

On the Dynamical Analysis of a Deterministic Typhoid Fever Infection Model

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Abstract

In this paper, we develop a deterministic model of typhoid fever. The existence and uniqueness of solutions of the model were examined by actual solutions. Mathematical analysis is carried out to determine the transmission dynamics of typhoid in a community. We conduct local stability analysis for the model. The results show that the disease-free equilibrium which is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Keyword: Typhoid, treatment, transmission, reproduction number, disease-free

1. INTRODUCTION

Typhoid is a major public health concern in tropical developing countries, especially in areas where access to clean water and other sanitation measures are limited [1-3]. Typhoid fever has complex pathogenesis and manifests as an acute febrile disease, with relatively long incubation period that involves transmigration of the microorganism through the Peyer's patch, localized multiplication in the mesenteric lymph nodes, and subsequent spread to the spleen prior to showing clinical symptoms [4]. It is a serious life-threatening infection characterised by false diagnosis due to similar symptoms with malaria, which leads to improper controls and management of the disease. Despite extensive work on typhoid, not much is understood about the biology of the human-adapted bacterial pathogen and the complexity of the disease in endemic areas, especially in Africa [5]. Globally, the burden of typhoid disease is estimated at 21 million cases and 222000 deaths annually with high rates reported among children and adolescents in South and Eastern Africa [6-8]. The symptoms are alleviated with antibiotic medications, however, a proportion of people treated for typhoid fever experience relapse, after a week of antibiotic treatment with symptoms which are milder and last for a shorter time compared with the original illness, requiring further treatment with antibiotics [9, 10]. Typhoid fever may be prevented using even though repeated mass vaccinations at intervals of 5 years interval may reduce the disease incidence, small gains re-observed at each subsequent vaccination [11]. The dynamics of typhoid fever involve multiple interactions between the human host, pathogen and environment, contributing to direct human-to-human and indirect environment-to-human transmission pathways [12, 13]. Typhoid fever produces long-term asymptomatic carriers which play a pivotal role in the disease transmission.

In order to gain in-depth understanding of the complex dynamics of typhoid fever a number of studies have been conducted and published. Cvjetancic [11] constructed an epidemic model for typhoid fever in a stable population to study the transmission of infection at different levels of control. Mushayabasa et al. [12] developed and analysed a deterministic mathematical model for assessment of the impact of treatment and educational campaigns in controlling typhoid out-break in Zimbabwe. Date et al. [6] reviewed various vaccination strategies using current typhoid vaccines to assess the acceptability, effectiveness, impact and implementation lessons in order to inform future public health typhoid control strategies. Watson and Edmond [5] carried out an intensive review of typhoid fever transmission dynamics models and economic evaluation of vaccination. Clinicians, microbiologists, and epidemiologists worldwide need full understanding and knowledge of typhoid fever to effectively control and manage the disease [5]. This present study investigates the criteria under which the effectiveness of treatment could lead to the stability of the equilibrium point. We establish conditions for existence and uniqueness of the solution of models, conducted local stability analysis of the models.

2.0 Model Formulation

Following [15], the equations describing typhoid fever epidemics are:

$$\frac{dS}{dt} = \Lambda - \frac{c\beta(I + k_1 I_r + k_2 T)}{N} S - \mu S \quad (1)$$

$$\frac{dI}{dt} = \frac{c\beta\rho(I + k_1 I_r + k_2 T)}{N} S + \alpha I_r - (\mu + \sigma + \delta_1) I \quad (2)$$

$$\frac{dI_r}{dt} = \frac{(1 - \rho)c\beta(I + k_1 I_r + k_2 T)}{N} S + rI - (\mu + \alpha) I_r \quad (3)$$

$$\frac{dT}{dt} = \alpha I - (\mu + \gamma + r + \delta_2) T \quad (4)$$

$$\frac{dR}{dt} = \gamma T - \mu R \quad (5)$$

$$N(t) = S(t) + I(t) + I_r(t) + T(t) + R(t) \quad (6)$$

As initial condition based on our assumptions, we choose (7)

$$S(0) = S_0, I(0) = I_0, I_r(0) = I_{r(0)}, T(0) = T_0, R(0) = R_0$$

Where

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Variables	Parameters
$S(t)$ - Susceptible human	Λ - Recruitment rate
$I(t)$ - Infectives human	μ - per capital death rate
$I_c(t)$ - Carriers human	δ_1, δ_2 - Disease-induced deaths
$T(t)$ - Treated infectives	C - effective contacts
$R(t)$ - Recovered human	β - Rate of transmission
	α - Progression to symptomatic state
	γ - Rate of recovery from treatment
	ρ - New infections becoming carriers
	σ - Rate of treatment
	τ - Proportion of treated individuals
	k_1, k_2 - Modification parameters

