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A THEORETICAL ASSESSMENT OF THE EFFECTS OF HOSPITAL RESOURCES ON A HOST-VECTOR DISEASE

ROSAIRE OUEDRAOGO, ALI TRAORÉ* AND HAMADOUM DICKO

ABSTRACT. This paper provides a mathematical analysis of a host vectors disease model with the influence of available hospital resources. We derive the basic reproduction number $\mathcal{R}_0^h$ of the model. We prove the existence of a unique disease-free equilibrium, which is stable when the basic reproduction number $\mathcal{R}_0^h$ is less than 1, indicating that the disease can be eradicated under these conditions. However, when $\mathcal{R}_0^h$ exceeds 1, the system exhibits multiple endemic equilibria, leading to the possible persistence of the disease into the population. The study also reveals the existence of bifurcations, indicating qualitative changes in the system's dynamics depending on certain critical parameter values. A sensitivity analysis of the parameters is carried out to assess the most influential parameters in managing the epidemic.

1. INTRODUCTION

Host vectors diseases, such as malaria, dengue and Zika, are significant public health challenges worldwide, especially in regions with limited healthcare infrastructure (see [19, 30]). These diseases are transmitted through vectors, primarily insects like mosquitoes, which carry pathogens from infected individuals to healthy ones. Managing the spread of such diseases is a complex task due to various environmental, biological, and social factors. Mathematical models play a crucial role in understanding the dynamics of vector-borne diseases and evaluating the impact of different intervention strategies. Over the years, various models have been developed to simulate the transmission process and provide insights into disease control (see [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 17, 18, 22, 20, 21, 23, 26, 27, 28, 31, 32]). These models often incorporate factors such as vector population dynamics, transmission rates, and human population movement. However, one important yet often overlooked factor in the management of outbreaks is the availability of hospital resources, which directly affects patient treatment and recovery rates. The recovery rate can be affected by many factors, among which we have the number of the health workforce including nurses, pharmacists and other healthcare workers, and the facilities

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*Corresponding author.

of the hospital, such as the number of hospital beds and medicines. Among these factors, the number of available hospital beds is used by health authorities as a method of estimating resource availability to the public. So, the study of a vector-borne disease model that takes into account the impact of hospital resources in terms of hospital bed-population ratio can be important for understanding and anticipating epidemic control. Parasitic diseases, primarily transmitted by insect vectors like mosquitoes, are public health challenges due to their complex transmission and potential rapid epidemic outbreaks. Integrating hospital resources into this type of model enables evaluation not only of disease spread but also of healthcare systems' capacity to respond effectively. This model examines how bed availability influences the dynamics of infection and epidemic severity, thus providing a framework for planning and optimizing public health resources. By offering a quantitative analysis of hospital capacity impact on the progression of vector-borne disease, this study informs policy decisions and strengthens the resilience of healthcare systems against future health crises. This paper is organized as follows: in Section 2, we provide a description of the epidemiological model. Section 3 is devoted to the study of the existence, positivity, and boundedness of the solutions. In Section 4, we analyze the stability of the equilibrium points. Section 5 is devoted to the study of bifurcation. A sensitivity analysis of the parameters is conducted in Section 6. The work is ended by a conclusion in Section 7.

2. Model Description

The dynamics of the infected humans and vectors populations over time are given by the following system of differential equations (see [25]) :

$$\begin{cases} \frac{dx(t)}{dt} = -\gamma x(t) + abm(1 - x(t))y(t), \\ \frac{dy(t)}{dt} = -\xi y(t) + ac(1 - y(t))x(t). \end{cases} \tag{2.1}$$

The variable x represents the proportion of infected humans, while y represents the proportion of infected vectors. The parameter γ is the recovery rate of infected humans, which is the rate at which they recover or become non-infectious. Similarly, ξ denotes the rate at which infected vectors lose their ability to transmit the infection, either through death or by losing the pathogen. The parameter a corresponds to the biting rate, while b represents the probability that a bite from an infected vector will infect a human. Additionally, c is the probability that a bite from a vector on an infected human will infect the vector, and m is the ratio of the number of vectors to the number of humans, indicating the relative density of vectors.

Considering medical resources q and the number of infected humans x, Shan (see [24]) established a type of recovery rate function as follows

$$g(x) = \mu_0 + (\mu_1 - \mu_0)\frac{q}{x + q}, \tag{2.2}$$

where μ_1 is the maximum per capita recovery rate due to the sufficient health care resource, and few infectious individuals, as well as the inherent property of a specific disease, and μ_0, is the minimum per capita recovery rate due to the function of basic clinical resources. Thus, $\mu_0 < \mu_1$. From an epidemic point of view, when the number of infected individuals is lower than the hospital resources at the initial stage of infection, the recovery rate decreases very slowly. When the number of infected individuals tends to zero, the recovery rate is still the maximum recovery rate μ_1, then

