Avian Malaria

E.R. Cara,
R. Natarajan,
E. Pinto,
R. Ximenes,
C. Simoncini,
HJB Njagarah

IFT-UNESP,II SSSMB 2013, grp 6

January 27, 2013

Outline

Introduction

What Avian Malaria is

- Avian Malaria is a parasitic disease of birds
- The etiologic agent is *Plasmodium relictum*
- The natural vector is mosquito *Culex pipiens*
- Some of the affected birds include; Hawaiian Amakihi, Liwi, Apapanes and Honeycreepers

Introduction

What Avian Malaria is

- Avian Malaria is a parasitic disease of birds
- The etiologic agent is *Plasmodium relictum*
- The natural vector is mosquito *Culex pipiens*
- Some of the affected birds include; Hawaiian Amakihi, Liwi, Apapanes and Honeycreepers

The evolution of the Avian malaria in the bird population and the equilibrium level of the both birds and mosquitoes is influenced by the state of interacting populations.

1. The mosquitoes (vectors) may be carrying the parasite or not
2. The birds (host) may be infected or uninfected.
3. Each class of vectors can bite both classes of the birds (host).

Vector Preference for the host

Two recent studies about Avian malaria indicate that the vector does not necessarily randomly bite the host;

a. According to Cornet *et al.*, 2012 [1], the vector prefers the infected host.

b. According to Lalubin *et al.*, 2012 [2], the uninfected host attracts the vectors.

Several studies evidently suggest that mosquitoes do not randomly feed with respect to the disease status of the host. According to Edman *et al.* 1985 [4], non random feeding by vectors may be expressed in three ways such as:

- attraction and penetration,
- probing and location of blood, and
- the intake of blood

Some studies performed on mice, hens infected with arbovirus as well as rift valley fever virus infected lambs, showed that mosquitoes feed more frequently on infected organisms compared to their uninfected counterparts [3].

Using different biting rates depending on the mosquito preference for the host (see Kingsolver, 1987) [3], we study the trajectories and equilibrium levels of the infection in both host and the vector.

Model

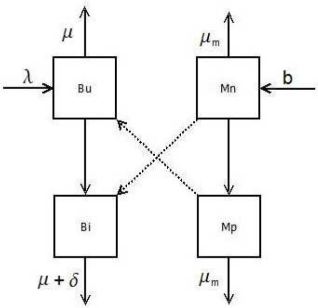


Figure: Schematic flow diagram for the model

Model

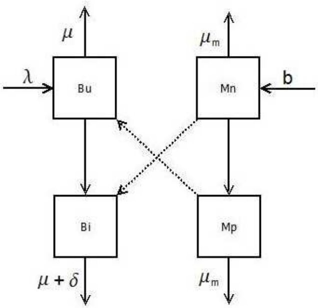


Figure: Schematic flow diagram for the model

Model system of equations

$$\frac{dB_u}{dt} = \lambda_1 - \kappa\beta\frac{B_u}{B_i + B_u}M_p - \mu B_u$$
$$\frac{dB_i}{dt} = \kappa\beta\frac{B_u}{B_i + B_u}M_p - (\mu+\delta)B_I$$
$$\frac{dM_n}{dt} = b - \beta\frac{B_i}{B_i + B_u}M_n - \mu_m M_n$$
$$\frac{dM_p}{dt} = \beta\frac{B_i}{B_i + B_u}M_n - \mu_m M_p. \tag{1}$$

Domain of biological significance

The domain of biological significance is defined as

$$\Omega := \left\{ (B_u, B_i, M_n, M_p) \in \mathbf{R}^4_+ : 0 < B_u + B_i \leq \frac{\lambda_1}{\mu}, M_n + M_p \leq \frac{b}{\mu_m} \right\}, \quad (2)$$

with initial conditions ($B_{u0} > 0,\ B_{i0} > 0,\ M_{n0} > 0,$ and $M_{p0} > 0$) is positively invariant and attracting with respect to the dynamical system described by system (1).

