

STABILITY AND SENSITIVITY ANALYSIS OF A SHIGELLA INFECTION EPIDEMIC MODEL AT DISEASE-FREE EQUILIBRIUM

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Abstract

In this study, we modified continuous mathematical model for the dynamics of shigella outbreak at constant recruitment rate π formulated by (Ojaswita et. al., 2014). In their model, they partitioned the population into Susceptible (S), Infected (I) and recovered (R) individuals. We incorporated a vaccinated class (V), educated class (G), exposed class (E), asymptomatic (A) hospitalized class (H) and Bacteria class (B) with their corresponding parameters. We analyzed a SVGEIAHRB compartmental nonlinear deterministic mathematical model of shigella epidemic in a community with constant population. Analytical studies were carried out on the model to: investigate the existence and uniqueness of solution of the model equations and explore the basic properties of the model equations (i.e. the positivity and boundedness of solutions of the model). The basic reproductive number R_0 that governs the disease transmission is obtained from the largest eigenvalue of the next-generation matrix. The disease-free equilibrium points of the model is computed and proved to be locally and globally asymptotically stable if $R_0 \leq 1$ and unstable if $R_0 > 1$. A sensitivity analysis of the epidemiological model of shigella epidemic is performed in order to determine which model parameters are the most important to disease transmission. Finally, we simulate the model system in MATLAB and obtained the graphical behavior of the variables in the model. From the simulation, we observed that the shigella infection was eradicated when $R_0 \leq 1$ while it persist in the environment when $R_0 > 1$.

Keywords: SVGEIAHRB Model, Basic reproduction number, Local stability, global stability, sensitivity analysis, numerical simulation

INTRODUCTION

Shigella dysenteriae is a species of the rod-shaped bacterial genus *Shigella* (Rodriguez, 2022). *Shigella* species can cause shigellosis (bacillary dysentery). It is also a genus of bacteria that is gram-negative, facultative anaerobic, non-spore-forming and non-motile (Hale, 1996) and genetically closely related to *E. coli*. The genus is named after Kiyoshi Shiga, who first discovered it in 1897 (Yabuuchi, 2002). The causative agent of human shigellosis, *Shigella* causes disease in primates, but not in other mammals (Ryan & Ray, 2004). It is only naturally found in humans and gorillas (Pond, 2005). During infection, it typically causes dysentery (Mims et. al., 2004). *Shigella* is heat sensitive and unable to survive dairy processes such as pasteurization and cooking temperatures.

Shigellosis is an infection of the intestines caused by *Shigella* bacteria (CDC, 2016). It is an acute infection which lasts for about 7 days in adults but may persist for longer and be more severe in infants and children. Death is more likely in children younger than 5 years. Abdominal pain, vomiting, diarrhea and fever are the main symptoms similar to other forms of gastroenteritis and

enteritis. Bloody diarrhea is a common distinguishing feature in shigellosis compared to similar bacterial infections like salmonellosis.

Mathematical model literatures

(Ojaswita et. al.,2014) developed a continuous mathematical model for shigella diarrhea outbreak. According to the pathogenesis of shigella, they partitioned the population into Susceptible (S), Infected (I) and recovered (R) individuals. They computed the disease-free equilibrium state and the basic reproduction number R_0 such that $R_0 < 1$ indicates the possibility of shigella diarrhea eradication in the community while $R_0 > 1$ represents uniform persistence of the disease. They also carried out numerical simulation with data that is based on demographics and disease outbreaks in Botswana which showed the variation of the population in different situations.

(Ebenezer & Patience, 2019) developed a compartmental mathematical model of (SITR) to investigate the effect of saturation treatment in the dynamical spread of diarrhea in the community. Their mathematical analysis showed that the disease free and the endemic equilibrium points of the model exist. They also showed that the disease-free equilibrium is locally and globally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. Numerical simulation results showed the effect of saturation treatment function on the spread of diarrhea. Efficacy of treatment also showed a great impact in the total eradication of diarrhea epidemic.

(Hailay et. al.,2019a) developed and investigated dysentery dynamics model with incorporating controls. The system is considered as SIRSB deterministic compartmental model with treatment and sanitation. They obtained the threshold number R_0 such that $R_0 \leq 1$ indicates the possibility of dysentery eradication in the community while $R_0 > 1$ represents uniform persistence of the disease. They used Lyapunov–LaSalle method to prove the global stability of the disease-free equilibrium. Moreover, they used geometric approach method to obtain the sufficient condition for the global stability of the unique endemic equilibrium for $R_0 > 1$. They carried out numerical simulation to justify the analytical results. They presented graphical results and discussed quantitatively. They found out that the aggravation of the disease can be decreased by using the constant controls treatment and sanitation.

Mathematical formulation

In this section, we formulate and analyze a mathematical model of Shigella disease. The modeled populations include humans and pathogens. The human population is subdivided into eight classes. These classes of individual are: Susceptible(S), Vaccinated (V), Education campaign (G), Exposed (E), Asymptomatic (A), Infected (I), Hospitalized (H) and Recovered (R). The pathogen population (concentration of shigella dysenteriae) is represented by B. The formulation of the model is based on the following assumptions:

Assumptions of the model

- i. the recruitment is through birth only and it is constant.
- ii. all individuals are born susceptible.
- iii. an individual can be infected through contact with the infectious individuals' faeces and contaminated water or food.
- iv. infected individuals die either naturally or due to the disease.
- v. vaccination is strictly on susceptible adult and susceptible children between the ages of 4 to 7years.
- vi. Vaccinated individuals move back to the susceptible class when they lose immunity due to

- the vaccine.
- vii. there is no permanent recovery.
- viii. there is homogenous mixture in the population.
- ix. the recruitment of bacteria in the environment is constant.
- x. Humans and primate animals are the only source of pathogens.
- xi. pathogen population in the environment diminishes through natural death and environmental contamination.
- xii. environmental sanitation will be enforced so that shigella pathogen death can be approximated to be constant at a rate σ_3 .

Flow diagram of the model with constant control

We demonstrate the dynamical transfer of the population with the flow diagram in Figure 1 below

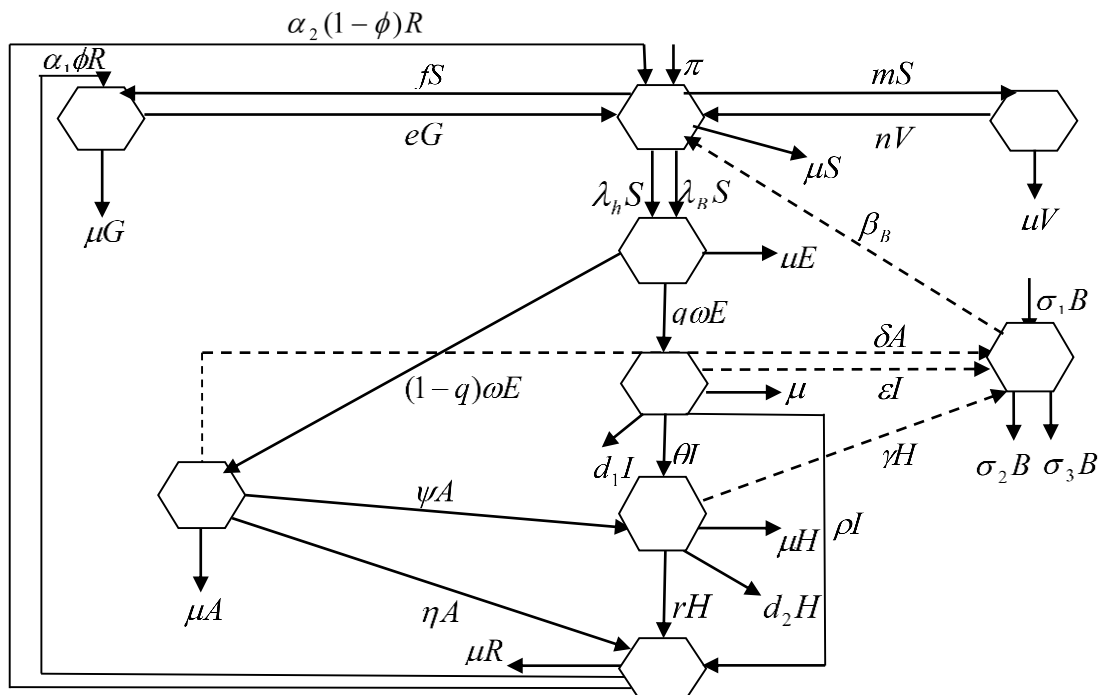


Figure 1. A schematic representation of flow of individuals (solid lines) among states and flow of pathogen in the environment (dotted lines) for the environmental infect transmission system (EITS) of the modified model.

Table 1: Description of the variables of the models

Variables	Description
	Number of susceptible individuals at time (t).
$V(t)$	Number of vaccinated individuals at time (t).
$G(t)$	Number of educated individuals at time (t).
$E(t)$	Number of exposed individuals at time (t).
$A(t)$	Number of asymptomatic individuals at time (t).
$I(t)$	Number of infected individuals at time (t).
$H(t)$	Number of hospitalized individuals at time (t).
$R(t)$	Number of Recovered individuals at time (t).
$B(t)$	Number of bacteria in the environment at time (t).

$N_h(t)$	The total human population size at time (t).
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Table 2: Description of the parameters of the models

Parameters	Description
	The recruitment rate.
m	The vaccination rate at which the susceptible individuals move to the vaccinated class.
n	The vaccine immunity loss rate at which the vaccinated individuals move to the susceptible class.
f	The education rate at which the susceptible individuals move to the educated class.
e	The recovering rate at which the educated individuals (who failed to adhere to the education they received) moved back to the susceptible class.
r	The rate at which the hospitalized individuals moved to the recovered class.
θ	The rate at which the infected individuals moved to the hospitalized class.
η	The rate at which the asymptomatic individuals moved to the recovered class.
μ	The natural death rate.
d_1	The death rate due to the disease in the infected class.
d_2	The death rate due to the disease in the hospitalized class.
ϕ	The proportion of the recovered individuals who moved to the educated class at a rate α_1 .
$(1 - \phi)$	The proportion of the recovered individuals who moved to the susceptible class at a rate α_2 .
q	The proportion of the exposed individuals who moved to the infected class at a rate ω .
$(1 - q)$	The proportion of the exposed individuals who moved to the asymptomatic class at a rate.
ω	The incubation rate (rate at which exposed individuals, $E(t)$, progress to either asymptomatic class $A(t)$ or infected $I(t)$).
ψ	The rate at which the asymptomatic individuals moved to the hospitalized class.
ρ	The recovering rate at which the infected individuals moved to the recovered class.
K	The concentration of <i>Shigella</i> in the environment that yields 50% chance of catching dysentery diarrhea (Berhe et. al., 2019).
λ_h	The force of infection in the human to human interaction.
λ_B	The force of infection in the environment to human interaction.
β_1	The transmission rate of shigella for the infected individuals due to human to human interaction.
β_2	The transmission rate of shigella for the asymptomatic individuals due to human to human interaction.
β_3	The transmission rate of shigella for the hospitalized individuals due to human to human interaction.

β_B	The ingestion rate of shigella by human from the environment.
ε	Shigella pathogen shedding rate for the infected individuals.
δ	Shigella pathogen shedding rate for the asymptomatic individuals.
γ	Shigella pathogen shedding rate for the hospitalized individuals.
σ_1	Shigella pathogen growth rate.
σ_2	Shigella pathogen natural death rate.
σ_3	Death rate of shigella pathogen due to environmental decontamination.

