DISCRETE AND CONTINUOUS
DYNAMICAL SYSTEMS SERIES B
Volume **19**, Number **10**, December **2014**

doi:10.3934/dcdsb.2014.19.3133

pp. **3133–3145**

A PERIODIC ROSS-MACDONALD MODEL IN A PATCHY ENVIRONMENT

Daozhou Gao

Francis I. Proctor Foundation for Research in Ophthalmology
University of California, San Francisco
San Francisco, CA 94143, USA

Yijun Lou

Department of Applied Mathematics
The Hong Kong Polytechnic University
Hung Hom, Kowloon, Hong Kong, China

Shigui Ruan

Department of Mathematics
University of Miami
Coral Gables, FL 33124, USA

Dedicated to Professor Chris Cosner on the occasion of his 60th birthday

Abstract. Based on the classical Ross-Macdonald model, in this paper we propose a periodic malaria model to incorporate the effects of temporal and spatial heterogeneity on disease transmission. The temporal heterogeneity is described by assuming that some model coefficients are time-periodic, while the spatial heterogeneity is modeled by using a multi-patch structure and assuming that individuals travel among patches. We calculate the basic reproduction number $\mathcal{R}_0$ and show that either the disease-free periodic solution is globally asymptotically stable if $\mathcal{R}_0 \leq 1$ or the positive periodic solution is globally asymptotically stable if $\mathcal{R}_0 > 1$. Numerical simulations are conducted to confirm the analytical results and explore the effect of travel control on the disease prevalence.

1. **Introduction.** Malaria, a widely prevalent vector-borne disease in tropical and subtropical areas, is caused by a parasite that is transmitted to humans and many other animals by the *Anopheles* mosquito. Once infected, people may experience a variety of symptoms, ranging from absent or very mild symptoms to severe complications and even death. It is one of the most deadly infectious diseases that causes major economic loss due to illness and death in humans.

The Ross-Macdonald model is the earliest and also simplest mathematical model describing malaria transmission between human and mosquito populations. It was initially proposed by Ross [31] in 1911 and later extended by Macdonald [23, 24, 25] in 1950s. The modeling framework is now widely used for malaria and some other

2010 *Mathematics Subject Classification.* Primary: 92D30; Secondary: 34D23.

Key words and phrases. Malaria, patch model, seasonality, threshold dynamics, basic reproduction number.

The work was supported in part by the Models of Infectious Disease Agent Study (MIDAS) (UCSF 1 U01 GM087728), NSFC (11301442), NIH (R01GM093345) and NSF (DMS-1022728, DMS-1412454).

mosquito-borne diseases. It captures the essential features of malaria transmission process, but ignores many factors of real-world ecology and epidemiology (see Ruan, Xiao and Beier [32]).

One omission in the classical Ross-Macdonald model is the temporal heterogeneity in the number of both populations and the human feeding rate of mosquitoes. In many nations like Niger, seasonal human migration has a long history, and destinations and reasons vary by community and ethnic group (Rain [29]). It is a common sense that there are more mosquitoes in the summer and fewer in the winter. The biological activity and geographic distribution of a malaria parasite and its vector are greatly influenced by climatic factors such as rainfall, temperature and humidity (Craig et al. [9], Gao et al. [12]). These influences can be investigated by assuming some parameters to be time dependent. In recent years, epidemic models with seasonal fluctuations have been proposed and explored by many researchers. A vector-borne model for epidemics of cutaneous leishmaniasis with a seasonally varying vector population and a distributed delay in humans was proposed and studied by Bacaër and Guernaoui [4]. Dembele, Friedman and Yakubu [10] introduced a new malaria model with periodic mosquito birth and death rates. Bai and Zhou [6] developed a SIRS model for bacillary dysentery with periodic coefficients. Using an ODE model with periodic transmission rates, Zhang et al. [38] considered the transmission dynamics of rabies from dogs to humans in China. Liu, Zhao and Zhou [17] used a compartmental model with periodic infection rate and reactivation rate to describe the TB transmission in China. For a detailed discussion of seasonal infectious diseases, we refer the reader to two excellent survey papers (Altizer et al. [1], Grassly and Fraser [13]) and the introduction of a recent paper (Lou, Lou and Wu [19]). Periodicity mainly occurs in the contact rate, birth or death rate, vaccination rate, etc.

Another omission is the spatial movements of hosts between different patches. The migration of humans can influence disease spread in a complicated way (Gao and Ruan [11]). To have a better understanding of the disease dynamics, it is necessary to incorporate periodic variations and population dispersal into epidemic models. These two issues are considered in (Lou and Zhao [20]) via a periodic reaction-diffusion-advection model. In this paper, we will formulate a periodic Ross-Macdonald model in a patchy environment and establish the threshold dynamics of the model in Section 2 and Section 3, respectively. The last section gives some numerical simulations and a brief discussion of our main results and future research directions.

2. **Model formulation.**

Most mosquitoes can only travel a couple of kilometers throughout their lifetime (Costantini et al. [8] and Midega et al. [26]), so we assume no movement for vector populations between patches (see Auger et al. [3]). For simplicity, the human vital dynamics are ignored and the population model for vectors is the same as that studied in Smith, Dushoff and Mckenzie [33]. Following the classical Ross-Macdonald model, we divide the adult female mosquito and human populations into two classes in each patch: susceptible and infectious. The total number of patches is p. We assume that the total populations of humans and mosquitoes at time t in patch i are $H_i(t)$ and $V_i(t)$, respectively. Let $h_i(t)$ and $v_i(t)$ denote the numbers of infectious humans and infectious mosquitoes in patch i, respectively. The interactions between humans and mosquitoes in patch i can be described by the following periodic system with non-negative initial conditions:

TABLE 1. The parameters in model (2.1) and their descriptions

Symbol	Description
$\varepsilon_i(t) > 0$	Recruitment rate of mosquitoes
$d_i(t) > 0$	Mortality rate of mosquitoes
$a_i(t) > 0$	Mosquito biting rate
$b_i > 0$	Transmission probability from infectious mosquitoes to susceptible humans
$c_i > 0$	Transmission probability from infectious humans to susceptible mosquitoes
$1/r_i > 0$	Human infectious period
$m_{ij}(t) \geq 0$	Human immigration rate from patch j to patch i for $i \neq j$
$-m_{ii}(t) \geq 0$	Human emigration rate from patch i

$$\frac{dH_i(t)}{dt} = \sum_{j=1}^{p} m_{ij}(t)H_j(t),\ 1 \leq i \leq p, \tag{2.1a}$$

$$\frac{dV_i(t)}{dt} = \varepsilon_i(t) - d_i(t)V_i(t),\ 1 \leq i \leq p, \tag{2.1b}$$

$$\frac{dh_i(t)}{dt} = b_i a_i(t)\frac{H_i(t) - h_i(t)}{H_i(t)}v_i(t) - r_i h_i(t) + \sum_{j=1}^{p} m_{ij}(t)h_j(t),\ 1 \leq i \leq p, \tag{2.1c}$$

$$\frac{dv_i(t)}{dt} = c_i a_i(t)\frac{h_i(t)}{H_i(t)}(V_i(t) - v_i(t)) - d_i(t)v_i(t),\ 1 \leq i \leq p. \tag{2.1d}$$

The model parameters and their descriptions are listed in Table 1. To incorporate the seasonal mosquito dynamics and human migration, all time-dependent parameters in system (2.1) are continuous and periodic functions with the same period $\omega = 365$ days. We assume that there is no death or birth during travel, so the emigration rate of humans in patch i, $-m_{ii}(t) \geq 0$, satisfies

$$\sum_{j=1}^{p} m_{ji}(t) = 0 \quad \text{for } i = 1, \ldots, p \quad \text{and} \quad t \in [0, \omega].$$

For travel rates between two patches, we assume there must be some travelers between different patches at some specific seasons. Mathematically, we assume that the matrix $(\int_0^\omega m_{ij}(t)dt)_{p\times p}$, which is related to the travel rates between different patches, is irreducible. The notation $H(t)$ will mean $(H_1(t), \ldots, H_p(t))$, with similar notations for other vectors. We will denote both zero value and zero vector by 0, but this should cause no confusion. The following theorem indicates that model (2.1) is mathematically and epidemiologically well-posed.

Theorem 2.1. *For any initial value z in*

$$\Gamma = \{(H, V, h, v) \in \mathbb{R}_+^{4p} : h_i \leq H_i, v_i \leq V_i, i = 1, \ldots, p\},$$

system (2.1) has a unique nonnegative bounded solution through z for all $t \geq 0$.

Proof. Let $G(t, z)$ be the vector field described by (2.1) with $z(t) \in \Gamma$. Then $G(t, z)$ is continuous and Lipschitzian in z on each compact subset of $\mathbb{R}^1 \times \Gamma$. Clearly, $G_k(t, z) \geq 0$ whenever $z \geq 0$ and $z_k = 0$, $k = 1, \ldots, 4p$. It follows from Theorem 5.2.1 in Smith [34] that there exists a unique nonnegative solution for system (2.1)

through $z \in \Gamma$ in its maximal interval of existence. The total numbers for hosts and vectors, $N^h(t) = \sum_{i=1}^{p} H_i(t)$ and $N^v(t) = \sum_{i=1}^{p} V_i(t)$, satisfy

$$\frac{dN^h(t)}{dt} = \sum_{i=1}^{p}\sum_{j=1}^{p} m_{ij}(t)H_j(t) = \sum_{i=1}^{p}\sum_{j=1}^{p} m_{ji}(t)H_i(t) = 0$$

and

$$\frac{dN^v(t)}{dt} = \sum_{i=1}^{p}(\varepsilon_i(t) - d_i(t)V_i(t)) \le \hat{\varepsilon} - \bar{d}N^v(t),$$

respectively, where $\hat{\varepsilon} = \max\limits_{0\le t\le\omega}\left(\sum\limits_{i=1}^{p}\varepsilon_i(t)\right)$ and $\bar{d} = \min\limits_{0\le t\le\omega}\left(\min\limits_{1\le i\le p} d_i(t)\right)$ are positive constants. Thus $N^h(t) \equiv N^h(0)$. The comparison principle (see Theorem B.1 in Smith and Waltman [35]) implies that $N^v(t)$ is ultimately bounded. Hence every solution of (2.1) exists globally. □

3. **Mathematical analysis.** In this section, we first show the existence of a unique disease-free periodic solution and then evaluate the basic reproduction number for the periodic system. By using the theory of monotone dynamical systems (Smith [34], Zhao [40]) and internally chain transitive sets (Hirsch, Smith and Zhao [15], Zhao [40]), we establish the global dynamics of the system. The following result is analogous to Lemma 1 in Cosner et al. [7] for the autonomous case.

Lemma 3.1. *The human migration model (2.1a) with $H_i(0) \ge 0$ for $i = 1,\dots,p$ and $N^h(0) > 0$ has a unique positive ω-periodic solution $H^*(t) \equiv (H_1^*(t),\dots,H_p^*(t))$, which is globally asymptotically stable. The mosquito growth model (2.1b) with $V_i(0) \ge 0$ for $i = 1,\dots,p$ has a unique positive ω-periodic solution $V^*(t) \equiv (V_1^*(t),\dots,V_p^*(t))$, which is globally asymptotically stable.*

Proof. Note that the travel rate matrix $M(t) \equiv (m_{ij}(t))_{p\times p}$ has nonnegative off-diagonal entries and the matrix $(\int_0^\omega m_{ij}(t)dt)_{p\times p}$ is irreducible. Let $\phi(t)$ be the fundamental matrix of system (2.1a) which satisfies $d\phi(t)/dt = M(t)\phi(t)$ and $\phi(0) = I_p$. Then the $p\omega$ period fundamental matrix $\phi(p\omega)$ is a strongly positive operator (Smith [34]). By using the $p\omega$ period fundamental matrix $\phi(p\omega)$ in the proof of Theorem 1 in Aronsson and Kellogg [2], we see that the $p\omega$ periodic system (2.1a) has a positive $p\omega$ periodic solution $H^*(t)$, which is globally asymptotically stable with respect to all nonzero solutions. By using the global attractivity of the $p\omega$ periodic solution, we can further show it is also ω periodic by using a similar argument in Weng and Zhao [37]. Moreover, it is easy to see that $\sum_{i=1}^{p} H_i^*(t) = N^h(0)$.

