

Mathematical modeling of typhoid fever disease incorporating unprotected humans in the spread dynamics.

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Abstract

A deterministic mathematical model of typhoid fever incorporating unprotected humans is formulated in this study and employed to study local and global stability of equilibrium points. The model incorporating Susceptible, unprotected, Infectious and Recovered humans which are analyzed mathematically and also result into a system of ordinary differential equations which are used for interpretations and comparison to the qualitative solutions in studying the spread dynamics of typhoid fever. Jacobian matrix was considered in the study of local stability of disease free equilibrium point and Castillo-Chavez approach used to determine global stability of disease free equilibrium point. Lyapunov function was used to study global stability of endemic equilibrium point. Both equilibrium points (DFE and EE) were found to be local and globally asymptotically stable. This means that the disease will be dependent on numbers of unprotected humans and other factors who contributes positively to the transmission dynamics.

.Key words: Basic reproduction number; Invariant region; Positivity of solution; Mathematical model; Unprotected humans; Disease Free Equilibrium; Endemic equilibrium point; Global stability.

1 Introduction

Typhoid fever is an endemic infectious disease that can be classified as enteritis diseases, and it is caused by presence of bacterium called *Salmonella Typhi* in the human body [15]. The disease is a common infectious disease in human beings and it's transmitted through food and water contaminated with faeces and urine of an infected person [3, 11, 12 and 17]. The disease is endemic in developing countries where it continuously causes illness and death. This is brought about by unsafe water supply, poor food hygiene and also wanting environmental sanitation. Incubation period is 7 to 14 days [3, 17]. General symptoms and effects of typhoid are the following; headache, stomachache, Joint ache, backache, muscle pain, loss of appetite, vomiting, diarrhea, rashes and fever. According to World Health Organization an estimated 17 million illness cases of typhoid fever were reported per year worldwide resulting to 0.6 million deaths annually[4,5]. Typhoid fever is an endemic disease that is classified as an enteritis disease. The disease is caused by a bacterium called *Salmonella Typhi*. It is a common infectious disease in human beings and is transmitted through food and water contaminated with faeces and urine of an infected person [3]. The disease is endemic in developing countries where it continuously causes illness and death. This is contributed by unsafe water supply, poor food hygiene and wanting environmental sanitation. According to World Health Organization an estimated 17 million illness cases of typhoid fever were reported per year worldwide resulting to 0.6 million deaths annually[4,5]. A lot of research has so far been done the last two decades, different researchers have come up with different mathematical models for instance[1,2,8]on other diseases among others and[3,5,6,7,11,12,15,17]for typhoid fever. In reference to [11,12] the author considered global stability of equilibrium points of typhoid fever model with protection, in their SPIT model they found out that the disease transmission can be kept minimal or manageable when protection is involved. Motivated by this work [11,12]; we considered a SEIR model incorporating the unprotected humans in the spread dynamics instead of protection basing our argument that the unprotected humans are also very important in the spread dynamics and contributes in spreading the infection when they interact with other population subclasses and also the environment.

2 Description and model formulation

We formulated a deterministic model for spread dynamics of typhoid fever that considers human population at time t . The model framework is divided into four compartments as follows. Susceptible(S), Unprotected (E), Infective (I) and Recovered(R). The model has the following flow. $S \rightarrow E \rightarrow I \rightarrow R \rightarrow S$.

We have used the following parameters in our model. (i) μ is the natural death rate (ii) α is the disease induced death rate. (iii) Λ human recruitment rate (birth). (iv) β disease interaction rate. (v) Ω unprotected symptoms showing rate (vi) γ Infective recovery rate and finally (vii) δ this is the rate at which recovered humans loses temporary immunity obtained through treatment and get the disease back again.

Since we are dealing with a population; all population compartments is positive $\forall t > 0$ in the feasible region $\varphi = \{S, E, I, R\} \in \varphi \subset R^4_+$ in. It can be shown that all the solutions are bounded

in φ , $\forall t > 0$ such that $0 \leq N \leq \frac{\Lambda}{\mu}$.Therefore the model is epidemiologically well posed in the region φ and is justified to be analyzed.

