A mathematical model analysis of the human melioidosis transmission dynamics with an asymptomatic case

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ABSTRACT

In this paper, we develop and examine a mathematical model of human melioidosis transmission with asymptomatic cases to describe the dynamics of the epidemic. The basic reproduction number ($R_0$) of the model is obtained. Disease-free equilibrium of the model is proven to be globally asymptotically stable when $R_0$ is less than the unity, while the endemic equilibrium of the model is shown to be locally asymptotically stable if $R_0$ is greater than unity. Sensitivity analysis is performed to illustrate the effect of the model parameters influencing on the disease dynamics. Furthermore, numerical experiments of the model are conducted to validate the theoretical findings.

1. Introduction

Melioidosis is a tropical infectious disease caused by an aerobic, gram-negative bacterium called *Burkholderia pseudomallei* (Ross et al., 2018; Mahikul et al., 2019; Saechan et al., 2022). It is reported mostly known as endemic, with a high number of cases and rate of mortality in numerous nations of the world including Thailand, Singapore, Malaysia, India, Bangladesh and China (Currie and Kaestli, 2016; Luangasanatip et al., 2019; Chowdhury et al., 2022). A recent report suggests that *Burkholderia pseudomallei* causes an estimated 165,000 human infections and 89,000 (54%) deaths annually all over the world (Limmathurosatskul et al., 2016; Wiersinga et al., 2018; Sullivan et al., 2020). *B. pseudomallei* is mainly found in contaminated environments (soil or water) (Currie and Kaestli, 2016; Luangasanatip et al., 2019). Infection commonly occurs by ingestion, percutaneous inoculation and inhalation of the organism from a contaminated environment (Luangasanatip et al., 2019; Chowdhury et al., 2022). Although human-to-human transmission is rare, it has been documented through contact with reproductive fluid, blood or other body fluids of an infected person (Benoit et al., 2015; Singh and Mahmood, 2017). Transmissions from humans to animals and vice versa are extremely uncommon and both animals and humans are susceptible to the *B. pseudomallei* (Currie, 2015; Phillips et al., 2016; Mahikul et al., 2019). However, we do not incorporate zoonotic infection of humans in this work.

Melioidosis is a serious infection in humans and it can be presented in a variety of clinical forms, septicemia, asymptomatic infections, localized with/without septicemia, visceral abscesses and can involve any organ (Benoit et al., 2015; Karunaratnha et al., 2018; Chakravorty and Heath, 2019). Currently, there is no vaccine available for the disease (Mahikul et al., 2019; Terefe and Kassa, 2020). Arise up from the clinical manifestation of the melioidosis, a two-phases therapy for the treatment of the *B. pseudomallei* is recommended. An intensive phase of intravenous antibiotics including cefazidime (CAZ), imipenem, or meropenem for a minimum of 10–14 days, followed by an eradication phase to prolonged oral trimethoprim-sulfamethoxazole (TMP-SMX) drug for 3-6 months (Ross et al., 2018; Mahikul et al., 2019; Fen et al., 2021). However, recent studies reported that *B. pseudomallei* is intrinsically susceptible to several classes of antimicrobial agents that are recommended for treatment of the disease including newer β-lactam antibiotics, especially to all intravenous antibiotics (Phillips et al., 2016; Dutta et al., 2017; Sengyee et al., 2017; Fen et al., 2021).

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Further, the epidemiology, clinical manifestations and risk factors of the disease are studied in (Tauran et al., 2015; Limmathurotsakul et al., 2016; Currie and Kenstli, 2016; Hinjoy et al., 2018; Libotte et al., 2020). Some compartmental models have been proposed to address the dynamics of melioidosis transmission from different perspectives. The authors in (Mahikul et al., 2019) studied a susceptible-exposed-infected-recovered-susceptible (SEIRS) model with an asymptomatic class to predict the burden and future trends of the disease incidence in Thailand taking into account population dynamics, seasonal movements, and incidence of diabetes in the human population. In their model the total population is sub grouped into eight classes namely, the susceptible, exposed, asymptomatic infected, symptomatic infected, recovered, diabetic susceptible, severe, and treatment. The authors determined key factors of the disease incidence patterns. The researchers in (Tavaen and Viriyapong, 2019) proposed a susceptible-latently infected-infectious-recovered (SEIR) model for melioidosis transmission by incorporating control factors such as hygiene care and treatment. The results of their work show that both hygiene care and treatment controls should be encouraged to reduce the spread of the disease. An SEIR model for the transmission dynamics of melioidosis is formulated and analyzed in (Terefe and Kassa, 2020). They were incorporated two recrudescence cases of the disease such as relapse and reinfection of individuals from the recovered class in their model.

Motivated by the literature mentioned above, we aim to propose and analyze a compartmental model for the dynamics of melioidosis transmission with an asymptomatic class. We also considered temporary immunity for recovered class in the disease transmission process. The remaining sections of the paper are structured as follows: we present the formulation of the model in Section 2. The qualitative properties of the model solutions, the basic reproduction number and the stability analysis of the steady states are given in Section 3. The sensitivity analysis of the model parameters is performed in Section 4. The numerical results are carried out in Section 5. The concluding results are provided in Section 6.

2. Model formulation

We formulate a compartmental model that describes the dynamic behavior of melioidosis. The model includes two population groups: the human population (host population) and the bacterial (pathogenic) population. The total human population at time $t$ represented by $N(t)$, is subdivided into five distinct classes: susceptible individuals ($S(t)$), latently-infected individuals ($E(t)$), infectious individuals without symptoms ($A(t)$), infectious individuals that are showing symptoms ($I(t)$), and recovered individuals ($R(t)$). Mathematically, the total human population is described as:

$$N(t) = S(t) + E(t) + A(t) + I(t) + R(t).$$

In the formulation of the model, the following assumptions are made:

(i) The new entry for the susceptible human population may be newborns or immigrants at a constant rate of $\Pi$.
(ii) The susceptible humans acquire infection of melioidosis through either percutaneous inoculation, inhalation and ingestion of the pathogen from the contaminated environments (soil or water) or direct contact with infectious (asymptomatic and symptomatic) individuals, and negligible transmission from infected animals.
(iii) The incidence from the environment to humans is assumed to be modeled logistically (saturating), and assumed homogeneous mixing for human to human interaction.
(iv) The symptomatic infectious are greater in number than asymptomatic infectious.

The probability of contact between susceptible humans and contaminated environment is represented by $\lambda_1(B_m) = \frac{B_m}{C+B_m}$, which is a nonlinear function in $B_m$. The constant $C$ is the pathogen concentration that yields 50% chance of catching melioidosis. Thus, the number of contact between the environment and susceptible humans is given by $\lambda_1(B_m)S$. Therefore, the number of infections per unit time due to the environment is given by $\beta_1\lambda_1(B_m)S$, where $\beta_1$ is the transmission rate due to the environment-to-susceptible human interaction. Whereas, the number of infections per unit time due the infectious individuals (asymptomatic and symptomatic) is given by $\beta_2(I + \sigma)A$, where $\beta_2$ is the transmission coefficient of the disease due to human-to-human interaction and $\sigma$ is the reduction in infectivity of $A$ with, $0 < \sigma < 1$. Therefore, the number of susceptible humans infected by the disease per unit time given by $\lambda S$ and join $E$, where $\lambda = \beta_1\lambda_1(B_m) + \beta_2(I + \sigma A)$ is the force of infection. The individuals in $E$ progress to $I$ with probability $\theta_e$ and to the $A$ with probability $\theta_a$, and the $A$ with probability $(1 - \theta)$. $B_m$ increases its size in the contaminated environment by $A$ and $I$ with the shedding rate $\eta$. Further, the description of the model parameters is summarized in Table 1. We obtained the following system of differential equations from schematic diagram of the melioidosis model in Fig. 1.

\[
\begin{align*}
\frac{dS}{dt} &= \Pi + aR - (\lambda + \mu)S, \\
\frac{dE}{dt} &= \lambda S - (\rho + \mu)E, \\
\frac{dA}{dt} &= (1 - \theta)\rho E - (\delta + \gamma_1 + \mu)A, \\
\frac{dI}{dt} &= \theta_\rho E - (\delta + \gamma_2 + \mu)I, \\
\frac{dR}{dt} &= \gamma_1 A + \gamma_2 I - (\alpha + \mu)R, \\
\frac{dB_m}{dt} &= \eta(A + I) - \mu_0 B_m.
\end{align*}
\]

Where, $\lambda = \frac{\beta_1\lambda_1(B_m)}{C+B_m} + \beta_2(I + \sigma A)$.

