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STABILITY ANALYSIS OF A DELAYED COVID-19 TRANSMISSION MODEL INVOLVING IMMIGRATION AND VACCINATION

MOHAMMED SEMLALI[1,*], KHALID HATTAF[2], MOHAMED SADIK[3], AIAD EL GOURARI[1]

[1]Laboratory of Partial Differential Equations, Algebra and Spectral Geometry (LEDPAGS), Faculty of Sciences, Ibn Tofail University, P.O.Box 133, Kenitra 14000, Morocco

[2]Equipe de Recherche en Modélisation et Enseignement des Mathématiques (ERMEM), Centre Régional des Métiers de l'Education et de la Formation (CRMEF), Casablanca, Morocco

[3]Laboratory of Applied Mathematics and Scientific Computing (LAMACS), Faculty of Sciences and Technologies, Sultan Moulay Slimane University, Beni Mellal, Morocco

Abstract. In this paper, we propose and analyze the dynamical behavior of a delayed COVID-19 transmission model with immigration, vaccination and general incidence function. The time delay into the proposed model represents the incubation period. Firstly, the well-posedness of the model is investigated. Moreover, we construct appropriate Lyapunov function to prove the global stability of equilibria. To support the theoretical results, numerical simulations are presented at the end of the study.

Keywords: COVID-19; time delay; immigration; vaccination; general incidence rate; stability analysis.

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1. INTRODUCTION

The mathematical modeling of epidemics is a very important tool in prediction, controlling the disease and understanding its transmission mechanism. Long ago, several epidemic models

*Corresponding author

E-mail address: semlali69@hotmail.com

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on theoretical developments are discussed by many researchers, they describe some mathematical models of epidemiology by dividing the total population into three classes: susceptible individuals S, infected individuals I and recovered individuals R [1, 2, 3]. Despite its simplicity, the SIR model in epidemiology is very important in today's analysis of diseases and presents the basic structure associated to the spread of a disease in a population. Many variants of SIR model have been studied in recent years to more model complex infectious diseases.

In many models in the literature, the transmission of the disease was assumed to be instantaneous and then it is formulated by ordinary differential equations without any time delay [4, 5]. Biologically, it is necessary to consider time delays in epidemic models. The consideration of temporal delays in epidemic modeling is important to describe a variety of factors. Moreover, the notion of delay helped to formulate the concept of latency, which represents the period of incubation [6, 7, 8, 9]. Cooke [10] considered the fact that an individual may not be infectious until some fixed time after becoming infected and proposed an SIR model with a discrete time delay. Beretta et al. [11] studied an SIR model with a distributed time delay which enables the infectivity to be a function of the duration since infection. To be precise, in this study we focus on the COVID-19 epidemic and we propose a new delayed SIR epidemic model for its transmission governed by delay differential equations with general incidence rate in presence of immigration and vaccination.

The present paper is organized as follows. In the next section, we first formulate our model and show the nonnegativity and boundedness of solutions. In Section 3, we analyze the stability of the model without infected immigrants. The analysis of the model with infected immigrants is established in Section 4. Numerical simulations are presented in Section 5 to illustrate and confirm the theoretical results. Finally, in the last section, a discussion and conclusion are given.

2. Model Formulation and Basic Results

In this section, we propose the following model

$$
\left\{
\begin{array}{ll}
\frac{dS}{dt} & = A + b - \mu S(t) - \mathscr{F}(S(t), I(t))I(t) - \nu S(t), \\
\frac{dI}{dt} & = c + \mathscr{F}(S(t-\tau), I(t-\tau))I(t-\tau)e^{-\mu\tau} - (\mu + d + r)I(t), \\
\frac{dR}{dt} & = rI(t) + \nu S(t) - \mu R(t),
\end{array}
\right. \tag{1}
$$

where the susceptible individuals are recruited at a rate A. The natural death rate in all classes is denoted by μ, while d is the death rate due to disease. The parameter r denotes recovery rate of the infected individuals. $\mathscr{F}(S,I)I$ is the rate of transmission and τ is the incubation period. Finally, the term $e^{-\mu\tau}$ is the probability of surviving from time $t-\tau$ to time t.

According to [6], we assume that the general incidence function $\mathscr{F}$ is continuously differentiable in the interior of $\mathbb{R}^2_+$ and satisfies the following hypotheses

(H_1) $\mathscr{F}(0,I)=0$, for all $I\geq 0$.

(H_2) $\frac{\partial \mathscr{F}}{\partial S}(S,I)>0$, for all $S>0$ and $I\geq 0$.

