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A Mathematical Model of the Transmission of COVID-19 in Ghana

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Abstract: The COVID-19 pandemic posed a serious threat to health and the global economy of the affected nations. Despite several measures to mitigate the transmission of the disease, there is a rise in the number of infections and death remain tremendous worldwide. This study used a deterministic model based on Susceptible-Latent-Infected-Hospitalized-Vaccinated-Recovered (SLIHVR) model to investigate the dynamics of the disease in Ghana. Data from daily reported cases of COVID-19 in Ghana between 15 March and 31 March 2021 were used to estimate the parameters of the model. Numerical simulations of the model were carried out by implementing the MATLAB ODE45 algorithm for solving non-stiff ordinary differential equations. The numerical simulation of the model was done to ascertain the long-run evolution of COVID-19. The findings indicated that the disease-free equilibrium was locally asymptotically stable whenever $R_n<1$ and the endemic equilibrium was asymptotically stable provided $R_n>1$. The was useful in understanding the dynamic mechanisms of the transmission and prevention of COVID-19 infection in Ghana. The study concluded that vaccinating a larger proportion of the populace was needed to control the disease.

Keywords: COVID-19 SLIHRV Transmission Dynamics, Stability Analysis, Simulation

1. Introduction

COVID-19, formerly known as the novel coronavirus (2019-nCoV), belongs to a group of justly wrapped non-segmental, single-stranded RNA viruses belonging to the Nidovirales order, the Coronavirus family and its Orthocoronavirus subfamily and is widely spread among mammals and humans [1, 2]. It is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [3, 4]. The disease was initially reported in Wuhan, Hubei province, China, at the end of 2019 [3, 5]. According to the World Health Organization (WHO), adults and people with cardiovascular diseases, diabetes, chronic respiratory diseases, and cancer are more likely to have life-threatening complications after contracting this disease.

The first confirmed death from COVID-19 occurred in Wuhan on 9th January, 2020 [6]. The first reported death outside of China occurred on 1st February in the Philippines, and the first reported death outside Asia was in the United States on 6th February [7]. By 28th February 2021, more than 113 million cases have been confirmed, with more than 2.52 million deaths attributed to COVID-19, making it one of the deadliest pandemics in history. The World Health Organization (WHO) declared the outbreak a public health emergency of international concern in January 2020 and a pandemic in March 2020 [8]. By 26th March 2020, 1.7 billion people worldwide were under some form of lockdown which increased to 3.9 billion people by the first week of April, which was more than half of the world's population [9].

The role of the Huanan Seafood Wholesale Market in the spread of the disease is unclear. However, many of the initial COVID-19 cases were related to this market, indicating that COVID-19 was transmitted from animals to humans [10]. A genomic study on the other hand, indicated that the virus was introduced to the market from another unknown location,

whilst the person-to-person transmission may have occurred earlier [11]. Person-to-person transmission is believed to occur between close contacts, primarily through respiratory droplets that are produced when an infected person coughs or sneezes.

A study by [12], found that COVID-19 aerosols, the main source of COVID-19 transmission could remain for up to 96 hours on the surface, in contrast with other coronaviruses, which can remain for only nine hours. This makes COVID-19 highly contagious and poses serious threats to the health and economies of developing countries with limited health infrastructure and resources to effectively contain its transmission. The longer people interact, the more likely they would transmit COVID-19. Closer distances can produce larger droplets and aerosols, whilst longer distances only involve aerosols. Larger droplets can also become aerosols through evaporation. However, it is unknown whether the virus can spread between rooms over long distances, such as through air ducts [13]. Airborne transmission can occur in high-risk indoor locations such as restaurants, choirs, stadiums, nightclubs, offices, and religious venues, and crowded or poorly ventilated areas. It can also occur in medical institutions, usually during aerosol-generating medical procedures for COVID-19 patients.

The effects of COVID-19 vary from mild symptoms to serious illnesses. The time interval from the onset of COVID-19 symptoms to death is 6 to 41 days, with a median of 14 days [14]. The most common symptoms at the onset of COVID-19 include fever, cough, dyspnoea, headache, sore throat, rhinorrhea, sputum production, haemoptysis, lymphopenia, loss of sense of smell and taste, study and runny nose, muscle pain, diarrhea and difficulty in breathing [15]. Pneumonia seems to be the most common manifestation of serious infections, and its main characteristics are fever, cough, dyspnoea, and bilateral infiltration on chest imaging [16].

Three groups of common symptoms including, respiratory symptoms of cough, sputum, shortness of breath, and fever; cough, sputum, shortness of breath; and fever have been identified. In addition to respiratory symptoms, gastrointestinal symptoms (such as nausea and diarrhea) have also been reported, and people with the same infection may have different symptoms. Their symptoms may change over time [17]. Digestive system symptoms including abdominal pain, vomiting, and diarrhea [18].

Like any other developing country, the COVID-19 outbreak has had seriously repercussions on people's daily lives, public health, and the economy of Ghana. The country recorded its first confirmed cases in Accra, on 12th March 2020 from two immigrants who visited the country, one from Norway and the other from Turkey [19]. Following the episodic transmission of the virus in the country, the Ghanaian government adopted aggressive measures such as social distancing, screening and diagnostic tools, quarantine and isolation, and adequate clinical management of patients to contain the spread of the virus. By 16th March 2020 schools and universities were closed [20], and public gatherings were banned, with the exception for essential public health and safety services. The Ministry of Health used every available medium including newspapers, radio, and TV stations to educate the public about the spread and prevention of COVID-19 infections [21].

