International Journal of Innovative Mathematics, Statistics & Energy Policies 6(1):24-39, Jan-Mar, 2018

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The Mathematical Dynamics of Screening and Treatment Failure in the Transmission of HIV/AIDS in Nigerian Economy

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ABSTRACT
This study proposed and analyzed two non-linear mathematical models for the dynamics of the effect of treatment failure, screening and migration in the transmission of HIV/AIDS. The equilibrium points of the models were found and their stability investigated. The models exhibited two equilibrium namely, the diseases-free and the endemic equilibra. It is found that if the effective reproduction number (R_T) is less than unity, the disease free equilibrium is local asymptotically stable (LAS) and globally asymptotically stable when $R_T \leq 1$. If $R_T>1$, a unique equilibrium exist which is locally asymptotically stable. Numerical simulations validated the analytical results and further reveal that the effective reproduction can be brought strictly less than one if infected pregnant mothers are properly managed.
Keywords: - Mathematical Dynamics, Transmission, HIV/AIDS, and Treatment Failure

INTRODUCTION

Globally, more than 30 million people are living with HIV/AIDS and over 23 million have died since 1981. About 95% of people with HIV live in developing and moderate-income nations and over 25 million people with HIV living in poor and moderate-income countries should be on antiretroviral medication. Of this number, only about 30% of these people are getting the treatment (Nasidi et al., 1986).

In Nigeria, AIDS was first diagnosed in 1985 in a female teenaged less than 14 years but was reported in 1986. This case was diagnosed in Lagos, one of the most populous cities in Nigeria (Abdulrahman, 2009). Twenty seven years after, the disease has become a massive epidemic which has become not only a health burden but also a socio-economic problem (Usman et al., 2012) .According to Margaret Lampe of the US Centres for Disease Control and Prevention, the number of people living with HIV/AIDS in Nigeria increased by almost 500,000 in three years, while the number of AIDS-related deaths also witnessed a marginal rise to 217,148 within the same period. Of particular interest to Jean Anderson of the Johns Hopkins Medical Institute, Maryland, was the high rate of infection through blood transfusion and mother-to-child transmission, despite the fact that such forms of transmission are easily preventable. A United Nations report last year had also described Nigeria as the country with the highest number of children living with the virus in the world. The report said in part, "Nigeria has the largest number of children acquiring HIV infection, nearly 60,000 in 2012 — a number that has remained unchanged since 2009" (Adebayo, 2014:15). In order to find an efficient way to control an infection, it is of great importance to establish its transmission dynamics. One main goal of mathematical epidemiology is to understand how to control and eradicate diseases (Akinwande, 2006). Mathematical models are used extensively in the study of ecological and epidemiological phenomena (Kaplan & Brandeau,1994). They

are particularly helpful as experimental tools with which to evaluate and compare control procedures and preventive strategies, and to investigate the relative effects of various sociological, biological and environmental factors on the spread of diseases. This is so because they can help in figuring out decisions that are of significance importance on the outcomes and provide comprehensive examinations that enter into decisions in a way that human reasoning and debate cannot.

Model

A mathematical model on the dynamics of the effect of treatment failure in horizontal and vertical transmission of HIV/AIDS was developed, improving on the existing model as explained in the literature review by incorporating the effect of treatment failure, screening and migration in horizontal and vertical transmission. Figure 1 is a schematic representation of the model.

