Research Article

Effect of fast migration on prey disease in a patchy system

Tanmay Chowdhury

Mrinalini Datta Mahavidyapith, Birati, Kolkata-700051, India

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Abstract

The effect of predator migration in the predator-prey system with disease in the prey population remains untouched. In this article, I have considered the individual-level migration of susceptible prey, infected prey, and predators between two different patches. I construct a couple of ODE models taking two different time scales. I consider that the individual migration of the species is faster than their demographic changes like birth, death, disease transmission, and interaction with predators. First I have study the model taking a large class of density-dependent migration rates. It has been proved that the fast equilibrium point is unique and asymptotically stable. Then I aggregate the model taking the advantage of two different time scales and construct a SIP model. The model has been investigated both analytically and numerically considering some particular type of density-dependent migrations. The theoretical study of the model includes evaluation of equilibrium points, local stability, and basic reproduction numbers in different situations. I found numerically the sensitivity of basic reproduction number with respect to migration ratios and the Switching of equilibrium points due to predator migration.

Key words: S-I-P model, fast migration, heterogeneous patches, basic reproduction number.

1. Introduction

Nature is naturally heterogeneous. Due to the heterogeneity of nature species needs migration. The effects of migration has been seen in many field ([1], [2], [3], [4]). In a region where two significantly different patches exist migration models better explore the system is there. These types of models comprise an important behavior of migration of species. There are several type of density-dependent migration like prey density-dependent migration of predator ([5], [6], [7], [8], [9]), predator density-dependent migration of prey ([10], [11]). In prey density-dependent migration of predators, predators moved towards a patch with a large prey density and leave the patch when it is small. On the other hand, in predator density-dependent prey dispersal, predators have a repulsive effect on prey i.e., prey leaves faster a given patch when more predators are there at that time.

In 2002 Charles *et al.* studied the effect of the migration behavior of susceptible hosts on the ability of the parasite to invade the system. But the existence of predators is natural as well as important to regulate the infection of parasitism in the prey population. Earlier researches are mainly focused on the effect of parasitism on the predator-prey system ([12], [13], [14], [15], [16]). In 2005 Roy and Chattopadhyay explore the conclusion of disease selective predation of predator in a predator-prey system with disease in prey population. In my treatise, I observe the impact of predator migration in an S-I-S system.

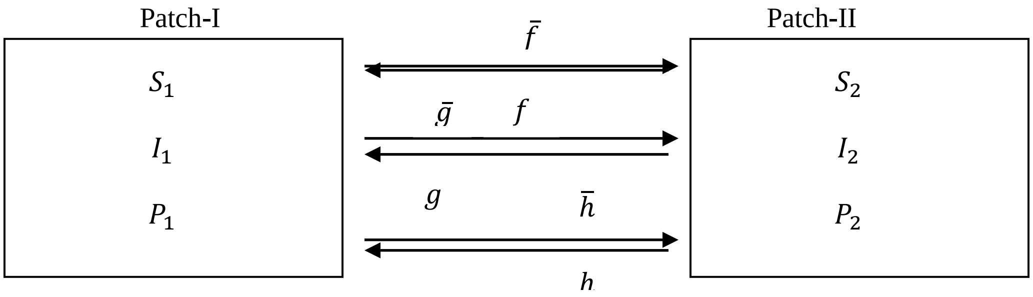
Here I consider a fast migration of prey and predators between two significantly different patches. I have studied an S-I-P model considering prey density- dependent migration of predators as well as predator density-dependent migration of both the susceptible and infected prey population. I study the situation when the infected remains in either patch losses their ability of migration by some parasitic infection. I observe the effect of predator migration on stability, population abundance, and the fitness of parasites in system. In all the cases I invent a huge impact of predator migration. In section 2, I have developed a slow-fast model and write down the model without migration which was studied by Asrul *et al.* [17]. Then in section 3, I have proved the asymptotic stability of the unique fast equilibrium point and the aggregated model. In section 4, the model has been studied taking a particular type of density-dependent migration. Section 5 and 6 are devoted for numerical analysis and conclusion.

2. Model Development

The following assumptions are made to formulate the model.

1. The migration of susceptible and infected prey population depends on the density of predator population in the patches.
2. The migration of predator population depends on the density of susceptible and infected prey population.
3. Migration is faster than the host growth, disease transmission and predator prey interactions.
4. Prey growth is regulated logistically by a density of both susceptible and infected host.
5. Predators growth rate due to predation of prey population follows Holling type-II functional response.

Schematic diagram of the migration



Under this assumption the following mathematical model has been developed.

$$\left.\begin{aligned}
\frac{dS_1}{d\tau} &= [f(P_2)S_2 - \bar{f}(P_1)S_1] + \epsilon\left[r_1(S_1+I_1)\left(1-\frac{S_1+I_1}{C_1}\right) - d_1S_1 + \gamma_1I_1 - \beta_1S_1I_1 - \frac{a_1S_1P_1}{1+b_1S_1}\right],\\
\frac{dS_2}{d\tau} &= [\bar{f}(P_1)S_1 - f(P_2)S_2] + \epsilon\left[r_2(S_2+I_2)\left(1-\frac{S_2+I_2}{C_2}\right) - d_2S_2 + \gamma_2I_2 - \beta_2S_2I_2 - \frac{a_2S_2P_2}{1+b_2S_2}\right],\\
\frac{dI_1}{d\tau} &= [g(P_2)I_2 - \bar{g}(P_1)I_1] + \epsilon\left[\beta_1S_1I_1 - d_1I_1 - \alpha_1I_1 - \gamma_1I_1 - \frac{a_1'I_1P_1}{1+b_1'I_1}\right],\\
\frac{dI_2}{d\tau} &= [\bar{g}(P_1)I_1 - g(P_2)I_2] + \epsilon\left[\beta_2S_2I_2 - d_2I_2 - \alpha_2I_2 - \gamma_2I_2 - \frac{a_2'I_2P_2}{1+b_2'I_2}\right],\\
\frac{dP_1}{d\tau} &= [h(S_2,I_2)P_2 - \bar{h}(S_1,I_1)P_1] + \epsilon\left[e\frac{a_1S_1P_1}{1+b_1S_1} + e'\frac{a_1'I_1P_1}{1+b_1'I_1} - m_1P_1\right],\\
\frac{dP_2}{d\tau} &= [\bar{h}(S_1,I_1)P_1 - h(S_2,I_2)P_2] + \epsilon\left[e\frac{a_2S_2P_2}{1+b_2S_2} + e'\frac{a_2'I_2P_2}{1+b_2'I_2} - m_2P_2\right],
\end{aligned}\right\} \quad (2.1)$$

where $S_1,\ I_1,\ P_1$ and $S_2,\ I_2,\ P_2$ are susceptible, infected, predator population density in patch-I and patch-II respectively.