With the initial conditions:

\[
S(0) = S_0 \geq 0, \quad E(0) = E_0 \geq 0, \quad A(0) = A_0 \geq 0, \quad I(0) = I_0 \geq 0, \quad R(0) = R_0 \geq 0, \quad B_m(0) = B_{m,0} \geq 0.
\]
### Table 1. Description of parameters of model.

| Parameter | Description |
|-----------|-------------|
| \( R \)  | Human recruitment rate. |
| \( \beta_1 \) | Transmission rate among environment and susceptible humans. |
| \( \beta_2 \) | Transmission rate among susceptible and infectious humans. |
| \( \mu \)  | Natural death rate of individuals. |
| \( \nu_1 \) | Natural death rate of bacteria. |
| \( \sigma \) | Disease waning immunity. |
| \( \delta \) | Disease-induced death rate of \( A \) and \( I \). |
| \( \rho \)  | Progression rate from latent infected to infectious classes. |
| \( \gamma_1 \) | Recovery rate from asymptomatic infectious. |
| \( \gamma_2 \) | Recovery rate from symptomatic infectious. |
| \( \eta \)  | Rate at which bacteria increase by \( A \) and \( I \). |

3. Model analysis

3.1. Positivity of solutions

For our model (2) to be epidemiologically meaningful, we have established the following nonnegativity result for all of its state variables.

**Theorem 3.1.** If \( S(0), E(0), A(0), I(0), R(0), \) and \( \text{B}_m(0) \) are positive initial conditions for the melioidosis model (2), then the solution \( (S(t), E(t), A(t), I(t), R(t), \text{B}_m(t)) \) of the model (2) is positive for all \( t > 0 \).

**Proof.** Let \( t_1 = \text{sup}\{ t > 0: S(t_1), E(t_1), A(t_1), I(t_1), R(t_1), \text{B}_m(t_1) \} \) are all positive, \( \forall t \in [0, t_1) \}. Note that \( t_1 > 0 \) for non-negative initial conditions. From the first equation of (2), we have

\[
\frac{dS}{dt} + (\lambda + \mu)S = \Pi + aR. \tag{3}
\]

Now using the variation formula to the equation (3) at \( t_1 > 0 \), we get

\[
S(t_1) = e^{\int_0^{t_1} (\lambda + \mu-s)(r)ds} \times \int_0^{t_1} e^{\int_s^{t_1} (\lambda + \mu-s)(r)dr} \times (\Pi + aR(s)ds + S(0)e^{-\int_0^{t_1} (\lambda + \mu-s)(r)dr} > 0.
\]

In the same manner, it can be demonstrated that \( E(t) > 0, A(t) > 0, I(t) > 0, R(t) > 0 \) and \( \text{B}_m(t) > 0, \forall t > 0 \). As a result, for all positive initial conditions, all solutions of the model (2) remain positive.

3.2. Invariant region

In this section, we need to establish a biologically feasible region in which the model (2) solution is bounded. The feasible region of the model equation (2) is stated as follows.

**Lemma 3.2.** Every solution of the model (2) remains in the closed set, \( \Omega_m = \{ (S, E, A, I, R, \text{B}_m) \in R^6_+: 0 \leq N(t) \leq \frac{H}{\mu} 0 \leq \text{B}_m(t) \leq \frac{aH}{\rho_2 \rho_3} \} \).

**Proof.** From the equations (1) and (2), we obtain

\[
\frac{dN}{dt} = H - \mu N - \delta (A + I) \leq H - \mu N = \mu (\frac{H}{\mu} - N). \tag{4}
\]
Note that if $N \leq \frac{\Pi}{\mu}$, then $\frac{dN}{dt} \geq 0$ and $\frac{dN}{dt} < 0$ whenever $N > \frac{\Pi}{\mu}$. Thus, by using the standard comparison theorem in (Lakshmikantham et al., 1989) and variation of formula to the differential inequality (4), we get

$$N(t) \leq N(0)e^{-\mu t} + \frac{\Pi}{\mu} (1 - e^{-\mu t}).$$

It follows that,

$$0 \leq \lim_{t \to \infty} \sup N(t) \leq \frac{\Pi}{\mu}.$$ 

In particular, if $N(0) \leq \frac{\Pi}{\mu}$, then $N(t) \leq \frac{\Pi}{\mu} \forall t > 0$. Similarly, from the last equation of (2), we found that

$$B_m(t) \leq B_m(0)e^{-\mu t} + \frac{\eta \Pi}{\mu \beta} (1 - e^{-\mu t}) \forall t > 0.$$ 

This implies that

$$0 \leq \lim_{t \to \infty} \sup B_m(t) \leq \frac{\eta \Pi}{\mu \beta}.$$ 

Therefore, $0 \leq B_m(t) \leq \frac{\eta \Pi}{\mu \beta}$ whenever, $0 \leq B_m(0) \leq \frac{\eta \Pi}{\mu \beta} \forall t > 0$.

Furthermore, if $N(0) > \frac{\Pi}{\mu}$ ($B_m(0) > \frac{\eta \Pi}{\mu \beta}$, respectively), then either the solution enters the region $\Omega_m$ in finite time or $N(t) \to \frac{\Pi}{\mu}$ ($B_m(t) \to \frac{\eta \Pi}{\mu \beta}$, respectively) asymptotically as $t \to \infty$. Consequently, the region is positively invariant and attracts all solutions of the system (2) and it suffices to consider the dynamics of the model (2) in $\Omega_m$.

### 3.3. Disease free equilibrium

The disease-free equilibrium (DFE) point is a point where no disease is present in the population. Since all states are considered to have a constant solution at the equilibrium point, we can then compute DFE by setting the right-hand equations in the system ODE (2) to zero and substituting zero for infective and causative agent classes. Therefore, the DFE point of the system (2) is given by

$$e_n^* = (S^*, 0, 0, 0, 0) = \left( \frac{\Pi}{\mu}, 0, 0, 0, 0 \right).$$

### 3.4. The basic reproductive number and local stability of the DFE

The basic reproduction (or reproductive) number ($R_n$) is a key concept in epidemiology that provides information on the status of the disease. To derive, $R_n$, we use the next-generation matrix approach introduced in (Van den Driessche and Watmough, 2002). Based on the method of Van den Driessche and Watmough in (Van den Driessche and Watmough, 2002) the infected compartments of our model are given in the following sub-system:

$$\begin{align*}
\frac{dE}{dt} &= \lambda S - (\rho + \mu)E, \\
\frac{dA}{dt} &= -(1-\theta)\rho E - (\delta + \gamma_1 + \mu)A, \\
\frac{dI}{dt} &= \theta \rho E - (\delta + \gamma_2 + \mu)I, \\
\frac{dB_m}{dt} &= \eta (A + I) - \mu \beta B_m. 
\end{align*}$$