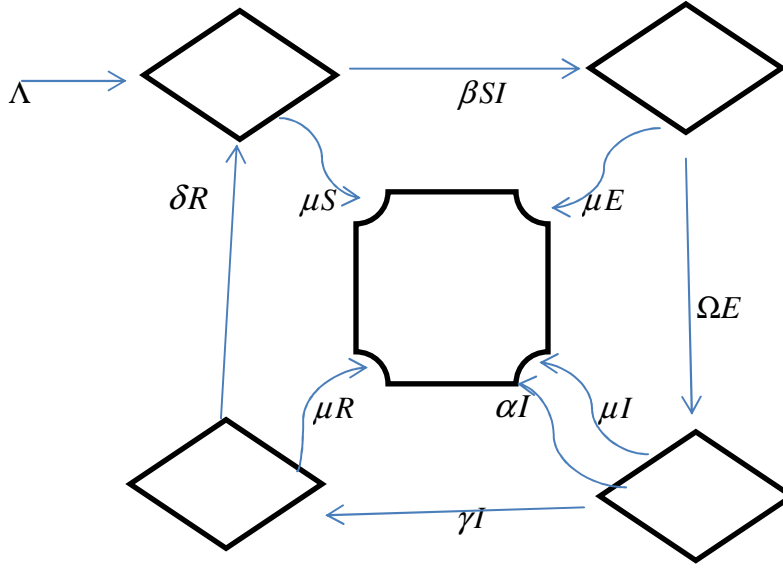


Fig 1.Compartmental diagram for an SEIR model of spread of typhoid fever with unprotected human compartment.

From the above model the transition between compartments can now be expressed into four non-linear differential equations defined as follows [20]

$$\begin{aligned}
 i) \frac{dS}{dt} &= \Lambda + \delta R - \beta SI - \mu S \\
 ii) \frac{dE}{dt} &= \beta SI - \Omega E - \mu E \\
 iii) \frac{dI}{dt} &= \Omega E - \gamma I - \alpha I - \mu I \\
 iv) \frac{dR}{dt} &= \gamma I - \delta R - \mu R
 \end{aligned} \tag{1}$$

Whereby $N(t) = S(t) + E(t) + I(t) + R(t)$

The model equations are non- linear and they describe the following. i) Describes dynamics of susceptible humans. ii) Describes dynamics of unprotected humans. iii) Describes dynamics of infected humans. iv) Describes dynamics of recovered humans.

3 Disease free equilibrium point (DFE)

At disease free equilibrium point given by $(E_1^*) = (S^* E^* I^* R^*)$; there is no disease in the population which implies absence of infective, unprotected and recovered humans. In our model is obtained by setting dynamical system of equations in 1 to zero as done by authors in [18]. At this point $E=I=R=0$, therefore $(E^* = 0, I^* = 0 \text{ and } R^* = 0)$ while $S \neq 0$ in all the differential equations.

Using the first equation of system 1, equating it to zero and making S the subject gives

$$\Lambda + \delta R - \beta SI - \mu S = 0.$$

$$\Lambda - \mu S = 0$$

$$S^* = \frac{\Lambda}{\mu}$$

The disease free equilibrium becomes $(S^* E^* I^* R^*) = \left(\frac{\Lambda}{\mu}, 0, 0, 0 \right)$

4. Basic reproductive number

The basic reproductive number (R_0) which is average number of secondary infections caused by one infectious individual introduced in a completely susceptible population is obtained using next generation matrix according to [9, 16, 20] as follows; Using the infected compartment E and I , their rate of change equations and considering the partial derivatives of m and n with respect to E and I leading to square matrices F and V respectively described as

$$F = \begin{pmatrix} 0 & 0 \\ \beta S & 0 \end{pmatrix} \text{ And } V = \begin{pmatrix} (\Omega + \mu) & -\Omega \\ 0 & (\alpha + \mu + \gamma) \end{pmatrix}$$

