

Effect of Climate on Malaria-Cholera Co-infection

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ABSTRACT

In this paper, we incorporate climate parameters in a model presented in 2014 by Okosun and Makinde, then the effect of climate variability on malaria-cholera co-infection is investigated. It is found that malaria infection contributes to increase in the reproduction number of cholera in the presence of climate variability. That is, under climate change, cholera is associated with an increase of malaria infection and also, that there is no association between malaria infection and an increased risk of cholera. Suggesting that the findings by the authors above will no longer hold when climate variability is put into consideration. Therefore, to effectively manage malaria and cholera co-infection in the presence of climate variability, the malaria and cholera control strategies must be carried out simultaneously by policy makers.

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1 Introduction

Malaria is a vector borne disease that is preventable and curable. Strategies to mitigate malaria infection include the use of mosquito nets, indoor spraying of insecticides and the drainage of stagnant water (Okosun, Oufiki and Marcus, 2011). Flooding provides excellent environmental predispositions for the spread of malaria and cholera and recurrent flooding in Africa and Asia pose serious challenges to a healthy environment and clean water (Agarwal and Verma, 2012).

Numerous models have been developed to understand the dynamics of diseases and inform decision makers to adopt appropriate intervention mechanisms for disease control (Reyburn, Kim, Emch, Khatib, von Seidlein and Ali, 2011; Tian and Wang, 2011; Mwasia and Tchuente, 2011; Makinde and Okosun, 2011; Bakare, 2015).

Rita et al (Reyburn et al., 2011) studied climate variability and the outbreak of cholera in Zanzibar. These authors focus was on the effects of climate change and ocean environmental variability on cholera outbreaks. They developed a prediction model for forecasting cholera outbreaks in Zanzibar. Other approaches include that of Koella and Anita (Koella and Anita, 2003) who considered a mosquitoes class. They explored various strategies to mitigate resistance and investigated parameters sensitivity to their results. Anderson and May (Anderson and May, 1991) derived a model of malaria dynamics which assumes that acquired immunity in malaria does not depend on the duration of exposure to the disease. Various control measures on the impact of the disease rate of transmission and prevalence were further studied. Semegni et al. (Semegni, Abiodun, Vyambura, Marcus and Witbooi, 2019) further investigated the sensitivity and optimal control of the disease parameters. Many authors have studied co-infection models of malaria with other infectious diseases such as tuberculosis, HIV/AIDS and hepatitis B (Mtisi and Tchuente, 2009; Kwenti, 2018; Kolawole and Kana, 2018). However, very few authors have investigated the co-infection dynamics of malaria and cholera (Okosun and Makinde, 2014; Boamah, Arma, Luginaah, Hambati, Chuenpagdee and Campbell, 2017). Climate factors have a huge impact on the environment and the spread of diseases (Yener and Altun, 2017). Several studies (Abiodun, Witbooi and Okosun, 2018; Abiodun, Witbooi, Okosun and Maharaj, 2018; Abiodun, Witbooi and Okosun, 2017) have developed climate-based mosquito-malaria model to investigate the population dynamics of mosquitoes and malaria transmission. However, these studies did not consider the effect of climate variables on the co-infection dynamics of malaria-cholera. In this paper, the effect of climate variability is investigated based on a model by Okosun and Makinde (Okosun and Makinde, 2014) in which we incorporated climate parameters.

2 Model Formulation

In this model the entire population of humans N_h , is sub-divided into susceptible human population S_h , malaria only infected human population I_m , cholera only infected human population R_c , both malaria and cholera co-infected human population G_{mc} , people who recovered from malaria only R_m , people who recovered from cholera only R_c , people who recovered from both malaria and cholera R_{mc} . Thus, $N_h = S_h + I_m + P_c + G_{mc} + R_c + R_m + R_{mc}$. The vector population N_v is partitioned into malaria infected mosquitoes population I_v and susceptible mosquitoes population S_v . Thus, $N_v = S_v + I_v$.