Consider that $F(t)$ is the rate of appearance of new infections in compartment $i$ and $V(t)$ is the rate of transfer of individuals into and out of compartment $i$, for, $i = 1, 2, 3, 4$. Thus, the column matrices $F(t)$ and $V(t)$ associated with the system ODE (6), are given by:

$$F(t) = \begin{bmatrix} F_1(t) \\ F_2(t) \\ F_3(t) \\ F_4(t) \end{bmatrix}, \quad V(t) = \begin{bmatrix} V_1(t) \\ V_2(t) \\ V_3(t) \\ V_4(t) \end{bmatrix}.$$

Thus, the associated Jacobian matrices of $F(t)$ and $V(t)$ at $e_n^*$ are found as follows:

$$F = \begin{bmatrix} \frac{\beta_1 \Pi}{\mu} & \frac{\beta_2 \Pi}{\mu} & \frac{\beta_3 \Pi}{\mu} & \frac{\beta_4 \Pi}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} \rho + \mu & 0 & 0 & 0 \\ 0 & \rho + \mu & 0 & 0 \\ 0 & 0 & \delta + \gamma_1 + \mu & 0 \\ 0 & 0 & 0 & \delta + \gamma_2 + \mu \end{bmatrix}.$$ 

Now, the next generation matrix of the model (2) is the product of $F$ and $V^{-1}$. Computing the product $FV^{-1}$, yields

$$FV^{-1} = \begin{bmatrix} 0 & \frac{\beta_1 \Pi}{\mu} & \frac{\beta_2 \Pi}{\mu} & \frac{\beta_3 \Pi}{\mu} & \frac{\beta_4 \Pi}{\mu} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ \frac{\rho + \mu}{\mu \beta} & \frac{\beta_1 \Pi}{\mu \beta} & \frac{\beta_2 \Pi}{\mu \beta} & \frac{\beta_3 \Pi}{\mu \beta} & \frac{\beta_4 \Pi}{\mu \beta} \end{bmatrix} = \begin{bmatrix} a_1 & a_2 & a_3 & a_4 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}.$$
\[ a_1 = \Pi \rho \left[ \theta \beta_1 (C \beta_2 \mu_1 + \eta \beta_1) + (1-\theta) x_2 (C \beta_2 \sigma \mu_2 + \eta \beta_1) \right], \quad a_2 = \frac{\Pi \beta_1 \eta + C \beta_2 \sigma \mu_2}{C \mu_2 \nu \epsilon_2 (\rho + \mu)}, \quad a_3 = \frac{\Pi \beta_1 \eta + C \beta_2 \mu_2 \nu \epsilon_1}{C \mu_2 \epsilon_2}, \quad a_4 = \frac{\Pi \beta_1}{C \mu_2}, \quad \epsilon_1 = \delta + \gamma_1 + \mu, \quad \epsilon_2 = \delta + \gamma_2 + \mu. \]

Thus, the eigenvalues of the next generation matrix \( (FV^{-1}) \) are
\[ \lambda_1 = \frac{\Pi \rho \left[ \theta \beta_1 (C \beta_2 \mu_1 + \eta \beta_1) + (1-\theta) x_2 (C \beta_2 \sigma \mu_2 + \eta \beta_1) \right]}{C \mu_2 \nu \epsilon_2 (\rho + \mu)}, \quad \lambda_2 = \lambda_3 = \lambda_4 = 0. \]

The required basic reproduction number of the model equation (2) is found through the spectral radius of the matrix \( R_0 = \rho(FV^{-1}) = \lambda_1 \). Hence,
\[ R_0 = \frac{\Pi \rho \beta_1 \left[ \theta (\delta + \gamma_1 + \mu) + \sigma (1-\theta) (\delta + \gamma_2 + \mu) \right]}{\mu (\rho \mu + \delta + \gamma_1 + \mu)(\delta + \gamma_2 + \mu)}. \]

The equation (7) can be written as
\[ R_0 = R_{0h} + R_{0b}. \]

Where,
\[ R_{0h} = \frac{\Pi \rho \beta_1 \left[ \theta (\delta + \gamma_1 + \mu) + \sigma (1-\theta) (\delta + \gamma_2 + \mu) \right]}{\mu (\rho + \mu)(\delta + \gamma_1 + \mu)(\delta + \gamma_2 + \mu)}, \]

is the basic reproduction number due to human-to-human transmission, and
\[ R_{0b} = \frac{\Pi \rho \beta_1 \left[ \theta (\delta + \gamma_1 + \mu) + (1-\theta) (\delta + \gamma_2 + \mu) \right]}{C \mu_2 (\rho + \mu)(\delta + \gamma_1 + \mu)(\delta + \gamma_2 + \mu)}, \]

is the basic reproduction number due to environment-to-human transmission.

Based on the Theorem 2 by (Van den Driessche and Watmough, 2002), we have the following standard result for the local stability of the DFE, \( \epsilon_0^* \).

**Theorem 3.3** (Local stability of the DFE). The DFE, \( \epsilon_0^* \), of the model (2) is locally asymptotically stable if \( R_0 < 1 \) and unstable if \( R_0 > 1 \).

### 3.5. Global stability of the DFE

We use the method presented in (Castillo-Chavez et al., 2002; Liao and Wang, 2011; Kanyi et al., 2021) to examine the global stability of the DFE of the model (2). We first denote the system (2) by
\[
\begin{align*}
\frac{dX_1}{dt} &= G_1(X_1, X_2), \\
\frac{dX_2}{dt} &= G_2(X_1, X_2), \quad G(X_1, 0) = 0,
\end{align*}
\]

where \( X_1 = (S, R) \) denotes uninfected classes and \( X_2 = (E, A, I, B_n) \) represents the infected classes including the bacterial population class. The DFE point of the model, \( \epsilon_0^* = (\frac{\epsilon}{\mu}, 0, 0, 0, 0, 0) \), is guaranteed to be globally asymptotically stable (GAS) if \( R_0 < 1 \) (which is locally asymptotically stable) and the following two conditions \( C_1 \) and \( C_2 \) hold:

\( C_1 \): For \( \frac{dX_1}{dt} = G_1(X_1, 0) \), if \( X_1^* = \left( \frac{\epsilon}{\mu}, 0 \right) \) is GAS, where \( X_1^* \) is DFE point of the system \( \frac{dX_1}{dt} \).

\( C_2 \): \( G_2(X_1, X_2) = AX_2 - G^*_2(X_1, X_2), G^*_2(X_1, X_2) \geq 0, \forall (X_1, X_2) \in \Omega \), where \( A \) is an M-matrix which is given by \( A = \frac{\partial G_2(X_1, 0)}{\partial X_2} \). Note that \( (X_1^*, 0) = \epsilon_0^* = (\frac{\epsilon}{\mu}, 0, 0, 0, 0, 0) \).

