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DETERMINING THE EFFECT OF CONTAMINATED ENVIRONMENT AND DIRECT TRANSMISSION ON THE DYNAMICS OF MONKEYPOX VIRUS

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Abstract. This study presents a deterministic mathematical model for direct and indirect transmission dynamics of Monkeypox disease. Direct transmission is through close contact with asymptomatic humans, symptomatic infectious human and infectious rodents while the indirect transmission is considered to be through contaminated environment. Four equilibrium states, that is, Monkeypox-Free equilibrium, E_0, Infected rodents only equilibrium state, E_1, Infected humans only equilibrium state, E_2, and Infected rodents and infected humans equilibrium state, E_3 is established. The global stability of the Monkeypox-Free equilibrium state is examined in terms of the reproduction ratio, R_0. The global stability of Infected rodents only equilibrium state is proved using Lyapunov-Kasovskii-Lasalle stability theorem while a Lyapunov function is constructed by adopting Voltera-Lyapunov matrix conditions and used to prove the Infected humans only equilibrium. Latin Hypercube Sampling technique and partial rank correlation coefficient is used to perform sensitivity analysis of the influence of various human parameters on R_{0h} and it is noted that human-to-human contact rate, environment-to-human contact rate, human virus shedding rate, virus decay rate from the environment, human recruitment rate and recovery rate of the symptomatic infectious humans were crucial parameters in the spread of Monkeypox infection in the human population. This is

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supported by the simulation results. Based on this, it recommended that policymakers, decision-makers and medical practitioners should pay much attention to these parameters and constitute control strategies that would increase on the recovery rate of the symptomatic humans, minimise human-to-human contact rate and human recruitment rate in order to minimize Monkeypox infections among human population.

Keywords: monkeypox virus; environmental transmission; basic reproduction number; Lyapunov-Kasovskii-Lasalle stability theorem; Voltera-Lyapunov matrix; sensitivity analysis.

2020 AMS Subject Classification: 92C60.

1. INTRODUCTION

Monkeypox commonly abbreviated as MPoX is a zoonotic disease caused by Monkeypox virus (MPoXV) of the family *Poxviridae* and genus *Orthopoxviridae* which causes illness in humans (Sepehrinezhad, Ahmadabad, & Sahab-Negah [1]). It is endemic in Central and West Africa. Recently, MPoX outbreak has been reported in Europe and North America (Sepehrinezhad, Ahmadabad, & Sahab-Negah [1], Falendysz et.al., [2]). Monkeypox which has a fatality rate of 10.6% and 3.6% for Central African and West Africa strains respectively was first reported in 1970 in Democratic Republic of Congo, formerly known as Zaire (Bunge et al., [3]). Since then outbreaks of Monkeypox have emerged in other parts of Africa as well as outside of Africa. This has therefore hinted on the relevance of this disease.

According to Center for Disease Control and Prevention [4], 13 African Union (AU) member states reported an outbreak of Monkeypox of which 11 had historically reported Monkey-pox outbreak prior to 2022. Accumulated total of 1,405 MPX cases and 62 deaths were reported in the first 5 months of 2022 from Cameroon, Central African Republic, the Democratic Republic of Congo and Nigeria (Center for Disease Control and Prevention [4]). As of the start of 2023, a total of 83,943 confirmed cases in over 111 countries globally (World Health Organization [5]).

Magnus et al., [6] identified Monkeypox as the responsible agent in two pox-like outbreaks in cynomolgus monkeys that were received in Copenhagen, Denmark at the Statens-Serum-Institut laboratory (Magnus et al., [6],Ladnyj, Ziegler, & Kima, [7]). It is from this background that the name Monkeypox came into use. Monkeypox virus reservoirs include: The Gambian porch rats, rope squirrels, rodents, prairies dogs, monkeys etc. (Falendysz et al., [2]). This zoonotic

disease can be transmitted from non-human primates, rodents, rope squirrels, etc to humans whenever humans come in contact with any of the infected animals. It can also be transmitted from an infected human to a healthy human whenever contact is made with the body fluids of the infected person either through body contacts or inhaling the respiratory droplets (Parker et al., [8]). Transmission can also be through contaminated formites and objects used by an infected person (Ajmera et al., [9]), and of recent there has been suggestions that it could also be transmitted through the placenta of a pregnant mother to the fetus (Mbala et al., [10], Center for Disease Control and Prevention [4]).

In humans, Monkeypox is characterized by high fever, body aches, headache, swelling on the lymph nodes, exhaustion and lesions on the skin (Usman et al., [11]). The lesions are usually filled with white fluid which later develops into abscesses and pustules (Bhunu, Mushayabasa, & Hymann [12]). It has also been noted that Monkeypox infection has three phases: (i) Incubation phase that last between 5-21 days (Guarner, Rio, & Malani, [13]), (ii) a prodromal phase which is the period at which signs and symptoms such as fever, headache, muscle aches are felt and surfaces on the patient and (iii) an exanthema phase which is phase of vesiculopustular rashes and pustules appearing on the body of the patient (Center for Disease Control and Prevention [4]). The last for 1-10 days from infection onset (Patauner, Gallo, & Durante-Mangoni [14]). In animals, there may be variation in the signs and symptoms of MPX depending on the animal species but most commonly includes cough, fever, clouding of the eyes, rashes, swelling on the limbs and lose of appetite (Reynolds et al., [15]). Many researchers have attempted to study and understand the dynamics of Monkeypox virus transmission in areas of biological and medical sciences as well as some work in the areas of mathematical sciences. Most of the models captured only direct route of transmission from humans to humans and from rodents/non-humans to humans. Models described by Emeka et al [16], Peter et al [17], Lasisi, Akinwande, & Oguntolu, [18], and Bankuru et al [19] incorporated controls in the model. Analysis of the models included finding the equilibrium points and understanding the stability of these equilibrium points as well as analysing the effective of incorporating controls as compartments in the models such as isolation of the infected humans was found to help in reducing the disease transmission (Peter et al [17]). Mathematical models described by Bhunu & Mushayabasa[20],

Lauko, Pinter, & TeWinkel [21] only described the dynamics of Monkeypox without considering the controls being practiced at that time. The analysis also included finding stability of the equilibrium states of the models.

A deterministic Monkeypox model with two sub-populations of human and non-humans(rodents) with environmental transmission as route of transmission was formulated (Madubueze et al [22]). The model was analyzed for effect of the virus shedding into the environment by both humans and rodents. It was noted that environmental transmission parameters are the main drivers of MPoX transmission. However, assumptions that the susceptible become infectious is unrealistic since both rodents and humans take some time before presentation of the signs and symptoms of MPoX (Guarner et al [13]). Therefore, this study incorporates the fact that both humans and rodents/non-humans take some time before presenting signs and symptoms of Monkeypox infection. We also extend the model to include humans who become asymptomatic upon infection (Guagliardo et al [23] since they have the potential of spreading the infection.

2. PRELIMINARIES

2.1. Model formulation. Many different mathematical models have been developed and used in epidemiology to understand the dynamics of different diseases. Among them is deterministic compartmental mathematical models which divide the population into groups defined by the possible disease states that one could be in over time (Naik et al [24]). Deterministic models are the foundation of mathematical epidemiology and provide a straightforward introduction to how models are built. Here, based on the assumptions that; (i) Recruitment into the susceptible population is by birth and immigration at a constant rate, (ii) Humans can be infected by close contact with infected humans, infected rodents and contaminated environment, (iii) Susceptible rodents can be infected by infected rodents only (Madubueze et al [22]), (iv) Susceptible humans can be infected via MPoXV concentration within the environment due to the shedding of the virus by infectious humans and rodents (World Health Organization [5]), (v) Once humans or rodents acquires the MPoXV, they take some time before eventually showing clinical signs and symptoms (Guarner et al [13]) and also it is assumed that there is homogeneous mixing in human and rodent sub-populations. A novel deterministic compartmental mathematical model

for the transmission dynamics of the Monkeypox disease is proposed which contains two sub-populations of the humans and the rodents with two transmission routes.

Motivated by works by Bhunu & Mushayabasa [20] and Madubueze et. al., [22],We consider a homogeneous mixing within the human and rodent population, i.e., individuals in the population have equal probability of contact with each other. Using a deterministic compartmental modeling approach to describe the disease transmission dynamics, at any time t, the total human and rodent population, $N_h(t)$ and $N_n(t)$ are subdivided into several epidemiological states depending on individuals' health status.

The human population. This is subdivided into seven compartments of Susceptible $S_h(t)$, Exposed $E_h(t)$, Quarantined J_h, Asymptomatic infected $I_a(t)$, Symptomatic infected $I_s(t)$, Hospitalized infected individuals $H_h(t)$, and the Recovered $R_h(t)$. The recruitment rate for the susceptible population is at a constant rate Π_h. The susceptible humans become infected, due to effective contact with asymptomatic infected and symptomatic infected humans at a rate β_{hh}; infected rodents at a rate β_{nh} and contaminated environment at a rate β_{ch}. The force of infection is given by, $\beta_{nh}I_n + \beta_{hh}(\theta_m I_a + I_s) + \beta_{ch}C_e$ with θ_m as the modification parameter for the transmission rate humans in the asymptotic class. μ_h is the natural death rate; ψ_1 is the rate at which the exposed humans become symptomatic infectious and ψ_2 is the rate at which exposed are put under surveillance through quarantine. The quarantine individuals who become asymptomatic infected move to the asymptomatic class at a rate ϕ_2, those who become symptomatically infectious move to symptomatic class at a rate ϕ_1 and while those who are a diagnosed to be health move to susceptible class at a rate ϕ_3. ψ_3 is the rate at which exposed individuals who were not identified or those who who did not identify themselves for having been in contact with an infected person become asymptomatic infectious. α_1 is the rate at which asymptomatic infected individuals recover while α_2 is the rate which they are hospitalized. ϕ_4 is the rate at which asymptomatic infected individuals recover due to natural immunity and the hospitalized infected individuals recover at a rate ν. The disease induced death is at a rate δ_h.

The rodent sub-population into three compartments of Susceptible, S_n, Exposed, E_n, and Infected, I_n. The recruitment rate of susceptible rodents at a rate Π_n. The susceptible rodents

become infected close contact with infected rodents at a rate, β_{nn} which is the product of the effective contact rate and probability of the rodents getting infected per contact with an infectious case. The force of infection is given by $\lambda_n = \beta_{nn} I_n$.

θ is the rate at which the exposed rodents become infectious and μ_n and δ_n are the natural and disease induced death of the rodents respectively.

The contaminated environment. The pathogens are released into the environment by the symptomatic infected humans and infected rodents at rates ω_1 and ω_2 respectively. This released pathogens into the environment contribute to the force of infection λ_h. Once the susceptible humans interact with the contaminated environment, they contract the virus at a rate β_{ch} which is the product of the effective contact rate and probability of the human getting infected per contact with a contaminated environment. The force of infection is given by $\beta_{ch} C_e$. The choice of this force of infection is motivated by works of Tsanou et al [25], who showed that mass action was good enough to model interaction of viral infectious from the environment. This pathogens decay from the environment at a rate μ_e.

The transfer relationships between the compartments is shown in the model diagram Figure 1.

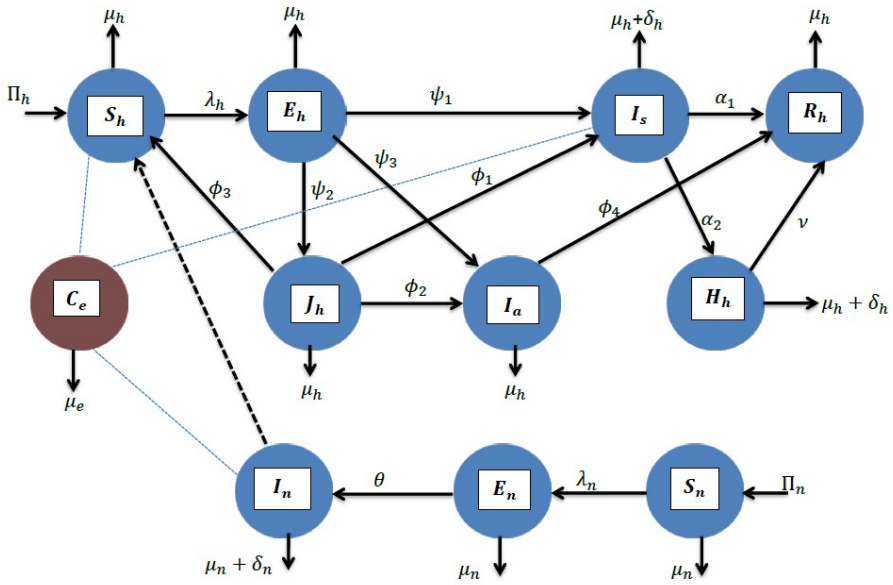

FIGURE 1. Schematic diagram for the transmission dynamics of MPoXV with both direct and environmental transmission.

2.2. Model Equations. Using the above assumptions and the flow diagram, the following system of equations are arrived at.

$$
\begin{cases}
\frac{dS_h}{dt} = & \Pi_h + \phi_3 J_h - \lambda_h S_h - \mu_h S_h \\
\frac{dE_h}{dt} = & \lambda_h S_h - (\psi_1 + \psi_2 + \psi_3 + \mu_h) E_h \\
\frac{dJ_h}{dt} = & \psi_2 E_h - (\phi_1 + \phi_2 + \phi_3 + \mu_h) J_h \\
\frac{dI_a}{dt} = & \psi_3 E_h + \phi_2 J_h - (\phi_4 + \mu_h) I_a \\
\frac{dI_s}{dt} = & \psi_1 E_h + \phi_1 J_h - (\alpha_1 + \alpha_2 + \mu_h + \delta_h) I_s \\
\frac{dH_h}{dt} = & \alpha_2 I_s - (\nu + \mu_h + \delta_h) H_h \\
\frac{dR_h}{dt} = & \phi_4 I_a + \alpha_1 I_s + \nu H_h - \mu_h R_h \\
\frac{dS_n}{dt} = & \Pi_n - \lambda_n S_n - \mu_n S_n \\
\frac{dE_n}{dt} = & \lambda_n S_n - (\theta + \mu_n) E_n \\
\frac{dI_n}{dt} = & \theta E_n - (\mu_n + \delta_n) I_n \\
\frac{dC_e}{dt} = & \omega_1 I_s + \omega_2 I_n - \mu_e C_e
\end{cases} \tag{1}
$$

The initial conditions are such that $S_h \geq 0, E_h \geq 0, J_h \geq 0 I_a \geq 0, I_s \geq 0, H_h \geq 0, R_h \geq 0, S_n \geq 0, E_n \geq 0, I_n \geq 0$ and $C_e \geq 0$.

