Transmission dynamics of Monkeypox virus: a mathematical modelling approach

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Received: 21 July 2021 / Accepted: 30 September 2021
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Abstract
Monkeypox (MPX), similar to both smallpox and cowpox, is caused by the monkeypox virus (MPXV). It occurs mostly in remote Central and West African communities, close to tropical rain forests. It is caused by the monkeypox virus in the Poxviridae family, which belongs to the genus Orthopoxvirus. We develop and analyze a deterministic mathematical model for the monkeypox virus. Both local and global asymptotic stability conditions for disease-free and endemic equilibria are determined. It is shown that the model undergo backward bifurcation, where the locally stable disease-free equilibrium co-exists with an endemic equilibrium. Furthermore, we determine conditions under which the disease-free equilibrium of the model is globally asymptotically stable. Finally, numerical simulations to demonstrate our findings and brief discussions are provided. The findings indicate that isolation of infected individuals in the human population helps to reduce disease transmission.

Keywords Monkeypox virus · Mathematical model · Stability · Backward bifurcation

Introduction

Monkeypox is a severe viral zoonotic disease (i.e., animal-to-human infection) that occurs sporadically, primarily in rural areas in Central and Western Africa, near tropical rain forests. This is caused by the monkeypox virus within the Poxviridae family that belongs to the genus Orthopoxvirus (Durski et al. 2018; Jezek et al. 1988). The genus Orthopoxvirus also comprises variola virus (the origin of smallpox), vaccinia virus (used for the eradication of smallpox in the vaccine), and cowpox virus (used in the earlier vaccine).

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Published online: 15 October 2021
monkeypox outbreaks in humans outside of Africa was a 2003 outbreak in the US. Monkeypox importation was later recognized in the United Kingdom and Israel. Mortality rate ranged from 1 percent to 10 percent in occurrences, with most deaths arising in younger populations (Ladnyj et al. 1972; CDC 2003). Monkeypox’s incubation period is typically about 6–16 days but can vary from 5 to 21 days. There are two facets of the contagious era, with an initial intrusive duration in the first 5 days, where the main signs are fever, lymphadenopathy (lymph node swelling), back pain, extreme headache, myalgia (muscle ache) and serious asthenia (energy shortage). A maculopapular rash (flat-based skin lesions) occurs 1–3 days after the onset of fever, and grows into small fluid-filled blisters (vesicles), which are pus-filled and then crust over in about ten days (Hutson et al. 2013).

Presently, there are no clear treatments available for monkeypox infection, though numerous novel antivirals, such as Brincindofovir, Tecovirimat and vaccinia immune globulin can be used to control the spread of the disease. There has been a significant increase in monkeypox in the last decade, associated with the decrease in herd immunity to smallpox. Vaccination against smallpox has been shown to be successful at 85 percent in the prevention of monkeypox but is no longer regularly available since global eradication of smallpox. The post-exposure vaccine can help prevent or decrease the severity of the disease (Rimoin et al. 2010; Meyer et al. 2020).

The disease has been given little attention in the past and this has contributed to insufficient knowledge on its mechanisms of transmission. Nevertheless, few studies have tried to research dynamics of monkeypox virus using a mathematical modelling technique. Study in Bhunu and Mushayabasa (2011) provides the basis for transmission analysis of pox-like dynamics of monkeypox virus as a case study. In Bhunu et al. (2009), the authors have shown that with the planned treatment intervention, the disease will be eradicated from both human and non-human primates in due time. The dynamics of monkeypox virus in human host and rodent with the stability analysis is studied in Usman and Adamu (2017). Other significant contributions can be found in TeWinkel (2019), Somma et al. (2019), Bankuru et al. (2020), Grant et al. (2020). Having gone through several works on the monkeypox virus and its mechanisms of transmission, we found that none considered the combination of isolated, exposed compartments in the human subpopulation and the effects of that contact rate with rodent population. Our aim is to investigate the various factors that could lead to reduction in the disease transmission and the effects of such factors on the basic reproduction number.

The rest of this paper is structured as follows: Method which includes model formulation and analysis are described in “Method” section. Next, “Backward bifurcation” section consists of the numerical simulations and results, discussion of results is given in “Results”, “Discussion” sections. Finally, in “Conclusion” section, we have provided conclusions of this article. Table 1 shows a detailed description of the parameters, while the model’s compartmental flow diagram is shown in Fig. 1.