Parameters description:

r_1 - Reproduction rate of prey population in patch - I (/time),
r_2 - Reproduction rate of prey population in patch - II (/time),
C_1 - Carrying capacity of patch - I (individual),
C_2 - Carrying capacity of patch - II (individual),
d_1 - Natural death rate of prey population in patch - I (/time),
d_2 - Natural death rate of prey population in patch - II (/time),
α_1 - Death rate due to disease in patch - I (/time),
α_2 - Death rate due to disease in patch - II (/time),
β_1 - Disease transmission rate in patch - I (/individual/time),
β_2 - Disease transmission rate in patch - II (/individual/time),
γ_1 - Recovery rate of infected prey population in patch - I (/time),
γ_2 - Recovery rate of infected prey population in patch - II (/time),
m_1 - Mortality rate of predators population in patch - I (/time),
m_2 - Mortality rate of predators population in patch - II (/time),
a_1 - Capture rate of predators to the susceptible prey in patch - I (/individual/time),
a_2 - Capture rate of predators to the susceptible prey in patch - II (/individual/time),
a_1' - Capture rate of predators to the infected prey in patch - I (/individual/time),
a_2' - Capture rate of predators to the infected prey in patch - II (/individual/time),
b_1 - half saturation constant of predator population in patch - I when predating susceptible prey (/individual),
b_2 - half saturation constant of predator population in patch - II when predating susceptible prey (/individual),
b_1' - half saturation constant of predator population in patch - I when predating infected prey (/individual),
b_2' - half saturation constant of predator population in patch - II when predating infected prey (/individual),
e - conversion rate of susceptible prey to predator (unit-less),
e' -conversion rate of infected prey to predator (unit-less),
and $0 < \epsilon \ll 1$.

Functions description:

$\bar{f}$ - Migration rate of susceptible prey from patch-I to patch-II which is a monotonic increasing positive valued function for all $P_1 > 0$,
f - Migration rate of susceptible prey from patch-II to patch-I which is a monotonic increasing positive valued function for all $P_2 > 0$,
$\bar{g}$ - Migration rate of infected prey from patch-I o patch-II which is a monotonic increasing positive valued function for all $P_1 > 0$,
g - Migration rate of infected prey from patch-II to patch-I which is a monotonic increasing positive valued function for all $P_2 > 0$,
$\bar{h}$ - Migration rate of predator from patch-I to patch-II which is a monotonic decreasing positive valued function for all $S_1 > 0$ and $I_1 > 0$,
h - Migration rate of predator from patch-II to patch-I which is a monotonic decreasing positive valued function for all $S_2 > 0$ and $I_2 > 0$,
I assume that $f, \bar{f}, g, \bar{g}, h, \bar{h} \in C^1(R_+^2)$.

If there is no migration then the system (2.1) becomes

$$\left.\begin{aligned}
\frac{dS_1}{dt} &= \left[r_1(S_1+I_1)\left(1-\frac{S_1+I_1}{C_1}\right)-d_1S_1+\gamma_1I_1-\beta_1S_1I_1-\frac{a_1S_1P_1}{1+b_1S_1}\right],\\
\frac{dI_1}{dt} &= \left[\beta_1S_1I_1-d_1I_1-\alpha_1I_1-\gamma_1I_1-\frac{a_1'I_1P_1}{1+b_1'I_1}\right],\\
\frac{dP_1}{dt} &= \left[e\frac{a_1S_1P_1}{1+b_1S_1}+e'\frac{a_1'I_1P_1}{1+b_1'I_1}-m_1P_1\right],
\end{aligned}\right\}\quad(2.2)$$

The analysis of the model (2.2) has been done in [17].

3. Equilibrium analysis of the fast model and aggregation of the model

As I see, the system (2.1) is mainly driven by the migration part; the demographic one is being only a small perturbation. I am now interested in the fast dynamics, and the corresponding fast model is obtained by neglecting the slow part i.e., taking $\epsilon = 0$.

$$\left.\begin{aligned}
\frac{dS_1}{d\tau} &= [f(P_2)S_2-\bar{f}(P_1)S_1],\\
\frac{dS_2}{d\tau} &= [\bar{f}(P_1)S_1-f(P_2)S_2],\\
\frac{dI_1}{d\tau} &= [g(P_2)I_2-\bar{g}(P_1)I_1],\\
\frac{dI_2}{d\tau} &= [\bar{g}(P_1)I_1-g(P_2)I_2],\\
\frac{dP_1}{d\tau} &= [h(S_2,I_2)P_2-\bar{h}(S_1,I_1)P_1],\\
\frac{dP_2}{d\tau} &= [\bar{h}(S_1,I_1)P_1-h(S_2,I_2)P_2],
\end{aligned}\right\}\quad(3.1)$$

where the total susceptible population is denoted by $S = S_1 + S_2$, the total infected population is denoted by $I = I_1 + I_2$ and total predator population is denoted by $P = P_1 + P_2$. These are the constants of motion of the fast system (3.1). So the fast equilibrium points and their stability are determined by the following system of equations.

$$\left.\begin{aligned}
\frac{dS_1}{d\tau} &= [f(P-P_1)(S-S_1)-\bar{f}(P_1)S_1],\\
\frac{dI_1}{d\tau} &= [g(P-P_1)(I-I_1)-\bar{g}(P_1)I_1],\\
\frac{dP_1}{d\tau} &= [h(S-S_1,I-I_1)(P-P_1)-\bar{h}(S_1,I_1)P_1],
\end{aligned}\right\}\quad(3.2)$$

