Mathematical model of COVID-19 transmission in the presence of waning immunity

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Abstract. We develop a new transmission model of COVID-19 in the presence of waning immunity with isolation and vaccination in humans. The spreading of the disease is determined by the basic reproduction number ($R_0$). Based on mathematical analysis, we found that the non-endemic equilibrium is locally asymptotically stable when $R_0 < 1$ whereas the endemic equilibrium is locally asymptotically stable when $R_0 > 1$. A numerical simulation is used to show the population dynamics. In conclusion, isolation, and vaccination (once it is available) are regarded as effective strategies for eliminating viruses, or at least to suppress the spread of the disease.

1. Introduction

This Coronavirus disease 2019 or commonly called COVID-19 that was caused by the virus named SARS-CoV-2 began in December 2019 in Wuhan city, Hubei province, China which then spread throughout the world rapidly and caused an outbreak [1]. The symptoms of the virus in humans include fever, dry cough, fatigue, dyspnoea, myalgia, normal or decrease leukocyte, and pneumonia [2]. These symptoms caused by COVID-19 are similar to the symptoms of infections by SARS-CoV and MERS-CoV [3]. Human-to-human transmission through droplets that are spread by coughing or sneezing from the infected. Also, transmission via the faecal-oral route possibly happens because SARS-CoV-2 RNA is not an inanimate virus detected in faeces [4].

The first report stated that the transmission of SARS-CoV-2 can occur from people who are infectious but asymptomatic [5]. In some cases, asymptomatic patients play a major role in the spread of this virus [6]. Therefore, asymptomatic patients are very important to be identified. Based on data, the absence of symptoms in these cases is unknown whether only at the beginning after contracting the disease or during their illness [7]. Health care workers are particularly at risk for nosocomial transmission because of the potential exposure to aerosol respiratory secretions during intubation, tracheal suctioning, bronchoscopy and termination of respiratory circuits, and environmental contamination [8,9]. Prevention that must be carried out in the ICU should ideally be isolated in the air pressure isolation room (AIIR) negative pressure with sufficient air changes and health workers have to use personal protective equipment (PPE) for air preventative measures [10,11]. If airborne prevention is not conducive due to limited facilities or excessive number of cases, other actions taken to reduce the risk of nosocomial transmission are physical distancing, supported by the use of disciplined PPE, universal contact, and water-drop prevention measures, and adequate ward ventilation [12,13].

Researchers are looking for effective and suitable vaccine and therapy candidates to control the deadly COVID-19. There is no effective vaccine or antiviral drug specifically for COVID-19. Therefore, controlling an outbreak depends exclusively on enforcing preventive measures and strict controls that
minimize the risk of possible transmission of the disease such as physical separation or physical distancing. The results obtained from a recent in vitro study of COVID-19 are promising because remdesivir and chloroquine drugs are found to be very effective in controlling infection [10]. According to WHO, research has shown, people infected with coronavirus build up antibodies, but they are not sure that the antibodies build up enough immunity to avoid reinfection. For some diseases, those who had infected after the first infection then recovered are immune for life. For other coronaviruses such as SARS, immunity lasted from a few months to a couple of years. In April, more than 100 reported cases by South Korean health officials. They say patients who had recovered could become reinfected as mentioned in https://www.sciencealert.com/those-positive-results-from-recovered-covid-19-patients-weren-t-reinfections-after-all. WHO said there is no study and research has evaluated whether antibodies can make someone immune to the infection of SARS-CoV-2 as of 24 April 2020 [7]. A study offer insight into potential reinfection. It is 38 out of 262, or almost 15% of the patients who had infected and recovered become positive again via PCR (polymerase chain reaction) tests in the southern Chinese city of Shenzhen as mentioned in https://www.time.com/5810454/coronavirus-immunity-reinfection.

Some mathematicians study about the mathematical model of COVID-19 to describe the dynamics of the evolution of the disease [14]. A key role in informing evidence-based decisions by health decision makers and policy makers is obtained through mathematical modelling [15]. Due to the emergence of a sudden outbreak of COVID-19, it is undeniable that both reported and unreported cases are very high. Therefore, it is very important to implement epidemic control measures. The SIR model with unreported cases is analyzed to understand the relation of unreported cases to reported cases [16,17]. Another mathematical model proposed by using the SEIR model obtained how high the reproductive value of control and the effect of interventions from quarantine and isolation [15].