The i-th equation of (2.1b) has a unique positive periodic solution

$$V_i^*(t) = e^{-\int_0^t d_i(s)ds}\left(V_i^*(0) + \int_0^t e^{\int_0^s d_i(\tau)d\tau}\varepsilon_i(s)ds\right) \text{ with } V_i^*(0) = \frac{\int_0^\omega e^{\int_0^s d_i(\tau)d\tau}\varepsilon_i(s)ds}{e^{\int_0^\omega d_i(s)ds} - 1},$$

which is globally asymptotically stable. □

Remark 3.1. We can relax the positivity assumption on $\varepsilon_i(t)$ to $[\varepsilon_i] > 0$ where $[\varepsilon_i] = \frac{1}{\omega}\int_0^\omega \varepsilon_i(t)dt$ is the average value of $\varepsilon_i(t)$ over $[0,\omega]$, or equivalently, $\varepsilon_i(\tilde{t}) > 0$

for some $\tilde{t} \in [0, 2\pi)$. See Lemma 2.1 in Zhang and Teng [39] for results on a general nonautonomous system of the form $dV_i(t)/dt = \varepsilon_i(t) - d_i(t)V_i(t)$.

The above result guarantees that system (2.1) admits a unique disease-free periodic solution

$$E_0(t) = (H_1^*(t), \ldots, H_p^*(t), V_1^*(t), \ldots, V_p^*(t), 0, \ldots, 0, 0, \ldots, 0).$$

Biologically, both human and mosquito populations in each patch are seasonally forced due to periodically changing human migration and seasonal birth, death and biting rates of mosquitoes, respectively. Now we consider the asymptotically periodic system for malaria transmission

$$\begin{aligned} \frac{dh_i(t)}{dt} &= b_i a_i(t)\frac{H_i^*(t) - h_i(t)}{H_i^*(t)}v_i(t) - r_i h_i(t) + \sum_{j=1}^{p} m_{ij}(t)h_j(t), \quad 1 \le i \le p, \\ \frac{dv_i(t)}{dt} &= c_i a_i(t)\frac{h_i(t)}{H_i^*(t)}(V_i^*(t) - v_i(t)) - d_i(t)v_i(t), \quad 1 \le i \le p. \end{aligned} \tag{3.1}$$

In what follows, we use the definition of Bacaër and Guernaoui [4] (see also Bacaër [5]) and the general calculation method in Wang and Zhao [36] to evaluate the basic reproduction number $\mathcal{R}_0$ for system (3.1). Then we analyze the threshold dynamics of system (3.1). Finally we study global dynamics for the whole system (2.1) by applying the theory of internally chain transitive sets (Hirsch, Smith and Zhao [15] and Zhao [40]).

Let $x = (h_1, \ldots, h_p, v_1, \ldots, v_p)$ be the vector of all infectious class variables. The linearization of system (3.1) at the disease-free equilibrium $P_0 = (0, \ldots, 0, 0, \ldots, 0)$ is

$$\frac{dx}{dt} = (F(t) - V(t))x, \tag{3.2}$$

where

$$F(t) = \begin{bmatrix} 0 & \mathcal{A} \\ \mathcal{B} & 0 \end{bmatrix} \text{ and } V(t) = \begin{bmatrix} \mathcal{C} & 0 \\ 0 & \mathcal{D} \end{bmatrix}.$$

Here $\mathcal{A} = (\delta_{ij}a_i(t)b_i)_{p\times p}$, $\mathcal{B} = (\delta_{ij}a_i(t)c_iV_i^*(t)/H_i^*(t))_{p\times p}$, $\mathcal{C} = (\delta_{ij}r_i - m_{ij}(t))_{p\times p}$, $\mathcal{D} = (\delta_{ij}d_i(t))_{p\times p}$, and δ_{ij} denotes the Kronecker delta function (i.e., 1 when $i = j$ and 0 elsewhere).

Let $Y(t, s), t \ge s$, be the evolution operator of the linear ω-periodic system

$$\frac{dy}{dt} = -V(t)y.$$

That is, for each $s \in \mathbb{R}^1$, the $2p \times 2p$ matrix $Y(t, s)$ satisfies

$$\frac{dY(t,s)}{dt} = -V(t)Y(t,s), \ \forall t \ge s, \ Y(s,s) = I_{2p},$$

where I_{2p} is the $2p \times 2p$ identity matrix.

Let C_ω be the ordered Banach space of all ω-periodic functions from $\mathbb{R}^1$ to $\mathbb{R}^{2p}$ equipped with the maximum norm. We define a linear operator $L : C_\omega \to C_\omega$ by

$$\begin{aligned} (L\phi)(t) &= \int_{-\infty}^{t} Y(t,s)F(s)\phi(s)ds \\ &= \int_{0}^{\infty} Y(t, t-a)F(t-a)\phi(t-a)da, \ \forall t \in \mathbb{R}^1, \ \phi \in C_\omega. \end{aligned} \tag{3.3}$$

It is easy to verify that conditions (A1)-(A7) in Wang and Zhao [36] are satisfied. Therefore, the basic reproduction number of the periodic system (3.1) is then defined

as $\mathcal{R}_0 := \rho(L)$, the spectral radius of L. The following lemma shows that the basic reproduction number $\mathcal{R}_0$ is the threshold parameter for local stability of the disease-free steady state.

Lemma 3.2 (Theorem 2.2 in Wang and Zhao [36]). *Let $\Phi_{F-V}(t)$ and $\rho(\Phi_{F-V}(\omega))$ be the monodromy matrix of system (3.2) and the spectral radius of $\Phi_{F-V}(\omega)$, respectively. The following statements are valid:*

(i) $\mathcal{R}_0 = 1$ *if and only if* $\rho(\Phi_{F-V}(\omega)) = 1$.
(ii) $\mathcal{R}_0 > 1$ *if and only if* $\rho(\Phi_{F-V}(\omega)) > 1$.
(iii) $\mathcal{R}_0 < 1$ *if and only if* $\rho(\Phi_{F-V}(\omega)) < 1$.

