Sensitivity Analysis of a Mathematical Modeling of Ebola Virus Population Dynamics in the Presence of Vaccine

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Abstract

The virus (Ebola virus) (EBV) belongs to the Filoviri-dae family which is a filovirus and is a serious disease which leads to hemorrhagic disease in human and non human such as chimpanzee, gorilla, porcupine, fruit bats etc. In this paper, a mathematical modeling for the population dynamics of EBV diseases in the presence of vaccination was developed. The research shows that, using the human control reproduction number (\Re_c) as response and infectious individual as response function, that the sensitive parameters in the formulated system (1) are the personal hygiene (ε), humans to human contact rate (β_1), modification parameter (η), human vaccination rate (ρ), proper burial (ϕ) and humans natural mortality rate (μ_h). The study shows that personal hygiene rate, effective contact rate of humans, natural mortality of humans' rate, vaccination rate and proper burial rate are very sensitive to both reproduction number and infectious humans.

Keywords: Ebola Virus, Mathematical Model, Population Dynamics, Optimal Control, Sensitivity Analysis

INTRODUCTION

The virus (Ebola virus) (EBV) belongs to the Filoviri-dae family which is a filovirus and is a serious disease which leads to hemorrhagic disease in human and non human such as chimpanzee, gorilla, porcupine, fruit bats etc (Zineb *et al.*,2018). According to Juga *et al.*(2021)

EBV instills panicking in all the society that are affected. The enormous much mortality and fast spread of the disease makes EBV a foremost problem for government and NGOs and health providers in West Africa. The symptoms of EVD are characterized by, high temperature, headache, malaise, pain abdominal, and asthenia. Averagely 8-10 days, a rash usually shows on the skin followed by hemorrhagic complications, leading to lost of life in 60%–90% of infected individuals (Racha and Torres,2015). Direct contact with body fluid, tissues and bodily secretions of death or infected individuals leads to successful transmissions, also, the disease can be contracted through nonhuman such as chimpanzee, gorilla, porcupine, fruit bats (Racha and Torres,2015).

Sensitivity analysis is an important analysis in mathematical epidemiology, so many authors considered this analysis in so many instance but this paper considered a sensitivity analysis on a novel model as formulated in Andrawus *et al.* (2022). The aim of this research is to find the sensitive parameter on basic reproduction number and infectious individuals of the model formulated in Andrawus *et al.* (2022), which the Authors did not address in there paper, they only address optimal control part analysis.

Model Construction

Mathematical modeling for the transmission dynamics of EVD by incorporating vaccine was developed in Andrawus *et al.*(2022). The model was subdivided into nine (9) compartments, eleven (11) state variables and nineteen (19) parameters as explained in Table 1.

Variable	Interpretation		
S_h	Susceptible humans		
L_h	Latently infected humans		
I_h	Infectious humans		
J_h	Isolated humans		
R_h	Remove individuals due to permanent recovery from infection		
D_h	Ebola-induced death Dead bodies (humans) before burial		
V	Virus in the environment		
N _b	Non career bats		
C_{b}	Career bats		
T_h	Total population of humans		
T_b	Total population of bats		
Parameter	Interpretation		
$\beta_1, \beta_2, \beta_3$	Human to human contact rate, contact rate of the virus in the environment to human and carrier bats to human contact rate respectively		
eta_4,eta_5	Bats to bats contact rate and virus in the environment to bats contact rate respectively.		
δ_1,δ_2	Disease induced of Infectious and Isolated humans		
δ_{b}	Death due to hunting		
γ	Natural recovery due to immune response		
φ	Isolation rate		
σ	Progression rate		
τ	Treatment rate of Isolated humans		
η	Modification parameter associated with reduced contact with the dead body of humans		
ε	Personal hygiene		

Table 1: Variable, parameter and interpretation of system (1)

$\alpha_1, \alpha_2, \alpha_3$	Shedding rate of Infectious, Dead body of humans and Carrier bats respectively
ρ	Vaccination rate
ϕ	Rate of proper burial of humans
Λ_h	Humans recruitment rate
Λ_b	Bats recruitment rate
μ_h	Humans natural mortality rate
μ_b	Bats natural mortality rate
ξ	Virus natural mortality rate

The system equation of the assumption above as it is given in (1).