In this paper, we propose a dynamic model of the spread of COVID-19 by modifying the SEIR model with waning immune factor. In terms of intervention, the model assumes the presence of vaccination and isolation as an effort to overcome the spread of COVID-19 which is now considered a global problem.

2. Method
In this paper, we assume that the type of the virus that spread are the same. The proposed model considers a total population \(N(t)\) that partitioned into five subclasses. Some individuals are susceptible \(S(t)\) is the individual that is yet to be infected, exposed \(E(t)\) as the individual that is infected asymptotic, infected \(I(t)\) is the individual that is contracted with SARS-CoV-2, isolated \(Q(t)\) is the individual that is contracted with SARS-CoV-2 and being isolated, and recovered \(R(t)\) is the individual that recovers from the disease. We study the effect of vaccination and isolation on the outbreaks which will be indicated by the isolation parameter \((h)\) and vaccination parameter is divided by \((p)\) as efficacy of vaccination and \((q)\) as proportion of vaccination where \(0 \leq p \leq 1\) and \(0 \leq q \leq 1\). The description of the SEIQR framework dynamic will be described in this following diagram.
The following differential equations are derived based on the assumption and using the compartment diagram where $A = \mu$:

$$\frac{dS}{dt} = A - \gamma S(t)(E(t) + I(t)) + cE(t) + bl(t) + aR(t) + eQ - \mu S(t) - pqS(t),$$

$$\frac{dE}{dt} = \gamma S(t)(E(t) + I(t)) - (c + \varepsilon + \mu)E(t),$$

$$\frac{dI}{dt} = \varepsilon E(t) - (\beta + b + \mu + h)I(t),$$

$$\frac{dQ}{dt} = hI(t) - (\mu + d + e)Q(t),$$

$$\frac{dR}{dt} = \beta I(t) - (\alpha + \mu)R(t) + pqS(t) + dQ(t).$$

Table 1 provides the parameters of the model.

| Parameter | Description |
|-----------|-------------|
| $A$       | Birth rate of susceptible |
| $\alpha$  | Rate at which the recovered become susceptible again |
| $\beta$   | Recovery rate |
| $\gamma$  | Infected contact rate |
| $\varepsilon$ | $\frac{1}{HP}$, HP is the incubation period |
| $\mu$     | Natural death rate |
| $b$       | Rate at which the infected become susceptible again |
| $c$       | Rate at which the exposed become susceptible again |
| $h$       | Rate at which the infected human to be isolated |
| $p$       | Efficacy of vaccination |
| $q$       | Proportion of vaccination |
| $d$       | Recovery rate from isolation |
| $e$       | Rate at which the isolated become susceptible again |
3. Result and Discussion

3.1. Dynamic Analysis

System (1) has two equilibrium points that the variables have non-zero values. The following equilibrium points are obtained from the system (1). The non-endemic equilibrium ($E_0$) and endemic equilibrium ($E_1$) are

$$E_0 = (S^0, E^0, I^0, Q^0, R^0) = \left( \frac{a+\mu}{pq+a+\mu}, 0, 0, 0, \frac{pq}{pq+a+\mu} \right),$$

$$E_1 = (S^*, E^*, I^*, Q^*, R^*),$$

where

$$S^* = \frac{(c+\varepsilon+\mu)(\beta+b+h+\mu)}{\gamma(\beta+b+h+\varepsilon+\mu)} = \frac{1}{\mathcal{R}_0} \left( \frac{a+\mu}{pq+a+\mu} \right),$$

$$E^* = \frac{(b+\beta+\mu+h)(d+\varepsilon+\mu)\mathcal{F}_1}{F_2},$$

$$I^* = \frac{e(d+\varepsilon+\mu)\mathcal{F}_1}{F_2},$$

$$Q^* = \frac{e\varepsilon\mathcal{F}_1}{F_2},$$

$$R^* = \frac{(b+h+\beta+\mu)(c+\varepsilon+\mu)}{\varphi(a+\mu)\omega} \left( pq\omega + \varphi \left( \frac{pq+a+\mu}{a+\mu} \mathcal{R}_0 - 1 \right) \right),$$

$$F_1 = \gamma(\beta+b+\varepsilon+h+\mu)(a+\mu) - (\beta+b+h+\mu)(c+\varepsilon+\mu)(pq+a+\mu) = (R_0 - 1)(\beta+b+h+\mu)(c+\varepsilon+\mu)(pq+a+\mu),$$

$$F_2 = \gamma(\beta+b+\varepsilon+h+\mu)((a+\mu)\omega + \varphi),$$

$$\omega = (b+h+\beta+\varepsilon+\mu)(d+\varepsilon+\mu) + eh,$$

$$\varphi = e(dh+d\beta+e\beta+\mu\beta).$$

Using the next-generation matrix method, the basic reproduction number from system (1) as equation (2).

