Mathematical Biosciences 281 (2016) 128–138

Contents lists available at ScienceDirect

Mathematical Biosciences

journal homepage: www.elsevier.com/locate/mbs

Vector-borne diseases models with residence times – A Lagrangian perspective

Derdei Bichara[a,b,*], Carlos Castillo-Chavez[c]

[a] Department of Mathematics, California State University, Fullerton, United States
[b] Center for Computational and Applied Mathematics, 800 N. State College Blvd, Fullerton, CA 92831, United States
[c] Simon A. Levin Mathematical, Computational and Modeling Science Center, Arizona State University, Tempe, AZ 85287, United States

ARTICLE INFO

Article history:
Received 23 September 2015
Revised 6 September 2016
Accepted 6 September 2016
Available online 10 September 2016

MSC:
92D30
34D23
34A34
34C12

Keywords:
Vector-borne diseases
Human dispersal
Basic reproduction number
Global stability
Nonlinear dynamical systems

ABSTRACT

A multi-patch and multi-group modeling framework describing the dynamics of a class of diseases driven by the interactions between vectors and hosts structured by groups is formulated. Hosts' dispersal is modeled in terms of patch-residence times with the nonlinear dynamics taking into account the *effective* patch-host size. The residence times basic reproduction number $\mathcal{R}_0$ is computed and shown to depend on the relative environmental risk of infection. The model is robust, that is, the disease free equilibrium is globally asymptotically stable (GAS) if $\mathcal{R}_0 \leq 1$ and a unique interior endemic equilibrium is shown to exist that is GAS whenever $\mathcal{R}_0 > 1$ whenever the configuration of host-vector interactions is irreducible. The effects of *patchiness* and *groupness*, a measure of host-vector heterogeneous structure, on the basic reproduction number $\mathcal{R}_0$, are explored. Numerical simulations are carried out to highlight the effects of residence times on disease prevalence.

1. Introduction

Vector-borne diseases, a major public health problem around the world, are responsible for over one million death and hundreds of millions cases each year [51,65] and so diminishing their impact is a worldwide priority. Travel, climate change and trade have significantly altered vector-borne diseases dynamics [10,26,38,52,53]. Ross [56] was the first to model a vector borne disease dynamics. Ross's paper [56] and follow up work [57–59] laid the foundation of what is known today as the field of mathematical or theoretical epidemiology. There is an extensive literature associated with the study of vector-host interactions in the context of human diseases ([2,4,6,14–16,20–24,31,40,41,43,44] and the references therein). Sparse theoretical results exist on the role of geographical heterogeneity on the spread of vector-borne diseases, mostly via metapopulation models [1,3,5,18,28,54,61,66,69], that assume that the movement of host is "permanent"; this approach has been referred as Eulerian [30,47,48]. A Lagrangian perspective considers the movement of individuals across patches in a framework where the hosts' origin or identity are never lost. This approach, useful in the study of the role of movement of individuals in highly connected settings albeit it has received limited attention [18,25,34,54,60].

The concept of Langragian and Eulerian approaches were implemented by Okubo et al. [47,48] in modeling the diffusion and aggregation of animal populations in ecology. This nomenclature has been used in the context of epidemic models by Cosner et al. [18]. The use of a Lagrangian approach in the study of the dynamics and control of vector-borne diseases has also been explored in [25,31] prior this work. Specifically, Dye and Hasibeder [25,31] considered the study of vector-born dynamics via $SIS-SI$ type host-vector models in the context of n patch systems. Rodriguez and Torres-Sorando [54] used a Lagrangian perspective via the incorporation of short-time visitations to multiple patches, also in the context of vector borne disease. In [60], authors also considered a patchy Ross–Macdonald model and derived patch specific basic reproduction number in order to identify which patch is a source or a sink. More recently, Iggidr et al. [34] introduced a general $SIR-SI$ multi group deriving necessary and sufficient conditions for the existence of a sharp threshold [34]. Their [34]

---

[*] Corresponding author.