The fast equilibrium point is the solution of the following system of equations:

$$\left.\begin{aligned}
&f(P-P_1)(S-S_1)-\bar{f}(P_1)S_1=0,\\
&g(P-P_1)(S-S_1)-\bar{g}(P_1)S_1=0,\\
&h(S-S_1,I-I_1)(P-P_1)-\bar{h}(S_1,I_1)P_1=0,\\
&S_1+S_2=S,\\
&I_1+I_2=I,\\
&P_1+P_2=P,
\end{aligned}\right\}\quad (3.3)$$

which gives $S_1=\eta(P_1)S$, $I_1=\mu(P_1)I$ and $P_1=\xi(S_1,I_1)P$ where P_1 is the solution of the equation

$$P_1=\phi(\bar{\phi}(P_1),\tilde{\phi}(P_1))\ \ldots\ldots\ldots\ldots\ldots\ldots\ldots(3.4)$$

where $\bar{\phi}(x)=\eta(x)S,\ \tilde{\phi}(x)=\mu(x)I,\ \phi(x,y)=\xi(x,y)P$ and

$\eta(x)=\frac{f(P-x)}{\bar{f}(x)+f(P-x)}$, $\mu(x)=\frac{g(P-x)}{\bar{g}(x)+g(P-x)}$, $\xi(x,y)=\frac{h(S-x,\ I-y)}{\bar{h}(x,\ y)+h(S-x,\ I-y)}$. Then

$$\bar{\phi}'(x)=-\frac{\bar{f}(x)f'(P-x)+f(P-x)\bar{f}'(x)}{[\bar{f}(x)+f(P-x)]^2}S,$$

$$\tilde{\phi}'(x)=-\frac{\bar{g}(x)g'(P-x)+g(P-x)\bar{g}'(x)}{[\bar{g}(x)+g(P-x)]^2}I,$$

$$\phi_x(x,y)=-\frac{\bar{h}(x,y)h_x(S-x,I-y)+h(S-x,I-y)\bar{h}_x(x,y)}{[\bar{h}(x,y)+h(S-x,I-y)]^2}P,$$

$$\phi_y(x,y)=-\frac{\bar{h}(x,y)h_y(S-x,I-y)+h(S-x,I-y)\bar{h}_y(x,y)}{[\bar{h}(x,y)+h(S-x,I-y)]^2}P,$$

Based on the assumption on the functions $f,\overline{f},g,\ \bar{g},\ h,\overline{h}$ it is clear that the function $\bar{\phi}$ and $\tilde{\phi}$ are decreasing for all $x>0$ and the function ϕ is increasing for all $x>0,y>0$. So the composite function $\phi\left(\bar{\phi}(P_1),\tilde{\phi}(P_1)\right)$ is decreasing and positive valued. Therefore if there exist a feasible solution of the equation (3.4) then it is unique. Let (S_1^*,I_1^*,P_1^*) be the fast equilibrium point. Then the characteristic equation of the system (3.2) is

$$\begin{vmatrix}-p_1-\lambda & 0 & -p_2\\ 0 & -p_3 & -p_4\\ p_5 & p_6 & -p_7-\lambda\end{vmatrix}=0\ \Rightarrow\ \lambda^3+A_1\lambda^2+A_2\lambda+A_3=0$$

where $A_1=p_1+p_3+p_7$,

$A_2=p_1p_7+p_3p_7+p_1p_3+p_4p_6+p_2p_5$,

$A_3 = p_1p_3p_7 + p_1p_4p_6 + p_2p_3p_5$

and $p_1 = f(P - P_1^*) + \bar{f}(P_1^*)$,

$p_2 = (S - S_1^*)f'(P - P_1^*) + S_1^*\bar{f}'(P_1^*)$,

$p_3 = g(P - P_1^*) + \bar{g}(P_1^*)$,

$p_4 = (I - I_1^*)g'(P - P_1^*) + I_1^*\bar{g}'(P_1^*)$,

$p_5 = (P - P_1^*)h_S(S - S_1^*,\ I - I_1^*) + \bar{h}_S(S_1^*, I_1^*)$,

$p_6 = (P - P_1^*)h_I(S - S_1^*,\ I - I_1^*) + \bar{h}_I(S_1^*, I_1^*)$,

$p_7 = \frac{P}{P_1^*}h(S - S_1^*,\ I - I_1^*)$.

where all p's are positive. Thus I have $A_1 > 0$ and $A_1A_2 > A_3$. Therefore the fast equilibrium is always asymptotically stable.

Now, I can obtain the global model at slow time scale $t = \epsilon\tau$ in terms of the aggregated variables S, I and P.

$$\left.\begin{aligned}
&\frac{dS}{dt} = \Big[r_1(S_1 + I_1)\left(1 - \frac{S_1+I_1}{C_1}\right) + r_2(S_2 + I_2)\left(1 - \frac{S_2+I_2}{C_2}\right) - d_1S_1 - d_2S_2 + \gamma_1I_1 + \gamma_2I_2 - \beta_1S_1I_1 - \beta_2S_2I_2 - \\
&\frac{a_1S_1P_1}{1+b_1S_1} - \frac{a_2S_2P_2}{1+b_2S_2}\Big],\\
&\frac{dI}{dt} = \left[\beta_1S_1I_1 + \beta_2S_2I_2 - d_1I_1 - d_2I_2 - \alpha_1I_1 - \alpha_2I_2 - \gamma_1I_1 - \gamma_2I_2 - \frac{a_1'I_1P_1}{1 + b_1'I_1} - \frac{a_2'I_2P_2}{1 + b_2'I_2}\right],\\
&\frac{dP}{dt} = \left[e\frac{a_1S_1P_1}{1 + b_1S_1} + e'\frac{a_1'I_1P_1}{1 + b_1'I_1} + e\frac{a_2S_2P_2}{1 + b_2S_2} + e'\frac{a_2'I_2P_2}{1 + b_2'I_2} - m_1P_1 - m_2P_2\right],
\end{aligned}\right\} \quad (3.5)$$

where $S_1, S_2, I_1, I_2, P_1, P_2$ are replaced by the fast equilibrium point.