$$\lim_{x \to 0^+} \frac{\partial g(x)}{\partial x} = 0.$$

Therefore, the recovery rate function (2.2) can be modified as

$$g(x) = \mu_0 + (\mu_1 - \mu_0)\,\frac{\theta}{x^2+\theta}.$$

If the number of infected individuals is higher than the hospital resources, the recovery rate decreases rapidly, and finally tends to the minimum recovery rate μ_0, then $\frac{\partial^2 g(x)}{\partial x^2}\Big|_{x=q} = 0$, so we have $\theta = 3q^2$. Then, function g takes the form

$$g(x) = \mu_0 + (\mu_1 - \mu_0)\,\frac{3q^2}{x^2+3q^2}. \tag{2.3}$$

Taking into account the healing function of human population due to the availability of hospital resources $g(x)$, model (2.1) becomes

$$\begin{cases} \frac{dx(t)}{dt} = -\gamma x(t) + abm(1-x(t))y(t) - \left(\mu_0 + (\mu_1-\mu_0)\,\frac{3q^2}{(x(t))^2+3q^2}\right)x(t), \\ \frac{dy(t)}{dt} = -\xi y(t) + ac(1-y(t))x(t). \end{cases} \tag{2.4}$$

3. Existence, positivity and boundedness

In this section, we demonstrate the existence, positivity, and boundedness of the solutions of the model (2.4).

Proposition 3.1. *The solutions of model (2.4) are contained in the region*

$$\Omega = \left\{(x,y) \in \mathbb{R}^2_+ \mid 0 \le x \le 1 \text{ and } 0 \le y \le 1\right\} \tag{3.1}$$

which is positively invariant.

Proof. We easily verify that when $x(t)$ and $y(t)$ reach the bounds 0 or 1, the respective derivatives $\frac{dx}{dt}$ and $\frac{dy}{dt}$ do not force $x(t)$ or $y(t)$ to go beyond these bounds.

- When $x = 0$ and $y \ge 0$, then $\frac{dx(t)}{dt}\Big|_{x=0} = abmy \ge 0$.
- When $y = 0$ and $x \ge 0$, then $\frac{dy(t)}{dt}\Big|_{y=0} = acx \ge 0$.
- When $x = 1$ and $y \ge 0$, then $\frac{dx}{dt}\Big|_{x=1,y\ge 0} = -\gamma - \left(\mu_0 + (\mu_1-\mu_0)\frac{3q^2}{1+3q^2}\right) \le 0$.
- When $y = 1$ and $x \ge 0$, then $\frac{dy}{dt}\Big|_{y=1,x\ge 0} = -\mu \le 0$.

The region Ω is, therefore, positively invariant for this epidemic model. This means that if the initial values $x(0)$ and $y(0)$ belong to this interval, the solutions of the system will remain in this interval for all time $t \ge 0$ □

Proposition 3.2. *For every initial value in Ω, solutions of system (2.4) exist for all time $t > 0$.*

Proof. Since the right-hand side of the system (2.4) is locally Lipschitz, thus the local existence of solutions follows. The global existence of the solutions is due to the fact that Ω is positively invariant and attracting all the solutions □

4. Stability analysis of the equilibrium points

In this section, we conduct an analysis of the stability of the model's equilibrium points, focusing first on the disease-free equilibrium point and then on the existence and stability

of the endemic equilibrium. This study allows us to better understand the conditions under which the disease dies out or persists within the population.

4.1. **Stability of the disease-free equilibrium.** The basic reproduction number is an important parameter in epidemiology. It is defined as the average number of secondary cases caused by an infected individual introduced into a susceptible population.
The disease-free equilibrium corresponds to the case where there are no infected components in a population and it is given by

$$\mathcal{E}_0 = (x_0, y_0) = (0, 0).$$

According to Van Den Driessche and Watmough (see [29]), the basic reproduction number of the model (2.4) is given by

$$\mathcal{R}_0^h = \sqrt{\frac{a^2bcm}{\xi\left(\gamma+\mu_1\right)}}.$$

Proposition 4.1. *The Disease-Free Equilibrium, denoted as $\mathcal{E}_0$, of model (2.4) is locally asymptotically stable if $\mathcal{R}_0^h < 1$ and unstable when $\mathcal{R}_0^h > 1$.*

Proof. The Jacobian matrix of the system (2.4) at any equilibrium point $\mathcal{E} = (x, y)$ is given by

$$J\left(\mathcal{E}\right) = \begin{pmatrix} -\gamma - \frac{a^2bcmx}{\xi+acx} - \frac{\mu_0x^4+9q^4\mu_1-3q^2x^2(\mu_1-3\mu_0)}{(x^2+3q^2)^2} & abm\left(1-x\right) \\ ac\left(1-y\right) & -\xi - acx \end{pmatrix}.$$

The characteristic polynomial of the matrix $J(\mathcal{E})$ at the trivial equilibrium $\mathcal{E}_0$ point is given by

$$Q(\alpha) = \alpha^2 + \left(\gamma+\xi+\mu_1\right)\alpha + \xi\left(\gamma+\mu_1\right) - a^2bcm.$$