2. Model Formulation

To fully understand the transmission dynamics of COVID-19 in Ghana, we formulated the Susceptible-Latent-Infected-Hospitalized-Vaccinated-Recovered (SLIHRV) model using country specific data and information on the biological mechanism through which infections spread in a population (see Figure 1). We divided the population of Ghana into six different categories based on the known characteristics of the COVID-19 pandemic, and assumed that each member of the population could be in one of the defined compartments (categories) (see Table 1).

Table 1. *Definitions of state of variables used in the model.*

Variables	State of Variables Definitions
$S(t)$	Susceptible population
$L(t)$	Latent population
$I(t)$	Infected population
$H(t)$	Hospitalized population
$R(t)$	Recovery population
$V(t)$	Vaccination population

The variables $S(t)$, $L(t)$, $I(t)$, $H(t)$, $R(t)$, and $V(t)$, represented the number of the individuals in each of the six classes at time t respectively.

The Susceptible population S(t) was made up of individuals who were not yet infected but could contract the virus if exposed to an infected individual. After exposure to the COVID-19 virus, the susceptible individuals, S enter the latent class, L where the disease incubates. The latent class is also called the asymptomatic class.

The Latent population L(t) consisted of individuals who have had the infection but do not show any clinical or noticeable symptoms even though they are infectious. They are capable of transmitting the coronavirus to other susceptible individuals. They stay in the L class before they become fully blown infectious with symptoms and move to the infectious class I, or identified through contact tracing and quarantined at class Q.

The Infected population I(t) consisted of individuals who were infectious and symptomatic with strong infectivity but have not yet been quarantined.

The Hospitalized population H(t) consisted of individuals who had been infected, and diagnosed and were in the hospitals.

The Recovered population R(t) was made up of individuals who had fully recovered from the infection.

The Vaccinated population $V(t)$ was made up of individuals who had been vaccinated to protect themselves from COVID-19 infection.

Figure 1 was formulated with α N being the recruitment into the susceptible population. It assumed a constant natural death rate of μ for all the classes. The susceptible population

is vaccinated at a rate of θ. The latent population increased by rate of probability of infection β and decreased by rate of progression from asymptomatic stage to infectiousness γ which later entered the infected class. The infected population became hospitalized at a rate of κ. In the hospitalized class, individuals died from the virus at rate of δ and recovered at a rate of ρ. The recovered population became susceptible at a rate of ω. Table 2 below shows the definition of the parameters used in the model.

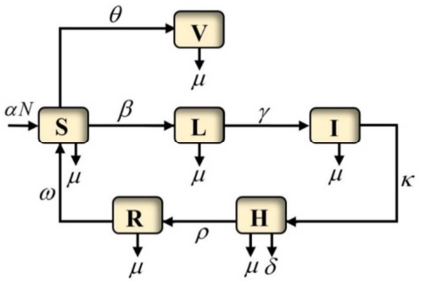

Figure 1. *SLIHVR Compartmental Model of COVID-19 Transmission.*

From the model formulated above (see Figure 1), the following non-linear equations were obtained.

$$\begin{cases} \dfrac{dS}{dt} = \alpha N - \dfrac{\beta(SL+SI)}{N} - \mu S - \theta S + \omega R \\ \dfrac{dL}{dt} = \dfrac{\beta(SL+SI)}{N} - \gamma L - \mu L \\ \dfrac{dI}{dt} = \gamma L - \kappa I - \mu I \\ \dfrac{dH}{dt} = \kappa I - \mu H - \delta H - \rho H \\ \dfrac{dR}{dt} = \rho H - \mu R - \omega R \\ \dfrac{dV}{dt} = \theta S - \mu V \end{cases} \tag{1}$$

Table 2. *Model Parameters and Definitions.*

Parameters	Definitions
β	Rate of probability of infection \
α	Recruitment rate
γ	Rate of progression from asymptomatic stage to infectiousness
K	Rate of hospitalization
ρ	Recovery rate
μ	Natural death rate
δ	Disease induced death rate
θ	Rate of vaccination
ω	Rate of loss of immunity

3. Model Analysis

3.1. Positivity of the Solution

Theorem 1

(Positivity) Suppose that

$S(0) \geq 0, L(0) \geq 0, I(0) \geq 0, H(0) \geq 0, R(0) \geq 0, V(0) \geq 0$

Then the solution $(S(t), L(t), I(t), H(t), R(t), V(t))$ of model Equation (1), is positively invariant set. That is $(S(t), L(t), I(t), H(t), R(t), V(t)) \in R_+^6$ *Proof*

We considered,

$$\frac{dS}{dt} = \alpha N - \frac{\beta(SL+SI)}{N} - \mu S - \theta S - \omega S \tag{2}$$

From Equation (2), we let $\Lambda = \alpha N$ and $\lambda_1 = \dfrac{\beta(SL+SI)}{N}$.