(H_3) $\frac{\partial \mathscr{F}}{\partial I}(S,I)\leq 0$, for all $S\geq 0$ and $I\geq 0$.

In addition to the assumptions above, we assume in this work that there are immigrants to susceptible individuals and immigrants to infected individuals denoted by b and c, respectively. The parameter ν represents the rate of vaccination.

It is very important to note that our model presented by system (1) includes many special cases. For instance, we get the model in [1] when $\tau=0$. Furthermore, the model introduced in [6] is a particular case of system (1), it suffices to ignore the immigration of infected individuals.

Since the first two equations in system (1) do not depend on the third one, then model (1) can be reduced to the following system

$$\left\{\begin{array}{ll} \frac{dS}{dt} & = A+b-\mu S(t)-\mathscr{F}(S(t),I(t))I(t)-\nu S(t), \\ \frac{dI}{dt} & = c+\mathscr{F}(S(t-\tau),I(t-\tau))I(t-\tau)e^{-\mu\tau}-(\mu+d+r)I(t). \end{array}\right. \tag{2}$$

We denote by $C=C([-\tau,0],\mathbb{R}^2)$ the Banach space of continuous functions mapping the interval $[-\tau,0]$ into $\mathbb{R}^2$ with the topology of uniform convergence. By the fundamental theory of functional differential equations (see, [12]), it is easy to show that there exists a unique solution $(S(t),I(t))$ of system (2) with initial data $(S_0,I_0)\in C$. In addition, for biological reasons, we assume that the initial conditions for system (2) satisfy

$$S_0(\theta)\geq 0,\quad I_0(\theta)\geq 0,\quad \theta\in[-\tau,0]. \tag{3}$$

As the model (2) describes population, it is important to prove that all solutions with nonnegative initial data will remain nonnegative and bounded for all time.

Theorem 2.1. *All solutions of the delayed system (2) satisfying conditions (3) remain nonnegative and bounded for all $t \geq 0$.*

Proof. Firstly, we prove by contradiction that the solution $S(t)$ is positive for all $t \geq 0$. Suppose not, let $t_1 > 0$ be the first time such that $S(t_1) = 0$, then by the first equation of system (2) under the hypothesis (H_1) we have $\frac{dS}{dt}(t_1) = A + b > 0$, it means there exists a sufficient small real number $\alpha > 0$ such that $S(t) < 0$ for $t \in (t_1 - \alpha, t_1)$. This contradicts the fact that $S(t) > 0$ for $t \in [0, t_1)$. Hence, $S(t) \geq 0$ for all $t \geq 0$.

Next, we prove the positivity of $I(t)$. From the second equation of system (2) we get

$$I(t) = I(0)e^{-at} + c\frac{1-e^{-at}}{a} + e^{-\mu\tau}\int_0^t \mathscr{F}(S(\theta-\tau), I(\theta-\tau))I(\theta-\tau)e^{-a(t-\theta)}d\theta, \tag{4}$$

where $a = \mu + d + r$.

Let $t \in [0, \tau]$, then $\theta - \tau \in [-\tau, 0]$ for all $\theta \in [0, \tau]$. According to (3) and (4), we deduce that $I(t) \geq 0$ for all $t \in [0, \tau]$. This method can be repeated to deduce nonnegativity of I on the interval $[\tau, 2\tau]$ and then on successive intervals $[n\tau, (n+1)\tau]$ for $n \geq 2$, to include all positive times. This proves the nonnegativity of solutions.

For boundedness of the solutions, we define the following function

$$G(t) = S(t) + e^{\mu\tau}I(t+\tau).$$

Then

$$\begin{aligned}
\frac{dG}{dt} &= A + b - (\mu+\nu)S(t) - \mathscr{F}(S(t), I(t))I(t) + e^{\mu\tau}\Big(c + \mathscr{F}(S(t), I(t))I(t)e^{-\mu\tau} - aI(t+\tau)\Big) \\
&= A + b - (\mu+\nu)S(t) + ce^{\mu\tau} - ae^{\mu\tau}I(t+\tau) \\
&= A + b + ce^{\mu\tau} - \mu G(t) - \nu S(t) - (d+r)e^{\mu\tau}I(t+\tau) \\
&\leq A + b + ce^{\mu\tau} - \mu G(t).
\end{aligned}$$

This implies that $G(t)$ is bounded, and so are $S(t)$ and $I(t)$. This completes the proof. ∎

