + \delta_1 A_1) + (\mu+\alpha_1)E_1^* \\ & + \frac{\beta_1 S_1^*}{\mu+\gamma_1}\{(1-p_1+\delta_1 p_1)\alpha_1 E_1 - (\mu+\gamma_1)(I_1+\delta A_1) \\ & - \frac{I_1^* + \delta_1 A_1^*}{I_1 + \delta_1 A_1}(1-p_1+\delta_1 p_1)\alpha_1 E_1 + (I_1^* + \delta_1 A_1^*)(\mu+\gamma_1)\Big\}. \end{aligned}$$

Note that $\lambda = \mu S_1^* + (\mu+\alpha_1)E_1^*$ and $\beta_1 S_1^*(I_1^* + \delta_1 A_1^*) = (\mu+\alpha_1)E_1^*$. By similar arguments to those in the proof of Theorem 3.2, we obtain

$$\begin{aligned} \frac{dV}{dt} = & \mu S_1^*\left(2 - \frac{S}{S_1^*} - \frac{S_1^*}{S}\right) + \beta_2(S_1^* - S_2^*)(I_2 + \delta_2 A_2) \\ & + (\mu+\alpha_1)E_1^*\left\{3 - \frac{S_1^*}{S} - \frac{\beta_1 S(I_1+\delta_1 A_1)}{E_1(\mu+\alpha_1)} - \frac{(1-p_1+\delta_1 p_1)\alpha_1 E_1}{(I_1+\delta_1 A_1)(\mu+\gamma_1)}\right\}. \end{aligned}$$

Let

$$D := \left\{(S, E_1, A_1, I_1, E_2, A_2, I_2) \in \text{int } R_+^4 \times R_+^3 : \frac{dV}{dt} = 0\right\}.$$

Since $R_0^1 > R_0^2 > 1$, by (3.9) we see that a solution of (2.2) in D for all t exhibits

$$A_2(t) \equiv I_2(t) \equiv 0.$$

It follows from the last equation of (2.2) that $E_2(t) \equiv 0$. Then it is easy to see that the maximal compact invariant set in D satisfies

$$S = S_1^*,\ \ E_1 = E_1^*,\ \ I_1 + \delta_1 A_1 = I_1^* + \delta_1 A_1^*,\ \ A_2 = 0,\ \ I_2 = 0,\ \ E_2 = 0.$$

Since $R_0^1 > R_0^2 > 1$, by similar arguments to those in (Wang & Chen, 1997; Wang & Zhao, 2004) we see that the boundary of R_+^7 with $E_1 = A_1 = I_1 = 0$ repels uniformly the positive solutions of model (2.2). Then by similar discussions to those in the proof of Theorem 3.2, we conclude the maximal compact invariant set in D satisfies

$$S = S_1^*,\ \ E_1 = E_1^*,\ \ A_1 = A_1^*,\ \ I_1 = I_1^*,\ \ E_2 = 0,\ \ A_2 = 0,\ \ I_2 = 0.$$

Therefore, the Lyapunov-LaSalle theorem (Hale & Verduyn Lunel, 1993) implies that $(S_1^*, E_1^*, A_1^*, I_1^*, 0, 0, 0)$ is globally stable. This proves the theorem. □

Let us consider an example to support the theoretical results. Motivated by (Ge & Wang, 2022), we fix the parameters by $\lambda = 0.1, \mu = 0.01, \delta_1 = \delta_2 = 0.5, \alpha_1 = \alpha_2 = 0.2, \gamma_1 = \gamma_2 = 0.1, p_1 = p_2 = 0.9, \beta_1 = 0.158, \beta_2 = 0.114$. Then $R_0^1 = 7.5238, R_0^2 = 5.4286$. It follows from Theorem 3.4 that the first strain is dominant and the second strain is excluded. Numerical computations confirm this result, which is shown in Fig. 2.

4. Discussions

In this paper, we study the mathematical model which includes the asymptomatic disease transmissions and consider the competition of two viral strains. Thus, the model captures the main features of COVID-19 spread. Moreover, the superinfection of different strains is neglected because the rate is small in practice. Indeed, infected individuals are much more likely quarantined due to onset of symptoms or nucleic acid test, which makes the probability of secondary infection from other strain quite small. Note that the different strains of COVID-19 exhibit the different levels of transmission ability, different mortality rates and different responses to vaccines (Ge & Wang, 2022). Hence, the prevention and control strategies vary with the characteristics of virus strain. More importantly, it is critical to know whether two strains coexist or one strain is dominant, because this information directs the deployment of the limited medical resources. The previous studies on this important issue use mainly numerical simulations to predict the trend of disease evolutions. The novelty of this paper is to analyze the dynamical behaviors of model (2.2) by rigor mathematical approach. Using the technique of comparison and Lyapunov functions, we show that the model has the property of competitive exclusion. That is, the viral strain with a larger basic reproduction number is dominant and the viral strain with the smaller reproduction number is excluded. This result precludes the possibility for coexistence of two viral strains of COVID-19, which is consistent with the progressions of COVID-19 evolutions.

It will be interesting to consider multiple strains in the model and study how vaccination affect the outcome of competition among viral strains. We leave these as future researches.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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