The system of differential equations describing the model is formulated as follows:

$$\left\{ \begin{array}{l} \frac{d}{dt} S_h = \Lambda_h + \kappa R_m + \omega R_c + \psi R_{mc} - \beta_h I_v S_h - \lambda S_h - \mu_h S_h \\ \frac{d}{dt} I_m = \beta_h I_v S_h - \lambda I_m - (\alpha + \mu_h + \phi) I_m \\ \frac{d}{dt} I_c = \lambda S_h - \beta_h I_v I_c - (\delta + \mu_h + m) I_c \\ \frac{d}{dt} G_{mc} = \beta_h I_v I_c + \lambda I_m - (\sigma + \mu_h + \eta + q) G_{mc} \\ \\ \frac{d}{dt} R_m = \alpha I_m - (\kappa + \mu_h) R_m + \epsilon(1 - \sigma) G_{mc} \\ \frac{d}{dt} R_c = \delta I_c - (\omega + \mu_h) R_c + (1 - \epsilon)(1 - \sigma) G_{mc} \\ \frac{d}{dt} R_{mc} = \sigma G_{mc} - (\psi + \mu_h) R_{mc} \\ \\ \frac{d}{dt} B_c = \rho(I_c + \theta G_{mc}) - \mu_b B_c \\ \frac{d}{dt} S_v = \Lambda_v - \beta_v(I_m + G_{mc}) S_v - \mu_v S_v \\ \frac{d}{dt} I_v = \beta_v S_v(I_m + G_{mc}) - \mu_v I_v \end{array} \right. \quad (2.1)$$

Here,

$$\lambda = \frac{B_c \nu}{KW(R_a, T) + B_c}, \quad (2.2)$$

where $W(R_a, T)$ is the water volume, B_c the population of bacteria, ν the rate of ingestion, K the concentration of bacteria, m and η are the respective death rates due to cholera alone, q and ϕ are the respective death rates due to malaria alone, ρ is the average contribution of each cholera infected individual to the aquatic population of *V. Cholerae*. The parameters κ , ω and ψ are respectively the immunity waning rates and α , σ and δ are the respective recovery rates. The term $\epsilon(1 - \sigma)$ is the rate at which co-infected people recover from malaria only and the term $(1 - \epsilon)(1 - \sigma)$ is the rate at which co-infected people recover from cholera only. Thus, $\sigma + (1 - \epsilon)(1 - \sigma) + \epsilon(1 - \sigma) = 1$. The parameters μ_h and μ_v represent the humans population and mosquitoes population mortality rates respectively and θ is the modification parameter.

Our model assumes that:

- The mosquitoes population does not suffer mosquito-induced death
- People co-infected with both cholera and malaria can only infect mosquitoes with malaria parasites.

3 Co-infection model analysis

The malaria-cholera co-infection model (1) has a disease free equilibrium (DFE) given by

$$\mathcal{E}_0 = (S_h^*, I_m^*, I_c^*, G_{mc}^*, R_m^*, R_c^*, R_{mc}^*, B_c^*, S_v^*, I_v^*) = \left(\frac{\Lambda_h}{\mu_v}, 0, 0, 0, 0, 0, 0, 0, \frac{\Lambda_v}{\mu_v}, 0 \right).$$

To establish the stability of the DFE $\mathcal{E}_0$, we calculated the basic reproduction number $\mathcal{R}_{mc}$ of the co-infection model (1) by applying the next operator method as described in Driessche and Watmough (Driessche and Watmough, 2002).

