

EXISTENCE OF EQUILIBRIUM POINTS OF THE MATHEMATICAL MODEL OF EBOLA DISEASE DYNAMICS INCORPORATING INFECTION-AGE STRUCTURE IN THE QUARANTINED COMPARTMENT WITH TREATMENT

^{1*} AZUABA E., ² AKINWANDE N.I., ³ ABDULRAHMAN S. AND ⁴ KUTA F. A.

^{1,2}Department of Mathematics, Federal University of Technology, Minna, Nigeria

⁴Department of Microbiology, Federal University of Technology, Minna, Nigeria

³Department of Mathematics, Federal University, Birnin Kebbi, Nigeria

E-mail: mlahaga35@gmail.com **Phone No:** +234-813-581-9787

Abstract

In this paper, we present a mathematical model of Ebola Virus Disease (EVD) dynamics incorporating infection-age structure in the compartment of the quarantined with treatment. The model equations consist of Ordinary and Partial Differential Equations and Integro-Differential Equation. We verified the feasible region and the positivity of solution of the model. There exist two equilibria; Disease Free Equilibrium (DFE) and Endemic Equilibrium (EE). The disease free equilibrium (DFE) points were obtained. The disease free equilibrium state describes the total absence of EVD in the studied population and shows the critical points of the model equations.

Keywords: Infection-age, Ebola Virus Disease, Disease Free Equilibrium, Endemic Equilibrium

Introduction

Ebola Virus Disease (EVD), also known as Ebola haemorrhagic fever is a rare disease caused by Ebola virus strains. Ebola can cause disease in humans and nonhuman primates. According to World Health Organisation (WHO, 2014), Ebola virus is one of the deadliest diseases caused by infection from the family of RNA (Ribonucleic Acid) virus called *Filovirus*. There are five identified Ebola virus strains. Four of the five virus strains have caused disease in the humans: Ebola virus (*Zaire ebolavirus*); Sudan virus (*Sudan ebolavirus*); Tai Forest virus (*Tai Forest ebolavirus* formerly known as Cote d'Ivoire *ebolavirus*); and Bundibugyo virus (*bundibugyo ebolavirus*). The fifth, Reston virus (*Reaton ebolavirus*), has caused disease in nonhuman primates such as monkeys, gorillas, fruit bats, forest antelope porcupines, and chimpanzees. In this paper, only the Zaire Ebola virus strain causing the actual outbreaks in West Africa that is considered. Kamalu *et al.* (2016) ascertained that Zaire Ebola virus was first discovered in 1976 near the Ebola River in what is now the Democratic Republic of the Congo. Since then, outbreaks of Ebola virus disease appeared sporadically in Africa. In March 2014, the Ebola virus was first reported in Guinea, now the virus has spread to other West African nations like Liberia, Sierra Leone, Senegal and Nigeria. Ebola signs and symptoms of infection typically start between two days and three weeks after contracting the virus with a fever, sore throat, muscle pain, and headache. Then, vomiting, diarrhea and rash usually follow along with decreased function of the liver and kidneys. At this time some people begin to bleed both internally and externally (WHO and Pan-AHO, 2014). The disease has a high risk of death, killing between 25 and 90 percent of those infected with an average of about 50 percent. This is often due to low blood pressure from fluid loss.

The natural reservoir hosts of Ebola viruses remain unknown but because of evidence and the nature of similarities in viruses, many researchers believe that the virus is animal-borne and that bats are the most likely reservoir. Therefore, the virus was initially transmitted to people

from wild animals and spreads in the human population through human-to-human transmission via blood and body fluids contact. People infected with Ebola virus can only spread the virus to other people once they have developed symptoms. Even if someone has symptoms, it is important to remember that the virus is only transmitted by direct contact with the blood or body fluids of an infected person. An infection can also occur through direct contact with contaminated dead body of Ebola victim or materials such as linens or clothing that are soiled with infected bodily fluids.