E-mail addresses: dbichara@fullerton.edu, bichara112@gmail.com (D. Bichara), ccchavez@asu.edu (C. Castillo-Chavez).

http://dx.doi.org/10.1016/j.mbs.2016.09.006
0025-5564/

abstract setting did not incorporate residence times explicitly, albeit their general infection terms technically may allow for their inclusion. The study in Iggidr et al. [34] and related papers, with the exception of [25,31], assume that hosts and vectors are residents or members of particular patch or group. Our framework can handle multiple levels of organization including the host's age or socio-economic structure (see [42,64] for the age factors and [8,37,49] for the socio-economics' role). Since vector transmission is often determined by the vectors' place of residence, it is often useful to decouple the host's structure from that of vectors' population whenever possible.

In this paper, we consider a vector-host model where the host population is structured by groups/classes that interact with non-mobile vectors living in multiple patches/environments. The hosts' groups may be defined by socioeconomic background, gender, or age. The vectors' patches represent the vectors' "space", which include schools, farms, workplaces etc. Hosts, in general, will distribute their time in a multitude of vectors' places of residence (patches). In our setup, we assume that the spatial scale under consideration is such that ignoring vector mobility across patches is acceptable. There are evidences that such an assumption is reasonable, for example, Dengue and Chikungunya's urban vectors *Aedes aegypti* rarely travel more than a few tens of meters during their lifespan [1,50]; the mainly rural but urban adapted vector *Aedes albopictus* have maximum dispersal of 400–600 m [33,45]; according to [9,45], the vectors *Aedes albopictus* are unlikely to travel long distance due to wind speed variability, in fact, they exhibit a tendency to fly closer to the ground, desisting to fly during heavy winds; the adult *Anopheles*(vector of malaria) does not fly more than 2 km [63]; and, *Anopheles gambiae*'s (the main malaria vector in Africa) maximal flight distance is 10 km [36]. In short, the spread of vector-borne diseases, in many instances, is primarily due to hosts' dispersal. Therefore, it is assumed here as in [5,69] that vectors do not abandon their geographical environment or patch. There are alternative modes of mosquitoes dispersal like those generated by trade, including the used-tires' trade [46,55].

The host population is structured into n groups with dispersal modeled via the residence times matrix $\mathbb{P} = (p_{ij})_{\substack{1\le i\le n, \\ 1\le j\le m}}$ where p_{ij} denotes the proportion of time that a host member of Groups i spends in Patch j. The use of this approach impacts the temporal dynamics of the *effective* host population size in each patch. Host *effective* population size *per* patch, that is the number of hosts of each group at time t in Patch j, $j = 1, 2, \dots, m$; is computed using the entries of the matrix $\mathbb{P}$ as weights. The density of *effective* infected host per patch account for both *effective* population and *effective* infected population size in each patch.

The host *effective* population size has not been incorporated in the literature using a Lagrangian approach in the context of vector-borne diseases before [18,54] (but see [11]). Our formulation generalize the case where vectors and hosts are defined by jointly inhabited patches [18,34,54]. We prove that the disease free equilibrium is GAS if $\mathcal{R}_0 \le 1$ and that a unique endemic equilibrium exists and is GAS if $\mathcal{R}_0 > 1$ whenever the multi-patch, multi-group system is irreducible. This approach has been used in the study of a general *SIS* model in the context of communicable diseases [7].

The paper is organized as follow. Section 2 is devoted to the derivation and basic properties of the model; Section 3 deals with the stability analysis of the disease free equilibrium (DFE) and the endemic equilibrium. Section 4, highlights the role of heterogeneity in term of patch and group variability on the basic reproduction number; Section 5 highlights tour results in the context of 2 groups, 2 patches and 2 groups and 3 patches via simulations. Section 6 collects our conclusions and thoughts on the usefulness of this approach and list possible extensions.