**Method**

We propose a deterministic compartmental model on the transmission dynamics of monkeypox consisting of two populations that is, humans and rodents. The human population is further subdivided into five compartments, susceptible humans $S_h(t)$, exposed humans $E_h(t)$, infected humans $I_h(t)$, isolated humans $Q_h(t)$ and recovered humans $R_h(t)$. The rodent population is subdivided into three compartments, susceptible rodents $S_r(t)$, exposed rodents $E_r(t)$ and infected rodents $I_r(t)$. Recruitment into human population is at a rate $\theta_h$. $\beta_1$ is the effective contact rate with the probability of human been infected with the virus per contact with an infected rodent and $\beta_2$ is the product of effective contact rate and the probability of human been infected with monkeypox virus after getting in contact with infectious human. The proportion of exposed individuals moving to highly infected class is $\alpha_2$ while the proportion identified is $\alpha_1$. After medical diagnosis, some suspected cases are confirmed, where others were not detected and returned back to susceptible humans a rate $\varphi$. The suspected cases are treated and moved to recovered class at a rate $\tau$. The recovery rate for human is at a rate $\gamma$. Natural death occurs in the humans and rodents population at the rates $\mu_h$ and $\mu_r$ respectively. $\beta_3$ is the effective contact rate with the probability of rodent been infected per contact with infected rodent. The infected rodent population decreased by natural mortality rate $\mu_r$ or by disease induced death rate $\delta_r$. The transition among various compartments considered in the model is illustrated in Fig. 1, the model is governed by the following set of nonlinear differential equations below:
Table 1 Parameter values used for the simulations

| Parameter | Value, Year⁻¹ | Source | Description |
|-----------|---------------|--------|-------------|
| $\theta_h$ | 0.029          | Bhunu et al. (2009) | Recruitment rate for humans |
| $\theta_r$ | 0.2           | Bhunu et al. (2009) | Recruitment rate for rodents |
| $\beta_1$ | 0.00025        | Bhunu and Mushayabasa (2011) | Rodent contact rate to humans |
| $\beta_2$ | 0.00006        | Bhunu and Mushayabasa (2011) | Human to humans contact rate |
| $\beta_3$ | 0.027          | Bhunu and Mushayabasa (2011) | Rodent to rodent contact rate |
| $\alpha_1$ | 0.2           | Assumed | Proportion of exposed human to infected humans |
| $\alpha_2$ | 2.0           | Estimated | Proportion identified as suspected case |
| $\varphi$ | 2.0           | Estimated | Proportion not detected after diagnosis |
| $\tau$    | 0.52          | Assumed | Progression from isolated to recovered class |
| $\gamma$  | 0.83          | Bhunu et al. (2009) | Humans recovery rate |
| $\mu_h$   | 1.5           | Bhunu and Mushayabasa (2011) | Natural death rate of human |
| $\mu_r$   | 0.002         | Bhunu and Mushayabasa (2011) | Natural death rate of rodents |
| $\delta_r$ | 0.5           | Assumed | Disease induced death rate for rodents |
| $\delta_h$ | 0.2           | Odom et al. (2009) | Disease induced death rate for humans |
The model analysis

For the human population, \( N_h = S_h + E_h + I_h + Q_h + R_h \), the differential equation is given as:

\[
\frac{dN_h}{dt} = \theta_h - \delta_h I_h - \mu_h N_h
\]  

(2)

Also, for the rodent population

\( N_r = S_r + E_r + I_r \), and the corresponding differential equations is given as:

\[
\frac{dN_r}{dt} = \theta_r - (\mu_r + \delta_r)N_r
\]  

(3)

**Theorem 1** Let \((S_h, E_h, I_h, Q_h, R_h, S_r, E_r, I_r)\) be the solution of 1 with the initial conditions in a biologically feasible region \( \Gamma = \Gamma_h \times \Gamma_r \) with:

\[
\Gamma_h = S_h, E_h, I_h, Q_h, R_h \in R^{5}_+ : N_h \leq \frac{\theta_h}{\mu_h}
\]  

(4)

and

\[
\Gamma_r = S_r, E_r, R_r \in R^{3}_+ : N_r \leq \frac{\theta_r}{\mu_r}
\]  

(5)

Then \( \Gamma \) is non-negative invariant

Following the approach of Somma et al. (2019), we have that:

\[
0 \leq N_h(t) \leq N_h(0) e^{-\mu_h t} + \frac{\theta_h}{\mu_r} (1 - e^{-\mu_r t})
\]  

(6)

also

\[
N_r(t) \leq N_r(0) e^{-(\mu_r + \gamma) t} + \frac{\theta_r}{\mu_r} (1 - e^{-(\mu_r + \gamma) t})
\]  

(7)

Hence, the set \( \Gamma \) is positive invariant and for \( t \).