Let $d_1 = \gamma+\xi+\mu_1$ and $d_2 = \xi\left(\gamma+\mu_1\right) - a^2bcm$.
The characteristic polynomial becomes

$$Q(\alpha) = \alpha^2 + d_1\alpha + d_2.$$

Hence, the roots of Q are

$$\alpha_1 = \frac{-d_1 - \sqrt{d_1^2 - 4d_2}}{2}, \quad \alpha_2 = \frac{-d_1 + \sqrt{d_1^2 - 4d_2}}{2},$$
$$\text{with } d_1 > 0 \text{ and } d_1^2 - 4d_2 > 0.$$

We observe that $\alpha_1 < 0$.
Let us now study the sign of α_2. If $\mathcal{R}_0^h < 1$, then $\xi\left(\gamma+\mu_1\right) - a^2bcm > 0$, that is $d_2 > 0$. Thus, $\sqrt{d_1^2 - 4d_2} < d_1$, which means that $\alpha_2 < 0$. Therefore, if $\mathcal{R}_0^h < 1$, both α_1 and α_2 are negative real numbers. On the other hand, if $\mathcal{R}_0^h > 1$, then $d_2 < 0$, and consequently, α_2 is a positive real number. Thus, the disease-free equilibrium is locally asymptotically stable if $\mathcal{R}_0^h < 1$, and unstable when $\mathcal{R}_0^h > 1$ □

We now state the global stability result of the disease-free equilibrium.
When $\mathcal{R}_0^h < 1$, the disease tends to disappear from the population. In this context, we assume that the recovery rate reaches its maximum value, that is, $g(x) = \mu_1$.

Proposition 4.2. *If $\mathcal{R}_0^h < 1$, then the disease-free equilibrium $\mathcal{E}_0$ is globally asymptotically stable.*

Proof. We construct the following Lyapunov function:

$$V(x,y) = acx + (\gamma+\mu_1)y.$$

Now, the derivative of V is given by

$$\begin{aligned}\frac{dV}{dt} &= -ac\gamma x + a^2bcm(1-x)y - ac\mu_1 x \\ &\quad - \xi(\gamma+\mu_1)y + ac(\gamma+\mu_1)(1-y)x \\ &= -a^2bcmxy - ac(\gamma+\mu_1)xy + a^2bcmy - \xi(\gamma+\mu_1)y \\ &= y\left(a^2bcm - \xi(\gamma+\mu_1)\right) - a^2bcmxy - ac(\gamma+\mu_1)xy \\ &= \xi(\gamma+\mu_1)\left((\mathcal{R}_0^h)^2 - 1\right) - \Big(a^2bcm + ac(\gamma+\mu_1)\Big)xy.\end{aligned}$$

Hence, if $\mathcal{R}_0^h < 1$ then $\frac{dV}{dt}$ is negative. In addition, the largest compact invariant subset of $\left\{(x,y)\in\mathbb{R}_+^2 \;\middle|\; \frac{dV}{dt}=0\right\}$ is the singleton set $\mathcal{E}_0$. Hence, LaSalle's invariant principle (see [15]) implies that $\mathcal{E}_0$ is globally asymptotically stable in Ω when $\mathcal{R}_0^h < 1$. □

4.2. **Existence of the endemic equilibrium.** In this subsection we provide the existence result of the endemic equilibrium. Denote by $\mathcal{E}^* = (x^*, y^*)$ an endemic equilibrium of model (2.4). Thus, $\mathcal{E}^*$ solves the following system

$$\begin{cases} -\gamma x^* + abm(1-x^*)y^* - \left(\mu_0 + (\mu_1-\mu_0)\,\frac{3q^2}{(x^*)^2+3q^2}\right)x^* = 0, \\ \\ -\xi y^* + ac(1-y^*)x^* = 0. \end{cases}$$

That is,

$$-\gamma x^* + abm(1-x^*)y^* - \left(\mu_0 + (\mu_1-\mu_0)\,\frac{3q^2}{(x^*)^2+3q^2}\right)x^* = 0,$$

which gives us

$$-\gamma x^* - \mu_0 x^* - abmx^*y^* - (\mu_1-\mu_0)\,\frac{3q^2x^*}{(x^*)^2+3q^2} + abmy^* = 0.$$

Factorizing by x^* gives

$$x^*\left(\gamma + \mu_0 + abmy^* + (\mu_1-\mu_0)\,\frac{3q^2}{(x^*)^2+3q^2}\right) = abmy^*$$

and

$$x^* = \frac{abmy^*}{\gamma+\mu_0+abmy^* + (\mu_1-\mu_0)\,\frac{3q^2}{(x^*)^2+3q^2}}.$$