Material and Methods

Model Formulation

The model equations are formulated using ordinary and partial differential equations and integro-differential equation. The model flow diagram is shown in figure 2.1. The total population is partitioned into five (5) compartments namely: Susceptible $S(t)$; Quarantine $P(t)$ under observation; Quarantine $Q(t)$ with treatment; Infected $I(t)$; fully recovered $R(t)$ individuals due to permanent immunity and Dead individuals $D(t)$ that are generated from $I(t)$ and $Q(t)$ only and is not a compartment among the living but dead individuals that are capable of causing subsequent reinfection if not properly handle. Therefore, it is not included in the total population. The $S(t)$ is a class in which members are EVD free but are open to infection through contacts with $I(t)$ and $D(t)$ respectively at the rate α_1 and $\alpha_2(1-\theta)$ where α_1 is the effective contact rate between $S(t)$ and $I(t)$, $\alpha_2(1-\theta)$ is the effective contact rate between $S(t)$ and $D(t)$, $(1-\theta)$ is the proportion of those who are not given proper burial and can cause subsequent reinfection, α_2 is the effective contact rate between $S(t)$ and $(1-\theta)$, hence $0 \leq \theta \leq 1$. $S(t)$ are generated through a natural birth rate Λ and they are reduced by a natural death rate μ . When $S(t)$ comes in contact with infected individuals $I(t)$ can become contaminated with the dead bodies at $(1-\theta)$ of Ebola victims, all the people who are suspected of having been infected usually by contacts tracing of the infected are then move into a class known as Quarantine $P(t)$ under observation.

After observation by healthcare workers if they are not infectious, meaning they are Ebola free then they can be removed back to join $S(t)$ population at the rate ϕ where ϕ is a fraction of individuals who are not infected with EVD and is confirmed after observation. While individuals who are infectious progress into $Q(t)$ (strict isolation zone) at the rate $(1-\phi)$ where $(1-\phi)$ is the probability of a newly observed individual to become infected and hence $0 \leq \phi \leq 1$. $P(t)$ are reduced at a natural death rate μ . $I(t)$ is a class of the individuals who are infected with EVD. This class is unavoidably present since Ebola infection is a severe disease and can cause death between two (2) to twenty one (21) days. Some of the infected individuals from $S(t)$ who are not suspected of having infection but suddenly become infected with EVD, they are automatically members of the infected class $I(t)$ and they are reduced due to μ, ϕ and δ_1 , where μ is the natural death rate, ϕ is the rate of quarantining $I(t)$ to $Q(t)$ and δ_1 is the disease induced death rate for $I(t)$. $D(t)$ is the compartment of dead individuals for both natural and Ebola induced death which are generated from $I(t)$ and $Q(t)$ through $\mu + \delta_1$ and $\mu + \delta_2$ respectively, where μ is the natural death rate, δ_1 and δ_2 are the disease induced death

rate of $I(t)$ and $Q(t)$ respectively. $D(t)$ is usually reduced by proper burial at the rate θ whereby θ is a fraction which is devoid of subsequent reinfection. This class exists because they are capable of spreading EVD through contaminated burial practices at the rate of $\alpha_2(1-\theta)$. This is possible because of factors such as political, economic situations, cultural, wars and lack of appropriate Personal Protection Equipment (PPE). To prevent the spread of Ebola virus disease, confirmed cases of individuals who are infectious of Ebola virus disease are isolated to remain in the Quarantine with treatment class $Q(t)$. $Q(t)$ is the class of individuals that are quarantined (strict isolation zone) and are receiving treatment. This is the second quarantine class. In this class, individuals are generated from $P(t)$ and $I(t)$ through $(1-\phi)$ and ϕ respectively. They are reduced by ω and $\mu + \delta_2$ where ω is the treatment rate and $\mu + \delta_2$ is natural and disease induced death rate of $Q(t)$. $R(t)$ is generated from $Q(t)$ via a treatment rate ω and is reduced by a natural death rate μ . The Quarantine with treatment class $Q(t)$ is structured by the infection age with the density function $q(t, \tau)$ following the idea by Akinwande (2005) where t is the time parameter and τ is the infection age. There is a maximum infection age T at which a member of the infected individuals from quarantine with treatment class $Q(t)$ must leave the compartment via death; and so $0 \leq \tau \leq T$. The death rate due to EVD infection is given by $\sigma(\tau) = \delta e^{-k(T-\tau)}$ where δ and k are constants. δ is the maximum death rate from infection while k is a control parameter which could be a measure of slowing down the death of the infected, this can be the measure of effectiveness of slowing down the death of the infected for example the effectiveness of ω . A high value of k will imply high effectiveness of such control measures and vice versa.