**Theorem 3.4.** The DFE, \( \epsilon_0^* \), given by (5), is GAS (2) provided that \( R_0 < 1 \).

**Proof.** We simply need to demonstrate that the criteria \( C_1 \) and \( C_2 \) are true when \( R_0 < 1 \). In the system of the model equation (2), we have
\[ G_1(X_1, 0) = \left[ \begin{array}{c} \Pi + aR - \mu S \\ -(a + \mu)R \end{array} \right], \quad X_1^* = \left( \frac{\epsilon}{\mu}, 0 \right). \]

We note that \( R(t) = R_0 e^{-(a+\mu)t} \). Also, \( S' = \Pi + aR - \mu S \), and equation (8) yields, \( S(t) = \Pi + aR_0 e^{-(a+\mu)t} - \mu S \) and its solution is given by
\[ S(t) = \frac{\Pi}{\mu} + S_0 e^{-\mu t} - R_0 e^{-(a+\mu)t}. \]

Now, consider \( t \to \infty \), to show \( X_1 \to X_1^* \). Clearly, \( R(t) \to 0 \) and \( S(t) \to \frac{\Pi}{\mu} \) as \( t \to \infty \), regardless of the values of \( R_0 \) and \( S_0 \). As a result, all points that satisfy these criteria converge to \( X_1^* = (\frac{\epsilon}{\mu}, 0) \). Hence, \( X_1^* = (\frac{\epsilon}{\mu}, 0) \) is GAS.
Next, consider

\[ G_2(X_1, X_2) = \begin{bmatrix} G_{21}(X_1, X_2) \\ G_{22}(X_1, X_2) \\ G_{23}(X_1, X_2) \end{bmatrix} = \begin{bmatrix} \beta_1 \left( \frac{B_m}{C + B_m} \right) S + \beta_2 (I + \sigma A) S - (\rho + \mu) E \\ (1 - \theta) \rho E - (\delta + \gamma_1 + \mu) A \\ \theta \rho E - (\delta + \gamma_2 + \mu) I \\ \eta(A + I) - \mu_B B_m \end{bmatrix}, \]

and \( G_2(X_1, X_2) = AX_1 + G_2^*(X_1, X_2) \). Where,

\[
A = \begin{bmatrix} -(\rho + \mu) & \frac{\rho \sigma B_m}{\mu} & \frac{\beta_1 B_m}{C} & \frac{\beta_1 B_m}{C} \\ (1 - \theta) \rho & -(\delta + \gamma_1 + \mu) & 0 & 0 \\ \theta \rho & 0 & -\left(\delta + \gamma_2 + \mu\right) & 0 \\ 0 & \eta & \eta & -\mu_B \end{bmatrix}, \quad \text{and} \quad G_2^*(X_1, X_2) = \begin{bmatrix} \Delta \\ 0 \\ 0 \\ 0 \end{bmatrix},
\]

with, \( \Delta = \beta_2 (I + \sigma A) \left( \frac{B_m}{I - S} \right) + \frac{\delta_1 B_m}{C} \left( \frac{B_m}{I - C + B_m} \right) \).

We have, \( 0 \leq \frac{CS}{C + B_m} \leq S \leq \frac{C}{\rho} (\frac{C}{C + B_m} \leq 1 \text{ and all parameters are nonnegative}) \). As a result, \( \left( \frac{B_m}{I - S} \right) \geq 0 \) and \( \left( \frac{B_m}{I - C + B_m} \right) \geq 0 \). Thus, \( G_2^*(X_1, X_2) \geq 0 \) \( \forall (X_1, X_2) \in \Omega_m \). Therefore, the DFE, \( e_0^* = (\mu, 0, 0, 0, 0) \), of the system (2) is GAS.

**Remark 1.** The model (2) does not show a backward bifurcation at \( R_0 = 1 \) when \( R_0 < 1 \). According to Theorem 3.4, the only positive (or stable) steady state for \( R_0 < 1 \) is DFE. This is because some typical cases of backward bifurcation in epidemic models weren’t considered in our model.

The common causes for the existence of backward bifurcation in some standard deterministic models including reinfection have been studied in (Elbashri et al., 2011; Gumel, 2012). For instance, backward bifurcation has been seen in the melioidosis epidemic model (Terefe and Kassa, 2020) due to reinfection and relapse of recovered individuals.

### 3.6. Endemic equilibrium

An endemic equilibrium (EE) point is a state where the disease remains in the population. By setting the system (2) equal to zero at steady state, the EE point of our model is obtained. Thus,

\[
\begin{aligned}
\frac{dS^*}{dt} &= \Pi + a R^* - \left( \beta_2 \frac{B_m}{C + B_m} + \beta_2 (I^* + \sigma A^*) + \mu \right) S^* = 0, \\
\frac{dE^*}{dt} &= (\beta_1 \frac{B_m}{C + B_m} + \beta_2 (I^* + \sigma A^*)) S^* - (\rho + \mu) E^* = 0, \\
\frac{dA^*}{dt} &= (1 - \theta) \rho E^* - (\delta + \gamma_1 + \mu) A^* = 0, \\
\frac{dI^*}{dt} &= \theta \rho E^* - (\delta + \gamma_2 + \mu) I^* = 0, \\
\frac{dB_m^*}{dt} &= \eta (A^* + I^*) - \mu_b B_m^*.
\end{aligned}
\]

From the equations in (9), solving the other state variables in terms of \( I^* \), we found the EE of the model (2) as:

\[
e_1^* = (S^*, E^*, A^*, I^*, R^*, B_m^*) = \left( \Pi + a \frac{R^*}{I^* + \lambda} \right) \left( \frac{1 - \theta}{\theta e_1} \right) I^* \left( \frac{\eta (1 - \theta) e_2 + \eta \theta e_1}{\mu B_m e_1} \right) I^* \left( \frac{\eta (1 - \theta) e_2 + \eta \theta e_1}{\mu B_m e_1} \right) I^*.
\]

Where, \( e_1 = (\delta + \gamma_1 + \mu), e_2 = (\delta + \gamma_2 + \mu) \). Then by substituting all the right-hand side expressions in (10) into the second equation of the system (9), we found the following quartic equation for \( I^* \):

\[
P_m(I^*) = I^* (A I^* + B I^* + C I^* + D) = 0.
\]

Where,

\[
A = -\beta_2 e_1 \theta^2 \eta^2 \left[ (\theta e_1 + \sigma (1 - \theta) e_2) \right] \left[ \sigma (\Pi - (1 - \theta) e_2 + \gamma_2 \theta e_1 - (\rho + \mu) (\sigma + \mu) e_1 e_2) \right],
\]

\[
B = -\beta_2 e_1 \eta^2 \left( \theta e_1 + \sigma (1 - \theta) e_2 \right) \left( \theta e_1 + \sigma (1 - \theta) e_2 \right),
\]

\[
C = -\beta_2 e_1 \eta^2 \left( \theta e_1 + \sigma (1 - \theta) e_2 \right),
\]

\[
D = \theta^3 e_1 (\sigma + \mu) (\rho + \mu) C^2 \mu e_1 e_2 (R_0 - 1) > 0 \quad \text{if} \quad R_0 > 1,
\]

with,
\[
\begin{align*}
\Psi_1 &= \alpha \rho \left( \gamma_1 (\delta + \mu) + \gamma_2 (1 - \theta) (\delta + \mu) + \epsilon_1 \epsilon_2 (\rho + \alpha + \mu) \right), \\
\Psi_2 &= \beta_1 \eta (\theta \epsilon_1 + (1 - \theta) \epsilon_2) + 2\beta_2 \mu \theta (\theta \epsilon_1 + \epsilon_2). \\
\Psi_3 &= \eta (\alpha + \mu) (\theta \epsilon_1 + (1 - \theta) \epsilon_2) (\rho + \mu) \mu \epsilon_1 \epsilon_2 (1 - R_0). \\
\Psi_4 &= \beta_1 \eta (\theta \epsilon_1 + (1 - \theta) \epsilon_2) + \beta_2 \mu \theta (\theta \epsilon_1 + \epsilon_2). \\
\Psi_5 &= \eta (\alpha + \mu) (\theta \epsilon_1 + (1 - \theta) \epsilon_2) (\rho + \mu) \mu \epsilon_1 \epsilon_2 (1 - R_0 + 1 - R_0). \\
\epsilon_1 &= (\delta + \gamma_1 + \mu), \quad \epsilon_2 = (\delta + \gamma_2 + \mu).
\end{align*}
\]

The zero root of the equation (11) corresponds to the DFE. It is worth noting that the coefficient A is always negative, the coefficients B and C are negative if \( R_0 \leq 1 \), and D is negative or positive if \( R_0 \) is less than unity or greater than unity, respectively. Moreover, when \( R_0 = 1 \), then D is zero (or has no sign) and the equation (11) is reduced to quadratic equation, \( A(T^*)^2 + B(T^*) + C = 0 \). So that the quartic equation (11) can be analyzed for the possibility of multiple equilibria. We used the Descartes’ rule of signs presented in (Levin, 2020) to analyze the existence of possible positive roots of the polynomial equation (11). This is described in Table 2. Hence, we have established the following result for the existence of the EE.