3. Analysis of the Model Without Immigration of Infected Individuals

In this section, we investigate the stability of model (2) without immigration of infected individuals. Hence, system (2) becomes

$$\begin{cases} \frac{dS}{dt} &= A+b-\mu S(t)-\mathscr{F}(S(t),I(t))I(t)-\nu S(t), \\ \frac{dI}{dt} &= \mathscr{F}(S(t-\tau),I(t-\tau))I(t-\tau)e^{-\mu\tau}-(\mu+d+r)I(t). \end{cases} \tag{5}$$

As in [6], system (5) has always one disease-free equilibrium $\mathscr{E}(\frac{A+b}{\mu+\nu},0)$. Then the basic reproduction number of the system (5) is given by

$$R_0 = \frac{\mathscr{F}(\frac{A+b}{\mu+\nu},0)e^{-\mu\tau}}{\mu+d+r}. \tag{6}$$

Based on the results in [6], we have the following theorems.

Theorem 3.1. *The disease-free equilibrium point of the system (5) is given by $\mathscr{E}(\frac{A+b}{\mu+\nu},0)$ and it exists for all parameter values. If $R_0>1$, then (5) has a unique endemic equilibrium $\mathscr{E}^*(S^*,I^*)$ with $S^*\in(0,\frac{A+b}{\mu+\nu})$ and $I^*>0$.*

Theorem 3.2. *The disease-free equilibrium $\mathscr{E}$ of the system (5) is globally asymptotically stable if $R_0\leq 1$ and unstable if $R_0>1$.*

Similarly to [6], we consider the following hypothesis for the case $R_0>1$

$$\left(1-\frac{\mathscr{F}(S,I)}{\mathscr{F}(S,I^*)}\right)\left(\frac{\mathscr{F}(S,I^*)}{\mathscr{F}(S,I)}-\frac{I}{I^*}\right)\leq 0 \text{ for all } S,I>0. \tag{H_4}$$

Theorem 3.3. *Assume that $R_0>1$ and (H_4) holds, then the endemic equilibrium $\mathscr{E}^*$ of the system (5) is globally asymptotically stable.*

4. Analysis of the Model With Immigration of Infected Individuals

Consider the case $c>0$, there is no disease-free equilibrium. In this section, we prove the existence of a unique equilibrium and analyze its global stability.

Theorem 4.1. *Assume that $c>0$. There exists a unique endemic equilibrium $\mathscr{E}_*(S_*,I_*)$ of the system (2), where $I_*\in(\frac{c}{\mu+d+r},\frac{A+b+ce^{\mu\tau}}{(\mu+d+r)e^{\mu\tau}})$ and $S_*=\frac{A+b+ce^{\mu\tau}-(\mu+d+r)e^{\mu\tau}I_*}{\mu+\nu}$.*

Proof. Solving $\frac{dS}{dt}=0$ and $\frac{dI}{dt}=0$, we obtain

$$(A+b-\mu S-\mathscr{F}(S,I)I-\nu S)e^{-\mu\tau}=0, \tag{7}$$

$$c+\mathscr{F}(S,I)Ie^{-\mu\tau}-(\mu+d+r)I=0. \tag{8}$$

Adding (7) and (8), we get $I = \frac{A+b+ce^{\mu\tau}-(\mu+\nu)S}{(\mu+d+r)e^{\mu\tau}}$, then $I \leq \frac{A+b+ce^{\mu\tau}}{(\mu+d+r)e^{\mu\tau}}$.

From (8), we have $\mathscr{F}(S,I)Ie^{-\mu\tau} = (\mu+d+r)I - c$. So, $I \geq \frac{c}{\mu+d+r}$. Consequently,

$$\frac{c}{\mu+d+r} \leq I \leq \frac{A+b+ce^{\mu\tau}}{(\mu+d+r)e^{\mu\tau}}.$$

If $I > \frac{A+b+ce^{\mu\tau}}{(\mu+d+r)e^{\mu\tau}}$ or $I < \frac{c}{\mu+d+r}$, then there is no positive equilibrium point.

Let us consider the function L defined on $[\frac{c}{\mu+d+r}, \frac{A+b+ce^{\mu\tau}}{(\mu+d+r)e^{\mu\tau}}]$ by

$$L(I) = c + \mathscr{F}(h(I),I)Ie^{-\mu\tau} - (\mu+d+r)I,$$

where $h(I) = \frac{A+b+ce^{\mu\tau}-(\mu+d+r)e^{\mu\tau}I}{\mu+\nu}$.