Equations of the model

$$\frac{dS}{dt} = \pi + nV + eG + \alpha_2(1 - \phi)R - (\lambda_h + \lambda_B)S - (m + f + \mu)S \quad (1)$$

$$\frac{dV}{dt} = mS - (n + \mu)V \quad (2)$$

$$\frac{dG}{dt} = fS + \alpha_1\phi R - (e + \mu)G \quad (3)$$

$$\frac{dE}{dt} = (\lambda_h + \lambda_B)S - (\omega + \mu)E \quad (4)$$

$$\frac{dA}{dt} = (1 - q)\omega E - (\eta + \psi + \mu)A \quad (5)$$

$$\frac{dI}{dt} = q\omega E - (\theta + \rho + d_1 + \mu)I \quad (6)$$

$$\frac{dH}{dt} = \theta I + \psi A - (r + d_2 + \mu)H \quad (7)$$

$$\frac{dR}{dt} = rH + \eta A + \rho I - \alpha_1\phi R - \alpha_2(1 - \phi)R - \mu R \quad (8)$$

$$\frac{dB}{dt} = \varepsilon I + \delta A + \gamma H + (\sigma_1 - \sigma_2 - \sigma_3)B \quad (9)$$

$$N = S + V + G + E + I + A + H + R \quad (10)$$

$$S(0) = S_0 > 0, V(0) = V_0 \geq 0, E(0) = E_0 \geq 0, G(0) = G_0 \geq 0, I(0) = I_0 \geq 0, A(0) = A_0 \geq 0,$$

$$H(0) = H_0 \geq 0, R(0) = R_0 \geq 0, B(0) = B_0 > 0.$$

The force of infection for human to human interaction (λ_h) and the force of infection for environment to human interaction (λ_B) are (11) and (12) respectively:

$$\lambda_h = \beta_1 I + \beta_2 A + \beta_3 H \quad (11)$$

$$\lambda_B = \frac{\beta_B B}{K + B} \quad (12)$$

$$\lambda_0 = \beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} \quad (13)$$

Where K is the shigella concentration that yields 25 – 50% chance of catching dysentery diarrhea (Cabral et. al., 2010). β_1, β_1 and β_1 are human to human interaction while β_B is the ingesting rate of shigella from the contaminated environment. Infected humans contribute to the concentration of

shigella at a rate of ε , asymptomatic humans contribute to the concentration of shigella at a rate of δ and hospitalized humans contribute to the concentration of shigella at a rate of γ . The pathogen population is growing at a rate σ_1 , natural death rate σ_2 and death rate of shigella pathogen due to environmental decontamination is σ_3 . We assume that $\sigma_1 - \sigma_2 - \sigma_3 > 0$ $\sigma_1 > \sigma_2 + \sigma_3$ represents the net death rate of the pathogen population in the environment (Bani-Yaghoub et. al., 2012).

MODEL ANALYSIS

Existence and uniqueness of solution for the model

Consider the initial value problem (IVP)

$$y' = f(t, y), \quad y(t_0) = y_0 \tag{14}$$

whose solution exist and unique.

In this subsection, we shall establish conditions for the existence and uniqueness of solution for the system of equations.

$$\text{Let } y' = f(t, y) = f(y) \tag{15}$$

such that

$$f_1(t, y) = f_1(y) = f_1 = \pi + nV + eG + \alpha_2(1 - \phi)R - \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} \right) S - (m + f + \mu)S \tag{16}$$

$$f_2(t, y) = f_2(y) = f_2 = mS - (n + \mu)V \tag{17}$$

$$f_3(t, y) = f_3(y) = f_3 = fS + \alpha_1 \phi R - (e + \mu)G \tag{18}$$

$$f_4 = \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} \right) S - (\omega + \mu)E \tag{19}$$

$$f_5 = (1 - q)\omega E - (\eta + \psi + \mu)A \tag{20}$$

$$f_6 = q\omega E - (\theta + \rho + d_1 + \mu)I \tag{21}$$

$$f_7 = \theta I + \psi A - (r + d_2 + \mu)H \tag{22}$$

$$f_8 = rH + \eta A + \rho I - \alpha_1 \phi R - \alpha_2(1 - \phi)R - \mu R \tag{23}$$

$$f_9 = \varepsilon I + \delta A + \gamma H + (\sigma_1 - \sigma_2 - \sigma_3)B \tag{24}$$

Theorem 1: (cauchy-lipchitz theorem)

Consider the initial value problem (IVP)

$$y' = f(t, y_1, y_2, y_3, \dots, y_n), \quad y(t_0) = y_0, \quad y_1(t_0) = y_{10}, \quad y_2(t_0) = y_{20}, \quad \dots, \quad y_n(t_0) = y_{n0} \tag{25}$$

Let R denote the region

$$|t - t_0| \leq a, \quad \|y - y_0\| \leq b, \quad y = (y_1, y_2, y_3, \dots, y_n), \quad y_0 = y_{10}, y_{20}, y_{30}, \dots, y_{n0} \tag{26}$$

Suppose that $f(t, y)$ satisfies the Lipchitz condition

$$\|f(t, y_n) - f(t, y_{n-1})\| \leq L \|y_n - y_{n-1}\| \tag{27}$$

whenever the pair (t, y_n) and (t, y_{n-1}) belong to R , where L is a Lipchitz positive constant, then there exist a constant number $\delta > 0$ such that there exists a unique continuous vector solution

$\bar{y}(t)$ of the system (14) in the interval $|t - t_0| < \delta$.

It is important to note that condition (16) is satisfied by the requirement that $\frac{\partial f_i}{\partial y_j}$, $\forall i, j = 1, 2, 3, \dots, n$ are continuous and bounded in the region R .

Lemma 1. If $f(t, y)$ has continuous partial derivative $\frac{\partial f_i}{\partial y_j}$ on a bounded closed convex domain R , then it satisfies a Lipchitz condition in R .

We are interested in the region $1 \leq \varepsilon \leq R$ (28)

We look for a bounded solution of the form $0 < R \leq \infty$. (29)

We shall prove the following existence theorem.

Theorem 2. Let D' denote the region defined in (27) such that (28) and (29) hold. Then there exist a solution of model system (16)-(24) which is bounded in the region D' .

Proof:

From (16)

$$\frac{dS}{dt} = \pi + nV + eG + \alpha_2(1-\phi)R - (m + f + \mu)S - \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} \right) S$$

Let $\frac{dS}{dt} = f_1(t, y_1) \equiv f_1(t, S)$

$$f_1(t, S) = \pi + nV + eG + \alpha_2(1-\phi)R - (m + f + \mu)S - \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} \right) S$$

$$\left| \frac{\partial f_1}{\partial S} \right| = \left| - \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} + m + f + \mu \right) \right| < \infty, \quad \left| \frac{\partial f_1}{\partial V} \right| = n < \infty, \quad \left| \frac{\partial f_1}{\partial G} \right| = e < \infty, \quad \left| \frac{\partial f_1}{\partial E} \right| = 0 < \infty,$$

$$\left| \frac{\partial f_1}{\partial A} \right| = |-\beta_2 S| = \beta_2 S < \infty, \quad \left| \frac{\partial f_1}{\partial I} \right| = |-\beta_1 S| = \beta_1 S < \infty, \quad \left| \frac{\partial f_1}{\partial H} \right| = |-\beta_3 S| = \beta_3 S < \infty, \quad \left| \frac{\partial f_1}{\partial R} \right| = \alpha_2(1-\phi) < \infty,$$

$$\left| \frac{\partial f_1}{\partial B} \right| = \left| - \frac{K\beta_B S}{(K + B)^2} \right| = \frac{K\beta_B S}{(K + B)^2} < \infty.$$

From (17)

$$\frac{dV}{dt} = mS - (n + \mu)V$$

Let $\frac{dV}{dt} = f_2(t, y_2) \equiv f_2(t, V)$

$$f_2(t, V) = mS - (n + \mu)V$$

$$\left| \frac{\partial f_2}{\partial S} \right| = m < \infty, \left| \frac{\partial f_2}{\partial V} \right| = -(n + \mu) = n + \mu < \infty, \left| \frac{\partial f_2}{\partial G} \right| = 0 < \infty, \left| \frac{\partial f_2}{\partial E} \right| = 0 < \infty, \left| \frac{\partial f_2}{\partial A} \right| = 0 < \infty,$$

$$\left| \frac{\partial f_2}{\partial I} \right| = 0 < \infty, \left| \frac{\partial f_2}{\partial H} \right| = 0 < \infty, \left| \frac{\partial f_1}{\partial R} \right| = 0 < \infty, \left| \frac{\partial f_1}{\partial B} \right| = 0 < \infty.$$

Similarly, we can also show that the remaining equations satisfy Lipchitz conditions. This completes the proof.

Since all f_i and their partial derivatives of the model equations with respect to each dependent variables (i.e. S, V, G, E, A, I, H, R and B) are continuous and bounded in the interval $0 < R < \infty$ by Lemma1, there exists a unique solution of (16) to (24) in the region R .

The positivity of solution of model

Theorem 3:

Let the initial values of the parameters be

$$\{S(0) = S_0 > 0, V(0) = V_0 \geq 0, E(0) = E_0 \geq 0, G(0) = G_0 \geq 0, I(0) = I_0 \geq 0, A(0) = A_0 \geq 0, H(0) = H_0 \geq 0, R(0) = R_0 \geq 0, B(0) = B_0 > 0\} \in R_+^9.$$

Then, the solution set $\{S(t), V(t), E(t), G(t), I(t), A(t), H(t), R(t), B(t)\}$ of the system (1) to (9) is non-negative for all $t > 0$.

Proof

From (1)

$$\frac{dS}{dt} = \pi + nV + eG + \alpha_2(1 - \phi)R - (m + f + \mu)S - \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} \right) S$$

It follows by comparison theorem that

$$\frac{dS}{dt} \geq - \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} + m + f + \mu \right) S \tag{30}$$

Solving (30) with the aid of separation of variables, we have

$$\frac{dS}{S} \geq - \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} + m + f + \mu \right) dt$$

$$\int \frac{dS}{S} \geq - \int \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} + m + f + \mu \right) dt \tag{31}$$

Integrating (31), we have

$$S(t) \geq S(0) e^{- \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K + B} + m + f + \mu \right) t} > 0$$

From (2)

$$\frac{dV}{dt} = mS - (n + \mu)V$$

$$\frac{dV}{dt} \geq -(n + \mu)V \tag{32}$$

Solving (32) with the aid of separation of variables, we have

$$\frac{dV}{V} \geq -(n + \mu)dt$$

$$\int \frac{dV}{V} \geq -\int (n + \mu)dt \tag{33}$$

Integrating (33), we have

$$V(t) \geq V(0)e^{-\int (n+\mu)dt}$$

$$V(t) \geq V(0)e^{-(n+\mu)t} > 0$$

Similarly, we can show that $G(t) \geq 0$, $E(t) \geq 0$, $A(t) \geq 0$, $I(t) \geq 0$, $H(t) \geq 0$, $R(t) \geq 0$ and $B(t) \geq 0$. This completes the proof.

The boundedness of solutions of the model

Theorem 4:

The closed set

$$\Omega = (\Omega_h; \Omega_B) = \left\{ \begin{array}{l} (S, V, G, E, A, I, H, R, B) \in R_+^9 : S + V + G + E + A + I + H + R + B = N_h; \\ 0 < N_h(t) \leq \frac{\pi}{\mu}; 0 < B(t) \leq \frac{\pi(\varepsilon + \delta + \gamma)}{\mu(\sigma_2 + \sigma_3 - \sigma_1)} \end{array} \right\} \tag{34}$$

is positively invariant.