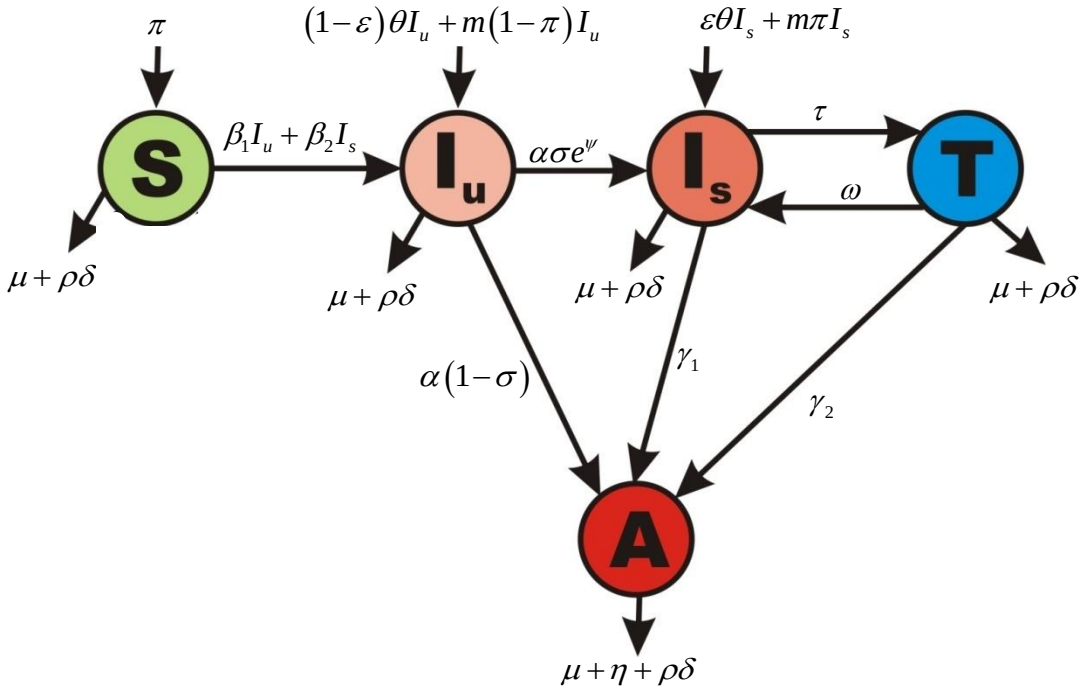

Figure 1 Schematic Diagram of the Model

Definition of Parameters of the Model

Parameter	Interpretation
π	Recruitment rate of susceptible individuals
μ	Natural death rate
η	AIDS-induced death
θ	Rate of giving birth to offspring by infected pregnant mothers I_u and I_s
ε	Proportion of HIV-positive birth by infected pregnant mothers I_u and I_s
m	Rate at which immigrants enters I_u and I_s
ψ	Rate of screening individuals in class I_u
α	Rate of progression from I_u to I_s or A
σ	Proportion of I_u which progresses to I_s while $1-\sigma$ is the proportion of I_u which progresses to A
γ_1	Rates of progression to I_s to A
γ_2	Rates of progression to T to A
ρ	Period of stay the immigrant is permitted to stay in the country
δ	Fraction of immigrants who left the country
τ	Rate of treating screened infected individuals
ω	Rate of treatment failure

Theorem:

Let D denotes the region $0 \le \xi \le R$

Then, the system (3.97) has a unique solution which is continuous and bounded in D. We now want to show that $\frac{\partial f_i}{\partial x_j}, i, j = 1, 2, 3, \ldots$ are continuous and bounded in D.

Proof

Let

$$f_1 = \pi - (\beta_1 I_u + \beta_2 I_s) S - k_1 S \quad (1.110a)$$

$$f_2 = \vartheta_1 I_u + (\beta_1 I_u + \beta_2 I_s) S - k_2 I_u \quad (1.110b)$$

$$f_3 = \vartheta_2 I_s + \alpha \vartheta_3 I_u + \omega T - k_3 I_s \quad (1.110c)$$

$$f_4 = \tau I_s - k_4 T \quad (1.110d)$$

$$f_5 = \alpha \vartheta_4 I_u + \gamma_1 I_s + \gamma_2 T - k_5 A \quad (1.110e)$$

From (1.110a), we have the partial derivatives below:

$$\left.\begin{aligned}
\left|\frac{\partial f_1}{\partial S}\right| &= \left|\beta_1 I_u + \beta_2 I_s - k_1\right| < \infty \\
\left|\frac{\partial f_1}{\partial I_u}\right| &= \left|\beta_1 S\right| < \infty \\
\left|\frac{\partial f_1}{\partial I_s}\right| &= \left|\beta_2 S\right| < \infty \\
\left|\frac{\partial f_1}{\partial T}\right| &= 0 < \infty \\
\left|\frac{\partial f_1}{\partial A}\right| &= 0 < \infty
\end{aligned}\right\} \qquad (1.111)$$

These partial derivatives of (1.111) exist, continuous and are bounded.