We have $L(\frac{c}{\mu+d+r}) = \frac{ce^{-\mu\tau}}{\mu+d+r}\mathscr{F}(\frac{A+b}{\mu+\nu}, \frac{c}{\mu+d+r}) > 0$ and $L(\frac{A+b+ce^{\mu\tau}}{(\mu+d+r)e^{\mu\tau}}) = -(A+b)e^{-\mu\tau} < 0$.

Therefore, there exists at least $I_* \in (\frac{c}{\mu+d+r}, \frac{A+b+ce^{\mu\tau}}{(\mu+d+r)e^{\mu\tau}})$ such that $L(I_*) = 0$.

Moreover, we have $L'(I_*) = [h'(I_*)\frac{\partial \mathscr{F}}{\partial S} + \frac{\partial \mathscr{F}}{\partial I}]I_* e^{-\mu\tau} + \mathscr{F}(h(I_*),I_*)e^{-\mu\tau} - (\mu+d+r)$.

Taking into account (H_2), (H_3) and (8), we get $L'(I_*) < 0$. Then I_* is the unique solution of the equation $L(I) = 0$. Consequently, system (2) has a unique endemic equilibrium $\mathscr{E}_*(S_*,I_*)$, where $I_* \in (\frac{c}{\mu+d+r}, \frac{A+b+ce^{\mu\tau}}{(\mu+d+r)e^{\mu\tau}})$ and $S_* = \frac{A+b+ce^{\mu\tau}-(\mu+d+r)e^{\mu\tau}I_*}{\mu+\nu}$. ■

Theorem 4.2. *The equilibrium $\mathscr{E}_*(S_*,I_*)$ of system (2) is globally asymptotically stable.*

Proof. Let g be the function defined from $\mathbb{R}_+^*$ to $\mathbb{R}$ by $g(x) = x - 1 - \ln(x)$. It is clear that $g(x) \geq 0$ for any $x > 0$ and $g(x) = 0$ if and only if $x = 1$. Hence, we define the following Lyapunov function Q by

$$Q(t) = S(t) - S_* - \int_{S_*}^{S(t)} \frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(X,I_*)}dX + e^{\mu\tau}I_* g\Big(\frac{I(t)}{I_*}\Big) + \mathscr{F}(S_*,I_*)I_* \int_{t-\tau}^{t} g\Big(\frac{\mathscr{F}(S(\theta),I(\theta))I(\theta)}{\mathscr{F}(S_*,I_*)I_*}\Big)d\theta.$$

As in [6], we will use the following notations: $X = X(t)$ and $X_\tau = X(t-\tau)$ for any $X \in \{S,I\}$, in order to simplify the presentation. Calculating the time derivative of Q along the positive solution of system (2), we get

$$\begin{aligned}\frac{dQ}{dt} &= [A+b-(\mu+\nu)S - \mathscr{F}(S,I)I](1 - \frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)}) + e^{\mu\tau}(c + \mathscr{F}(S_\tau,I_\tau)I_\tau e^{-\mu\tau} - aI)(1 - \frac{I_*}{I}) \\ &\quad + \mathscr{F}(S_*,I_*)I_*\Big[g\Big(\frac{\mathscr{F}(S,I)I}{\mathscr{F}(S_*,I_*)I_*}\Big) - g\Big(\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S_*,I_*)I_*}\Big)\Big].\end{aligned}$$

Since $A+b=(\mu+\nu)S_*+\mathscr{F}(S_*,I_*)I_*$ and $\mathscr{F}(S_*,I_*)I_*=(aI_*-c)e^{\mu\tau}$, we have

$$\begin{aligned}\frac{dQ}{dt} &= [(\mu+\nu)S_*(1-\frac{S}{S_*})+\mathscr{F}(S_*,I_*)I_*-\mathscr{F}(S,I)I](1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})\\ &+e^{\mu\tau}(1-\frac{I_*}{I})[c(1-\frac{I}{I_*})+\mathscr{F}(S_\tau,I_\tau)I_\tau e^{-\mu\tau}-\mathscr{F}(S_*,I_*)Ie^{-\mu\tau}]\\ &+\mathscr{F}(S_*,I_*)I_*[\frac{\mathscr{F}(S,I)I}{\mathscr{F}(S_*,I_*)I_*}-\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S_*,I_*)I_*}+\ln(\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S,I)I})].\end{aligned}$$