Finding inverse of V and multiplying it with F

$$V^{-1} = \begin{pmatrix} \frac{1}{(\Omega + \mu)} & \frac{\Omega}{(\Omega + \mu)(\alpha + \mu + \gamma)} \\ 0 & \frac{1}{(\alpha + \mu + \gamma)} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} 0 & 0 \\ \frac{\beta S}{(\Omega + \mu)} & \frac{\beta S \Omega}{(\Omega + \mu)(\alpha + \mu + \gamma)} \end{pmatrix}$$

Introducing Eigen values and solving the determinant gives two Eigen values as follows $\lambda = 0$ and $\lambda = \frac{\beta S \Omega}{(\Omega + \mu)(\alpha + \mu + \gamma)}$. The most dominant eigenvalue is $\lambda = \frac{\beta S \Omega}{(\Omega + \mu)(\alpha + \mu + \gamma)}$ which

forms our basic reproductive number. At disease free equilibrium $R_0 = \frac{\beta \Lambda \Omega}{\mu(\Omega + \mu)(\alpha + \mu + \gamma)}$

Theorem 2

Disease free equilibrium is locally asymptotically stable if less than unity and unstable if greater than unity.

Proof

Basic reproductive number is $R_0 = \frac{\beta \Lambda \Omega}{\mu(\Omega + \mu)(\alpha + \mu + \gamma)}$

At Disease Free Equilibrium $R < 1$ hence $\frac{\beta \Lambda \Omega}{\mu(\Omega + \mu)(\alpha + \mu + \gamma)} < 1$

Making Ω the subject

$$\Omega < \frac{\mu^2 (\alpha + \mu + \gamma)}{\beta \Lambda - \mu (\alpha + \mu + \gamma)}.$$

Therefore if $\Omega < \frac{\mu^2 (\alpha + \mu + \gamma)}{\beta \Lambda - \mu (\alpha + \mu + \gamma)}$, disease free equilibrium will be locally stable.

Lemma 1

If $R_0 > 1$ then it follows that $\frac{\beta \Lambda \Omega}{\mu(\Omega + \mu)(\alpha + \mu + \gamma)} > 1$. this implies that $\Omega > \frac{\mu^2 (\alpha + \mu + \gamma)}{\beta \Lambda - \mu (\alpha + \mu + \gamma)}$

.Which means that DFE is locally asymptotically unstable.

5. Endemic equilibrium point (EE).

At Endemic equilibrium point (E_2^*); disease exists. The variables are all nonzero, evaluating the state variables of equations of the system 2, the endemic equilibrium points of dynamical systems given as follows according to authors [12, 14].

$$E_2^* = \{S^{**}, E^{**}, I^{**}, R^{**}\} \text{ Where } S^{**} > 0, E^{**} > 0, I^{**} > 0, \text{ and } R^{**} > 0.$$

And

$$\begin{aligned}
S^{**} &= \frac{(\Omega + \mu)(\gamma + \alpha + \mu)}{\Omega\beta} \\
E^{**} &= \frac{(\gamma + \alpha + \mu)(\delta + \mu)\{\Lambda\Omega\beta - \mu\{(\Omega + \mu)(\gamma + \alpha + \mu)\}\}}{\beta\Omega\{(\delta + \mu)(\Omega + \mu)(\gamma + \alpha + \mu)\} - \gamma\Omega\delta} \\
I^{**} &= \frac{(\delta + \mu)}{\beta} \cdot \frac{\Lambda\Omega\beta - \mu\{(\Omega + \mu)(\gamma + \alpha + \mu)\}}{\{(\delta + \mu)(\Omega + \mu)(\gamma + \alpha + \mu)\} - \gamma\Omega\delta} \\
R^{**} &= \frac{1}{\beta} \left\{ \frac{\{\gamma\Lambda\Omega\beta - \gamma\mu\{(\Omega + \mu)(\gamma + \alpha + \mu)\}\}}{\{(\delta + \mu)(\Omega + \mu)(\gamma + \alpha + \mu)\} - \gamma\Omega\delta} \right\}
\end{aligned}$$

5 Global Stability of the disease free equilibrium

This stability is obtained by using Castillo-Chavez et al (2002) approach, whereby the model is first rewritten as follows according to [9, 10 and 12]

$$\frac{dM}{dt} = H(M, N) \text{ and } \frac{dN}{dt} = G(M, N), G(M, 0) = 0$$

Where $M = (S)$ and $N = (E, I)$ with components of $M \in R$ denoting the susceptible population and components of $N \in R^2$ denotes the unprotected (E) and infected (I).