Positivity of Solution

We show that is the system starts with non-negative initial conditions ($B_{u0} > 0,\ B_{i0} > 0,\ M_{n0} > 0,$ and $M_{p0} > 0$), the solutions/trajectories of (1) will remain non-negative for all $t \in [0, \infty)$. This is an ideal condition to check since the model monitors birds and mosquito populations. Then we have the following theorem

Theorem

Given that the initial conditions of the system (1) ($B_{u0} > 0,\ B_{i0} > 0,\ M_{n0} > 0,$ *and* $M_{p0} > 0$), *the resulting solutions* (B_u, B_i, M_n *and* M_p) *re all non-negative for all* $t \in [0, \infty)$.

Boundedness of solutions

We show that the state space variables ($B_u,\ B_i,\ M_n,$ and M_p) with initial conditions
($B_{u0}\ B_{i0},\ M_{n0},$ and M_{p0}) are non-negative for all $t \in [0, \infty)$.

Theorem

Given that the initial conditions of the system (1) ($B_{u0} > 0,\ B_{i0} > 0,\ M_{n0} > 0,$ and $M_{p0} > 0$), the resulting solutions ($B_u,\ B_i,\ M_n,$ and M_p) are all non-negative for all $t \in [0, \infty)$.

Disease free equilibrium

The model has a disease free equilibrium (DFE) given by

$$\mathbb{E}_0 := \left(B_u^*, B_i^*, M_n^*, M_p^*\right) = \left(\frac{\lambda_1}{\mu}, 0, \frac{b}{\mu_m}, 0\right) \tag{3}$$

Reproduction number

$$\mathcal{R}_0 = \sqrt{\mathcal{R}_e}, \quad \text{where} \quad \mathcal{R}_e = \frac{\kappa \beta^2 \mu b}{(\mu + \delta)\mu_m^2 \lambda_1} \tag{4}$$

The terms $1/(\mu + \delta)$ and $1/\mu_m$ indicate the maximum life expectancy of the infected birds and the mosquitoes respectively.

The reproduction number given in (4) describes the number of infected birds (mosquito) that an infected mosquito (bird) infects throughout out the infectious period when introduced to a fully susceptible bird (mosquito) population.

Local stability of the DFE

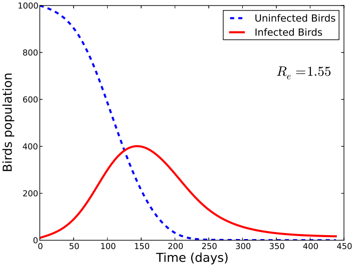
We linearise the system of equation (1) at the disease free equilibrium,to obtain a characteristic polynomial

$$P(\lambda) = (\lambda+\mu)(\lambda+\mu_m)\left(\lambda^2 + (\mu+\delta+\mu_m)\lambda + \mu_m(\mu+\delta)[1-\mathcal{R}_e]\right) \quad (5)$$

For $P(\lambda) = 0$, the roots $\lambda_1 = -\mu$, $\lambda_2 = -\mu_m$ and the roots of the third factor λ_3 and λ_4 will be negative only when $\mathcal{R}_e < 1$.

- The DFE is locally asymptotically stable when $\mathcal{R}_e < 1$.
- When $\mathcal{R}_e > 1$ atleast one root is positive thus the DFE is unstable.

Simulation



(a)

Simulation

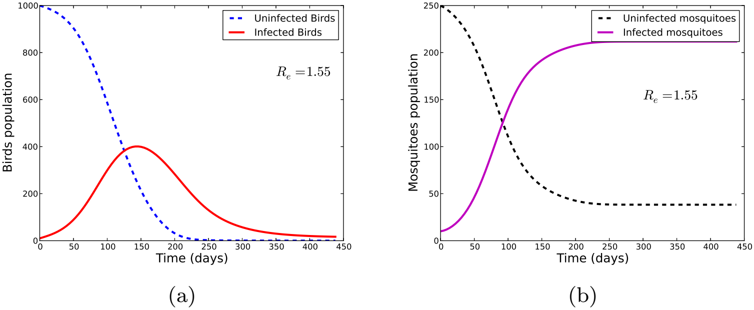


Figure: $\mu = 1/(365\times12)$, $\lambda_1 = B_{u0}\mu$, $\mu_m = 1/40$, $b = M_{n0}\mu_m$, $\beta = 0.07$, $\kappa = 0.64$, $\delta = 0.02$

Summary

Figure 2, is obtained from model system (1) where the mosquitoes are assumed to randomly bite the hosts without preference to the disease status of the host.