**Monkeypox-free equilibrium state**

This occurs in the absence of disease. Thus, in the absence of infection, we set \( E_h, I_h, Q_h, R_h, E_r, I_r \) to zero in 1 and the resulting solution gives the monkeypox-free equilibrium states given as:

\[
\Phi_{MFE} (S_h^*, E_h^*, I_h^*, Q_h^*, R_h^*, S_r^*, E_r^*, I_r^*)
\]  

(8)

**Endemic equilibrium**

This occurs when the infection persist in the population represented by \( \Phi_{MEE} (S^*_h, E^*_h, I^*_h, Q^*_h, R^*_h, S^*_r, E^*_r, I^*_r) \). Thus,

\[
S^*_h = \frac{k_1 k_3 \theta_h}{\mu_h k_1 k_3 - \alpha_2 \phi \phi_h + k_1 k_3 \phi_h}
\]

\[
E^*_h = \frac{k_3 \phi_h \theta_h}{\mu_h k_1 k_3 - \alpha_2 \phi \phi_h + k_1 k_3 \phi_h}
\]

\[
I^*_h = \frac{k_3 \alpha_1 \phi \phi_h}{k_2 (\mu_h k_1 k_3 - \alpha_2 \phi \phi_h + k_1 k_3 \phi_h)}
\]

\[
Q^*_h = \frac{\mu_h k_1 k_3 - \alpha_2 \phi \phi_h + k_1 k_3 \phi_h}{(\alpha_1 \gamma + \alpha_2 \kappa) \phi \phi_h \theta_h}
\]

\[
R^*_h = \frac{\mu_h k_1 k_3 - \alpha_2 \phi \phi_h + k_1 k_3 \phi_h}{(\alpha_1 \gamma + \alpha_2 \kappa) \phi \phi_h \theta_h}
\]

\[
S^*_r = \frac{\theta_r}{\mu_r + \phi_r}
\]

\[
E^*_r = \frac{\phi_r \alpha_3 \theta_r}{k_3 k_5 (\mu_r + \phi_r)}
\]

\[
I^*_r = \frac{\theta_r}{k_3 k_5 (\mu_r + \phi_r)}
\]

where \( k_1 = \alpha_1 + \alpha_2 + \mu_h \), \( k_2 = \mu_h + \delta_h + \gamma \), \( k_3 = \phi + \tau + \delta_r + \mu_r \), \( k_4 = \mu_r + \alpha_3 \), \( k_5 = \mu_r + \delta_r \), \( \phi_h = \frac{\beta_h}{k_3 k_5 \mu_r + \phi_r} \), \( \phi_r = \frac{\beta_r}{k_3 k_5 \mu_r + \phi_r} \)

**Basic reproduction number**

In our proposed model 1, compartments \( S_h, R_h \) and \( S_r \) are the disease free states whereas the compartments \( E_h, I_h, Q_h, E_r \) and \( I_r \) are the infection class.

Hence the monkeypox-free equilibrium state can be given as:

\[
\Phi_{MFE} = \left( \frac{\theta_h}{\mu_h}, 0, 0, 0, 0, \frac{\theta_r}{\mu_r}, 0, 0 \right)
\]  

(10)
The basic reproduction number is one of the critical parameters to examine the long-term behaviour of an epidemic. It can be defined as the number of secondary cases produced by a single infected individual in its entire life span as infectious agent. We have used next-generation matrix technique explained in Diekmann et al. (2010), Peter et al. (2020), to obtain the expression of reproduction number \( R_0 \). It was first introduced by Driessche and Watmough van den Driessche and Watmough (2008), where this technique is discussed in detail for the estimation of \( R_0 \). Also, there are various articles available in literature where the next-generation matrix technique has been used to estimate the expression for the basic reproduction number (Samui et al. 2020; Kumar et al. 2021).