4. Study of the model taking particular type of density-dependent migration

Let $f(P_2) = f_pP_2 + f_0$ and $\bar{f}(P_1) = \bar{f}_pP_1 + \bar{f}_0$ be a particular type of density-dependent migration rate of susceptible prey population from patch-II to patch-I and patch-I to patch-II respectively where $f_p,\ f_0\ ,\ \bar{f}_p,\ \bar{f}_0$ are positive. Let the predator density-dependent migration of infected prey from patch-II to patch-I and patch-I to patch-II are of the form $g(P_2) = g_pP_2 + g_0$ and $\bar{g}(P_1) = \bar{g}_pP_1 + \bar{g}_0$ respectively where $g_p,\ g_0\ ,\ \bar{g}_p,\ \bar{g}_0$ are positive. I also assume that the density-dependent migration rate of predators from patch-II to patch-I and patch-I to patch-II are $h(S_2, I_2) = \frac{1}{h_sS_2 + h_iI_2 + h_0}$ and $\bar{h}(S_1, I_1) = \frac{1}{\bar{h}_sS_1 + \bar{h}_iI_1 + \bar{h}_0}$ respectively where $h_s, h_i,\ h_0\ ,\ \bar{h}_s,\ \bar{h}_i,\ \bar{h}_0$ are positive. It is clear that all the functions $f, \bar{f}, g, \bar{g}, h, \bar{h}$ satisfy the conditions described in the section of model formulation. So our model (2.1) with the above stated density-dependent migration rates becomes

$$\frac{dS_1}{d\tau} = [(f_pP_2 + f_0)S_2 - (\bar{f}_pP_1 + \bar{f}_0)S_1] + \epsilon\left[r_1(S_1 + I_1)\left(1 - \frac{S_1 + I_1}{C_1}\right) - d_1S_1 + \gamma_1I_1 - \beta_1S_1I_1 - \frac{a_1S_1P_1}{1 + b_1S_1}\right],$$

$$
\begin{aligned}
\frac{dS_2}{d\tau} &= [(\bar{f}_p P_1 + \bar{f}_0)S_1 - (f_p P_2 + f_0)S_2] + \epsilon\left[r_2(S_2+I_2)\left(1-\frac{S_2+I_2}{C_2}\right) - d_2 S_2 + \gamma_2 I_2 - \beta_2 S_2 I_2 - \frac{a_2 S_2 P_2}{1+b_2 S_2}\right],\\
\frac{dI_1}{d\tau} &= [(g_p P_2 + g_0)I_2 - (\bar{g}_p P_1 + \bar{g}_0)I_1] + \epsilon\left[\beta_1 S_1 I_1 - d_1 I_1 - \alpha_1 I_1 - \gamma_1 I_1 - \frac{a_1' I_1 P_1}{1+b_1' I_1}\right], \qquad (4.1)\\
\frac{dI_2}{d\tau} &= [(\bar{g}_p P_1 + \bar{g}_0)I_1 - (g_p P_2 + g_0)I_2] + \epsilon\left[\beta_2 S_2 I_2 - d_2 I_2 - \alpha_2 I_2 - \gamma_2 I_2 - \frac{a_2' I_2 P_2}{1+b_2' I_2}\right],\\
\frac{dP_1}{d\tau} &= [\frac{1}{h_s S_2 + h_i I_2 + h_0}P_2 - \frac{1}{\bar{h}_s S_1 + \bar{h}_i I_1 + \bar{h}_0}P_1] + \epsilon\left[e\frac{a_1 S_1 P_1}{1+b_1 S_1} + e'\frac{a_1' I_1 P_1}{1+b_1' I_1} - m_1 P_1\right],\\
\frac{dP_2}{d\tau} &= [\frac{1}{\bar{h}_s S_1 + \bar{h}_i I_1 + \bar{h}_0}P_1 - \frac{1}{h_s S_2 + h_i I_2 + h_0}P_2] + \epsilon\left[e\frac{a_2 S_2 P_2}{1+b_2 S_2} + e'\frac{a_2' I_2 P_2}{1+b_2' I_2} - m_2 P_2\right],
\end{aligned}
$$

The aggregated system looks like (3.5) where $S_1, S_2, I_1, I_2, P_1, P_2$ are replaced by the fast equilibrium point $(S_1^*, S_2^*, I_1^*, I_2^*, P_1^*, P_2^*,)$ given below.

$$
\left.
\begin{aligned}
S_1^* &= \frac{f_p P_2^* + f_0}{\bar{f}_p P_1^* + \bar{f}_0 + f_p P_2^* + f_0} S\,,\\
S_2^* &= \frac{\bar{f}_p P_1^* + \bar{f}_0}{\bar{f}_p P_1^* + \bar{f}_0 + f_p P_2^* + f_0} S\,,\\
I_1^* &= \frac{g_p P_2^* + g_0}{\bar{g}_p P_1^* + \bar{g}_0 + g_p P_2^* + g_0} I\,,\\
I_2^* &= \frac{\bar{g}_p P_1^* + \bar{g}_0}{\bar{g}_p P_1^* + \bar{g}_0 + g_p P_2^* + g_0} I\,,\\
P_2^* &= \frac{\bar{h}_s S_1 + \bar{h}_i I_1 + \bar{h}_0}{\bar{h}_s S_1 + \bar{h}_i I_1 + \bar{h}_0 + h_s S_2 + h_i I_2 + h_0} P\,,\\
P_2^* &= \frac{h_s S_2 + h_i I_2 + h_0}{\bar{h}_s S_1 + \bar{h}_i I_1 + \bar{h}_0 + h_s S_2 + h_i I_2 + h_0} P\,,
\end{aligned}
\right\} \quad (4.2)
$$

If there is no infected prey then the system becomes

$$
\left.
\begin{aligned}
\frac{dS_1}{d\tau} &= [(f_p P_2 + f_0)S_2 - (\bar{f}_p P_1 + \bar{f}_0)S_1] + \epsilon\left[r_1 S_1\left(1-\frac{S_1}{C_1}\right) - d_1 S_1 - \frac{a_1 S_1 P_1}{1+b_1 S_1}\right],\\
\frac{dS_2}{d\tau} &= [(\bar{f}_p P_1 + \bar{f}_0)S_1 - (f_p P_2 + f_0)S_2] + \epsilon\left[r_2 S_2\left(1-\frac{S_2}{C_2}\right) - d_2 S_2 - \frac{a_2 S_2 P_2}{1+b_2 S_2}\right],\\
\frac{dP_1}{d\tau} &= [\frac{1}{h_s S_2 + h_0}P_2 - \frac{1}{\bar{h}_s S_1 + \bar{h}_0}P_1] + \epsilon\left[e\frac{a_1 S_1 P_1}{1+b_1 S_1} - m_1 P_1\right],\\
\frac{dP_2}{d\tau} &= [\frac{1}{\bar{h}_s S_1 + \bar{h}_0}P_1 - \frac{1}{h_s S_2 + h_0}P_2] + \epsilon\left[e\frac{a_2 S_2 P_2}{1+b_2 S_2} - m_2 P_2\right],
\end{aligned}
\right\} \quad (4.3)
$$

The analysis of the model (4.3) has been done in [11] taking $d_1 = d_2 = 0$ and Holling type-I functional response $b_1 = b_2 = 0$ for predation rates.