Thus,

$$\begin{aligned}\frac{dQ}{dt} &= (\mu+\nu)S_*(1-\frac{S}{S_*})(1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})+(\mathscr{F}(S_*,I_*)I_*-\mathscr{F}(S,I)I)(1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})\\ &+(1-\frac{I_*}{I})[\mathscr{F}(S_\tau,I_\tau)I_\tau-\mathscr{F}(S_*,I_*)I]-\frac{c(I-I_*)^2}{II_*}e^{\mu\tau}\\ &+\mathscr{F}(S_*,I_*)I_*[\frac{\mathscr{F}(S,I)I}{\mathscr{F}(S_*,I_*)I_*}-\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S_*,I_*)I_*}+\ln(\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S,I)I})].\end{aligned}$$

This leads to

$$\begin{aligned}\frac{dQ}{dt} &= (\mu+\nu)S_*(1-\frac{S}{S_*})(1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})-\frac{c(I-I_*)^2}{II_*}e^{\mu\tau}-\mathscr{F}(S_*,I_*)I_*[-1+\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)}-\frac{\mathscr{F}(S,I)}{\mathscr{F}(S,I_*)}\frac{I}{I_*}\\ &+\frac{I}{I_*}+\frac{\mathscr{F}(S_\tau,I_\tau)}{\mathscr{F}(S_*,I_*)}\frac{I_\tau}{I}-1-\ln(\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S,I)I})].\\ &= (\mu+\nu)S_*(1-\frac{S}{S_*})(1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})-\frac{c(I-I_*)^2}{II_*}e^{\mu\tau}+\mathscr{F}(S_*,I_*)I_*[\frac{\mathscr{F}(S,I)}{\mathscr{F}(S_*,I_*)}-\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S_*,I_*)I}\\ &+\ln(\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S,I)I})-1-\frac{I}{I_*}+\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}+\frac{\mathscr{F}(S,I)}{\mathscr{F}(S,I_*)}\frac{I}{I_*}+3-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)}-\frac{\mathscr{F}(S,I)}{\mathscr{F}(S_*,I_*)}-\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}]\\ &= (\mu+\nu)S_*(1-\frac{S}{S_*})(1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})-\frac{c(I-I_*)^2}{II_*}e^{\mu\tau}+\mathscr{F}(S_*,I_*)I_*[-1-\frac{I}{I_*}+\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}\\ &+\frac{\mathscr{F}(S,I)}{\mathscr{F}(S,I_*)}\frac{I}{I_*}]+\mathscr{F}(S_*,I_*)I_*[\frac{\mathscr{F}(S,I)}{\mathscr{F}(S_*,I_*)}-\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S_*,I_*)I}+\ln(\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S,I)I})]\\ &+\mathscr{F}(S_*,I_*)I_*[3-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)}-\frac{\mathscr{F}(S,I)}{\mathscr{F}(S_*,I_*)}-\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}].\end{aligned}$$

Then

$$\begin{aligned}\frac{dQ}{dt} &= (\mu+\nu)S_*(1-\frac{S}{S_*})(1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})-\frac{c(I-I_*)^2}{II_*}e^{\mu\tau}+\mathscr{F}(S_*,I_*)I_*[-1-\frac{I}{I_*}\\ &+\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}+\frac{\mathscr{F}(S,I)}{\mathscr{F}(S,I_*)}\frac{I}{I_*}]-\mathscr{F}(S_*,I_*)I_*[\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)}-1-\ln(\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})+\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}-1\\ &-\ln(\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)})+\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S_*,I_*)I}-1-\ln(\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S_*,I_*)I})]\end{aligned}$$

$$= (\mu+\nu)S_*(1-\frac{S}{S_*})(1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})-\frac{c(I-I_*)^2}{II_*}e^{\mu\tau}+\mathscr{F}(S_*,I_*)I_*[-1-\frac{I}{I_*}+\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}$$
$$+\frac{\mathscr{F}(S,I)}{\mathscr{F}(S,I_*)}\frac{I}{I_*}]-\mathscr{F}(S_*,I_*)I_*[g(\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)})+g(\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)})+g(\frac{\mathscr{F}(S_\tau,I_\tau)I_\tau}{\mathscr{F}(S_*,I_*)I})].$$

According to (H_4), we have

$$-1-\frac{I}{I_*}+\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}+\frac{\mathscr{F}(S,I)}{\mathscr{F}(S,I_*)}\frac{I}{I_*}=\left(1-\frac{\mathscr{F}(S,I)}{\mathscr{F}(S,I_*)}\right)\left(\frac{\mathscr{F}(S,I_*)}{\mathscr{F}(S,I)}-\frac{I}{I_*}\right)\leq 0.$$