Furthermore,

$$-\xi y^* + ac(1-y^*)x^* = 0 \;\Rightarrow\; y^* = \frac{acx^*}{\xi + acx^*}.$$

By substituting y^* into the expression of x^*, we get

$$x^*\Big(\gamma + \mu_0 + \frac{a^2bcm}{\xi+acx^*}(x^*-1) + (\mu_1-\mu_0)\,\frac{3q^2}{(x^*)^2+3q^2}\Big) = 0,$$

that is
$x^* = 0$ or

$$\gamma + \mu_0 + \frac{a^2bcm}{\xi + acx^*}(x^* - 1) + (\mu_1 - \mu_0)\frac{3q^2}{(x^*)^2 + 3q^2} = 0. \tag{4.1}$$

The solution $x^* = 0$ gives us the disease-free equilibrium $\mathcal{E}_0$ defined above.
By developing (4.1) we obtain

$$\begin{aligned}&-\left(a^2bcm + ac\left(\gamma + \mu_0\right)\right)(x^*)^3 + \xi\Big(\left(\gamma + \mu_1\right)\left((\mathcal{R}_0^h)^2 - 1\right) + (\mu_1 - \mu_0)\Big)(x^*)^2\\ &- 3q^2ac\left(abm + \gamma + \mu_1\right)x^* + 3q^2\xi\left(\gamma + \mu_1\right)\left((\mathcal{R}_0^h)^2 - 1\right) = 0.\end{aligned}$$

Setting

$$\begin{aligned}A_3 &= -\left(a^2bcm + ac\left(\gamma + \mu_0\right)\right),\\ A_2 &= \xi\left(\gamma + \mu_1\right)\left((\mathcal{R}_0^h)^2 - 1\right) + \xi(\mu_1 - \mu_0),\\ A_1 &= -3q^2ac\left(abm + \gamma + \mu_1\right),\\ A_0 &= 3q^2\xi\left(\gamma + \mu_1\right)\left((\mathcal{R}_0^h)^2 - 1\right).\end{aligned}$$

We obtain the following equation

$$\mathcal{P}(x^*) = A_3(x^*)^3 + A_2(x^*)^2 + A_1x^* + A_0 = 0, \tag{4.2}$$

Clearly $A_3 < 0$ and $A_1 < 0$.
Further, since $\mu_1 > \mu_0$ and $\mathcal{R}_0^h > 1$, thus $A_2 > 0$.
The number of positive real root(s) of $\mathcal{P}\left(x^*\right)$ depend on the signs of A_3, A_2, A_1 and A_0. This can be analyzed by applying Descarte's rule of sign (see [16]). The various possibilities has been shown in the Table 1.

Table 1: Number of possible positive roots of polynomial $\mathcal{P}\left(x^*\right)$.

Cases	A_3	A_2	A_1	A_0	$\mathcal{R}_0^h$	changes in sign	Total possible positive roots
1	-	+	-	+	$\mathcal{R}_0^h > 1$	3	1,3
2	-	+	-	-	$\mathcal{R}_0^h < 1$	2	0,2
3	-	-	-	-	$\mathcal{R}_0^h < 1$	0	0

The results can be summarized as follows.

Proposition 4.3. *The model (2.4),*
(i) one or three endemic equilibria when $\mathcal{R}_0^h > 1$ and case 1 is satisfied,
(ii) has two endemic equilibria when $\mathcal{R}_0^h < 1$ and cases 2 is satisfied,
(iii) does not have any endemic equilibrium when $\mathcal{R}_0^h < 1$ and case 3 is satisfied.

4.3. **Stability of the endemic equilibrium.** In this subsection, we analyze the stability of the endemic equilibrium. We state the following result:

Proposition 4.4. *If $\mathcal{R}_0^h > 1$, the endemic equilibrium (x^*, y^*) of model (2.4) is globally asymptotically stable whenever $|x|\mu_1 < abm|y|x$.*

Proof. Defining

$$\begin{cases}\tilde{x} = x - x^*,\\ \\ \tilde{y} = y - y^*.\end{cases}$$

Therefore,

$$\begin{cases} \dot{\tilde{x}} = -\gamma\,(\tilde{x}+x^*) + abm(1-\tilde{x}-x^*)(\tilde{y}+y^*) - \frac{\mu_0(\tilde{x}+x^*)^3+3q^2\mu_1(\tilde{x}+x^*)}{(\tilde{x}+x^*)^2+3q^2}, \\ \dot{\tilde{y}} = -\xi(\tilde{y}+y^*) + ac(1-\tilde{y}-y^*)(\tilde{x}+x^*). \end{cases}$$

By setting $\tilde{x} = x$ and $\tilde{y} = y$, we obtain

$$\begin{cases} \dot{x} = abmy^*(1-x^*) - \gamma x^* + abm(1-x-x^*)y - abmy^*x - \gamma x - \frac{\mu_0(x+x^*)^3+3q^2\mu_1(x+x^*)}{(x+x^*)^2+3q^2}, \\ \dot{y} = ac(1-y^*)x^* - \xi y^* + ac(1-y-y^*)x - acyx^* - \xi y. \end{cases}$$

Since (x^*, y^*) is an endemic equilibrium, we have

$$\begin{cases} -\gamma x^* + abm(1-x^*)y^* = \frac{\mu_0(x^*)^3+3q^2\mu_1 x^*}{(x^*)^2+3q^2}, \\ ac(1-y^*) - \xi y^* = 0. \end{cases}$$