4.1 Analysis of the model (4.1) in particular case

If I consider the constant migration and the constant $b_1 = b_2 = 0$ then the aggregated system looks like

$$\left.\begin{aligned} \frac{dS}{dt} &= r_sS + r_iI - k_sS^2 - k_iI^2 - k_{si}SI - d_sS + \bar{\gamma}I - \bar{\beta}SI - \bar{a}SP, \\ \frac{dI}{dt} &= \bar{\beta}SI - (d_i + \bar{\alpha} + \bar{\gamma})I - \bar{a}'IP, \\ \frac{dP}{dt} &= e\bar{a}SP + e'\bar{a}'IP - \bar{m}P, \end{aligned}\right\} \qquad (4.4)$$

where $r_s = r_1\eta_1 + r_2\eta_2$, $r_i = r_1\mu_1 + r_2\mu_2$, $k_s = \frac{r_1}{C_1}{\eta_1}^2 + \frac{r_2}{C_2}{\eta_2}^2$, $k_i = \frac{r_1}{C_1}{\mu_1}^2 + \frac{r_2}{C_2}{\mu_2}^2$, $k_{si} = 2\frac{r_1}{C_1}\eta_1\mu_1 + 2\frac{r_2}{C_2}\eta_2\mu_2$, $\bar{\beta} = \beta_1\eta_1\mu_1 + \beta_2\eta_2\mu_2$, $d_s = d_1\eta_1 + d_2\eta_2$, $d_i = d_1\mu_1 + d_2\mu_2$, $\bar{\gamma} = \gamma_1\mu_1 + \gamma_2\mu_2$, $\bar{\alpha} = \alpha_1\mu_1 + \alpha_2\mu_2$, $\bar{a} = a_1\eta_1\xi_1 + a_2\eta_2\xi_2$, $\bar{a}' = a_1'\mu_1\xi_1 + a_2'\mu_2\xi_2$, $\bar{m} = m_1\xi_1 + m_2\xi_2$ and $\eta_1 = \frac{f_0}{\bar{f}_0 + f_0}$, $\eta_2 = \frac{\bar{f}_0}{\bar{f}_0 + f_0}$, $\mu_1 = \frac{g_0}{\bar{g}_0 + g_0}$, $\mu_2 = \frac{\bar{g}_0}{\bar{g}_0 + g_0}$, $\xi_1 = \frac{\bar{h}_0}{\bar{h}_0 + h_0}$, $\xi_2 = \frac{h_0}{\bar{h}_0 + h_0}$.

Equilibrium points of the model (4.4):

1. The trivial equilibrium point $E_0 = (0,0,0)$.
2. The axial equilibrium point $E_1 = (\bar{S}, 0,0)$ where $\bar{S} = \frac{r_s - d_s}{k_s}$.
3. The planer equilibrium point $E_2^I = (\tilde{S}, \tilde{I}, 0)$ where $\tilde{S} = \frac{d_i + \bar{\alpha} + \bar{\gamma}}{\beta}$ and $\tilde{I}$ is the roots of the equation $k_iI^2 + \left(k_{si}\tilde{S} + d_i - r_i + \bar{\alpha}\right)I + \left(k_s\tilde{S}^2 + d_s\tilde{S} - r_s\tilde{S}\right) = 0$.
4. Another planer equilibrium point $E_2^{II} = (S', 0, P')$ where $S' = \frac{\bar{m}}{e\bar{a}}$ and $P' = \frac{r_s - d_s}{\bar{a}} - \frac{k_s}{\bar{a}}S'$.
5. The interior equilibrium $E^*(S^*, I^*, P^*)$ is the solution of

$$\left.\begin{aligned} r_sS + r_iI - k_sS^2 - k_iI^2 - k_{si}SI - d_sS + \bar{\gamma}I - \bar{\beta}SI - \bar{a}SP &= 0, \\ \bar{\beta}S - (d_i + \bar{\alpha} + \bar{\gamma}) - \bar{a}'P &= 0, \\ e\bar{a}S + e'\bar{a}'I - \bar{m} &= 0. \end{aligned}\right\} \qquad (4.5)$$

4.2 Basic reproduction number

The concept of basic reproduction number is fundamental to study the epidemic of infectious diseases. The basic reproductive number is the average number of secondary infections produced when one infected individual is introduced into a host virgin population. The basic reproductive number measures the fitness of the parasite in an ecological system. There are two basic reproductions number first one in absence of predator denoted by $\bar{R}_0$ and the second one in presence of predator denoted by R_0. The effect of prey migration on basic reproduction ratio in absence of predator has been analyzed by Charles *et al.* (2002). Here I have found both the basic reproduction numbers using the next-generation matrix method.

$$\mathcal{F} = \begin{bmatrix} 0 \\ \bar{\beta}SI \\ 0 \end{bmatrix}, \mathcal{V} = \begin{bmatrix} -r_sS - r_iI + k_sS^2 + k_iI^2 + k_{si}SI + d_sS - \bar{\gamma}I + \bar{\beta}SI + \bar{\alpha}SP \\ (d_i + \bar{\alpha} + \bar{\gamma})I + \bar{\alpha}'IP \\ -e\bar{\alpha}SP - e'\bar{\alpha}'IP + \bar{m}P \end{bmatrix}$$

Basic reproduction number in absence of predator:

Here the new infection matrix $F(E_1) = \left[\frac{\partial \mathcal{F}_i(E_1)}{\partial x_j}\right]$ and the transfer matrix $V(E_1) = \left[\frac{\partial \mathcal{V}_i(E_1)}{\partial x_j}\right]$ at the equilibrium point $E_1 = (\bar{S}, 0,0)$ where $\bar{S} = \frac{r_s - d_s}{k_s}$.