2. Derivation of the model

We consider the dynamics of human-vector interactions within a population composed of n social groups and m environments or patches. We denote by $N_{h,\,i}$ the host population in social group i, $i = 1, \dots, i$, and $N_{v,j}$ vector population in Patch j, $j = 1, \dots, m$. The susceptible and infected host populations in group i, $i = 1, \dots, n$, at time t, are denoted by $S_{h,\,i}(t)$ and $I_{h,\,i}(t)$, respectively. It is assumed that the total host population in each group is constant, that is $N_{h,i} = S_{h,i}(t) + I_{h,i}(t)$; that the disease in the host is captured by an *SIS* epidemic model while the vectors' dynamics follows an *SI* framework. The vector population in each patch is composed by $S_{v,j}$ and $I_{v,j}$, the susceptible and infected vector populations in Patch j, $j = 1, \dots, m$, respectively.

The entries of the residence times matrix $\mathbb{P}$ denote the proportion of time that individuals of different groups spend in each patches; specifically p_{ij} represents the proportion of time that members of group i spend in Patch j ($p_{ij} \ge 0$ for all j and $\sum_{j=1}^m p_{ij} = 1$ for all i). The susceptible individuals of group i ($S_{h,\,i}$) are generated through birth at the per-capita rate μ_i and they recover from infection at the per-capita rate γ_i. It is assumed that all offsprings are susceptible and that the disease does not confer immunity. The birth of susceptible individuals in group i is compensated by deaths, maintaining constant host population size in each group. The host population is at risk of infection in every patches from its interaction with local infected vectors ($I_{v,j}$, $j = 1, \dots, m$). Hence, the dynamics of the the susceptible host of group i, for $i = 1, \dots, n$, is given by:

$$\dot{S}_{h,i} = \mu_i N_{h,i} + \gamma_i I_{h,i} - \sum_{j=1}^{m} b_j(N_h, N_{v,j})\beta_{v,h} p_{ij} S_{h,i}\frac{I_{v,j}}{N_{v,j}} - \mu_i S_{h,i}$$

where $b_j(N_h, N_{v,j})$ is the number of mosquito bites per human per unit of time [13,15,27,29] in Patch j. $b_j(N_h, N_{v,j})$ is assumed to be a function of the number of host in Patch j; a population that includes visitors from other patches.

The dynamics of infected hosts of group i, $i = 1, \dots, n$, is modeled as follows

$$\dot{I}_{h,i} = \sum_{j=1}^{m} b_j(N_h, N_{v,j})\beta_{vh} p_{ij} S_{h,i}\frac{I_{v,j}}{N_{v,j}} - (\mu_i + \gamma_i)I_{h,i} \tag{1}$$

The susceptible vectors in Patch j are replenished via constant recruitment $\Lambda_{v,j}$, subject to death at the per-capita rate μ_v and removed (through harvesting and spraying) at the per-capita rate δ_j. We suppose that the natural per-capita vectors' death rates are the same in all patches. Though, the vectors do not move across patches, the susceptible mosquitoes in Patch j ($S_{v,j}$) may, of course, be infected by infected hosts of any group while visiting Patch j. The *effective* proportion of infected individuals in Patch j is therefore given by

$$\frac{\sum_{i=1}^{n} p_{ij} I_{h,i}}{\sum_{k=1}^{n} p_{kj} N_{h,k}}$$

Hence, the dynamics of susceptible vector in Patch j, $j = 1, \dots, m$ in patch j at time t is given by

$$\dot{S}_{v,j} = \Lambda_{v,i} - a_j \beta_{hv} S_{v,j}\frac{\sum_{i=1}^{n} p_{ij} I_{h,i}}{\sum_{k=1}^{n} p_{kj} N_{h,k}} - (\mu_v + \delta_j)S_{v,j}$$

where a_j is the number of bites per mosquito per unit of time in Patch j, assumed to be constant.

The dynamics of infected vectors in Patch j is given by

$$\dot{I}_{v,j} = a_j \beta_{hv} S_{v,j}\frac{\sum_{i=1}^{n} p_{ij} I_{h,i}}{\sum_{k=1}^{n} p_{kj} N_{h,k}} - (\mu_v + \delta_j)I_{v,j} \tag{2}$$

We know that the total number of bites by mosquitoes ($a_j N_{v,j}$ in Patch j) should equal the total number of bites received by