It follows that

$$\mathcal{R}_{mc} = \max\{\mathcal{R}_m, \mathcal{R}_c\}$$

where

$$\mathcal{R}_m = \sqrt{\frac{\Lambda_v \Lambda_h \beta_h \beta_v}{\mu_h \mu_v^2 (\alpha + \phi + \mu_h)}}, \quad (3.1)$$

and

$$\mathcal{R}_c = \frac{\nu \rho \Lambda_h}{\mu_b \mu_h K W(R_a, T)} \left(\frac{(\eta + q + \sigma + \mu_h) + \theta(m + \delta + \mu_h)}{(m + \delta + \mu_h)(\eta + q + \sigma + \mu_h)} \right). \quad (3.2)$$

Applying the same method as in (Okosun and Makinde, 2014), it can be shown that:

Theorem 3.1. *The disease free equilibrium $\mathcal{E}_0$ is locally asymptotically stable if $\mathcal{R}_{mc} < 1$ and unstable otherwise.*

3.1 Influence of cholera on malaria

To investigate the impact of malaria of cholera and vice versa, we express $\mathcal{R}_c$ as a function of $\mathcal{R}_m$ first by solving the expression (3.1) for μ_h . We get

$$\mu_h = \frac{-D_1 \mathcal{R}_m + \sqrt{D_1^2 \mathcal{R}_m^2 + 4D_2}}{2\mu_v \mathcal{R}_m}$$

where,

$$D_1 = \mu_v(\alpha + \phi), \quad D_2 = \Lambda_v \Lambda_h \beta_v \beta_h,$$

and letting,

$$\sqrt{D_1^2 \mathcal{R}_m^2 + 4D_2} = D_3 \mathcal{R}_m + D_4,$$

we get,

$$\mu_h = \frac{\mathcal{R}_m(D_3 - D_1) + D_4}{2\mu_v \mathcal{R}_m} \quad (3.3)$$

substituting (3.3) into the expression (3.2), we obtain

$$\mathcal{R}_c = \frac{\mathcal{R}_{0c}(D_4 + (D_3 - D_1)\mathcal{R}_m + 2(\eta + q + \sigma)\mu_v \mathcal{R}_m + \theta(D_4 + (D_3 - D_1)\mathcal{R}_m + 2(m + \delta)\mu_v \mathcal{R}_m))}{D_4 + (D_3 - D_1)\mathcal{R}_m + 2(\eta + q + \sigma)\mu_v \mathcal{R}_m}. \quad (3.4)$$

Differentiating $\mathcal{R}_c$ with respect to $\mathcal{R}_m$ yields

$$\frac{\partial \mathcal{R}_c}{\partial \mathcal{R}_m} = \frac{2D_4\theta(m + \delta - (\eta + q + \sigma))\mu_v \mathcal{R}_{0c}}{[D_4 + \mathcal{R}_m(D_3 - D_1 + 2(\eta + q + \sigma)\mu_v)]^2} \quad (3.5)$$

Thus $\frac{\partial \mathcal{R}_c}{\partial \mathcal{R}_m}$ is strictly positive whenever $\eta + q + \sigma \leq m + \delta$. This implies that the spread of cholera infection will be enhanced with an increase of malaria infection. In other words if $\frac{\partial \mathcal{R}_c}{\partial \mathcal{R}_m} > 0$, an increase in malaria cases will result in a proliferation of cholera in the population. If $\frac{\partial \mathcal{R}_c}{\partial \mathcal{R}_m} = 0$, this will imply that malaria infection has no noticeable impact on the spread of cholera. In the same manner, expressing μ_h as a function of $\mathcal{R}_c$ yields

$$\mu_h = \frac{F_1 - F_2 \mathcal{R}_c + \sqrt{F_3 \mathcal{R}_c^2 + F_4 \mathcal{R}_c + F_5}}{2\mathcal{R}_c} \quad (3.6)$$

where

$$F_1 = (1 + \theta)\mathcal{R}_{0c}, \quad F_2 = \eta + m + q + \sigma + \delta, \quad F_3 = q + \sigma + \eta - m - \delta$$

$$F_4 = 2(\theta - 1)(m + \delta - \eta - \sigma - q)\mathcal{R}_{0c}, \quad F_5 = (1 + \theta)^2\mathcal{R}_{0c}^2$$

also let $\sqrt{F_3\mathcal{R}_c^2 + F_4\mathcal{R}_c + F_5} = F_6\mathcal{R}_c + F_7$.