Therefore, $F(E_1) = \begin{bmatrix} 0 & 0 & 0 \\ 0 & \bar{\beta}\bar{S} & 0 \\ 0 & 0 & 0 \end{bmatrix}$ and $V(E_1) = \begin{bmatrix} \bar{A} & \bar{B} & \bar{C} \\ 0 & D & 0 \\ 0 & 0 & \bar{E} \end{bmatrix}$

where $\bar{A} = -r_s + 2k_s\bar{S} + d_s$, $\bar{B} = -r_i + k_{si}\bar{S} + \bar{\beta}\bar{S} - \bar{\gamma}$, $\bar{C} = \bar{\alpha}\bar{S}$, $\bar{D} = d_i + \bar{\alpha} + \bar{\gamma}$, $\bar{E} = -e\bar{\alpha}\bar{S} + \bar{m}$.

So, the next generation matrix is $FV^{-1} = \frac{1}{|V|}\begin{bmatrix} 0 & 0 & 0 \\ 0 & \bar{\beta}\bar{S}\bar{A}\bar{E} & 0 \\ 0 & 0 & 0 \end{bmatrix}$

Thus the eigenvalues of FV^{-1} are $\left\{0, \frac{\bar{\beta}\bar{S}}{\bar{D}}, 0\right\}$.

The basic reproduction number is the largest eigenvalue of FV^{-1} ([18], [19]) which is

$$\bar{R}_0 = \varrho(FV^{-1}) = \frac{\bar{\beta}\bar{S}}{d_i + \bar{\alpha} + \bar{\gamma}} \text{ .... (4.6)}$$

Basic reproduction number in presence of predator:

In this article, I am interested to explore the influence of predator migration on basic reproduction number. So I have to calculate the basic reproduction number at the equilibrium point $E_2^{II} = (S', 0, P')$ where $S' = \frac{\bar{m}}{e\bar{\alpha}}$ and $P' = \frac{r_s - d_s}{\bar{\alpha}} - \frac{k_s}{\bar{\alpha}}S'$.

I evaluate the new infection matrix $F(E_2^{II}) = \left[\frac{\partial \mathcal{F}_i(E_2^{II})}{\partial x_j}\right]$ and the transfer matrix $V(E_2^{II}) = \left[\frac{\partial \mathcal{V}_i(E_2^{II})}{\partial x_j}\right]$ at the disease-free equilibrium point $E_2^{II} = (S', 0, P')$.

Therefore, $F(E_1) = \begin{bmatrix} 0 & 0 & 0 \\ 0 & \bar{\beta}S' & 0 \\ 0 & 0 & 0 \end{bmatrix}$ and $V(E_1) = \begin{bmatrix} A & B & C \\ 0 & D & 0 \\ E & F & G \end{bmatrix}$

where $A = -r_s + 2k_sS' + \bar{\alpha}P' + d_s$, $B = -r_i + k_{si}S' + \bar{\beta}S' - \bar{\gamma}$, $C = \bar{\alpha}S'$, $D = d_i + \bar{\alpha} + \bar{\gamma} + \bar{\alpha}'P'$, $E = -e\bar{\alpha}P'$, $F = -e'\bar{\alpha}'P'$, $G = -e\bar{\alpha}S' + \bar{m}$.

So, the next generation matrix is $FV^{-1} = \frac{1}{|V|}\begin{bmatrix} 0 & 0 & 0 \\ 0 & \bar{\beta}\bar{S}(AG - EC) & 0 \\ 0 & 0 & 0 \end{bmatrix}$

Thus the eigenvalues of FV^{-1} are $\left\{0, \frac{\bar{\beta}S'}{D}, 0\right\}$.

The basic reproduction number is the largest eigenvalue of FV^{-1} ([18], [19]) which is

$$R_0 = \varrho(FV^{-1}) = \frac{\bar{\beta}S'}{d_i + \bar{\alpha} + \bar{\gamma} + \bar{\alpha}'P'} \text{ .... (4.7)}$$

Similarly Local basic reproduction number of patch-I is $LR_{01} = \frac{\beta_1 S_1'}{d_1+\alpha_1+\gamma_1+a_1' P_1'}$ where $S_1' = \frac{m_1}{ea_1}$ and $P_1' = \frac{r_1-d_1}{a_1} - \frac{r_1}{C_1 a_1} S_1'$.

Also the local basic reproduction number of patch-II is $LR_{02} = \frac{\beta_2 S_2'}{d_2+\alpha_2+\gamma_2+a_2' P_2'}$ where $S_2' = \frac{m_2}{ea_2}$ and $P_2' = \frac{r_2-d_2}{a_2} - \frac{r_2}{C_2 a_2} S_2'$.

4.3 Local stability of the equilibrium points

1. The trivial equilibrium point $E_0 = (0,0,0)$ is stable if $r_s < d_s$ that is reproduction rate of prey population is lesser than the death rate in the aggregated system and otherwise unstable.

2. The axial equilibrium point $E_1 = (\bar{S}, 0,0)$ is stable if E_0 is unstable and $\bar{R}_0 < 1$ and $\bar{m} > e\bar{a}\bar{S}$ that means basic reproduction number in absence of predator is less than unity and mortality rate of predator in aggregated system is sufficiently small. Otherwise E_1 is unstable.

3. The planer equilibrium point $E_2^I = (\tilde{S}, \tilde{I}, 0)$ is stable if $\bar{m} > e\bar{a}\tilde{S} + e'\bar{a}'\tilde{I}$ and $r_s < 2k_s\tilde{S} + k_{si}\tilde{I} + \bar{\beta}\tilde{I}$, $r_i < 2k_i\tilde{I} + k_{si}\tilde{S} + d_i + \bar{\alpha}$ which implies predator mortality and prey reproduction in the aggregated system is sufficiently small. Otherwise E_2^I is unstable.

