Mathematical Biosciences 277 (2016) 89–107

Contents lists available at ScienceDirect

Mathematical Biosciences

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

Mathematical models of Ebola—Consequences of underlying assumptions

Zhilan Feng[a,*], Yiqiang Zheng[a], Nancy Hernandez-Ceron[b], Henry Zhao[a], John W. Glasser[c], Andrew N. Hill[c]

[a] Department of Mathematics, Purdue University, West Lafayette, IN 47907, USA
[b] University of Michigan, Ann Arbor, MI 48109, USA
[c] Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

ARTICLE INFO

Article history:
Received 8 December 2015
Revised 16 March 2016
Accepted 9 April 2016
Available online 26 April 2016

Keywords:
Mathematical models
Ebola
Arbitrarily distributed disease stage
Exponential waiting time
Model assumptions

ABSTRACT

Mathematical models have been used to study Ebola disease transmission dynamics and control for the recent epidemics in West Africa. Many of the models used in these studies are based on the model of Legrand et al. (2007), and most failed to accurately project the outbreak's course (Butler, 2014). Although there could be many reasons for this, including incomplete and unreliable data on Ebola epidemiology and lack of empirical data on how disease-control measures quantitatively affect Ebola transmission, we examine the underlying assumptions of the Legrand model, and provide alternate formulations that are simpler and provide additional information regarding the epidemiology of Ebola during an outbreak. We developed three models with different assumptions about disease stage durations, one of which simplifies to the Legrand model while the others have more realistic distributions. Control and basic reproduction numbers for all three models are derived and shown to provide threshold conditions for outbreak control and prevention.

1. Introduction

Mathematical models have been very helpful in evaluating and identifying alternative strategies for infectious disease control and prevention. However, for the recent epidemics of Ebola in West Africa, the success of mathematical models has been very limited. As pointed out in Butler [2], "mathematical models have failed to accurately project the outbreak's course". Although various reasons may explain why "on-the-ground data contradict the projections of published models", including incomplete and unreliable data on Ebola epidemiology (especially in the hardest-hit areas) and lack of empirical data on how disease-control measures quantitatively affect Ebola transmission, it is important to examine the appropriateness of assumptions made in the models on which the projections are based. This is the objective of the current paper. There have been various modeling approaches, including deterministic and stochastic models, or relatively simple models consisting of ordinary differential equations (ODEs) and more complicated agent-based models, among others. Many of the ODE models are variations of the model studied by Legrand et al. [8], to which we refer as the Legrand model. It has been pointed out that some of the assumptions made in the Legrand model may not have clear justifications (see, for example, Rivers et al. [11]). Thus, it is important to examine the critical assumptions made in this model and better understand their possible impact on model outcomes.

It often happens that, when a model is formulated, certain assumptions are made without consideration of their consequences. One of the most common assumptions made in ODE models is the exponential waiting time in disease stages. That is, the survival probability is described by a negative exponential function. For example, if the model assumes that an infected individual will recover at a constant per-capita rate γ, then it implicitly assumes that the infectious period is exponentially distributed, and the probability that an individual is still infectious $s > 0$ units of time since onset is given by

$$P_I(s) = e^{-\gamma s}.$$

That is, if X_I denotes the random variable for the waiting time in the infectious class I before exiting, then

$$\mathbb{P}[X_I > s] = P_I(s) = e^{-\gamma s}.$$

In this case, the average waiting time before recovery (or the mean infectious period) is given by

$$\mathbb{E}[X_I] = \int_0^\infty P_I(s)ds = \frac{1}{\gamma}.$$

* Corresponding author. Tel.: +1 765 494 1901; fax: +1 765 494 0548.
E-mail address: fengz@purdue.edu (Z. Feng).

http://dx.doi.org/10.1016/j.mbs.2016.04.002
0025-5564/