The equations for rates of change of total human is given by

$$\frac{dN_h}{dt} = \Pi_h + \phi_3 J_h - \mu_h N_h - \delta_h (I_s + J_h) \tag{2}$$

and for rodent sub-population is given by

$$\frac{dN_n}{dt} = \Pi_n - \mu_n N_n - \delta_n I_n \tag{3}$$

The state variables and model parameter descriptions and values used in the numerical simulations are represented in Table 1 and Table 2 respectively.

TABLE 1. Model Variables and their definitions

Symbol	Definition
S_h	Susceptible human population
E_h	Exposed human population
J_h	Quarantined humans
I_a	Asymptomatic infected human population
I_s	Symptomatic infected human population
H_h	Hospitalized infected humans
R_h	Recovered human population
S_n	Susceptible rodent population
E_n	Exposed rodent population
I_n	Infected rodent population
C_e	Contaminated environment

TABLE 2. Model parameters descriptions and estimations for simulations

Symbol	Definition	Value	Source
Π_h	Recruitment rates into the susceptible human	0.029	[20]
Π_n	Rodents recruitment rate	0.2	[22]
β_{hh}	Human to human contact rate	0.00006	[20, 11]
β_{nh}	Rodent to human contact rate	0.0027	[11]
β_{ch}	Contaminated environment to human contact rate	0.01	[22]
β_{nn}	Rodents to rodents contact rate	0.027	[11, 20]
μ_h	Humans natural mortality rate	0.01794	[26]
μ_n	Rodents natural mortality rate	0.0006	[17]
δ_h	Human Monkeypox-induced mortality rate	0.0247	[26]
δ_n	Rodents Monkeypox-induced mortality rate	0.4	[20]
ψ_1	Progression rate of exposed humans to symptomatic class	0.095	[26]
ψ_2	Progression rate of exposed humans to quarantined class	0.481	[26]
ψ_3	Progression rate of exposed humans to asymptomatic class	0.020	Assumed
ϕ_3	Proportion of quarantined individuals who are susceptible	0.283	[26]
ϕ_2	Proportion of quarantined humans who become asymptomatic	0.050	Assumed
ϕ_1	Rate at which quarantined humans become symptomatic infected	0.52	[17, 22]
ϕ_4	Asymptomatic infected humans recovery rate	0.020	Assumed
α_1	Recovery rate of symptomatic infected humans	0.14	Assumed
α_2	Rate at which the symptomatic infected humans are hospitalized	0.03	Assumed
ν	Recovery rate of the hospitalized infected humans	0.036	[27]
θ	Rate at which the exposed rodents become infected	0.3	[11]
ω_1	symptomatic infected humans virus shedding rate into the environment	0.04	[25]
ω_2	Rodents Virus shedding rate into the environment	0.02	[22]
μ_e	Pathogen decay rate from the environment	0.003	[22]

3. Analysis of Monkeypox Model

3.1. Feasible region and Monkeypox-Free equilibruim point, E_0. To determine whether the Monkeypox model is biologically meaningful, the Monkeypox model is analyzed for positivity and boundedness, that is, to show that all the Monkeypox model state variables are non-negative at all time $t > 0$.

Theorem 1. *The solutions $S_h(t), E_h(t), J_h(t) I_a(t), I_s(t), H_h(t), R_h(t), S_n(t), E_n(t), I_n(t)$ and $C_e(t)$ of the Monkeypox model Equation* (1) *with non-negative initial conditions, remains non-negative for all time $t > 0$.*

Proof. Suppose that

$$\begin{aligned} t^* &= sup\{t > 0 \quad | \quad S_h(t) > 0, E_h(t) > 0, J_h(t) > 0, I_a(t) > 0, I_s(t) > 0, H_h(t) > 0, R_h(t) > 0, \\ &\quad S_n(t) > 0, E_n(t) > 0, I_n(t) > 0, C_e(t) > 0\} > 0 \end{aligned}$$

then it follows from Equation (1) that

$$\begin{aligned} \frac{dS_h}{dt} &= \Pi_h + \phi_3 J_h - \lambda_h S_h - \mu_h S_h \\ &\geq \Pi_h - \lambda_h S_h - \mu_h S_h \end{aligned}$$

which can written as

$$\frac{d}{dt}\left(S_h(t)\exp\left[\mu_h t + \int_0^t \lambda_h(u)du\right]\right) \geq \Pi_h \exp\left[\mu_h t + \int_0^t \lambda_h(u)du\right]$$

Hence

$$S_h(t^*)\exp\left[\mu_h t^* + \int_0^{t^*} \lambda_h(u)du\right] - S_h(0) \geq \int_0^{t^*}\left(\Pi_h \exp\left[\mu_h t^* + \int_0^y \lambda_h(u)du\right]\right)dy$$

so that

$$\begin{aligned} S_h(t^*) &\geq S_h(0)\exp\left[-\mu_h t^* - \int_0^{t^*} \lambda_h(u)du\right] + \exp\left[-\mu_h t^* - \int_0^{t^*} \lambda_h(u)du\right] \times \\ &\quad \int_0^{t^*}\left(\Pi_h \exp\left[\mu_h t^* + \int_0^y \lambda_h(u)du\right]\right)dy > 0 \end{aligned}$$

□

Similarly, it can be shown that $E_h(t), J_h(t), I_a(t), I_s(t), H_h(t), R_h(t), S_n(t), E_n(t), I_n(t), C_e(t) \geq 0$ for all $t > 0$.

Therefore, this shows that, all the solutions to the Monkeypox model Equation (1) remain non-negative for all non-negative initial conditions.

Theorem 2. *The feasible region*

$$\Omega = \left\{ (S_h, E_h, J_h, I_a, I_s, H_h, R_h, S_n, E_n, I_n, C_e) \in \Re_+^{11} | N_h \leq \frac{\Pi_h}{\mu_h}, N_n \leq \frac{\Pi_n}{\mu_n}, C_e \leq \frac{\omega_1 \Pi_h}{\mu_e \mu_h} + \frac{\omega_2 \Pi_n}{\mu_e \mu_n} \right\}$$

is positively invariant with respect to the MPoX model Equation (1)

Proof. From Equation (2), in the absence of the disease

$$\frac{dN_h}{dt} = \Pi_h - \mu_h N_h$$

Upon integrating gives a solution

$$N_h = \frac{\Pi_h}{\mu_h} + \left(N_h(0) - \frac{\Pi_h}{\mu_h} \right) \exp(-\mu_h t)$$

which implies that

$$\limsup_{t \longrightarrow \infty} N_h(t) \leq \frac{\Pi_h}{\mu_h}$$

Hence

$$\Omega_{N_h} = \left\{ N_h(t) \in \Re_+ | N_h(t) \leq \frac{\Pi_h}{\mu_h} \right\}$$

Similarly from Equation (3), $\frac{dN_n}{dt} = \Pi_n - \mu_n N_n - \delta_n I_n$, in the absence of the disease,

$$\frac{dN_n}{dt} = \Pi_n - \mu_n N_n$$

Upon integrating gives a solution

$$N_n = \frac{\Pi_n}{\mu_n} + \left(N_n(0) - \frac{\Pi_n}{\mu_n} \right) \exp(-\mu_n t)$$

which implies that

$$\limsup_{t \longrightarrow \infty} N_n(t) \leq \frac{\Pi_n}{\mu_n}$$

Hence

$$\Omega_{N_n} = \left\{ N_n(t) \in \Re_+ | N_n(t) \leq \frac{\Pi_n}{\mu_n} \right\}$$

Also with $I_a \leq N_h$, $I_s \leq N_h$ and $I_n \leq N_n$,

$$\frac{dC_e}{dt} \leq \omega_1 \frac{\Pi_h}{\mu_h} + \omega_2 \frac{\Pi_n}{\mu_n} - \mu_e C_e$$

upon integrating gives

$$C_e(t) \leq \frac{\omega_1 \frac{\Pi_h}{\mu_h} + \omega_2 \frac{\Pi_n}{\mu_n}}{\mu_e} + \left(C_e(0) - \frac{\omega_1 \frac{\Pi_h}{\mu_h} + \omega_2 \frac{\Pi_n}{\mu_n}}{\mu_e} \right) \exp(-\mu_e t)$$

implying that

$$\limsup_{t \longrightarrow \infty} C_e(t) \leq \frac{\omega_1 \frac{\Pi_h}{\mu_h} + \omega_2 \frac{\Pi_n}{\mu_n}}{\mu_e}$$

Therefore, the feasible region

$$\Omega = \left\{ (S_h, E_h, J_h I_a, I_s, H_h, R_h, S_n, E_n, I_n, C_e) \in \Re_+^{11} | N_h \leq \frac{\Pi_h}{\mu_h}, N_n \leq \frac{\Pi_n}{\mu_n}, C_e \leq \frac{\omega_1 \Pi_h}{\mu_e \mu_h} + \frac{\omega_2 \Pi_n}{\mu_e \mu_n} \right\}$$

is positively invariant with respect to the Monkeypox model. □

In this region, Ω, the Monkeypox model can be considered as epidemiologically meaningful, positively invariant and mathematically well-posed [28]. Thus, every solution of the system with initial conditions in Ω always remains in Ω for all $t > 0$.

3.1.1. *Local stability of Monkeypox-Free Equilibrium Point, E_0.* This is achieved when there is no Monkeypox disease persisting in both the human and rodent sub-populations. In this case there is only one possible equilibrium point. Let $E_0 = (S_h^0, E_h^0, J_h^0, I_a^0, I_s^0, H_h^0, R_h^0, S_n^0, E_n^0, I_n^0, C_e^0)$ be the Monkeypox-Free equilibrium point of the Monkeypox model Equation (1), where $S_h^0 > 0, E_h^0 = 0, J_h^0 = 0, I_a^0 = 0, I_s^0 = 0, H_h^0 = 0, R_h^0 = 0, S_n^0 > 0, E_n^0 = 0, I_n^0 = 0, C_e^0 = 0$, then solving the model Equation (1) at E_0 gives

$$E_0 = (S_h^0, E_h^0, J_h^0, I_a^0, I_s^0, H_h^0, R_h^0, S_n^0, E_n^0, I_n^0, C_e^0) = \left(\frac{\Pi_h}{\mu_h}, 0, 0, 0, 0, 0, 0, \frac{\Pi_n}{\mu_n}, 0, 0, 0 \right)$$

Definition 1. *The basic reproduction ratio is the mean number of secondary infections produced by a single infectious human/rodent when introduced into a completely susceptible population (Diekmann, Heesterbeek, & Roberts* [29]*).*

The local stability of the Monkeypox-Free equilibrium point is governed and controlled by the basic reproduction ratio, R_0. This is computed using the next generation matrix operator approach (Van den Driessche & Watmough [30]).

Consider the disease compartments $E_h, J_h, I_a, I_s, H_h, E_n, I_n$ & C_e of the MPoX model Equation (1). From the model, it can be observed that the rate of appearance of new infections into the disease compartments is given by

$$\mathscr{F} = \begin{pmatrix} \lambda_h S_h \\ 0 \\ 0 \\ 0 \\ 0 \\ \lambda_n S_n \\ 0 \\ 0 \end{pmatrix} \tag{4}$$

The Jacobian F of Equation (4) at the Monkeypox-Free equilibrium is given by

$$F = \begin{pmatrix} 0 & 0 & \frac{\beta_{hh}\theta_m\Pi_h}{\mu_h} & \frac{\beta_{hh}\Pi_h}{\mu_h} & 0 & 0 & \frac{\beta_{nh}\Pi_h}{\mu_h} & \frac{\beta_{ch}\Pi_h}{\mu_h} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_{nn}\Pi_n}{\mu_n} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{5}$$

The difference between rates of transfer out and in to the disease compartments is given by

$$\mathscr{V} = \mathscr{V}^- - \mathscr{V}^+ = \begin{pmatrix} \pi_1 E_h \\ \pi_2 J_h - \psi_2 E_h \\ \pi_3 I_a - \phi_2 J_h - \psi_3 E_h \\ \pi_4 I_s - \psi_1 E_h - \phi_1 J_h \\ \pi_5 H_h - \alpha_2 I_s \\ \pi_6 E_n \\ \pi_7 I_n - \theta E_n \\ \mu_e C_e - \omega_1 I_s - \omega_2 I_n \end{pmatrix} \tag{6}$$

where

$$\pi_1 = \psi_1 + \psi_2 + \psi_3 + \mu_h, \quad \pi_2 = \phi_1 + \phi_2 + \phi_3 + \mu_h, \quad \pi_3 = \phi_4 + \mu_h$$

$$\pi_4 = \alpha_1 + \alpha_2 + \mu_h + \delta_h, \quad \pi_5 = \nu + \mu_h + \delta_h, \quad \pi_6 = \theta + \mu_n, \quad \pi_7 = \mu_n + \delta_n.$$

