Chaos, Solitons and Fractals 104 (2017) 575–579

Contents lists available at ScienceDirect

Chaos, Solitons and Fractals

Nonlinear Science, and Nonequilibrium and Complex Phenomena

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

Transmission dynamics of Ebola virus disease with human mobility in Sierra Leone

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ARTICLE INFO

Article history:
Received 14 August 2017
Revised 8 September 2017
Accepted 16 September 2017

Keywords:
EVD
Sierra Leone
Basic reproduction number
Human mobility

ABSTRACT

Ebola virus disease outbreak in West Africa in 2014, especially serious in Sierra Leone. In order to reveal the transmission mechanisms of ebola virus disease, we present a mathematical model to estimate the basic reproduction number in Sierra Leone. It was found that if effective control strategies are not taken, then ebola virus disease will outbreak in Sierra Leone. What is more, it was revealed that human mobility may paly an important role on the outbreak of ebola virus disease.

1. Introduction

Ebola virus disease (EVD) is originally identified in 1976 in Yambuku, the Democratic Republic of Congo (old Zaire), and Nzara, South Sudan, which is caused by an RNA virus in the filovirus family [1,2]. It can cause Ebora hemorrhagic fever in humans and primate with high mortality rate and typical symptoms are nausea, vomiting, diarrhea, skin tone, body aches, internal bleeding, fever and so on. EVD is mainly distributed in tropical rain forest in Central Africa and tropical grassland in Southeast Africa.

An outbreak of EVD in 2014 is the largest EVD outbreak to date, which occurred suddenly in West Africa and brought about more than 1000 lives to lose life. The first case in West Afica was reported in three southeastern districts (Gueckedou, Macenta, and Kissidougou) of Guinea and in the capital city of Conakry [3]. After then, EVD spread to West Africa and the first cases identified in Sierra Leone were reported in May. Up to now, more than 8000 people are infected by EVD and more than 3000 cases died in Sierra Leone [4]. To well describe the information about the appraisal of EVD in Sierra Leone, we show the number of the newly infected cases from May 19th, 2014 to January 11th, 2015 in Fig. 1. The public health impact of the current EVD outbreak in Sierra Leone has been far greater than case counts. For such reason, we will figure out the transmission mechanisms of EVD in Sierra Leone.

Dynamical modeling has being one of the most important tools in analyzing the epidemiological characteristics of infectious diseases and various models have been used to study different aspects of diseases spread including EVD in Sierra Leone [5–15]. Based on a transmission model, Kucharski et al. evaluated the benefits and risks of introducing community care centers (CCCs) into Sierra Leone's Western Area and found that use of CCCs may cause a decline in cases [9]. Khan et al. developed a SEIR (susceptible-exposed-infected-recovered) type deterministic model and used data to estimate the basic reproductive ratio of EVD in Sierra Leone as 1.492 and 1.362 [12]. Rivers et al. used existing data from Sierra Leone to parameterize a dynamical model of EVD and evaluated the efficacy of interventions of EVD in Sierra Leone [14]. We refer to a review by Chowell and Nishiura [5] for more detailed discussions on EVD spread in Sierra Leone.

Although some work has been done on transmission dynamics of EVD in Sierra Leone, there are still lots of issues need to be well addressed. In Ref. [8], Park et al. suggested that transmission has primarily been within country, not between-country in Sierra Leone. As a result, the main purpose of this study is to reveal the influences of human mobility on EVD spread in Sierra Leone.