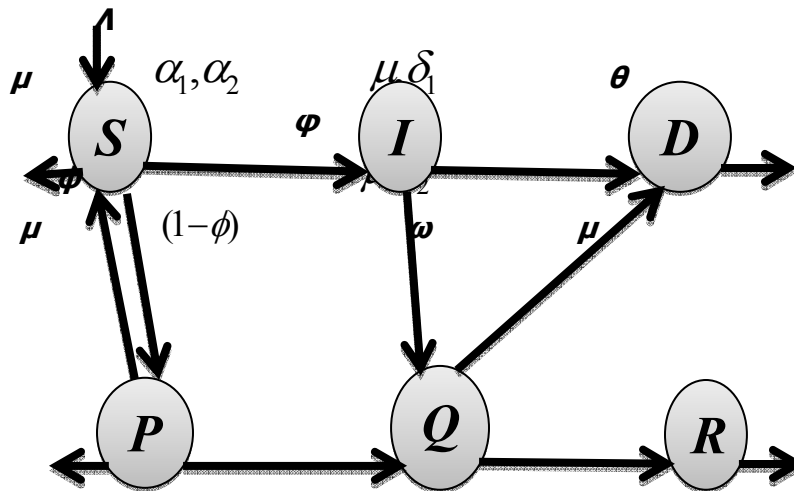


Figure 2.1: Model Diagram

Table 2.1: Notation and definition of variables and parameters in Model Diagram are represented as follows

Symbol	Description
$S(t)$	Susceptible individuals at time t
$P(t)$	Quarantine under observation individuals at time t
$I(t)$	Infected individuals at time t
$D(t)$	Dead individuals resulting from $I(t)$ and $Q(t)$ at time t
$R(t)$	Recovered individuals due to permanent recovery from infection at time t
$Q(t)$	Quarantine individuals with treatment at time t
Λ	Birth rate into $S(t)$ only
μ	Natural death rate
δ_1	Disease induced death rate of infected class $I(t)$
δ_2	Disease induced death rate of quarantine with treatment $Q(t)$
α_1	Effective contact rate between $I(t)$ and $S(t)$
α_2	Effective contact rate between $D(t)$ and $S(t)$
γ	Quarantine rate of suspected individuals from $S(t)$ to $P(t)$
ϕ	Quarantine rate from $I(t)$ to $Q(t)$
ϕ	Proportion of individuals that move back from $P(t)$ to $S(t)$ after observation
θ	Proportion of those who are given proper burial, $0 \leq \theta \leq 1$
ω	Treatment rate,

Model Equations

$$\frac{dS}{dt} = \Lambda - \frac{\alpha_1 IS}{N} - \frac{\alpha_2 (1-\theta)DS}{N} + \phi P - (\mu + \gamma)S \quad (2.1)$$

$$\frac{dP}{dt} = \gamma S - (\phi + \mu)P \quad (2.2)$$

$$\frac{dI}{dt} = \frac{\alpha_1 IS}{N} + \frac{\alpha_2 (1-\theta)DS}{N} - (\mu + \delta_1 + \phi)I \quad (2.3)$$

$$\frac{dD}{dt} = (\mu + \delta_1)I + (\mu + \delta_2)Q - \theta D \quad (2.4)$$

$$\frac{dR}{dt} = \omega Q - \mu R \quad (2.5)$$

$$\frac{\partial q(t, \tau)}{\partial t} + \frac{\partial q(t, \tau)}{\partial \tau} + (\mu + \sigma(\tau))q(t, \tau) = 0 \quad (2.6)$$