We rewrite equation (2) further as equation (3)

$$\frac{dS}{dt} + (\lambda_1 + \mu + \theta) S = \Lambda + \omega R \tag{3}$$

Solving Equation (3) using the method of integrating factors, we find the integrating factor defined by Equation (4)

$$I.F = e^{\int (\lambda_1 + \mu + \theta) dt} = e^{\int \lambda_1 dt + (\mu+\theta) dt} \tag{4}$$

We multiply through Equation (3) by (4) and simplifying gives Equation (5)

$$\frac{d}{dt}\left(S(t) e^{\int_0^t \lambda_1(s) ds + (\mu+\theta)t} \right) \geq (\Lambda + \omega R) e^{\int_0^t \lambda_1(s) ds + (\mu+\theta)t} \tag{5}$$

Which implies

$$S(t) e^{\int_0^t \lambda_1(s) ds + (\mu+\theta)t} - S(0) \geq \int_0^t (\Lambda + \omega R) e^{\int_0^t \lambda_1(s) ds + (\mu+\theta)t} dw \tag{6}$$

$$S(t) e^{\int_0^t \lambda_1(s) ds + (\mu+\theta)t} \geq S(0) + \int_0^t (\Lambda + \omega R) e^{\int_0^t \lambda_1(s) ds + (\mu+\theta)t} dw \tag{7}$$

Therefore, we have

$$S(t) \geq S(0)e^{-\int_0^t \lambda_1(s)ds+(\mu+\theta)t} + e^{-\int_0^t \lambda_1(s)ds+(\mu+\theta)t} \int_0^t (\Lambda+\omega R) e^{\int_0^t \lambda_1(s)ds+(\mu+\theta)t} dw \quad (8)$$

Hence, $\forall t \in J$, $S(t)$ is positive. Now considering the second equation of the system (1) gives;

$$\frac{dL}{dt} = \lambda_1 S - (\gamma+\mu)L \quad (9)$$

We rewrite Equation (9) as

$$\frac{dL}{dt} + (\gamma+\mu)L = \lambda_1 S \quad (10)$$

Multiplying through equation (10) by the integrating factor, $e^{(\gamma+\mu)}$ and simplifying leads to (11)

$$\frac{d}{dt}\left(L(t)e^{(\gamma+\mu)t}\right) \geq \lambda_1 S e^{(\gamma+\mu)t} \quad (11)$$

Which implies

$$L(t)e^{(\gamma+\mu)t} - L(0) \geq \int_0^w \lambda(w)S(w)e^{(\gamma+\mu)t}dw \quad (12)$$

$$L(t)e^{(\gamma+\mu)t} \geq L(0) + \int_0^w \lambda(w)S(w)e^{(\gamma+\mu)t}dw \quad (13)$$

Therefore,

$$L(t)e^{(\gamma+\mu)t} \geq L(0)e^{-(\gamma+\mu)t} + e^{-(\gamma+\mu)t}\int_0^w \lambda(w)S(w)e^{(\gamma+\mu)t}dw \quad (14)$$

Hence, $\forall t \in J$, $L(t)$ is positive. Similarly, considering the third equation of the system (1) gives;

$$\frac{dI}{dt} = \gamma L - (\kappa+\mu)I \quad (15)$$

$$\frac{dI}{dt} + (\kappa+\mu)I = \gamma L \quad (16)$$

$$\frac{d}{dt}\left(Ie^{(\kappa+\mu)t}\right) \geq \gamma L e^{(\kappa+\mu)t} e^{(\kappa+\mu)t} \quad (17)$$

$$Ie^{(\kappa+\mu)t} - I(0) \geq \gamma\int_0^t L(s)e^{(\kappa+\mu)s}ds \quad (18)$$

$$I(t)e^{(\kappa+\mu)t} \geq I(0) + \gamma\int_0^t L(s)e^{(\kappa+\mu)s}ds \quad (19)$$

$$T(t) \geq I(0)e^{-(\kappa+\mu)t} + \gamma e^{-(\kappa+\mu)t}\int_0^t L(s)e^{(\kappa+\mu)s}ds \quad (20)$$

Hence, $\forall t \in J$, $I(t)$ is positive. Now considering the fourth equation of the system (1) gives;

$$\frac{dH}{dt} = \kappa I - (\mu+\delta+\rho)H \quad (21)$$

$$\frac{dH}{dt} + (\mu+\delta+\rho)H = \kappa I \quad (22)$$

$$\frac{d}{dt}\left(He^{(\mu+\delta+\rho)t}\right) \geq \kappa I e^{(\mu+\delta+\rho)t} \quad (23)$$

$$H(t)e^{(\mu+\delta+\rho)t} - H(0) \geq \kappa\int_0^t I(w)e^{(\mu+\delta+\rho)w}dw \quad (24)$$

$$H(t) \geq H(0)e^{-(\mu+\delta+\rho)t} + \kappa e^{-(\mu+\delta+\rho)t}\int_0^t I(w)e^{(\mu+\delta+\rho)w}dw \quad (25)$$