$$\mathcal{R}_0 = \frac{\gamma(a+\mu)(\beta+b+\mu+h+\varepsilon)}{(pq+a+\mu)(c+\varepsilon+\mu)(\beta+b+\mu+h)} = \mathcal{R}_1 \mathcal{R}_2,$$

where $\mathcal{R}_1 = \frac{\gamma(a+\mu)}{(pq+a+\mu)(c+\varepsilon+\mu)}$ and $\mathcal{R}_2 = \frac{(\beta+b+\mu+h+\varepsilon)}{(\beta+b+\mu+h)}$.

When $\mathcal{R}_0 > 0$, then $F_1 > 0$, so that the endemic equilibrium point exists. It can be seen from $\mathcal{R}_1$ that the vaccination parameter $p$ and $q$ decreases $\mathcal{R}_0$. Also $\mathcal{R}_2$ shows that the greater the rate of isolation ($h$) the smaller $\mathcal{R}_0$, with the condition of the virus incubation period $\varepsilon > 0$.

To analyze the stability of the equilibrium, we first linearize the system so that the Jacobian matrix obtained. After that, substitute the equilibrium point to the Jacobian matrix. The Jacobian matrix of the non-endemic equilibrium is as following equation (3).

$$J = \begin{bmatrix}
-\mu - pq & \frac{-\gamma(a+\mu)}{pq+a+\mu} + c & \frac{-\gamma(a+\mu)}{pq+a+\mu} + b & e & a \\
0 & \frac{\gamma(a+\mu)}{pq+a+\mu} - c - \varepsilon - \mu & 0 & 0 & 0 \\
0 & \varepsilon & -b - \beta - h - \mu & 0 & 0 \\
0 & 0 & h & -d - e - \mu & 0 \\
0 & 0 & \beta & d & -a - \mu
\end{bmatrix}$$

The following eigenvalues obtained from the Jacobian matrix:

$$\lambda_1 = -\mu.$$
\[ \lambda_2 = -(d + e + \mu), \]
\[ \lambda_3 = -(pq + a + \mu), \]
\[ \lambda_4 = -\frac{1}{2} \left( L - \frac{\gamma(a + \mu) + \sqrt{L^2 + 4G}}{pq + a + \mu} \right), \]
\[ \lambda_5 = -\frac{1}{2} \left( L - \frac{\gamma(a + \mu) - \sqrt{L^2 + 4G}}{pq + a + \mu} \right), \]

where \( L = (b + \beta + h + c + \varepsilon + 2\mu) > 0, \ G = \gamma(a + \mu)(\beta + b + \mu + h + \varepsilon) - (pq + a + \mu)(c + \varepsilon + \mu)(\beta + b + \mu + h). \) It is clear that \( \lambda_1, \lambda_2, \lambda_3 \) are negative. If \( R_0 < 1, \) then \( G < 0. \) It means \( \lambda_4, \lambda_5 < 0. \) So the non-endemic equilibrium point is locally asymptotically stable when \( R_0 < 1. \)

The Jacobian matrix of the endemic equilibrium is as following equation (4).

\[
J = \begin{bmatrix}
-\gamma(E^* + I^*) - \mu - pq & -\gamma S^* + c & -\gamma S^* + b & e & a \\
\gamma(E^* + I^*) & \gamma S^* - c - \varepsilon - \mu & \gamma S^* & 0 & 0 \\
0 & \varepsilon & -b - \beta - h - \mu & 0 & 0 \\
0 & pq & 0 & h & -d - e - \mu \\
pq & 0 & \beta & d & -a - \mu \\
\end{bmatrix}
\]

Based on the Jacobian matrix, we get the characteristic polynomial as equation (5).

\[
(\lambda + \mu)(a_4\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0) = 0
\]

The endemic equilibrium will be locally asymptotically stable with the condition \( a_0, a_1, a_2, a_3 > 0 \) and \( R_0 > 1. \)

3.2. Numerical Simulation

The numerical simulation is used to show the population dynamics. We divided the numerical simulation into two scenarios, Worst Case Scenario and Isolation & Vaccination Scenario. The results of numerical simulation are displayed in Figure 2, Figure 3, Figure 4, and Figure 5.