Thus, the disease-free equilibrium P_0 of system (3.1) is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$.

Lou and Zhao [20] presented a global qualitative analysis for system (3.1) with a single patch. We will show that the system with multiple patches does not exhibit more complicated dynamics.

Lemma 3.3. *Let $\mathbb{D}_t = \{(h, v); 0 \le h \le H^*(t), 0 \le v \le V^*(t)\}$. For each $x(0) = (h(0), v(0)) \in \mathbb{R}^{2p}_+$, system (3.1) admits a unique solution $x(t) = (h(t), v(t)) \in \mathbb{R}^{2p}_+$ through $x(0)$ for all $t \ge 0$. Moreover, $x(t) \in \mathbb{D}_t$, $\forall t \ge 0$, provided that $x(0) \in \mathbb{D}_0$.*

Proof. Let $K(t, x)$ denote the vector field described by (3.1). Since $K(t, x)$ is continuous and locally Lipschitizan in x in any bounded set. By Theorem 5.2.1 in Smith [34] and Theorem 2.1, system (3.1) has a unique solution $(h(t), v(t))$ through $x(0) \in \mathbb{R}^{2p}_+$ which exists globally.

To prove the second statement, we let $u(t) = H^*(t) - h(t)$ and $w(t) = V^*(t) - v(t)$, where $(h(t), v(t))$ is the solution through $x(0) \in \mathbb{D}_0$. Then $(u(t), w(t))$ satisfies the following system with $u(0) = H^*(0) - h(0) \ge 0$ and $w(0) = V^*(0) - v(0) \ge 0$:

$$\frac{du_i(t)}{dt} = -a_i(t)b_i\frac{u_i(t)}{H_i^*(t)}(V_i^*(t) - w_i(t)) - r_iu_i(t) + r_iH_i^*(t) + \sum_{j=1}^{p} m_{ij}(t)u_j(t),$$

$$\frac{dw_i(t)}{dt} = \varepsilon_i(t) - a_i(t)c_i\frac{H_i^*(t) - u_i(t)}{H_i^*(t)}w_i(t) - d_i(t)w_i(t),$$

for $i = 1, \dots, p$. It then follows from Theorem 5.1.1 in Smith [34] that $(u(t), w(t)) \ge 0$. That is, the solution for system (3.1) $x(t) = (h(t), v(t)) \le (H^*(t), V^*(t))$ holds for all $t \ge 0$ whenever $x(0) \in \mathbb{D}_0$. □

Theorem 3.1. *System (3.1) admits a unique positive ω-periodic solution, denoted by $P^*(t) = (h^*(t), v^*(t)) = (h_1^*(t), \dots, h_p^*(t), v_1^*(t), \dots, v_p^*(t))$, which is globally asymptotically stable with initial values in $\mathbb{D}_0 \backslash \{0\}$ if $\mathcal{R}_0 > 1$ and the disease-free equilibrium P_0 is globally asymptotically stable in $\mathbb{D}_0$ if $\mathcal{R}_0 \le 1$.*

Proof. To show the global asymptotic stability of $P^*(t)$ or P_0, it suffices to verify that $K(t, x) : \mathbb{R}^1_+ \times \mathbb{D}_0 \to \mathbb{R}^{2p}$ satisfies (A1)-(A3) in Theorem 3.1.2 in Zhao [40].

For every $x = (h, v) \ge 0$ with $h_i = 0$ or $v_i = 0$, $t \in \mathbb{R}^1_+$, we have

$$K_i(t, x) = a_i(t)b_iv_i + \sum_{1 \le j \le p, j \ne i} m_{ij}(t)h_j \ge 0$$

or

$$K_{p+i}(t, x) = a_i(t)c_i\frac{h_i}{H_i^*(t)}V_i^*(t) \ge 0,$$

for $i = 1, \dots, p$. So (A1) is satisfied.

By Lemma 3.3, the system (3.1) is cooperative in $\mathbb{D}_t$, and the ω-periodic semiflow is monotone. We can further prove that the $p\omega$-periodic semiflow is strongly monotone in $\mathrm{Int}\mathbb{D}_0$, the interior of $\mathbb{D}_0$, due to the irreducibility of $(\int_0^\omega m_{ij}(t)dt)_{p\times p}$.

For each $t \geq 0$, $i = 1, \ldots, p$, there hold

$$\begin{aligned} K_i(t, \alpha x) &= a_i(t)b_i\frac{H_i^*(t) - \alpha h_i}{H_i^*(t)}\alpha v_i - r_i\alpha h_i + \sum_{j=1}^{p} m_{ij}(t)\alpha h_j \\ &> \alpha\left(a_i(t)b_i\frac{H_i^*(t) - h_i}{H_i^*(t)}v_i - r_i h_i + \sum_{j=1}^{p} m_{ij}(t)h_j\right) = \alpha K_i(t, x) \end{aligned}$$

and

$$\begin{aligned} K_{p+i}(t, \alpha x) &= a_i(t)c_i\frac{\alpha h_i}{H_i^*(t)}(V_i^*(t) - \alpha v_i) - d_i(t)\alpha v_i \\ &> \alpha\left(a_i(t)c_i\frac{h_i}{H_i^*(t)}(V_i^*(t) - v_i) - d_i(t)v_i\right) = \alpha K_{p+i}(t, x) \end{aligned}$$

for each $x \gg 0, \alpha \in (0, 1)$. That is, $K(t, \cdot)$ is strictly subhomogeneous on $\mathbb{R}_+^{2p}$.

Moreover, $K(t, 0) \equiv 0$ and all solutions are ultimately bounded. Therefore, by Theorem 3.1.2 in Zhao [40] or Theorem 2.3.4 in Zhao [40] as applied to the $p\omega$ solution map associated with (3.1), the proof is complete. □

Using the theory of internally chain transitive sets (Hirsch, Smith and Zhao [15] or Zhao [40]), as argued in Lou and Zhao [22], we find that the disease either dies out or persists and stabilizes at a periodic state.