Similarly, from (1.110b), we have the partial derivatives thus:

$$\left.\begin{aligned}
\left|\frac{\partial f_2}{\partial S}\right| &= \left|\beta_1 I_u + \beta_2 I_s\right| < \infty \\
\left|\frac{\partial f_2}{\partial I_u}\right| &= \left|\vartheta_1 - k_2\right| < \infty \\
\left|\frac{\partial f_2}{\partial I_s}\right| &= \left|\beta_2 S\right| < \infty \\
\left|\frac{\partial f_2}{\partial T}\right| &= 0 < \infty \\
\left|\frac{\partial f_2}{\partial A}\right| &= 0 < \infty
\end{aligned}\right\} \qquad (1.112)$$

Similarly, from (3.110c), we have the partial derivatives thus:

$$\left.\begin{aligned}
\left|\frac{\partial f_3}{\partial S}\right| &= 0 < \infty \\
\left|\frac{\partial f_3}{\partial I_u}\right| &= \left|\alpha\vartheta_3\right| < \infty \\
\left|\frac{\partial f_3}{\partial I_s}\right| &= \left|\vartheta_2 - k_3\right| < \infty \\
\left|\frac{\partial f_3}{\partial T}\right| &= \left|\omega\right| < \infty \\
\left|\frac{\partial f_3}{\partial A}\right| &= 0 < \infty
\end{aligned}\right\} \qquad (1.113)$$

Similarly, from (1.110d), we have the partial derivatives thus:

$$\left.\begin{aligned}
\left|\frac{\partial f_4}{\partial S}\right| &= 0 < \infty \\
\left|\frac{\partial f_4}{\partial I_u}\right| &= 0 < \infty \\
\left|\frac{\partial f_4}{\partial I_s}\right| &= |\tau| < \infty \\
\left|\frac{\partial f_4}{\partial T}\right| &= |-k_4| < \infty \\
\left|\frac{\partial f_4}{\partial A}\right| &= 0 < \infty
\end{aligned}\right\} \qquad (1.114)$$

Lastly, from equation (1.110e), we have the partial derivatives thus:

$$\left.\begin{aligned}
\left|\frac{\partial f_5}{\partial S}\right| &= 0 < \infty \\
\left|\frac{\partial f_5}{\partial I_u}\right| &= |\alpha \vartheta_4| < \infty \\
\left|\frac{\partial f_5}{\partial I_s}\right| &= |\gamma_1| < \infty \\
\left|\frac{\partial f_5}{\partial T}\right| &= |\gamma_2| < \infty \\
\left|\frac{\partial f_5}{\partial A}\right| &= |-k_5| < \infty
\end{aligned}\right\} \qquad (1.115)$$

As clearly shown above, the partial derivatives of the whole system(1.110) exist, they are finite and bounded as shown in (1.111) – (1.115) above. Hence, by Theorem 1, the model system (1.97) has a unique solution.

Existence of Equilibria, E^*

The long term behaviour of the solutions of the ODEs (1.97a) – (1.97e) above can be examined at equilibrium states since the solutions are independent of time.

At equilibrium state the rate of change of each variable is equal to zero.

$$\text{i.e.}\ \frac{dS}{dt} = \frac{dI_u}{dt} = \frac{dI_s}{dt} = \frac{dT}{dt} = \frac{dA}{dt} = 0 \qquad (1.116)$$

At any arbitrary equilibrium state, let

$$\begin{pmatrix} S \\ I_u \\ I_s \\ T \\ A \end{pmatrix} = \begin{pmatrix} S^* \\ I_u^* \\ I_s^* \\ T^* \\ A^* \end{pmatrix} \tag{1.117}$$

Thus from system (1.107), we have

$$\pi - \left(\beta_1 I_u^* + \beta_2 I_s^*\right) S^* - k_1 S^* = 0 \tag{1.118a}$$

$$\vartheta_1 I_u^* + \left(\beta_1 I_u^* + \beta_2 I_s^*\right) S^* - k_2 I_u^* = 0 \tag{1.118b}$$

$$\vartheta_2 I_s^* + \alpha\vartheta_3 I_u^* + \omega T^* - k_3 I_s^* = 0 \tag{1.118c}$$

$$\tau I_s^* - k_4 T^* = 0 \tag{1.118d}$$

$$\alpha\vartheta_4 I_u^* + \gamma_1 I_s^* + \gamma_2 T^* - k_5 A^* = 0 \tag{1.118e}$$