$E_1^* = G(M^*, 0)$ Represent disease free equilibrium.

The following are conditions.) i) $\frac{dM}{dt} = H(M, 0)$, M^* is globally asymptotically stable

(GAS) ii) $G(M, N) = AN - \bar{G}(M, N)$, $\bar{G}(M, 0) = 0$ for $(M, N) \in \varphi$

Where $G(M, N) = A = D_N G(W^*, 0)$ is M- matrix (the off diagonal elements of A are non-negative) and φ is the region where the model lies.

$$H(M, N) = (\Lambda + \delta R - \beta SI - \mu S) \text{ and } G(M, N) = \begin{pmatrix} \beta SI - \Omega E - \mu E \\ \Omega E - \gamma I - \alpha I - \mu I \end{pmatrix}$$

At disease free equilibrium (DFE); $E=0$, $I=0$ and $R=0$ while $\varphi = R^4$

Further $\frac{dM}{dt} = H(M, 0)$ which is also equal to $\Lambda + \delta R - \mu S$.

$M^* = (S^*, 0, 0, 0)$ is globally stable hence condition 1 satisfied.

For condition 2

$$\bar{G}(M, N) = \begin{pmatrix} \beta SI \\ 0 \end{pmatrix} \text{ and } A = \begin{pmatrix} -a - \lambda & \beta S^* \\ \Omega & -b - \lambda \end{pmatrix}.$$

$$\text{AN- } \bar{G}(M, N) = \begin{pmatrix} (-a - \lambda)E + \beta S^*I - \beta SI \\ \Omega E + (-b - \lambda)I - 0 \end{pmatrix}$$

$$= \begin{pmatrix} (-a - \lambda)E + \beta SI \\ \Omega E + (-b - \lambda)I \end{pmatrix} \quad (9)$$

Replacing a and b, the equation 9 become

$$\begin{pmatrix} \beta SI - \Omega E - \mu E \\ \Omega E - \gamma I - \alpha I - \mu I \end{pmatrix} \text{ This also gives } G(M, N)$$

Hence $G(M, N)$ is satisfied and proofed to be globally asymptotically stable

7. Global stability of endemic equilibrium

Proof: By the use of lyapunov function defined by LaSalle [1976] and also in [13, 16, and 18 and 19], we have determined global stability as follows

$$L(S^{**}, E^{**}, I^{**}, R^{**}) = (S - S^{**} - S^{**} \ln(\frac{S^{**}}{S})) + \left(E - E^{**} - E^{**} \ln(\frac{E^{**}}{E}) \right) + (I - I^{**} - I^{**} \ln(\frac{I^{**}}{I})) + (R - R^{**} - R^{**} \ln(\frac{R^{**}}{R}))$$

computing the derivative of L along the solutions of the system is directly:

$$\frac{dL}{dt} = \left(\frac{s - s^{**}}{s} \right) \frac{dS}{dt} + \left(\frac{E - E^{**}}{E} \right) \frac{dE}{dt} + \left(\frac{I - I^{**}}{I} \right) \frac{dI}{dt} + \left(\frac{R - R^{**}}{R} \right) \frac{dR}{dt} \quad (10)$$

Substituting the equations of system 1 in equation 10, the equation becomes

$$\frac{dL}{dt} = \left[\left(\frac{s - s^{**}}{s} \right) \Lambda + \delta R - (\beta I + \mu) S \right] + \left[\left(\frac{E - E^{**}}{E} \right) \beta SI - (\Omega + \mu) E \right] +$$

$$\left[\left(\frac{I - I^{**}}{I} \right) \Omega E - (\gamma + \alpha + \mu) I \right] + \left[\left(\frac{R - R^{**}}{R} \right) \gamma I - (\delta + \mu) R \right] \quad (11)$$