Proof

From the model equations (1) to (9), the total population is given by

$$N_h = S + V + G + E + A + I + H + R \tag{35}$$

Differentiating the total human population $N_h(t)$ in (35) with respect to time t , we have

$$\frac{dN_h}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dG}{dt} + \frac{dE}{dt} + \frac{dA}{dt} + \frac{dI}{dt} + \frac{dH}{dt} + \frac{dR}{dt} \tag{36}$$

Substituting the differential equations (1) to (8) in (36), we have

$$\frac{dN_h}{dt} = \pi - \mu S - \mu V - \mu G - \mu E - \mu A - \mu I - \mu H - \mu R - d_1 I - d_2 H \tag{37}$$

$$\frac{dN_h}{dt} = \pi - \mu(S - V - G - E - A - I - H - R) - d_1 I - d_2 H \tag{38}$$

Substitute (35) in (38), we have

$$\frac{dN_h}{dt} = \pi - \mu N_h - d_1 I - d_2 H \tag{39}$$

In the absence of shigella pathogen, there is no death due to shigella pathogen (i.e. $d_1 = 0, d_2 = 0$) then (39) becomes

$$\frac{dN_h}{dt} = \pi - \mu N_h$$

$$\frac{dN_h}{dt} + \mu N_h = \pi \tag{40}$$

$$I.F = e^{\int \mu dt} = e^{\mu t} \tag{41}$$

Multiply both sides of (40) by (41)

$$e^{\mu t} \frac{dN_h}{dt} + \mu N_h e^{\mu t} = \pi e^{\mu t} \tag{42}$$

Equation (42) becomes

$$\lim_{t \rightarrow \infty} N_h(t) = \lim_{t \rightarrow \infty} \frac{\pi}{\mu} + C \lim_{t \rightarrow \infty} e^{-\mu t} \Rightarrow \lim_{t \rightarrow \infty} N_h(t) = \frac{\pi}{\mu} + C(0)$$

$$\lim_{t \rightarrow \infty} N_h(t) = \frac{\pi}{\mu} \tag{43}$$

This result implies that if there is no disease, $N_h = \frac{\pi}{\mu}$. It also means that we have a steady state population. Therefore, the feasible solution set of the population of the system (40) exist in the region

$$\Omega_h = \left\{ (S, V, G, E, A, I, H, R) \in \mathbb{R}_+^8 : S + V + G + E + A + I + H + R = N_h > 0, 0 \leq N_h(t) \leq \frac{\pi}{\mu} \right\}$$

Similarly, considering equation (9) in the system of equation (1) to (9)

$$\frac{dB}{dt} = \varepsilon I + \delta A + \gamma H - (\sigma_2 + \sigma_3 - \sigma_1)B$$

Let the total shigella pathogen population be $B(t)$. We have

$$\frac{dB}{dt} = \varepsilon I + \delta A + \gamma H - (\sigma_1 + \sigma_2 + \sigma_3)B$$

$$\frac{dB}{dt} \leq (\varepsilon + \delta + \gamma)N_h - (\sigma_1 + \sigma_2 + \sigma_3)B \tag{44}$$

Put equation (43) in (44), we have

$$\frac{dB}{dt} \leq (\varepsilon + \delta + \gamma) \frac{\pi}{\mu} - (\sigma_2 + \sigma_3 - \sigma_1)B$$

$$\frac{dB}{dt} + (\sigma_2 + \sigma_3 - \sigma_1)B \leq (\varepsilon + \delta + \gamma) \frac{\pi}{\mu} \tag{45}$$

$$I.F = e^{\int (\sigma_2 + \sigma_3 - \sigma_1) dt} = e^{(\sigma_2 + \sigma_3 - \sigma_1)t} \tag{46}$$

Multiply both sides of (45) by (46), we have

$$\frac{dB}{dt} e^{(\sigma_1 + \sigma_2 + \sigma_3)t} + (\sigma_1 + \sigma_2 + \sigma_3) B e^{(\sigma_1 + \sigma_2 + \sigma_3)t}$$

$$\leq (\varepsilon + \delta + \gamma) \frac{\pi}{\mu} e^{(\sigma_1 + \sigma_2 + \sigma_3)t}$$

$$\frac{d}{dt} [B e^{(\sigma_2 + \sigma_3 - \sigma_1)t}] \leq (\varepsilon + \delta + \gamma) \frac{\pi}{\mu} e^{(\sigma_2 + \sigma_3 - \sigma_1)t}$$

$$\int d [B e^{(\sigma_2 + \sigma_3 - \sigma_1)t}] \leq (\varepsilon + \delta + \gamma) \frac{\pi}{\mu} \int e^{(\sigma_2 + \sigma_3 - \sigma_1)t} dt + C B e^{(\sigma_2 + \sigma_3 - \sigma_1)t} \leq \frac{\pi(\varepsilon + \delta + \gamma)}{\mu(\sigma_2 + \sigma_3 - \sigma_1)} e^{(\sigma_2 + \sigma_3 - \sigma_1)t} + C$$

$$\lim_{t \rightarrow \infty} B(t) \leq \lim_{t \rightarrow \infty} \frac{\pi(\varepsilon + \delta + \gamma)}{\mu(\sigma_2 + \sigma_3 - \sigma_1)} + C \lim_{t \rightarrow \infty} e^{-(\sigma_2 + \sigma_3 - \sigma_1)t}$$

$$0 \leq B(t) \leq \frac{\pi(\varepsilon + \delta + \gamma)}{\mu(\sigma_2 + \sigma_3 - \sigma_1)} \quad (47)$$

provided that $\sigma_2 + \sigma_3 > \sigma_1$

Therefore, the feasible solution set of the shigella pathogen population of the system (45) exist in the region

$$\Omega_B = \left\{ B(t) \in R_+^1 : 0 < B(t) \leq \frac{\pi(\varepsilon + \delta + \gamma)}{\mu(\sigma_2 + \sigma_3 - \sigma_1)} \right\} \quad (48)$$

Thus, the feasible set for the modified model system (1) to (9) is given by

$$\Omega = (\Omega_h; \Omega_B) = \left\{ \begin{array}{l} (S, V, G, E, A, I, H, R) \in R_+^8 : S + V + G + E + A + I + H + R = N_h, \\ 0 < N_h(t) \leq \frac{\pi}{\mu}; B(t) \in R_+^1 : B = N_B, 0 < B(t) \leq \frac{\pi(\varepsilon + \delta + \gamma)}{\mu(\sigma_2 + \sigma_3 - \sigma_1)} \end{array} \right\}$$

This is a positive invariant set of the model which shows that the model is both biologically and mathematically meaningful in the domain $\Omega = (\Omega_h; \Omega_B)$

Disease-free equilibrium points of the model

The equilibrium points of the system of non-linear ordinary differential equation are obtained by setting the derivatives of the model equation to zero (0).

$$\left(\text{i.e. } \frac{dS}{dt} = \frac{dV}{dt} = \frac{dG}{dt} = \frac{dE}{dt} = \frac{dA}{dt} = \frac{dI}{dt} = \frac{dH}{dt} = \frac{dR}{dt} = \frac{dB}{dt} = 0 \right)$$

Thus, at equilibrium point, the system of equation (3.1) to (3.9) becomes

$$\pi + nV^\circ + eG^\circ + \alpha_2(1-\phi)R^\circ - (m + f + \mu)S^\circ - \left(\beta_1 I^\circ + \beta_2 A^\circ + \beta_3 H^\circ + \frac{\beta_B B^\circ}{K + B^\circ} \right) S^\circ = 0 \quad (49)$$

$$mS^\circ - (n + \mu)V^\circ = 0 \quad (50)$$

$$fS^\circ + \alpha\phi R^\circ - (e + \mu)G^\circ = 0 \quad (51)$$

$$\left(\beta_1 I^\circ + \beta_2 A^\circ + \beta_3 H^\circ + \frac{\beta_B B^\circ}{K + B^\circ} \right) S^\circ - (\omega + \mu)E^\circ \quad (52)$$

$$(1 - q)\omega E^\circ - (\eta + \psi + \mu)A^\circ = 0 \quad (53)$$

$$q\omega E^\circ - (\theta + \rho + d_1 + \mu)I^\circ = 0 \quad (54)$$

$$\theta I^\circ + \psi A^\circ - (r + d_2 + \mu)H^\circ = 0 \quad (55)$$

$$rH^\circ + \eta A^\circ + \rho I^\circ - (\alpha_1\phi + \alpha_2(1-\phi) + \mu)R^\circ = 0 \quad (56)$$

$$\varepsilon I^\circ + \delta A^\circ + \gamma H^\circ - (\sigma_2 - \sigma_3 - \sigma_1)B^\circ = 0 \quad (57)$$

At disease-free equilibrium (in the absence of infection), there will be no exposed individuals

$$E^\circ = 0 \quad (58)$$

Substitute (58) in (53), we have

$$A^\circ = 0 \tag{59}$$

Substitute (58) in (54), we have

$$I^\circ = 0 \tag{60}$$

Substitute (59) and (60) in (55), we have

$$H^\circ = 0 \tag{61}$$

Substitute (59), (60) and (61) in (56), we have

$$R^\circ = 0 \tag{62}$$

Substitute (59), (60) and (61) in (57), we have

$$B^\circ = 0 \tag{63}$$

Substitute (62) in (51), we have

$$fS^\circ - (e + \mu)G^\circ = 0 \tag{64}$$

Similarly, substitute (59), (60), (61), (62) and (63) in (49), we have

$$\pi + nV^\circ + eG^\circ - (m + f + \mu)S^\circ = 0 \tag{65}$$

From (50),

$$mS^\circ - (n + \mu)V^\circ = 0$$

$$V^\circ = \frac{m}{n + \mu} S^\circ \tag{66}$$

Substitute (66) in (65), we have

$$\pi + \frac{m}{n + \mu} S^\circ + eG^\circ - (m + f + \mu)S^\circ = 0 \tag{67}$$

From (64)

$$G^\circ = \frac{f}{e + \mu} S^\circ \tag{68}$$

Substitute (68) in (67), we have

$$\pi + \frac{mn}{n + \mu} S^\circ + \frac{ef}{e + \mu} S^\circ - (m + f + \mu)S^\circ = 0$$

$$S^\circ = \frac{\pi(e + \mu)(n + \mu)}{(m + f + \mu)(e + \mu)(n + \mu) - mn(e + \mu) - ef(n + \mu)} \tag{69}$$

Substitute (69) in (68), we have

$$G^\circ = \frac{f(n + \mu)\pi}{(m + f + \mu)(e + \mu)(n + \mu) - mn(e + \mu) - ef(n + \mu)}$$

Similarly, substitute (69) in (66), we have

$$V^\circ = \frac{m(e + \mu)\pi}{(m + f + \mu)(e + \mu)(n + \mu) - mn(e + \mu) - ef(n + \mu)} \tag{70}$$

Therefore, the disease-free equilibrium point is denoted by $E^\circ = (S^\circ, V^\circ, G^\circ, E^\circ, A^\circ, I^\circ, H^\circ, H^\circ, R^\circ)$

$$E^\circ = \left\{ \begin{array}{l} \left(\frac{\pi(e + \mu)(n + \mu)}{(m + f + \mu)(e + \mu)(n + \mu) - mn(e + \mu) - ef(n + \mu)}, \frac{m(e + \mu)\pi}{(m + f + \mu)(e + \mu)(n + \mu) - mn(e + \mu) - ef(n + \mu)}, \right. \\ \left. \frac{f(n + \mu)\pi}{(m + f + \mu)(e + \mu)(n + \mu) - mn(e + \mu) - ef(n + \mu)}, 0, 0, 0, 0, 0 \right) \end{array} \right\} \tag{71}$$

Computation of the basic reproduction number R_0

The basic reproduction number R_0 is the average number of new infections that one infected case will generate during their entire infectious lifetime (Nelson & Williams, 2013), (Addo, 2009), (Heffernan et. al., 2012).

It is very important in determining whether the disease persists in the population or die out. We use the next generation matrix to compute the basic reproduction number R_0 which is formulated in (Van den Driessche & Watmough, 2002). Let us assume that there are n compartments of which the first m compartments correspond to infected individuals.

Let

- $F_i(y)$ be the rate of appearance of new infections in compartment i ,
- $V_i^+(y)$ be the rate of transfer of individuals into compartment i by all other means, and
- $V_i^-(y)$ be the rate of transfer of individuals out of compartments i .