**Theorem 3.5 (Existence of the EE).** The model (2)
(i) has a unique positive endemic equilibrium if the case (1, 2, or 3) is satisfied,
(ii) has a unique positive endemic equilibrium or three positive endemic equilibria if the case 4 is satisfied,
(iii) has no positive endemic equilibrium if \( R_0 \leq 1 \).

**Theorem 3.6 (Local stability of the EE).** The endemic equilibrium, \( e_1^*, e_2^* \), of the model (2), described in the equation (14), is locally asymptotically stable for \( R_0 > 1 \).

**Proof.** We use the technique presented in (Castillo-Chavez and Song, 2004), to show the existence of forward bifurcation. The following change for the state variables of the model (3) is performed to implement the procedure. Suppose, \( S = x_1, E = x_2, A = x_3, I = x_4, R = x_5, \) and \( B_a = x_6 \).

Thus, the vector notation for the variables is given by

\[
X = (x_1, x_2, x_3, x_4, x_5, x_6)^T.
\]  

Using the vector notation in (12), the system (2) can be expressed as

\[
\frac{dX}{dt} = F(X), \quad \text{where} \quad F = (f_1, f_2, f_3, f_4, f_5, f_6)^T.
\]  

Hence, the equation (13) can be rewritten as:

\[
\begin{align*}
\frac{dx_1}{dt} &= \Pi + \alpha x_5 - \left( \beta_1 \frac{x_5}{x_5 + x_6} + \beta_2 (x_4 + \sigma x_3) + \mu \right) x_1 = f_1, \\
\frac{dx_2}{dt} &= \left( \beta_1 \frac{x_5}{x_5 + x_6} + \beta_2 (x_4 + \sigma x_3) \right) x_1 - (\rho + \mu) x_2 = f_2, \\
\frac{dx_3}{dt} &= (1 - \theta) \rho x_2 - (\delta + \gamma_1 + \mu) x_3 = f_3, \\
\frac{dx_4}{dt} &= \theta \rho x_2 - (\delta + \gamma_2 + \mu) x_4 = f_4, \\
\frac{dx_5}{dt} &= (\gamma_1 + \gamma_2) x_4 - (\alpha + \mu) x_5 = f_5, \\
\frac{dx_6}{dt} &= \eta (x_3 + x_4) - \mu_0 x_6 = f_6.
\end{align*}
\]  

Suppose that \( \beta_1 = \beta_1^* \) is chosen as bifurcation parameter and computing for \( \beta_1^* \) for \( R_0 = 1 \), we found that

\[
\beta_1^* = \frac{(\rho + \mu) \mu \alpha \epsilon_1 \epsilon_2 - C \mu \beta_1 \Pi \rho \theta \epsilon_1 + \sigma(1 - \theta) \epsilon_2)}{\Pi \rho \theta \epsilon_1 + (1 - \theta) \epsilon_2}.
\]

Then, the Jacobian matrix of the system of equations (14) computed at \( (e_1^*, \beta_1^*) \) is given by

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**Table 2.** Possible positive roots of \( P_n(T^*) \) for \( R_0 > 1, R_0 < 1 \) and \( R_0 = 1 \).

| Cases | A | B | C | D | \( R_0 \) | No. of sign changes | No. of possible positive real roots |
|-------|---|---|---|---|--------|-------------------|-----------------------------------|
| 1     | - | + | + | + | \( R_0 > 1 \) | 1                 | 1                                 |
| 2     | - | - | + | + | \( R_0 > 1 \) | 1                 | 1                                 |
| 3     | - | + | + | + | \( R_0 > 1 \) | 1                 | 1                                 |
| 4     | - | + | - | + | \( R_0 > 1 \) | 3                 | 1, 3                             |
| 5     | - | - | - | - | \( R_0 < 1 \) | 0                 | 0                                 |
| 6     | - | - | - | 0 | No sign | \( R_0 = 1 \) | 0                                 |

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where, $J_1 = \frac{e_0 + H}{\mu}$, $J_2 = \frac{2}{\mu}$, $J_3 = \frac{e_0 \rho}{\mu}$, $J_4 = (\rho + \mu)$, $J_5 = (1 - \theta)\rho$, $J_6 = \delta + \gamma_1 + \mu$, $J_7 = \theta\rho$, $J_8 = \delta + \gamma_2 + \mu$, $J_9 = (\alpha + \mu)$.

The characteristic polynomial equation of $J(e_{\lambda}^0, \beta_1^*)$ is obtained as

$$P(\lambda) = |J(e_{\lambda}^0, \beta_1^*) - \lambda I| = \lambda^3 + B_1 \lambda^2 + B_2 \lambda + B_3.$$  \hfill (15)

With,

$$B_1 = J_4 + J_6 + J_8 + \mu_b,$$

$$B_2 = J_3 J_8 + J_4 H_3 + J_6 H_3 + J_8 J_6 - J_1 J_8 - J_2 J_7,$$

$$B_3 = J_3 J_6 J_8 + J_4 J_6 H_3 + J_6 J_5 H_3 - J_1 J_3 J_8 - J_2 J_2 J_7 - J_1 J_3 J_6 - J_2 J_2 J_5 - J_4 H_4 - J_3 J_7.$$  

Obviously, $\lambda_1 = 0$, $\lambda_2 = -\mu$, $\lambda_3 = -\alpha - \mu$ are the three eigenvalues of $J(e_{\lambda}^0, \beta_1^*)$. The other eigenvalues are the roots the polynomial $P_3(\lambda)$. Based on the Routh’s criterion in Equation 5.1 by Martcheva (2015), for the roots of the polynomial $P_3(\lambda)$ in (15) to have negative real parts the following conditions must be satisfied: $B_1 > 0$, $B_2 > 0$, $B_3 > 0$ and $B_1 B_2 - B_3 > 0$. Clearly, the first condition, $B_1 = J_4 + J_6 + J_8 + \mu_b = (\delta + \gamma_1 + \mu) + (\delta + \gamma_2 + \mu) + (\rho + \mu) + (\rho + \mu) + (\rho + \mu) > 0$.