$$\mu_h = \frac{(F_6 - F_2)\mathcal{R}_c + F_7 + F_1}{2\mathcal{R}_c}$$

$$\mathcal{R}_m^2 = \frac{4\Lambda_v\Lambda_h\beta_v\beta_h\mathcal{R}_c^2}{[F_1 + F_7 + (F_6 - F_2)\mathcal{R}_c][F_1 + F_7 + 2(\alpha + \phi)\mathcal{R}_c + (F_6 - F_2)\mathcal{R}_c]\mu_v} \quad (3.7)$$

now differentiating $\mathcal{R}_m$ with respect to $\mathcal{R}_c$, we get

$$\frac{\partial\mathcal{R}_m}{\partial\mathcal{R}_c} = \frac{4(F_1 + F_7)\Lambda_v\Lambda_h\mathcal{R}_c[F_1 + F_7 + (\alpha + \phi + F_6 - F_2)\mathcal{R}_c]\beta_v\beta_h}{[F_1 + F_7 + (F_6 - F_2)\mathcal{R}_c]^2[F_1 + F_7 + (2(\alpha + \phi) + F_6 - F_2)\mathcal{R}_c]^2\mu_v} \quad (3.8)$$

Thus whenever equation (3.8) is greater than zero, meaning that should the number of cholera cases increase in the population, then number of malaria cases will increase as well. To evaluate the influence of malaria treatment on cholera infection, we differentiate $\mathcal{R}_m$ with respect to α and get

$$\frac{\partial\mathcal{R}_m}{\partial\alpha} = -\frac{\alpha}{\alpha + \phi + \mu_h} \quad (3.9)$$

Since $\mathcal{R}_m$ is a decreasing function of α , treating cholera will positively impact on the progression of malaria.

3.2 Stability of the disease-free equilibrium $\mathcal{E}_0$

It follows that the reproductive number of cholera as a function of malaria reproductive number can be expressed as follows:

$$\mathcal{R}_c = \frac{HG(\mathcal{R}_m^2)_m \left(GG\mathcal{R}_m + (1+\theta) \left(-(D_1\mathcal{R}_m) + \sqrt{4D_2 + D_1^2(\mathcal{R}_m^2)_m} \right) \right) \mu_v^2}{K \left(-(D_1\mathcal{R}_m) + \sqrt{4D_2 + D_1^2(\mathcal{R}_m^2)_m} \right) \left(BG\mathcal{R}_m - D_1\mathcal{R}_m + \sqrt{4D_2 + D_1^2(\mathcal{R}_m^2)_m} \right) \left(PG\mathcal{R}_m - D_1\mathcal{R}_m + \sqrt{4D_2 + D_1^2(\mathcal{R}_m^2)_m} \right) \mu_b} \quad (3.10)$$

where,

$$D_1 = \mu_v(\alpha + \phi), \quad D_2 = \Lambda_h\Lambda_v\beta_v\beta_h$$

$$GG = 2(qm + r\phi + (m + \delta)\theta + \sigma)\mu_v^2, \quad HG = 4\nu\rho\Lambda_h\mu_v^2 \quad (3.11)$$

$$BG = 2(m + \delta)\mu_v^2, \quad PG = 2(qm + r\phi + \sigma)\mu_v^2$$

Similarly, it follows that the reproductive number of malaria as a function of cholera reproductive number can be expressed as follows:

$$\mathcal{R}_m = \sqrt{\frac{4\Lambda_v\Lambda_h\beta_v\beta_h\mathcal{R}_c^2}{[F_1 + \sqrt{F_3\mathcal{R}_c^2 + F_4\mathcal{R}_c + F_5} - F_2\mathcal{R}_c][F_1 + \sqrt{F_3\mathcal{R}_c^2 + F_4\mathcal{R}_c + F_5} + 2(\alpha + \phi) - F_2\mathcal{R}_c]\mu_v}} \quad (3.12)$$