It is assumed that each function is continuously differentiable at least twice in each variable. The disease transmission model consists of nonnegative initial conditions together with the following system of equations:

$$\frac{dy_i}{dt} = f_i(y) = F_i(y) - V_i(y), \quad i = 1, 2, 3, \dots, n \quad (72)$$

$$\text{where } V_i(y) = V_i^-(y) - V_i^+(y). \quad (73)$$

$$\frac{d}{dt} = F - V = \begin{pmatrix} (\lambda_h + \lambda_B)S \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} - \begin{pmatrix} (\omega + \mu)E \\ (\eta + \psi + \mu)A - (1 - q)\omega E \\ (\theta + \rho + d_1 + \mu)I - q\omega E \\ (r + d_2 + \mu)H - \theta I - \psi A \\ (\sigma_2 + \sigma_3 - \sigma_1)B - \varepsilon I - \delta A - \gamma H \end{pmatrix}$$

$$R_0 = \rho(FV^{-1}) = \rho \left(\left(\frac{\partial F_i}{\partial y_j} \Big|_{E^0} \right) \left(\frac{\partial V_i}{\partial y_j} \Big|_{E^0} \right)^{-1} \right) \quad (74)$$

where F are the new infection transfer terms and V is the non-singular matrix of the remaining transfer terms. The basic reproduction number R_0 of the model (1) – (9) is calculated using the next generation matrix (Van den Driessche & Watmough, 2002). In using their approach (Van den Driessche & Watmough, 2002), we have:

$$F = \left(\frac{\partial F_i}{\partial y_j} \Big|_{E^0} \right) = \begin{pmatrix} 0 & \beta_2 S^\circ & \beta_1 S^\circ & \beta_3 S^\circ & \frac{\beta_B S^\circ}{K} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \Rightarrow F = \begin{pmatrix} 0 & y_1 & y_2 & y_3 & y_4 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \quad (75)$$

$$\text{Let } y_1 = \beta_2 S^\circ, \quad y_2 = \beta_1 S^\circ, \quad y_3 = \beta_3 S^\circ \quad \text{and} \quad y_4 = P_{30} = \frac{\beta_B S^\circ}{K}$$

$$\text{Similarly, } V = \begin{pmatrix} \omega + \mu & 0 & 0 & 0 & 0 \\ -(1-q)\omega & \eta + \psi + \mu & 0 & 0 & 0 \\ -q\omega & 0 & \theta + \rho + d_1 + \mu & 0 & 0 \\ 0 & -\psi & -\theta & r + d_2 + \mu & 0 \\ 0 & -\delta & -\varepsilon & -\gamma & \sigma_2 + \sigma_3 - \sigma_1 \end{pmatrix}$$

$$|V| = T_{15} = P_2 P_4 P_5 P_8 P_{13}$$

$$V^{-1} = \frac{1}{|V|} \cdot \text{Adj}V \Rightarrow V^{-1} = \frac{1}{T_{15}} \begin{pmatrix} T_1 & 0 & 0 & 0 & 0 \\ T_2 & T_6 & 0 & 0 & 0 \\ T_3 & 0 & T_9 & 0 & 0 \\ T_4 & T_7 & T_{10} & T_{12} & 0 \\ T_5 & T_8 & T_{11} & T_{13} & T_{14} \end{pmatrix} \quad (76)$$

Substitute (75) and (76) in (74), we have

$$FV^{-1} = \begin{pmatrix} \frac{T_2 y_1}{T_{15}} + \frac{T_3 y_2}{T_{15}} + \frac{T_4 y_3}{T_{15}} + \frac{T_5 y_4}{T_{15}} & \frac{T_6 y_1}{T_{15}} + \frac{T_7 y_3}{T_{15}} + \frac{T_8 y_4}{T_{15}} & \frac{T_9 y_2}{T_{15}} + \frac{T_{10} y_3}{T_{15}} + \frac{T_{11} y_4}{T_{15}} & \frac{T_{12} y_3}{T_{15}} + \frac{T_{13} y_4}{T_{15}} & \frac{T_{14} y_4}{T_{15}} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$T_{16} = \frac{T_2 y_1}{T_{15}} + \frac{T_3 y_2}{T_{15}} + \frac{T_4 y_3}{T_{15}} + \frac{T_5 y_4}{T_{15}}, \quad T_{17} = \frac{T_6 y_1}{T_{15}} + \frac{T_7 y_3}{T_{15}} + \frac{T_8 y_4}{T_{15}}, \quad T_{18} = \frac{T_9 y_2}{T_{15}} + \frac{T_{10} y_3}{T_{15}} + \frac{T_{11} y_4}{T_{15}},$$

$$T_{19} = \frac{T_{12} y_3}{T_{15}} + \frac{T_{13} y_4}{T_{15}} \text{ and } T_{20} = \frac{T_{14} y_4}{T_{15}}$$

$$FV^{-1} = \begin{pmatrix} T_{16} & T_{17} & T_{18} & T_{19} & T_{20} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$|FV^{-1} - \lambda I| = \begin{vmatrix} T_{16} - \lambda & T_{17} & T_{18} & T_{19} & T_{20} \\ 0 & -\lambda & 0 & 0 & 0 \\ 0 & 0 & -\lambda & 0 & 0 \\ 0 & 0 & 0 & -\lambda & 0 \\ 0 & 0 & 0 & 0 & -\lambda \end{vmatrix} = 0 \quad \lambda^4 (T_{16} - \lambda) = 0 \Rightarrow T_{16} - \lambda = 0 \Rightarrow \lambda = T_{16}$$

$$\lambda = \rho(FV^{-1}) = R_0 = T_{16} = \frac{T_2 y_1}{T_{15}} + \frac{T_3 y_2}{T_{15}} + \frac{T_4 y_3}{T_{15}} + \frac{T_5 y_4}{T_{15}}$$

$$R_0 = \frac{T_2 y_1}{T_{15}} + \frac{T_3 y_2}{T_{15}} + \frac{T_4 y_3}{T_{15}} + \frac{T_5 y_4}{T_{15}}$$

$$R_0 = \frac{(1-q)\omega\beta_2 S^\circ}{(\eta+\psi+\mu)(\omega+\mu)} + \frac{q\omega\beta_1 S^\circ}{(\theta+\rho+d_1+\mu)(\omega+\mu)} + \frac{((1-q)\omega(\theta+\rho+d_1+\mu)\psi + (\eta+\psi+\mu)q\omega\theta)\beta_3 S^\circ}{(\eta+\psi+\mu)(\theta+\rho+d_1+\mu)(r+d_2+\mu)(\omega+\mu)}$$

$$+ \frac{(1-q)\omega((\theta+\rho+d_1+\mu)(\psi\gamma + (r+d_2+\mu)\delta) + (\eta+\psi+\mu)q\omega(\theta\gamma + (r+d_2+\mu)\varepsilon))\beta_B S^\circ}{K(\eta+\psi+\mu)(\theta+\rho+d_1+\mu)(r+d_2+\mu)(\sigma_2+\sigma_3-\sigma_1)(\omega+\mu)}$$

The local stability analysis of the disease-free equilibrium

To examine the local stability of the disease-free (E°) equilibrium, we obtain the Jacobian matrix by differentiating the functions ($f_i; i = 1, 2, 3, \dots, 9$) partially with respect to the variables in the system of the modified equations. The Jacobian matrix from the partial derivatives of (1) to (9) at disease-free (J_{E°) is given by:

$$J_{E^\circ} = \begin{pmatrix} -P_{10} & n & e & 0 & -P_{26} & -P_{27} & -P_{28} & P_7 & -P_{30} \\ m & -P_{11} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ f & 0 & -P_{12} & 0 & 0 & 0 & 0 & P_6 & 0 \\ 0 & 0 & 0 & -P_{13} & P_{26} & P_{27} & P_{28} & 0 & P_{30} \\ 0 & 0 & 0 & P_1 & -P_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & P_3 & 0 & -P_4 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \psi & \theta & -P_5 & 0 & 0 \\ 0 & 0 & 0 & 0 & \eta & \rho & r & -P_{31} & 0 \\ 0 & 0 & 0 & 0 & \delta & \varepsilon & \gamma & 0 & -P_8 \end{pmatrix}$$

where $P_1 = (1-q)\omega$, $P_2 = \eta + \psi + \mu$, $P_3 = q\omega$, $P_4 = \theta + \rho + d_1 + \mu$, $P_5 = r + d_2 + \mu$, $P_6 = \alpha_1\phi$,

$$P_8 = \sigma_2 + \sigma_3 - \sigma_1, P_9 = \beta_1 I^* + \beta_2 A^* + \beta_3 H^* + \frac{\beta_B B^*}{K+B^*}, P_{10} = m + f + \mu, P_{11} = n + \mu,$$

$$P_{13} = \omega + \mu, P_{26} = \beta_2 S^\circ, P_{27} = \beta_1 S^\circ, P_{28} = \beta_3 S^\circ, P_{30} = \frac{\beta_B S^\circ}{K} = y_4, P_{31} = \alpha_1\phi + \alpha_2(1-\phi) + \mu$$

$$|J_{E^\circ} - \lambda I| = \begin{vmatrix} -P_{10} - \lambda & n & e & 0 & -P_{26} & -P_{27} & -P_{28} & P_7 & -P_{30} \\ m & -P_{11} - \lambda & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ f & 0 & -P_{12} - \lambda & 0 & 0 & 0 & 0 & P_6 & 0 \\ 0 & 0 & 0 & -P_{13} - \lambda & P_{26} & P_{27} & P_{28} & 0 & P_{30} \\ 0 & 0 & 0 & P_1 & -P_2 - \lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & P_3 & 0 & -P_4 - \lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \psi & \theta & -P_5 - \lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & \eta & \rho & r & -P_{29} - \lambda & 0 \\ 0 & 0 & 0 & 0 & \delta & \varepsilon & \gamma & 0 & -P_8 - \lambda \end{vmatrix} = 0$$

$$(P_{31} + \lambda) \left[mn(P_{12} + \lambda) + (P_{11} + \lambda)(ef - (P_{12} + \lambda)(P_{10} + \lambda)) \right] \begin{vmatrix} -P_{13} - \lambda & P_{26} & P_{27} & P_{28} & P_{30} \\ P_1 & -P_2 - \lambda & 0 & 0 & 0 \\ P_3 & 0 & -P_4 - \lambda & 0 & 0 \\ 0 & \psi & \theta & -P_5 - \lambda & 0 \\ 0 & \delta & \varepsilon & \gamma & -P_8 - \lambda \end{vmatrix} = 0$$

$$\begin{aligned} P_{31} + \lambda = 0 &\Rightarrow \lambda = -P_{31} \Rightarrow \lambda_1 = -(\alpha_1\phi + \alpha_2(1-\phi) + \mu) \\ mn(P_{12} + \lambda) + (P_{11} + \lambda)(ef - (P_{12} + \lambda)(P_{10} + \lambda)) &= 0 \\ mnP_{12} + mn\lambda + (P_{11} + \lambda)(ef - (P_{10}P_{12} + (P_{10} + P_{12})\lambda) + \lambda^2) &= 0 \\ mnP_{12} + mn\lambda + efP_{11} - P_{10}P_{11}P_{12} - (P_{10} + P_{12})P_{11}\lambda - P_{11}\lambda^2 + ef\lambda - P_{10}P_{12}\lambda - (P_{10} + P_{12})\lambda^2 - \lambda^3 &= 0 \\ \lambda^3 + (P_{11} + P_{10} + P_{12})\lambda^2 + (P_{11}(P_{10} + P_{12}) + P_{10}P_{12} - mn - ef)\lambda + P_{10}P_{11}P_{12} - mnP_{12} - efP_{11} &= 0 \quad (77) \end{aligned}$$

We applied Routh-Hurwitz criterion for stability to investigate the stability of (77).