From (1.118d)

$$T^* = \frac{\tau I_s^*}{k_4} \tag{1.119}$$

Substituting (3.119) into (3.118c) gives

$$\left(k_4\vartheta_2 + \tau\omega - k_3k_4\right) I_s^* + k_4\alpha\vartheta_3 I_u^* = 0 \tag{1.120}$$

From (1.120)

$$I_s^* = \left(\frac{k_4\alpha\vartheta_3}{k_3k_4 - k_4\vartheta_2 - \tau\omega}\right) I_u^* \tag{1.121}$$

Substituting (3.121) into (3.119) gives

$$T^* = \left(\frac{k_4\tau\alpha\vartheta_3}{k_3k_4 - k_4\vartheta_2 - \tau\omega}\right) I_u^* \tag{1.122}$$

Substituting (1.121) and (1.122) into (1.118e) gives

$$A^* = \left(\frac{\alpha\vartheta_4\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right) + k_4\gamma_1\alpha\vartheta_3 + k_4\gamma_2\tau\alpha\vartheta_3}{k_5\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)}\right) I_u^* \tag{1.123}$$

Substituting (1.121) into (1.118b) gives

$$\left(\frac{\left(\vartheta_1 + \beta_1 S^* - k_2\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right) + k_4\alpha\vartheta_3\beta_2 S^*}{k_3k_4 - k_4\vartheta_2 - \tau\omega}\right) I_u^* = 0 \tag{1.124}$$

This means that either

$$I_u = 0 \tag{1.125}$$

Or

$$\frac{\left(\vartheta_1 + \beta_1 S^* - k_2\right)\left(k_3 k_4 - k_4 \vartheta_2 - \tau\omega\right) + k_4 \alpha \vartheta_3 \beta_2 S^*}{k_3 k_4 - k_4 \vartheta_2 - \tau\omega} = 0 \tag{1.126}$$

(1.126) will greater than zero if

$$\frac{\left[\beta_1\left(k_3 k_4 - k_4 \vartheta_2 - \tau\omega\right) + k_4 \alpha \vartheta_3 \beta_2\right] S^* - \left(k_2 - \vartheta_1\right)\left(k_3 k_4 - k_4 \vartheta_2 - \tau\omega\right)}{k_3 k_4 - k_4 \vartheta_2 - \tau\omega} = 0$$

$$\frac{\dfrac{\left[\beta_1\left(k_3 k_4 - k_4 \vartheta_2 - \tau\omega\right) + k_4 \alpha \vartheta_3 \beta_2\right] S^*}{\left(k_2 - \vartheta_1\right)\left(k_3 k_4 - k_4 \vartheta_2 - \tau\omega\right)} - 1}{k_3 k_4 - k_4 \vartheta_2 - \tau\omega} = 0$$

$$\frac{R_0 - 1}{k_3 k_4 - k_4 \vartheta_2 - \tau\omega} = 0 \tag{1.127}$$

which resulted into an equilibrium state where each of the sub-population is greater than zero.

Therefore, the system (1.97) has two different equilibrium states, namely: the disease-free equilibrium in which all the infected compartments are zero and the endemic equilibrium in which all the compartments are greater than zero.

Linearization

Linearization of the system (1.97) at the disease-free equilibrium point $\left(E^0\right)$ gives the Jacobian matrix

$$J\left(E^0\right) = \begin{pmatrix} -k_1 & -\beta_1 S^0 & -\beta_2 S^0 & 0 & 0 \\ 0 & \vartheta_1 - k_2 + \beta_1 S^0 & \beta_2 S^0 & 0 & 0 \\ 0 & \alpha\vartheta_3 & \vartheta_2 - k_3 & \omega & 0 \\ 0 & 0 & \tau & -k_4 & 0 \\ 0 & \alpha\vartheta_4 & \gamma_1 & \gamma_2 & -k_5 \end{pmatrix} \tag{1.128}$$

Remark: Simplifying (1.118b) and (1.118c), gives

$$\left.\begin{aligned} k_2 &> \vartheta_1 \\ k_2 &> \beta_1 S \\ k_3 &> \vartheta_2 \\ k_3 k_4 &> \tau\omega \end{aligned}\right\} \qquad (1.129)$$

The Jacobian matrix (1.129) shall be used in the local stability analysis of both the disease-free and endemic equilibria.