The Jacobian V of Equation (6) is given by

$$V = \begin{pmatrix} \pi_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\psi_2 & \pi_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\psi_3 & -\phi_2 & \pi_3 & 0 & 0 & 0 & 0 & 0 \\ -\psi_1 & -\phi_1 & 0 & \pi_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -\alpha_2 & \pi_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \pi_6 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\theta & \pi_7 & 0 \\ 0 & 0 & 0 & -\omega_1 & 0 & 0 & -\omega_2 & \mu_e \end{pmatrix} \tag{7}$$

and computing FV^{-1} from Equations (5) and (7) gives

$$FV^{-1} = \begin{pmatrix} B_{11} & B_{12} & \frac{\beta_{hh}\Pi_h\theta_m}{\pi_3\mu_h} & \frac{\beta_{hh}\Pi_h}{\pi_4\mu_h} - \frac{\beta_{ch}\Pi_h\omega_1}{\pi_4\mu_h\mu_e} & 0 & B_{16} & B_{17} & -\frac{\beta_{ch}\Pi_h}{\mu_h\mu_e} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{\beta_{nn}\,\theta\Pi_n}{mu_n\pi_6\pi_7} & \frac{\beta_{nn}\Pi_n}{\mu_n\pi_7} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{8}$$

$$B_{11} = \frac{\beta_{hh}\Pi_h\theta_m(\psi_3\pi_2+\phi_2\psi_2)}{\mu_h\pi_1\pi_2\pi_3} + \frac{\beta_{hh}\Pi_h(\pi_2\psi_1+\phi_1\psi_2)}{\mu_h\pi_1\pi_2\pi_4} + \frac{\beta_{ch}\Pi_h\omega_1(\phi_1\psi_2+\pi_2\psi_1)}{\pi_1\pi_2\pi_4\mu_h\mu_e}$$

$$B_{12} = \frac{\beta_{hh}\theta_m\Pi_h\phi_2}{\mu_h\pi_2\pi_3} + \frac{\beta_{hh}\Pi_h\phi_1}{\mu_h\pi_2\pi_4} + \frac{\beta_{ch}\Pi_h\omega_1\phi_1}{\pi_2\pi_4\mu_h\mu_e}$$

$$B_{16} = \frac{\beta_{nh}\Pi_h\mu_n\theta}{\mu_h\pi_6\pi_7} + \frac{\beta_{ch}\Pi_h\omega_2\theta}{\pi_6\pi_7\mu_h\mu_e}$$

$$B_{17} = \frac{\beta_{nh}\Pi_h}{\pi_7\mu_h} + \frac{\beta_{ch}\Pi_h\omega_2}{\pi_7\mu_h\mu_e}$$

Computing the spectral radius of Equation (8), i.e., $\rho(FV^{-1})$ gives

$$\left(0,0,0,0,0,0, \frac{\beta_{hh}\Pi_h\theta_m(\psi_3\pi_2+\phi_2\psi_2)}{\mu_h\pi_1\pi_2\pi_3} + \frac{\beta_{hh}\Pi_h(\pi_2\psi_1+\phi_1\psi_2)}{\mu_h\pi_1\pi_2\pi_4} + \frac{\beta_{ch}\Pi_h\omega_1(\phi_1\psi_2+\pi_2\psi_1)}{\pi_1\pi_2\pi_4\mu_h\mu_e}, \frac{\beta_{nn}\,\theta\Pi_n}{\mu_n\pi_6\pi_7}\right)$$

The basic reproduction number is given by the dominant eigenvalue. Hence

$$R_0 = \max\{R_{0h}, R_{0n}\} \tag{9}$$

where

$$R_{0n} = \frac{\beta_{nn}\,\theta\Pi_n}{\mu_n\pi_6\pi_7}$$

$$R_{0h} = \frac{\beta_{hh}\Pi_h\theta_m(\psi_3\pi_2+\phi_2\psi_2)}{\mu_h\pi_1\pi_2\pi_3} + \frac{\beta_{hh}\Pi_h(\pi_2\psi_1+\phi_1\psi_2)}{\mu_h\pi_1\pi_2\pi_4} + \frac{\beta_{ch}\Pi_h\omega_1(\phi_1\psi_2+\pi_2\psi_1)}{\pi_1\pi_2\pi_4\mu_h\mu_e} \tag{10}$$

which can be written as $R_{0h} = R^a_{0h} + R^s_{0h} + R^e_{0h}$

with

$$R^a_{0h} = \frac{\beta_{hh}\Pi_h\theta_m(\psi_3\pi_2 + \phi_2\psi_2)}{\mu_h\pi_1\pi_2\pi_3} \quad R^s_{0h} = \frac{\beta_{hh}\Pi_h(\pi_2\psi_1 + \phi_1\psi_2)}{\mu_h\pi_1\pi_2\pi_4} \quad R^e_{0h} = \frac{\beta_{ch}\Pi_h\omega_1(\phi_1\psi_2 + \pi_2\psi_1)}{\pi_1\pi_2\pi_4\mu_h\mu_e}$$

The terms $\frac{1}{\pi_1}$ and $\frac{1}{\pi_6}$ are the average time spent by an individual human and rodent in the exposed classes, $\frac{1}{\pi_2}$, $\frac{1}{\pi_3}$, $\frac{1}{\pi_4}$, $\frac{1}{\pi_5}$ are the average time spent by individual human in the quarantine, asymptomatic, symptomatic and hospitalization classes respectively while $\frac{1}{\pi_7}$ is the average time spent by rodents in the infectious class and $\frac{1}{\mu_e}$ is the average time spent by the pathogen in the environment.

The reproduction ratio R_{0h} is the reproduction ratio for human to human and environment to human transmission while R_{0n} is the reproduction ratio for rodent to rodent transmission.
The reproduction ratios R^a_{0h}, and R^s_{0h} are for human to human transmission when contact is made with asymptomatic infected, and symptomatic infected humans while R^e_{0h} is the reproduction ratio for contaminated environment to human transmission.

Therefore, the quantity R_0 measures the average number of new cases generated by a single Monkeypox infected human, infected Rodent in a population throughout its life time and a single Monkeypox Virus contaminated environment. R_0 is very useful in describing the magnitude of transmission (Bani-Yaghoub, et al [31]) in a Monkeypox epidemic . If $R_0 < 1$, then Monkeypox Virus infection will disappear from the population in both human and rodent population whereas Monkeypox outbreak generate an epidemic if $R_0 > 1$. This gives a biological interpretation of R_0 (Diekmann, Heesterbeek, & Roberts [29]).

Theorem 3. *The Monkeypox-free equilibrium, E_0, of model system* (1) *is locally asymptotically stable if $R_0 < 1$, otherwise it is unstable if $R_0 > 1$.*

Proof. To prove the local stability of the Monkeypox-free equilibrium, E_0, it is sufficient to show that the Jacobian matrix of the model system (1) evaluated at Monkeypox-free equilibrium E_0 has negative eigenvalues.

The Jacobian matrix at E_0 is given by

(11)
$$J(E_0) = \begin{pmatrix} -\mu_h & 0 & \phi_3 & -\beta_{hh}\frac{\Pi_h}{\mu_h}\theta_m & -\beta_{hh}\frac{\Pi_h}{\mu_h} & 0 & 0 & 0 & 0 & -\frac{\beta_{nh}\Pi_h}{\mu_h} & -\frac{\beta_{ch}\Pi_h}{\mu_h} \\ 0 & -\pi_1 & 0 & \beta_{hh}\theta_m\frac{\Pi_h}{\mu_h} & \beta_{hh}\frac{\Pi_h}{\mu_h} & 0 & 0 & 0 & 0 & \frac{\beta_{nh}\Pi_h}{\mu_h} & \frac{\beta_{ch}\Pi_h}{\mu_h} \\ 0 & \psi_2 & -\pi_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \psi_3 & \phi_2 & -\pi_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \psi_1 & \phi_1 & 0 & -\pi_4 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \alpha_2 & -\pi_5 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \phi_4 & \alpha_1 & \nu & -\mu_h & 0 & 0 & 0 & \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\mu_n & 0 & -\beta_{nn}\frac{\Pi_n}{\mu_n} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\pi_6 & \beta_{nn}\frac{\Pi_n}{\mu_n} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \theta & -\pi_7 & 0 \\ 0 & 0 & 0 & 0 & \omega_1 & 0 & 0 & 0 & 0 & \omega_2 & -\mu_e \end{pmatrix}$$

The Monkeypox-free equilibrium point E_0 of the model Equation (1) is locally asymptotically stable if all the eigenvalues λ_i; for $i = 1,2,...,11$ of the Jacobian matrix $J(E_0)$ are negative or have negative real parts if $R_0 < 1$ using Routh-Hurwitz criterion (Capo-Lugo & Bainum, [32]). The eigenvalues can be computed from the characteristic polynomial using

$$|J(E_0) - \lambda I|$$

where $I_{11\times 11}$ is an identity matrix.

Therefore, the characteristic polynomial is of the form

(12)
$$\begin{aligned} P(\lambda) = [(\mu_h+\lambda)^2][\lambda^2 + (\pi_1+\pi_2)\lambda + (\pi_1\pi_2][\lambda^2 + (\pi_3+\pi_4)\lambda + \pi_3\pi_4][\lambda^2 \\ + (\mu_n+\pi_5)\lambda + \mu_n\pi_5][\lambda^2 + (\pi_6+\pi_7)\lambda + \pi_7\pi_6 - \beta_{nn}\frac{\Pi_n}{\mu_n}\theta][\lambda+\mu_e] \end{aligned}$$

The polynomial $P(\lambda)$ in Equation (12) can be written as

$$P(\lambda) = a_1(\lambda) \times a_2(\lambda) \times a_3(\lambda) \times a_4(\lambda) \times a_5(\lambda) \times a_6(\lambda)$$

where

$$a_1(\lambda) = \mu_h + \lambda$$

$$a_2(\lambda) = \lambda^2 + (\pi_1+\pi_2)\lambda + (\pi_1\pi_2)$$

$$a_3(\lambda) = \lambda^2 + (\pi_3 + \pi_4)\lambda + \pi_3\pi_4$$

$$a_4(\lambda) = \lambda^2 + (\mu_n + \pi_5)\lambda + \mu_n\pi_5$$

$$a_5(\lambda) = \lambda^2 + (\pi_6 + \pi_7)\lambda + \pi_7\pi_6 - \beta_{nn}\frac{\Pi_n}{\mu_n}\theta$$

$$a_6(\lambda) = \lambda + \mu_e$$

It can be seen from $a_5(\lambda)$ that $\pi_6\pi_7 - \beta_{nn}\theta = \pi_6\pi_7\left(1 - \dfrac{\beta_{nn}\Pi_\theta}{\mu_n\pi_6\pi_7}\right) = \pi_6\pi_7(1 - R_{0n}) > 0$ if $R_{0n} < 1$.

Therefore, following from the Routh–Hurwitz criterion for second order polynomials, which requires that all the coefficients in the polynomials be positive and, thus, all the eigenvalues are negative numbers, it is clear that the condition is satisfied and hence the Monkypox-Free equilibrium point E_0 is locally asymptotically stable provided $R_0 < 0$. This completes the proof.

□

3.1.2. *Global stability of Monkeypox-Free equilibruim point.*

Definition 2. *The Monkeypox-Free equilibrium point E_0 is said to be globally stable if all solutions of the model system* (1) *that begin any where in Ω remain near E_0 over an indefinite time.*

Using the approach applied by Chien, Fengsheng & Shatey[33], We consider the Monkeypox model system of ordinary differential Equation (1) be written in the form

$$\begin{aligned} \frac{dx}{dt} &= f_1(x,y) \\ \frac{dy}{dt} &= f_2(x,y) \end{aligned} \tag{13}$$

where $x \in \Re^m$ denotes the number of uninfected individuals and $y \in \Re^n$ denotes the infected individuals with $f_2(x^0,0) = 0$, $x \in \Re^m$ and $y \in \Re^n$ and $E_0 = (x^0,0)$ the Monkeypox-Free equilibrium state. Then the following conditions are established.

- Condition $[C_1]$: For $\dfrac{dx}{dt} = f_1(x,0)$, x^0 is globally asymptotically stable.
- Condition $[C_2]$: $f_2(x,y) = Ay - \hat{f}_2(x,y)$, with $\hat{f}_2(x,y) \geq 0$ for $(x,y) \in \Omega$, where the Jacobian matrix $A = \dfrac{\partial f_2}{\partial y}(x^0,0)$ is a matrix with all its off diagonal entries non-negative

(M-matrix). Then the Monkeypox-Free equilibrium, E_0 is globally asymptotically stable provided that $\mathrm{R}_0 < 1$ and conditions (C_1) and (C_2) are satisfied.

Theorem 4. *The Monkeypox-Free equilibrium point E_0 is globally asymptotically stable if $R_0 < 1$.*

Proof. Rewriting the model Equation (1) in the form (13), we have $x = [S_h, R_h, S_n]^T$ and $y = [E_h, J_h, I_a, I_s, H_h E_n, I_n, C_e]^T$.

When $E_h = J_h = I_a = I_s = H_h = E_n = I_n = C_e = 0$, the uninfected MPX model system changes to

$$\begin{aligned} \frac{dS_h}{dt} &= \Pi_h - \mu_h S_h \\ \frac{dR_h}{dt} &= 0 \\ \frac{dS_n}{dt} &= \Pi_n - \mu_n S_n \end{aligned} \tag{14}$$

Equation (14) has the solutions as below

$$S_h(t) = \frac{\Pi_h}{\mu_h} + \left(S_h(0) - \frac{\Pi_h}{\mu_h}\right)\exp(-\mu_h t), \quad R_h = 0, \quad S_n(t) = \frac{\Pi_n}{\mu_n} + \left(S_n(0) - \frac{\Pi_n}{\mu_n}\right)\exp(-\mu_n t) \tag{15}$$

From Equation (15), its clear that irrespective of the initial values $S_h(0)$ and $S_n(0)$, we obtain

$$\lim_{t \longrightarrow \infty} S_h(t) = \frac{\Pi_h}{\mu_h}$$

and

$$\lim_{t \longrightarrow \infty} S_n(t) = \frac{\Pi_n}{\mu_n}$$

this therefore confirms that $x^0 = \left(\frac{\Pi_h}{\mu_h}, 0, \frac{\Pi_h}{\mu_h}\right)$ is globally asymptotically stable, hence condition C_1 holds for the MPX model system.