$$a_0 = 1, a_1 = (P_{11} + P_{10} + P_{12}), a_2 = P_{11}(P_{10} + P_{12}) + P_{10}P_{12} - mn - ef, a_3 = P_{10}P_{11}P_{12} - mnP_{12} - efP_{11}$$

For order one,

$$\Delta_1 = a_1 = P_{11} + P_{10} + P_{12} > 0$$

For order two,

$$a_0\lambda^2 + a_1\lambda + a_2 = 0$$

$$\Delta_2 = \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} \Rightarrow \Delta_2 = a_1a_2 - a_0a_3$$

$$\Delta_2 = a_1a_2 - a_0a_3 > 0 \Rightarrow a_1a_2 > a_3$$

$$\Delta_2 = (P_{11} + P_{10} + P_{12})(P_{11}(P_{10} + P_{12}) + P_{10}P_{12} - mn - ef) - (P_{10}P_{11}P_{12} - mnP_{12} - efP_{11}) > 0$$

$$\text{iff } (P_{11} + P_{10} + P_{12})(P_{11}(P_{10} + P_{12}) + P_{10}P_{12} - mn - ef) > P_{10}P_{11}P_{12} - mnP_{12} - efP_{11}$$

For order three,

$$a_0\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$$

$$\Delta_3 = \begin{vmatrix} a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 \\ a_5 & a_4 & a_3 \end{vmatrix} \Rightarrow \Delta_3 = a_1(a_2a_3 - a_1a_4) - a_0(a_3^2 - a_1a_5) > 0$$

$$a_0 = 1, a_4 = 0, a_5 = 0$$

$$\Delta_3 = a_1a_2a_3 - a_3^2 > 0 \Rightarrow a_3(a_1a_2 - a_3) > 0 \Rightarrow a_1a_2 > a_3$$

$$\Delta_3 = \begin{vmatrix} P_{11} + P_{10} + P_{12} & 1 & 0 \\ P_{10}P_{11}P_{12} - mnP_{12} - efP_{11} & P_{11}(P_{10} + P_{12}) + P_{10}P_{12} - mn - ef & P_{11} + P_{10} + P_{12} \\ 0 & 0 & P_{10}P_{11}P_{12} - mnP_{12} - efP_{11} \end{vmatrix} > 0$$

$$\Delta_3 = (P_{10}P_{11}P_{12} - mnP_{12} - efP_{11})((P_{11} + P_{10} + P_{12})(P_{11}(P_{10} + P_{12}) + P_{10}P_{12} - mn - ef) - (P_{10}P_{11}P_{12} - mnP_{12} - efP_{11})) > 0$$

$$\text{iff } (P_{10}P_{11}P_{12} - mnP_{12} - efP_{11})((P_{11} + P_{10} + P_{12})(P_{11}(P_{10} + P_{12}) + P_{10}P_{12} - mn - ef)) > (P_{10}P_{11}P_{12} - mnP_{12} - efP_{11})$$

Similarly,

$$\begin{vmatrix} -P_{13} - \lambda & P_{26} & P_{27} & P_{28} & P_{30} \\ P_1 & -P_2 - \lambda & 0 & 0 & 0 \\ P_3 & 0 & -P_4 - \lambda & 0 & 0 \\ 0 & \psi & \theta & -P_5 - \lambda & 0 \\ 0 & \delta & \varepsilon & \gamma & -P_8 - \lambda \end{vmatrix} = 0$$

$$\begin{aligned} & \lambda^5 + [P_2 + P_4 + P_5 + P_{13} + P_8] \lambda^4 + [P_1 P_{26} + P_3 P_{27} + P_2 (P_4 + P_5 + P_{13} + P_8) + P_4 P_5 + (P_4 + P_5)(P_{13} + P_8) + P_{13} P_8] \lambda^3 \\ & + [\psi P_1 P_{28} + P_1 P_{26} (P_4 + P_5 + P_8) + \delta P_1 P_{30} - \theta P_3 P_{28} - P_3 P_{27} (P_2 + P_5 + P_8) - \varepsilon P_3 P_{20} + P_4 P_5 (P_{13} + P_8) \\ & + P_{13} P_8 (P_4 + P_5) + P_2 (P_4 P_5 + (P_4 + P_5)(P_{13} + P_8) + P_{13} P_8)] \lambda^2 + [\psi P_1 P_{28} (P_4 + P_8) + \psi \gamma P_1 P_{30} \\ & + P_1 P_{26} (P_4 (P_5 + P_8) + P_5 P_8) + \delta P_1 P_{30} (P_4 + P_5) - \theta P_3 P_{28} (P_2 + P_8) - \theta \gamma P_3 P_{20} - P_3 P_{27} (P_5 P_8 + P_2 (P_5 + P_8)) \\ & - \varepsilon P_3 P_{20} (P_2 + P_5) + P_4 P_5 P_8 P_{13} + P_2 (P_4 P_5 (P_{13} + P_8) + P_8 P_{13} (P_4 + P_5))] \lambda + \psi P_1 P_{28} P_4 P_8 \\ & + P_1 P_{26} P_4 P_5 P_8 + \delta P_1 P_{30} P_4 P_5 + P_2 P_4 P_5 P_{13} P_8 - \theta P_3 P_{28} P_2 P_8 - \theta \gamma P_3 P_{20} P_2 - P_3 P_{27} P_2 P_5 P_8 \\ & - \varepsilon P_3 P_{20} P_2 P_5 = 0 \end{aligned} \tag{78}$$

We also adopted Routh- Hurwitz criterion for stability to investigate the stability of (78).

$$a_0 \lambda^5 + a_1 \lambda^4 + a_2 \lambda^3 + a_3 \lambda^2 + a_4 \lambda^1 + a_5 = 0$$

$$a_0 = 1 > 0$$

$$a_1 = P_2 + P_4 + P_5 + P_{13} + P_8 > 0$$

$$a_2 = P_1 P_{26} + P_3 P_{27} + P_2 (P_4 + P_5 + P_{13} + P_8) + P_4 P_5 + (P_4 + P_5)(P_{13} + P_8) + P_{13} P_8 > 0$$

$$\begin{aligned} a_3 = & \psi P_1 P_{28} + P_1 P_{26} (P_4 + P_5 + P_8) + \delta P_1 P_{30} - \theta P_3 P_{28} - P_3 P_{27} (P_2 + P_5 + P_8) - \varepsilon P_3 P_{20} + P_4 P_5 (P_{13} + P_8) \\ & + P_{13} P_8 (P_4 + P_5) + P_2 (P_4 P_5 + (P_4 + P_5)(P_{13} + P_8) + P_{13} P_8) > 0 \end{aligned}$$

$$\begin{aligned} a_4 = & \psi P_1 P_{28} (P_4 + P_8) + \psi \gamma P_1 P_{30} + P_1 P_{26} (P_4 (P_5 + P_8) + P_5 P_8) + \delta P_1 P_{30} (P_4 + P_5) - \theta P_3 P_{28} (P_2 + P_8) \\ & - \theta \gamma P_3 P_{20} - P_3 P_{27} (P_5 P_8 + P_2 (P_5 + P_8)) - \varepsilon P_3 P_{20} (P_2 + P_5) + P_4 P_5 P_8 P_{13} \\ & + P_2 (P_4 P_5 (P_{13} + P_8) + P_8 P_{13} (P_4 + P_5)) > 0 \end{aligned}$$

$$\begin{aligned} \text{Iff } & \psi P_1 P_{28} (P_4 + P_8) + \psi \gamma P_1 P_{30} + P_1 P_{26} (P_4 (P_5 + P_8) + P_5 P_8) + \delta P_1 P_{30} (P_4 + P_5) + P_4 P_5 P_8 P_{13} \\ & + P_2 (P_4 P_5 (P_{13} + P_8) + P_8 P_{13} (P_4 + P_5)) P_1 P_{28} > \theta P_3 P_{28} (P_2 + P_8) - \theta \gamma P_3 P_{20} - P_3 P_{27} (P_5 P_8 + P_2 (P_5 + P_8)) \\ & - \varepsilon P_3 P_{20} (P_2 + P_5) \end{aligned}$$

$$\begin{aligned} a_5 = & \psi P_1 P_{28} P_4 P_8 + P_1 P_{26} P_4 P_5 P_8 + \delta P_1 P_{30} P_4 P_5 + P_2 P_4 P_5 P_{13} P_8 - \theta P_3 P_{28} P_2 P_8 - \theta \gamma P_3 P_{20} P_2 - P_3 P_{27} P_2 P_5 P_8 \\ & - \varepsilon P_3 P_{20} P_2 P_5 > 0 \end{aligned}$$

$$\begin{aligned} \text{Iff } & \psi P_1 P_{28} P_4 P_8 + P_1 P_{26} P_4 P_5 P_8 + \delta P_1 P_{30} P_4 P_5 + P_2 P_4 P_5 P_{13} P_8 > \theta P_3 P_{28} P_2 P_8 + \theta \gamma P_3 P_{20} P_2 + P_3 P_{27} P_2 P_5 P_8 \\ & + \varepsilon P_3 P_{20} P_2 P_5 \end{aligned}$$

For order one,

$$\Delta_1 = a_1 = P_2 + P_4 + P_5 + P_{13} + P_8 > 0$$

For order two,

$$a_0 \lambda^2 + a_1 \lambda + a_2 = 0$$

$$\Delta_2 = \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} \Rightarrow \Delta_2 = a_1 a_2 - a_0 a_3 > 0$$

$$= \left(\begin{array}{l} (P_2 + P_4 + P_5 + P_{13} + P_8) \times \\ (P_1 P_{26} + P_3 P_{27}) \\ + P_2 (P_4 + P_5 + P_{13} + P_8) + P_4 P_5 \\ + (P_4 + P_5)(P_{13} + P_8) + P_{13} P_8 \end{array} \right) - \left(\begin{array}{l} (\psi P_1 P_{28} + P_1 P_{26} (P_4 + P_5 + P_8) + \delta P_1 P_{30} - \theta P_3 P_{28}) \\ - P_3 P_{27} (P_2 + P_5 + P_8) - \varepsilon P_3 P_{20} + P_4 P_5 (P_{13} + P_8) \\ + P_{13} P_8 (P_4 + P_5) + P_2 (P_4 P_5 + (P_4 + P_5)(P_{13} + P_8) + P_{13} P_8) \end{array} \right) > 0$$

For order three,

$$a_0 \lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3 = 0$$

$$\Delta_3 = \begin{vmatrix} a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 \\ a_5 & a_4 & a_3 \end{vmatrix} > 0 \Rightarrow \Delta_3 = a_1(a_2 a_3 - a_1 a_4) - a_0(a_3^2 - a_1 a_5) > 0$$

$$a_0 = 1, a_4 = 0, a_5 = 0$$

For order four,

$$a_0 \lambda^4 + a_1 \lambda^3 + a_2 \lambda^2 + a_3 \lambda + a_4 = 0$$

$$a_0 = 1, a_5 = 0, a_6 = 0, a_7 = 1$$

$$\Delta_4 = a_1 \{ (a_4(a_2 a_3 - a_1 a_4)) - a_5(a_2^2 - a_0 a_4) \} - a_0 \{ (a_4(a_3^2 - a_1 a_5)) - a_5(a_2 a_3 - a_0 a_5) \} > 0$$

$$\text{Iff } \Delta_4 = a_1 \{ (a_4(a_2 a_3 - a_1 a_4)) - a_5(a_2^2 - a_0 a_4) \} > a_0 \{ (a_4(a_3^2 - a_1 a_5)) - a_5(a_2 a_3 - a_0 a_5) \}$$

For order five,

$$a_0 \lambda^5 + a_1 \lambda^4 + a_2 \lambda^3 + a_3 \lambda^2 + a_4 \lambda + a_5 = 0$$

$$a_0 = 1, a_6 = 0, a_7 = 0, a_8 = 0, a_9 = 0$$

$$\Delta_5 = a_5 \Delta_4 > 0$$

The global stability analysis of the disease-free equilibrium

We investigated the global asymptotic stability of the disease-free equilibrium of shigella using Castillo-Chavez theorem (Castillo-Chavez & Song, 2004). We write the model equations (1) - (9) in the form:

$$\frac{dX}{dt} = F(X, Z) \tag{79}$$

$$\frac{dY}{dt} = G(X, Z), G(X, 0) = 0 \tag{80}$$

where $X = (S, V, G, R) \in R_+^4$ represents the uninfected individuals and $Z = (E, A, I, H, B) \in R_+^5$ represents the infected individuals. Let $E^\circ = (X^*, 0)$ represents the disease-free equilibrium point of the system.