where,

$$\begin{aligned} F_1 &= (1 + \theta)\mathcal{R}_{0c}, \quad F_2 = m + q + \eta + \delta + \sigma \\ F_3 &= \eta + \sigma + q - \delta - m, \quad F_4 = 2(\theta - 1)(\delta + m - \eta - \sigma - q)\mathcal{R}_{0c} \\ F_5 &= (1 + \theta)^2\mathcal{R}_{0c}^2 \end{aligned} \quad (3.13)$$

and

$$\mathcal{R}_{0c} = \frac{4\nu\rho\Lambda_v\mathcal{R}_c^2}{\mu_b K[F_1 - F_2\mathcal{R}_c + \sqrt{F_3\mathcal{R}_c^2 + F_4\mathcal{R}_c + F_5}][2(m + \delta)\mathcal{R}_c + \sqrt{F_3\mathcal{R}_c^2 + F_4\mathcal{R}_c + F_5}]} \quad (3.14)$$

The impact of cholera on malaria is given by;

$$\mathcal{R}_m = \frac{\partial \mathcal{R}_m}{\partial \mathcal{R}_c} = \frac{4F_1\Lambda_v\Lambda_h\mathcal{R}_c[F_1 + \sqrt{F_3\mathcal{R}_c^2 + F_4\mathcal{R}_c + F_5} + (\alpha + \phi - F_2)\mathcal{R}_c]\beta_v\beta_h}{[F_1 + \sqrt{F_3\mathcal{R}_c^2 + F_4\mathcal{R}_c + F_5} - F_2\mathcal{R}_c]^2\mathcal{K}} \quad (3.15)$$

where $\mathcal{K} = F_1 + \sqrt{F_3\mathcal{R}_c^2 + F_4\mathcal{R}_c + F_5} + (2(\alpha + \phi) - F_2)\mathcal{R}_c]^2\mu_v$

Whereas the impact of malaria on cholera is calculated as;

$$\mathcal{R}_c = \frac{\partial \mathcal{R}_c}{\partial \mathcal{R}_m} = \frac{2\theta(m + \delta - (\eta + q + \sigma))\mu_v\mathcal{R}_{0c}}{[\sqrt{D_1^2\mathcal{R}_m^2 + 4D_2} - D_1\mathcal{R}_m + 2(\eta + q + \sigma)\mu_v]^2} \quad (3.16)$$

4 Numerical results and discussions

We begin the numerical analysis by simulating the spatial distribution of the reproduction number of cholera and malaria over Nigeria in Fig. 1 and Fig. 3 respectively. To achieve this, we used the seasonal climate data of the study region to simulate the annual variation from 2000-2015. The impact of climate variable on the reproduction number of malaria and cholera co-infection was also investigated as shown in Fig. 2 and Fig. 4 respectively. We begin the co-infection simulations with the reproduction number of malaria on cholera for all the seasons as shown in Fig. 2. The same analysis was repeated on the reproduction number of cholera on malaria as shown in Fig. 4. It is noticed in Fig. 2 that the reproduction number is higher between March to May and between September to November than other seasons. However, there is no much noticeable difference in the case of cholera on malaria as shown in Fig. 4. This implies that malaria infection contributes to increase in the reproduction number of cholera in the presence of climate variability, but cholera not necessarily have much impact on malaria transmission.