2. Dynamical model

The data on EVD in Sierra Leone are reported by 14 administrative areas (see Fig. 2), and thus we regard each administrative area as a single patch and, in each patch, the submodel structure follows the SEIHFR model based on the framework by Rivers et al. [14] (see Fig. 3). For patch *i*, the total population is divided

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https://doi.org/10.1016/j.chaos.2017.09.022
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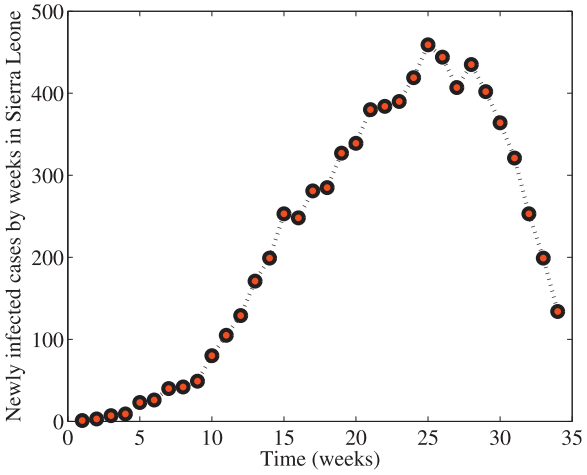

Fig. 1. Newly infected cases in Sierra Leone as a function of weeks. The fist week is from 19 to 25, May 2014 and the 34th week (last data point) is from 5 to 11, January 2015. Data for the ebola outbreak in West Africa can be found in http://github.com/ebola.

into six compartments: Susceptible (S_i), Exposed (E_i), Infectious (I_i), Hospitalized (H_i), Funeral (F_i) and Recovered/Removed (R_i). Our assumptions on the dynamical transmission of EVD in Sierra Leone are demonstrated in the flowchart (see Fig. 3). The model is a system of the following ordinary differential equations:

$$\begin{cases} \dfrac{dS_i}{dt} = -(\beta_i^I S_i I_i + \beta_i^H S_i H_i + \beta_i^F S_i F_i) + \sum\limits_{j=1}^{n} a_{ij} S_j, \\ \dfrac{dE_i}{dt} = \beta_i^I S_i I_i + \beta_i^H S_i H_i + \beta_i^F S_i F_i - \alpha_i E_i + \sum\limits_{j=1}^{n} b_{ij} E_j, \\ \dfrac{dI_i}{dt} = \alpha_i E_i - [\gamma_i^H \theta_i + \gamma_i^R (1-\theta_i)(1-\delta_i) + \gamma_i^F (1-\theta_i)\delta_i] I_i + \sum\limits_{j=1}^{n} c_{ij} I_j, \\ \dfrac{dH_i}{dt} = \gamma_i^H \theta_i I_i - [\eta_i \rho_i + \xi_i (1-\rho_i)] H_i + \sum\limits_{j=1}^{n} d_{ij} H_j, \\ \dfrac{dF_i}{dt} = \gamma_i^F (1-\theta_i)\delta_i I_i + \eta_i \rho_i H_i - \omega_i^F F_i + \sum\limits_{j=1}^{n} f_{ij} F_j, \\ \dfrac{dR_i}{dt} = \gamma_i^R (1-\theta_i)(1-\delta_i) I_i + \xi_i (1-\rho_i) H_i + \omega_i^F F_i + \sum\limits_{j=1}^{n} l_{ij} R_j, \end{cases} \tag{2.1}$$

where β_i^I (β_i^H or β_i^F) represents transmission coefficient between the susceptible and the infectious (hospitalized or funeral) in patch i and $\beta_i^I S_i I_i$ ($\beta_i^I S_i H_i$ or $\beta_i^I S_i F_i$) describes the transmission of EVD from the infectious (hospitalized or funeral) to the susceptible in this patch; $1/\alpha_i$ represents the incubation period of the infectious in patch i; $1/\gamma_i^H$ represents the time until hospitalization in patch i; $1/\gamma_i^R$ represents the duration of infection in patch i; $1/\gamma_i^F$ represents the time from infection to death in patch i; θ_i represents the fraction of infected hospitalized in patch i; δ_i represents the case fatality rate (unhospitalized) in patch i; ρ_i represents the case fatality rate (hospitalized) in patch i; $1/\eta_i$ represents the time from hospitalization to death in patch i; $1/\xi_i$ represents the time from hospitalization to recovery in patch i.