Figure 2. Population Dynamics of the worst-case scenario as \( R_0 < 1 \)

Figure 2 shows that population dynamics of the worst-case scenario as \( R_0 < 1 \) for \( a = 0.35, \ \beta = 0.5, \ b = 0.025, \ c = 0.35, \ \varepsilon = 0.15, \ \gamma = 0.1, \ e = 0.35, p = 0, q = 0, d = 0, \mu = 0.015 \) and initial condition \( (S(0), E(0), I(0), Q(0), R(0)) = (0.02, 0.06, 0.03, 0.015, 0.01). \) We get \( R_0 = 0.24811219 < 1. \) In this scenario, the non-endemic equilibrium \( E_0 \) is locally asymptotically stable. The
exposed $E(t)$, the infected $I(t)$ and the isolated $Q(t)$ of solutions approaches to 0 as $t$ approaches to positive infinity. It means the disease will not spread in the population or dies out.

Figure 3. Population Dynamics of the worst-case scenario as $R_0 > 1$

Figure 3 shows that population dynamics of the worst-case scenario as $R_0 > 1$ for $a = 0.35$, $\beta = 0.33$, $b = 0.025$, $c = 0.35$, $\epsilon = 0.1$, $\gamma = 0.55$, $e = 0.35$, $p = 0$, $q = 0$, $d = 0$, $\mu = 0.075$ and initial condition $(S(0), E(0), I(0), Q(0), R(0)) = (0.01, 0.01, 0.01, 0.005, 0.01)$. We get $R_0 = 1.291251384 > 1$. In this scenario, the endemic equilibrium $E_1$ is locally asymptotically stable. The exposed $E(t)$ and the infected $I(t)$ approach to 0.15 and 0.04 respectively as $t$ approaches to positive infinity. It means the disease will spread or remains in the population.

Figure 4. Population Dynamics of the isolation and vaccination scenario as $R_0 < 1$

Figure 4 shows that the population dynamics of the isolation and vaccination scenario as $R_0 < 1$ for $a = 0.35$, $\beta = 0.5$, $b = 0.025$, $c = 0.35$, $\epsilon = 0.15$, $\gamma = 0.1$, $e = 0.35$, $p = 0.2$, $q = 0.2$, $h = 0.5$, $d = 0.5$, $\mu = 0.015$ and initial condition $(S(0), E(0), I(0), Q(0), R(0)) = (0.02, 0.06, 0.03, 0.015, 0.01)$. We get $R_0 = 0.2002369560 < 1$. In this scenario, the non-endemic equilibrium $E_0$ is locally asymptotically stable. The exposed $E(t)$ and the infected $I(t)$ approach to 0 and the recovered $R(t)$ approaches to 0.03 as $t$ approaches to positive infinity. It means the disease will not spread in the population or dies out.
Figure 5. Population Dynamics of the isolation and vaccination scenario as $\mathcal{R}_0 > 1$

Figure 5 shows the population dynamics of the isolation and vaccination scenario as $\mathcal{R}_0 > 1$ for $a = 0.35$, $\beta = 0.33$, $b = 0.025$, $c = 0.35$, $\epsilon = 0.1$, $\gamma = 0.55$, $e = 0.35$, $p = 0.2$, $q = 0.2$, $h = 0.5$, $d = 0.5 \mu = 0.075$ and initial condition $(S(0), E(0), I(0), Q(0), R(0)) = (0.01, 0.01, 0.01, 0.005, 0.01)$. We get $\mathcal{R}_0 = 1.083488291 < 1$. In this scenario, the endemic equilibrium $E_1$ is locally asymptotically stable. The exposed $E(t)$, the infected $I(t)$, the recovered $R(t)$ approach 0.05, 0.01, and 0.07 respectively, as $t$ approaches to positive infinity. It means the disease will spread or remains in the population. Also, the isolation & vaccination is effective to suppress the spread of the disease.

4. Conclusion

In this paper, a new transmission model of COVID-19 in the presence of waning immunity with isolation and vaccination in humans is developed. The basic reproduction number $\mathcal{R}_0$ is the threshold condition that determines the propagation dynamics. The system has two equilibrium. A non-endemic equilibrium $E_0$ is locally asymptotically stable when $\mathcal{R}_0 < 1$, it means the disease will not spread in the population or dies out. Whereas the endemic equilibrium $E_1$ is locally asymptotically stable when $\mathcal{R}_0 > 1$. It means the disease will spread or remains in the population. The isolation and vaccination is effective to suppress the spreading of COVID-19 although there is waning immunity in the population.

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