The following malaria parameters values were considered

Parameter	Description	value	Reference
Malaria Parameters			
$\epsilon(T)$	Mosquito biting rate	$0.000203D_1D_2$	(Ngarakana-Gwasira, Bhunu and Mashonjowa, 2013; Paaijmans, Cator and Thomas, 2013)
		$D_1 = T^2 - 11.7T$	
		$D_2 = \sqrt{42.3 - T}$	
$\mu_v(T)$	Mosquito death rate	$\frac{1}{(-4.4 + 1.31T - 0.03T^2)}$	(Alonso, Bouma and Pascual, 2011; Martens, Niessen and Rotmans, 1995)
$\eta_v(T)$	Progression rate of mosquitoes	$\frac{(T - T_{min})}{111}$	(Ngarakana-Gwasira et al., 2013; Paul and Edwin, 2010; McDonald, 1957)
$W(R_a, T)$	Water volume	$R_{a0}T_0 \left(1 + R_{a1}T_1 \sin\left(\frac{2\pi T}{365}\right) \right)$	(Ngarakana-Gwasira et al., 2013; Paul and Edwin, 2010; McDonald, 1957)
ϕ	malaria related death	0.502	(Okosun, Ouifki and Marcus, 2013)
q	malaria related death among co-infected	0.45	assumed
β_h	probability of human getting infected	0.07833	(Mukandavire, Garira and Tchuente, 2009)
β_v	probability of mosquitoes getting infected	0.07833	(Mukandavire et al., 2009)
μ_h	Natural death rate in humans	0.000049132	(Okosun et al., 2013)
κ	malaria immunity waning rate	100, 1/17	(Mukandavire et al., 2009)
ψ	malaria-cholera immunity waning rate	0.001	assumed
Λ_h	human birth rate	0.00099	(Mukandavire et al., 2009)
Λ_v	mosquitoes birth rate	0.0089	(Mukandavire et al., 2009)
σ	co-infected population recovery rate	0.0000134	assumed
α	malaria infected population recovery rate	$1/(2*365)$	(Okosun and Makinde, 2014)
ϵ	co-infected who recovered from malaria only	0.0001	assumed

Table 1: Description of malaria parameters and their values in the co-infection model (1).

Further the following bacteria and cholera parameters values were used

Parameter	Description	value	Reference
Cholera and Bacteria Parameters			
ν	ingestion rate	0.5	(Nielan, Schaefer, Gaff, Fister and Lenhart, 2010)
K	concentration of bacteria in water	1000	(Sanches, Ferreira and Kraenkel, 2011)
η	cholera related death rate among co-infected patients	0.03	assumed
m	cholera infection death rate	0.02407	(Shuai, Tien and van den Driessche, 2012)
ρ	cholera infection death rate due to the aquatic environment	0.7	assumed
θ	modification parameter	1.2	(Mushayabasa and Bhunu, 2009)
μ_b	bacteria mortality rate	0.033	(Nielan et al., 2010)
λ	bacteria contact rate with humans	0.05	assumed
ω	cholera immunity waning rate	0.001	(Sanches et al., 2011)
δ	rate of recovery of cholera infected individuals	0.07	(Sanches et al., 2011)

Table 2: Description of bacteria and cholera parameters and their values in the co-infection model (1).