Moreover, we have

$$\left(1-\frac{S}{S_*}\right)\left(1-\frac{\mathscr{F}(S_*,I_*)}{\mathscr{F}(S,I_*)}\right)\leq 0.$$

Consequently, $\frac{dQ}{dt}\leq 0$ with equality if and only if $S=S_*$ and $I=I_*$. From LaSalle invariance principle [13], it follows that $\mathscr{E}_*$ is globally asymptotically stable. ■

5. Numerical Simulations

In this section, we apply our results to the following model

$$\text{(9)}\qquad \begin{cases} \frac{dS}{dt} &= A+b-\mu S(t)-\frac{\beta S(t)I(t)}{1+\alpha_1 S(t)+\alpha_2 I(t)}-\nu S(t),\\ \frac{dI}{dt} &= c+\frac{\beta S(t-\tau)I(t-\tau)}{1+\alpha_1 S(t-\tau)+\alpha_2 I(t-\tau)}e^{-\mu\tau}-(\mu+d+r)I(t), \end{cases}$$

which is a special case of system (2) by choosing $\mathscr{F}(S,I)=\frac{\beta S}{1+\alpha_1 S+\alpha_2 I}$, where β is the rate of infection, α_1 and α_2 measuring the effects of saturation.

Firstly, we choose $A=6$, $b=1$, $\beta=0.01$, $d=0.01$, $\mu=0.01$, $\nu=0.01$, $r=0.01$, $\alpha_1=0.1$, $\alpha_2=0.1$ and $\tau=5.6$.

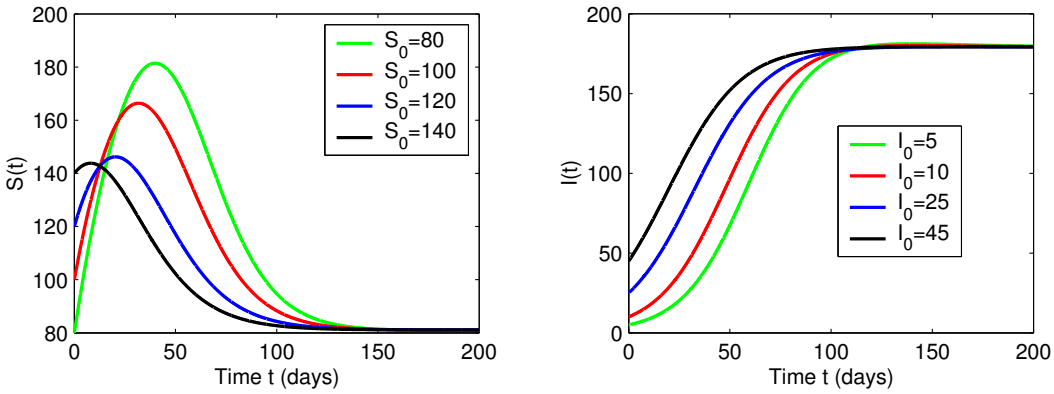

FIGURE 1. The dynamical behavior of system (2) when $c=0$.

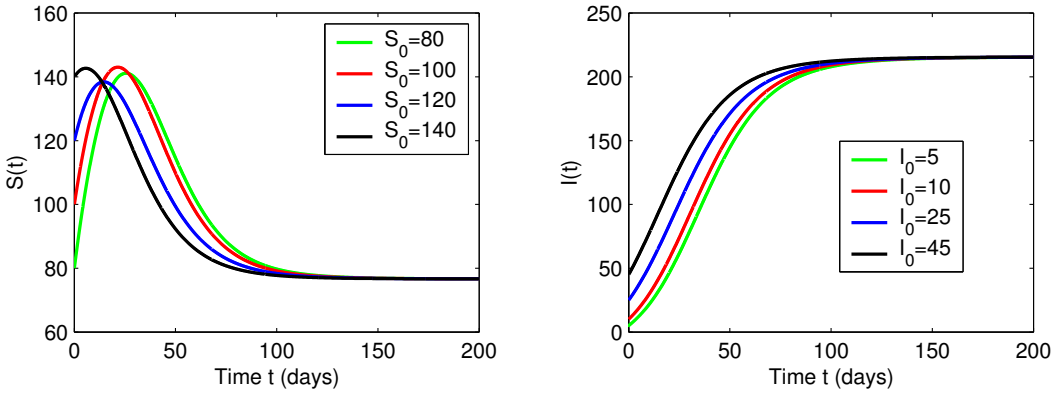

FIGURE 2. The dynamical behavior of system (2) when $c = 1$.