3.0 Method of Solution

3.1 Positivity of Solutions

It is necessary to prove that all solutions of system (1) – (5) with positive initial data will remain positive for all times (t). This will be established following theorem:

Lemma 1: Let the closed set

$$\left\{ \begin{matrix} S \\ I \\ I_c \\ T \\ R \end{matrix} \in \mathbb{R}^+ \mid \begin{matrix} S(0) \geq 0 \\ I(0) \geq 0 \\ I_c(0) \geq 0 \\ T(0) \geq 0 \\ R(0) \geq 0 \\ S + I + I_c + T + R \leq \frac{\Lambda}{\mu} \end{matrix} \right.$$

Then, the solution of $(S(t), I(t), I_c(t), T(t), R(t))$ of the equations (1) to (5) are positive for all $t \geq 0$

Proof-

from equation (1) we have that

$$\frac{dS}{dt} = \Lambda - \beta S - \mu S$$

$$\frac{dS}{dt} \geq -\mu S$$

$$\frac{dS}{S} \geq -\mu dt$$

$$\int_0^t \frac{1}{S} dS \geq -\mu \int_0^t dt$$

$$S(t) \geq e^{-\mu t} S(0) \geq 0$$

Similarly,

$$I(t) \geq e^{-(\mu + \sigma + \delta_1)t} I(0) \geq 0$$

$$I_c(t) \geq e^{-(\mu + \alpha)t} I_c(0) \geq 0$$

$$T(t) \geq e^{-(\mu + \gamma + \tau + \delta_2)t} T(0) \geq 0$$

$$R(t) \geq e^{-\mu t} R(0) \geq 0$$

Hence, the solution of $(S(t), I(t), I_c(t), T(t), R(t))$ of equation (1) to (5) are positive for all $t \geq 0$

3.2 Existence and Uniqueness of Solution

Lemma 2: Let $\delta_1 = \delta_2 = 0$, then the equation (1) to (6) with the initial condition has a unique solution for all $t \geq 0$

Proof: Let $\delta_1 = \delta_2 = 0$, $\Phi(t) = S(t) + I(t) + I_c(t) + T(t) + R(t)$. We obtain

$$\frac{d\Phi}{dt} = \Lambda - \Phi\mu, \Phi(0) = S(0) + I(0) + I_c(0) + T(0) + R(0) = \Phi_0 \tag{8}$$

By direct integration, we obtain the solution of problem (8) as

$$\Phi(t) = \frac{\Lambda}{\mu} (1 - e^{-\mu t}) + \Phi_0 e^{-\mu t} \tag{9}$$

Then, we obtain

$$S(t) = \left(\frac{\Lambda}{\mu} + (1 - e^{-\mu t}) e^{-\mu t}\right) - (I(t) + I_c(t) + T(t) + R(t)) \tag{10}$$

$$I(t) = \left(\frac{\Lambda}{\mu} + (1 - e^{-\mu t}) e^{-\mu t}\right) - (S(t) + I_c(t) + T(t) + R(t)) \tag{11}$$

$$I_c(t) = \left(\frac{\Lambda}{\mu} + (1 - e^{-\mu t}) e^{-\mu t}\right) - (S(t) + I(t) + T(t) + R(t)) \tag{12}$$

$$T(t) = \left(\frac{\Lambda}{\mu} + (1 - e^{-\mu t}) e^{-\mu t}\right) - (S(t) + I(t) + I_c(t) + R(t)) \tag{13}$$

$$R(t) = \left(\frac{\Lambda}{\mu} + (1 - e^{-\mu t}) e^{-\mu t}\right) - (S(t) + I(t) + I_c(t) + T(t)) \tag{14}$$

Hence, there exists a unique solution of problem (1) – (6). This completes the proof.