Table 2.2: Notation and definition of variables and parameters that are not in the Model Diagram as follows

Symbol	Description
$B(t)$	Boundary conditions at time t
$q(t, \tau)$	Density functions of infection-age
$\psi(\tau)$	Initial condition of Infection-age
$\sigma(\tau)$	Death rate from infection
δ	Maximum death rate from infection
k	Measure of the effectiveness of efforts at slowing down the death of infected members
t	Time parameter
τ	Infection age
T	Maximum age of infection
Ω	The feasible set or Invariant region

The boundary conditions are given as:

$$q(t,0) = B(t) = \frac{\alpha_1 IS}{N} + \frac{\alpha_2 (1-\theta)DS}{N} + \phi I + (1-\phi)P \quad (2.7)$$

$$q(t,T) = 0 \quad (2.8)$$

Where, T is the maximum infection age; i.e. when $\tau = T$ the infected member dies of EVD.

$$\text{The total population size } N \text{ is given by: } N(t) = S(t) + P(t) + I(t) + R(t) + Q(t) \quad (2.9)$$

The total population of infected individuals from quarantine with treatment is given as:

$$Q(t) = \int_0^T q(t, \tau) d\tau \quad (2.10)$$

According to Akinwande (2006) the death rate via infection is given by (2.11)

$$\sigma(\tau) = \delta e^{-k(T-\tau)} \quad (2.11)$$

The initial conditions are:

$$S(0) = S_0, P(0) = P_0, I(0) = I_0, D(0) = I_0, R(0) = R_0, Q(0) = Q_0, N(0) = N_0 \quad (2.12)$$

$$q(0, \tau) = \psi(\tau) \quad (2.13)$$

Integrating (2.6) over τ gives:

$$\frac{dQ}{dt} + q(t,T) - q(t,0) = -\mu \int_0^T q(t, \tau) d\tau - \int_0^T \sigma(\tau) q(t, \tau) d\tau \quad (2.14)$$

Let,

$$\int_0^T \sigma(\tau) q(t, \tau) d\tau = \delta \int_0^T e^{-k(T-\tau)} q(t, \tau) d\tau \quad (2.15)$$

Where, $\sigma(\tau)$ and $\int_0^T q(t, \tau) d\tau$ are as defined in (2.11) and (2.10) respectively.

Applying integration by parts on R. H.S. of (2.15) we get:

$$\int_0^T \sigma(\tau)q(t, \tau)d\tau = 0 \tag{2.16}$$

Substituting equations (2.7), (2.8), (2.10) and (2.16) into (2.14) yields

$$\frac{dQ}{dt} = \frac{\alpha_1 IS}{N} + \frac{\alpha_2(1-\theta)DS}{N} + \phi I + (1-\phi)P - \mu Q \tag{2.17}$$

Invariant Region of the Model

The invariant region describes the region in which the solution of the system makes biological sense.

Lemma 2.1: The region Ω is positively-invariant and all solutions are contained in $\Omega \in \mathfrak{R}_+^6$

Proof:

Let, $\Omega = (S, P, I, D, R, Q) \in \mathfrak{R}_+^6$ be any solution of the system with non-negative initial conditions. We determined the total population sizes $N(t)$ from the differential equations of the model system.

Adding (2.1) to (2.5) and (2.17) gives

$$\frac{dN(t)}{dt} = \Lambda - \mu N + j(t) + b(t) \tag{2.18}$$

Where, $j(t) = (\delta_2 + \omega)Q(t)$ (2.19)

$$b(t) = \frac{\alpha_1 I(t)S(t)}{N(t)} + \frac{\alpha_2(1-\theta)D(t)S(t)}{N(t)} + (1-\phi)P(t) - \theta D(t) \tag{2.20}$$

With, $\Omega = \left\{ (S, P, I, D, R, Q) \in \mathfrak{R}_+^6 \mid S + P + I + D + R + Q \leq \frac{\Lambda}{\mu} \right\}$ (2.21)

From (2.18), in the absence of EVD infection equation (2.19) equals to zero and equation (2.20) equals to $P(t)$ since all the infected classes are zero and the population is made up of susceptible $S(t)$ and quarantine under observation $P(t)$.

