Transmission dynamic and backward bifurcation of Middle Eastern respiratory syndrome coronavirus

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Abstract. Middle East respiratory syndrome coronavirus (MERS-CoV) remains an emerging disease threat with regular human cases on the Arabian Peninsula driven by recurring camels to human transmission events. In this paper, we present a new deterministic model for the transmission dynamics of (MERS-CoV). In order to do this, we develop a model formulation and analyze the stability of the proposed model. The stability conditions are obtained in term of $R_0$, we find those conditions for which the model become stable. We discuss basic reproductive number $R_0$ along with sensitivity analysis to show the impact of every epidemic parameter. We show that the proposed model exhibits the phenomena of backward bifurcation. Finally, we show the numerical simulation of our proposed model for supporting our analytical work. The aim of this work is to show via mathematical model the transmission of MERS-CoV between humans and camels, which are suspected to be the primary source of infection.

Keywords: epidemic model, reproductive number, stability analysis, backward bifurcation, numerical simulation.

1 Introduction

A new coronavirus was identified in Saudi Arabia in September 2012 known as Middle Eastern respiratory syndrome coronavirus (MERS-CoV) \cite{5,11}. MERS-CoV is associated with an animal source in the Middle East. Besides human, MERS-CoV has been found in camel in several countries \cite{1}. Since its emergence in 2012, the Middle East
respiratory coronavirus (MERS-CoV) has caused spill over from the dromedary camel population into the human population. This virus also spread from an infected person’s respiratory secretion such as through coughing. MERS-CoV has spread from ill people to others through closed contacts such as caring for or living with an infected person [3]. Since April 2012 till date, there have been a total of 536 cases with 145 deaths, a case fatality rate of 27 percent with the majority being reported in the Middle East (Saudi Arabia, Jordan, and Qatar) [2]. For the forecast of dynamics of infectious diseases, see [8,10,18].

One of the largest outbreaks of MERS-CoV has been described by Assire et al. [4] with the description that the virus is transmissible from human to human. Zumla et al. [19] pointed out in a review article that the reason for the camel to human transmission could be the indirect exposure, e.g., it was possible that the patient’s exposure to MERS-CoV was consumption of unpasteurized camel milk, which is very common practice in Saudi Arabia.

Poletto et al. [15] believed that peoples movement and maxing during Hajj and Umrah were mainly responsible for MERS-CoV transmission. Besides, camel racing, closing and the opening again of camel market along with climatic factors could have an impact on the transmission of MERS-CoV from camels to humans and then among humans.

In this paper, we take the human and camel population. We construct a compartmental model for the transmission dynamics of MERS-CoV. The model is consisting of human population, that is: susceptible human $S_h$, exposed or latent human $E_h$, symptomatic and infectious human $I_h$, infectious but asymptomatic class human $A_h$, hospitalized class $H_h$, and recovery class human $R_h$. Camel population, which consists of susceptible camel $S_c$, asymptomatic infected camel $X_c$, and symptomatic infected camel $Y_c$. We analyze the stability of the proposed model. The stability conditions are obtained in terms of basic reproductive number. To find the transmission potential of diseases, we investigate a formula for the basic reproduction number of camel to human population and from human to human population by using next-generation matrix method. For local stability of the proposed model (1), we use Routh–Hurwitz criteria. When the basic reproductive number is less than one, the disease-free equilibrium of the model is locally asymptotically stable, therefore, the disease dies out after some period of time. While when the basic reproduction number is greater than one, the disease will prevail and persist in the population. We also investigate the model for global stability by using Lyapunov function theory. Sensitivity analysis was carried out on the model parameters to analyze their impact on disease transmission. The backward bifurcation in a disease model has an important qualitative implications. We find backward bifurcation and endemic equilibria. Numerical simulation of the proposed model (1) was carried out, and the results are displayed.

This article is arranged as follows. Section 2 represents the mathematical construction of epidemic model. In Section 3, we show the positivity and boundedness of the proposed model. In Section 4, we analyzed the stability of the proposed model. Equilibria and basic reproductive number of model (1) are presented in Sections of 4.1 and 4.2. Section 5 deal with backward bifurcation and endemic equilibria. In Section 6, we present the global asymptotic stability of endemic equilibrium by using Lyapunov function theory. Numerical simulation results of the proposed model are presented in Section 7.
2 Model formulation