Figures 1 and 2 show the dynamics of system (2) for four different initial conditions. We observe that the solutions of model (2) in both cases $c = 0$ and $c = 1 > 0$, converge from a certain time to the unique endemic equilibrium. This confirms the global stability results given in sections 3 and 4. From a biological point of view, the disease will persist in the population but it will be under control.

Next, we study the impact of delay, vaccination as well as immigration on dynamical behavior of COVID-19 model.

5.1. Impact of delay. Now, we take different values of τ and the same other parameters as above except $\mu = 0.02$, $\alpha_1 = 0.2$ and $\alpha_2 = 0.2$.

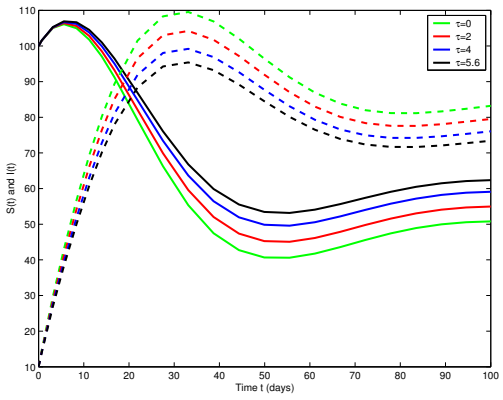

FIGURE 3. The numerical simulation of paths $S(t)$ (the continuous line trajectories) and $I(t)$ (the dashed line trajectories) of our model (2) for different values of τ.

The consideration of temporal delays in epidemic modeling is important to describe a variety of factors. Moreover, the notion of delay helped to formulate the concept of latency, which represents the period of incubation. Figure 3 shows that considering temporal delays creates the difference.

5.2. Impact of vaccination. Next, we take different values of ν and the same other parameters as above.

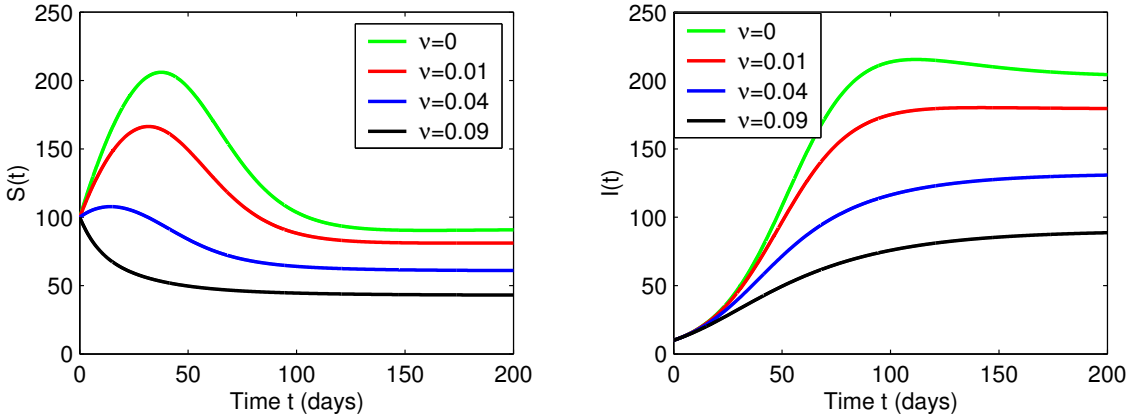

FIGURE 4. The dynamical behavior of system (2) for different values of ν.

One can see that Figure 4 shows that the vaccination rate has a very important impact on the dynamical behavior of the system (2) and also prove that intensifying the vaccination significantly decreases the number of confirmed cases. This tells us that vaccine plays a critical role in reducing the number of infected individuals.

5.3. Impact of susceptible individuals immigration. For this simulation, we take different values of b and the same other parameters as above except $c = 2$ and $\alpha_2 = 0.2$.