Thus, $\frac{dN}{dt} = \Lambda - \mu N$ (2.22)

Where, $N = S + P$ (2.23)

We apply both the Birkhoff and Rota (1982) theorem of differential inequality and separation of variables of differential inequality on equation (2.22), we get

$$\frac{dN}{\Lambda - \mu N} \leq d(t) \tag{2.24}$$

Integrating both sides of equation (2.24) gives

$$\Lambda - \mu N \geq Ae^{-\mu t} \tag{2.25}$$

Where, A is a constant. We apply the initial conditions in equation (2.25); i.e. $t = 0, N(0) = N_0$

We obtained, $A = \Lambda - \mu N_0$ (2.26)

Substituting (2.26) in (2.25), we have

$$\Lambda - \mu N \geq (\Lambda - \mu N_0)e^{-\mu t} \tag{2.27}$$

Hence,
$$N(t) \leq \frac{\Lambda}{\mu} - \left(\frac{\Lambda - \mu N_0}{\mu} \right) e^{-\mu t} \tag{2.28}$$

Thus as $t \rightarrow \infty$, we have:
$$0 \leq N(t) \leq \left(N(0) - \frac{\Lambda}{\mu} \right) e^{-\mu t} + \frac{\Lambda}{\mu}, \forall t \geq 0 \tag{2.29}$$

We have $\lim_{t \rightarrow \infty} N(t) < \frac{\Lambda}{\mu}$ when $N(0) \leq \frac{\Lambda}{\mu}$. However, if $N(0) \geq \frac{\Lambda}{\mu}$,

$N(t)$ will decrease to $\frac{\Lambda}{\mu}$. So $N(t)$ is a bounded function of time. The system (2.1) to (2.6) has

solutions which are contained in the feasible region Ω and at limiting equilibrium $\lim_{t \rightarrow \infty}$

$N(t) = \frac{\Lambda}{\mu}$ besides, any sum or difference of variables in Ω with positive initial values will remain

in Ω or in a neighbourhood of Ω . Thus Ω is positively invariant (i.e. solutions remain positive for all times, t) and attracting with respect to the flow of the system (2.1) to (2.6) which are epidemiologically meaningful and mathematically well posed.

Positivity of Solutions

The positivity of solutions describe non-negativity of solutions of system.

Lemma 2.2: All the solution of the equations (2.1) to(2.6) are positive for all time $t \geq 0$ provided that the initial conditions are positive.

Proof:

Let the initial data be: $\{(S(0), P(0), I(0), D(0), R(0), Q(0)) \geq 0\} \in \mathbb{R}_+^6$

Then, the solution set

$\{S(t), P(t), I(t), D(t), R(t), Q(t)\}$ of the system (2.1) to (2.6) is positive for all $t > 0$

From (2.1), we have

$$\frac{dS}{S} \geq -(\mu + \gamma)dt \tag{2.30}$$

Integrating (2.30) gives

$$S(t) \geq S(0)e^{-(\mu+\gamma)t} \tag{2.31}$$

Similarly, from (2.2)

$$\frac{dP}{P} \geq -(\mu + \phi)dt \tag{2.32}$$

Integrating (2.32) gives

$$P(t) \geq P(0)e^{-(\mu+\phi)t} \tag{2.33}$$

From (2.3), we have that

$$\frac{dI}{I} \geq -(\mu + \delta_1 + \varphi)dt \tag{2.34}$$

Solving (2.34) gives

$$I(t) \geq I(0)e^{-(\mu+\delta_1+\varphi)t} \tag{2.35}$$

Similarly, from (2.4), we have

$$\frac{dD}{D} \geq -\theta dt \tag{2.36}$$

Integrating (2.36) gives:

$$D(t) \geq D(0)e^{-\theta t} \geq 0 \tag{2.37}$$

From (2.5), we have

$$\frac{dR}{R} \geq -\mu dt \tag{2.38}$$

Solving (2.38) gives

$$R(t) \geq R(0)e^{-\mu t} \tag{2.39}$$

Similarly, from (2.17), we have

$$\frac{dQ}{Q} \geq -\mu dt \tag{2.40}$$

Integrating (2.40) we have the following

$$Q(t) \geq Q(0)e^{-\mu t} \tag{2.41}$$

Therefore, all the solution of equations of system (2.1) to (2.6) are positive for all $t > 0$

Existence of Equilibrium Points of the Model

Equations (2.1) to (2.13) are re-written as follows:

$$\frac{dS}{dt} = \Lambda - \frac{\alpha_1 S}{N} \int_0^T q(t, \tau) d\tau - \frac{\alpha_2 k_1 DS}{N} + \phi P - k_2 S \tag{2.42}$$

$$\frac{dP}{dt} = \gamma S - k_3 P \tag{2.43}$$

$$\frac{dI}{dt} = \frac{\alpha_1 S}{N} \int_0^T q(t, \tau) d\tau + \frac{\alpha_2 k_1 DS}{N} - k_4 \int_0^T q(t, \tau) d\tau \tag{2.44}$$

$$\frac{dD}{dt} = (k_5 + k_6) \int_0^T q(t, \tau) d\tau - \theta D \tag{2.45}$$

$$\frac{dR}{dt} = \omega \int_0^T q(t, \tau) d\tau - \mu R \tag{2.46}$$

$$\frac{\partial q(t, \tau)}{\partial t} + \frac{\partial q(t, \tau)}{\partial \tau} + (\mu + \sigma(\tau))q(t, \tau) = 0 \tag{2.47}$$

The boundary conditions are given as:

$$q(t,0) = B(t) = \frac{\alpha_1 S}{N} \int_0^T q(t,\tau) d\tau + \frac{\alpha_2 k_1 DS}{N} + k_7 P + \phi \int_0^T q(t,\tau) d\tau \quad (2.48)$$

Where, $Q(t) = I(t) = \int_0^T q(t,\tau) d\tau$ (2.49)

$$k_1 = (1 - \theta), k_2 = (\mu + \gamma), k_3 = (\mu + \phi), k_4 = (\mu + \phi + \delta_1), k_5 = (\mu + \delta_1), k_6 = (\mu + \delta_2), k_7 = (1 - \phi) \quad (2.50)$$

And the initial conditions are:

$$N(0) = N_0, S(0) = S_0, P(0) = P_0, I(0) = I_0, D(0) = D_0, R(0) = R_0, q(0, \tau) = \psi(\tau) \quad (2.51)$$

Disease-free Equilibrium State (E^0)

The disease-free equilibrium state describes the total absence of EVD in the studied population. At this state all the infected classes will be zero and the population will be made up of the susceptible and quarantine under observation populations only.

Lemma 2.3: A disease-free equilibrium state of the model equations (2.42) to (2.48) exists at the point:

$$\begin{pmatrix} S \\ P \\ I \\ D \\ R \\ Q \end{pmatrix} = \begin{pmatrix} \left(\frac{(\mu + \phi)\Lambda}{(\mu + \gamma)(\mu + \phi) - \phi\gamma} \right) \\ \left(\frac{\gamma\Lambda}{(\mu + \gamma)(\mu + \phi) - \phi\gamma} \right) \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} = E^0 \quad (2.52)$$

Proof:

According to Medlock (2010) equilibria are the points where the variables do not change with time. That is $\frac{dS}{dt} = \frac{dP}{dt} = \frac{dI}{dt} = \frac{dD}{dt} = \frac{dR}{dt} = 0$.