In this section, we develop a compartmental epidemic model of Middle Eastern respiratory syndrome coronavirus (MERS-CoV). According to biological characteristics of the MERS-CoV, we divide the total population into human and camel populations. $S_h(t)$ is susceptible human, $E_h(t)$ is the exposed human, $I_h(t)$ is symptomatic and infectious human, infectious but asymptotic class human $A_h(t)$, hospitalized human $H_h(t)$, recovery class $R_h(t)$, $S_c(t)$ is susceptible camel, $X_c(t)$ is asymptomatic infected camel, and $Y_c(t)$ is symptomatic infected camel. Keeping the characteristic of Middle Eastern respiratory syndrome coronavirus (MERS-CoV) along with the above characterization leads to the following system of ordinary differential equations:

\[
\begin{align*}
\frac{dS_h}{dt} &= b_h - \frac{\beta_1 X_c + \beta_2 Y_c + \beta_3 I_h + \beta_4 q H_h}{N_h} S_h - \mu_0 S_h, \\
\frac{dE_h}{dt} &= \frac{\beta_1 X_c + \beta_2 Y_c + \beta_3 I_h + \beta_4 q H_h}{N_h} S_h - (\gamma + \mu_0) E_h, \\
\frac{dI_h}{dt} &= \rho_\gamma E_h - (\phi_a + \phi_1) I_h - (\mu_0 + \mu_1) I_h, \\
\frac{dA_h}{dt} &= \gamma (1 - \rho) E_h - (\mu_0 + \mu_2) A_h, \\
\frac{dH_h}{dt} &= \phi_a I_h - \phi_\phi H_h - \mu_0 H_h, \\
\frac{dR_h}{dt} &= \phi_1 I_h + \phi_\phi H_h - \mu_0 R_h, \\
\frac{dS_c}{dt} &= b_c - \frac{\beta_5 X_c + \beta_6 Y_c}{N_c} S_c - k_1 S_c, \\
\frac{dX_c}{dt} &= \frac{\beta_5 X_c + \beta_6 Y_c}{N_c} S_c - (k_2 + \gamma_c) X_c, \\
\frac{dY_c}{dt} &= \gamma_c X_c - (k_3 + \alpha_c) Y_c
\end{align*}
\]  

with initial size of population

\[
S_h(0) > 0, \quad E_h(0) \geq 0, \quad I_h(0) \geq 0, \quad A_h(0) \geq 0, \quad H_h(0) \geq 0, \\
R_h(0) \geq 0, \quad S_c(0) \geq 0, \quad X_c(0) \geq 0, \quad Y_c(0) \geq 0.
\]

Here $b_h$ is the birth rate of human population, $\beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \beta_6$ show the transmission rate per unit time, $q$ show the approximate transmission rate of hospitalized patient. The rate at which individuals leave the exposed class by becoming infectious is $\gamma$. $\rho$ is the proportion of progression from exposed class $E_h(t)$ to symptomatic infectious class $I_h(t)$, $1 - \rho$ is that of progression to asymptotic class $A_h(t)$, $\phi_a$ is the average rate at which symptomatic individuals hospitalize, and $\phi_1$ is the recovery rate without being hospitalized. $\phi_\phi$ is the recovery rate of the hospitalized patient. $\mu_0$ is the natural death rate, $\mu_1, \mu_2$ are death rate due to MERS-CoV.
The camel population is represented as \( SI \) model, where \( b_c \) is the birth rate of camel population, \( S_c \) represents susceptible camels, \( X_c \) represents asymptomatic infected camels, and \( Y_c \) represents symptomatic camels. \( \gamma_c \) is the moving rate from asymptomatic camel to symptomatic camel population. \( k_1, k_2, k_3 \) are the natural death rate of susceptible, asymptomatic camel, and symptomatic infected camels. \( \alpha_c \) is the death rate due to MERS-CoV. \( N_h \) and \( N_c \) are human and camel populations, respectively.

### 3 Positivity and boundedness

**Lemma 1.** All the variables given in model (1) are positive and bounded.

**Proof.** The positivity follow from the standard argument [16] with which we can show that if \( R_{10}^n = (s_1, s_2, \ldots, s_n) \in R_{+}^n, s_i \geq 0, \) for all \( i \in 1, \ldots, n \), then \( R_{10}^n \) is positively invariant under the flow induced by model (1).