Hence, $\forall t \in J$, $H(t)$ is positive. Now considering the recovered equation of the system (1) gives;

$$\frac{dR}{dt} = \rho H - (\mu+\omega)R \quad (26)$$

$$\frac{dR}{dt} + (\mu+\omega)R = \rho H \quad (27)$$

$$\frac{d}{dt}\left(\mathrm{Re}^{(\mu+\omega)t}\right) \geq \rho H\, \mathrm{e}^{(\mu+\omega)t} \quad (28)$$

$$R(t)\,\mathrm{e}^{(\mu+\omega)t} - R(0) \geq \rho\int_0^t H(w)\,\mathrm{e}^{(\mu+\omega)w}\,dw \quad (29)$$

$$R(t) \geq R(0)\,\mathrm{e}^{-(\mu+\omega)t} + \rho\,\mathrm{e}^{-(\mu+\omega)t}\int_0^t H(w)\,\mathrm{e}^{(\mu+\omega)w}\,dw \quad (30)$$

Hence, $\forall t \in J$, $R(t)$ is positive. Considering the Vaccination class, we have

$$\frac{dV}{dt} + \mu V = \theta S \quad (31)$$

$$\frac{d}{dt}\left(Ve^{\mu t}\right) \geq \theta S e^{\mu t} \quad (32)$$

$$V(t)e^{\mu t} - V(0) \geq \theta\int_0^w S(w)e^{\mu t}dw \quad (33)$$

$$V(t) \geq V(o)e^{-\mu t} + \theta e^{-\mu t}\int_0^w S(w)e^{\mu t}dw \quad (34)$$

Hence, $\forall t \in J$, $V(t)$ is positive. Hence it has been shown that $S(t) > 0, L(t) > 0, I(t), H(t) > 0$, $R(t) > 0$, and $V(t) > 0$ for all $t > 0$.

3.2. Disease-Free Equilibrium

Disease-free equilibrium points (DFE) are steady-state solutions or equilibrium points where there was no infection of COVID-19. We set the disease-free equilibrium at $L \quad I \quad H \quad R \quad 0$ in the model.

$$\begin{cases} \alpha N - (\mu+\theta)S^* = 0 \\ \theta S^* - \mu V^* = 0 \end{cases} \tag{35}$$

Solving equation (35) gives Equation (36)

$$\text{DFE} = \left[\frac{\alpha N}{\mu+\theta}, 0, 0, 0, 0, \frac{\alpha\theta N}{\mu(\mu+\theta)} \right] \tag{36}$$

3.3. Disease-Endemic Equilibrium

The endemic equilibrium state is the state where the disease cannot be totally eradicated but remains in the population.

$$\begin{cases} \alpha N - \dfrac{\beta S^*(L^* + I^*)}{N} - (\mu+\theta)S^* + \omega R^* = 0 \\ \dfrac{\beta S^*(L^* + I^*)}{N} - (\gamma+\mu)I^* = 0 \\ \gamma L^* - (\kappa+\mu)I^* = 0 \\ \kappa I^* - (\mu+\delta+\rho)H^* = 0 \\ \rho H^* - (\mu+\omega)R^* = 0 \\ \theta S^* - \mu V = 0 \end{cases} \tag{37}$$

Solving equation (35) gives the solutions below

$$\text{EE} = \left[S^*, L^*, I^*, H^*, R^*, V^* \right] \tag{38}$$

where

$$\begin{cases} S^* = \dfrac{\alpha N}{(\mu+\theta)\ {}_0} \\ L^* = \dfrac{\eta_2(\ {}_0 - 1)\eta_3}{\eta_1} \\ I^* = \dfrac{\gamma\eta_2(\ {}_0 - 1)(\mu+\omega)(\mu+\delta+\rho)}{\eta_1} \\ H^* = \dfrac{\gamma\kappa\eta_2(\ {}_0 - 1)(\mu+\omega)}{\eta_1} \\ R^* = \dfrac{\gamma\kappa\eta_2(\ {}_0 - 1)}{\eta_1} \\ V^* = \dfrac{\alpha\theta N}{\mu(\mu+\theta)\ {}_0} \end{cases} \tag{39}$$

3.4. Basic Reproduction Number

Reproduction number is an important topic in epidemiological models which is usually denoted by R_0. It is an important parameter that predicts whether an infection will spread throughout the population or not. To obtain R_0, we used the next generation matrix technique [22]. When an infected person is introduced into a susceptible population, the total number of infectives as a result of this infected person during the epidemic is referred to as Basic Reproduction Number R_0.

$$= \begin{pmatrix} \dfrac{\beta S(L+I)}{N} \\ 0 \\ 0 \end{pmatrix} \text{ and } = \begin{pmatrix} (\gamma+\mu)L \\ -\gamma L + (\kappa+\mu)I \\ (\delta+\mu+\rho)H - \kappa I \end{pmatrix} \tag{40}$$

Partially differentiating with respect to L, I, and H gives

$$\partial_{\ L,I,H} = \begin{pmatrix} \frac{\beta S}{N} & \frac{\beta S}{N} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \tag{41}$$

and

$$\partial_{\ L,I,H} = V = \begin{pmatrix} \mu+\gamma & 0 & 0 \\ -\gamma & \kappa+\mu & 0 \\ 0 & -\kappa & \delta+\mu+\rho \end{pmatrix} \tag{42}$$

Substituting the Disease-Free equilibrium into Equations (41) and (42) produces equations (43) and (44)

$$F = \begin{pmatrix} \frac{\alpha\beta}{\mu+\theta} & \frac{\alpha\beta}{\mu+\theta} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \tag{43}$$

and

$$V = \begin{pmatrix} \mu+\gamma & 0 & 0 \\ -\gamma & \kappa+\mu & 0 \\ 0 & -\kappa & \delta+\mu+\rho \end{pmatrix} \tag{44}$$