At the disease-free equilibrium state, we set

$$S(t) = x^0; P(t) = u^0; I(t) = y^0; D(t) = f^0; R(t) = r^0; Q(t) = z^0; \text{ and } N(t) = n^0; \quad (2.53)$$

$$q(t, \tau) = q(\tau); \quad (2.54)$$

Where,

$$n^0 = x^0 + u^0 + y^0 + f^0 + r^0 + z^0, n = x + u + y + f + r + z \quad (2.55)$$

And from equations (2.49), (2.53) and (2.54), we obtain:

$$z^0 = y^0 = \int_0^T q(\tau) d\tau \quad (2.56)$$

Equations (2.42) to (2.48) give:

$$\Lambda - \frac{\alpha_1 x^0 z^0}{n^0} - \frac{\alpha_2 k_1 f^0 x^0}{n^0} + \phi u^0 - k_2 x^0 = 0 \quad (2.57)$$

$$\gamma x^0 - k_3 u^0 = 0 \quad (2.58)$$

$$\frac{\alpha_1 x^0 z^0}{n^0} + \frac{\alpha_2 k_1 f^0 x^0}{n^0} - k_4 z^0 = 0 \quad (2.59)$$

$$(k_5 + k_6) z^0 - \theta f^0 = 0 \quad (2.60)$$

$$\omega z^0 - \mu r^0 = 0 \quad (2.61)$$

$$\frac{dq(\tau)}{d\tau} + (\mu + \sigma(\tau))q(\tau) = 0 \quad (2.62)$$

$$q(0) = B_0 = \frac{\alpha_1 x^0 z^0}{n^0} + \frac{\alpha_2 k_1 x^0 f^0}{n^0} + \phi z^0 + k_7 u^0 \quad (2.63)$$

Solving (2.62) for $q(\tau)$ gives

$$q(\tau) = q(0) e^{-\int_0^\tau (\mu + \sigma(s)) ds} \quad (2.64)$$

$$\text{Let, } \pi(\tau) = e^{-\int_0^\tau (\mu + \sigma(s)) ds} \quad (2.65)$$

Substituting (2.65) into (2.64) we obtain:

$$q(\tau) = q(0)\pi(\tau) \quad (2.67)$$

Integrating both sides of (2.67) gives:

$$\int_0^\tau q(\tau) d\tau = q(0) \int_0^\tau \pi(\tau) d\tau \quad (2.68)$$

Equation (2.68) is re-written in the form:

$$z^0 = q(0)\bar{\pi} \quad (2.69)$$

Where,

$$\bar{\pi} = \int_0^\tau \pi(\tau) d\tau \quad (2.70)$$

Using (2.63) in (2.69) gives:

$$\frac{\alpha_1 x^0 z^0}{n^0} \bar{\pi} + \frac{\alpha_2 k_1 x^0 f^0}{n^0} \bar{\pi} + \phi z^0 \bar{\pi} + k_7 u^0 \bar{\pi} = z^0 \quad (2.71)$$

Factorizing the L.H.S of (2.71) gives:

$$\left[\frac{\alpha_1 x^0 z^0}{n^0} + \frac{\alpha_2 k_1 x^0 f^0}{n^0} + \phi z^0 + k_7 u^0 \right] \bar{\pi} = z^0 \quad (2.72)$$

From (2.72), either

$$\bar{\pi} = z^0 \quad (2.73)$$

Or

$$\left[\frac{\alpha_1 x^0 z^0}{n^0} + \frac{\alpha_2 k_1 x^0 f^0}{n^0} + \phi z^0 + k_7 u^0 \right] = z^0 \quad (2.74)$$

If and only if $\bar{z} = z^0$, then equation (2.69) yields

$$z^0 = 0, \quad q(0) = 1 \quad (2.75)$$

And so (2.69) to (2.74) equal zero.

