



Assessing the effects of daily commuting in two-patch dengue dynamics: A case study of Cali, Colombia

Edwin Barrios^a, Sunmi Lee^b, Olga Vasilieva^{a,*}

^a Department of Mathematics, Universidad del Valle, Calle 13 No. 100-00, Cali 760032, Colombia

^b Department of Applied Mathematics, University Kyung Hee, 1732 Deokyoungdaero, Giheung-gu, Yongin-si, Gyeonggi-do 446-701, Republic of Korea

ARTICLE INFO

Article history:

Received 4 July 2017

Revised 7 May 2018

Accepted 10 May 2018

Keywords:

Dengue dynamics

Two-patch model

Residence times

Effective population sizes

Effective vectorial density

ABSTRACT

There are many infectious diseases that can be spread by daily commuting of people and dengue fever is one of them. The absence of vaccine and irregularities in ongoing vector control programs make this disease the most frequent and persistent in many tropical and subtropical regions of the world. This paper targets to access the effects of daily commuting on dengue transmission dynamics by using a deterministic two-patch model fitted to observed data gathered in Cali, Colombia where dengue fever is highly persistent and exhibits endemo-epidemic patterns.

The two-patch dengue transmission model with daily commuting of human residents between patches (that is, between the city and its suburban areas) is presented using the concept of residence times, which certainly affect the disease transmission rates by inducing variability in human population sizes and vectorial densities at each patch.

The same modeling framework is applied to two primary scenarios (epidemic outbreaks and endemic persistence of the disease) and for each scenario two coupling cases (one-way and asymmetric commuting) with different inflow and outflow intensities are analyzed.

The concept of *effective vectorial density*, introduced in this paper, allows to explain in very simple terms why the daily commuting affects quite differently the dengue morbidity among human residents in both patches. In particular, residents of the patch with a greater share of incoming than outgoing commuters may actually "benefit" from inflow of daily commuter by avoiding a considerable number of infections. However, residents of the patch with a greater share of outgoing than incoming commuters, especially those who stay at home patch, incur more risk of getting infected. Additionally, the model shows that daily commuting enhance the total number of human infections acquired in both patches and may even provoke an epidemic outbreak in one patch while moderately lowering the level of the disease persistence in another patch.

© 2018 Elsevier Ltd. All rights reserved.

1. Introduction

Among vector-borne viral infections, dengue fever has been ranked by the World Health Organization (WHO) as the most frequent and persistent in the world (WHO, 2009). Dengue morbidity is strongly correlated with the presence and abundance of *Aedes aegypti* mosquitoes which act as the principal transmitters of five serotypes (or strains) of the dengue virus (DENV1–5)¹. The

pathogen of DENV is transmitted from female mosquitoes to human hosts (and vice versa) during their cycle of blood-feeding since only females need to ingest human blood in order to mature their eggs (male mosquitoes do not bite people).

In recent decades, the incidence of dengue has increased dramatically worldwide, and this is attributed to various reasons, among which many scholars point out:

- the global warming that provides more favorable conditions for mosquito reproduction and stimulate their expansion into new geographic areas;
- mosquitoes abilities to develop resistance to pesticides that jeopardizes the established vector control programs;
- uncontrolled urbanization and poor sanitation conditions of growing metropolitan areas in many tropical countries;

* Corresponding author.

E-mail addresses: edwin.barrios@correounivalle.edu.co (E. Barrios), sunmilee@khu.ac.kr (S. Lee), olga.vasilieva@correounivalle.edu.co (O. Vasilieva).

¹ While four serotypes of dengue virus (DENV1–4) are currently circulating in various tropical countries worldwide, the discovery of the fifth dengue strain DENV5 has been recently claimed by Normile (2013).

- people mobility that facilitates the DENV expansion and persistence in human populations.

People mobility is one of the factors that had historically favored the spread of various infectious diseases, including “indirectly” transmitted diseases such as water-borne or vector-borne infections. In this context, the arrival of chikungunya and Zika viruses to the Americas in 2014 is a good example of how people’s long-distance travels contribute to the spread of new vector-borne diseases (Gatherer and Kohl, 2016; Staples and Fischer, 2014). On the other hand, people mobility is becoming more and more habitual in terms of daily commuting (short-distance travels) since many former residents of big cities decide to move out to nearby towns and suburbs in order to avoid overpopulation, higher leasing costs, heavy traffics, etc. typical for big cities. What can be the effects of daily commuting on dissemination of infectious diseases which are considered persistent? Does daily commuting increase or reduce the overall disease incidence?

In this paper, we try to give answers to these questions in reference to dengue propagation in the city of Cali, Colombia and its nearby localities since this geographic area is considered hyper-endemic with regards to dengue fever (Mendez et al., 2006; Ocampo and Wesson, 2004). It is worth noting that in all tropical regions of the Americas (including Colombia), dengue has endemo-epidemic patterns with outbreaks every 2–4 years (Dick et al., 2012). In Colombia, such patterns are attributed to simultaneous circulation of four serotypes of the dengue virus DENV1–4 during epidemic periods and to a strong predominance of one particular DENV strain during inter-epidemic or endemic periods (Mendez et al., 2006; Ocazonez et al., 2006). Therefore, this paper is focused on analysis of two primary scenarios – epidemic and endemic – which are studied separately using the observed data on dengue incidence collected during high-transmission period (epidemic scenario) or low-transmission period (endemic scenario).