Theorem 3.2. *For system (2.1), if $\mathcal{R}_0 > 1$ then there is a unique positive ω-periodic solution, denoted by $E^*(t) = (H^*(t), V^*(t), h^*(t), v^*(t))$, which is globally asymptotically stable; if $\mathcal{R}_0 \leq 1$ then the disease-free periodic solution $E_0(t)$ is globally asymptotically stable.*

Proof. Let P be the Poincaré map of the system (2.1) on $\mathbb{R}_+^{4p}$, that is,

$$P(H(0), V(0), h(0), v(0)) = (H(\omega), V(\omega), h(\omega), v(\omega)).$$

Then P is a compact map. Let $\Omega = \Omega(H(0), V(0), h(0), v(0))$ be the omega limit set of $P^n(H(0), V(0), h(0), v(0))$. It then follows from Lemma 2.1′ in Hirsch, Smith and Zhao [15] (see also Lemma 1.2.1′ in Zhao [40]) that Ω is an internally chain transitive set for P. Based on Lemma 3.1, we have

$$\lim_{t\to\infty}(H(t), V(t)) = (H^*(t), V^*(t))$$

for any $H(0) > 0$ and $V(0) > 0$. Thus, $\Omega = \{(H^*(0), V^*(0))\} \times \Omega_1$ for some $\Omega_1 \subset \mathbb{R}_+^{2p}$ and

$$P^n|_\Omega(H^*(0), V^*(0), h(0), v(0)) = (H^*(0), V^*(0), P_1^n(h(0), v(0))),$$

where P_1 is the Poincaré map associated with the system (3.1). Since Ω is an internally chain transitive set for P^n, then Ω_1 is an internally chain transitive set for P_1^n. Next, we will discuss different scenarios when $\mathcal{R}_0 \leq 1$ and $\mathcal{R}_0 > 1$.

Case 1. $\mathcal{R}_0 \leq 1$. In this case, the zero equilibrium P_0 is globally asymptotically stable for system (3.1) according to Theorem 3.1. It then follows from Theorem 3.2 and Remark 4.6 of Hirsch, Smith and Zhao [15] that $\Omega_1 = \{(0, 0)\}$, which further

implies that $\Omega = \{(H^*(0), V^*(0), 0, 0)\}$. Therefore, the disease free periodic solution $(H^*(t), V^*(t), 0, 0)$ is globally asymptotically stable.

Case 2. $\mathcal{R}_0 > 1$**.** In this case, there are two fixed points for the map P_1, $(0,0)$ and $(h^*(0), v^*(0))$. We claim that $\Omega_1 \neq \{(0,0)\}$ for all $h(0) > 0$ or $v(0) > 0$. Assume that, by contradiction, $\Omega_1 = \{(0,0)\}$ for some $h(0) > 0$ or $v(0) > 0$. Then $\Omega = \{(H^*(0), V^*(0), 0, 0)\}$ and we have

$$\lim_{t\to\infty} (H(t), V(t), h(t), v(t)) = (H^*(t), V^*(t), 0, 0).$$

Since $\mathcal{R}_0 > 1$, there exists some $\delta > 0$ such that the following linear system is unstable

$$\begin{aligned} \frac{dh_i(t)}{dt} &= b_i a_i(t)(1-\delta)v_i(t) - r_i h_i(t) + \sum_{j=1}^{p} m_{ij}(t)h_j(t), \quad 1 \le i \le p, \\ \frac{dv_i(t)}{dt} &= c_i a_i(t)(1-\delta)\frac{V_i^*(t)}{H_i^*(t)}h_i(t) - d_i(t)v_i(t), \quad 1 \le i \le p. \end{aligned} \tag{3.4}$$

Moreover, there exists some $T_0 > 0$ such that

$$|(H(t), V(t), h(t), v(t)) - (H^*(t), V^*(t), 0, 0)| < \delta \min_{0\le t\le\omega}\{H^*(t), V^*(t)\}, \ \forall t > T_0.$$

Hence we have

$$\begin{aligned} \frac{dh_i(t)}{dt} &\ge b_i a_i(t)(1-\delta)v_i(t) - r_i h_i(t) + \sum_{j=1}^{p} m_{ij}(t)h_j(t), \quad 1 \le i \le p, \\ \frac{dv_i(t)}{dt} &\ge c_i a_i(t)(1-\delta)\frac{V_i^*(t)}{H_i^*(t)}h_i(t) - d_i(t)v_i(t), \quad 1 \le i \le p, \end{aligned}$$

when $t > T_0$. According to the instability of system (3.4) and the comparison principle, $h_i(t)$ and $v_i(t)$ will go unbounded as $t \to \infty$, which contradicts the boundedness of solutions (Theorem 2.1).

Since $\Omega_1 \neq \{(0,0)\}$ and $(h^*(0), v^*(0))$ is globally asymptotically stable for P_1^n in $\mathbb{R}_+^{2p} \setminus \{(0,0)\}$, it follows that $\Omega_1 \bigcap W^s((h^*(0), v^*(0))) \neq \emptyset$, where $W^s((h^*(0), v^*(0)))$ is the stable set for $(h^*(0), v^*(0))$. By Theorem 3.1 and Remark 4.6 in Hirsch, Smith and Zhao [15], we then get $\Omega_1 = \{(h^*(0), v^*(0))\}$. Thus, $\Omega = \{(H^*(0), V^*(0), h^*(0), v^*(0))\}$, and hence the statement for the case when $\mathcal{R}_0 > 1$ is valid. □

4. **Simulations and discussions.** In this section, we provide some numerical simulations for the two-patch case to support our analytical conclusions. The following matrix and lemma will be used in numerical computation for the basic reproduction number $\mathcal{R}_0$. Let $W(t, \lambda)$ be the monodromy matrix (see Hale [14]) of the homogeneous linear ω-periodic system

$$\frac{dx}{dt} = \Big(-V(t) + \frac{F(t)}{\lambda}\Big)x, \ t \in \mathbb{R}^1$$

with parameter $\lambda \in (0, \infty)$.