3.3 Equilibrium State of the Model

At equilibrium,

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dT}{dt} = \frac{dR}{dt} = 0$$

$$\Lambda - \frac{c\beta(I+k_1I_1+k_2T)}{N}S - \mu S = 0 \tag{15}$$

$$\frac{c\beta(I+k_1I_1+k_2T)}{N}S + \alpha I_1 - (\mu + \sigma + \delta_1)I = 0 \tag{16}$$

$$\frac{(1-\rho)c\beta(I+k_1I_1+k_2T)}{N}S + rT - (\mu + \alpha)I = 0 \tag{17}$$

$$\alpha I - (\mu + \gamma + r + \delta_2)T = 0 \tag{18}$$

$$\gamma T - \mu R = 0 \tag{19}$$

3.4 The Disease Free Equilibrium (DFE)

The equilibrium state in the absence of infection is known as Disease Free Equilibrium (DFE). Therefore the disease free equilibrium exists if $I = 0$

Putting $I = 0$ into the above equations, the Disease free equation is

$$(S, I, T, R) = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right) \tag{22}$$

3.5 The Basic Reproduction Number, (R_0)

We compute the effective reproduction number of the model using the next generation operator method by van den Driessche and Watmough [16]. effective reproduction number is defined as the average number of secondary infections generated by primary cases under a specific control (treatme this case) strategy. Distinguishing new infections from other transitions in (1) – (5), we obtain the two matrices F and V of generation of new infection transition terms respectively expressed as

$$F = \begin{bmatrix} \rho c\beta & \rho k_1 c\beta & \rho k_2 c\beta \\ (1-\rho)c\beta & (1-\rho)k_1 c\beta & (1-\rho)k_2 c\beta \\ 0 & 0 & 0 \end{bmatrix}$$

and

$$V = \begin{bmatrix} k_1 & -\alpha & 0 \\ 0 & k_2 & -r \\ -\sigma & 0 & k_3 \end{bmatrix} \tag{24}$$

Where,

$$k_1 = \mu + \sigma + \delta_1$$

$$k_2 = \mu + \alpha$$

$$k_3 = \mu + \gamma + r + \delta_2 \tag{25}$$

The effective reproduction number of the model is the dominant eigenvalue or spectral radius of the matrix FV^{-1} . thus

$$R_0 = \frac{(\rho\mu + \alpha)k_1 c\beta}{(k_1 k_2 k_3 - r\alpha\sigma)} + \frac{k_2 \rho r \alpha c\beta}{(k_1 k_2 k_3 - r\alpha\sigma)} + \frac{k_1 (1-\rho)c\beta}{k_2} + \frac{k_3 k_1 \rho \alpha c\beta}{(k_1 k_2 k_3 - r\alpha\sigma)} \tag{26}$$

3.6 The Stability Results

The Jacobian Matrix of the system is given by:

$$J(E^*) = \begin{bmatrix} -\frac{c\beta}{N}(I+k_1I_1+k_2T) - \mu & c\beta & c\beta k_1 & c\beta k_2 & 0 \\ \frac{\rho c\beta}{N}(I+k_1I_1+k_2T) & \rho c\beta - k_1 & \rho c\beta k_1 + \alpha & \rho c\beta k_2 & 0 \\ (1-\rho)c\beta(I+k_1I_1+k_2T) & (1-\rho)c\beta & [(1-\rho)c\beta k_1 - k_1] & (1-\rho)c\beta k_2 + r & 0 \\ 0 & \sigma & 0 & -k_2 & 0 \\ 0 & 0 & 0 & \gamma & -\mu \end{bmatrix} \tag{27}$$

We evaluate the jacobian at the disease free equilibrium to determine the local stability of the system. We obtain

$$J(E^*) = \begin{bmatrix} -\mu & c\beta & c\beta k_1 & c\beta k_2 & 0 \\ 0 & (\rho c\beta - k_1) & (\rho c\beta k_1 + \alpha) & \rho c\beta k_2 & 0 \\ 0 & (1-\rho)c\beta & [(1-\rho)c\beta k_1 - k_1] & [(1-\rho)c\beta k_2 + r] & 0 \\ 0 & \sigma & 0 & -k_2 & 0 \\ 0 & 0 & 0 & \gamma & -\mu \end{bmatrix} \tag{28}$$

Using elementary row transformation, the matrix (28) becomes

$$J(E^*) = \begin{bmatrix} -\mu & c\beta & c\beta k_1 & c\beta k_2 & 0 \\ 0 & -(\rho c\beta - k_1) & (\rho c\beta k_1 + \alpha) & \rho c\beta k_2 & 0 \\ 0 & 0 & A_1 & A_1 & 0 \\ 0 & 0 & 0 & A_1 & 0 \\ 0 & 0 & 0 & 0 & -\mu \end{bmatrix} \tag{29}$$