For boundedness, we call total human population in model (1) by \( N_h(t) \) and camel population by \( N_c(t) \). Let \( N_h(t) \) represents the total human population at time \( t \), i.e.,

\[
N_h(t) = S_h(t) + E_h(t) + I_h(t) + A_h(t) + H_h(t) + R_h(t).
\]

The time differentiation of \( N_h(t) \) and the use of equations in model (1) give

\[
\frac{dN_h}{dt} = b_h - \mu_0 S_h - \mu_0 E_h - (\mu_0 + \mu_1) I_h - (\mu_0 + \mu_2) A_h - \mu_0 H_h - \mu_0 R_h \\
\leq b_h - \mu_0 N_h.
\]

This means that there exists \( \limsup_{t \to \infty} b_h/\mu_0 \).

Let \( N_c(t) \) represents the total camels population at time \( t \),

\[
N_c(t) = S_c(t) + X_c(t) + Y_c(t),
\]

\[
\frac{dN_c}{dt} = b_c - k_1 S_c - k_2 X_c - k_3 Y_c - \alpha_c Y_c \leq b_c - k_1 N_c.
\]

This means that there exists \( \limsup_{t \to \infty} b_c/k_1 \).
From the above results it follows that \( S_h(t), E_h(t), I_h(t), A_h(t), H_h(t), R_h(t), S_c(t), X_c(t), Y_c(t) \) are bounded on their maximal domain. Therefore, for biological feasibility, we study (1) in the closed set

\[
\Omega = \left\{ (S_h, E_h, I_h, A_h, H_h, R_h, S_c, X_c, Y_c) \in R_+^9: \right. \\
0 < S_h + E_h + I_h + A_h + H_h + R_h + S_c + X_c + Y_c \leq \frac{b_h}{\mu_0} + \frac{b_c}{k_1} \left. \right\}.
\]

The Jacobian of model (1) is given by

\[
J_0 = \begin{pmatrix}
-A_2 & 0 & -A_3 & 0 & -A_4 & 0 & 0 & -A_5 & -A_6 \\
A_1 & -A_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & C_1 & -C_2 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & C_3 & 0 & -C_4 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \phi_a & 0 & -D_1 & 0 & 0 & 0 & 0 \\
0 & 0 & \phi_1 & 0 & \phi & -\mu_0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & D_5 & E_2 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_c & -E_3 \\
\end{pmatrix}.
\]

Here

\[
A_2 = -\frac{b_1 X_c + b_2 Y_c + b_3 I_h + b_4 q H_h}{N_h} - \mu_0, \quad A_3 = \frac{b_3 S_h}{N_h}, \quad A_4 = -\frac{b_4 q S_h}{N_h}, \]

\[
A_5 = \frac{b_2 S_h}{N_h}, \quad A_6 = \frac{\beta_2 S_h}{N_h}, \quad B_2 = \frac{\beta_1 X_c + \beta_2 Y_c + \beta_3 I_h + \beta_4 q H_h}{N_h},
\]

\[
B_3 = \frac{\beta_1 X_c + \beta_2 Y_c + \beta_3 I_h + \beta_4 q H_h}{N_h}, \quad B_5 = \frac{\beta_4 q S_h}{N_h}, \quad B_6 = \frac{\beta_2 S_h}{N_h},
\]

\[
B_7 = \frac{\beta_2 S_h}{N_h}, \quad C_1 = \rho \gamma, \quad C_2 = -(\phi_a + \phi_1 + \mu_0 + \mu_1), \quad C_3 = \gamma (1 - \rho),
\]

\[
C_4 = \mu_0 + \mu_2, \quad D_1 = \phi_\phi + \mu_0, \quad D_2 = -\frac{\beta_5 X_c + \beta_6 Y_c + \beta_7 I_h - k_3}{N_c},
\]

\[
D_3 = -\frac{\beta_5 S_c}{N_c}, \quad D_4 = \frac{\beta_6 S_c}{N_c}, \quad D_5 = \frac{\beta_5 X_c + \beta_6 Y_c + \beta_7 I_h - k_3}{N_c},
\]

\[
E_2 = \frac{\beta_5 S_c}{N_c} - (k_3 + \alpha_c) - \frac{\beta_6 S_c}{N_c}, \quad E_3 = k_3 + \alpha_c.
\]

\[
4 \quad \text{Stability analysis}
\]

We investigate the positivity and boundedness of the proposed model. We then study the qualitative behaviour of the proposed model (1). For this, first, we find equilibria and the threshold quantity \( R_0 \).
4.1 Equilibrium analysis and threshold quantity

For disease-free equilibria, we set all the variables and rate of change equal to zero except \( S_h = S_{h0}, S_c = S_{c0} \), the disease-free equilibrium of the proposed model (1) become

\( d_0 = (b_h/\mu_0, 0, 0, 0, 0, b_c/k_1, 0, 0) \).