$$\frac{dS_{h}}{dt} = \Lambda_{h} - \lambda_{h}S_{h} - (\rho + \mu_{h})S_{h}$$

$$\frac{dL_{h}}{dt} = \lambda_{h}S_{h} - (\sigma + \gamma + q + \mu_{h})L_{h}$$

$$\frac{dI_{h}}{dt} = \sigma L_{h} - (\varphi + \delta_{1} + \mu_{h})I_{h}$$

$$\frac{dJ_{h}}{dt} = \sigma Q_{h} + \varphi I_{h} - (\tau + \delta_{2} + \mu_{h})J_{h}$$

$$\frac{dR_{h}}{dt} = \gamma L_{h} + \rho S_{h} + \tau J_{h} - \mu_{h}R_{h}$$

$$\frac{dD_{h}}{dt} = (\delta_{1} + \mu_{h})I_{h} + (\delta_{2} + \mu_{h})J_{h} - \phi D_{h}$$

$$\frac{dV}{dt} = \alpha_{1}I_{h} + \alpha_{2}D_{h} + \alpha_{3}C_{b} - \xi V$$

$$\frac{dN_{b}}{dt} = \Lambda_{b} - \lambda_{b}N_{b} - (\delta_{b} + \mu_{b})N_{b}$$

$$\frac{dC_{b}}{dt} = \lambda_{b}N_{b} - (\delta_{b} + \mu_{b})C_{b}$$
(1)

where

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$$\lambda_{h} = \frac{\beta_{1}(1-\varepsilon)(I_{h}+\eta D_{h})}{T_{h}} + \frac{\beta_{2}(1-\varepsilon)V}{T_{h}} + \frac{\beta_{3}(1-\varepsilon)C_{b}}{T_{h}}$$
(2)

and

$$\lambda_b = \frac{\beta_4 C_b}{T_b} + \frac{\beta_5 V}{T_b} \tag{3}$$

The invariant region

The total population of human T_h is deduced by adding the first seven equations of the model (1) this gives $\frac{dT_h}{dt} = \Lambda_h - \mu_h (T_h - I_h - J_h) - \phi D_h$, so that $T_h \rightarrow \frac{\Lambda_h}{\mu_h}$ as $t \rightarrow \infty$. Thus, $T_h(t)$ is bounded above with $\frac{\Lambda_h}{\mu_h}$ provided that $T_h(0) \leq \frac{\Lambda_h}{\mu_h}$. Furthermore, considering $T_h(0) > \frac{\Lambda_h}{\mu_h}$, then $T_h(t)$ will decrease to this level. Similarly, calculation for the bats equations shows that $T_b \rightarrow \frac{\Lambda_b}{\mu_b}$ as $t \rightarrow \infty$. Thus, the following feasible region: $\Omega = \left\{ (S_h, \mathcal{L}_h, \mathcal{I}_h, \mathcal{D}_h, \mathcal{R}_h, V, \mathcal{N}_b, \mathcal{C}_b) \in \mathbb{R}^9_+ : T_h \leq \frac{\Lambda_h}{\mu_h}, T_b \leq \frac{\Lambda_b}{K_8} \right\}$ (4)

is invariantly positive set in the flow explained in system (1). Therefore, there is no path of solution that leaves from beginning to end of Π . Also, no path of solution paths can leave Π , trajectories remain positive for positive starting conditions. Trajectories exist at any given time t. In Π , system (1) is said to be epidemiologically and mathematically well posed.

As in Van den Driessche and Watmough (2002) the *F* and *V* matrices for the newly infected influx terms and the remainder terms of infected compartments respectively, the reproduction number is given by

$$\Re_{c} = \frac{\Re_{0}^{bbv} + \Re_{0}^{hhv1} + \sqrt{\left(\Re_{0}^{bbv} - \Re_{0}^{hhv1}\right)^{2} + 4\Re_{0}^{bv1}\Re_{0}^{hvb}}}{2}$$
(5)

where

$$\begin{split} \Re_{0}^{hhv1} &= \frac{\sigma\beta_{1}(1-\varepsilon)\mu_{h}}{K_{1}K_{2}K_{3}} + \frac{\sigma\eta\beta_{1}(1-\varepsilon)\mu_{h}\left(\varphi K_{6}+K_{4}K_{5}\right)}{\varphi K_{1}K_{2}K_{3}K_{4}} + \frac{\sigma\beta_{2}(1-\varepsilon)\mu_{h}\left(\varphi\alpha_{1}K_{4}+\varphi\alpha_{2}K_{6}+\alpha_{2}K_{4}K_{5}\right)}{\varphi\xi K_{1}K_{2}K_{3}K_{4}}, \\ \Re_{0}^{hvb} &= \frac{\beta_{2}(1-\varepsilon)\mu_{h}\alpha_{3}}{\xi K_{1}K_{7}} + \frac{\beta_{3}(1-\varepsilon)\mu_{h}}{K_{1}K_{7}}, \\ \Re_{0}^{bv1} &= \frac{\sigma\beta_{5}\left(\varphi\alpha_{1}K_{4}+\varphi\alpha_{2}K_{6}+\alpha_{2}K_{4}K_{5}\right)}{\varphi\xi K_{2}K_{3}K_{4}}, \\ \Re_{0}^{bv2} &= \frac{\beta_{5}\left(\varphi\alpha_{1}K_{4}+\varphi\alpha_{2}K_{6}+\alpha_{2}K_{4}K_{5}\right)}{\varphi\xi K_{3}K_{4}}, \text{ and } \\ \Re_{0}^{bbv} &= \frac{\beta_{5}\alpha_{3}}{\xi K_{7}} + \frac{\beta_{4}}{K_{7}} \end{split}$$

also, $K_1 = \rho + u_2 + \mu_h$, $K_2 = \sigma + \gamma + u_3 + \mu_h$, $K_3 = \varphi + \delta_1 + \mu_h$), $K_4 = \tau + u_4 + \delta_2 + \mu_h$,