The evolution of the populations is obtained for $R_e = 1.55 > 1$ indicating that Avian malaria remains prevalent in the population.

Consistent Host preference

The models system of equations is given by

$$\begin{aligned}
\frac{dB_u}{dt} &= \lambda_1 - \kappa\beta\frac{B_u}{B_u + QB_i}M_p - \mu B_u \\
\frac{dB_i}{dt} &= \kappa\beta\frac{B_u}{B_u + QB_i}M_p - (\mu + \delta)B_i \\
\frac{dM_n}{dt} &= b - \beta\frac{QB_i}{B_u + QB_i}M_n - \mu_m M_n \\
\frac{dM_p}{dt} &= \beta\frac{QB_i}{B_u + QB_i}M_n - \mu_m M_p.
\end{aligned} \tag{6}$$

Reproduction number

Using the next generation method as in the first model, the basic reproduction number for model system (6) is given by

$$\mathcal{R}_{02} = \sqrt{\mathcal{R}_{e2}}, \quad \text{where} \quad \mathcal{R}_{e2} = \frac{\kappa \beta^2 \mu b Q}{(\mu + \delta)\mu_m^2 \lambda_1} \tag{7}$$

We note that $\mathcal{R}_{e2}$ is directly proportional to Q, the mosquito preference for the infected host.

Therefore, increasing Q consequently increases the value of $\mathcal{R}_{e2}$ and hence the severity of avian malaria in the bird population as well as presence of the pathogen in the mosquito population.

Simulation

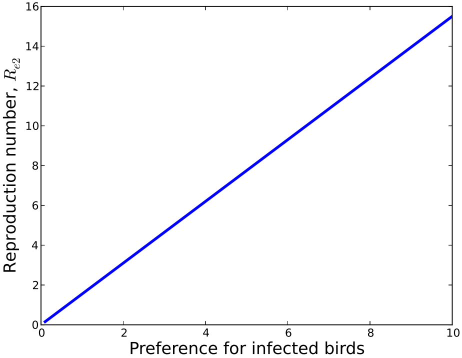


Figure: Reproduction number as a function of preference of mosquitoes for the infected birds

Simulation

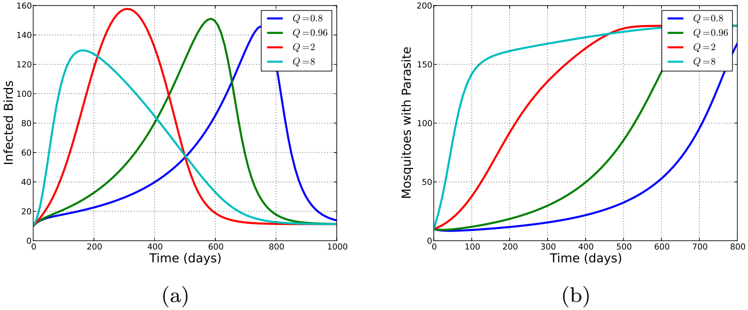
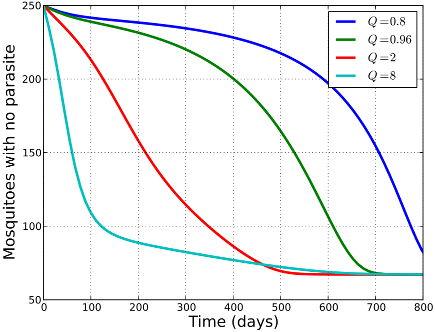