Where,

$$\lambda_1 = \frac{(\rho\mu + \alpha)k_1 c\beta - k_1 k_2 k_3 + \alpha\tau\sigma}{c_1 \rho \beta k_1 k_2 + \rho \alpha \beta - c_1 \rho \beta k_1 - c_1 \beta k_2 k_3 + k_1 k_2} \tag{30}$$

$$\lambda_2 = \frac{\rho \alpha \beta k_1 k_2 + \rho \alpha \beta \sigma - \rho \alpha \beta k_1 - c_1 \beta k_2 k_3 - c_1 \rho \alpha + k_1^2 k_2}{\rho \alpha \beta - k_1 k_2}$$

$$\lambda_3 = \frac{k_1 k_2 k_3 \rho \alpha \beta \sigma + k_1 k_2 (1 - \rho) c_1 \beta (k_1 k_2 k_3 - \tau \alpha \sigma) + k_1 k_2^2 k_3 \rho \alpha \beta - k_1 k_2 (k_1 k_2 k_3 - \tau \alpha \sigma)}{\rho \alpha \beta \sigma - \rho \alpha \beta k_1 k_2 - \rho \alpha \beta k_1 k_2 k_3 - \rho \alpha \beta k_1 k_2}$$

The characteristics equation of the upper triangular jacobian is

$$J(E^*) = \begin{pmatrix} -(\mu + \lambda) & c\beta & c\beta k_1 & c\beta k_2 & 0 \\ 0 & -(\lambda + \rho \alpha \beta + \lambda) & (\rho \alpha \beta k_1 + \alpha) & \rho \alpha \beta k_2 & 0 \\ 0 & 0 & (\lambda - \lambda) & \lambda_1 & 0 \\ 0 & 0 & 0 & (\lambda - \lambda) & 0 \\ 0 & 0 & 0 & 0 & -(\mu + \lambda) \end{pmatrix} \tag{31}$$

Therefore, the eigenvalues are;

$$\lambda_1 = -\mu < 0 \tag{32}$$

$$\lambda_2 = -(\lambda + \rho \alpha \beta) < 0 \tag{33}$$

$$\lambda_3 = \lambda_4 = \frac{(\rho\mu + \alpha)k_1 c\beta - k_1 k_2 k_3 + \alpha\tau\sigma}{c_1 \rho \beta k_1 k_2 + \rho \alpha \beta - c_1 \rho \beta k_1 - c_1 \beta k_2 k_3 + k_1 k_2} \tag{34}$$

For λ_3 to be negative, then

$$\frac{(\rho\mu + \alpha)k_1 c\beta}{k_1 k_2 k_3 + \alpha\tau\sigma} < 1 \tag{35}$$

$$R_{c1} < 1 \tag{36}$$

$$\lambda_4 = \lambda_5 = \frac{k_1 k_2 k_3 \rho \alpha \beta \sigma + k_1 k_2 (1 - \rho) c_1 \beta (k_1 k_2 k_3 - \tau \alpha \sigma) + k_1 k_2^2 k_3 \rho \alpha \beta - k_1 k_2 (k_1 k_2 k_3 - \tau \alpha \sigma)}{c_1 \beta \tau \rho k_1 k_2 - k_1 c_1 \beta \rho \alpha - k_1 k_2 c_1 \rho \beta - k_1 c_1 \beta \rho \alpha} \tag{37}$$

For λ_4 to be negative, then we have

$$\frac{k_1 k_2 k_3 \rho \alpha \beta \sigma + k_1 k_2 (1 - \rho) c_1 \beta (k_1 k_2 k_3 - \tau \alpha \sigma) + k_1 k_2^2 k_3 \rho \alpha \beta - k_1 k_2 (k_1 k_2 k_3 - \tau \alpha \sigma)}{c_1 \beta \tau \rho k_1 k_2 - k_1 c_1 \beta \rho \alpha - k_1 k_2 c_1 \rho \beta - k_1 c_1 \beta \rho \alpha} < 0 \tag{38}$$

$$\left(\frac{k_1 \rho \alpha \beta \sigma}{k_1 k_2 k_3 - \tau \alpha \sigma} + \frac{k_1 (1 - \rho) c_1 \beta}{k_2} + \frac{k_1 k_2 \rho \alpha \beta}{k_1 k_2 k_3} \right) < 1 \tag{39}$$

$$R_{c1} + R_{c2} < 1 \tag{40}$$

$$\lambda_5 = -\mu < 0 \tag{41}$$

This implies that, $\lambda_3 < 0$ if $R_{c1} < 1$ and $\lambda_4 < 0$ if $R_{c1} + R_{c2} < 1$

The quantity R_c denotes the reproduction number of the model for a population consisting entirely of infected individuals, R_i represents the reproduction number of the model for a population consisting entirely of carrier individuals, while R_r is the reproduction number of the model for a population consisting entirely of treated individuals.