The disease-free equilibrium E° to be globally asymptotically stable equilibrium for the model, the conditions (H1) and (H2) shown below should be satisfied:

H1: For $\frac{dX}{dt} = F(X, 0)$, X^* globally asymptotically stable.

H2: For $\frac{dZ}{dt} = D_Z G(X^*, 0)Z - \bar{G}(X, Z)$, $\bar{G}(X, Z) \geq 0$ for all $(X, Z) \in \Omega$, where $D_Z G(X^*, 0)$ is the Jacobian of $G(X, Z)$ evaluated at $(X^*, 0)$.

Theorem 5:

The equilibrium point $E^\circ = (X^*, 0)$ of the system (79) and (80) is globally asymptotically stable if $R_0 < 1$ and the conditions (H1) and (H2) are satisfied.

Proof:

We partitioned the modified model system into two subsystems. These are $X = (S, V, G, R) \in R_+^4$ and $Z = (E, A, I, H, B) \in R_+^5$. From equation (79) and (80) we have two functions: $F(X, Z)$ and $G(X, Z)$, where

Condition H1:

$$\frac{dX}{dt} = F(X, Z) = \begin{pmatrix} \frac{dS}{dt} = \pi + nV + eG + \alpha_2(1-\phi)R - \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K+B} \right) S - (m + f + \mu)S \\ \frac{dV}{dt} = mS - (n + \mu)V \\ \frac{dG}{dt} = fS + \alpha_1 \phi R - (e + \mu)G \\ \frac{dR}{dt} = rH + \eta A + \rho I - (\alpha_1 \phi + \alpha_2(1-\phi) + \mu)R \end{pmatrix}$$

$$\frac{dX}{dt} = F(X, 0) = \begin{pmatrix} \left. \frac{dS}{dt} \right|_{E^\circ} = \pi + nV + eG - (m + f + \mu)S \\ \left. \frac{dV}{dt} \right|_{E^\circ} = mS - (n + \mu)V \\ \left. \frac{dG}{dt} \right|_{E^\circ} = fS - (e + \mu)G \\ \left. \frac{dR}{dt} \right|_{E^\circ} = 0 \end{pmatrix} \tag{81}$$

Therefore, the convergence of the solutions of the reduced system equation (81) is globally asymptotically stable in Ω .

Condition H2: $\frac{dZ}{dt} = G(X, Z) =$

$$\begin{pmatrix} \frac{dE}{dt} = \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K+B} \right) S - (\omega + \mu)E \\ \frac{dA}{dt} = (1-q)\omega E - (\eta + \psi + \mu)A \\ \frac{dI}{dt} = q\omega E - (\theta + \rho + d_1 + \mu)I \\ \frac{dH}{dt} = \theta I + \psi A - (r + d_2 + \mu)H \\ \frac{dB}{dt} = \varepsilon I + \delta A + \gamma H - (\sigma_2 - \sigma_3 - \sigma_1)B \end{pmatrix}$$

$$\frac{dZ}{dt} = G(X, 0) = \begin{pmatrix} \left. \frac{dE}{dt} \right|_{E^\circ} = 0 \\ \left. \frac{dA}{dt} \right|_{E^\circ} = 0 \\ \left. \frac{dI}{dt} \right|_{E^\circ} = 0 \\ \left. \frac{dH}{dt} \right|_{E^\circ} = 0 \\ \left. \frac{dB}{dt} \right|_{E^\circ} = 0 \end{pmatrix} = 0$$

More so,

$$G(X, Z) = AZ - \hat{G}(X, Z)$$

$$\hat{G}(X, Z) = AZ - G(X, Z)$$

where

$$A = \frac{\partial G}{\partial Z}(X^*, 0) = D_Z(X^*, 0) \text{ is a Metzler matrix.}$$

Let

$$\frac{dE}{dt} = f_1 = \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K+B} \right) S - (\omega + \mu) E$$

$$\frac{dA}{dt} = f_2 = (1-q)\omega E - (\eta + \psi + \mu) A$$

$$\frac{dI}{dt} = f_3 = q\omega E - (\theta + \rho + d_1 + \mu) I$$

$$\frac{dH}{dt} = f_4 = \theta I + \psi A - (r + d_2 + \mu) H$$

$$\frac{dB}{dt} = f_5 = \varepsilon I + \delta A + \gamma H - (\sigma_2 - \sigma_3 - \sigma_1) B$$

The Jacobian matrix from the partial derivatives of (4), (5), (6), (7) and (9) with respect to the infected variables at disease-free ($A = J_{E^0}$) is given by:

$$A = J_{E^0} = \begin{pmatrix} -(\omega + \mu) & \beta_2 S^0 & \beta_1 S^0 & \beta_3 S^0 & \frac{\beta_B S^0}{K} \\ (1+q)\omega & -(\eta + \psi + \mu) & 0 & 0 & 0 \\ q\omega & 0 & -(\theta + \rho + d_1 + \mu) & 0 & 0 \\ 0 & \psi & \theta & -(r + d_2 + \mu) & 0 \\ 0 & \delta & \varepsilon & \gamma & -(\sigma_2 + \sigma_3 - \sigma_1) \end{pmatrix}$$

Let $y_1 = \beta_2 S^0$, $y_2 = \beta_1 S^0$, $y_3 = \beta_3 S^0$ and $y_4 = P_{30} = \frac{\beta_B S^0}{K}$

$$\Rightarrow A = J_{E^0} = \begin{pmatrix} -P_{14} & y_1 & y_2 & y_3 & y_4 \\ P_1 & -P_2 & 0 & 0 & 0 \\ P_3 & 0 & -P_4 & 0 & 0 \\ 0 & \psi & \theta & -P_5 & 0 \\ 0 & \delta & \varepsilon & \gamma & -P_8 \end{pmatrix}$$

$$\hat{G}(X, Z) = AZ - G(X, Z)$$

$$= \begin{pmatrix} -P_{14} & y_1 & y_2 & y_3 & y_4 \\ P_1 & -P_2 & 0 & 0 & 0 \\ P_3 & 0 & -P_4 & 0 & 0 \\ 0 & \psi & \theta & -P_5 & 0 \\ 0 & \delta & \varepsilon & \gamma & -P_8 \end{pmatrix} \begin{pmatrix} E \\ A \\ I \\ H \\ B \end{pmatrix} - \begin{pmatrix} \left(\beta_1 I + \beta_2 A + \beta_3 H + \frac{\beta_B B}{K+B} \right) S - (\omega + \mu) E \\ (1-q)\omega E - (\eta + \psi + \mu) A \\ q\omega E - (\theta + \rho + d_1 + \mu) I \\ \theta I + \psi A - (r + d_2 + \mu) H \\ \varepsilon I + \delta A + \gamma H - (\sigma_2 - \sigma_3 - \sigma_1) B \end{pmatrix}$$

$$\hat{G}_1(X, Z) = -P_{14}E + y_1A + y_2I + y_3H + y_4B - \left(\left(\beta_1I + \beta_2A + \beta_3H + \frac{\beta_B B}{K+B} \right) S - (\omega + \mu)E \right)$$

$$\hat{G}_1(X, Z) = (\beta_1I + \beta_2A + \beta_3H)(S^\circ - S) + \left(\frac{S^\circ}{K} - \frac{S}{K+B} \right) \beta_B B$$

$$\hat{G}_2(X, Z) = P_1E + P_2A - ((1-q)\omega E - (\eta + \psi + \mu)A)$$

$$\hat{G}_2(X, Z) = (1-q)\omega E - (\eta + \psi + \mu)A - ((1-q)\omega E - (\eta + \psi + \mu)A) = 0$$

$$\hat{G}_3(X, Z) = P_3E - P_4I - (q\omega E - (\theta + \rho + d_1 + \mu)I)$$

$$\hat{G}_3(X, Z) = q\omega E - (\theta + \rho + d_1 + \mu)I - (q\omega E - (\theta + \rho + d_1 + \mu)I) = 0$$

$$\hat{G}_4(X, Z) = \psi A + \theta I - P_5H - (\theta I + \psi A - (r + d_2 + \mu)H)$$

$$\hat{G}_4(X, Z) = \theta I + \psi A - (r + d_2 + \mu)H - (\theta I + \psi A - (r + d_2 + \mu)H) = 0$$

$$\hat{G}_5(X, Z) = \delta A + \varepsilon I + \gamma H - P_8B - (\varepsilon I + \delta A + \gamma H - (\sigma_2 - \sigma_3 - \sigma_1)B)$$

$$\hat{G}_5(X, Z) = \delta A + \varepsilon I + \gamma H - (\sigma_2 - \sigma_3 - \sigma_1)B - (\varepsilon I + \delta A + \gamma H - (\sigma_2 - \sigma_3 - \sigma_1)B) = 0$$

$$\hat{G}(X, Z) = \begin{pmatrix} \hat{G}_1(X, Z) \\ \hat{G}_2(X, Z) \\ \hat{G}_3(X, Z) \\ \hat{G}_4(X, Z) \\ \hat{G}_5(X, Z) \end{pmatrix} \Rightarrow \hat{G}(X, Z) = \begin{pmatrix} (\beta_1I + \beta_2A + \beta_3H)(S^\circ - S) + \left(\frac{S^\circ}{K} - \frac{S}{K+B} \right) \beta_B B \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

$$\hat{G}(X, Z) = (\beta_1I + \beta_2A + \beta_3H)(S^\circ - S) + \left(\frac{S^\circ}{K} - \frac{S}{K+B} \right) \beta_B B \geq 0$$

$$\hat{G}(X, Z) \geq 0 \quad \forall (X, Z) \in \Omega, \text{ provided that } S^\circ \geq S.$$

Sensitivity analysis

The sensitivity indices of the basic reproduction number R_0 with respect to each parameter in the extended model equations of shigella infection was analyzed using the numerical values in Table 3 below

Table 3: Parameter values for the shigella model.