a_{ij} (b_{ij}, c_{ij}, d_{ij}, f_{ij} and l_{ij}) with ($i \neq j$) represents the immigration rate of susceptible (exposed, infected, hospitalized, funeral and recovered) individuals from jth patch to ith patch. a_{ii} (b_{ii}, c_{ii}, d_{ii}, f_{ii} and l_{ii}) is non-positive and represents the emigration rate of susceptible individuals in the ith patch. During the dispersal process between patches, we assume that no death and birth events. Consequently, we have that:

$$\sum_{j=1}^{n} a_{ji} = 0, \quad \sum_{j=1}^{n} b_{ji} = 0, \quad \sum_{j=1}^{n} c_{ji} = 0, \quad \sum_{j=1}^{n} d_{ji} = 0,$$
$$\sum_{j=1}^{n} f_{ji} = 0, \quad \sum_{j=1}^{n} l_{ji} = 0, \quad \forall 1 \leq i \leq n.$$

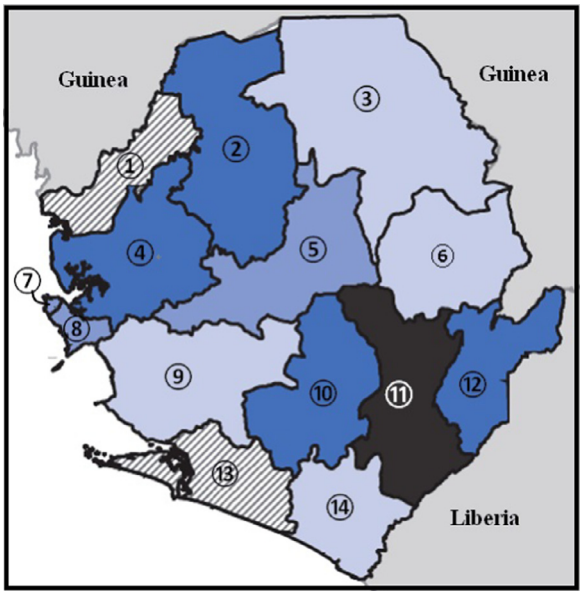

Fig. 2. Sierra Leone consists of 14 administrative areas. 1: Kambia; 2: Bombali; 3: Koinadugu; 4: Port Loko; 5: Tonkolili; 6: Kono; 7: Western Urban; 8: Western Rural; 9: Moyamba; 10: Bo; 11: Kenema; 12: Kailahun; 13: Bonthe; 14: Pujehun. The map is drawn by Matlab R2011a and lines are added by Microsoft Office Word 2010.

3. Basic reproduction number of EVD in Sierra Leone

Denote

$$c_i^1 = \beta_i^I, \quad c_i^2 = \beta_i^H, \quad c_i^3 = \beta_i^F, \quad c_i^4 = \alpha_i, \quad c_i^5 = \gamma_i^H \theta_i,$$
$$c_i^6 = \gamma_i^R (1-\theta_i)(1-\delta_i), \quad c_i^7 = \gamma_i^F (1-\theta_i)\delta_i, \quad c_i^8 = \eta_i \rho_i,$$
$$c_i^9 = \xi_i (1-\rho_i), \quad c_i^{10} = \omega_i^F.$$

We have the following matrix:

$$\mathcal{F} = \begin{pmatrix} c_i^1 S_i I_i + c_i^2 S_i H_i + c_i^3 S_i F_i \\ 0 \\ 0 \\ 0 \end{pmatrix},$$

$$\mathcal{V} = \begin{pmatrix} c_i^4 E_i \\ -(c_i^4 E_i - c_i^5 I_i - c_i^6 I_i - c_i^7 I_i) \\ -(c_i^5 I_i - c_i^8 H_i - c_i^9 H_i) \\ -(c_i^7 I_i + c_i^8 H_i - c_i^{10} F_i) \end{pmatrix},$$

where $\mathcal{F}$ represents the rate of appearance of new infection and $\mathcal{V}$ denotes the rate of transfer of individuals. Calculating the derivative of $x = (E_i, I_i, H_i, F_i)$, then substituting disease-free equilibrium