The dynamic of this equilibrium will be discuss with the help of linear stability analysis theory. On the basis of stability theory, we find those condition for which the model become stable and disease spreading will be under control. We state the dynamic of the proposed model around disease-free equilibrium with the help of the following result.

**Theorem 1.** The disease-free equilibrium point \((b_h/\mu_0, 0, 0, 0, 0, b_c/k_1, 0, 0)\), is locally stable if \( R_0 < 1 \), otherwise, the disease-free equilibrium is unstable when \( R_0 > 1 \).

In epidemiology the basic reproduction ratio of an infection can be thought of as the expected number of cases directly generated by one case in a population when all the population are susceptible to infection. We use next-generation matrix method to find the basic reproductive number [6]. In Eq. (3) the matrices \( \bar{F} \) and \( \bar{V} \) contain the nonlinear and linear terms, respectively, that is,

\[
\bar{F} = \begin{pmatrix}
    \frac{(\beta_1 X_c + \beta_2 Y_c + \beta_3 I_h + \beta_4 q H_h)S_h}{N_h} \\
    0 \\
    0 \\
    \frac{(\beta_5 X_c + \beta_6 Y_c)S_c}{N_c} \\
    0
\end{pmatrix},
\]

\[
\bar{V} = \begin{pmatrix}
    (\gamma + \mu_0)E_h \\
    \rho \gamma E_h - (\phi_a + \phi_1)I_h - (\mu_0 + \mu_1)I_h \\
    \phi_a I_h - \phi_d H_h - \mu_0 H_h \\
    (k_2 + \gamma_c)X_c \\
    \gamma_c X_c - (k_3 + \alpha_c)Y_c
\end{pmatrix}.
\]

The Jacobian matrices of \( \bar{F} \) and \( \bar{V} \) at disease-free equilibrium \( d_0 \) are the following:

\[
F = \begin{pmatrix}
    0 & \beta_2 S_h & \beta_4 q S_h & \beta_5 S_h & \beta_6 S_h \\
    0 & 0 & 0 & 0 & 0 \\
    0 & 0 & 0 & 0 & 0 \\
    0 & 0 & 0 & \beta_5 S_c & \beta_6 S_c \\
    0 & 0 & 0 & 0 & 0
\end{pmatrix},
\]

\[
V = \begin{pmatrix}
    M_1 & 0 & 0 & 0 & 0 \\
    -M_2 & M_3 & 0 & 0 & 0 \\
    0 & -\phi_a & M_4 & 0 & 0 \\
    0 & 0 & 0 & M_5 & 0 \\
    0 & 0 & 0 & -\gamma_c & M_6
\end{pmatrix},
\]

where \( M_1 = \gamma + \mu_0, M_2 = \rho \gamma, M_3 = (\phi_a + \phi_1) + (\mu_0 + \mu_1), M_4 = \phi_d + \mu_0, \) and \( M_5 = k_2 + \gamma_c, M_6 = k_3 + \alpha_c. \)
The basic reproduction number $R_0$ is therefore the spectral radius of next-generation matrix $\bar{H} = FV^{-1}$. $R_0 = R_h + R_c$, where

$$R_h = \frac{\gamma \beta_2 \rho S_h}{N_h(\gamma + \mu_0)(\phi_a + \phi_1 + \mu_0 + \mu_1)} + \frac{\gamma \phi_3 q \rho S_h}{N_h(\phi_1 + \mu_0)(\phi_a + \mu_0)(\phi_1 + \phi_3 + \mu_0 + \mu_1)}$$

$$R_c = \frac{\beta_6 S_c}{N_c(k_3 + \alpha_c)}.$$

### 4.2 Sensitivity analysis

We present analysis of the sensitivity of a few parameters using in the proposed model. This make it easier for us to know the parameters that have a significant effect on reproductive number. We apply the technic given in [9]. Sensitivity index of basic reproductive number $R_0$ is given by $\Delta R_0 = \frac{\partial R_0}{\partial h} \frac{h}{R_0}$, where $h$ is parameter.

Both Figs. 2 and 3 show the sensitivity of $R_0$. They show the importance of different parameters in the transmission of disease and also allow to measure the change in the

![Figure 2](https://www.journals.vu.lt/nonlinear-analysis)

Figure 2. The graphs show the variation of different parameters and its effect on the basic reproductive number.
reproduction number with the change in a parameter. Using these indices, we find the parameters that highly affect the reproduction number (see Table 1).