The inverse of V is calculated and given below.

$$V^{-1} = \begin{pmatrix} \dfrac{1}{\mu+\gamma} & 0 & 0 \\ \dfrac{\gamma}{(\mu+\gamma)(\mu+\kappa)} & \dfrac{1}{\kappa+\mu} & 0 \\ \dfrac{\gamma\kappa}{(\mu+\gamma)(\mu+\kappa)(\delta+\mu+\rho)} & \dfrac{\kappa}{(\mu+\kappa)(\delta+\mu+\rho)} & \dfrac{1}{(\delta+\mu+\rho)} \end{pmatrix} \tag{45}$$

Therefore, the next generation matrix, G is given as

$$G = FV^{-1} = \begin{pmatrix} \frac{\alpha\beta(\kappa+\mu)+\alpha\beta\gamma}{(\mu+\gamma)(\mu+\theta)(\kappa+\mu)} & \frac{\alpha\beta}{(\mu+\gamma)(\kappa+\mu)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \tag{46}$$

Evaluating the eigenvalues of G gives

$$\lambda_1 = 0, \lambda_2 = 0 \text{ and } \lambda_3 = \frac{\alpha\beta(\kappa+\mu+\gamma)}{(\mu+\gamma)(\mu+\theta)(\kappa+\mu)} \quad (47)$$

Therefore, the basic reproduction number, R_0 which is the dominant eigenvalue of the next generation matrix is found in Equation (48)

$$_0 = \frac{\alpha\beta(\kappa+\mu+\gamma)}{(\mu+\gamma)(\mu+\theta)(\kappa+\mu)} \quad (48)$$

3.5. Stability of the Disease-Free Equilibrium Point

Theorem 1:

The disease-free state DFE is locally asymptotically stable if $J(DFE)<1$ and unstable if $J(DFE)>1$ [20].

Proof: The Jacobian matrix of the system (1) denoted by J is obtained in Equation (49)

$$J = \begin{pmatrix} -\frac{\beta(L+I)}{N}-\mu-\theta & -\frac{\beta S}{N} & -\frac{\beta S}{N} & 0 & \omega & 0 \\ \frac{\beta(L+I)}{N} & \frac{\beta S}{N}-\gamma-\mu & \frac{\beta S}{N} & 0 & 0 & 0 \\ 0 & \gamma & -\kappa-\mu & 0 & 0 & 00 \\ 0 & 0 & \kappa & -\delta-\mu-\rho & 0 & 0 \\ 0 & 0 & 0 & \rho & -\mu-\omega & 0 \\ 0 & 0 & \theta & 0 & 0 & -\mu \end{pmatrix} \quad (49)$$

Evaluating the Jacobian matrix (49) at the disease-free equilibrium is obtained as

$$J(\text{DFE}) = \begin{pmatrix} -\mu-\theta & -\frac{\beta\alpha}{\mu+\theta} & -\frac{\beta\alpha}{\mu+\theta} & 0 & \omega & 0 \\ 0 & \frac{\beta\alpha}{\mu+\theta}-\gamma-\mu & \frac{\beta\alpha}{\mu+\theta} & 0 & 0 & 0 \\ 0 & \gamma & -\kappa-\mu & 0 & 0 & 0 \\ 0 & 0 & \kappa & -\delta-\mu-\rho & 0 & 0 \\ 0 & 0 & 0 & \rho & -\mu-\omega & 0 \\ \theta & 0 & 0 & 0 & 0 & -\mu \end{pmatrix} \quad (50)$$

We needed to show that the eigenvalues of Equation (53) were all negative. Solving for the eigenvalues, we get.

$$\begin{cases} \lambda_1 = -\theta-\mu \\ \lambda_2 = -\delta-\mu-\rho \\ \lambda_3 = -\mu-\omega \\ \lambda_4 = -\mu \\ \lambda_5 = -\frac{1}{2(\mu+\theta)}\left(Y-\sqrt{W}\right) \\ \lambda_6 = -\frac{1}{2(\mu+\theta)}\left(Y+\sqrt{W}\right) \end{cases} \quad (51)$$

where

$$Y = -\alpha\beta+\gamma\mu+\gamma\theta+\kappa\mu+\kappa\theta+2\mu^2+2\mu\theta \quad (52)$$

and

$$W = \mu^2\begin{cases} \alpha^2\beta^2+2\alpha\beta\gamma\mu+2\alpha\beta\gamma\theta+2\alpha\beta\kappa\mu+2\alpha\beta\kappa\theta \\ +\gamma^2\mu^2+2\gamma^2\mu\theta+\gamma^2\theta^2-2\gamma\kappa\mu^2-4\gamma\kappa\mu\theta- \\ 2\gamma\kappa\theta^2+\kappa^2\mu^2+2\kappa^2\mu\theta+\kappa^2\theta^2 \end{cases} \quad (53)$$

It can be observed that all the eigenvalues of the Jacobian matrix were are strictly negative with the exception of λ_5. However, for $R_0 < 1$ all eigenvalues must be non-positive.