The model system 1 can be written as:

\[
\frac{dx}{dt} = F(x) - V(x)
\]

\[
F = \begin{pmatrix}
0 & \beta_2 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
\end{pmatrix}
\]

\[
V = \begin{pmatrix}
-\theta_h + \frac{(\beta_1 + \beta_h)S_h}{N_h} + \mu_hS_h - \phi Q_h \\
(\alpha_1 + \alpha_2 + \mu_h)E_h \\
-\alpha_1E_h + (\mu_h + \delta_h + \gamma)I_h \\
-\alpha_2E_h + (\phi + \tau + \delta_h + \mu_h)Q_h \\
-\gamma I_h - \tau Q_h + \mu_hR_h \\
-\theta_e + \frac{\beta_2S_h}{N_e} + \mu_iS_t \\
-\frac{\beta_2S_t}{N_t} + (\mu_e + \alpha_3)E_t \\
-\alpha_3E_t + (\mu_e + \delta_e)I_t \\
\end{pmatrix}
\]

Progression from \( E_h \) to \( I_h \) or \( Q_h \) are not considered to be new infections, but rather the progression of infected individuals through various compartments. Hence, the transmission matrix \( F \) and transitions matrix \( V \) can be given as:

\[
F = \begin{pmatrix}
0 & \beta_2 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
\end{pmatrix}
\]

\[
V = \begin{pmatrix}
\alpha_1 + \alpha_2 + \mu_h & 0 & 0 & 0 \\
-\alpha_1 & \mu_h + \delta_h + \gamma & 0 & 0 \\
-\alpha_2 & 0 & \phi \tau + \delta_h + \mu_h & 0 \\
0 & 0 & 0 & \mu_e + \delta_e \\
\end{pmatrix}
\]

For simplicity, let \( Y_1 = \alpha_1 + \alpha_2 + \mu_h, Y_2 = \mu_h + \delta_h + \gamma, Y_3 = \phi \tau + \delta_h + \mu_h \) and \( Y_4 = \mu_e + \delta_e \)

Now:

\[
V^{-1} = \begin{pmatrix}
Y_2 Y_3 Y_4 & 0 & 0 & 0 \\
\alpha_1 Y_3 Y_4 & Y_1 Y_3 Y_4 & 0 & 0 \\
\alpha_2 Y_2 Y_4 & 0 & Y_1 Y_2 Y_4 & 0 \\
0 & 0 & 0 & Y_1 Y_2 Y_3 \\
\end{pmatrix}
\]

(12)

Now, after much simplification we obtain:

\[
FV^{-1} = \begin{pmatrix}
\beta_2 \alpha_1 Y_3 Y_4 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
\end{pmatrix}
\]

(13)

Now, the basic reproduction number is defined as the largest eigenvalue (spectral radius) of the next generation matrix \( FV^{-1} \) and can be obtained as:

\[
R_0 = \rho(FV^{-1}) = \frac{\beta_2 \alpha_1 Y_3 Y_4}{Y_1 Y_2 Y_3 Y_4} = \frac{\beta_2 \alpha_1 Y_3 Y_4}{Y_1 Y_2 Y_3 Y_4}
\]

(14)

Hence,

\[
R_0 = \frac{\alpha_1 \beta_2}{(\alpha_1 + \alpha_2 + \mu_h)(\mu_h + \delta_h + \gamma)}
\]

(15)

**Stability of disease-free equilibrium**

To obtain the conditions for the global stability for \( E_0 \), we have used the approach set out in Castillo-Chavez and Song (2004), which states that if the model system can be written in the following form:

\[
\frac{dX}{dt} = F(X, Z)
\]

\[
\frac{dZ}{dt} = G(X, Z), G(X, 0) = 0
\]

here \( X \in \mathbb{R}^n \) are the uninfected individuals and \( Z \in \mathbb{R}^n \) describes the infected individuals. According to this notation, the disease-free equilibrium is given by \( Q_0 = (X_0, 0) \)

Now, the following two conditions guarantees the global stability of the disease free equilibrium.

**K1**: For \( \frac{dX}{dt} = F(X, 0) \), \( X_0 \) is globally asymptotically stable.

**K2**: \( G(X, Z) = BZ - \tilde{G}(X, Z) \) where \( \tilde{G}(X, Z) \geq 0 \) for \( X, Z \in \Omega \).

here \( B = D \tilde{G}(X_0, 0) \) is a \( M \)-matrix and \( \Omega \) is the feasible of the model. The following theorem then defines the global stability of \( E_0 \).

**Lemma 1** The equilibrium point \( Q_0 = (X_0, 0) \) is a globally asymptotically stable when \( R_0 \leq 1 \) and assumptions \( K_1 \) and \( K_2 \) are satisfied.
Now, the following theorem establishes the global stability of the disease free equilibrium \( E_0 \) for our proposed model system.