The infectious subsystem $[E_h, J_h, I_a, I_s, H_h, E_n, I_n, C_e]$ in Equation (13) is equivalent to

$$\frac{dy}{dt} = \begin{pmatrix} \lambda_h S_h - (\psi_1 + \psi_2 + \psi_3 + \mu_h)E_h \\ \psi_2 E_h - (\phi_1 + \phi_2 + \phi_3 + \mu_h)J_h \\ \psi_3 E_h + \phi_2 J_h - (\phi_4 + \mu_h)I_a \\ \psi_1 E_h + \phi_2 J_h - (\alpha_1 + \alpha_2 + \mu_h + \delta_h +)I_s \\ \alpha_2 I_s - (\nu + \mu_h - \delta_h)J_h \\ \lambda_n S_n - (\theta + \mu_n)E_n \\ \theta E_n - (\mu_n + \delta_n)I_n \\ \omega_1 I_s + \omega_2 I_n - \mu_e C_e \end{pmatrix} \tag{16}$$

Matrix in Equation (16) can be written as

$$\frac{dy}{dt} = \begin{pmatrix} -\pi_1 & 0 & \beta_{hh}\theta_m S_h^0 & \beta_{hh} S_h^0 & 0 & 0 & \beta_{nh} S_h^0 & \beta_{ch} S_h^0 \\ \psi_2 & -\pi_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ \psi_3 & \phi_2 & -\pi_3 & 0 & 0 & 0 & 0 & 0 \\ \psi_1 & \phi_2 & 0 & -\pi_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \alpha_2 & -\pi_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\pi_6 & \beta_{nn} S_n^0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \theta & -\pi_7 & 0 \\ 0 & 0 & 0 & \omega_1 & 0 & 0 & \omega_2 & -\mu_e \end{pmatrix} \begin{pmatrix} E_h \\ J_h \\ I_a \\ I_s \\ H_h \\ E_n \\ I_n \\ C_e \end{pmatrix} \tag{17}$$

$$- \begin{pmatrix} \beta_{hh}(\theta_m I_a + I_s)(S_h^0 - S_h) + \beta_{nh}(S_h^0 - S_h) + \beta_{ch}(S_h^0 - S_h) \\ 0 \\ 0 \\ 0 \\ 0 \\ \beta_{nn} I_n (S_n^0 - S_n) \\ 0 \\ 0 \end{pmatrix}$$

which is in the form

$$\frac{dy}{dt} = Ay - \hat{f}_2(x, y)$$

as in Condition, C_2 with

$$A = \begin{pmatrix} -\pi_1 & 0 & \beta_{hh}\theta_m S_h^0 & \beta_{hh} S_h^0 & 0 & 0 & \beta_{nh} S_h^0 & \beta_{ch} S_h^0 \\ \psi_2 & -\pi_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ \psi_3 & \phi_2 & -\pi_3 & 0 & 0 & 0 & 0 & 0 \\ \psi_1 & \phi_2 & 0 & -\pi_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \alpha_2 & -\pi_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\pi_6 & \beta_{nn} S_n^0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \theta & -\pi_7 & 0 \\ 0 & 0 & 0 & \omega_1 & 0 & 0 & \omega_2 & -\mu_e \end{pmatrix}$$

and

$$\hat{f}_2(x,y) = \begin{pmatrix} \beta_{hh}(\theta_m I_a + I_s)(S_h^0 - S_h) + \beta_{nh} I_n (S_h^0 - S_h) + \beta_{ch} C_e (S_h^0 - S_h) \\ 0 \\ 0 \\ 0 \\ 0 \\ \beta_{nn} I_n (S_n^0 - S_n) \\ 0 \\ 0 \end{pmatrix}$$

If $y(0) > 0$, then $y(t) \geq 0$. Since A is an M-matrix, therefore, using variation formula, we have

$$0 \leq y(t) = e^{At} y(0) - \int_0^t e^{A(t-r)} \hat{f}_2(x(r) - y(r)) dr \leq e^{At} y(0)$$

Since A is M-matrix, when $R_0 < 1$ then A has a negative dominant eigenvalue and we have

$$\lim_{t \longrightarrow \infty} ||e^{At}|| = 0$$

thus

$$\lim_{t \longrightarrow \infty} y(t) = 0$$

Therefore, E_0 is globally stable whenever $R_0 < 1$, otherwise it is unstable. □

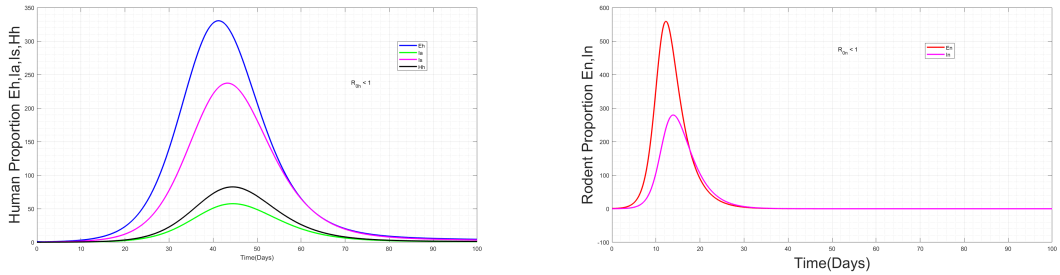

FIGURE 2. Global stability of Monkeypox-Free equilibrium state when $R_0 < 1$

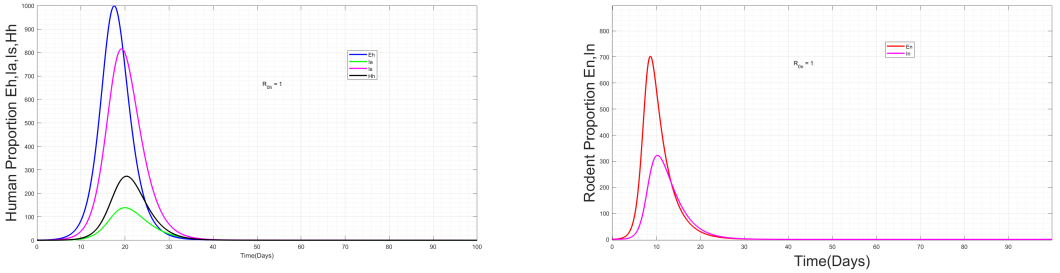

FIGURE 3. Global stability of Monkeypox-Free equilibrium state when $R_0 = 1$

Figure 2 shows a validation of the global stability of the Monkeypox-Free equilibrium state, E_0 when both R_{0n} and R_{0n} are less than unity (< 1) with all parameter values as indicated in Table 2 except for $\beta_{nn} = 0.003$ and $\beta_{hh} = 0.00023$ while in Figure 3 shows validation of global stability of Monkeypox-Free equilibrium point when $R_{0h} = 1$ and $R_{0n} = 1$ which is obtained provided $\beta_{hh} = 0.000488$ and $\beta_{nn} = 0.0050535$ respectively with the rest of the parameters as incicated in Table 2.

3.2. Monkepox Endemic equilibruim point. Monkeypox endemic equilibrium state is achieved when the disease persist in the population. For the case of Monkeypox model, the disease can persist in the non-human population only, the disease can persist in the human population only or when there is persistence in both human and non-human population. This would give rise to two semi-endemic equilibrium points and one co-existence endemic equilibrium state. The semi-endemic equilibrium is when there is infected rodents only or infected humans only while the co-existence endemic equilibrium point is when there is infection in both human and rodent population.

3.2.1. *Infected rodent only equilibrium state, E_1.* This equilibrium state occurs where there is only rodent to rodent infection and no human to human infection and no rodent to human infection, that is, $\beta_{ch} = \beta_{hh} = \beta_{nh} = 0$ and hence $S_h^* = \dfrac{\Pi_h}{\mu_h}$. The nature of S_h^* shows that $R_{0h} < 1$.

To determine the remaining components of E_1, we consider the system of equations with rodents and contaminated environment only with $\lambda_n^* = \beta_{nn} I_n^*$.

$$\begin{cases} \Pi_n - \beta_{nn} I_n^* S_n^* - \mu_n S_n^* & = 0 \\ \beta_{nn} I_n^* S_n^* - (\theta + \mu_n) E_n^* & = 0 \\ \theta E_n^* - (\mu_n + \delta_n) I_n^* & = 0 \\ \omega_2 I_n^* - \mu_e C_e^* & = 0 \end{cases} \tag{18}$$

From the third Equation in (18), we have

$$E^* = \frac{(\mu_n + \delta_n)}{\theta} I_n^*$$

Substituting in the second equation, gives

$$\beta_{nn} S_n^* = \frac{(\theta + \mu_n)(\mu_n + \delta_n)}{\theta}$$

Implying that

$$S_n^* = \frac{(\theta + \mu_n)(\mu_n + \delta_n)}{\beta_{nn}\theta}$$

From the first Equation in (18), we have

$$I_n^* = \frac{\Pi_n}{\beta_{nn} S_n^*} - \frac{\mu_n}{\beta_{nn}} = \frac{\Pi_n \theta \beta_{nn}}{(\theta + \mu_n)(\mu_n + \delta_n)} - \frac{\mu_n}{\beta_{nn}}$$

which gives

$$I_n^* = \frac{\mu_n}{\beta_{nn}} (R_{0n} - 1)$$

therefore,

$$E_n^* = \frac{(\mu_n + \delta_n)\mu_n}{\theta \beta_{nn}} (R_{0n} - 1)$$

and

$$C_e^* = \frac{\omega_2 \mu_n}{\mu_e \beta_{nn}} (R_{0n} - 1)$$

Hence $E_1 = \left(\dfrac{\Pi_h}{\mu_h}, 0, 0, 0, 0, 0, 0, 0, S_n^*, E_n^*, I_n^*, C_e^* \right)$.

3.2.2. *Global Stability of Infected rodent only equilibrium state E_1.* Many techniques have been used to show the global stability of epidemic models Shuai & Van den Driessche [34]). Among the notable ones is Lyapunov-Kasovskii-Lasalle stability theorem (Martcheva [35]). To utilize this this technique, we shall need the following definitions, Theorems and Lemmas.

Definition 3. *A function $\mathscr{L}(p,q)$ on an open interval containing the origin is said to be a Lyapunov function for a dynamical system $\frac{dp}{dt} = f(p,q)$ and $\frac{dq}{dt} = g(p,q)$ if and only if*

- $\mathscr{L}(p,q) > 0$*, for all* $(x,y) \in U - \{0,0\}$
- $\mathscr{L}(0,0) = 0$
- $\frac{d\mathscr{L}}{dt} \leq 0$*, for all* $(p,q) \in U - \{0,0\}$

Consider $(p^*,q^*) = (0,0)$ as an equilibrium point of the system $\frac{dp}{dt} = f(p,q)$ and $\frac{dq}{dt} = g(p,q)$ and $\mathscr{L}(p,q)$ be a continuous differentiable positive definite function in the neighborhood of the origin, then

- If $\frac{d\mathscr{L}}{dt} \leq 0$, for all $(p,q) \in U - \{0,0\}$, where $U \subset \mathbf{R}^+$ then origin is stable.
- If $\frac{d\mathscr{L}}{dt} < 0$, for all $(p,q) \in U - \{0,0\}$, then origin is uniformly asymptotically stable.
- If $\frac{d\mathscr{L}}{dt} > 0$, for all $(p,q) \in U - \{0,0\}$, then origin is unstable.

Theorem 5. *Lyapunov stability theorem (Liapunov* [36]*, Martcheva* [35]*).*
If a function $\mathscr{L}(p,q)$ is radially unbounded and positive definite and its time derivative is negative, $\mathscr{L}' < 0$, for all $(p,q) \neq (p^*,q^*)$, then the equilibrium point (p^*,q^*) is globally stable.

Theorem 6. *Krasovskii-Lasalle theorem (Krasovskii* [37]*, Lasalle* [38]*).*
Let (p^*,q^*) be the equilibrium point of an autonomous system $\frac{dp}{dt} = f(p,q)$ and $\frac{dq}{dt} = g(p,q)$, that is, $f(p^*,q^*) = 0$ and $g(p^*,q^*) = 0$. Suppose there exist a continuous differentiable function $\mathscr{L} : \mathscr{R}^n \longrightarrow \mathscr{R}$ and that it is radially bounded and positive definite and satisfies $\mathscr{L}' \leq 0$, for all time, t and all $(p,q) \in \mathscr{R}^n$. Then the equilibrium point (p^*,q^*) is globally stable.

Lemma 1. *(Martcheva* [35]*) Assume that $x_1,...,x_n$ are positive numbers. Then their arithmetic mean is greater than or equal to the geometric mean. i.e.,*

$$\frac{x_1 + ... + x_n}{n} \geq (x_1 \times ... \times x_n)^{\frac{1}{2}}$$

Now for the Infected rodent only system with assumption that rodents are not affected by the dynamics of Monkeypox in the environment (Madubueze [22]), we ignore the equation for contaminated environment and deal with only the rodent equations and consider Lyapunov function of the form

$$\begin{aligned}\mathscr{L}_1 &= \frac{1}{b_1}(S_n - S_n^* - S_n^* \ln \frac{S_n}{S_n^*}) + \frac{1}{b_2}(E_n - E_n^* - E_n^* \ln \frac{E_n}{E_n^*}) \\ &+ \frac{1}{b_3}(I_n - I_n^* - I_n^* \ln \frac{I_n}{I_n^*}) + \frac{1}{b_4}(S_h - S_h^* - S_h^* \ln \frac{S_h}{S_h^*}) \end{aligned} \tag{19}$$

where b_1, b_2, b_3, b_4 are positive constants. The time derivative of $\mathscr{L}_1$ is given by

$$\begin{aligned}\frac{d\mathscr{L}_1}{dt} &= \frac{1}{b_1}\left(1 - \frac{S_n^*}{S_n}\right)\frac{dS_n}{dt} + \frac{1}{b_2}\left(1 - \frac{E_n^*}{E_n}\right)\frac{dE_n}{dt} \\ &+ \frac{1}{b_3}\left(1 - \frac{I_n^*}{I_n}\right)\frac{dI_n}{dt} + \frac{1}{b_4}\left(1 - \frac{S_h^*}{S_h}\right)\frac{dS_h}{dt} \end{aligned} \tag{20}$$

Substituting Equation (1) in (20), we have

$$\begin{aligned}\frac{d\mathscr{L}_1}{dt} &= \frac{1}{b_1}\left(1 - \frac{S_n^*}{S_n}\right)(\Pi_n - \beta_{nn} I_n S_n - \mu_n) + \frac{1}{b_2}\left(1 - \frac{E_n^*}{E_n}\right)(\beta_{nn} I_n S_n - (\theta + \mu_h)E_n) \\ &+ \frac{1}{b_3}\left(1 - \frac{I_n^*}{I_n}\right)(\theta E_n - (\mu_n + \delta_n)I_n) + \frac{1}{b_4}\left(1 - \frac{S_h^*}{S_h}\right)(\Pi_h - \mu_h S_h) \end{aligned} \tag{21}$$