4. The planer equilibrium point $E_2^{II} = (S', 0, P')$ is stable if $R_0 < 1$ and unstable otherwise.

4.4 Effect of predator migration on basic reproduction number

The basic reproduction number in presence of predator can be written as follows

$$R_0 = \frac{\bar{\beta} S'}{d_i+\bar{\alpha}+\bar{\gamma}+\bar{a}' P'} = \frac{\bar{\beta}\bar{m}\bar{a}}{e(d_i+\bar{\alpha}+\bar{\gamma})\bar{a}^2+\bar{a}'[e(r_s-d_s)\bar{a}-k_s\bar{m}]} = \frac{D_1}{N_1+N_2} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{(4.8)}$$

where $D_1 = (\beta_1\eta_1\mu_1 + \beta_2\eta_2\mu_2)(m_1\xi_1 + m_2\xi_2)(a_1\eta_1\xi_1 + a_2\eta_2\xi_2)$,

$N_1 = e[(d_1 + \alpha_1 + \gamma_1)\mu_1 + (d_2 + \alpha_2 + \gamma_2)\mu_2]\ (a_1\eta_1\xi_1 + a_2\eta_2\xi_2)^2$,

$N_2 = (a_1'\mu_1\xi_1 + a_2'\mu_2\xi_2)[e\{(r_1 - d_1)\eta_1 + (r_2 - d_2)\eta_2\}(a_1\eta_1\xi_1 + a_2\eta_2\xi_2) - \left(\frac{r_1}{C_1}{\eta_1}^2 + \frac{r_2}{C_2}{\eta_2}^2\right)(m_1\xi_1 + m_2\xi_2)]$,

If the predators migrate more to patch-I then we can take $\xi = \frac{\xi_2}{\xi_1} \to 0$. In this case

$$\tilde{R}_0 = \frac{\tilde{D}_1}{\tilde{N}_1+\tilde{N}_2} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots.. \text{(4.9)}$$

where $\tilde{D}_1 = (\beta_1\eta_1\mu_1 + \beta_2\eta_2\mu_2)m_1 a_1\eta_1$,

$\tilde{N}_1 = e[(d_1 + \alpha_1 + \gamma_1)\mu_1 + (d_2 + \alpha_2 + \gamma_2)\mu_2]a_1^2\eta_1^2$,

$\tilde{N}_2 = a_1'\mu_1[e\{(r_1 - d_1)\eta_1 + (r_2 - d_2)\eta_2\}a_1\eta_1 - \left(\frac{r_1}{C_1}{\eta_1}^2 + \frac{r_2}{C_2}{\eta_2}^2\right)m_1]$, Further if the infected prey migrate more to patch-I then we can take $\mu = \frac{\mu_2}{\mu_1} \to 0$. In this case

$$R_{01} = \frac{\beta_1 m_1 a_1 \eta_1^2}{e(d_1+\alpha_1+\gamma_1)a_1^2\eta_1^2 + a_1'[e\{(r_1-d_1)\eta_1+(r_2-d_2)\eta_2\}a_1\eta_1 - \left(\frac{r_1}{C_1}{\eta_1}^2+\frac{r_2}{C_2}{\eta_2}^2\right)m_1]} \quad \ldots\ldots. (4.10)$$

Again if the infected prey migrate more to patch-II then we can take $\frac{1}{\mu} = \frac{\mu_1}{\mu_2} \to 0$. In this case

$$R_{01} = \frac{\beta_2 m_1 \eta_2}{e(d_2+\alpha_2+\gamma_2)a_1}. \quad \ldots\ldots\ldots\ldots (4.11)$$

5. Numerical Results

In this section, I have numerically simulated the theoretical results of our model. The hypothetical parameter values are mainly taken from [1] and [17]. The values of the new parameters which appear due to inclusion of predator in the system are taken on the basis of biological feasibility. I have used MATLAB version R2016a for numerical simulation of the model.

Table-1

parameter	values	units
r_1	0.18	/days
r_2	0.2	/days
d_1	0.15	/days
d_2	0.16	/days
C_1	180	number
C_2	130	number
α_1	0.1	/days
α_2	0.1	/days
γ_1	0.5	/days
γ_2	0.5	/days
β_1	0.4	/number/days
β_2	0.3	/number/days
a_1	0.08	/number/days
a_2	0.01	/number/days
a_1'	0.1	/number/days
a_2'	0.1	/number/days
e	0.1	unit-less
e'	0.1	unit-less
m_1	0.02	/days
m_2	0.01	/days
f_0	10	/days
$\bar{f}_0$	4	/days
g_0	4	/days
$\bar{g}_0$	4	/days
h_0	4	/days
$\bar{h}_0$	4	/days

Table-2

parameter	values	units
r_1	5.2	/days
r_2	5.5	/days
d_1	0.15	/days
d_2	0.16	/days
C_1	880	number
C_2	830	number
α_1	5.8	/days
α_2	5.8	/days
γ_1	0.5	/days
γ_2	0.5	/days
β_1	0.05	/number/days
β_2	0.05	/number/days
a_1	0.05	/number/days
a_2	0.05	/number/days
a_1'	0.1	/number/days
a_2'	0.1	/number/days
e	0.01	unit-less
e'	0.01	unit-less
m_1	0.01	/days
m_2	0.01	/days
f_0	10	/days
$\bar{f}_0$	4	/days
g_0	4	/days
$\bar{g}_0$	4	/days
h_0	4	/days
$\bar{h}_0$	4	/days

5.1 Numerical sensitivity analysis

Definition: The normalized forward sensitivity index of a variable, m that depends differentiably on a parameter n, is defined as $\Gamma_{\mathrm{n}}^{\mathrm{m}} = \frac{\partial m}{\partial n} \times \frac{n}{m}$

For R_0 the analytical expression of the sensitivity becomes $\Gamma_{\mathrm{n}}^{R_0} = \frac{\partial R_0}{\partial n} \times \frac{n}{R_0}$ where n is a parameters involved in R_0. I have computed the sensitivity of R_0 with respect to the three parameters $\xi = \frac{\xi_2}{\xi_1}$ related to predator migration, $\mu = \frac{\mu_2}{\mu_1}$ related to infected prey migration and $\eta = \frac{\eta_2}{\eta_1}$related to susceptible prey migration. It has been found that $\Gamma_{\xi}^{R_0} = 0.7731, \Gamma_{\mu}^{R_0} = -0.2556$ and $\Gamma_{\eta}^{R_0} = 0.5130$with respect to the set of parameters given in Table-1. So I have found that the parameter is $\xi = \frac{\xi_2}{\xi_1} = \frac{h_0}{\bar{h}_0}$ is more sensitive than the other two. Thus we can say that predator migration is more sensitive than the migration of susceptible and infected prey to changing the basic reproduction number.