Expanding equation 11, it produces

$$\frac{dL}{dt} = \Lambda + \delta R - (\beta I + \mu) S - \Lambda \frac{S^{**}}{S} - \delta R \frac{S^{**}}{S} + (\beta I + \mu) S^{**} + \beta SI - (\Omega + \mu) E - \beta SI \frac{E^{**}}{E} +$$

$$(\Omega + \mu) E^{**} + \Omega E - (\gamma + \alpha + \mu) I - \Omega E \frac{I^{**}}{I} + (\gamma + \alpha + \mu) I^{**} + \gamma I - (\delta + \mu) R - \gamma I \frac{R^{**}}{R} + (\delta + \mu) R^{**}$$

Further simplification result to

$$\begin{aligned} \frac{dL}{dt} = & \left[\Lambda + \delta R + (\beta I + \mu) S^{**} + \beta SI + (\Omega + \mu) E^{**} + \Omega E + (\gamma + \alpha + \mu) I^{**} + \gamma I + (\delta + \mu) R^{**} \right] \\ & - \left[(\beta I + \mu) S + \Lambda \frac{S^{**}}{S} + \delta R \frac{S^{**}}{S} + (\Omega + \mu) E + \beta SI \frac{E^{**}}{E} + (\gamma + \alpha + \mu) I + \Omega E \frac{I^{**}}{I} + (\delta + \mu) R + \gamma I \frac{R^{**}}{R} \right] \end{aligned}$$

From equation it's clear that ; $\frac{dL}{dt} = A - B$. Where A are the positive terms and B are the negative ones, such that;

$$A = \Lambda + \delta R + (\beta I + \mu) S^{**} + \beta SI + (\Omega + \mu) E^{**} + \Omega E + (\gamma + \alpha + \mu) I^{**} + \gamma I + (\delta + \mu) R^{**}$$

$$B = (\beta I + \mu) S + \Lambda \frac{S^{**}}{S} + \delta R \frac{S^{**}}{S} + (\Omega + \mu) E + \beta SI \frac{E^{**}}{E} + (\gamma + \alpha + \mu) I + \Omega E \frac{I^{**}}{I} + (\delta + \mu) R + \gamma I \frac{R^{**}}{R}$$

$$\text{If } A < B \text{ then } \frac{dL}{dt} \leq 0$$

$$\frac{dL}{dt} = 0 \text{ Only if } S = S^{**}, E = E^{**}, I = I^{**}, R = R^{**}$$

The largest invariant set in $\{(S, E, I, R) \in \varphi : \frac{dL}{dt} = 0\}$ is a singleton E_2^* . Where E_2^* is the endemic equilibrium. Therefore, the endemic equilibrium is globally asymptotically stable in the invariant region φ if $A < B$.

6 Discussion.

In this research we modeled unprotected human compartment the in the spread dynamics of typhoid fever in humans. Global stability of both equilibrium point (Disease Free Equilibrium point and Endemic Equilibrium point) was carried out. From our findings of stability analysis of equilibrium points is stable when $R_0 < 1$ and unstable when $R_0 > 1$. This shows that unprotected humans have great impact in the spread dynamics and need to be considered amongst other protective factors if typhoid fever is to be effectively eradicated from human population. Our model clearly portrays direct variation between the unprotected and infected compartment.

From our finding if $\Omega < \frac{\mu^2 (\alpha + \mu + \gamma)}{\beta \Lambda - \mu (\alpha + \mu + \gamma)}$, there disease equilibrium will be stable and typhoid

disease will not have a hand in the population. However if $\Omega > \frac{\mu^2 (\alpha + \mu + \gamma)}{\beta \Lambda - \mu (\alpha + \mu + \gamma)}$, then disease will be dependent on the unprotected humans as well as other prevailing circumstances.

7. Conclusion and recommendation

We conclude that there is direct variation relationship between the unprotected and infectious compartments, therefore the unprotected humans contribute significantly to the spread dynamics of typhoid fever disease. Therefore we recommend policy makers in health sectors to incorporate protection measures to avoid the disease prevailing in the population. Deaths due to typhoid will

be low if the unprotected group is managed properly by providing periodic oral protection doses or vaccines at birth.

Competing interest

No competing interest exist from the authors.

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