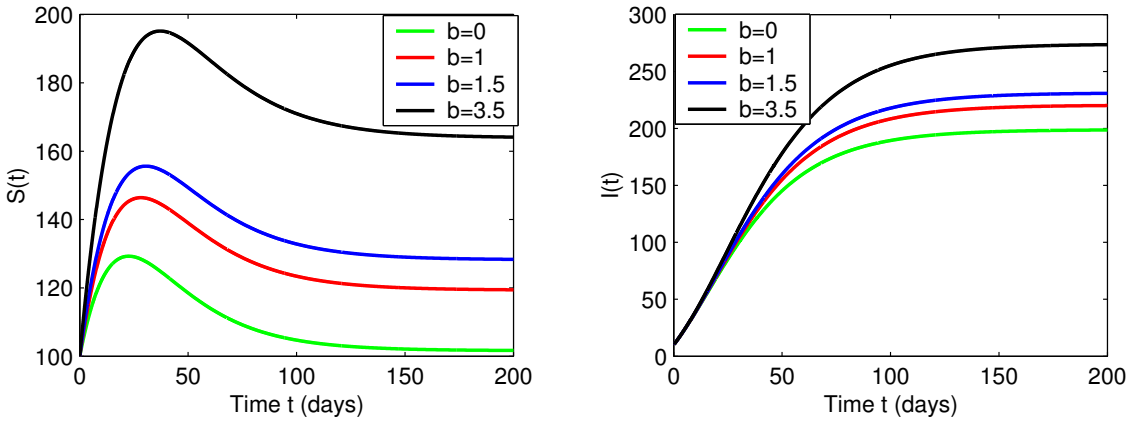

FIGURE 5. The dynamical behavior of system (2) for different values of b.

Figure 5 shows the dynamical behavior of system (2) for different values of b.

5.4. Impact of infected individuals immigration. In this case, we take different values of c and the same other parameters as above except $\alpha_2 = 0.2$.

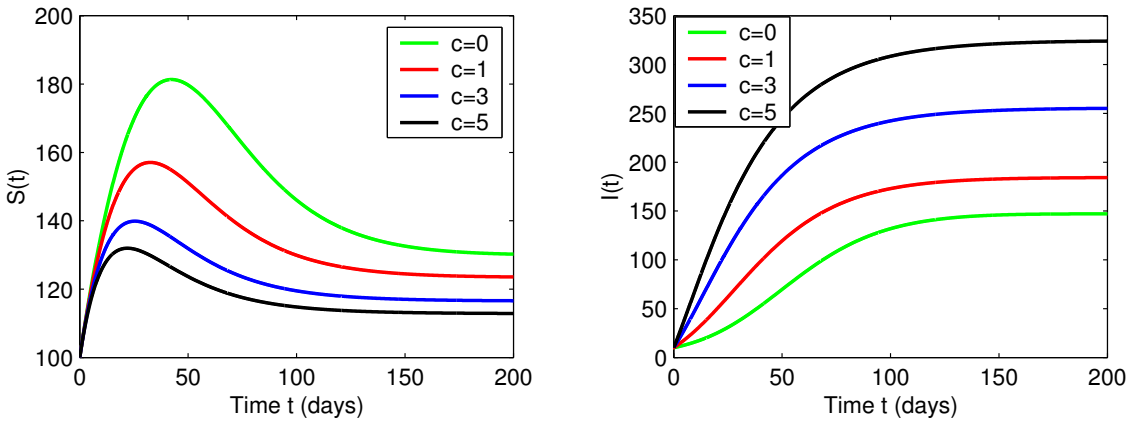

FIGURE 6. The dynamical behavior of system (2) for different values of c.

Figure 6 shows that the immigration of infected individuals has a great effect on the solutions of system (2). Because of this immigration, the disease will persist in and its elimination will be a very painful task. To eliminate the infection, we have to either control the immigration of infected individuals or uproot the disease in all regions.

6. Discussion and Conclusion

In this study, we have developed a new delayed SIR epidemic model to well describe the behavior of the COVID-19 disease epidemic. The model takes into account the immigration, vaccination and general incidence function. We have first provided the result regarding the well-posedness of the proposed model in terms of nonnegativity and boundedness of the solutions. In the case where $c = 0$, we found the results obtained in [6] (the model has the disease-free equilibrium which is globally asymptotically stable when $R_0 \leq 1$ and the disease is finally extinguished. When $R_0 > 1$, the disease persists and the model has a unique endemic equilibrium which is globally asymptotically stable). When $c > 0$, we have shown that the model has no disease-free equilibrium and we proved that there exists a unique endemic equilibrium which is globally asymptotically stable. Furthermore, we have investigated the impact of vaccination on the spread of the disease by showing that the vaccination decreases the number of confirmed cases while the disease will persist because of the immigration of infected individuals. To eliminate the infection, we can to either control the immigration of infected individuals or uproot the disease in all regions.

On the other hand, the study of the memory effect by using the new generalized Hattaf fractional derivative [14, 15] and also the impact of stochastic perturbations [16] on the dynamics of our developed model will be the main aim of our future works.

Conflict of Interests

The authors declare that there is no conflict of interests.

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