Lemma 4.1 (Theorem 2.1 in Wang and Zhao [36])**.** *The following statements are valid:*

(i) *If $\rho(W(\omega, \lambda)) = 1$ has a positive solution λ_0, then λ_0 is an eigenvalue of L and hence $\mathcal{R}_0 > 0$, where L is the next generation operator defined in (3.3);*
(ii) *If $\mathcal{R}_0 > 0$, then $\lambda = \mathcal{R}_0$ is the unique solution of $\rho(W(\omega, \lambda)) = 1$;*
(iii) *$\mathcal{R}_0 = 0$ if and only if $\rho(W(\omega, \lambda)) < 1$ for all $\lambda > 0$.*

According to Lemma 4.1(ii), we can show that the basic reproduction number for (3.1) is proportional to the biting rate, that is, $\tilde{\mathcal{R}}_0 = k\mathcal{R}_0$ if $\tilde{\beta}_i(t) = k\beta_i(t)$ for $k > 0$ and $1 \le i \le p$ (see Lou and Zhao [21] or Liu and Zhao [18]).

To implement numerical simulations, we choose the baseline parameter values as follows: $b_i = 0.2, r_i = 0.02, c_i = 0.3, d_i(t) = 0.1$ for $i = 1, 2$. For the first patch, $\varepsilon_1(t) = 12.5-(5\cos(\frac{2\pi t}{365})+2.5\sin(\frac{2\pi t}{365}))-(5\cos(\frac{4\pi t}{365})-2.5\sin(\frac{4\pi t}{365})) \ge 12.5-5\sqrt{5} > 0$, $a_1(t) = 0.028\varepsilon_1(t) > 0$. In the second patch, $\varepsilon_2(t) = 15 - 12\cos(\frac{2\pi t}{365})$, $a_2(t) = 0.18 - 0.12\cos(\frac{2\pi t}{365})$. Then, using Lemma 4.1, we can numerically compute that the respective reproduction numbers of the disease in patches 1 and 2 are $\mathcal{R}_{10} = 1.7571 > 1$ and $\mathcal{R}_{20} = 0.8470 < 1$ and the disease persists in the first patch but dies out in the second patch (see Figure 1(a)). When humans migrate between these two patches with $m_{12}(t) = 0.006 - 0.004\cos(\frac{2\pi t}{365})$ and $m_{21}(t) = 0.006 + 0.004\cos(\frac{2\pi t}{365})$, the basic reproduction number is $\mathcal{R}_0 = 1.3944 > 1$. Thus, the disease becomes endemic in both patches (see Figure 1(b)).

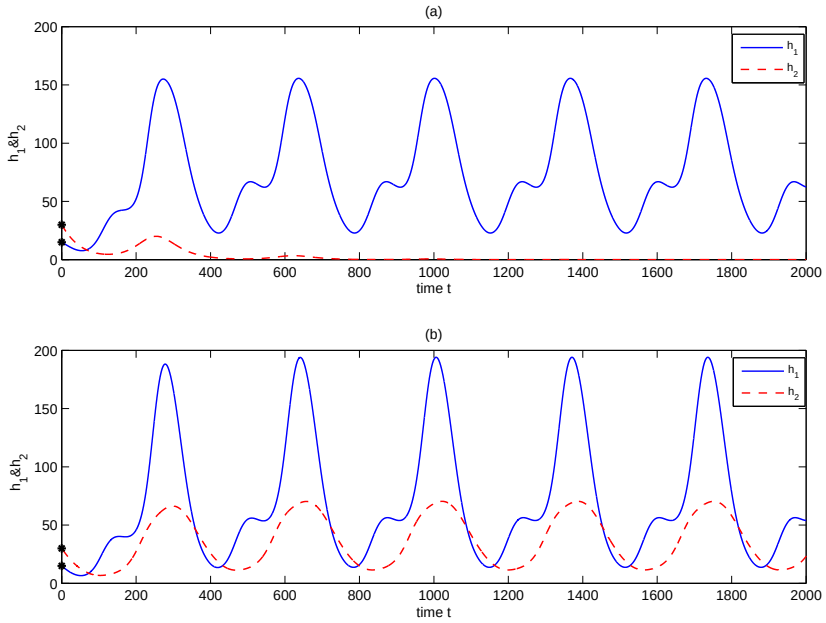

FIGURE 1. Numerical solution of system (3.1) with initial conditions: $H_1(0) = 200, V_1(0) = 50, h_1(0) = 15, v_1(0) = 10$ and $H_2(0) = 300, V_2(0) = 30, h_2(0) = 30, v_2(0) = 5$. The curves of the number of infected humans in patches 1 and 2, respectively, are blue solid and red dashed. (a) when there is no human movement, $\mathcal{R}_{10} = 1.7571 > 1$ and $\mathcal{R}_{20} = 0.8470 < 1$ indicate the disease persists in patch 1 but dies out in patch 2; (b) when human movement presents, $\mathcal{R}_0 = 1.3944 > 1$ indicates the disease persists in both patches, and will stabilize in a seasonal pattern.

The basic reproduction number for the corresponding time-averaged autonomous system (see Wang and Zhao [36] and Zhang et al. [38]) is $\bar{\mathcal{R}}_0 = 1.2364$. By Lemma

4.1 or the linearity of $\mathcal{R}_0$ in the mosquito biting rates, we can multiply the biting rates by an appropriate constant such that $\bar{\mathcal{R}}_0$ below 1 while $\mathcal{R}_0$ above 1. Thus, the autonomous malaria model may underestimate disease severity in some transmission settings.

In order to investigate the effect of possible travel control on the malaria risk, we determine the disease risk when shifting the phases of the movement functions, while keeping their respective mean values and forcing strengths to be the same. With the same parameter values and initial data except that the migration rates $m_{12}(t) = 0.006 - 0.004\cos(\frac{2\pi t}{365} + \phi_1)$ and $m_{21}(t) = 0.006 + 0.004\cos(\frac{2\pi t}{365} + \phi_2)$, we evaluate the annual malaria prevalence over the two patches for $\phi_1, \phi_2 \in [0, 2\pi]$. Then Figure 2 presents the effect of phase shifting for movement functions on disease prevalence. The approximate range of malaria prevalence is from 17% to 23%. This result indicates that appropriate travel control can definitely reduce the disease risk, and therefore, an optimal travel control measure can be proposed.