**Theorem 2** The DFE point \( E_0 \) is globally asymptotically stable provided \( R_0 \leq 1 \).

**Proof** First, we will prove \( \mathcal{K}_1 \) as:

\[
F(X,0) = \begin{bmatrix}
\theta_h - \mu_h S_h \\
-\mu_h R_h \\
-(\mu_t + \alpha_3) E_t 
\end{bmatrix}
\]

The characteristic polynomial of \( F(X,0) \) is:

\[
(\lambda + \mu_h)^2(\lambda + \mu_t + \alpha_3)
\]

\Rightarrow \lambda_1 = \lambda_2 = -\mu_h, \lambda_3 = -\mu_t, \text{ and } \lambda_4 = -\mu_t - \alpha_3.

Hence, \( X = X_0 \) is globally asymptotically stable.

Now, we have:

\[
G(X,Z) = BZ - \hat{G}(X,Z)
\]

\[
= \begin{bmatrix}
-(a_1 + a_2 + \mu_h) \\
\frac{\beta_3}{N_h} \\
a_1 \\
-\mu_t - \alpha_3 \\
0 \\
\end{bmatrix}
\]

\[
\times \begin{bmatrix}
E_h \\
I_h \\
Q_h \\
I_t \\
\end{bmatrix}
\]

\[
= \begin{bmatrix}
\frac{(\beta_3 S_h + \beta_4 I_h)}{N_h} \\
\frac{S_h}{N_h} \\
0 \\
\frac{(\mu_t + \alpha_3) E_t}{N_t} \\
\end{bmatrix}
\]

Here, one can easily observe that \( B \) satisfies all conditions explained in K2.

**Stability of endemic equilibrium**

We will use the Routh–Hurwitz criterion to prove the local stability of the endemic equilibria. Here, we will derive the conditions under which the endemic equilibria is locally asymptotically stable.

The Jacobian matrix about the endemic equilibria \( \phi_{\text{MEE}} \) is given as:

\[
J = \begin{bmatrix}
a_{11} & a_{12} & a_{13} & 0 & 0 & a_{18} \\
a_{21} & a_{22} & a_{23} & 0 & 0 & 0 & a_{28} \\
0 & a_{32} & a_{33} & 0 & 0 & 0 & 0 \\
0 & a_{42} & 0 & a_{44} & 0 & 0 & 0 \\
0 & 0 & a_{53} & a_{54} & a_{55} & 0 & 0 \\
0 & 0 & 0 & 0 & a_{66} & a_{68} & 0 \\
0 & 0 & 0 & 0 & a_{76} & a_{77} & a_{78} \\
0 & 0 & 0 & 0 & 0 & a_{87} & a_{88} \\
\end{bmatrix}
\]

Here,

\[
a_{11} = -\left(\frac{\beta_1 I_t + \beta_2 I_h}{N_h}\right) - \mu_h, \quad a_{13} = -\frac{\beta_2 S_h}{N_h}
\]

\[
a_{21} = \frac{\beta_1 I_t + \beta_2 I_h}{N_h}, \quad a_{22} = -(a_1 + a_2 + \mu_h)
\]

\[
a_{23} = \frac{\beta_2 S_h}{N_h}, \quad a_{28} = \frac{\beta_2 S_h}{N_h}
\]

\[
a_{32} = a_1, \quad a_{33} = -(\mu_h + \delta_h + \gamma)
\]

\[
a_{42} = a_2, \quad a_{44} = -(\varphi + \tau + \delta_h + \mu_h)
\]

\[
a_{53} = \gamma, \quad a_{54} = \tau, \quad a_{55} = -\mu_h
\]

\[
a_{66} = -(\mu_t + \delta_t), \quad a_{68} = -\frac{\beta_1 S_t}{N_t}
\]

\[
a_{76} = \frac{\beta_3 I_t}{N_t}, \quad a_{77} = -(\mu_t + \alpha_3)
\]

\[
a_{78} = \frac{\beta_3 S_t}{N_t}, \quad a_{87} = \alpha_3, \quad a_{88} = -(\mu_t + \delta_t)
\]