Substituting for Π_h and Π_n using the equilibrium state conditions in Equation (21) gives

$$\begin{aligned}\frac{d\mathscr{L}_1}{dt} &= \frac{1}{b_1}\left(1 - \frac{S_n^*}{S_n}\right)(\beta_{nn} I_n^* S_n^* + \mu_n S_n^* - \beta_{nn} I_n S_n - \mu_n S_n) + \frac{1}{b_2}\left(1 - \frac{E_n^*}{E_n}\right)(\beta_{nn} I_n S_n - (\theta + \mu_h)E_n) \\ &+ \frac{1}{b_3}\left(1 - \frac{I_n^*}{I_n}\right)(\theta E_n - (\mu_n + \delta_n)I_n) + \frac{1}{b_4}\left(1 - \frac{S_h^*}{S_h}\right)(\mu_h S_h^* - \mu_h S_h) \end{aligned} \tag{22}$$

After opening the brackets, collecting some like terms and multiplying the fraction terms with equilibrium values, we have

$$\begin{aligned}\frac{d\mathscr{L}_1}{dt} &= \frac{-\mu_n}{b_1}\frac{(S_n - S_n^*)^2}{S_n} + \frac{1}{b_1}\beta_{nn} I_n^* S_n^* - \frac{1}{b_1}\beta_{nn} I_n S_n - \frac{1}{b_1}\beta_{nn}\frac{I_n^* S_n^{*^2}}{S_n} + \frac{1}{b_1}\beta_{nn} I_n S_n^* \\ &+ \frac{1}{b_2}\beta_{nn} I_n S_n - \frac{1}{b_2}(\theta + \mu_n)E_n - \frac{1}{b_2}\beta_{nn} I_n S_n \frac{E_n^* I_n^* S_n^*}{E_n I_n^* S_n^*} + \frac{1}{b_2}(\theta + \mu_n)E_n^* \\ &+ \frac{1}{b_3}\theta E_n - \frac{1}{b_3}(\mu_n + \delta_n)I_n - \frac{1}{b_3}\theta E_n \frac{I_n^* E_n^*}{I_n E_n^*} + \frac{1}{b_3}(\mu_n + \delta_n)I_n^* - \frac{\mu_h}{b_4}\frac{(S_h - S_h^*)^2}{S_h} \end{aligned} \tag{23}$$

If $b_1 = b_2$, then $-\frac{1}{b_1}\beta_{nn} I_n S_n$ cancels $\frac{1}{b_2}\beta_{nn} I_n S_n$ and we have

$$\begin{aligned}\frac{d\mathscr{L}_1}{dt} &= \frac{-\mu_n}{b_1}\frac{(S_n-S_n^*)^2}{S_n}+\frac{1}{b_1}\beta_{nn}I_n^*S_n^*-\frac{1}{b_1}\beta_{nn}\frac{I_n^*S_n^{*^2}}{S_n}+\frac{1}{b_1}\beta_{nn}I_nS_n^*\\ &-\frac{1}{b_2}(\theta+\mu_n)E_n-\frac{1}{b_2}\beta_{nn}I_nS_n\frac{E_n^*I_n^*S_n^*}{E_nI_n^*S_n^*}+\frac{1}{b_2}(\theta+\mu_n)E_n^*\\ &+\frac{1}{b_3}\theta E_n-\frac{1}{b_3}(\mu_n+\delta_n)I_n-\frac{1}{b_3}\theta E_n\frac{I_n^*E_n^*}{I_nE_n^*}+\frac{1}{b_3}(\mu_n+\delta_n)I_n^*-\frac{\mu_h}{b_4}\frac{(S_h-S_h^*)^2}{S_h}\end{aligned}$$

Since $b_1=b_2$, then $\beta_{nn}I_n^*S_n^*=(\theta+\mu_n)E_n^*$, from the equilibrium equation. Now we need to choose b_3 such that

$$\frac{1}{b_3}(\mu_n+\delta_n)I_n^*=\frac{1}{b_2}(\theta+\mu_n)E_n^*$$

This gives

$$b_3=b_2\left(\frac{\theta}{\theta+\mu_n}\right)$$

Factorizing $\beta_{nn}I_n^*S_n^*$ gives

$$\begin{aligned}\frac{d\mathscr{L}_1}{dt} &= \frac{-\mu_n}{b_1}\frac{(S_n-S_n^*)^2}{S_n}-\frac{\mu_h}{b_5}\frac{(S_h-S_h^*)^2}{S_h}+\frac{1}{b_1}\beta_{nn}I_n^*S_n^*\left[-\frac{S_n^*}{S_n}-\frac{E_n^*I_nS_n}{E_nI_n^*S_n^*}-\frac{I_n^*E_n}{E_n^*I_n}\right]\\ &+\frac{1}{b_1}\beta_{nn}S_n^*I_n-\frac{1}{b_3}(\mu_n+\delta_n)I_n+\frac{1}{b_3}\theta E_n-\frac{1}{b_2}(\theta+\mu_n)E_n \qquad (24)\end{aligned}$$

substituting for S_n^* by its equilibrium value and using $b_3=b_2\left(\frac{\theta}{\theta+\mu_n}\right)$, we see that

$$\left(\frac{1}{b_1}\beta_{nn}S_n^*-\frac{1}{b_3}(\mu_n+\delta_n)\right)I_n=0$$

and

$$\left(\frac{1}{b_3}\theta-\frac{1}{b_2}(\theta+\mu_n)\right)E_n=0$$

If $b_1=b_2=\mu_n, b_4=\mu_h$, then $b_3=\mu_n\left(\frac{\theta}{\theta+\mu_n}\right)$ and we have

$$\frac{d\mathscr{L}_1}{dt} = -\frac{(S_n-S_n^*)^2}{S_n}-\frac{(S_h-S_h^*)^2}{S_h}+\frac{1}{b_1}\beta_{nn}I_n^*S_n^*\left[3-\frac{S_n^*}{S_n}-\frac{E_n^*I_nS_n}{E_nI_n^*S_n^*}-\frac{I_n^*E_n}{E_n^*I_n}\right] \qquad (25)$$

From Equation (25), $\frac{d\mathscr{L}_1}{dt}<0$ provided we can show that $\frac{1}{b_1}\beta_{nn}I_n^*S_n^*\left[3-\frac{S_n^*}{S_n}-\frac{E_n^*I_nS_n}{E_nI_n^*S_n^*}-\frac{I_n^*E_n}{E_n^*I_n}\right]<0$. Let $a_1=\frac{S_n}{S_n^*}, a_2=\frac{E_n^*I_nS_n}{E_nI_n^*S_n^*}$ and $a_3=\frac{I_n^*E_n}{I_nE_n^*}$, then $a_1a_2a_3=1$ and

$$a_1+a_2+a_3=\frac{S_n}{S_n^*}+\frac{E_n^*I_nS_n}{E_nI_n^*S_n^*}+\frac{I_n^*E_n}{I_nE_n^*}\geq 3$$

Therefore, utilizing Lemma 1, the arithmetic mean is larger than the geometric mean. Hence, $\frac{d\mathscr{L}_1}{dt} < 0$. This proves that equilibrium point E_1 is globally asymptotically stable. The implication is that solutions that begin near the equilibrium point E_1 remain near E_1 for an indefinite time.

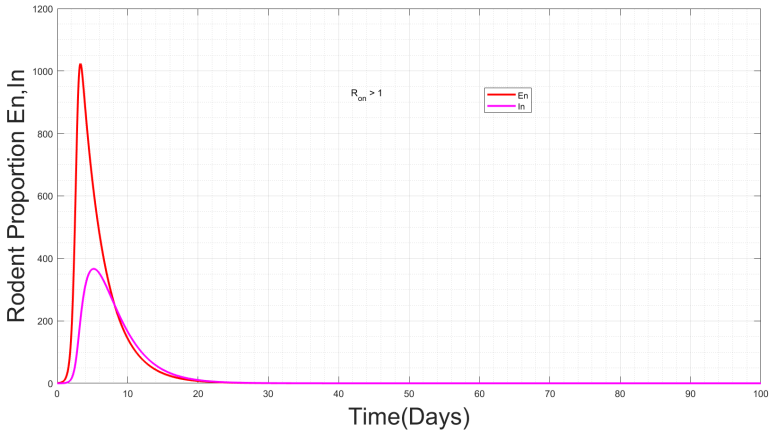

FIGURE 4. Global stability of Infected Rodents only equilibrium state when $R_{0n} > 1$

Figure 4 shows a validation of global stability of the Infected rodents only equilibrium state with $R_{0n} = 5.3429 > 1$ and all parameter values are as indicated in Table 2.

3.2.3. *Infected human only equilibrium state, E_2.* This is achieved whenever the Monkeypox disease is persistent in the human population only, that is $E_n = I_n = 0$. Therefore, from the Monkeypox model system, $S_n^{**} = \dfrac{\Pi_n}{\mu_n}$.
For co-existence of the infected rodent-free equilibrium with the human population, the human and environmental compartments are solved simultaneously as follows,

$$\begin{aligned}
\Pi_h + \phi_3 J_h^{**} - \lambda_h^{**} S_h^{**} - \mu_h S_h^{**} &= 0 \\
\lambda_h^{**} S_h^{**} - \pi_1 E_h^{**} &= 0 \\
\psi_2 E_h^{**} - \pi_2 J_h^{**} &= 0 \\
\psi_3 E_h^{**} + \phi_2 J_h^{**} - \pi_3 I_a^{**} &= 0 \\
\psi_1 E_h^{**} + \phi_1 J_h^{**} - \pi_4 I_s^{**} &= 0
\end{aligned} \tag{26}$$

$$\alpha_2 I_s^{**} - \pi_5 H_h^{**} = 0$$

$$\phi_4 I_a^{**} + \alpha_1 I_s^{**} + \nu H_h^{**} - \mu_h R_h^{**} = 0$$

$$\omega_1 I_s^{**} - \mu_e C_e^{**} = 0.$$

Solving (26) gives,

(27)

$$\begin{cases}
S_h^{**} &= \dfrac{\pi_2 \Pi_h (\pi_1 + \mu_h)}{\lambda_h^{**}(\pi_1\pi_2 + \pi_2\mu_h - \phi_3\psi_2) + \pi_2\mu_h(\pi_1+\mu_h)} \\
E_h^{**} &= \dfrac{\pi_2 \Pi_h \lambda_h^{**}}{\lambda_h^{**}(\pi_1\pi_2 + \pi_2\mu_h - \phi_3\psi_2) + \pi_2\mu_h(\pi_1+\mu_h)} \\
I_a^{**} &= \dfrac{\lambda_h^{**}\Pi_h(\psi_2\phi_2 + \psi_3\pi_2)}{\pi_3\lambda_h^{**}(\pi_1\pi_2 + \pi_2\mu_h - \phi_3\psi_2) + \pi_3\pi_2\mu_h(\pi_1+\mu_h)} \\
I_s^{**} &= \dfrac{\lambda_h^{**}\Pi_h(\psi_2\phi_1 + \psi_1\pi_2)}{\pi_4\lambda_h^{**}(\pi_1\pi_2 + \pi_2\mu_h - \phi_3\psi_2) + \pi_4\pi_2\mu_h(\pi_1+\mu_h)} \\
H_h^{**} &= \dfrac{\alpha_2\lambda_h^{**}\Pi_h(\psi_2\phi_1 + \psi_1\pi_2)}{\pi_4\pi_5\lambda_h^{**}(\pi_1\pi_2 + \pi_2\mu_h - \phi_3\psi_2) + \pi_4\pi_5\pi_2\mu_h(\pi_1+\mu_h)} \\
R_h^{**} &= \dfrac{\lambda_h^{**}\Pi_h(\psi_2\pi_4\pi_5\phi_4\phi_2 + \psi_2\alpha_2\nu\pi_3\phi_1 + \pi_4\pi_5\phi_4\psi_3\pi_2 + \psi_2\pi_3\alpha_1\pi_5\phi_1 + \alpha_2\nu\pi_3\psi_1\pi_2 + \pi_3\alpha_1\pi_5\psi_1\pi_2)}{\lambda_h^{**}\pi_5\pi_3\pi_4\mu_h(\pi_1\pi_2 + \pi_2\mu_h - \phi_3\psi_2) + \pi_5\pi_3\pi_4\mu_h\pi_2\mu_h(\pi_1+\mu_h)} \\
C_e^{**} &= \dfrac{\lambda_h^{**}\Pi_h\omega_1(\psi_2\phi_1 + \psi_1\pi_2)}{\pi_4\mu_e\lambda_h^{**}(\pi_1\pi_2 + \pi_2\mu_h - \phi_3\psi_2) + \pi_4\mu_e\pi_2\mu_h(\pi_1+\mu_h)}
\end{cases}$$

Therefore, the infected human only equilibrium state is given by

$$E_2 = (S_h^{**}, E_h^{**}, J_h^{**}, I_a^{**}, I_s^{**}, H_h^{**}, R_h^{**}, \frac{\Pi_n}{\mu_n}, 0, 0, C_e^{**}).$$