Now, we need to show the remaining three conditions. After several algebraic manipulations for the parameters of the coefficients $B_2$, $B_3$, and of the expression $B_1 B_2 - B_3$, we found

$$B_2 = Q_1 + Q_2 + Q_3 > 0, \text{ if } R_0 \leq 1 \text{ where, } Q_1 = \mu(J_4 + J_6 + J_8) + J_6 J_8 > 0,$$

$$Q_2 = \frac{1}{\mu} \left( \mu J_6 J_8 - \mu J_7 \right) > 0 \text{ if } R_0 \leq 1, \quad Q_3 = \frac{1}{\mu} \left( \mu J_3 J_8 - \mu J_5 \right) > 0 \text{ if } R_0 \leq 1,$$

$$B_3 = P_1 + P_2 + P_3 + P_4 > 0, \text{ for } R_0 \geq 1 \text{ where, } P_1 = J_6 J_8 \mu_b > 0,$$

$$P_2 = \frac{1}{C_{\mu_b}} \left( C_{\mu_b} \mu J_3 J_7 - \mu J_8 \right), \text{ for } R_0 \leq 1,$$

$$P_3 = \frac{1}{C_{\mu_b}} \left( C_{\mu_b} \mu J_5 J_8 - \mu J_7 \right) \text{ for } R_0 \leq 1,$$

$$P_4 = \frac{1}{\mu} \left( \mu J_3 J_7 \mu_b - \mu J_4 \right) \text{ for } R_0 \leq 1,$$

$$B_1 B_2 - B_3 = A_3 (J_5 + \mu_b) + J_5 (J_6 \mu_b + J_8 \mu_b + J_6 J_8) + \mu(J_7 + J_5 J_7) + J_8 (J_6 \mu_b + J_8 \mu_b + J_6 J_8) > 0 \text{ if } R_0 \leq 1.$$

Consequently, zero is a simple eigenvalue of $J(e_{\lambda}^0, \beta_1^*)$ and all other eigenvalues of $J(e_{\lambda}^0, \beta_1^*)$ have negative real numbers or real parts. Therefore, the center manifold theory (Carr, 2012) can be used to study the dynamics of (14) near $\beta_1^*$. Furthermore, it can be computed that $J(e_{\lambda}^0, \beta_1^*)$ has a right eigenvector corresponding to zero eigenvalue, given by $U = (u_1, u_2, u_3, u_4, u_5, u_6)^T$, where

$$u_1 = -\frac{u_2 (\rho + \mu) J_6 J_8}{\mu J_6 J_8 (a \rho J_6 J_8 + (\rho + \mu) J_6 J_8 + \rho J_6 J_8 + \rho (a J_6 J_8 + J_6 J_8)) < 0,}

$$u_2 = 0, \quad u_3 = \frac{(1 - \theta) J_8}{\theta J_8}, \quad u_4 = \frac{(1 - \theta) J_8}{\theta J_8},

$$u_5 = \frac{\gamma_1 \rho J_6 J_8 + \gamma_2 \rho J_6 J_8}{(a + \mu) J_6 J_8}, \quad u_6 = \frac{\eta \rho J_6 J_8 + (1 - \theta) J_8}{\eta J_6 J_8 J_8}.$$

Where, $J_8 = \delta + \gamma_1 + \mu$, $J_9 = \delta + \gamma_2 + \mu$.

Likewise, $J(e_{\lambda}^0, \beta_1^*)$ has a left eigenvector, $V = (v_1, v_2, v_3, v_4, v_5, v_6)^T$ associated with $\lambda = 0$, satisfying the condition $U^T V = 1$, with

$$v_1 = 0, \quad v_2 = v_2 > 0, \quad v_3 = \frac{\Pi (\beta_1 J_6 C + \beta_1^* \eta)}{C_{\beta_1 C} J_6}, \quad v_4 = \frac{\Pi (\beta_1 J_6 C + \beta_1^* \eta)}{C_{\beta_1 C} J_6}, \quad v_5 = 0, \quad v_6 = \frac{\beta_1^* \Pi}{C_{\beta_1 C} \beta_1 J_6}.$$

Computations of $a$ and $b$: The local stability of $e_{\lambda}^*$ for $R_0 > 1$, but near to the unity is determined by the signs of two associated constants $a$ and $b$, where

$$a = \sum_{k=1}^{6} v_k u_k u_k \frac{\partial^2 f_k}{\partial x_k \partial x_k}(e_{\lambda}^0, \beta_1^*),$$

$$b = \sum_{k=1}^{6} v_k u_k \frac{\partial^2 f_k}{\partial x_k \beta_1^*}(e_{\lambda}^0, \beta_1^*).$$
Since $R_0 = 1$, $v_2 > 0$, $1 - \theta > 0$, and all parameters are positive. After some algebraic manipulations, we obtained:

$$a = -v_2\beta_2 \left( \frac{\mu + \alpha}{\mu} \right) \left( \frac{\eta \rho [\theta(\delta + \gamma_1 + \mu) + (1 - \theta)(\delta + \gamma_2 + \mu)]}{\mu \beta_2 + \gamma_1 + \mu(\delta + \gamma_2 + \mu)} \right) < 0, \quad \text{always}$$

where,

$$\phi = \frac{\eta \rho \beta_2 \left[ \theta(\delta + \gamma_1 + \mu) + (1 - \theta)(\delta + \gamma_2 + \mu) \right]}{\mu \beta_2 + \gamma_1 + \mu(\delta + \gamma_2 + \mu)} > 0,$$

and,

$$\frac{\partial^2 f_2}{\partial \alpha \partial \beta_1} (\varepsilon^*_0, \beta^*_0) = v_2 \beta_2 \left( \frac{\eta \rho \beta_2 \left[ \theta(\delta + \gamma_1 + \mu) + (1 - \theta)(\delta + \gamma_2 + \mu) \right]}{\mu \beta_2 + \gamma_1 + \mu(\delta + \gamma_2 + \mu)} \right) > 0, \quad \text{always}.$$  

Based on the computed value of $a$ and $b$, and with the help of Theorem 4.1 by Chavez and Song in (Castillo-Chavez and Song, 2004), the model exhibits a forward bifurcation at $R_0 = 1$ (see Fig. 2), and hence, the EE is locally asymptotically stable for $R_0 > 1$, but close to 1. The biological consequence of this is that the melioidosis disease can be eliminated from a community as long as $R_0 < 1$. This completes the proof.

4. Sensitivity analysis

The sensitivity analysis for the basic reproduction number, $R_0$, of the melioidosis model parameters is performed following the approach in (Chitnis et al., 2008; Rosa and Torres, 2018; Aldila and Angelina, 2021; Purwati et al., 2020; Engida et al., 2022). This helps us to identify the parameters with a high impact on $R_0$ and also helps in providing appropriate intervention strategies. To measure the sensitivity of $R_0$ with respect to the model parameters we use a normalized forward sensitivity index of $R_0$, which is defined as the ratio of the relative change in the $R_0$ to the relative change in the parameter.

**Definition 4.1.** The normalized forward sensitivity index of the basic reproduction number, $R_0$, of the model (2), which is differentiable with respect to a given parameter $\alpha$, is given by the relation

$$Y_{\alpha} = \frac{\partial R_0}{\partial \alpha} \times \frac{a}{R_0},$$

Therefore, using the equation (16) in the above Definition 4.1, we can easily derive an analytical expression for the sensitivity index of $R_0$, using the explicit formula (7), to each parameter that it includes.