Then,

$$\begin{cases} \dot{x} = -(abmy^*+\gamma)x + abm(1-x-x^*)y - \frac{\mu_0(x+x^*)^3+3q^2\mu_1(x+x^*)}{(x+x^*)^2+3q^2} + \frac{\mu_0(x^*)^3+3q^2\mu_1 x^*}{(x^*)^2+3q^2}, \\ \dot{y} = ac(1-y-y^*)x - (acx^*+\xi)y. \end{cases}$$

This can be rewritten as:

$$\begin{cases} \dot{x} = -abm\frac{xy^*}{x^*} + abm(1-x-x^*)y + \frac{\left(\mu_0(x^*)^2+3q^2\mu_1\right)(x+x^*)}{(x^*)^2+3q^2} - \frac{\mu_0(x+x^*)^3+3q^2\mu_1(x+x^*)}{(x+x^*)^2+3q^2}, \\ \dot{y} = ac(1-y-y^*)x - ac\frac{x^*}{y^*}y. \end{cases}$$

There are two equilibria: $(0,0)$, which is the endemic equilibrium, and the disease-free equilibrium $(-x^*, -y^*)$, which are written in the new coordinates. Clearly, one can verify that in the new coordinates:

$$-x^* \le x \le 1-x^* \quad \text{and} \quad -y^* \le y \le 1-y^*.$$

We introduce the following Lyapunov function:

$$V(x,y) = ac|x| + abm\frac{y^*}{x^*}|y|.$$

We define ε_x and ε_y by

$$\varepsilon_x = \begin{cases} -1 & \text{if } x<0, \\ 0 & \text{if } x=0, \\ 1 & \text{if } x>0. \end{cases} \quad \text{and} \quad \varepsilon_y = \begin{cases} -1 & \text{if } y<0, \\ 0 & \text{if } y=0, \\ 1 & \text{if } y>0. \end{cases}$$

Thus,

$$|x| = \varepsilon_x x, \ |y| = \varepsilon_y y.$$

The derivation of the function V with respect to the time t is given by:

$$\frac{dV}{dt} = ac\varepsilon_x\dot{x} + abm\frac{y^*}{x^*}\varepsilon_y\dot{y}.$$

By replacing $\dot{x}$ and $\dot{y}$ after a rearrangement, we obtain

$$\begin{aligned}\frac{dV}{dt} =& - a^2bcm\frac{y^*}{x^*}\varepsilon_x x + ac\varepsilon_x x\left(\frac{\mu_0\left(x^*\right)^2+3q^2\mu_1}{\left(x^*\right)^2+3q^2}\right) + a^2bcm\varepsilon_x(1-x-x^*)y\\ &- ac\varepsilon_x\left(\frac{\mu_0\left(x+x^*\right)^3+3q^2\mu_1\left(x+x^*\right)}{\left(x+x^*\right)^2+3q^2}\right) + ac\varepsilon_x\left(\frac{\mu_0\left(x^*\right)^3+3q^2\mu_1x^*}{\left(x^*\right)^2+3q^2}\right)\\ &+ a^2bcm\frac{y^*}{x^*}\varepsilon_y(1-y-y^*)x - a^2bcm\varepsilon_y y.\end{aligned}$$

Clearly, it is easy to verify that

$$\varepsilon_x\varepsilon_y|x| = \varepsilon_y x \text{ and } \varepsilon_x\varepsilon_y|y| = \varepsilon_x y.$$

Therefore,

$$\begin{aligned}\frac{dV}{dt} =& a^2bcm\frac{y^*}{x^*}\Big(-1+\varepsilon_x\varepsilon_y\left(1-y-y^*\right)\Big)|x| + a^2bcm\Big(-1+\varepsilon_x\varepsilon_y\left(1-x-x^*\right)\Big)|y|\\ &+ ac\varepsilon_x\left(x+x^*\right)\left(\frac{\mu_0\left(x^*\right)^2+3q^2\mu_1}{\left(x^*\right)^2+3q^2} - \frac{\mu_0\left(x+x^*\right)^2+3q^2\mu_1}{\left(x+x^*\right)^2+3q^2}\right).\end{aligned}$$

Since $\varepsilon_x\varepsilon_y < 1$, then

$$\begin{aligned}\frac{dV}{dt} \leq& - a^2bcm\frac{y^*}{x^*}\left(y+y^*\right)|x| - a^2bcm\left(x+x^*\right)|y|\\ &+ ac\varepsilon_x\left(x+x^*\right)\left(\frac{\mu_0\left(x^*\right)^2+3q^2\mu_1}{\left(x^*\right)^2+3q^2} - \frac{\mu_0\left(x+x^*\right)^2+3q^2\mu_1}{\left(x+x^*\right)^2+3q^2}\right).\end{aligned}$$