The characteristic equation of \( J \) is given as:

\[
\frac{1}{N_h N_t} \left[ (-x - \mu_h)(-\phi_2 (I_t \beta_1 + I_h \beta_2) \\
(x + \gamma + \delta_h + \mu_h) + (-x - \tau - \varphi - \delta_h - \mu_h) \\
(S_h \alpha_1 \beta_2 (x + \mu_h) - (x + \alpha_1 + \alpha_2 + \mu_h) \\
(x + \gamma + \delta_h + \mu_h) (I_t \beta_1 + I_h \beta_2 + N_h (x + \mu_h))) \\
(S_h \alpha_1 \beta_2 (x + \mu_t) - (x + \alpha_3 + \mu_t) \\
(I_t \beta_1 + N_t (x + \mu_t)) (x + (\mu_t + \delta_t)) \right] = 0
\]

which can be further written as:

\[
x^8 + A_1 x^7 + A_2 x^6 + A_3 x^5 + A_4 x^4 \\
+ A_5 x^3 + A_6 x^2 + A_7 x + A_8 = 0
\]

where \( A_i \)’s are the coefficients of \( x^{8-i}; i = 1, 2, \ldots 8 \) after converting the polynomial in standard form.

Note: To obtain the condition for the stability of \( \phi_{\text{MEE}} \) we will made the following substitution:
The analysis conducted in the previous section on the occurrence of endemic equilibrium \( E^* \) suggests the probability of backward bifurcation. It can be defined as the state when a stable endemic equilibrium coexist with a stable disease-free equilibrium when the associated reproduction number is less than unity. We use the center manifold based result (theorem 4.1) given in Castillo-Chavez and Song (2004), to check the occurrence of backward bifurcation.

Let:

\[
\begin{align*}
S_h &= y_1, & E_h &= y_2, & I_h &= y_3, & Q_h &= y_4, \\
R_h &= y_5, & S_e &= y_6, & E_e &= y_7, & I_e &= y_8.
\end{align*}
\]

Consider, \( U = (y_1, y_2, y_3, y_4, y_5, y_6, y_7, y_8)^T \), then the given system (1) can be written as:

\[
\frac{dU}{dt} = \begin{pmatrix} f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8 \end{pmatrix}^T
\]

where,

\[
\begin{align*}
f_1 &= \theta_h - \frac{(\beta_1 y_8 + \beta_2 y_3)S_h}{N_h} - \mu_h y_1 + \phi y_4 \\
f_2 &= \frac{(\beta_1 y_8 + \beta_2 y_3)S_h}{N_h} - (\alpha_1 + \alpha_2 + \mu_h) y_2 \\
f_3 &= \alpha_1 y_2 - (\mu_h + \delta_h + \gamma) y_3 \\
f_4 &= \alpha_2 y_2 - (\nu + \gamma + \delta_h + \mu_h) y_4 \\
f_5 &= \gamma y_3 + \nu y_4 - \mu_h y_5 \\
f_6 &= \theta_i - \frac{\beta_3 y_6 y_8}{N_i} - \mu_i y_6 \\
f_7 &= \frac{\beta_3 y_6 y_8}{N_i} - (\mu_i + \alpha_3) y_7 \\
f_8 &= \alpha_3 y_7 - (\mu_i + \delta_i) y_8
\end{align*}
\]

From the expression of \( R_0 \), we can observe that \( R_0 \) is highly influenced by \( \beta_2 \), the product of effective contact rate and the probability of human been infected with monkey pox virus after getting in contact with infectious human. Therefore, we will consider \( \beta_2 \) as our bifurcation parameter.

Hence, when \( R_0 = 1 \), we have:

\[
\beta_2^* = \frac{(\alpha_1 + \alpha_2 + \mu_h)(\mu_h + \delta_h + \gamma)}{\alpha_1}
\]  

(25)

Now, the above system at monkeypox-free equilibrium state \( \phi_{MFE} \) is given by:

\[
J_0(\phi_{MFE}, \beta_2^*) = \begin{bmatrix}
-\mu_h & 0 & -\beta_2 & 0 & 0 & 0 & 0 & -\beta_1 \\
0 & -\alpha_1 & -\beta_2 & 0 & 0 & 0 & 0 & 0 \\
0 & \alpha_1 & -\alpha_2 & 0 & 0 & 0 & 0 & 0 \\
0 & \sigma_2 & 0 & -A_3 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & -\gamma & -\tau & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & -\mu_i & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & -A_4 & \beta_3 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & -\alpha_i & -A_3
\end{bmatrix}
\]