Parameter	Description	Values per day	Source
π	Recruitment rate.	500	(Edward <i>et al.</i> , 2018)
m	The rate at which the susceptible individuals move to the vaccinated class.	0.02	Assumed
n	The rate at which the vaccinated individuals move to the susceptible class.	0.027	Assumed

f	The rate at which susceptible individuals move to the sensitized class.	0.7	Assumed
e	The rate at which sensitized individuals (who failed to adhere to the sensitization they received) moved back to the susceptible class.	0.42	Assumed
θ	The rate at which the infected individuals moved to hospitalized class.	0.03	Assumed
r	The rate at which hospitalized individuals moved to the recovered class.	0.06	Assumed
η	The rate at which the asymptomatic individuals moved to the recovered class.	0.41	Assumed
μ	Natural death rate.	0.45	Assumed
d_1	The death rate due to the disease in the infected class.	0.02	(Edward <i>et al.</i> , 2018)
d_2	The death rate due to the disease in the hospitalized class.	0.025	Assumed
q	The proportion of the exposed individuals who moved to the infected class at a rate ω .	0.9	(Edward <i>et al.</i> , 2018)
$(1 - q)$	The proportion of the exposed individuals who moved to the asymptomatic class at a rate ω .	0.1	Assumed
ψ	The rate at which Asymptomatic individuals moved to the hospitalized class.	0.04	Assumed
ρ	The rate at which infected individuals moved to the recovered class.	0.14	Assumed
κ	The concentration of <i>Shigella</i> in the environment that yields 50% chance of catching dysentery diarrhea	600	Assumed
β_1	The transmission rate of shigella for the infected individuals due to human to human interaction.	0.095	Assumed
β_2	The transmission rate of shigella for the asymptomatic individuals due to human to human interaction.		0.075
Assumed			
β_3	The transmission rate of shigella for the hospitalized individuals due to human to human interaction.	0.055	Assumed
β_B	The ingestion rate of shigella by human from the environment.	0.00039	Assumed

ε	Shigella pathogen shedding rate for the infected individuals.	80	(Edward <i>et al.</i> , 2018)
δ	Shigella pathogen shedding rate for the asymptomatic individuals.	70	(Edward <i>et al.</i> , 2018)
γ	Shigella pathogen shedding rate for the hospitalized individuals.	90	Assumed
σ_1	Shigella pathogen growth rate.	0.73	Assumed
σ_2	Shigella pathogen natural death rate.	0.83	(Edward <i>et al.</i> , 2018)
σ_3	Death rate of shigella pathogen due to environmental contamination.	1.60	(Edward <i>et al.</i> , 2018)

Table 4: The sensitivity indices of the basic reproduction number R_0 with respect to each parameter in R_0 of the extended model equations of shigella infection.

Parameters	Sensitivity indices
π	$U_{\pi}^{R_0} = \frac{\partial R_0}{\partial \pi} \times \frac{\pi}{R_0} = +1.0000$
m	$U_m^{R_0} = \frac{\partial R_0}{\partial m} \times \frac{m}{R_0} = \frac{P_{12}(n - P_{11})}{F_4} = -0.0227$
n	$U_n^{R_0} = \frac{\partial R_0}{\partial n} \times \frac{n}{R_0} = \frac{[\pi F_4 P_{12} - F_3(P_{10} P_{12} - m P_{12} - ef)]n}{F_3 F_4} = +0.0013$
e	$U_e^{R_0} = \frac{\partial R_0}{\partial e} \times \frac{e}{R_0} = \frac{[\pi F_4 P_{11} - F_3(P_{10} P_{11} - mn - f P_{11})]e}{F_3 F_4} = +0.2104$
f	$U_f^{R_0} = \frac{\partial R_0}{\partial f} \times \frac{f}{R_0} = \frac{-f P_{11}(P_{12} - e)}{F_4} = -0.4357$
β_1	$U_{\beta_1}^{R_0} = \frac{\partial R_0}{\partial \beta_1} \times \frac{\beta_1}{R_0} = \frac{K P_2 P_3 P_5 P_8 \beta_1}{F_1} = +0.9101$
β_2	$U_{\beta_2}^{R_0} = \frac{\partial R_0}{\partial \beta_2} \times \frac{\beta_2}{R_0} = \frac{K P_1 P_4 P_5 P_8 \beta_2}{F_1} = +0.0568$
β_3	$U_{\beta_3}^{R_0} = \frac{\partial R_0}{\partial \beta_3} \times \frac{\beta_3}{R_0} = \frac{K(P_1 P_4 \psi + P_2 P_3 \theta) P_8 \beta_2}{F_1} = +0.0327$
β_B	$U_{\beta_B}^{R_0} = \frac{\partial R_0}{\partial \beta_B} \times \frac{\beta_B}{R_0} = \frac{[P_1 P_4 (\psi \gamma + P_5 \delta) + P_2 P_3 (\theta \gamma + P_5 \varepsilon)] \beta_B}{F_1} = +0.0005$
κ	$U_K^{R_0} = \frac{\partial R_0}{\partial K} \times \frac{K}{R_0} = \frac{[[P_1 P_4 P_5 P_8 \beta_2 + P_2 P_3 P_5 P_8 \beta_1 + (P_1 P_4 \psi + P_2 P_3 \theta) \beta_3 P_8] \times F_2 - F_1 \times P_2 P_4 P_5 P_8 P_{13}] K}{F_1 F_2} = -0.0005$

$$\omega \quad U_{\omega}^{R_0} = \frac{\partial R_0}{\partial \omega} \times \frac{\omega}{R_0} = \frac{\left[\frac{\left[\left[(1-q)\beta_2 KP_4 P_5 P_8 + q\beta_1 KP_2 P_5 P_8 + \right] + \left[(1-q)P_4 \psi + qP_2 \theta \right] K\beta_3 P_8}{\left[(1-q)P_4 (\psi\gamma + P_5 \delta) + qP_2 (\theta\gamma + P_5 \varepsilon) \right] \beta_B} \right] F_2 - F_1 \times KP_2 P_4 P_5 P_8}{F_1 F_2} \right] \omega}{F_1 F_2}$$

$$= +0.5625$$

$$q \quad U_q^{R_0} = \frac{\partial R_0}{\partial q} \times \frac{q}{R_0} = \frac{\left[\frac{\left[-\omega\beta_2 KP_4 P_5 P_8 + \omega\beta_1 KP_2 P_5 P_8 + \right] + \left[-\omega P_4 (\psi\gamma + P_5 \delta) + \omega P_2 (\theta\gamma + P_5 \varepsilon) \right] \beta_B}{\left[-\omega P_4 \psi + \omega P_2 \theta \right] K\beta_3 P_8} \right] q}{F_1}$$

$$= +0.3996$$

$$\eta \quad U_{\eta}^{R_0} = \frac{\partial R_0}{\partial \eta} \times \frac{\eta}{R_0} = \frac{\left[\left[K\beta_1 P_3 P_5 P_8 + K\beta_3 P_3 P_8 \theta + P_3 (\theta\gamma + P_5 \varepsilon) \beta_B \right] F_2 - F_1 \left[KP_4 P_5 P_8 P_{13} \right] \right] \eta}{F_1 F_2}$$

$$= -0.0274$$

$$\psi \quad U_{\psi}^{R_0} = \frac{\partial R_0}{\partial \psi} \times \frac{\psi}{R_0} = \frac{\left[\left[K\beta_1 P_3 P_5 P_8 + K\beta_3 P_1 P_4 P_8 + K\beta_3 P_3 P_8 \theta + P_1 P_4 \gamma \beta_B + P_3 (\theta\gamma + P_5 \varepsilon) \beta_B \right] F_2 - F_1 \left[KP_4 P_5 P_8 P_{13} \right] \right] \psi}{F_1 F_2}$$

$$= +0.0005805$$

$$\theta \quad U_{\theta}^{R_0} = \frac{\partial R_0}{\partial \theta} \times \frac{\theta}{R_0} = \frac{\left[\left[K\beta_2 P_1 P_5 P_8 + K\beta_3 P_1 P_8 \psi + K\beta_3 P_2 P_3 P_8 + P_2 P_3 \gamma \beta_B + P_1 (\psi\gamma + P_5 \delta) \beta_B \right] F_2 - F_1 \left[KP_2 P_5 P_8 P_{13} \right] \right] \theta}{F_1 F_2}$$

$$= -0.0145$$

$$\rho \quad U_{\rho}^{R_0} = \frac{\partial R_0}{\partial \rho} \times \frac{\rho}{R_0} = \frac{\left[\left[K\beta_2 P_1 P_5 P_8 + K\beta_3 P_1 P_8 \psi + P_1 (\psi\gamma + P_5 \delta) \beta_B \right] F_2 - F_1 \left[KP_2 P_5 P_8 P_{13} \right] \right] \rho}{F_1 F_2}$$

$$= -0.2056$$

$$d_1 \quad U_{d_1}^{R_0} = \frac{\partial R_0}{\partial d_1} \times \frac{d_1}{R_0} = \frac{\left[\left[K\beta_2 P_1 P_5 P_8 + K\beta_3 P_1 P_8 \psi + P_1 (\psi\gamma + P_5 \delta) \beta_B \right] F_2 - F_1 \left[KP_2 P_5 P_8 P_{13} \right] \right] d_1}{F_1 F_2}$$

$$= -0.0294$$

$$d_2 \quad U_{d_2}^{R_0} = \frac{\partial R_0}{\partial d_2} \times \frac{d_2}{R_0} = \frac{\left[\left[K\beta_2 P_1 P_4 P_8 + K\beta_1 P_2 P_3 P_8 + (P_1 P_4 \delta + P_2 P_3 \varepsilon) \beta_B \right] F_2 - F_1 \left[KP_2 P_4 P_8 P_{13} \right] \right] d_2}{F_1 F_2}$$

$$= -0.0015$$

$$r \quad U_r^{R_0} = \frac{\partial R_0}{\partial r} \times \frac{r}{R_0} = \frac{\left[\left[K\beta_2 P_1 P_4 P_8 + K\beta_1 P_2 P_3 P_8 + (P_1 P_4 \delta + P_2 P_3 \varepsilon) \beta_B \right] F_2 - F_1 \left[KP_2 P_4 P_8 P_{13} \right] \right] r}{F_1 F_2}$$

$$= -0.0037$$

$$\delta \quad U_{\delta}^{R_0} = \frac{\partial R_0}{\partial \delta} \times \frac{\delta}{R_0} = \frac{-\left[KP_2 P_4 P_5 P_8 \right] \omega}{F_2} = -0.4375$$

$$\varepsilon \quad U_{\varepsilon}^{R_0} = \frac{\partial R_0}{\partial \varepsilon} \times \frac{\varepsilon}{R_0} = \frac{-\left[KP_2 P_4 P_5 P_8 \right] \omega}{F_2} = -0.4375$$

$$\gamma \quad U_{\gamma}^{R_0} = \frac{\partial R_0}{\partial \gamma} \times \frac{\gamma}{R_0} = \frac{-\left[KP_2 P_4 P_5 P_8 \right] \omega}{F_2} = -0.4375$$

$$\sigma_1 \quad U_{\sigma_1}^{R_0} = \frac{\partial R_0}{\partial \sigma_1} \times \frac{\sigma_1}{R_0} = \frac{\left[-K\beta_2 P_1 P_4 P_5 - K\beta_1 P_2 P_3 P_5 - (P_1 P_4 \psi + P_2 P_3 \theta) K\beta_3 \right] F_2 + F_1 \left[KP_2 P_4 P_5 P_{13} \right] \sigma_1}{F_1 F_2}$$

$$\begin{aligned}
 &= +0.0002010 \\
 \sigma_2 \quad U_{\sigma_2}^{R_0} &= \frac{\partial R_0}{\partial \sigma_2} \times \frac{\sigma_2}{R_0} = \frac{[[K\beta_2 P_1 P_4 P_5 + K\beta_1 P_2 P_3 P_5 + (P_1 P_4 \psi + P_2 P_3 \theta) K\beta_3] F_2 - F_1 [K P_2 P_4 P_5 P_{13}]] \sigma_2}{F_1 F_2} \\
 &= -0.0002286 \\
 \sigma_3 \quad U_{\sigma_3}^{R_0} &= \frac{\partial R_0}{\partial \sigma_3} \times \frac{\sigma_3}{R_0} \\
 &= \frac{[[K\beta_2 P_1 P_4 P_5 + K\beta_1 P_2 P_3 P_5 + (P_1 P_4 \psi + P_2 P_3 \theta) K\beta_3] F_2 - F_1 [K P_2 P_4 P_5 P_{13}]] \sigma_3}{F_1 F_2} = -0.0004406 \\
 \mu \quad U_{\mu}^{R_0} &= \frac{\partial R_0}{\partial \mu} \times \frac{\mu}{R_0} = \left[\frac{F_1' F_2 - F_1 F_2'}{F_1^2} \right] \times \frac{F_3}{F_4} + \left[\frac{F_4 F_3' - F_3 F_4'}{F_4^2} \right] \times \frac{F_1}{F_2} = -2.0342
 \end{aligned}$$

where; $F_1 = K\beta_2 P_1 P_4 P_5 P_8 + K\beta_1 P_2 P_3 P_5 P_8 + (P_1 P_4 \psi + P_2 P_3 \theta) K\beta_3 P_8 + [P_1 P_4 (\psi \gamma + P_5 \delta) + P_2 P_3 (\theta \gamma + P_5 \varepsilon)] \beta_B$,
 $F_1 = 5.003962$; $F_2 = K P_2 P_4 P_5 P_{13} = 27.46617754$; $F_4 = P_{10} P_{11} P_{12} - mn P_{12} - ef P_{11} = 0.3448$;
 $F_3 = \pi P_{11} P_{12} = 207.495$; $F_1' = 28.1873319$, $F_2' = 171.4656762$, $F_3' = 5.103$ and $F_4' = 1.6851$.