5 Endemic equilibria and backward bifurcation

We will find the endemic equilibria of system (1), where at least one of the infected component is non zero. Let \( D_1 = (S_h^*, E_h^*, I_h^*, A_h^*, H_h^*, R_h^*, X_c^*, Y_c^*, S_c^*) \) represent any endemic equilibrium point. Solving equations of (1) at steady state gives

\[
S_h^* = \frac{\gamma_c \beta_5 (Q_1 + b \beta_6 \gamma_c + Q_2^2 Q_1 \beta_5) I_h^*}{\beta_1 Q_1 Q_3 + \beta_2 Q_3 (1 - R_0)}, \\
E_h^* = \frac{\gamma_c \beta_5 (Q_3 + \beta_6 \gamma_c + Q_2^2 Q_1 \beta_5 + Q_2 Q_1 \beta_6 \gamma_c) I_h^*}{(\gamma + \mu_0) (\beta_1 Q_1 Q_3 + \beta_2 Q_3 + \beta_4 Q_2 \phi_a) (Q_1 + \beta_0 \gamma_c Q_2^2 Q_3 \beta_5 - Q_2 Q_3 \beta_6 \gamma_c)}, \\
A_h^* = \frac{\gamma (1 - \rho) (\gamma_c \beta_5) (Q_1 + \beta_6 \gamma_c) I_h^*}{(\mu_0 + \mu_2) (\gamma + \mu_0) (\beta_1 Q_1 Q_3 + \beta_2 Q_3 + \beta_4 Q_3 \phi_a) (1 - R_0)}, \\
H_h^* = \frac{\phi_a I_h^*}{\phi_d + \mu_0}, \\
R_h^* = \frac{\phi_1 (\phi_d + \mu_0) + \phi_a \phi_d) I_h^*}{\mu_0 (\phi_d + \mu_0)},
\]

Figure 3. The graphs show the variation of different parameters and its effect on the basic reproductive number.

Table 1. Values of parameters obtained in the sensitivity analysis.

| Parameter | Sensitivity indices | Parameter | Sensitivity indices |
|-----------|---------------------|-----------|---------------------|
| \( \alpha_c \) | -0.8091519 | \( \beta_2 \) | 0.002044 |
| \( \gamma \) | 0.0014879 | \( \rho \) | 0.00204588 |
| \( \mu_0 \) | -0.0025667 | \( \mu_1 \) | -0.0001346 |
| \( b_h \) | 0.0820448 | \( b_c \) | 0.9979541 |
| \( \phi_1 \) | -0.000124034 | \( \phi_a \) | 0.0023932 |
| \( N_h \) | -1.1975449 | \( N_c \) | -0.00204588 |
| \( \phi_\phi \) | -0.0095502 | \( \beta_3 \) | 0.00010744 |
| \( N_\phi \) | -1.1975449 | \( N_c \) | -0.00204588 |
| \( \kappa_3 \) | -0.1888021 | \( \beta_6 \) | 0.4975411 |

Nonlinear Anal. Model. Control, 27(1):54–69, 2022
\[
X_c^* = \frac{Q_1Q_2(\beta_5\gamma_c b\beta_6\gamma_c)I_h^*}{\gamma_c b \beta_5 + (1 - R_{0c})}, \quad Y_c^* = \frac{\gamma_c Q_1Q_2(\beta_5\gamma_c \beta_4\gamma_c)I_h^*}{Q_1(\gamma_c \beta_5 Q_1 + b\beta_6\gamma_c + Q_2Q_1\beta_5Q_2)}, \\
S_c^* = \frac{bN_c(\beta_1Q_3 + \beta_2Q_3 + \beta_4Q_2\phi_a)(1 - R_{0c})}{b\gamma_c \beta \beta_5(Q_3 + b\beta)},
\]

where \(Q_1 = k_3 + \alpha_c, Q_2 = k_2 + \alpha_c, Q_3 = (Q_2Q_3\beta_6\gamma_c - \beta_6\gamma_c)I_h^*\). The significance of backward bifurcation in the epidemiological model is that the classical requirement of the basic reproduction number \(R_{0c}\) should be less than one [13], while it is necessary for the elimination of the MERS-CoV virus from the population. The presence of backward bifurcation in the proposed model suggests that the feasibility of MERS virus elimination when the basic reproduction number is less than one depends on the initial size of the subpopulation of the model.