Multiplying equation (52) by itself, we get gives Equation (54)

$$Y^2 = \begin{pmatrix} \alpha^2\beta^2 - 2\alpha\beta\gamma\mu - 2\alpha\beta\gamma\theta - 2\alpha\beta\kappa\mu - 2\alpha\beta\kappa\theta - 4\alpha\beta\mu^2 - 4\alpha\beta\mu\theta + \gamma^2\mu^2 \\ +2\gamma^2\mu\theta + \gamma^2\theta^2 + 2\gamma\kappa\mu^2 + 4\gamma\kappa\mu\theta + 2\gamma\kappa\theta^2 + 4\gamma\mu^3 + 8\gamma\mu^2\theta + 4\gamma\mu\theta^2 \\ +\kappa^2\mu^2 + 2\kappa^2\mu\theta + \kappa^2\theta^2 + 4\kappa\mu^3 + 8\kappa\mu^2\theta + 4\kappa\mu\theta^2 + 4\mu^4 8\mu^3\theta + 4\mu^2\theta^2 \end{pmatrix} \tag{54}$$

$$W - Y^2 = \begin{pmatrix} 4\alpha\beta\gamma\mu + 4\alpha\beta\gamma\theta + 4\alpha\beta\kappa\mu + 4\alpha\beta\kappa\theta + 4\alpha\beta\mu^2 + \\ 4\alpha\beta\mu\theta - 4\gamma\kappa\mu^2 - 8\gamma\kappa\mu\theta - 4\gamma\kappa\theta^2 - 4\gamma\mu^3 - 8\gamma\mu^2\theta \\ -4\gamma\mu\theta^2 - 4\kappa\mu^3 - 8\kappa\mu^2\theta - 4\kappa\mu\theta^2 - 4\mu^4 - 8\mu^3\theta - 4\mu^2\theta^2 \end{pmatrix} \tag{55}$$

which can be simplify as

$$Z = P_0 + N_0 \tag{56}$$

where

$$p_0 = 4(\theta+\mu)^2(\gamma+\kappa+\mu) \tag{57}$$

and

$$N_0 = -4(\theta+\mu)^2(\mu+\kappa)(\gamma+\mu) \tag{58}$$

and Hence, upon further simplification R_0 is given by the Equation (59).

$$_0 = -\frac{\beta\alpha(\gamma+\kappa+\mu)}{(\theta+\mu)(\mu+\kappa)(\gamma+\mu)} \tag{59}$$

Since $R_0 < 1$, implies the disease-free equilibrium is locally asymptotically stable.

3.6. Local Stability of the Endemic Equilibrium

A corollary of Gershgorin circle theorem was used to investigate the local stability of the endemic equilibrium points of the model. Using the Corollary of Gershgorin Circle Theorem, let A be an $n \times n$ matrix with real entries, if the diagonal elements a_{ii} of A satisfy;

$$a_{ii} < r_i \tag{60}$$

where

$$r_i = \sum_{j=1, j\neq i}^{n} |a_{ii}| \tag{61}$$

for $i+1,\ldots,n$ then the eigenvalues of are negative or have negative real parts.

Theorem 2

The Endemic equilibrium (EE) is locally asymptotically stable if $R_0 <$ s1.

Proof: The Jacobian matrix evaluated at the Endemic equilibrium (EE) is given Equation (62)

$$\begin{pmatrix} -\frac{\beta(\ _0-1)(h_2+h_3)}{N} - \mu - \theta & -\frac{\beta h_1}{_0 N} & -\frac{\beta h_1}{_0 N} & 0 & \omega & 0 \\ \frac{\beta(\ _0-1)(h_2+h_3)}{N} & \frac{\beta h_1}{_0 N} - \gamma - \mu & \frac{\beta h_1}{_0 N} & 0 & 0 & 0 \\ 0 & \gamma & -\kappa-\mu & 0 & 0 & 0 \\ 0 & 0 & \kappa & -\delta-\mu-\rho & 0 & 0 \\ \theta & 0 & 0 & \rho & -\mu-\omega & 0 \\ 0 & 0 & 0 & 0 & 0 & -\mu \end{pmatrix} \tag{62}$$

where $h_2 = -\frac{\eta_2\eta_3}{\eta_1}$, $h_3 = -\frac{\eta_2\eta_3}{\eta_1(\kappa+\mu)}$

The matrix can be reduced to matrix (63) below since $-\mu$ is an eigenvalue.

$$\begin{pmatrix} -\frac{\beta(\ _0-1)(h_2+h_3)}{N}-\mu-\theta & -\frac{\beta h_1}{\ _0N} & -\frac{\beta h_1}{\ _0N} & 0 & \omega \\ \frac{\beta(\ _0-1)(h_2+h_3)}{N} & \frac{\beta h_1}{\ _0N}-\gamma-\mu & \frac{\beta h_1}{\ _0N} & 0 & 0 \\ 0 & \gamma & -\kappa-\mu & 0 & 0 \\ \theta & 0 & \kappa & -\delta-\mu-\rho & 0 \\ 0 & 0 & 0 & \rho & -\mu-\omega \end{pmatrix} \tag{63}$$