Let $\phi_0 = \Pi \rho \beta_1 \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2) + C \mu \beta_2 \theta(\epsilon_1 + (1 - \theta)\epsilon_2)$, $\psi_1 = (\rho + \mu)C \mu \epsilon_1 \epsilon_2$, $\epsilon_1 = \delta + \gamma_1 + \mu$, and $\epsilon_2 = \delta + \gamma_2 + \mu$. Thus,

$$Y_{\beta_1} = \frac{\beta_1 \Pi \rho \beta_1 \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\beta_2} = \frac{C \mu \beta_2 \Pi \rho \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_1} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}.$$  

$$Y_{\beta_1} = \frac{C \mu \beta_2 \Pi \rho \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_1} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}.$$  

$$Y_{\epsilon_1} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_1} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0},$$

$$Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0},$$

$$Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}, \quad Y_{\epsilon_2} = \frac{\beta_1 \Pi \rho \eta \theta(\epsilon_1 + (1 - \theta)\epsilon_2)}{\phi_0}. \quad \text{(17)}$$
Table 3. Sensitivity indices of $R_0$ to the model parameter values.

| Parameter | Value | Sensitivity index | Source |
|-----------|-------|-------------------|--------|
| $I$       | $\mu \times N_0$ | 1 | (Terefe and Kassa, 2020) |
| $\beta_1$ | 0.00077 | 0.9437 | Assumed |
| $\mu$     | 0.000396 | -1.0089 | (Tavaen and Viriyapong, 2019) |
| $\theta$  | 0.5125 | 0.2238 | Assumed |
| $\delta$  | 0.0732 | -0.8148 | (Terefe and Kassa, 2020) |
| $\gamma_1$| 0.0157 | -0.1498 | (Mahikul et al., 2019) |
| $\gamma_2$| 0.0183 | 0.0563 | Assumed |
| $\mu_0$   | 0.0185 | -0.0563 | (Tavaen and Viriyapong, 2019) |
| $C$       | 5000 | 0.0563 | Assumed |
| $\sigma$  | 0.13 | 0.0563 | Assumed |
| $\rho$    | 0.0493 | 0.0047 | Assumed |
| $\eta$    | 0.0248 | -0.0147 | (Mahikul et al., 2019) |
| $\phi_0$  | 0.088 | 0.0045 | (Tavaen and Viriyapong, 2019) |

Table 4. Values and description of parameters of the model.

| Parameter | Description | Value | Unit | Source |
|-----------|-------------|-------|------|--------|
| $I$       | Human recruitment rate | $\mu \times N_0$ | Humans day$^{-1}$ | (Terefe and Kassa, 2020) |
| $\beta_1$ | Human transmission rate due to pathogen | 0.00183 | Day$^{-1}$ | Assumed |
| $\beta_2$ | Human transmission rate due to A & I | 0.00077 | (Humans days)$^{-1}$ | Assumed |
| $\theta$  | Probability of progress of E to I | 0.5125 | Dimensionless | Assumed |
| $\mu$     | Natural death rate of humans | 0.000396 | Day$^{-1}$ | (Tavaen and Viriyapong, 2019) |
| $\delta$  | Disease-induced death rate of A & I | 1 | Day$^{-1}$ | (Terefe and Kassa, 2020) |
| $\gamma_1$| Recovery rate from A | 0.0248 | Day$^{-1}$ | (Mahikul et al., 2019) |
| $\gamma_2$| Recovery rate from I | 0.0157 | Day$^{-1}$ | (Mahikul et al., 2019) |
| $\rho$    | The progression rate of E to A & I | 0.088 | Day$^{-1}$ | (Tavaen and Viriyapong, 2019) |
| $\sigma$  | Reduction rate of infectivity A | 0.0493 | Dimensionless | Assumed |
| $a$       | Disease waning immunity | 0.0726 | Day$^{-1}$ | Assumed |
| $\eta$    | Rate at which bacteria increase by A & I | 0.13 | No. of B. pseudomallei cell human$^{-1}$ day$^{-1}$ | (Tavaen and Viriyapong, 2019) |
| $\mu_0$   | Natural death rate of bacteria | 0.0185 | Day$^{-1}$ | (Tavaen and Viriyapong, 2019) |
| $C$       | Concentration of B. pseudomallei | 5000 | No. of B. pseudomallei cell | Assumed |

In particular, the sensitivity index of $R_0$ related to the recruitment rate, $I$, is found in (17) using (16) as $\frac{dR_0}{dI} = \frac{dR_0}{dy^0 \frac{dy}{dx^0}} \times R_0 = 1$.

Similarly, the detailed sensitivity indices of $R_0$ to the parameter values are described in Table 3 from the most sensitive parameter to the least sensitive parameter. In Table 3, the positive sign of $Y^i_{R_0}$ shows a positive impact of the parameter $a$ on $R_0$ (directly proportional). Whereas the negative sign of $Y^i_{R_0}$ shows a negative impact of $a$ on $R_0$ (indirectly proportional). For instance, decreasing $\beta_1$ by 10% results in a decrease in 9.44%. Similarly, increasing (or decreasing) $\beta_2$ by 15% results in an increase (or decrease, respectively) the value of $R_0$ by 14.16%. This suggests that preventive measures should be provided to reduce the spread of the disease. In contrast, increasing $\gamma_1$ by 10% results in decreases in 9.67%.

In view of the results of the sensitivity analysis, the most influencing parameters are human recruitment rate ($II$), human transmission rate ($\beta_1$), the human natural death rate ($\mu$), and disease-induced death rate ($\delta$) among other parameters. This demonstrates that melioidosis spread can be controlled by reducing the human transmission rate, $\beta_0$, on susceptible humans. As a result, preventive intervention efforts should be provided to combat the burden of the disease in the population. Moreover, when the value of reduction rate of A ($\sigma$) is 0.5, then the value of $R_0$ will increase by 35.22% and if the value of $\sigma$ is 1, the value of will increase by 74.28%. Therefore, although the asymptomatic infections are difficult to diagnose they have a great impact on the spread of the disease in the population. Also, it has a great role in increasing the growth of Burkholderia pseudomallei in the environment.

5. Numerical results and discussions

The model (2) is numerically simulated to show the effect of the most influencing parameters on disease dynamics. To accomplish this, the fourth-order Runge-Kutta method is applied in the Matlab. The parameter values used for simulations are described in Table 4 and the initial conditions are considered as ($S_0$, $E_0$, $A_0$, $E_0$, $R_0$, $B_{0,n}$) = (700, 20.0, 10.0, 300). We used these parameter values and the initial conditions in all simulations of the model. In Figs. 3 and 4, it is noted that all model solution trajectories ultimately remain in the positively invariant region $\Omega_n$ whenever the initial values are in $\Omega_n$. The basic reproduction number of the model (2) is obtained as $R_0 \approx 3.5482 > 1$. From the equation (15), we found the unique positive endemic equilibrium, $\epsilon^*_1 = (205.7844, 2.976, 1.2975, 1.503, 0.7641, 19.6794)$ for $R^*_1 \approx 1.503$, which is locally asymptotically stable for $R_0 > 1$ and the others are negative (unstable). As a result, all model solution trajectories move towards the steady-state $\epsilon^*_1$ as demonstrated in Figs. 3 (a) - (3) (e). In addition, the graphs show that the number of infected classes endures in population and that each one gradually goes to the small positive constant (to the corresponding component of $\epsilon^*_1$). However, if we modify the values of $\beta_1$, $\beta_2$, $\gamma_1$ and $\gamma_2$ into 0.015, 0.00027, 0.058 and 0.0527, respectively, it gives $R_0 \approx 0.951 < 1$. Thus, $\epsilon^*_1$ is unstable since the model in this case contains a DFE that is globally asymptotically stable. As a result,
of other impacts 5.2. \( \eta \) for could parameter’s Fig. 6(a), parameters 5.1. eliminate the components Fig. 3. In susceptible community Impact Impacts 2 on susceptible, as Fig. 5 (a) - 5 (c), observed of the infectious (both symptomatic or asymptomatic) as confirmed in Figs. 6 (b) - 6 (d). In addition, reducing the value of \( \beta_2 \) reduces the value of \( R_0 \). As a result, the infectious classes could finally vanish by considerably lowering the value of \( \beta_2 \). This can be accomplished by providing appropriate personal preventive interventions for susceptible humans and by treating infectious classes. Similarly, in Figs. 5 (a) - 5 (c), we observed the impact of the transmission rate, \( \beta_1 \), on classes of susceptible, infectious and bacterial. Furthermore, from the findings of the impacts of the transmission rates, we conclude that reducing \( \beta_1 \) on susceptible humans is essential for minimizing the spread of disease infection.