From the sensitivity analysis, it was discovered that the following parameters have high impact on the transmission of the diseases. They are: the transmission rate β_1 of the asymptomatic individuals and the rate at which the exposed individuals moved to either asymptomatic or infected class ω . Table 4 presented the sensitivity index of the shigella model with respect to R_0 . The result of the sensitivity index presented above in Table 4 shows that the recruitment rate π has the highest positive sensitivity index with value $U_{\pi}^{R_0} = +1.0000$, which indicates that an increase (a decrease) in the rate π by 10% will increase (decrease) the basic reproduction number R_0 by 10%. Similarly, increase in the other positive values of the sensitivity indices will increase the basic reproduction number.

Moreover, the natural death rate of human μ has the highest negative sensitivity index with value $U_{\mu}^{R_0} = -2.0342$ which indicates that an increase in μ by 10% will decrease the basic reproduction number R_0 by 10% and a decrease in μ by 10% will increase the basic reproduction number R_0 by 10%.

The conclusion is that the natural death rate of human μ has the highest sensitivity index with value $U_{\mu}^{R_0} = -2.0342$.

Numerical results

In this section, we carried out the numerical solution of the system (1) – (9) using the Runge-Kutta order four scheme. The numerical results are shown in Figure 2 and 3. Figure 2, represented the graph of the model when the basic reproduction number is greater than one and Figure 3, represented the graph of the model when the value of the basic reproduction number is less than or equal to one.

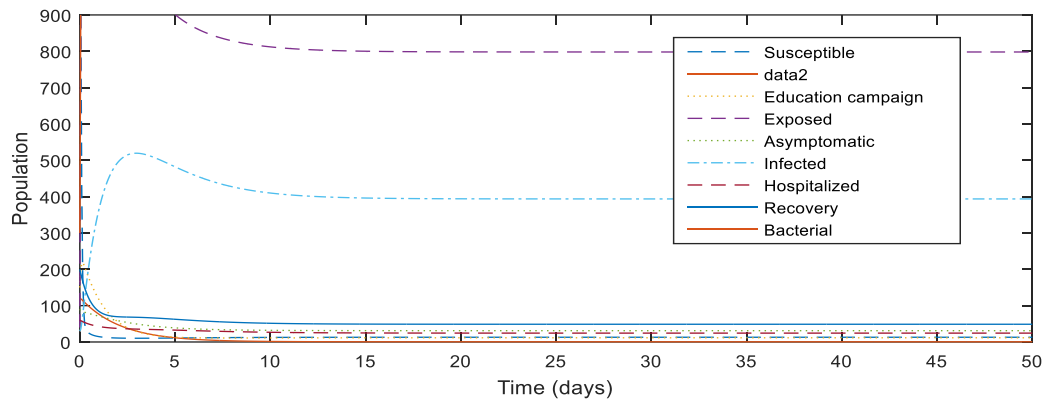


Figure2: The graphical behaviour of the dynamic system (1) – (9) with a given initial condition and parameter values: when $R_0 = 3.8643 > 1$, the endemic equilibrium point is locally asymptotically stable.

Where $\pi = 500, m = 0.02, n = 0.027, e = 0.42, f = 0.7, \beta_1 = 0.095, \beta_2 = 0.075, \beta_3 = 0.055, K = 600, \beta_B = 0.00039, \omega = 0.35, q = 0.9, \eta = 0.41, \psi = 0.04, \theta = 0.03, \rho = 0.14, d_1 = 0.02, d_2 = 0.025, r = 0.06, \delta = 70, \varepsilon = 80, \gamma = 90, \sigma_1 = 0.73, \sigma_2 = 0.83, \sigma_3 = 1.60, \mu = 0.45, \alpha_1 = 0.65, \alpha_2 = 0.98, \phi = 0.029$.

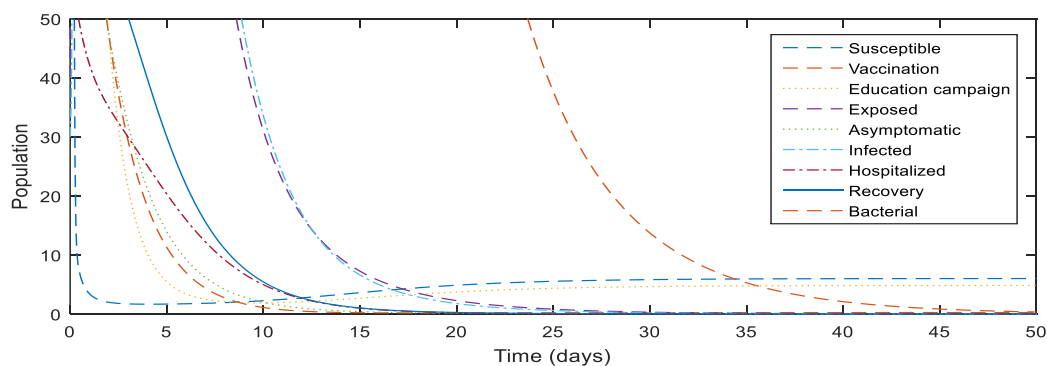


Figure3: The graphical behaviour of the dynamic system (1) – (9) with a given initial condition and parameter values: when $R_0 = 0.0388 < 1$, the disease-free equilibrium point is locally asymptotically stable.

Where $\pi = 5, m = 0.02, n = 0.027, e = 0.42, f = 0.7, \beta_1 = 0.0095, \beta_2 = 0.0075, \beta_3 = 0.0055, K = 60, \beta_B = 0.000039, \omega = 0.35, q = 0.9, \eta = 0.41, \psi = 0.04, \theta = 0.03, \rho = 0.14, d_1 = 0.02, d_2 = 0.025, r = 0.06, \delta = 70, \varepsilon = 80, \gamma = 90, \sigma_1 = 0.73, \sigma_2 = 0.83, \sigma_3 = 1.60, \mu = 0.45, \alpha_1 = 0.65, \alpha_2 = 0.98, \phi = 0.029$.

CONCLUSION

In this Paper, we formulated a mathematical model equation of shigella infection with the aid of system of ordinary differential equations to study the dynamics of shigella infection by incorporating a vaccinated class (V), educated class (G), exposed class (E), asymptomatic (A) hospitalized class (H) and Bacteria class (B) with their corresponding parameters. We investigated the existence and uniqueness of solution for the dynamic system using the Lipchitz condition to ascertain the effectiveness of the model as well as the positively invariant region of the system. The next generation matrix approach was used to determine the basic reproduction number R_0 . The disease free equilibrium (DFE) was obtained. We also obtained the local and global stability of the disease free equilibrium. We obtained the numerical solution of the model system in MATLAB. From the simulation, we observed that the shigella infection persist in the environment with the original parameter values whose $R_0 = 3.8643 > 1$ and was eradicated when some of the parameter values were varied and $R_0 = 0.0388 < 1$.

REFERENCES

- Ojaswita, C., Tiny, M., Shedden, M. (2014), A Continuous Mathematical Model for Shigella outbreaks, *American Journal of Biomedical Engineering*, Vol. 4 No. 1, pp. 10-16. doi: 10.5923/j.ajbe.20140401.02.
- Rodriguez, Margret (2022). " Gram negative bacilli and coccobacilli: Entero bacteriaceae, Shigella". *Microbiology for Surgical Technologists* (3rd ed.). Cengage. pp. 222–224. ISBN 978-0-357-62624-5.
- Yabuuchi, E. (2002). "Bacillus dysentericus (sic) 1897 was the first taxonomic rather than Bacillus dysenteriae 1898". *International Journal of Systematic and Evolutionary Microbiology*. **52** (Pt 3): 1041. doi:10.1099/00207713-52-3-1041. PMID 12054222.
- Ryan, K.J. & Ray, C.G. (2004). *Sherris medical microbiology: an introduction to infectious diseases* (4th ed.). McGraw-Hill Professional Med/Tech. ISBN 978-0-8385-8529-0.
- Pond, K (2005). "Shigella". *Water recreation and disease. Plausibility of associated infections: Acute effects, sequelae and mortality*. WHO. pp. 113–8. ISBN 978-92-4-156305-5.
- Mims, C., Dockrell, H., Goering, R., Roitt, I., Wakelin, D., Zuckerman, M eds. (2004). *Medical Microbiology* (3rd ed.). Mosby. p. 287. ISBN 978-0-7234-3259-3. <https://researchonline.lshtm.ac.uk/id/eprint/14346>
- Centers for Disease Control and Prevention (2016). "Shigella – Shigellosis". Archived from the Original on 24 July 2016. Retrieved 29 July.
- Ebenezer, B. G. T. and Patience, P. G. (2019), Mathematical analysis of diarrhea model with Saturated incidence rate. *An open journal of mathematical sciences*. DOI:10.30538/oms2019.0046
- Hailay, W. B., Oluwole, D. M. & David, M. T. (2019a) Modelling the dynamics of direct and pathogens-induced dysentery diarrhoea epidemic with controls, *Journal of Biological*

Dynamics, 13:1, 192-217, DOI: 10.1080/17513758.2019.1588400.

- Berhe, H. W., Makinde, O. D., and Theuri, D. M. (2019) "Co-dynamics of measles and dysentery diarrhea diseases with optimal control and cost-effectiveness analysis," *Applied Mathematics and Computation*, vol. 347, pp. 903–921. DOI: 10.1016/j.amc.2018.11.049
- Cabral, Joao P. S., (2010) Water Microbiology. Bacterial Pathogens and Water, International Journal of Environmental Research and Public Health, Vol. 7, No. 10, pp. 3657-3703. Doi: 10.3390/ijerph7103657
- Bani-Yaghoub, Majid and Gautam, Raju and Shuai, Zhisheng and van den Driessche, P. and Ivanek, Renata (2012) Reproduction Numbers for Infections with Free-Living Pathogens Growing in the Environment, *Journal of Biological Dynamics*, Vol. 6, No. 2, pp. 923-940. <https://doi.org/10.1080/17513758.2012.693206>
- Nelson, K. E. & Williams, C. (2013). *Infectious disease epidemiology*, Jones & Bartlett Publishers. doi: 10.1007/978-0-387-09834-0_34
- Addo, D. (2009). Mathematical model for the control of malaria, Ph.D. thesis, University Of Cape Coast. <http://hdl.handle.net/123456789/1436>
- Heffernan, J., Smith, R. & Wahl, L. (2005). Perspectives on the basic reproductive ratio, *Journal of the Royal Society Interface* 2 (4) 281–293. doi: 10.1098/rsif.2005.0042
- Van den Driessche, P. & Watmough, J. (2002) Reproduction numbers and subthreshold endemic equilibria for compartmental models of disease transmission, *Mathematical biosciences* 180 (1), 29–48. DOI: 10.1016/s0025-5564(02) 00108-6
- Castillo-Chavez, C. and Song, B.(2004) Dynamical models of Tuberculosis and their applications. *Math. Biosci.Eng*, 1(2):361- 404. DOI: 10.3934 /mbe.2004. 1.361