Now if \(I_h \neq 0\), then putting \(S_c^*, X_c^*, Y_c^*, H_h^*\) in the first equation of model (1) at steady state and using of simple algebraic manipulation, we obtain the equation

\[
f(I_h) = aI_h^2 + bI_h + c = 0.
\]

In Eq. (4), \(a, b, \) and \(c\) are defined as

\[
a = b\gamma_c \beta_5 Q_2Q_3 + Q_3^2\beta_2 + b\beta_6\gamma_c Q_3^2, \\
b = b\beta_1Q_2Q_3^2(1 - R_0)\beta_6, \\
c = b\beta_6\gamma_c Q_3^2 + \beta_3gQ_1Q_2.
\]

In Eq. (5), \(Q = N_h(\gamma + \mu_0)(\phi_a + \phi_1 + \mu_0 + \mu_1) + N_c(k_3 + \alpha_c)\). Clearly, the coefficient \(a\) is always positive, while \(b\) is positive or negative depend on the value of \(R_0\). As \(a > 0\), the existence of positive solution of Eq. (4) depend on the sign of \(b, c\), which shows that the equilibrium depend continuously on the basic reproductive number. For \(b^2 < 4ac\), Eq. (4) has no positive solutions, and there is no endemic equilibrium.

For \(R_0 = 1\), the following result holds.

**Lemma 2.** If \(R_0 = 1\), model (1) posses the phenomena of backward bifurcation when \(c < 0\); (see Fig. 4).

![Figure 4. Bifurcation diagram of model (1) showing backward bifurcation.](https://www.journals.vu.lt/nonlinear-analysis)
6 Stability of endemic equilibrium

We prove the local stability of model (1) at endemic equilibria (EE). For this, we have the following result.

Theorem 2. The endemic equilibrium point \( E_2 = (S_h^*, E_h^*, I_h^*, A_h^*, H_h^*, R_h^*, X_c^*, Y_c^*, S_c^*) \) is locally asymptotically stable if \( R_0 > 1 \), and it is unstable for \( R_0 < 1 \).

Proof. By applying the row operation and some simplification to the matrix (2) we have the following result. We prove the local stability of model (1) at endemic equilibria (EE). For this, we have the following Jacobian matrix:

\[
J_0 = \begin{pmatrix}
-A_2 & 0 & -\frac{\beta_3 S_h}{N_h} & 0 & -\frac{\beta_4 q S_h}{N_h} & 0 & 0 & -\frac{\beta_1 S_h}{N_h} & -\frac{\beta_2 S_h}{N_h} \\
0 & -A_2 & T_1 & 0 & T_2 & 0 & 0 & T_3 & T_4 \\
0 & 0 & -T_5 & T_6 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & -C_2 T_5 & T_3 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & -T_7 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & -T_8 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & -D_2 & T_7 & -\frac{\beta_3 S_h}{N_h} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & -E_2 & -\frac{\beta_2 S_h}{N_h} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\gamma_c - T_9
\end{pmatrix}. \tag{6}
\]

In Eq. (6), the values of \( T_i \) for \( i = 1, 2, \ldots, 8 \) are given as

\[
T_1 = \frac{\beta_3 S_h}{N_h} A_2 - \frac{\beta_3 S_h}{N_h} B_2, \quad T_2 = \frac{\beta_4 q S_h}{N_h} A_2 - \frac{\beta_4 q S_h}{N_h} B_2,
\]
\[
T_3 = \frac{\beta_1 S_h A_2}{N_h} - \frac{\beta_1 S_h B_2}{N_h}, \quad T_4 = \frac{\beta_2 S_h A_2}{N_h} - \frac{\beta_2 S_h B_2}{N_h},
\]
\[
T_5 = \gamma (1 - \rho), \quad T_6 = (\mu_0 + \mu_2) \gamma \rho,
\]
\[
T_7 = (\mu_0 + \mu_2) \gamma \rho \phi_a, \quad T_8 = \phi_\phi (\phi_\phi + \mu + \mu_0) + (\phi_\phi + \mu_0) \phi_a, \quad T_9 = k_3 + \alpha_c.
\]

Thus the eigenvalues of the Jacobian matrix (6) become

\[
\lambda_1 = -G < 0, \quad \lambda_2 = -((\gamma + \mu_0) A_2 < 0,
\]
\[
\lambda_3 = -C_2 \gamma (1 - \rho) = -T_5 < 0, \quad \lambda_4 = -C_2 \gamma (1 - \rho) < 0,
\]
\[
\lambda_5 = -(\mu_0 + \mu_2) \gamma \rho \phi_a < 0, \quad \lambda_6 = -\phi_\phi (\phi_\phi + \mu + \mu_0) + (\phi_\phi + \mu_0) \phi_a < 0,
\]
\[
\lambda_7 < 0, \quad \lambda_8 < 0, \quad \lambda_9 < 0.
\]