Figure: $\mu = 1/(365{\times}12)$, $\lambda_1 = B_{u0}\mu$, $\mu_m = 1/40$, $b = M_{n0}\mu_m$, $\beta = 0.07$, $\kappa = 0.64$, $\delta = 0.02$



(a)

Figure: $\mu = 1/(365 \times 12)$, $\lambda_1 = B_{u0} * \mu$, $\mu_m = 1/40$, $b = M_{n0} * \mu_m$, $\beta = 0.07$, $\kappa = 0.64$, $C = 2$, $\delta = 0.02$

Switching host preference

The models system of equations is given by

$$\begin{aligned}
\frac{dB_u}{dt} &= \lambda_1 - \kappa\beta \frac{(1+\alpha)e^{-Q\frac{B_i}{B_i+B_u}}}{1+\alpha e^{-Q\frac{B_i}{B_i+B_u}}} M_p - \mu B_u, \\
\frac{dB_I}{dt} &= \kappa\beta \frac{(1+\alpha)e^{-Q\frac{B_i}{B_i+B_u}}}{1+\alpha e^{-Q\frac{B_i}{B_i+B_u}}} M_p - (\mu+\delta)B_i, \\
\frac{dM_n}{dt} &= b - \beta \frac{\left(1-e^{-Q\frac{B_i}{B_i+B_u}}\right)}{1+\alpha e^{-Q\frac{B_i}{B_i+B_u}}} M_n - \mu_m M_n \\
\frac{dM_p}{dt} &= \beta \frac{\left(1-e^{-Q\frac{B_i}{B_i+B_u}}\right)}{1+\alpha e^{-Q\frac{B_i}{B_i+B_u}}} M_n - \mu_m M_p.
\end{aligned} \tag{8}$$

Reproduction number

The values α, Q and β are non negative constants. The parameters α and Q are chosen such that the biting rate of infected birds approaches unity as the fraction of infected host approaches one. The

parameter α affects the switching position and Q affects both the *switch point* and the rate at which the switch occurs. The basic reproduction number for model system (8) is given by

$$\mathcal{R}_{03} = \sqrt{\mathcal{R}_{e3}}, \quad \text{where} \quad \mathcal{R}_{e3} = \frac{\kappa\mu b Q\beta^2}{(\mu+\delta)(1+\alpha)\mu_m\lambda_1} \tag{9}$$

Similar to $\mathcal{R}_{e2}$, $\mathcal{R}_{e3}$ is also directly proportional to the mosquito preference for infected host

For the model system (8), we are yet to obtain fine trajectories owing to the challenge in fixing the parameters.

Summary

From the model with consistent preference for the infected host, we observe that increasing preference for the infected host;

- the trajectory of the infected birds reaches equilibrium levels at a faster rate.
- the level of the parasite in the birds population increases.

The influence of mosquito preference for infected birds on the level of infection in birds is an indirect process. We can not therefore make a conclusive statement regarding the maximum level of infection in the population with respect to preference.

Some suggested reasons for mosquito preference for the infected hosts [1] include;

1. The preference behaviour could be adaptive for the mosquitoes.
2. the preference of mosquitoes for infected hosts is a result of the parasite manipulating the host with the aim of maximising its own transmission.

References I

S. Cornet, A. Nicot, A. Rivero and S. Gandon (2012)
Malaria infection increases bird attractiveness to uninfected mosquitoes.
Ecol. Lett.

F. Lalubin, P. Bize, J van Rooyen, P. Christe and O. Glaizot (2012)
Potential evidence of parasite avoidance in an avian malarial vector.
Anim. Behav. 84,539-545

J. G. Kingsolver (1987)
Mosquito host choice and the epidemiology of Malaria.
Am. Nat. 130, 811-827

J. Edman, J. Day and E. Walker, (1985)
Vector-host interplay -factors affecting disease transmission.
pages 273-285 in L.P. Lounibos, J.R. Ray and J.H Frank, eds Ecology of Mosquitoes. Chapman & Hall, New York

Thank you for your attention