Clearly, ‘0’ is an eigenvalue of \( J_0(\phi_{MFE}, \beta_2^*) \). Let \( W = (w_1, w_2, w_3, w_4, w_5, w_6, w_7, w_8) \) be the associated right eigenvector corresponding to zero eigenvalue, and can be attained by simplifying:

\[
\begin{align*}
-\mu_h w_1 - \beta_2 w_3 - \beta_1 w_8 &= 0 \\
-A_1 w_2 + \beta_2 w_3 + \beta_1 w_8 &= 0 \\
\alpha_1 w_2 - A_2 w_3 &= 0 \\
\alpha_2 w_2 - A_3 w_4 &= 0 \\
\gamma w_5 + \nu w_4 - \mu_h w_5 &= 0 \\
-\mu_i w_6 - \beta_3 w_8 &= 0 \\
-A_4 w_7 + \beta_3 w_8 &= 0 \\
\alpha_3 w_7 - A_3 w_8 &= 0
\end{align*}
\]

(26)

On evaluation, \( W \) can be given as:
\[ w_1 = \frac{A_1 A_3}{a_1 \mu_h} \quad w_2 = \frac{A_2}{a_1} \quad w_3 = 1 \]

\[ w_4 = \frac{\alpha_2 A_2}{\alpha_1 A_3} \quad w_5 = \frac{1}{\mu_h} \left( \gamma + \frac{\tau \alpha_2 A_2}{\alpha_1 A_3} \right) \]

\[ w_6 = \frac{\beta_3}{\beta_1 \mu_1} \left( \frac{A_1 A_2}{\alpha_1} + \beta_2 \right) \]

\[ w_7 = -\frac{A_5}{\alpha_5 \beta_1} \left( \frac{A_1 A_2}{\alpha_1} + \beta_2 \right) \]

\[ w_8 = -\frac{1}{\beta_1} \left( \frac{A_1 A_2}{\alpha_1} + \beta_2 \right) \]

Now, let \( V = (v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8) \) be the associated left eigenvector of \( J_0 \) corresponding to zero eigenvalue and satisfying \( V \cdot W = 0 \). Then \( V \) can be given as:

\[ v_1 = 0, \]

\[ v_2 = \left( \frac{A_2}{a_1} + \frac{\beta_2}{A_2} - \left( \frac{A_1 A_3}{\alpha_1} + \beta_2 \right) \right)^{-1} \times \left( \frac{A_5}{\alpha_5} + \frac{\beta_2}{A_2} \right), \]

\[ v_3 = \frac{\beta_1}{A_2} v_2, \quad v_4 = v_5 = v_6 = 0, \]

\[ v_7 = \frac{\beta_2}{A_2} v_2, \quad v_8 = \frac{\beta_2}{A_2} v_7 \]

As discussed in theorem 4.1 (Castillo-Chavez and Song 2004), we have:

\[ a = \sum_{k,j=1}^{8} v_k w_i \frac{\partial^2 f_k}{\partial y_i \partial y_j} (\phi_{MFE}, \beta_2^2) \]  \hspace{1cm} (27)

\[ b = \sum_{k,j=1}^{8} v_k w_i \frac{\partial^2 f_k}{\partial y_i \partial \beta_2} (\phi_{MFE}, \beta_2^2) \]  \hspace{1cm} (28)

Algebraic calculations show that:

\[ \frac{\partial^2 f_2}{\partial x_1 x_3} = N_h \frac{\partial^2 f_2}{\partial x_1 x_1} = N_h \frac{\partial^2 f_1}{\partial x_1 x_8} = N_h \frac{\partial^2 f_2}{\partial x_8 x_1} \]

\[ \frac{\partial^2 f_7}{\partial x_8 x_6} = N_r \frac{\partial^2 f_7}{\partial x_8 x_8} \]

Now, substituting all the above values in the expressions for ‘a’ and ‘b’, we obtain:

\[ a = 2v_2 w_i (w_3 \beta_2 + w_8 \beta_1) + 2v_4 w_6 w_8 \]  \hspace{1cm} (29)

\[ b = v_2 w_2 \frac{\theta}{\mu_h N_h} \]  \hspace{1cm} (30)

Now, to persist backward bifurcation in the proposed model, both the values of ‘α’ and ‘β’ has to be simultaneously positive.

### Results

A sensitivity analysis determines how different values of an independent variable affect a particular dependent variable under a given set of assumptions (Kalyan et al. 2021; Victor et al. 2020). The normalized forward sensitivity index of a variable to a parameter is the ratio of the relative change in the variable to the relative change in the parameter. When variable is a differentiable function of the parameter, the sensitivity index may be alternatively defined using partial derivatives. The parameter values have been taken from literature as given in Table 1.