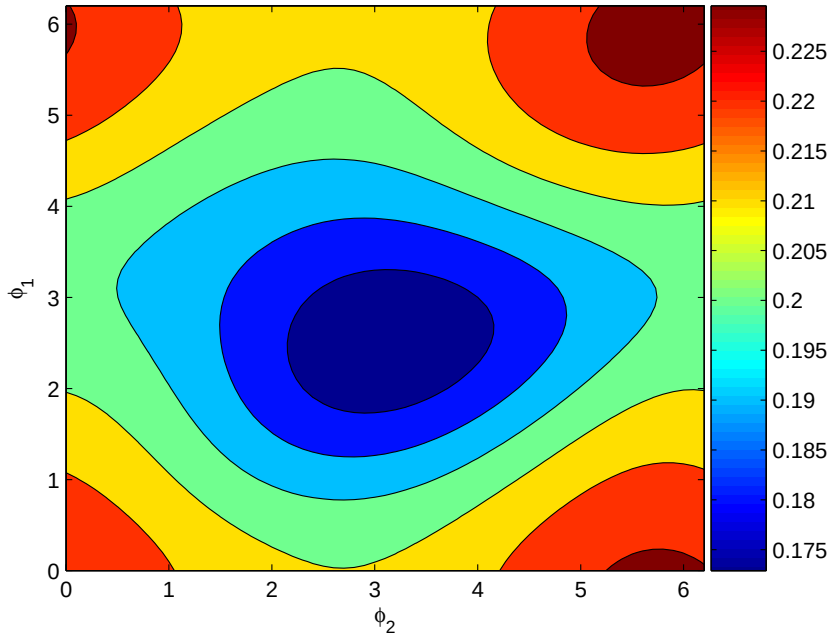

FIGURE 2. Effect of phase shift for movement rates between two patches on disease risk.

In this project, we have developed a compartmental model to address seasonal variations of malaria transmission among different regions by incorporating seasonal human movement and periodic changing in mosquito ecology. We then derive the basic reproduction number and establish the global dynamics of the model. Mathematically, we generalize the model and results presented in Cosner et al. [7] and Auger et al. [3] from a constant environment to a periodic environment. Biologically, our result gives a possible explanation to the fact that malaria incidence show seasonal peaks in most endemic areas (Roca-Feltrer et al. [30]). The numerical examples suggest that a better understanding of seasonal human migration can

help us to prevent and control malaria transmission in a spatially heterogeneous environment.

It would be interesting to assess the impacts of climate change on the emerging and reemerging of mosquito-borne diseases, especially malaria. It is believed that global warming would cause climate change, while climatic factors such as precipitation, temperature, humidity and wind speed affect the biological activity and geographic distribution of the pathogen and its vector. It sometimes even affects human behavior through sea-level rise, more extreme weather events, etc.

The current and potential future impact of climate change on human health has attracted considerable attention in recent years. Many of the early studies (see Ostfeld [27] and the references cited therein) claimed that recent and future trends in climate warming were likely to increase the severity and global distribution of vector-borne diseases, while there is still substantial debate about the link between climate change and the spread of infectious diseases (Lafferty [16]). The controversy is partially due to the fact that although there is massive work using empirical-statistical models to explore the relationship between climatic factors and the distribution and prevalence of vector-borne diseases, there are very few studies incorporating climatic factors into mathematical models to describe disease transmission.

The research that comes closest to what we expect to do has been conducted by Parham and Michael in [28], where they used a system of delay differential equations to model malaria transmission under varying climatic and environmental conditions. Model parameters are assumed to be temperature-dependent or rainfall-dependent or both. Due to the complexity of their model, mathematical analysis was not possible and only numerical simulations were carried out. Furthermore, the basic reproduction number is also difficult to project through their model. We would like to extend our model to a mathematically tractable climate-based model in the future.

Acknowledgments. Part of this work was done while the first author was a graduate student in the Department of Mathematics, University of Miami. We thank Drs. Chris Cosner, David Smith and Xiao-Qiang Zhao for helpful discussions on this project.

REFERENCES

[1] S. Altizer, A. Dobson, P. Hosseini, P. Hudson, M. Pascual and P. Rohani, Seasonality and the dynamics of infectious diseases, *Ecol. Lett.*, **9** (2006), 467–484.

[2] G. Aronsson and R. B. Kellogg, On a differential equation arising from compartmental analysis, *Math. Biosci.*, **38** (1973), 113–122.

[3] P. Auger, E. Kouokam, G. Sallet, M. Tchuente and B. Tsanou, The Ross-Macdonald model in a patchy environment, *Math. Biosci.*, **216** (2008), 123–131.

[4] N. Bacaër and S. Guernaoui, The epidemic threshold of vector-borne diseases with seasonality, *J. Math. Biol.*, **53** (2006), 421–436.

[5] N. Bacaër, Approximation of the basic reproduction number R_0 for vector-borne diseases with a periodic vector population, *Bull. Math. Biol.*, **69** (2007), 1067–1091.

[6] Z. Bai and Y. Zhou, Threshold dynamics of a Bacillary Dysentery model with seasonal fluctuation, *Discrete Contin. Dyn. Syst., Ser. B*, **15** (2011), 1–14.

[7] C. Cosner, J. C. Beier, R. S. Cantrell, D. Impoinvil, L. Kapitanski, M. D. Potts, A. Troyo and S. Ruan, The effects of human movement on the persistence of vector-borne diseases, *J. Theoret. Biol.*, **258** (2009), 550–560.