5.1. Impacts of the parameters \( \beta_1, \beta_2 \) on transmission process of the disease

In this section, we demonstrate the effects of the parameters \( \beta_1 \) and \( \beta_2 \) on the dynamics of melioidosis transmission by varying their values. These parameters significantly contribute to the spread of the disease by enhancing the force of infection in the transmission process of the epidemic. From Fig. 6 (a), we observed that increasing the value of \( \beta_2 \) will significantly increase the number of susceptible individuals getting infected (or reduce the number of susceptible humans). In other words, the number of susceptible individuals is inversely proportional to \( \beta_2 \). However, decreasing this parameter’s value will gradually decrease both the size of the bacterial population and the number of infectious humans (both symptomatic or asymptomatic) as confirmed in Figs. 6 (b) - 6 (d). In addition, reducing the value of \( \beta_2 \) reduces the value of \( R_0 \). As a result, the infectious classes could finally vanish by considerably lowering the value of \( \beta_2 \). This can be accomplished by providing appropriate personal preventive interventions for susceptible humans and by treating infectious classes. Similarly, in Figs. 5 (a) - 5 (c), we observed the impact of the transmission rate, \( \beta_1 \), on classes of susceptible, infectious and bacterial. Furthermore, from the findings of the impacts of the transmission rates, we conclude that reducing \( \beta_1 \) on susceptible humans is essential for minimizing the spread of disease infection.

5.2. Impact of the shedding rate of Burkholderia pseudomallei (\( \eta \))

By releasing the organism into the environment, infectious individuals (both asymptomatic and symptomatic) contribute significantly to the growth of \( B. pseudomallei \), which in turn increases the rate at which the disease spreads from the environment. Fig. 7 (a) and 7 (b), show the impacts of \( \eta \) on populations of susceptible individuals and bacterial, respectively. As illustrated in Fig. 7 (b), it is noted that increasing the value of \( \eta \) increases the size of the bacterial population dramatically. Whereas in Fig. 7 (a), the size of susceptible individuals increases as \( \eta \) diminishes over time. This demonstrates that in order to decrease the rate of shedding of the \( B. pseudomallei \), a control intervention strategy (typically treatment control) should be applied to infectious individuals. As a result, there will be a decrease in the growth of \( B. pseudomallei \) in the environment. In other words, the number of susceptible individuals getting infected will be diminished.
Fig. 4. Simulations illustrating the global asymptomatic stability of the DFE = (730, 0, 0, 0, 0, 0) of the system (2) for $R_0 < 1$. (a) The stability behavior of the human population components of DFE over the simulation period, (b) The stability behavior of the bacterial population component of DFE over the simulation period, (c) The stability behavior of the susceptible human component of DFE as $t$ gets large, (d) The stability behavior of the infected and recovered individual components of DFE as $t$ gets large, and (e) The stability behavior of the bacterial population component of DFE as $t$ gets large.

Fig. 5. Simulations illustrating the changing effect of $\beta_i$ on the model (2); (a) variation of susceptible individuals for different values of $\beta_i$, (b) variation of infectious individuals ($I + A$) for different values of $\beta_i$ and (c) variation of bacterial population for different values of $\beta_i$.

5.3. Impacts of the recovery rates ($\gamma_1$ & $\gamma_2$)

In Figs. 8 (a) & 8 (d), and in Figs. 9 (a) & 9 (e), we observed that the populations of susceptible and recovered humans decrease as recovery rates decrease. On the other hand, in Figs. 8 (b), 8 (c) & 8 (e), and Figs. 9 (b) - 9 (d) & 9 (f), we noted that the recovery rates are indirectly related to the number of infectious individuals (symptomatic and asymptomatic) and bacterial population. This shows that the number of infectious humans will be greatly diminished (or recovered humans will be increased) by providing the intervention control measure (treatment) in the population. However, the population of susceptible individuals increases as recovery rates increase because of the disease waning immunity as confirmed in Fig. 8 (a) and Fig. 9 (a). Thus, in addition, a preventive intervention strategy should be provided to diminish the disease spread.
Fig. 6. Simulations illustrating the changing effect of $\beta_2$ on the model (2); (a) variation of susceptible individuals for different values of $\beta_2$, (b) variation of infectious individuals ($I + A$) for different values of $\beta_2$, (c) variation of recovered individuals for different values of $\beta_2$ and (d) variation of bacterial population for different values of $\beta_2$.

Fig. 7. Simulations illustrating the changing effect of $\eta$ on the model (2); (a) variation of susceptible individuals for different values of $\eta$ and (b) variation of bacterial population for different values of $\eta$. 
6. Conclusion

Transmission of disease infection in humans that usually occur due to interaction with a contaminated environment can be reduced by avoiding contact with the contaminated sources or using treated water for drinking, which, as in the case of melioidosis. In this paper, we proposed a compartmental model that explains the dynamics of melioidosis transmission with an asymptomatic class in the human population. The formulated model has a disease-free equilibrium (DFE), which is globally asymptotically stable (GAS) whenever the basic reproduction number \( R_0 \) is less than unity. Whereas the endemic equilibrium of the model is shown to be locally asymptotically stable when \( R_0 \) is greater than unity. Sensitivity analysis results indicate that the recruitment rate \( (\beta_1) \) is the most influential parameter followed by the transmission coefficient \( (\beta_2) \). Thus, the parameter \( \beta_2 \) plays an important role to minimize the spread of disease infection. Furthermore, the numerical simulations of the steady state deduced that every solution of the model approaches the unique positive endemic equilibrium, \( e^*_A \), over time for \( R_0 \approx 3.5482 > 1 \), as confirmed in Figs. 3 (a) - 3 (e). From numerical findings, we also noted that the populations of infectious individuals (both asymptomatic and symptomatic) and bacterial diminish when transmission rates decrease, see, Figs. 5 (a) - 5 (c) and Figs. 6 (b) - 6 (d). While these population groups increase as the recovery rates of infectious individuals decrease. In contrast, the number of susceptible individuals increases as the recovery rates increase due to the disease waning immunity (see Fig. 8 (a) and Fig. 9 (a)). Our study suggests that in order to minimize the spread of the disease in the population, treatment of both asymptomatic and symptomatic infected individuals needs to be scaled up and human transmission coefficients should be reduced.

Declarations

Author contribution statement

Habtamu Ayalew Engida: Conceived and designed the experiments; Performed the experiments; Analyzed and interpreted the data; Wrote the paper.

David Mwangi Theuri, Duncan Gathungu, John Gachohi: Contributed reagents, materials, analysis tools or data; Analyzed and interpreted the data.

Haileyesus Tessema Alemneh: Conceived and designed the experiments; Contributed reagents, materials, analysis tools or data.
Fig. 9. Simulations illustrating the changing effect of $\gamma$ on the model (2); (a) variation of susceptible individuals for different values of $\gamma$, (b) variation of asymptomatic infectious individuals $A$ for different values of $\gamma$, (c) variation of symptomatic infectious individuals $I$ for different values of $\gamma$, (d) variation of infectious individuals $(I + A)$ for different values of $\gamma$, (e) variation of recovered individuals for different values of $\gamma$ and (f) variation of bacterial population for different values of $\gamma$.

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Data included in article/supplementary material/referenced in article.

Declaration of interests statement

The authors declare no conflict of interest.

Additional information

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