We start by formulating a customary (normalized) dengue transmission model of SEI-SEIR(S) type with homogeneous mixing in one single patch (see, e.g. Derouich et al., 2003; Erickson et al., 2010; Lee and Castillo-Chavez, 2015), describing its underlying parameters, and stating the necessary assumptions (Section 2). The same modeling framework is further applied to both scenarios of the disease transmission. For epidemic scenario, we admit that all recovered human individuals can be reinfected with another DENV strain and, therefore, we apply the SEI-SEIRS variant of the model. In case endemic scenario, we suppose that all recovered human individuals acquire immunity and, thence, we apply the SEI-SEIR variant of the model.

For both scenarios, we estimate the key model parameters which are directly related to the disease transmission via effective contacts between the mosquitoes and human hosts. These estimations are performed in Section 3 by fitting the model to the daily incidence data collected by the Municipal Secretariat of Public Health (MSPH) of Cali, Colombia in 2013 (epidemic year) and in 2014 (endemic year).

In order to assess the effects of daily commuting from suburban areas to (and, to a lesser extent, from) Cali on dengue transmission, we should incorporate the elements of spatial heterogeneity into the single-patch model by extending it over two patches: Patch 1 (city of Cali) and Patch 2 (suburban areas and nearby towns outside Cali) with coupling, which refers to people mobility between two patches and can be unidirectional or bi-directional. The two-patch dengue transmission model is presented in Section 4 with additional details available in Appendix B and Appendix C.

This model was derived by applying the so-called *Lagrangian approach* (see more details in Bichara and Castillo-Chavez, 2016; Cosner et al., 2009; Falcón-Lezama et al., 2016; Iggidr et al., 2016; Ruktanonchai et al., 2016) which can be regarded as the

most convenient and appropriate way for expressing mathematically the daily commuting of people between two patches. Under this approach, all human individuals are identified as residents of either one or another patch, while their temporary dispersals (i.e., daily commuting) are expressed in terms of *residence times* formally introduced in Lee and Castillo-Chavez (2015) for a two-patch model and further developed in Bichara and Castillo-Chavez (2016) for a multi-patch model (however, see (Cosner et al., 2009; Rodríguez and Torres-Sorando, 2001; Ruktanonchai et al., 2016; Torres-Sorando and Rodríguez, 1997) where residence times had been referred to as “fractions of time”). It is worth noting that besides residence times (or fractions of time), people mobility has been modeled by other authors by using the dispersal matrix (Xiao and Zou, 2014), probabilistic gravity-type approach (Stone et al., 2017), host-vector contact network (Iggidr et al., 2016), transfer rates (Auger et al., 2008; Falcón-Lezama et al., 2016) or rates of travel (Adams and Kapan, 2009; Arino et al., 2012), as well as emigration and immigration rates between patches (Gao and Ruan, 2012).

In our setting, only human individuals may commute between the major city (Cali) and its suburban areas, so we suppose that mosquitoes do not leave their patches² In other words, the total population sizes of mosquitoes in both patches remain essentially invariant in time during the observation periods. On the other hand, daily commuting affects the temporal dynamics of human population sizes in the sense that the number of people effectively present at Patch i ($i = 1, 2$) is not equal to the number of residents of this patch for all $t \geq 0$. The latter is attributed to the incoming and outgoing commuters (or inflow and outflow, respectively) who, being formally assigned to one patch, spend a share of their time in another patch. This situation is modeled using the concept of *effective populations sizes* introduced in Bichara and Castillo-Chavez (2016). Additionally, we presume that the average vectorial density (i.e., an average number of vectors per one human host) at each patch can also be affected by commuting. Namely, if the inflow to one patch is greater (less) than its respective outflow, the vectorial density in this patch decreases (increases). By introducing the explicit concept of *effective vectorial density* (which was indirectly used in Bichara and Castillo-Chavez (2016) inside the effective contact rate), the impact of residence times on the disease transmission becomes clearly visible since the rate of the infection spreading positively correlates with the vectorial density.

Section 5 is devoted to the case studies and underlying analysis of the effects of daily commuting (or coupling between two patches) on the disease transmissibility across both patches. Here, for each scenario (epidemic and endemic) we revise several cases with regards to coupling (one-way versus asymmetric coupling) and its underlying intensity (weak versus strong) and compare them with an “uncoupled case” where daily commuting is ignored. We have focused on these particular cases since they mimic the most realistic situations regarding the daily commuting between Cali and its suburban areas.

Finally, Section 6 resumes the results of this paper and provides solid arguments for revision of existent vector control policies in the city of Cali and its suburban localities.

Before proceeding, we would like to convey that this paper has been strongly motivated by the previous work (Lee and Castillo-Chavez, 2015) of its second author. There are some similarities and differences in both works. Both works studied dengue transmission dynamics in a two-patch system. However, there are some signif-

² However, several scholars had considered models where only vectors were allowed to move between patches (Dye and Hasibeder, 1986; Hasibeder and Dye, 1988; Smith et al., 2004) while other authors designed models where both vectors and human hosts were allowed to travel across patches (see, e.g., Gao and Ruan, 2012; Ruktanonchai et al., 2016).

Download English Version:

<https://daneshyari.com/en/article/8876600>

Download Persian Version:

<https://daneshyari.com/article/8876600>

[Daneshyari.com](https://daneshyari.com)