[8] C. Costantini, S. G. Li, A. D. Torre, N. Sagnon, M. Coluzzi and C. E. Taylor, Density, survival and dispersal of *Anopheles gambiae* complex mosquitoes in a West African Sudan savanna village, *Med. Vet. Entomol.*, **10** (1996), 203–219.
[9] M. H. Craig, I. Kleinschmidt, J. B. Nawn, D. Le Sueur and B. L. Sharp, Exploring 30 years of malaria case data in KwaZulu-Natal, South Africa: Part I. The impact of climatic factors, *Trop. Med. Int. Health*, **9** (2004), 1247–1257.
[10] B. Dembele, A. Friedman and A.-A. Yakubu, Malaria model with periodic mosquito birth and death rates, *J. Biol. Dynam.*, **3** (2009), 430–445.
[11] D. Gao and S. Ruan, A multi-patch malaria model with logistic growth populations, *SIAM J. Appl. Math.*, **72** (2012), 819–841.
[12] H. Gao, L. Wang, S. Liang, Y. Liu, S. Tong, J. Wang, Y. Li, X. Wang, H. Yang, J. Ma, L. Fang and W. Cao, Change in rainfall drives malaria re-emergence in Anhui province, China, *PLoS ONE*, **7** (2012), e43686.
[13] N. C. Grassly and C. Fraser, Seasonal infectious disease epidemiology, *Proc. R. Soc. B.*, **273** (2006), 2541–2550.
[14] J. K. Hale, *Ordinary Differential Equations*, Wiley-Interscience, New York, 1980.
[15] M. W. Hirsch, H. L. Smith and X.-Q. Zhao, Chain transitivity, attractivity, and strong repellors for semidynamical systems, *J. Dyn. Differ. Equ.*, **13** (2001), 107–131.
[16] K. D. Lafferty, The ecology of climate change and infectious diseases, *Ecology*, **90** (2009), 888–900.
[17] L. Liu, X.-Q. Zhao and Y. Zhou, A tuberculosis model with seasonality, *Bull. Math. Biol.*, **72** (2010), 931–952.
[18] X. Liu and X.-Q. Zhao, A periodic epidemic model with age structure in a patchy environment, *SIAM J. Appl. Math.*, **71** (2011), 1896–1917.
[19] J. Lou, Y. Lou and J. Wu, Threshold virus dynamics with impulsive antiretroviral drug effects, *J. Math. Biol.*, **65** (2012), 623–652.
[20] Y. Lou and X.-Q. Zhao, The periodic Ross-Macdonald model with diffusion and advection, *Appl. Anal.*, **89** (2010), 1067–1089.
[21] Y. Lou and X.-Q. Zhao, A climate-based malaria transmission model with structured vector population, *SIAM J. Appl. Math.*, **70** (2010), 2023–2044.
[22] Y. Lou and X.-Q. Zhao, Modelling malaria control by introduction of larvivorous fish, *Bull. Math. Biol.*, **73** (2011), 2384–2407.
[23] G. Macdonald, The analysis of sporozoite rate, *Trop. Dis. Bull.*, **49** (1952), 569–585.
[24] G. Macdonald, Epidemiological basis of malaria control, *Bull. World Health Organ.*, **15** (1956), 613–626.
[25] G. Macdonald, *The Epidemiology and Control of Malaria*, Oxford University Press, London, 1957.
[26] J. T. Midega, C. M. Mbogo, H. Mwambi, M. D. Wilson, G. Ojwang, J. M. Mwangangi, J. G. Nzovu, J. I. Githure, G. Yan and J. C. Beier, Estimating dispersal and survival of *Anopheles gambiae* and *Anopheles funestus* along the Kenyan coast by using mark-release-recapture methods, *J. Med. Entomol.*, **44** (2007), 923–929.
[27] R. S. Ostfeld, Climate change and the distribution and intensity of infectious diseases, *Ecology*, **90** (2009), 903–905.
[28] P. E. Parham and E. Michael, Modeling the effects of weather and climate change on malaria transmission, *Environ. Health Perspect.*, **118** (2010), 620–626.
[29] D. Rain, *Eaters of the Dry Season: Circular Labor Migration in the West African Sahel*, Westview Press, Boulder, CO, 1999.
[30] A. Roca-Feltrer, J. R. Armstrong Schellenberg, L. Smith and I. Carneiro, A simple method for defining malaria seasonality, *Malaria J.*, **8** (2009), 276.
[31] R. Ross, *The Prevention of Malaria*, 2nd edn., Murray, London, 1911.
[32] S. Ruan, D. Xiao and J. C. Beier, On the delayed Ross-Macdonald model for malaria transmission, *Bull. Math. Biol.*, **70** (2008), 1098–1114.
[33] D. L. Smith, J. Dushoff and F. E. McKenzie, The risk of a mosquito-borne infection in a heterogeneous environment, *PLoS Biology*, **2** (2004), 1957–1964.
[34] H. L. Smith, *Monotone Dynamical Systems: An Introduction to the Theory of Competitive and Cooperative Systems*, Mathematical Surveys and Monographs, vol. 41, A.M.S., Providence, RI, 1995.
[35] H. L. Smith and P. Waltman, *The Theory of the Chemostat*, Cambridge University Press, Cambridge, 1995.

[36] W. Wang and X.-Q. Zhao, Threshold dynamics for compartmental epidemic models in periodic environments, *J. Dyn. Differ. Equ.*, **20** (2008), 699–717.
[37] P. Weng and X.-Q. Zhao, Spatial dynamics of a nonlocal and delayed population model in a periodic habitat, *Discrete Contin. Dyn. Syst. Ser. A*, **29** (2011), 343–366.
[38] J. Zhang, Z. Jin, G. Sun, X. Sun and S. Ruan, Modeling seasonal Rabies epidemics in China, *Bull. Math. Biol.*, **74** (2012), 1226–1251.
[39] T. Zhang and Z. Teng, On a nonautonomous SEIRS model in epidemiology, *Bull. Math. Biol.*, **69** (2007), 2537–2559.
[40] X.-Q. Zhao, *Dynamical Systems in Population Biology*, Springer-Verlag, New York, 2003.

Received July 2013; 1st revision January 2014; 2nd revision January 2014.

E-mail address: daozhou.gao@ucsf.edu
E-mail address: yijun.lou@polyu.edu.hk
E-mail address: ruan@math.miami.edu