Thus,

$$\frac{dV}{dt} \leq -a^2bcm\frac{y^*}{x^*}(y+y^*)|x| - a^2bcm(x+x^*)|y| + ac\varepsilon_x(x+x^*)\left(\frac{\mu_0\left(x^*\right)^2+3q^2\mu_1}{\left(x^*\right)^2+3q^2}\right).$$

Since $\mu_0 < \mu_1$, we get

$$\frac{dV}{dt} \leq a\left(x+x^*\right)\left(-abm|y| + \varepsilon_x\mu_1\right) - a^2bcm\frac{y^*}{x^*}(y+y^*)|x|.$$

Clearly, if $\varepsilon_x\mu_1 \leq abm|y|$, we get $\frac{dV}{dt} \leq 0$ for all $(x,y) \in \mathbb{R}^2_+$. Moreover, the largest invariant subset of $\left\{(x,y) \in \mathbb{R}^2_+ \mid \frac{dV}{dt} = 0\right\}$ is equal to the singleton $\{\mathcal{E}^*\}$. Then, by LaSalle invariant principle we conclude that the endemic equilibrium $\mathcal{E}^*$ is globally asymptotically stable, when $\mathcal{R}_0^h > 1$ (see [15]) □

5. BIFURCATIONS ANALYSIS

Bifurcation analysis contribute to understand qualitative changes in epidemic dynamics which may have important implications for public health decision-making.
Let b be the bifurcation parameter.
When $\mathcal{R}_0^h = 1$, we get

$$b = \frac{\xi\left(\gamma+\mu_1\right)}{a^2cm}.$$

Consider

$$\begin{cases} \frac{dx(t)}{dt} = f_1(x,y) = -\gamma x(t) + abm(1-x(t))y(t) - \left(\mu_0 + (\mu_1 - \mu_0)\,\frac{3q^2}{(x(t))^2+3q^2}\right)x(t), \\ \\ \frac{dy(t)}{dt} = f_2(x,y) = -\xi y(t) + ac(1-y(t))x(t). \end{cases} \tag{5.1}$$

The linearization of system (2.4) at the disease-free equilibrium gives

$$J\left(\mathcal{E}_0\right) = \begin{pmatrix} -\gamma - \mu_1 & abm \\ \\ ac & -\xi \end{pmatrix}.$$

The right eigenvalues (u_1, u_2) of $J\left(\mathcal{E}_0\right)$ of associated to 0 are given by

$$\begin{pmatrix} -\gamma - \mu_1 & abm \\ \\ ac & -\xi \end{pmatrix} \begin{pmatrix} u_1 \\ \\ u_2 \end{pmatrix} = \begin{pmatrix} 0 \\ \\ 0 \end{pmatrix}. \tag{5.2}$$

We obtain

$$\begin{cases} -\left(\gamma + \mu_1\right)u_1 + abmu_2 = 0, \\ \\ acu_1 - \xi u_2 = 0. \end{cases} \tag{5.3}$$

Since $b = \frac{\xi(\gamma+\mu_1)}{a^2cm}$, the first equation of system (5.3) becomes $acu_1 - \xi u_2 = 0$, therefore

$$u_2 = \frac{ac}{\xi}u_1.$$

Hence,

$$\begin{cases} u_1 > 0, \\ \\ u_2 = \frac{ac}{\xi}u_1 > 0. \end{cases}$$

The left eigenvectors (v_1, v_2) of $J(\mathcal{E}_0)$ associated to 0 are given by

$$\begin{pmatrix} -\gamma - \mu_1 & ac \\ \\ abm & -\xi \end{pmatrix} \begin{pmatrix} v_1 \\ \\ v_2 \end{pmatrix} = \begin{pmatrix} 0 \\ \\ 0 \end{pmatrix}, \tag{5.4}$$

that is

$$\begin{cases} -\left(\gamma + \mu_1\right)v_1 + acv_2 = 0, \\ \\ abmv_1 - \xi v_2 = 0. \end{cases} \tag{5.5}$$

Since $b = \frac{\xi(\gamma+\mu_1)}{a^2cm}$, the first equation of system (5.5) becomes $abmv_1 - \xi v_2 = 0$, therefore

$$v_2 = \frac{\gamma + \mu_1}{ac}v_1.$$

Hence,

$$\begin{cases} v_1 > 0, \\ \\ v_2 = \frac{\gamma+\mu_1}{ac}v_1 > 0. \end{cases} \tag{5.6}$$