The matrix (63) satisfies the corollary of Gershgorin's circle theorem, if the following inequalities hold;

$$\begin{cases} -\frac{\beta(\ _0-1)(h_2+h_3)}{N}-\mu-\theta<\frac{2\beta h_1}{\ _0N} \quad \Leftrightarrow \frac{\beta(\ _0-1)(h_2+h_3)}{N}+\mu+\theta>\frac{2\beta h_1}{\ _0N} \\ \frac{2\beta h_1}{\ _0N}-\gamma-\mu<-\frac{\beta(\ _0-1)(h_2+h_3)}{N}-\frac{\beta h_1}{\ _0N} \Leftrightarrow \frac{2\beta h_1}{\ _0N}<-\frac{\beta(\ _0-1)(h_2+h_3)}{N}+\gamma+\mu \\ -\kappa-\mu<-\gamma \\ -\delta-\mu-\rho<-\kappa \\ -\mu-\omega<-\rho \end{cases} \tag{64}$$

From Equation (64) substituting the second equation into the first equation yields Equation (65)

$$\frac{\beta(\mathcal{R}_0-1)(h_2+h_3)}{N}+\mu+\theta>-\frac{\beta(\mathcal{R}_0-1)(h_2+h_3)}{N}+\gamma+\mu \tag{65}$$

Simplifying (65) gives

$$\frac{2\beta(\mathcal{R}_0-1)(h_2+h_3)}{N}+\mu+\theta>\gamma+\mu \tag{66}$$

Equation (66) can only hold if and only if

$$\mathcal{R}_0-1>0 \tag{67}$$

which implies that

$$\mathcal{R}_0>1 \tag{68}$$

Since $R_0 > 1$, it implied that the endemic equilibrium (EE) was locally asymptotically stable.

3.7. Simulation of the Model

We carried out some numerical simulations for the model and studied the dynamics of the COVID-19 outbreak disease model in Ghana. Although the disease was not yet fully understood, the Government of Ghana had collected much data during the COVID-19 epidemic which was useful in the simulation. Based on the cumulative number of confirmed cases in Ghana, we derived the following parameters in Table 3.

Table 3. *Values and Source of Parameters Used.*

Parameter	Value	Source
β	0.071649 per day	Estimated
α	0.000079452 per day	Estimated
γ	0.125 per day	Estimated
K	0.1 per day	Estimated
ρ	0.07143 per day	Estimated
μ	0.000019726 per day	Estimated
δ	0.008145 per day	Estimated

Parameter	Value	Source
θ	0.000014 per day	Estimated
ω	0.004464 per day	Estimated

4. Discussion

4.1. Susceptible Population

There was a rapid decrease in the Susceptible population due to the occurrence of the disease in Ghana (Figure 2). However, with the introduction of containment measures such as social distancing and isolation, coupled with improved treatment, the susceptible population began to increase. This increase can also be attributed to the increased immunity of the recovered individuals from the first wave of infections. However, as the Susceptible Population increased, many people felt they were free from infection and hence failed to adequately follow preventive measures. Hence the number of infections began to surge rapidly leading to a decrease in the Susceptible population. This was followed by an increase in the Susceptible population due to a decrease in infections which could be attributed to the introduction of vaccines which moved individuals to the vaccinated class. This oscillatory behavior repeats until the disease becomes extinct or endemic, meaning the disease has now come to stay.

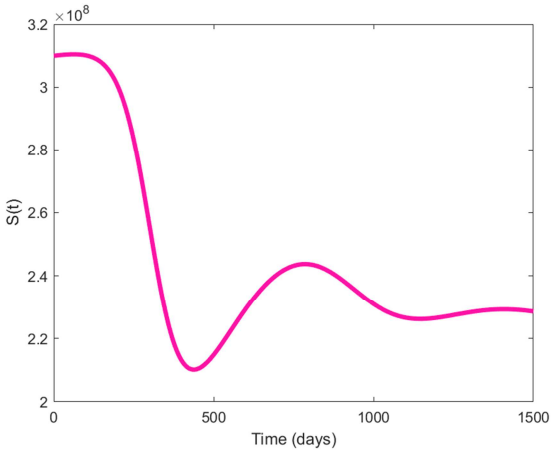

Figure 2. *Susceptible Population.*

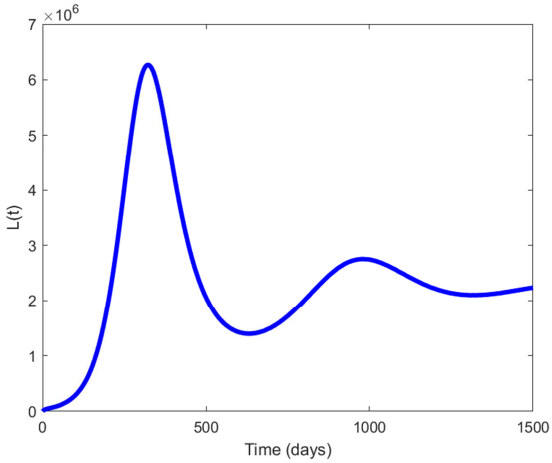

Figure 3. *Latent Population.*

4.2. Latent Population

Individuals who left the susceptible population entered the latent class because of exposure to the virus. This is where the virus begins to incubate inside them. This increases the population as seen in Figure 3. It oscillated due to tightening measures to control the disease.

4.3. Infected Population

As individuals in the population became symptomatic, they progressed to the infected class, thereby increasing the infected population. Figure 4 shows a sharp increase by entry of the latent class individuals into the infected population. This population increased until containment measures were implemented. The introduction of containment measures, and the movement of individuals into the hospitalized class caused the infected population to fall.