Hence, the disease free equilibrium (DFE) of the equation (1) to (5) is locally asymptotically stable if $R_c < 1$ and unstable otherwise.

4.0 Conclusion

We presented deterministic model for typhoid transmission model and we determined conditions for existence and stability of equilibrium state characterized in terms of the effective reproduction number. The study showed that there is a disease free equilibrium which is locally asymptotically stable if $R_c < 1$ and unstable if otherwise.

5.0 References

- [1] Crump J. A. and Mintz E. D. (2010): Global trends in typhoid and paratyphoid fever, *Emerging Infections* CID 50, pp241-246. DOI: 10.1093/infdis/jip128.
- [2] Mutua, J. M., Wang, W. and Vaidya, N. K. (2015). Modelling malaria and typhoid fever co-infection dynamics, *Mathematical Biosciences* 264, pp128-144.
- [3] Pitzer, V. E., Feasey, N. A., Msefula, C., Mallewa, J., Kennedy, N., Dube, Q., Denis, B., Gordon, M. A. and Heyerman, R. S. (2015): Mathematical modelling to assess the drivers of the recent emergence of typhoid fever in Blantyre, Malawi, *CID*: 61(4), pp251-258.
- [4] Thompson, L. J., Dunstan, S. J., Dolecek, C., Perkins, T., House, D., Dougan, G., Nguyen, T. H., Tran, T. P., Doan, C. D., Le, T. P., Nguyen, T. D., Tran, T. H., Farrar, J. J., Monack, D., Lynn, D. J., Popper, S. J. and Falkow, S. (2009): Transcriptional response in the peripheral blood of patients infected with *Salmonella enterica* serovar Typhi, *106(52)*, 22433-22438.
- [5] Wain, J., Hendriksen, R. S., Mikoleit, M. L., Keddy, K. H. and Ochia, R. L. (2015): Typhoid fever, the *Lancet* 385, pp1136-1145.
- [6] Date, K. A., Bentsi-Enchill, A., Marks, F. and Fox, K. (2015): Typhoid fever vaccination strategies, *Vaccine* 33, pp55-61.
- [7] Mogasale, V., Maskery, B., Ochiai, R. L., Lee, J. S., Mogasale, V. V., Ramani, E., Kim, Y. E., Park, J. K. and Wierzb, T. F. (2014): Burden of typhoid fever in low-income and middle-income countries: A systematic, literature-based update with risk-factor adjustment, *Lancet Glob. Health* 2, pp570-580.
- [8] Qamar, F. N., Azmatullah, A. and Bhutta, A. A. (2015): Challenges in measuring complications and death due to invasive *Salmonella* infections, *Vaccine* 33, pp16-20.
- [9] Basnyat, B. (2007): The treatment of enteric fever, *J. of the Royal Soc. of Med.* 100, pp161-162.
- [10] Zaki, S. (2011): Re-infection of typhoid fever and typhoid vaccine (comment on an imported enteric fever caused by a quinolone-resistant *Salmonella typhi*), *Ann. Saudi Med.* 31(2), 203-204. doi:10.4103/0256-4947.77505.
- [11] Mushayabasa, S., Bhunu, C. P. and Mhlanga, N. A. (2014): Modelling the transmission dynamics of typhoid in malaria endemic settings, *Appl. Math. Int. J.* 6(1), pp121-140.
- [12] Gonzalez-Guzman, J. (1989): An epidemiological model for direct and indirect transmission of typhoid fever, *Maths. Biosci.* 96, pp33-46.
- [13] Pitzer, V. E., Bowles, C. C., Baker, S., Kang, G., Balaji, V., Farrar, J. J. and Grenfell, B. T. (2014): Predicting the impact of vaccination on the transmission dynamics of typhoid in South Asia: A mathematical modeling study, *PLOS Negl. Trop. Dis.* 8(1), e2642. doi:10.1371/journal.pntd.0002642.
- [14] Mushayabasa, S., Bhunu, C. P. and Mhlanga, N. A. (2014): Modeling the transmission dynamics of typhoid in malaria endemic settings, *Appl. Math. Int. J.* 6(1), pp121-140.
- [15] Watson, C. H. and Edmunds, W. J. (2015): A review of typhoid fever transmission dynamic models and economic evaluations of vaccination, *Vaccine* 33, 42-54. <http://dx.doi.org/10.1016/j.vaccine.04.013>.
- [16] Moatlhodi, K. and Gosalamang, R. K. (2016): Mathematical analysis of typhoid infection with treatment, *Journal of mathematical sciences: advances and applications*, vol. 40, pp75-91.