 $K_5 = \delta_1 + \mu_h$, $K_6 = \delta_2 + \mu_h$ and $K_7 = \delta_b + \mu_b$

Sensitivity and uncertainty analysis

Uncertainties are anticipated to occur in the process of estimating the values of these parameters. Sensitivity and uncertainty analysis have to be done on system (1) in order to check the impact of the small perturbation and to each parameter's sensitivity of system (1). Effect of uncertainties will be thoroughly checked on the trajectories obtained, Latin Hypercube Sampling technique (LHS) will be use to check uncertainty analysis. Additionally, impact of the variation and each parameter's sensitivity of system (1) will be carried out globally using partial rank correlation coefficient (Blower and Dowlatabadi, 1994; Nwankwo and Okuonghae, 2019 and McLeod *et al.*, 2006). We carry out the uncertainty and sensitivity analysis using the values as given in Table 1 of Andrawus *et al.* (2022).

Using the human control reproduction number (\Re_c) and total number of infectious humans (I_h) as response functions, it is shown in Table 2 that the top PRCC-ranked parameters of the model (1) are the personal hygiene (ε), humans to human contact rate (β_1) modification

parameter (η), human vaccination rate (ρ), proper burial (ϕ) and humans natural mortality rate (μ_h).

Parameter	\mathfrak{R}_{c}	I_h
Λ_h	-0.0087	-0.0347
μ_h	0.6117	0.6161
β_1	0.7388	0.7316
ε	-0.9684	-0.9706
η_1	0.5023	0.5084
β_2	-0.0298	-0.0291
ρ	-0.5871	-0.6001
σ	0.2010	0.1709
γ	-0.1037	-0.1550
<i>q</i>	-0.2182	-0.1759
φ	-0.3461	-0.3508
δ_1	-0.0354	-0.0886
τ	-0.2946	-0.2959
δ_2	0.3134	0.2989
ϕ	-0.4939	-0.5219
Λ_b	-	-0.0590
β_3	-	0.0429
δ_{b}	-	0.0004
μ_{b}	-	-0.0191

Table.2. Partial rank correlation coefficient values of system (1) parameters using \Re_c and I_h as response functions

As expected, these results suggest that proper burial, personal hygiene and vaccination should be taken into consideration to menace the disease in the society.



Fig. 1. Sensitivity analysis with \mathfrak{R}_c as a response function

Fig 1 is showing global sensitive parameters to human control reproduction number, it shows that personal hygiene rate, effective contact rate of humans, vaccination rate and proper burial rate are very sensitive to human control reproduction number.



Fig. 2. Sensitivity analysis with I_h as a response function

Fig 2. is showing global sensitive parameters to infectious humans, it shows that personal hygiene rate, effective contact rate of humans, natural mortality of humans rate, vaccination rate and proper burial rate are very sensitive to Infectious humans.

DISCUSSION

The virus (Ebola virus) (EBV) belongs to the Filoviri-dae family which is a filovirus and is a serious disease which leads to hemorrhagic disease in human and non human such as chimpanzee, gorilla, porcupine, fruit bats. Also, a mathematical modeling of EVD for the transmission dynamics and control was introduced as in Andrawus *et al.*(2022), the model consist of both humans and bats population. The population human was subdivided into seven (7) classes which consist of susceptible humans, latently infected humans, infectious humans, dead body of humans, isolated humans and removed humans. The bats population was subdivided into two which consist of non-carrier bats and carrier bats also, with virus in the environment compartment. The boundedness of the solution was carried out, global uncertainty and sensitivity analysis was performed which shows that personal hygiene rate, effective contact rate of humans, natural mortality of humans' rate, vaccination rate and proper burial rate are very sensitive to both reproduction number and infectious humans.

CONCLUSION

This research has been examined, using deterministic mathematical modeling of EVD for the transmission dynamics and control in a population, the model has various control strategies that could be implemented to bring down the burden of EBV in a society. The research shows that, using the human control reproduction number (\Re_c) and I_h as response functions, as in Table 2 that system one has personal hygiene (ε), humans to human contact rate (β_1), modification parameter (η), human vaccination rate (ρ), proper burial (ϕ) and humans natural mortality rate (μ_h) as the top Partial rank correlation coefficient ranked parameters. This means that concentrating on these sensitive parameters can help greatly in eradicating EBV in the environment.

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