By differentiation, we obtain

$$\frac{\partial f_1}{\partial x}(\mathcal{E}_0) = -\gamma - \mu_1,\ \frac{\partial f_1}{\partial y}(\mathcal{E}_0) = abm,\ \frac{\partial f_2}{\partial x}(\mathcal{E}_0) = ac,\ \frac{\partial f_2}{\partial y}(\mathcal{E}_0) = -\xi,$$

$$\frac{\partial^2 f_1}{\partial x^2}(\mathcal{E}_0) = \frac{\partial^2 f_2}{\partial x^2}(\mathcal{E}_0) = \frac{\partial^2 f_1}{\partial y^2} = \frac{\partial^2 f_2}{\partial y^2} = 0,$$

$$\frac{\partial^2 f_1}{\partial x \partial y}(\mathcal{E}_0) = \frac{\partial^2 f_1}{\partial y \partial x}(\mathcal{E}_0) = -abm, \quad \frac{\partial^2 f_2}{\partial y \partial x}(\mathcal{E}_0) = \frac{\partial f_2}{\partial x \partial y}(\mathcal{E}_0) = -ac,$$
$$\frac{\partial^2 f_1}{\partial x \partial b} = \frac{\partial^2 f_2}{\partial x \partial b} = \frac{\partial^2 f_2}{\partial y \partial b} = 0, \ \frac{\partial^2 f_1}{\partial y \partial b} = am.$$

As in [6], we now calculate the values of e_1 and e_2 defined by

$$e_1 = \sum_{k,i,j=1}^{2} v_k u_i u_j \frac{\partial^2 f_k}{\partial x_i \partial x_j} \text{ and } e_2 = \sum_{k;i=1}^{2} v_k \omega_i \frac{\partial^2 f_k}{\partial x_i \partial b}.$$

We have,

$$\begin{aligned} e_1 = & \sum_{k,j=1}^{2} v_k u_1 u_j \frac{\partial^2 f_k}{\partial x_j x_j} + \sum_{k,j=1}^{2} v_k u_2 u_j \frac{\partial^2 f_k}{\partial y_j x_i} \\ = & -2u_1 u_2 a \left(v_1 bm + v_2 c\right) < 0, \end{aligned} \tag{5.7}$$

and

$$\begin{aligned} e_2 = & \sum_{k;i=1}^{2} v_k \omega_i \frac{\partial^2 f_k}{\partial x_i \partial b} \\ = & \sum_{k=1}^{2} v_k u_1 \frac{\partial^2 f_k}{\partial x \partial b} + \sum_{k=1}^{2} v_k u_2 \frac{\partial^2 f_k}{\partial y \partial b} \\ = & v_1 u_2 am > 0. \end{aligned} \tag{5.8}$$

Thus, $e_1 < 0$ and $e_2 > 0$.
By using Theorem 4.1 in [6], the following result hold.

Proposition 5.1. *For $\mathcal{R}_0^h = 1$, the system (2.4) exhibits a backward transcritical bifurcation.*

6. Sensitivity analysis of the parameters

This section aims to examine the impact of several parameters on the basic reproduction number $\mathcal{R}_0^h$, an essential indicator for assessing the potential spread of an infection.
By differentiating $\mathcal{R}_0^h$ with respect to the rates b (the probability of infectious bites per vector), a (the biting rate of humans by a single vector), c (the probability that an infectious bite produces an infectious vector), and m (the average number of vectors per person), we obtain the following partial derivatives:

$$\frac{\partial \mathcal{R}_0^h}{\partial b} = \frac{1}{2\sqrt{b}} \sqrt{\frac{a^2 cm}{\xi\left(\gamma + \mu_1\right)}} > 0, \quad \frac{\partial \mathcal{R}_0^h}{\partial a} = \sqrt{\frac{bcm}{\xi\left(\gamma + \mu_1\right)}} > 0,$$
$$\frac{\partial \mathcal{R}_0^h}{\partial c} = \frac{1}{2\sqrt{c}} \sqrt{\frac{a^2 bm}{\xi\left(\gamma + \mu_1\right)}} > 0, \quad \text{and} \quad \frac{\partial \mathcal{R}_0^h}{\partial m} = \frac{1}{2\sqrt{m}} \sqrt{\frac{a^2 bc}{\xi\left(\gamma + \mu_1\right)}} > 0.$$

The positivity of these partial derivatives show that an increase of the probability of infectious bites per vector b, the biting rate of humans by a single vector a, the probability that an infectious bite produces an infectious vector c, the average number of vectors per person m, contribute to an increase of the basic reproduction number $\mathcal{R}_0^h$. This situation indicates a high spread of the disease, and this can make disease control more challenging.

By differentiating $\mathcal{R}_0^h$ with respect to the rates ξ, μ_1, and γ, we obtain

$$\frac{\partial \mathcal{R}_0^h}{\partial \xi} = -\frac{1}{2\sqrt{\xi}}\sqrt{\frac{a^2bcm}{\gamma+\mu_1}} < 0, \quad \frac{\partial \mathcal{R}_0^h}{\partial \mu_1} = -\frac{1}{2\left(\gamma+\mu_1\right)\sqrt{\gamma+\mu_1}}\sqrt{\frac{a^2bcm}{\xi}} < 0 \text{ and}$$

$$\frac{\partial \mathcal{R}_0^h}{\partial \gamma} = -\frac{1}{2\left(\gamma+\mu_1\right)\sqrt{\gamma+\mu_1}}\sqrt{\frac{a^2bcm}{\xi}} < 0.$$

These show that an increase of the mosquito mortality rate ξ, the maximum per capita recovery rate μ_1, the recovery rate of infected humans γ leads to a decrease of the basic reproduction number $\mathcal{R}_0^h$. Therefore, an increase of these parameters has a positive impact on disease control.