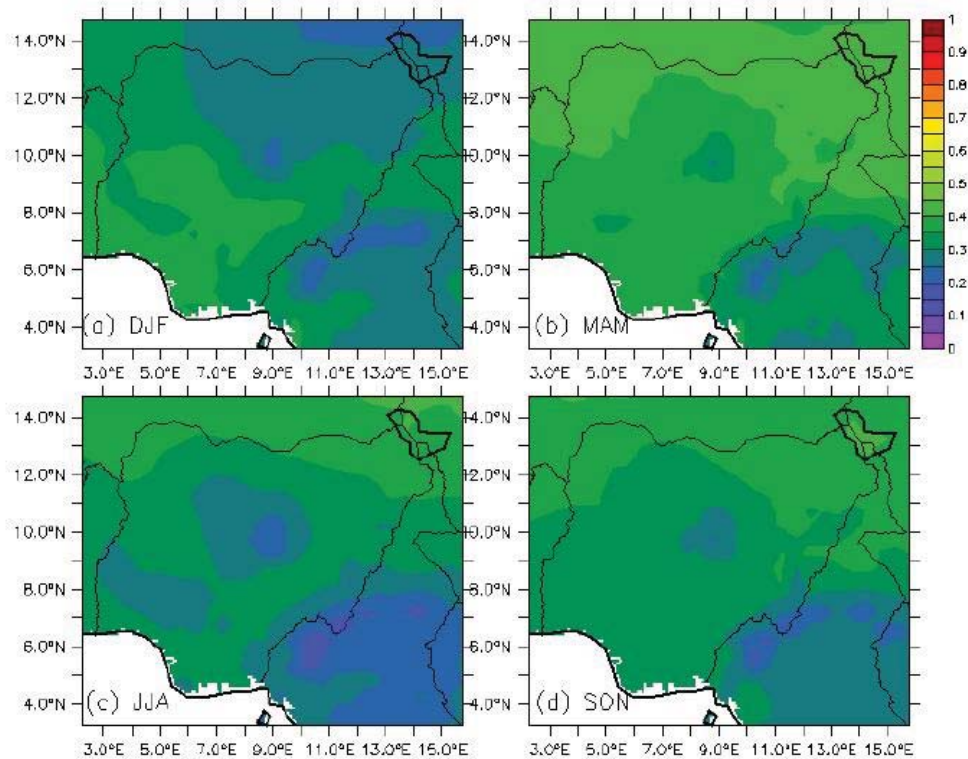


Figure 1: Spatial distribution of the cholera reproductive number over Nigeria

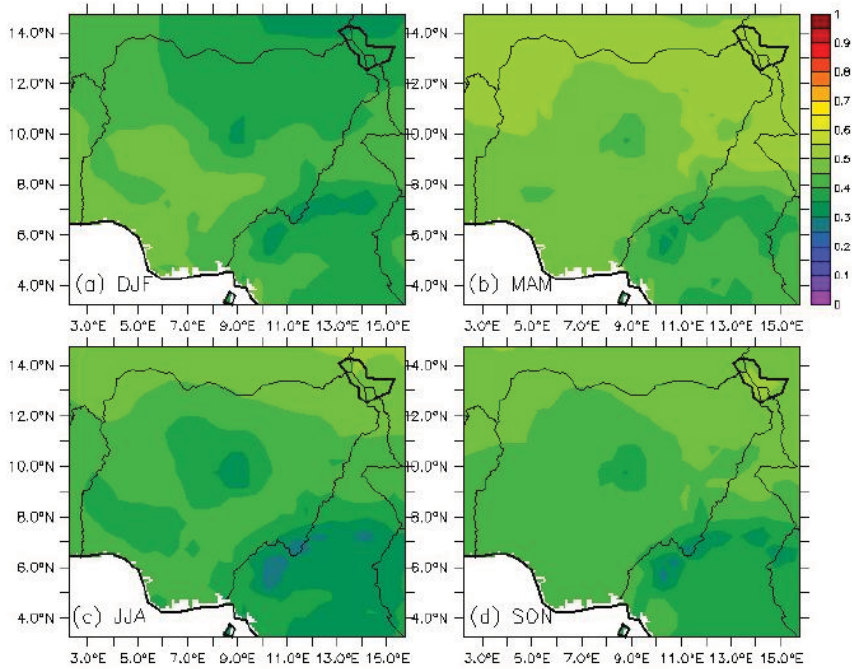


Figure 2: Spatial distribution of the impact of malaria on cholera reproductive number over Nigeria