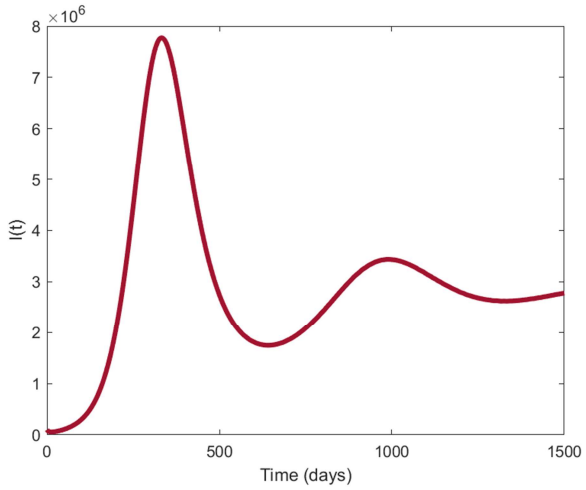

Figure 4. *Infected Population.*

4.4. Hospitalized Population

The increase in the number of infected individuals led to a drastic increase in the hospitalized population as seen in Figure 5. The population of this classes decreases afterwards due to the recovery of individuals in the class.

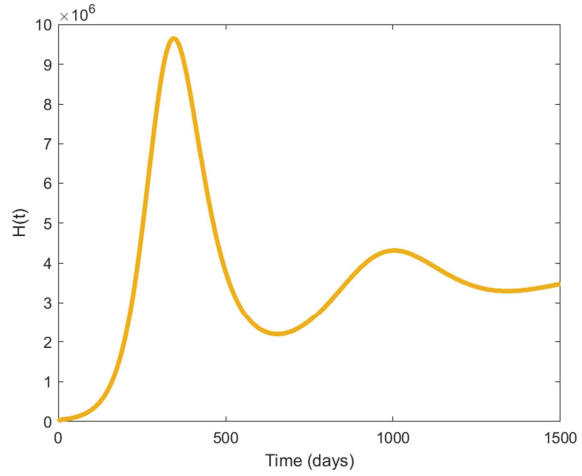

Figure 5. *Hospitalized Population.*

4.5. Recovered Population

As people recovered and left the hospitals, the recovered class increased. Ghana recorded about 98 percent recovery rate, resulting from effective implementation of containment measures which resulted in a steady increase in COVID-19 cases (see Figure 6).

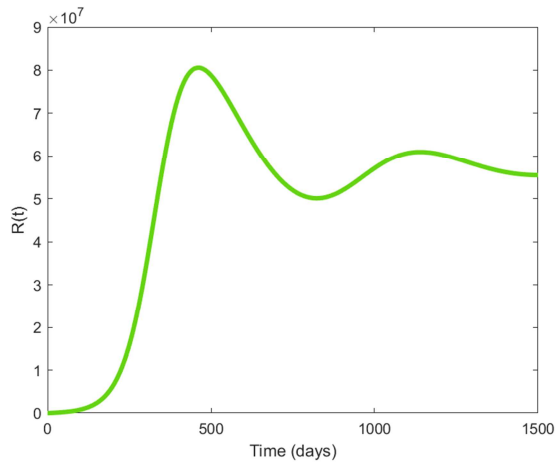

Figure 6. *Recovered Population.*

4.6. Vaccinated Population

The introduction of vaccines led to an exponential growth of the vaccinated population, even though the vaccines received in Ghana were woefully inadequate (see Figure 7).

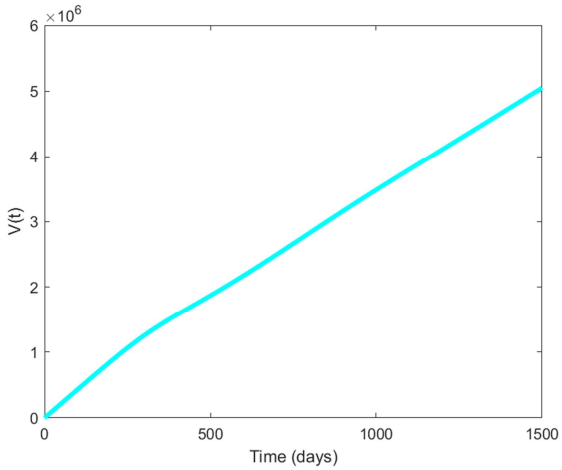

Figure 7. *Vaccinated Population.*

5. Conclusion

The Susceptible-Latent-Infected-Hospitalized-Recovered-Vaccinated (SLIHRV) was useful in understanding the dynamic mechanisms of the transmission and prevention of COVID-19 infection in Ghana. The model confirmed the stability of the endemic equilibrium, indicating that COVID-19 would persist in the Ghanaian population. The model also manifested that the disease-free equilibrium was stable, which means a reduction of COVID-19 infection among the population due to the introduction of strict containment measures. The findings of the study indicated that if the Ghanaian government continued with measures to keep the basic reproduction number below 1, it is highly likely that they would be able to effectively control the virus and possibly eliminate COVID-19 from the population in the future. The achieve this goal, the government must make every effort to vaccinate more people to immunize the population and move most of the people into the vaccinated class. The education and awareness about COVID-19 transmission and prevention must be ongoing to keep the population constantly informed to follow preventive measures to avoid infection from the virus.

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