Here

\[
G = \frac{\gamma \beta_2 \rho}{(\gamma + \mu_0)(\phi_a + \phi_1 + \mu_0 + \mu_1)} - \frac{\gamma \phi_a \beta_3 q \rho}{(\phi_1 + \mu_0)(R_0 - 1)}.
\]

If \( R_0 > 1 \), all the eigenvalues have negative real parts. \( \lambda_1 < 0 \) if \( R_0 > 1 \), which prove the result. \( \square \)
6.1 Global stability of endemic equilibrium

**Theorem 3.** For $R_0 > 1$, the endemic equilibrium point $D_1$ of model (1) is stable globally, and it is unstable for $R_0 < 1$.

**Proof.** We define the Lyapunov function as \([7, 17]\)

$$U(t) = \frac{1}{2} \left[ (S_h - S_h^*) + (E_h - E_h^*) + (I_h - I_h^*) + (A_h - A_h^*) 
+ (H_h - H_h^*) + (S_c - S_c^*) + (X_c - X_c^*) + (Y_c - Y_c^*) \right]^2.$$  \(7\)

Differentiating (7) with respect to time, we obtain

$$U'(t) = \left[ (S_h - S_h^*) + (E_h - E_h^*) + (I_h - I_h^*) + (A_h - A_h^*) 
+ (H_h - H_h^*) + (S_c - S_c^*) + (X_c - X_c^*) + (Y_c - Y_c^*) \right] \times \left[ \frac{dS_h}{dt} + \frac{dE_h}{dt} + \frac{dI_h}{dt} + \frac{dA_h}{dt} + \frac{dH_h}{dt} + \frac{dS_c}{dt} + \frac{dX_c}{dt} + \frac{dY_c}{dt} \right].$$

After some rearrangement and using the values of system (1), we have

$$U'(t) = -\left[ (S_h - S_h^*) + (E_h - E_h^*) + (I_h - I_h^*) + (A_h - A_h^*) 
+ (H_h - H_h^*) + (S_c - S_c^*) + (X_c - X_c^*) + (Y_c - Y_c^*) \right] \times \left[ \mu_0(S_h - S_h^*) + \mu_0(E_h - E_h^*) + (\mu_0 + \mu_1)(I_h - I_h^*) 
+ \frac{\phi_a + \phi_1(\mu_0 + \mu_1)}{\gamma \rho} + \frac{\gamma \beta_2 \rho S_h}{N_h(\gamma + \mu_0)} + k_1 S_c 
+ (k_2 + \alpha_c) X_c^*(R_0 - 1) + \frac{\gamma \beta_2 \rho S_h}{N_h(\gamma + \mu_0)(\phi_a + \phi_1 + \mu_0 + \mu_1)} \right].$$

The last equation implies that $U'(t) < 0$ for all $t$, while $U'(t) = 0$ if $S_h = S_h^*$, $S_c = S_c^*$, and $R_0 > 1$, which prove the global stability of model (1) around the endemic equilibrium [14].

**7 Numerical simulation**

To study the dynamical behavior of the MERS-CoV model, a numerical algorithm was developed and implemented in an extensive numerical simulations by using Runge–Kutta fourth-order method using the parameter values listed in Table 2. For the simulation purpose, some parameters are chosen, and some are taken from the published data. The choice of parameters are taken in such a way that would be more biological feasible.

This numerical results are given in Figs. 5–6.
Transmission dynamic and backward bifurcation of MERS-CoV

Figure 5. The plots demonstrate the time dynamics of different compartmental population susceptible, exposed, symptomatic and infected, infected but asymptomatic, hospitalized when $R_0 < 1$. 

Nonlinear Anal. Model. Control, 27(1):54–69, 2022
Figure 6. The plots demonstrate the time dynamics of different compartmental population recover, susceptible camels, undetected infected camels, detected infected camels when $R_0 < 1$.