3.2.4. *Global stability of the Infected humans only equilibrium state, E_2.* Adopting a Voltera-Lyapunov matrix conditions (Chien,Fengsheng & Shateyi[33], Madubueze et al [22]), a Lyapunov function is constructed to determine the global stability of the infected humans only equilibrium state, E_2. Consider $\mathscr{L}_2$ to be the Volterra-Lyapunov function defined in the region Ω for the Monkeypox model system. Then the global stability of the infected humans only Infected-humans only equilibrium state, E_2 holds if $\dfrac{d\mathscr{L}_2}{dt} < 0$. Let the Volterra-Lyapunov function be of the form

$$\begin{aligned}
\mathscr{L}_2 &= e_1(S_h - S_h^{**})^2 + e_2(E_h - E_h^{**})^2 + e_3(J_h - J_h^{**})^2 + e_4(I_a - I_a^{**})^2 \\
&+ e_5(I_s - I_s^{**})^2 + e_6(H_h - H_h^{**})^2 + e_7(R_h - R_h^{**})^2 + e_8(S_n - S_n^{**})^2 + e_9(C_e - C_e^{**})^2,
\end{aligned} \tag{28}$$

where $e_1, e_2, e_3, e_4, e_5, e_6, e_7, e_8$, and e_9 are positive constants. Differentiating $\mathscr{L}_2$ with respect to the state variables yields

$$\frac{d\mathscr{L}_2}{dt} = 2e_1(S_h - S_h^{**})\frac{dS_h}{dt} + 2e_2(E_h - E_h^{**})\frac{dE_h}{dt} + 2e_3(J_h - J_h^{**})\frac{dJ_h}{dt} + 2e_4(I_a - I_a^{**})\frac{dI_a}{dt}$$

$$+ 2e_5(I_s - I_s^{**})\frac{dI_s}{dt} + 2e_6(H_h - H_h^{**})\frac{dH_h}{dt} + 2e_7(R_h - R_h^{**})\frac{dR_h}{dt} \tag{29}$$

$$+ 2e_8(S_n - S_n^{**})\frac{dS_n}{dt} + 2e_9(C_e - C_e^{**})\frac{dC_e}{dt}. \tag{30}$$

Substituting for $\frac{dS_h}{dt}, \frac{dE_h}{dt}, \frac{dJ_h}{dt}, \frac{dI_a}{dt}, \frac{dI_s}{dt}, \frac{dH_h}{dt}, \frac{dR_h}{dt}, \frac{dS_n}{dt}$ and $\frac{dC_e}{dt}$ and using the conditions for endemic equilibrium gives

$$\begin{aligned}
\frac{d\mathscr{L}_2}{dt} &= 2e_1(S_h - S_h^{**})\left[\Pi_h + \phi_3 J_h - \lambda_h S_h - \mu_h S_h - \Pi_h - \phi_3 J_h^{**} + \lambda_h^{**} S_h^{**} + \mu_h S_h^{**}\right] \\
&+2e_2(E_h - E_h^{**})\left[\lambda_h S_h - \pi_1 E_h - \lambda_h^{**} S_h^{**} + \pi_1 E_h^{**}\right] + 2e_3(J_h - J_h^{**})\left[\psi_2 E_h - \pi_2 J_h - \psi_2 E_h^{**} + \pi_2 J_h^{**}\right] \\
&+2e_4(I_a - I_a^{**})\left[\psi_3 E_h + \phi_2 J_h - \pi_3 I_a - \psi_3 E_h^{**} - \phi_2 J_h^{**} + \pi_3 I_a^{**}\right] \\
&+2e_5(I_s - I_s^{**})\left[\psi_1 E_h + \phi_1 J_h - \pi_4 I_s - \psi_1 E_h^{**} - \phi_1 J_h^{**} + \pi_4 I_s^{**}\right] \qquad (31) \\
&+2e_6(H_h - H_h^{**})\left[\alpha_2 I_s - \pi_5 H_h - \alpha_2 I_s^{**} + \pi_5 H_h^{**}\right] \\
&+2c_7(R_h - R_h^{**})\left[\phi_4 I_a + \alpha_1 I_s + \nu H_h - \mu_h R_h - \phi_4 I_a^{**} - \alpha_1 I_s^{**} - \nu H_h^{**} + \mu_h R_h^{**}\right] \\
&+2e_8(S_n - S_n^{**})\left[-\mu_n(S_n - S_n^{**})\right] + 2e_9(C_e - C_e^{**})\left[\omega_1 I_s - \mu_e C_e - \omega_1 I_s^{**} + \mu_e C_e^{**}\right].
\end{aligned}$$

Introducing $\lambda_h S_h^{**}$ in the first two terms of Equation (31) and simplifying gives

$$\begin{aligned}
\frac{d\mathscr{L}_2}{dt} &= 2e_1(S_h - S_h^{**})\left[-(\mu_h + \lambda_h)(S_h - S_h^{**}) + \phi_3(J_h - J_h^{**}) - S_h^{**}(\lambda_h - \lambda_h^{**})\right] \\
&+2e_2(E_h - E_h^{**})\left[-\pi_1(E_h - E_h^{**}) + \lambda_h(S_h - S_h^{**}) + S_h^{**}(\lambda_h - \lambda_h^{**})\right] \\
&+2e_3(J_h - J_h^{**})\left[\psi_2(E_h - E_h^{**}) - \pi_2(J_h - J_h^{**})\right] \\
&+2e_4(I_a - I_a^{**})\left[-\pi_3(I_a - I_a^{**}) + \phi_2(J_h - J_h^{**}) + \psi_3(E_h - E_h^{**})\right] \\
&+2e_5(I_s - I_s^{**})\left[\psi_1(E_h - E_h^{**}) + \phi_1(J_h - J_h^{**}) - \pi_4(I_s - I_s^{**})\right] \qquad (32) \\
&+2e_6(H_h - H_h^{**})\left[\alpha_2(I_s - I_s^{**}) - \pi_5(H_h - H_h^{**})\right] \\
&+2c_7(R_h - R_h^{**})\left[\phi_4(I_a - I_a^{**}) + \alpha_1(I_s - I_s^{**}) + \nu(H_h - H_h^{**}) - \mu_h(R_h - R_h^{**})\right] \\
&+2e_8(S_n - S_n^{**})\left[-\mu_n(S_n - S_n^{**})\right] \\
&+2e_9(C_e - C_e^{**})\left[\omega_1(I_s - I_s^{**}) - \mu_e(C_e - C_e^{**})\right].
\end{aligned}$$

Equation (33) is given by

$$\frac{d\mathscr{L}_2}{dt} = X(YZ + Z^T Y^T)X^T$$

with

$$X = \begin{pmatrix} (S_h - S_h^{**}) & (E_h - E_h^{**}) & (J_h - J_h^{**}) & (I_a - I_a^{**}) & (I_s - I_s^{**}) & (H_h - H_h^{**}) \\ & (R_h - R_h^{**}) & (S_n - S_n^{**}) & (C_e - C_e^{**}), & & \end{pmatrix}$$

$$Y = \begin{pmatrix} e_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & e_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & e_3 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & e_4 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & e_5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & e_6 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & e_7 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & e_8 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & e_9 \end{pmatrix}$$

and

(33)

$$Z = \begin{pmatrix} -(\mu_h + \lambda_h) & 0 & \phi_3 & -\beta_{hh}\theta_m S_h^{**} & -\beta_{hh} S_h^{**} & 0 & 0 & 0 & -\beta_{ch} S_h^{**} \\ \lambda_h & -\pi_1 & 0 & \beta_{hh}\theta_m S_h^{**} & \beta_{hh} S_h^{**} & 0 & 0 & 0 & \beta_{ch} S_h^{**} \\ 0 & \psi_2 & -\pi_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \psi_3 & \phi_2 & -\pi_3 & 0 & 0 & 0 & 0 & 0 \\ 0 & \psi_1 & \phi_1 & 0 & -\pi_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \alpha_2 & -\pi_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & \phi_4 & \alpha_1 & \nu & -\mu_h & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\mu_n & 0 \\ 0 & 0 & 0 & 0 & \omega_1 & 0 & 0 & 0 & -\mu_e \end{pmatrix}$$

Showing that Z is Lyapunov stable or $-Z$ is diagonal stable would imply global asymptotic stability when $X \neq X^{**}$. This can be achieved in a similar manner as shown by Chien, Fengsheng & Shateyi [33], using the following notations, definitions and Lemmas.

Notation 1. Matrix M have the property of symmetry and positive definite (negative), i.e., $M > 0 (M < 0)$.

Notation 2. For any $n \times n$ matrix M, we shall use $\widetilde{M}$ to denote the $(n-1) \times (n-1)$ matrix which is obtained by deleting the last row and last column of matrix M.

Definition 4. *Cross* [39] *A non-singular matrix $M_{n\times n}$ is Voltera-Lyapunov stable if there exist a positive matrix $R_{n\times n}$ such that*

$$RM + M^T R^T < 0$$

Definition 5. *Chien, Fengsheng & Shateyi* [33] *Matrix $M_{n\times n}$ is diagonally stable if there exist a diagonal matrix $R_{n\times n}$ such that*

$$RM + M^T R^T > 0$$

Lemma 2. [39]

Let $M = \begin{pmatrix} m_{11} & m_{12} \\ m_{21} & m_{22} \end{pmatrix}$ *be a* 2×2 *matrix. Then* $M_{2\times 2}$ *is Voltera-Lyapunov stable if*

$$\begin{cases} m_{11} & < 0 \\ m_{22} & < 0 \\ det(M) & = m_{11}m_{22} - m_{21}m_{12} > 0 \end{cases}$$

Lemma 3. [39, 33] *Let $M = [m_{ij}]$ be a non-singular $n \times n$ matrix $(n \geq 2)$ and $R = diag(r_1, r_2, ..., r_n)$ be positive diagonal $n \times n$ matrix. Let $P = M^{-1}$ and if*

$$\begin{cases} m_{nn} & > 0 \\ \widetilde{R}\widetilde{M} + (\widetilde{R}\widetilde{M})^T & > 0 \\ \widetilde{R}\widetilde{P} + (\widetilde{R}\widetilde{P})^T & > 0 \end{cases}$$

then there exist $r_n > 0$ such that $RM + M^T R^T > 0$.

Lemma 4. *The matrix Z in Equation* (33) *is Voltera-Lyapunov stable.*

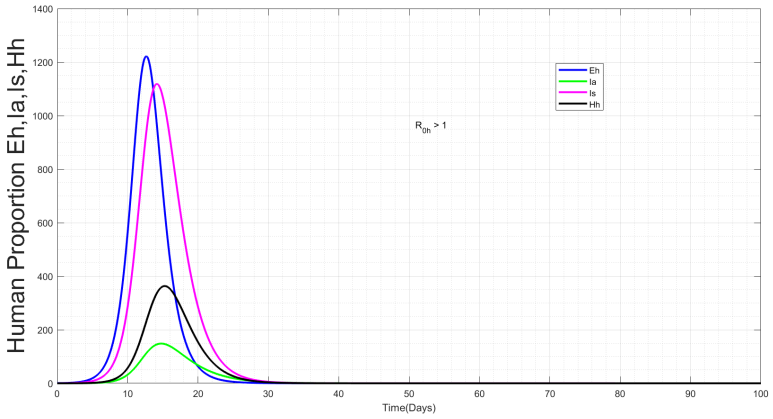

FIGURE 5. Global stability of Infected humans only equilibrium state when $R_{0h} > 1$

Proof. It is clear from (33) that $-z_{99} > 0$ from matrix Z and Lemma 2 and Lemma 3 are satisfied, then there exists a positive 9×9 diagonal matrix Y such that

$$Y(-Z) + (-Z)^T Y^T > 0$$

which implies that

$$Y(Z) + (Z)^T Y^T < 0$$

Therefore, $\frac{d\mathscr{L}_2}{dt} < 0$ when $X \neq X^{**}$ and this ensures the global stability of the infected humans only endemic equilibrium point. Thus, applying LaSalle's invariant principle, the global stability of Infected humans only equilibrium state is stated in the next theorem below. □

Theorem 7. *The Infected humans only endemic equilibrium point, E_2 of the model system* (1) *is globally asymptotically stable if $R_{0h} > 0$ and unstable otherwise.*

Figure 5 shows a validation of global stability of Infected humans only equilibrium state, E_2 with $R_{0h} = 1.505$ in accordance to Theorem 7 and parameters values are as indicated in Table 2. It is to be noted that the same argument can be used to understand the Co-existence of Infected humans and infected rodents equilibrium state.

4. Numerical Results and Discussion

4.1. Sensitivity Analysis. The effect of direct and environmental transmission on R_0 is carried out using sensitivity analysis. Sensitivity analysis is important in finding the relative importance of each model parameter on a given response function which in this case is taken to be R_0 (Mugabi et al. [40]). Thus, in addition to finding the effects of these routes on R_0, the effects of other parameters in the Monkeypox model (1) on R_0 are also determined. Therefore, this analysis will help to determine where to best allocate resources which are scarce in times of Monkeypox outbreak by focusing control measures on the parameters with the highest influence. The Latin Hypercube Sampling (LHS) method is used for the sensitivity analysis. Latin Hypercube Sampling method requires selecting a range and baseline value for each model parameter and generating N multiple runs for R_0 (Helton [41]). Here we used $N = 1000$ Parameters are assumed all to follow a uniform distribution (Simpson & Gumel [42]). From the LHS method the partial rank correlation coefficients (PRCCs) which is a value that measures the strength of relationship between two variables while controlling the effects of the other variables (Gomero [43]) is calculated and depicted in Table 3 and Figure 6 for case of the Monkeypox model (1). The effect of a given parameter on the transmission dynamics of Monkeypox disease is determined by the sign and magnitude of the partial rank correlation coefficients. A parameter with a negative partial rank correlation coefficient value has the potential of minimising Monkeypox infection when increased while parameter with a positive partial rank correlation coefficient value has the potential of minimising Monkeypox infection when decreased (Madubueze et al [22]). The parameters with partial rank correlation coefficient values greater than 0.5 or less than -0.5 are the most sensitive to R_0 (Taylor [44]). A plot of PRCCs of the model parameters for range of values as in Table 2 is shown by the Tornado plot in Figure 6. It can also be observed that parameters $\beta_{hh}, \beta_{ch}, \omega_1$ have positive PRCCs which are greater than 0.5. This means that whenever these parameters are increased, there shall be an increase in the Monkeypox infection while parameter $\alpha_1, \mu_e, \& \mu_h$ is negative and less than -0.5 meaning that increasing it would reduce on the Monkeypox infection. Therefore, as indicated in Table 3 and Figure 6,

Parameters	PRCC values	
Π_h	0.3914	
β_{nh}	0.0257	
β_{hh}	0.5756	
θ_m	0.2109	
β_{ch}	0.5331	
μ_h		-0.8042
ψ_1	0.1080	
ψ_2		-0.0747
ψ_3		-0.0591
ϕ_1	0.0036	
ϕ_2	0.0005	
ϕ_3		-0.0616
ϕ_4		-0.1720
α_1		-0.6411
α_2		-0.0388
δ_h		-0.1361
ω_1	0.5123	
μ_e		-0.5462

TABLE 3. Model parameters and their corresponding PRCC values

these parameters influence the transmission dynamics of the Monkeypox infection and in order to control the spread of Monkeypox in the human population decision makers and health practitioners should target these parameters.