Since the basic reproduction number \( R_0 \) helps us to predict the future course of the disease, the sensitivity analysis is performed to understand which parameters involved in the model effect the value of \( R_0 \) relatively more. We have used the following expression of the sensitivity for \( R_0 \) which depends upon parameter \( v \):

\[ \psi_{R_0} = \frac{v}{R_0} \times \frac{\partial R_0}{\partial v} \]  \hspace{1cm} (31)

A negative index of sensitivity shows that the parameter and \( R_0 \) are inversely proportional. A positive sensitivity index, however, denotes that the value of \( R_0 \) increases with an increase in the value of the parameter concerned.

The estimated sensitivity indices for \( R_0 \) are presented in Table 2. From Table 2, we can see that an increase in the values of \( a_2, \mu_h, \delta_h \) and \( \gamma \) will result in a decrease in the value of \( R_0 \). On the other hand, an increase in the value of \( a_1 \) and \( \beta_2 \) will increase the monkey-pox cases.

### Table 2: Sensitivity index of parameters

| Parameter     | Expression of the sensitivity index | Value       |
|---------------|-------------------------------------|-------------|
| \( a_1 \)     | \( \frac{a_1 + \mu_h}{a_1 + a_2 + \mu_h} \) | 0.945946   |
| \( a_2 \)     | \( \frac{\mu_h}{a_1 + a_2 + \mu_h} \) | -0.540541  |
| \( \beta_2 \) | \( 1 \)                              | 1           |
| \( \mu_h \)   | \( \frac{\mu_h (\gamma + a_1 + \delta_h + \gamma_0)}{(a_1 + a_2 + \mu_h)(\gamma + a_1 + \gamma_0)} \) | -0.998291  |
| \( \delta_h \)| \( \frac{\delta}{\gamma + a_1 + \gamma_0} \) | -0.0790514 |
| \( \gamma \)  | \( \frac{\gamma}{\gamma + a_1 + \gamma_0} \) | -0.328063  |
Discussion

The basic reproduction number is a crucial parameter in disease dynamics which gives us major information about the disease. To understand the effect of various disease transmission parameters on the basic reproduction number, we have obtained the surface plots showing variation of $R_0$ with sensitive parameters. From Fig. 2, it can be observed that as the value of $\alpha_2$ increases, it leads to reduced disease transmission. Similarly, it can be easily seen from Fig. 3 that contact rate with rodent population directly affects the transmission of monkey-pox. Similarly, the simultaneous effect of $\beta_2, \alpha_2, \mu_h$ and $\gamma$ on the basic reproduction number has been shown in Figs. 4 and 5.

Further, we have performed numerical experiments to detect effect of change in sensitive parameters on the number of infected individuals. This has been investigated in Figs. 6, 7 and 8. Now we have incorporated a compartment $Q_h$ in the model, which consists of the isolated proportion of the infected humans. Through numerical simulations, we have shown how the infected population would behave in the absence of isolated interventions. In Fig. 9, we show that the isolation of infected individuals helps to reduce disease transmission.

Conclusion

A non-linear compartmental model has been proposed to understand the transmission of Monkey pox disease. The proposed model consist of eight mutually exclusive compartments. The human population has been divided into five compartments, where we has introduced the exposed ($E_h$) and isolated human ($Q_h$) compartments along with standard compartments of exposed population ($E_h$), infected humans ($I_h$) and recovered humans ($R_h$). Similarly, the rodent population is also divided into three compartments; exposed...
Further, we have established the fundamental properties of the proposed model. Basic reproduction number has been estimated using next-generation matrix technique. The proposed model exhibit two equilibrium points; disease free equilibrium ($E_0$), susceptible ($S_t$) and infected rodents ($I_t$). Further, we have established the fundamental properties of the proposed model.
point and endemic equilibrium point. We have obtained the stability conditions for both of the equilibrium points. Further, the existence of the endemic equilibrium implies the possibility of the backward bifurcation. We have also derived the condition for the existence of the backward bifurcation. Further we have shown the sensitivity of various parameters involved in the model. The sensitivity index has been provided in Table 2. We found that $\alpha_2$, which is human to human contact rate is the most sensitive parameter in the transmission of the disease. Also, with the help of numerical
simulations, we have shown the simultaneous effect of various parameters on the basic reproduction number $R_0$. Our analysis suggests that isolation of infected humans helps to reduce disease transmission. It is, therefore, realised from the simulation that isolation of the infected humans, is playing significant roles in the management and control of monkeypox virus.

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