5.2 Basic reproduction number versus migration

In (4.8), I have expressed \$R_0\$ in terms of the migration rate of susceptible prey, infected prey, and predator species. I have found the limiting expression of basic reproduction number in (4.9) when the migration rate of predators from patch-II to patch-I is very larger than from patch-I to patch-II. In Figure-1(a) we can observe how the infection increases in the system and crosses the epidemic threshold value when ξ increase. I have also found the limiting expression of basic reproduction number in (4.10) and (4.11) when the migration rate of infected prey from patch-II to patch-I is very larger than from patch-I to patch-II and the opposite respectively. In Figure-1(b) we can observe how the infection decrease in the system and become below the epidemic threshold value when μ increase.

I observe numerically that the basic reproduction in absence of predator is $R_0 = 6.8449$ which is much higher than the basic reproduction in presence of predator $R_0 = 0.6215$. I calculate the local basic reproduction number for both patches. The local basic reproduction number for patch-I and patch-II are $LR_{01} = 0.6375$ and $LR_{02} = 1.9878$ respectively.

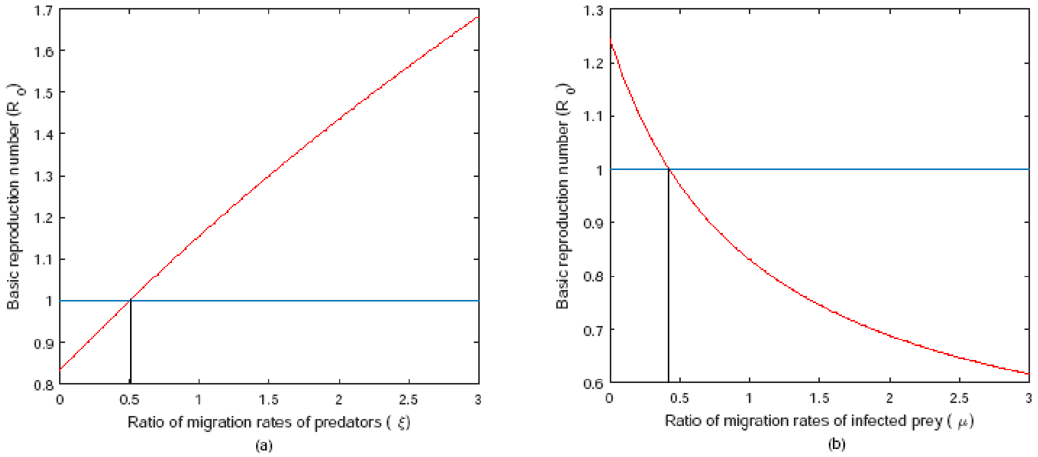
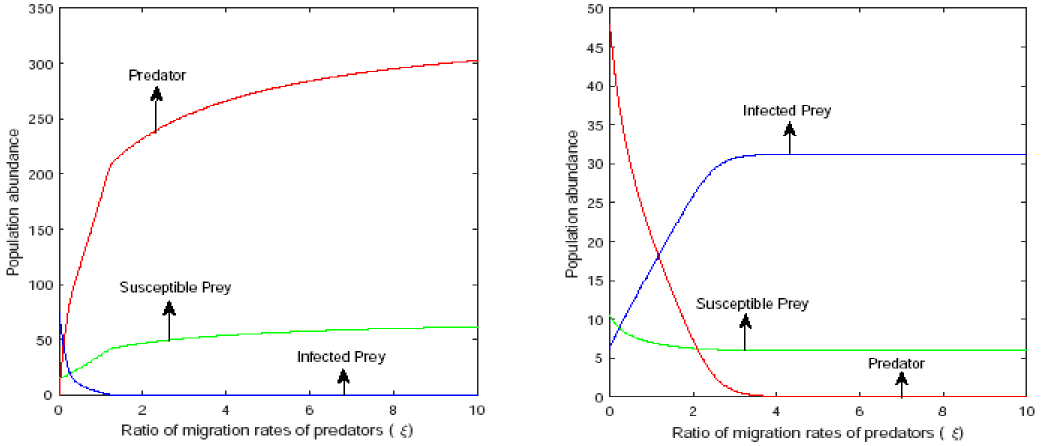


Figure-1 : (a) Basic reproduction number is increasing when ξ increase. (b) Basic reproduction number is decreasing when μ increase. Parameter values are taken from Table-1

My numerical investigation over the model (4.4) explores the switching of the equilibrium points due to migration of predator population when the infected prey lives in one of the patches losing their mobility due to infection. From Figure 2(a) we can observe that when $g_0 = 0$ that is the infected prey does not migrate to patch-I in other words the infected prey remains in patch-II then E^* switches to E_2^{II} as ratio of migration rates of predators increases from 0 to 10. Again From Figure 2(b) we can observe that when $\bar{g}_0 = 0$ that is the infected prey does not migrate to patch-II in other words the infected prey remains in patch-I then E^* switches to E_2^{I} as Ratio of migration rates of predators increases from 0 to 10.



(a) For g_0=0

(b) For $\bar{g}_0$=0

Figure-2 : Switching of equilibrium points when ξ increase. Parameter values are taken from Table-2

6. Conclusion

In this article, I intend to explore the effect of the migration of predators on a two-patch predator-prey model with disease in the prey population. Here I consider the migration of susceptible prey, infected prey, and predator population between two different patches. An ODE models has been constructed taking two different time scales. I consider that the individual migration of the species is faster than their demographic changes like birth, death, disease transmission, and interaction with predators. The model has been studied taking a large class of density-dependent migration rates. I have proved that the fast equilibrium point is unique and asymptotically stable. Then I aggregate the model taking the advantage of two different time scales and construct a SIP model. The model has been investigated both analytically and numerically considering some particular type of density-dependent migrations. I investigate the effect of predator migration on stability, population abundance, and fitness of parasites in the system. In all the cases I invent a huge impact of predator migration. I observe that if the infected prey lives in one of the patches losing their mobility due to infection then for the fast migration of predators the stable endemic equilibrium E^* can switch to E_2^{II} or E_2^{I} according to the infected prey lies in patch-II or in patch-I respectively. Thus if the infected prey lives in one of the patches due to the migration of the predator the system will be either disease-free or predator-free. I establish theoretically that the disease-free equilibrium is stable if $R_0 < 1$ and otherwise unstable. I observe numerically that the predator migration is more sensitive than the migration of susceptible and infected prey to changing the basic reproduction number.

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