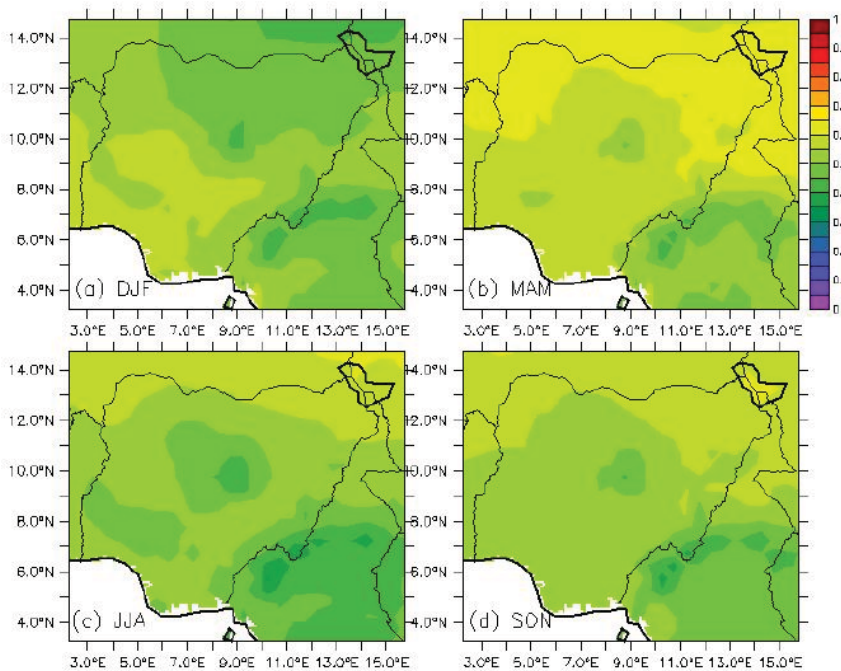


Figure 3: Spatial distribution of the malaria reproductive number over Nigeria

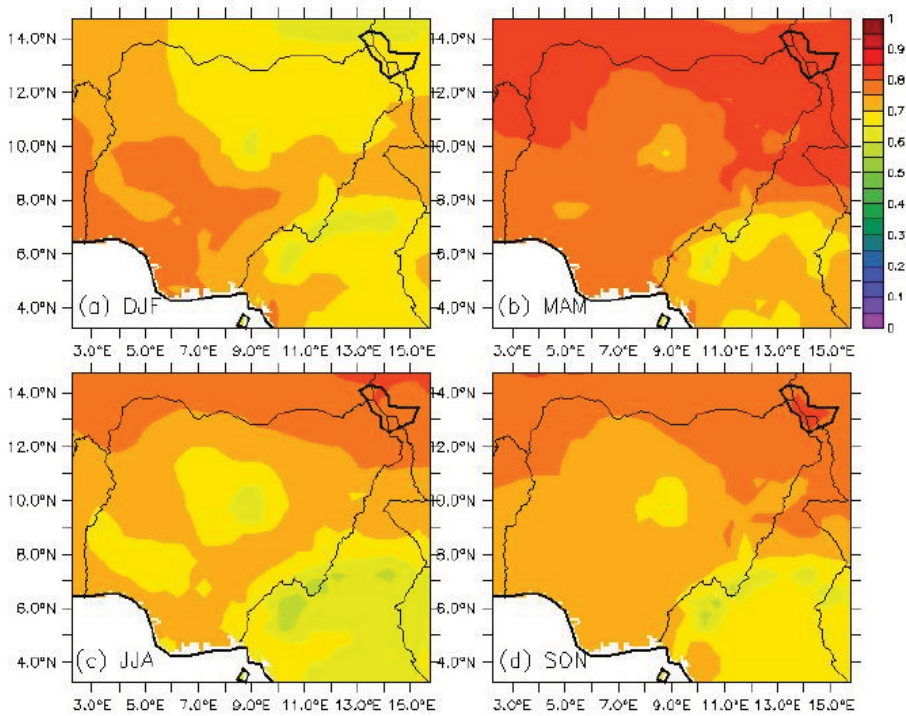


Figure 4: Spatial distribution of the impact of cholera on malaria reproductive number over Nigeria

5 Concluding remarks

In this study, a climate-based mathematical model to investigate the impact of temperature and rainfall on the co-infection of malaria and cholera transmission is developed and analysed. Analyses show that fluctuations of the climate variables will cause both increases and decreases in the areas suitable for co-infection of malaria and cholera transmission. Climate change has a huge effect on the distribution of environmental suitability for malaria and cholera co-infection transmission with changes in temperature and rainfall patterns. However, the global and local impacts of climate change on the co-infection dynamics of malaria and cholera transmission remain uncertain. We showed that an increase in malaria infection will result in an increase of cholera infection and that treating cholera will positively impact on the spread of malaria. The model however provides a numerical basis for further refinement and prediction of the impact of environmental variability on the co-infection of malaria and cholera.

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