We now focus on identifying the most influential parameters of the model using the partial rank correlation coefficient (PRCC) method. Figure 1 shows the partial rank correlation coefficients for the parameters of model (2.4). A positive value indicates a positive correlation and a negative value indicates a negative correlation. We observe that the most

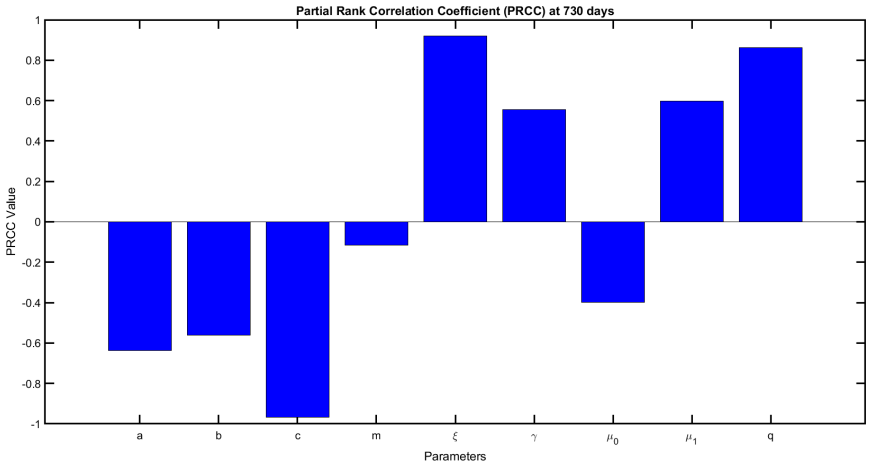

FIGURE 1. Sensitivity of model (2.4) parameters.

influential parameters in the model are the mosquito mortality rate ξ, the recovery rate of infected humans γ, the maximum per capita recovery rate μ_1, and the rate of available medical resources q. This implies that eventual control will depend on these epidemic parameters. These informations can guide health authorities in implementing effective strategies to prevent and control host-vector diseases.

7. CONCLUSION

In this paper, we present a mathematical analysis of a host vectors model that takes into account hospital resources. Many existing models of vector-borne diseases in the literature do not consider hospital resources, even though their inclusion can be essential for a better understanding of the transmission of host vectors diseases. Incorporating hospital resources not only improves the understanding of the mechanisms of disease spread but also offers valuable recommendations to health authorities for the design and implementation of control strategies. The analysis of the model shows the existence of a unique disease-free equilibrium and several endemic equilibria. The disease-free equilibrium is stable if

$\mathcal{R}_0^h$ is less than 1 and unstable when $\mathcal{R}_0^h$ is greater than 1, and in this case, the study reveals the emergence of multiple endemic equilibria, indicating the persistence of the disease despite control efforts. The analysis of the transcritical bifurcation shows changes in stability between equilibrium points. Sensitivity analysis is derived and we found that the most important parameters are the maximum per capita recovery rate due to the sufficient health care resource μ_1, the rate at which infected vectors loose their ability to transmit the infection ξ, the recovery rate of infected humans γ and the rate of available medical resources q. By solving equation $\mathcal{R}_0^h = 1$, we derived a critical recovery rate due to the sufficient health care resource $\mu_1^c = \frac{a^2bcm}{\xi} - \gamma$. If the maximum per capita recovery rate due to the sufficient health care resource μ_1 is greater than μ_1^c, the disease will die out into the population. By integrating the knowledge gained from mathematical modeling with the practical realities of hospital management, we hope to pave the way for more effective and sustainable strategies to host-vectors disease. The current paper constitutes a first step of the work and the future step will be devoted to its validation using real-world data, which can be essential to evaluate the accuracy of the predictions and provide recommendations to optimize control strategies.

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ROSAIRE OUEDRAOGO
LABORATOIRE DE MATHÉMATIQUES ET INFORMATIQUE, UNIVERSITÉ JOSEPH KI-ZERBO, 03 BP 7021 OUAGADOUGOU 03, BURKINA FASO.
ORCID: 0009-0009-8035-9999
Email address: rosaireouedraogo@gmail.com

ALI TRAORÉ
LABORATOIRE DE MATHÉMATIQUES ET INFORMATIQUE, UNIVERSITÉ JOSEPH KI-ZERBO, 03 BP 7021 OUAGADOUGOU 03, BURKINA FASO
ORCID: 0000-0001-6647-7985
Email address: traoreali.univ@yahoo.fr

HAMADOUM DICKO
LABORATOIRE DE MATHÉMATIQUES, INFORMATIQUE ET APPLICATIONS, UNIVERSITÉ NORBERT ZONGO, BP 376 KOUDOUGOU, BURKINA FASO
ORCID: 0009-0006-0153-9042
Email address: dickoh507@gmail.com