Table 2. Parameters and its values.

| Notation | Value | Source | Parameter | Value | Source |
|----------|-------|--------|-----------|-------|--------|
| $b_h$    | 0.09  | estimated | $b_c$     | 0.022 | estimated |
| $\beta_1$ | 0.09 | estimated | $\beta_2$ | 0.022 | estimated |
| $\beta_3$ | 0.09 | estimated | $\beta_4$ | 0.022 | estimated |
| $\mu_0$  | 0.09  | estimated | $k_1$     | 0.022 | estimated |
| $\phi_0$ | 0.09  | estimated | $\gamma_c$ | 0.022 | estimated |
| $\phi_0$ | 0.09  | estimated | $\mu_0$   | 0.022 | estimated |
| $\gamma$ | 0.026 | estimated | $k_2$     | 0.0002 | [15] |
| $k_3$    | 0.05  | estimated | $\rho$    | 0.065 | estimated |
| $\mu_c$  | 0.023 | estimated | $\alpha_c$ | 0.04  | [11] |
| $q$      | 0.004 | estimated | $\phi_0$  | 0.014 | estimated |
| $\mu_1$  | 0.01  | estimated | $\mu_2$   | 0.008 | estimated |
| $\beta_6$ | 0.0001 | estimated | $\beta_7$ | 0.008 | estimated |
8 Conclusion

In this work, we showed using a deterministic model the transmission of MERS-CoV between human population and camel population. We developed a model formulation and discussed the stability of the proposed model. The stability conditions are obtained in terms of $R_0$. We found those condition under which the model become stable. The threshold quantity $R_0$ measures transmission potential of disease. We found $R_0$ by using next-generation matrix method. We performed sensitivity analysis of the basic reproductive number in order to find the most sensitive parameter. We shown that the proposed model exhibits the phenomena of backward bifurcation. Finally, to support our analytical work, we have shown the numerical simulation for our proposed model.

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Appendix: Proof of Theorem 1

The Jacobian matrix of the system at $(F_0, 0, 0, 0, 0, 0, E_0, 0, 0)$ is given by

$$J_0 = \begin{pmatrix}
-\mu_0 & 0 & -\frac{\beta_3 S_h}{N_h} & 0 & -\frac{\beta_4 S_h}{N_h} & 0 & 0 & -\frac{\beta_1 S_h}{N_h} & -\frac{\beta_2 S_h}{N_h} \\
0 & -(\gamma + \mu_0) & \frac{\beta_3 N_h}{N_H} & 0 & \frac{\beta_4 q S_h}{N_h} & 0 & 0 & \frac{\beta_1 N_h}{N_H} & \frac{\beta_2 S_h}{N_h} \\
0 & \rho \gamma & -C_3 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & L_1 & 0 & -L_2 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \phi_a & 0 & -L_3 & 0 & 0 & 0 & 0 \\
0 & 0 & \phi_1 & 0 & \phi_a & -\mu_0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & D_4 & -\frac{k_3}{N_c} & -\frac{k_5}{N_c} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_5 S_c}{N_c} & \frac{\beta_6 S_c}{N_c} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_c & -T_9 \\
\end{pmatrix},$$

where $L_1 \gamma (1 - \rho), L_2 = \mu_0 + \mu_2$, and $L_3 = \phi + \mu_0$.

After elementary row operation, we get the characteristic equation of the Jacobian matrix (3):

$$(\zeta + \mu_0)(\zeta + \gamma + \mu_0)(\zeta + C_3(\gamma + \mu_0))(\zeta + C_3 \gamma (1 - \rho))$$

$$(\zeta + C_4)(\zeta + \mu_0 \phi_a)(\zeta^2 + a_1 \zeta^2 + a_2 \zeta + a_3) = 0,$$

where

$$a_1 = k_3 + 2 \frac{k_3}{N_c} + k_3 + \alpha_c, \quad a_2 = 2 \frac{k_3^2}{N_c} + 2 \frac{k_3}{N_c} \alpha_c + \frac{\beta_5 S_c}{N_c} D_4,$$

$$a_3 = \frac{k_3^3}{N_c^2} \alpha_c + \frac{\gamma_c \beta_6 S_c}{N_c D_4} + \frac{\frac{\beta_5 S_c}{N_c} D_4}{\alpha_c},$$

$$a_1 a_2 = \frac{k_3}{N_c} \left[ 2 k_3^2 + 2 k_3 + \beta_5 S_c D_4 + 2 \frac{k_3^2}{N_c} + 4 \frac{k_3}{N_c} \alpha_c + 2 k_5 S_c D_4 \right]$$

$$+ 2 \frac{k_3}{N_c} \alpha_c + 2 \alpha_c^2 + \frac{\beta_5 D_4 \alpha_c}{k_3}.$$
The application of Routh–Hurwitz criteria [12]

\[(H_1) \ a_i > 0 \text{ for } i = 1, 2, 3 \text{ and } a_1a_2 > a_3\]

implies that the eigenvalues have negative real parts, thus model (1) is locally asymptotically stable at DFE.

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