4.2. Simulation results. Simulation results for the Monkeypox model system 1 are carried out using MATLAB $R2019a$ inbuilt ODE45 solver and the parameter values as indicated in Table 2, except where they are stated otherwise. The simulations illustrate and support the analytical results already established in section 3. The following initial conditions, $S_h(0) = 5000, J_h = 100, I_a = 5, I_s = 20, H_h = 5, R_h = 0, S_n = 1350, E_n = 20, I_n = 1, C_e = 10$ are

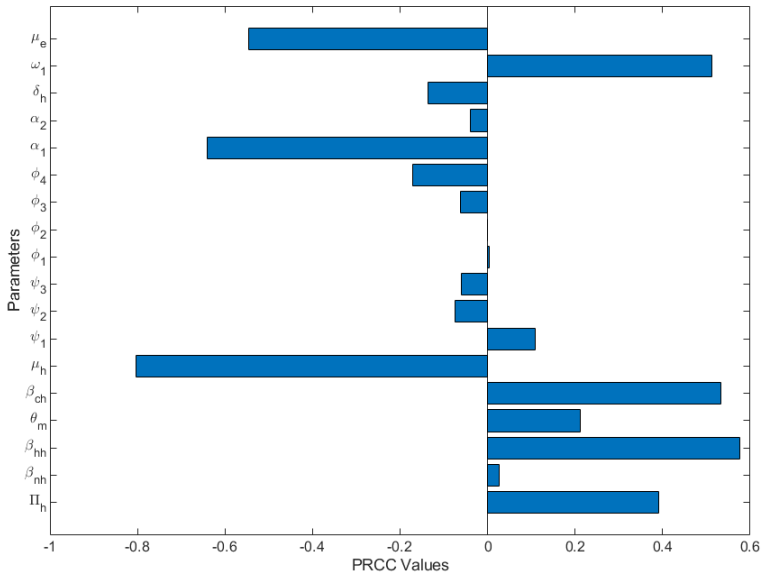

FIGURE 6. Tornado plot of Partial Rank Correlation Coefficient (PRCC) values for some important parameters of R_{0h}

used for the simulations. The impacts of the most sensitive parameters are illustrated in Table 3 and Figure 6 is its visual representation. Figure 7 is a graphical representation of the effect of varying the human to human contact rate, β_{hh}. Figure 7 (a), (b) , (c) and (d) show a decrease in the number of Exposed humans, Asymptomatic infectious, symptomatic infectious and Hospitalized humans as a result of an decrease in the human to human contact rate. This in turn decreases the basic reproduction ratio R_{0h} from $R_{0h} = 2.5119$ (for $\beta_{hh} = 0.00063$(green line)) to $R_{0h} = 0.5389$ (for $\beta_{hh} = 0.00013$(yellow line)). This is consistent with the findings of Bhunu & Mushayabasa [20]. This implication of is that Monkeypox infection can be reduced whenever the contact between susceptible humans and infectious humans whether symptomatic or asymptomatic can be reduced below 0.00013. Therefore, efforts such as sensitization should be aimed at educating people on human to avoid or reduce close contacts in case of Monkeypox outbreak.

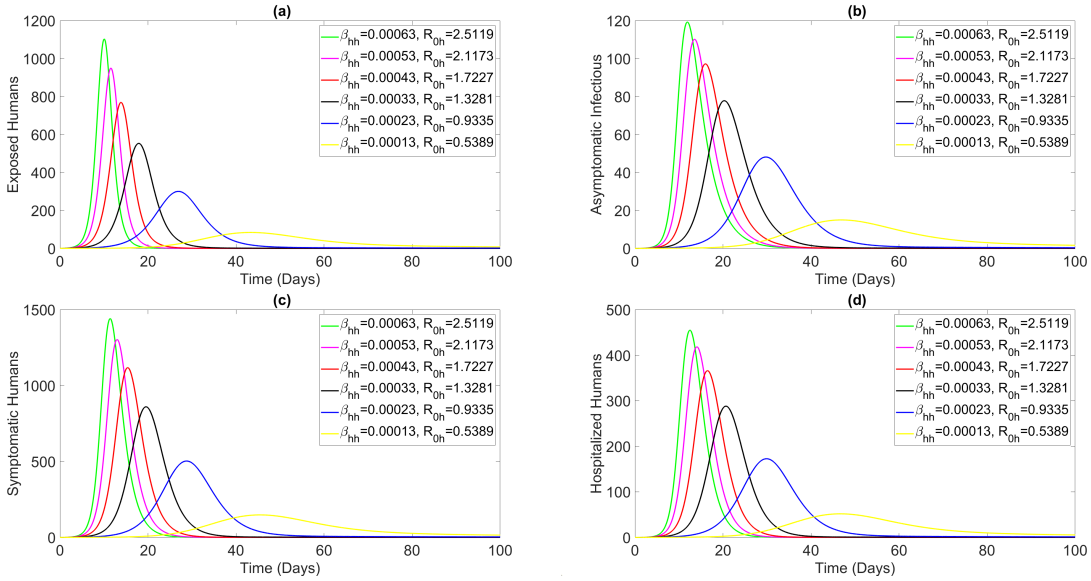

FIGURE 7. Effect of decreasing human-human transmission rate, β_{hh} on Human Disease compartments and corresponding basic reproduction number R_{0h}

Figure 8 shows the effect of increasing α_1 on the trend of the human disease classes. It is observed that this leads to a reduction in the number of exposed, asymptomatic, symptomatic infectious and hospitalized humans which in turn reduces the basic reproduction ratio, R_{0h} from 1.2833 to 0.9670. This is crucial in minimizing Monkeypox infection as an increase in the number of asymptomatic and symptomatic infectious humans would increase Monkeypox infection (World Health Organization [5]). Therefore, medical practitioners should target α_1 as one of the key parameters so that $R_{0h} < 1$. Figure 8 also shows how an increase in the recovery rate would reduce on the exposure rate as many would gain immunity from Monkeypox infection therefore reducing the Basic Reproduction number. The above shows that increase in the recovery rate α_1 leads to a slow reduction in R_{0h}. This means relying on it alone would not guarantee fast control of Monkeypox infection. This is in agreement with results from studies by Madubueze et al. [22] and Emeka et al. [16].

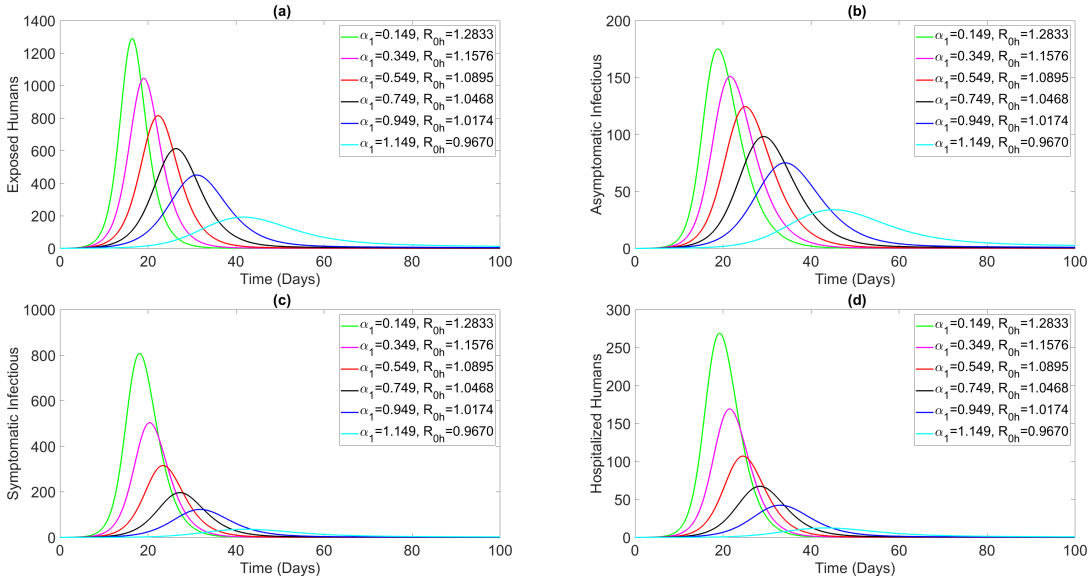

FIGURE 8. Effect of increasing α_1 on Human Disease compartments and corresponding basic reproduction number R_{0h}

Figure 9 shows how the human disease compartments changes with an increase in the human recruitment rate. It is observed that more humans would be exposed (Figure 9(a)), asymptomatic infectious (Figure 9(b)), symptomatic infectious (Figure 9(b)), and Hospitalized (Figure 9(b)) whenever there is an increase in the recruitment rate above the baseline value. This is an indication that even the basic reproduction number would increase far above unity. Therefore, to ensure a reduction in the basic reproduction ratio, $R_{0h} < 1$, efforts should be made to reduce on the human recruitment rate below the baseline value.

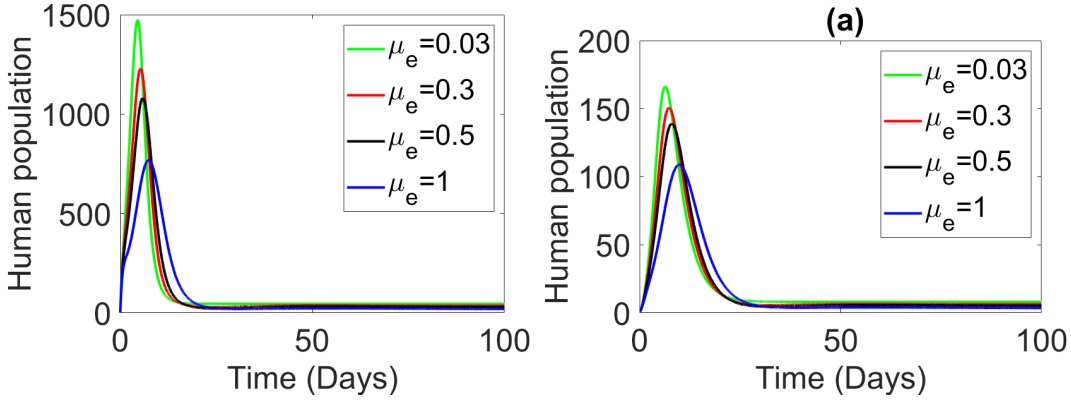

FIGURE 10. Effect of increasing Virus decay rate μ_e from the Contaminated Environment on Exposed and Asymptomatic Infectious Human population

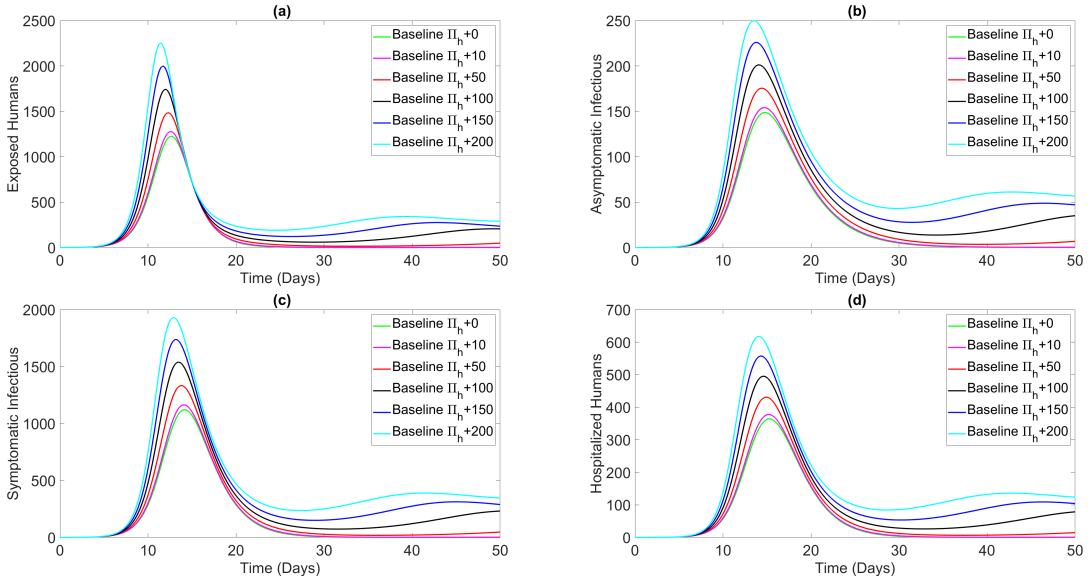

FIGURE 9. Effect of increasing Π_h on Human Disease compartments and corresponding basic reproduction number R_{0h}

From Figure 6, Figure 7, Figure 8, Figure 9, it shows that all the key parameters must be taken into consideration in order to achieve $R_{0h} < 1$. The first plot in Figure 10 shows the effect of increasing the virus decay rate from the environment on the exposed human population while the second shows how the Asymptomatic infected humans would decrease in number as a result of an increase in the virus decay rate. In both cases it is also noted that as the decay rate approaches 1 i.e $\mu_e = 1$, the basic reproduction number falls below 1 i.e $R_{0h} < 1$. Figure 11 shows the

effect of decreasing environment-to-human transmission rate, β_{ch} and virus shedding rate, ω_1 from symptomatic humans to the environment on the proportion of exposed, asymptomatic and symptomatic infectious humans. It is observed that a decrease in β_{ch} and ω_1 significantly reduces on the proportion of Exposed, Asymptomatic and Symptomatic infectious humans and also reduces on the basic reproduction number to below unity is is very vital in minimizing and controlling of Monkeypox infection.