Substituting (2.75) into (2.56) and (2.61) gives:

$$z^0 = y^0 = r^0 = 0 \quad (2.76)$$

Solving (2.60) for f^0 gives:

$$f^0 = \frac{(k_5 + k_6)z^0}{\theta} \quad (2.77)$$

Substituting (2.76) into (2.77) we obtain:

$$f^0 = 0 \quad (2.78)$$

Solving (2.58) for u^0 yields:

$$u^0 = \frac{\gamma x^0}{k_3} \quad (2.79)$$

Substituting (2.76) and (2.78) into (2.57) gives:

$$\Lambda + \phi u^0 - k_2 x^0 = 0 \quad (2.80)$$

Substituting (2.79) into (2.80) and isolating x^0 , gives

$$x^0 = \left(\frac{(\mu + \phi)\Lambda}{(\mu + \gamma)(\mu + \phi) - \phi\gamma} \right) \quad (2.81)$$

Substituting (2.81) into (2.79) we obtain:

$$u^0 = \left(\frac{\gamma\Lambda}{(\mu + \gamma)(\mu + \phi) - \phi\gamma} \right) \quad (2.82)$$

Substituting (2.76), (2.78) (2.81) and (2.82) into (2.55) and simplifying gives:

$$n^0 = \left(\frac{\Lambda((\mu + \phi) + \gamma)}{(\mu + \gamma)(\mu + \phi) - \phi\gamma} \right) \quad (3.132)$$

Result and Discussion

Thus, a Disease Free-Equilibrium (DFE) exists for the model of equations (2.1) to (2.6).

$\left(\frac{\gamma\Lambda}{(\mu + \gamma)(\mu + \phi) - \phi\gamma} \right)$ represents the total number of individuals who are quarantined under observation and are free of EVD infection after confirmation. $\left(\frac{(\mu + \phi)\Lambda}{(\mu + \gamma)(\mu + \phi) - \phi\gamma} \right)$ represents the total number of susceptible individuals in the absence of EVD and $\left(\frac{\Lambda((\mu + \phi) + \gamma)}{(\mu + \gamma)(\mu + \phi) - \phi\gamma} \right)$

represents the total population in the absence of infection while $\pi(\tau) = e^{-\int_0^\tau (\mu + \sigma(s)) ds}$ is the survival probability as a function of infection age τ in the quarantined with treatment compartment. $\left(\frac{k_5 + k_6}{\theta}\right) z^0$ represents the total dead bodies both naturally and disease induced death caused by $I(t)$ and $Q(t)$ only.

Conclusion

The feasible set Ω of the model (2.1) to (2.6) is positively invariant (i.e. solutions remain positive for all times, t) and the model is epidemiologically meaningful and mathematically well posed. Equation (2.72) showed the existence of two equilibria in the model; equation (2.75) showed the disease free equilibrium (DFE) and equation (2.74) showed the endemic equilibrium (EE). We went further to obtain the disease-free equilibrium points of the model as given by equation (2.52). This implies that at the disease free equilibrium Ebola can be wiped out otherwise persists when is endemic.

References

- Akinwande, N. I. (2005). A mathematical model of the chaotic dynamics of the AIDS disease pandemic. *Journal of the Nigerian Mathematical Society*, 24, 8-16.
- Akinwande, N. I. (2006). A mathematical model of the dynamics of the HIV/AIDS disease pandemic. *Journal of the Nigerian Mathematical Society*, 25, 99-108.
- Birkhoff, G., & Rota, G. C. (1982). *Ordinary differential equations*. Ginn: Oxford University Press.
- Kamalu, C. I.O., Dozie, N.S., Oghome, P., Nwakaudu, M.S., Uzundu, F. N., & Obijianku, J. C. (2016). S-I-S Compartmental modelling and predictive analysis of Ebola outbreak in Central and West Africa. *World Journal of Engineering Research and Technology*, 2(3), 13-36.
- Medlock, J. (2010). Mathematical analysis of epidemiological models. *Journal of Emerging Infectious Diseases*, 11(9), 1355-1362.
- WHO & Pan AHO. (2014). Ebola Virus Disease (EVD), implication of introduction in the Americas, Corrigendum, Pan American Health Organisation and World Health Organisation.
- World Health Organisation (WHO, 2014). *Facts sheets on Ebola outbreaks*.