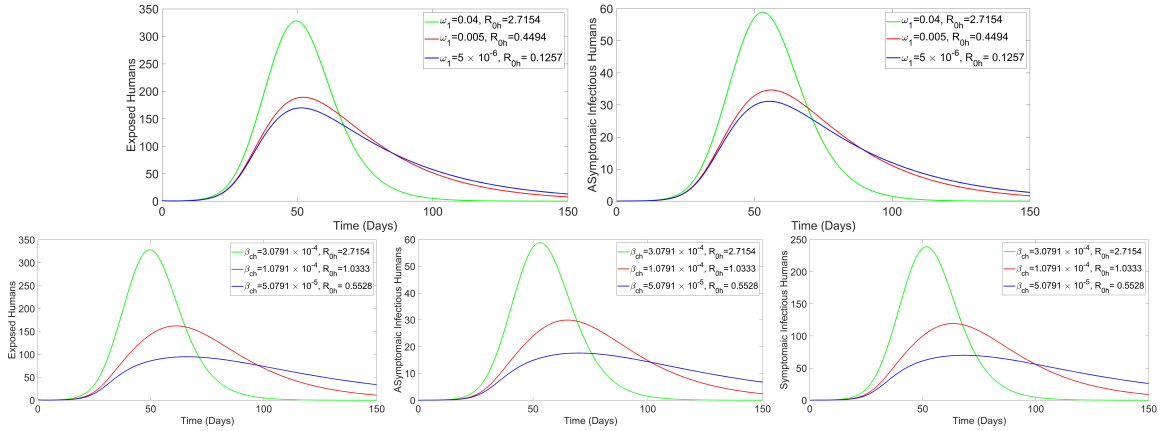

FIGURE 11. Effect of varying ω_1 and β_{ch} on the proportion of Exposed, Asymptomatic and Symptomatic Infectious humans and corresponding Basic reproduction numbers

5. CONCLUSION

An epidemiological mathematical model for the direct and indirect transmission dynamics of Monkeypox in two sub-populations of humans and rodents is formulated and analyzed. The Basic reproduction ratio, R_0, a quantity which measures the average number of secondary infections which result from an introduction of a single infectious individual in a completely susceptible population, is computed using Next-generation matrix approach. Two basic reproduction ratios that correspond to the two sub-populations of rodents and humans were arrived at, that is, R_{0n} and R_{0h} respectively. The basic reproduction ratio, R_0 is used to establish the local and global stability of the Monkeypox-Free equilibrium state, E_0 and the results is validated by Figure 2 and Figure 3.

The formulated Monkeypox model 1 has three Endemic equilibrium states, that is, the Infected rodent only, Infected humans only and coexistence of infected rodents and humans equilibrium states. The global stability of Infected rodents only equilibrium state is proved using Lyapunov-Kasovskii-Lasalle stability theorem and validating using Figure 4 while a Lyapunov function was constructed by adopting Voltera-Lyapunov matrix conditions and used to prove the Infected humans only equilibrium state which can in turn be used to prove the coexistence of Infected rodents and humans equilibrium point. Figure 5 is used to validate global stability of Infected humans only equilibrium state. Latin Hypercube Sampling technique and partial rank correlation coefficient is used to perform sensitivity analysis of the various human parameters on R_{0h} and it is noted that human-to-human contact rate β_{hh}, environment-to-human contact rate, β_{ch}, virus shedding rate from symptomatic infectious humans, ω_1, virus decay rate from the environment, μ_e, human recruitment rate Π_h and recovery rate of symptomatic infected humans α_1, were key parameters in the spread of Monkeypox infection in the human population. Some other parameters that play important roles are as indicated in Table 3. Simulations results in Figure 6 - Figure 11 support this findings. This also suggest that policymakers, decision makers and medical practitioners should pay much attention to these parameters in order to minimize Monkeypox infections especially among the human population. This can be done through sensitization of the public, hand washing, use of personal protective gears by medics.

Difficulty in estimating some key parameters such the proportion of humans who are asymptomatic, the virus shedding rate of symptomatic humans into the environment and the rate of virus decay are some of the limitations of this study. This is because there are no real-life data of some of these parameters and we rely of sourced parameters values from literature on the transmission dynamics of Monkeypox.

The model may be extended to incorporate trans-placental transmission as there is little known about the vertical transmission of Monkeypox virus. A stochastic mathematical model of Monkeypox can be formulated and used to understand the probability of persistence of the disease in different environmental conditions and an optimal control analysis with different interventions aimed at reducing both environmental and direct transmission may be a good contribution for future work.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

REFERENCES

[1] A. Sepehrinezhad, R.A. Ahmadabad, S. Sahab-Negah, Monkeypox virus from neurological complications to neuroinvasive properties: current status and future perspectives, J. Neurol. 270 (2022), 101–108. https://doi.org/10.1007/s00415-022-11339-w.

[2] E.A. Falendysz, J.G. Lopera, J.B. Doty, et al. Characterization of Monkeypox virus infection in African rope squirrels (Funisciurus sp.), PLoS Negl. Trop. Dis. 11 (2017), e0005809. https://doi.org/10.1371/journal.pntd.0005809.

[3] E.M. Bunge, B. Hoet, L. Chen, et al. The changing epidemiology of human monkeypox–A potential threat? A systematic review, PLoS Negl. Trop. Dis. 16 (2022), e0010141. https://doi.org/10.1371/journal.pntd.0010141.

[4] CDC, 2022 outbreak cases and data, (2022). https://www.cdc.gov/poxvirus/mpox/response/2022.

[5] WHO, Joint monthly surveillance report on SARS-CoV-2 and mpox in animals in the European Region, December 2022, (2023). https://www.who.int/europe/publications/i/item/WHO-EURO-2023-6616-46382-67849.

[6] P. von Magnus, E.K. Andersen, K.B. Petersen, et al. A pox-like disease in cynomolgus monkeys, Acta Pathol. Microbiol. Scand. 46 (1959), 156–176.

[7] I.D. Ladnyj, P. Ziegler, E. Kima, A human infection caused by monkeypox virus in Basankusu territory, Democratic Republic of the Congo, Bull. World Health Organ. 46 (1972), 593–597.

[8] S. Parker, A. Nuara, R.M.L. Buller, et al. Human monkeypox: An emerging zoonotic disease, Future Microbiol. 2 (2007), 17–34. https://doi.org/10.2217/17460913.2.1.17.

[9] K.M. Ajmera, L. Goyal, T. Pandit, et al. Monkeypox - An emerging pandemic, IDCases 29 (2022), e01587. https://doi.org/10.1016/j.idcr.2022.e01587.

[10] P.K. Mbala, J.W. Huggins, T. Riu-Rovira, et al. Maternal and fetal outcomes among pregnant women with human monkeypox infection in the Democratic Republic of Congo, J. Infect. Dis. 216 (2017), 824–828. https://doi.org/10.1093/infdis/jix260.

[11] S. Usman, I. Isa Adamu, Modeling the transmission dynamics of the monkeypox virus infection with treatment and vaccination interventions, J. Appl. Math. Phys. 05 (2017), 2335–2353. https://doi.org/10.4236/jamp.2017.512191.

[12] C.P. Bhunu, S. Mushayabasa, J.M. Hyman, Modelling HIV/AIDS and monkeypox co-infection, Appl. Math. Comput. 218 (2012), 9504–9518. https://doi.org/10.1016/j.amc.2012.03.042.

[13] J. Guarner, C. del Rio, P.N. Malani, Monkeypox in 2022–What clinicians need to know, JAMA. 328 (2022), 139–140. https://doi.org/10.1001/jama.2022.10802.

[14] F. Patauner, R. Gallo, E. Durante-Mangoni, Monkeypox infection: An update for the practicing physician, Eur. J. Intern. Med. 104 (2022), 1–6. https://doi.org/10.1016/j.ejim.2022.08.022.

[15] M.G. Reynolds, J.B. Doty, A.M. McCollum, et al. Monkeypox re-emergence in Africa: a call to expand the concept and practice of One Health, Expert Rev. Anti-Infect. Therapy. 17 (2019), 129–139. https://doi.org/10.1080/14787210.2019.1567330.

[16] PC Emeka, M.O. Ounorah, F.Y. Eguda, Mathematical model for monkeypox virus transmission dynamics, Epidemiology. 08 (2018), 1000348. https://doi.org/10.4172/2161-1165.1000348.

[17] O.J. Peter, S. Kumar, N. Kumari, et al. Transmission dynamics of Monkeypox virus: a mathematical modelling approach, Model. Earth Syst. Environ. 8 (2021), 3423–3434. https://doi.org/10.1007/s40808-021-01313-2.

[18] N.O. Lasisi, N.I. Akinwande, F.A. Oguntolu, Development and exploration of a mathematical model for transmission of monkey-pox disease in humans, Math. Models Eng. 6 (2020), 23–33. https://doi.org/10.21595/mme.2019.21234.

[19] S.V. Bankuru, S. Kossol, W. Hou, et al. A game-theoretic model of Monkeypox to assess vaccination strategies, PeerJ. 8 (2020), e9272. https://doi.org/10.7717/peerj.9272.

[20] C.P. Bhunu, S. Mushayabasa, Modelling the transmission dynamics of pox-like infections, IAENG Int. J. Appl. Math. 41 (2011), 2.

[21] I. Lauko, G. Pinter, R. TeWinkel, Equilibrium analysis for an epidemic model with a reservoir for infection, Lett. Biomath. 5 (2018), 255–274.

[22] C.E. Madubueze, I.O. Onwubuya, G.N. Nkem, et al. The transmission dynamics of the monkeypox virus in the presence of environmental transmission, Front. Appl. Math. Stat. 8 (2022), 1061546. https://doi.org/10.3389/fams.2022.1061546.

[23] S.A.J. Guagliardo, B. Monroe, C. Moundjoa, et al. Asymptomatic orthopoxvirus circulation in humans in the wake of a monkeypox outbreak among chimpanzees in Cameroon, Amer. J. Trop. Med. Hyg. 102 (2020), 206–212. https://doi.org/10.4269/ajtmh.19-0467.

[24] P.A. Naik, J. Zu, M.B. Ghori, et al. Modeling the effects of the contaminated environments on COVID-19 transmission in India, Results Phys. 29 (2021), 104774. https://doi.org/10.1016/j.rinp.2021.104774.

[25] T. Berge, M. Chapwanya, J.M.S. Lubuma, et al. A mathematical model for ebola epidemic with self-protection measures, J. Biol. Syst. 26 (2018), 107–131. https://doi.org/10.1142/s0218339018500067.

[26] U.E. Michael, L.O. Omenyi, E. Kafayat, et al. Monkeypox mathematical model with surveillance as control, Commun. Math. Biol. Neurosci. 2023 (2023), 6. https://doi.org/10.28919/cmbn/7781.

[27] S. Okyere, J. Ackora-Prah, Modeling and analysis of monkeypox disease using fractional derivatives, Results Eng. 17 (2023), 100786. https://doi.org/10.1016/j.rineng.2022.100786.

[28] H.W. Hethcote, The mathematics of infectious diseases, SIAM Rev. 42 (2000), 599–653. https://doi.org/10.1137/s0036144500371907.

[29] O. Diekmann, J.A.P. Heesterbeek, M.G. Roberts, The construction of next-generation matrices for compartmental epidemic models, J. R. Soc. Interface. 7 (2009), 873–885. https://doi.org/10.1098/rsif.2009.0386.

[30] P. van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci. 180 (2002), 29–48. https://doi.org/10.1016/s0025-5564(02)00108-6.

[31] M. Bani-Yaghoub, R. Gautam, Z. Shuai, et al. Reproduction numbers for infections with free-living pathogens growing in the environment, J. Biol. Dyn. 6 (2012), 923–940. https://doi.org/10.1080/17513758.2012.693206.

[32] P. A. Capó-Lugo, P. M. Bainum, Orbital mechanics and formation flying: A digital control perspective, Elsevier, Amsterdam, 2011.

[33] F. Chien, S. Shateyi, Volterra-Lyapunov stability analysis of the solutions of babesiosis disease model, Symmetry. 13 (2021), 1272. https://doi.org/10.3390/sym13071272.

[34] Z. Shuai, P. van den Driessche, Global stability of infectious disease models using Lyapunov functions, SIAM J. Appl. Math. 73 (2013), 1513–1532. https://doi.org/10.1137/120876642.

[35] M. Martcheva, An introduction to mathematical epidemiology, Vol. 61, Texts in Applied Mathematics, Springer, New York, 2015. https://doi.org/10.1007/978-1-4899-7612-3.

[36] A.M. Liapunov, Stability of motion, Vol. 30, Mathematics in Science and Engineering, Elsevier, Amsterdam, 2016.

[37] N. Krasovskii, Nekotorye zadachi teorii ustoichivosti dvizheniya (certain problems in the theory of stability of motion), Gosudarstv. Izdat. Fiz.-Mat. Lit. 1959.

[38] J. LaSalle, Some extensions of Liapunov's second method, IRE Trans. Circuit Theory. 7 (1960), 520–527. https://doi.org/10.1109/tct.1960.1086720.

[39] G.W. Cross, Three types of matrix stability, Linear Algebra Appl. 20 (1978), 253–263. https://doi.org/10.1016/0024-3795(78)90021-6.

[40] F. Mugabi, K.J. Duffy, J.Y.T. Mugisha, et al. Determining the effects of transplacental and direct transmission on the probability of persistence in a bluetongue virus model in temperate and tropical regions, Results Appl. Math. 7 (2020), 100120. https://doi.org/10.1016/j.rinam.2020.100120.

[41] J.C. Helton, Uncertainty and sensitivity analysis techniques for use in performance assessment for radioactive waste disposal, Reliab. Eng. Syst. Safe. 42 (1993), 327–367. https://doi.org/10.1016/0951-8320(93)90097-i.

[42] L. Simpson, A.B. Gumel, Mathematical assessment of the role of pre-exposure prophylaxis on HIV transmission dynamics, Appl. Math. Comput. 293 (2017), 168–193. https://doi.org/10.1016/j.amc.2016.07.043.

[43] B. Gomero, Latin hypercube sampling and partial rank correlation coefficient analysis applied to an optimal control problem, Master's Thesis, University of Tennessee, 2012.

[44] R. Taylor, Interpretation of the correlation coefficient: A basic review, J. Diagn. Med. Sonography. 6 (1990), 35–39. https://doi.org/10.1177/875647939000600106.