Disease-free Equilibrium State $\left(E^0\right)$

At the disease-free equilibrium state there is absence of disease. Thus, all the infected classes will be zero and the entire population will be made up of susceptible individuals.

Proof: At the disease-free equilibrium state, let

$$\begin{pmatrix} S \\ I_u \\ I_s \\ T \\ A \end{pmatrix} = \begin{pmatrix} S^0 \\ I_u{}^0 \\ I_s{}^0 \\ T^0 \\ A^0 \end{pmatrix} \qquad (1.131)$$

Substituting (1.125) into (1.121), (1.122) and (1.123) gives

$$I_s{}^0 = T^0 = A^0 = 0 \qquad (1.132)$$

Now, substituting (1.125) and (1.132) into (1.118a) gives

$$\pi - k_1 S^0 = 0$$

$$S^0 = \frac{\pi}{k_1} \qquad (1.133)$$

Substituting the value of k_1 from (3.98) gives

$$S^0 = \frac{\pi}{(\mu + \rho\delta)} \qquad (1.134)$$

Hence, from (1.125), (1.132) and (1.134) the lemma is proved.

Basic Reproduction Number, R_T

The basic reproduction number, R_T is a measure of the number of infections produced, on average, by an infected individual in the early stages of an epidemic, when virtually all contacts are

susceptible.When $R_T < 1$, then on average, an infected individual produces less than one newly infected individual over the course of its infection period, and hence, the infection may die out in the long run. If $R_T < 1$, each infected individual produces, on average more than one new infection, the infection will be able to spread in a population, thus becoming an epidemic. A

The next generation operator approach described by Van de Driessche and Watmough (2002) is a better method used in finding R_T and it is widely accepted because it reflects the biological meaning of R_0. Using this method we obtained the basic reproduction number, R_T of the system (3.97) which is the spectral radius (ρ) of the next generation matrix, G, i.e $R_0 = \rho\left(FV^{-1}\right)$. F is the matrix of the new infection terms and V the matrix of the transition terms.

Then,

$$F = \begin{pmatrix} \beta_1 S^0 & \beta_2 S^0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \qquad (1.135)$$

and

$$V = \begin{pmatrix} k_1 - \vartheta_1 & 0 & 0 & 0 \\ -\alpha\vartheta_3 & k_3 - \vartheta_2 & -\omega & 0 \\ 0 & -\tau & k_4 & 0 \\ -\alpha\vartheta_4 & -\gamma_1 & -\gamma_2 & k_5 \end{pmatrix} \qquad (1.136)$$

In order to determine the matrix V^{-1}, we use the Gauss-Jordan elimination method as explained Kreyszig (2005) and Stroud and Booth (2003).

i.e.

$$V^{-1} = \begin{pmatrix} \frac{1}{k_2 - \vartheta_1} & 0 & 0 & 0 \\ \frac{k_4\alpha\vartheta_3}{(k_2-\vartheta_1)(k_3k_4 - k_4\vartheta_2 - \tau\omega)} & \frac{k_4}{(k_2-\vartheta_1)(k_3k_4 - k_4\vartheta_2 - \tau\omega)} & \frac{\omega}{(k_2-\vartheta_1)(k_3k_4 - k_4\vartheta_2 - \tau\omega)} & 0 \\ \frac{k_4\alpha\vartheta_3}{(k_2-\vartheta_1)(k_3k_4 - k_4\vartheta_2 - \tau\omega)} & \frac{\tau}{(k_2-\vartheta_1)(k_3k_4 - k_4\vartheta_2 - \tau\omega)} & \frac{k_3 - \vartheta_2}{(k_2-\vartheta_1)(k_3k_4 - k_4\vartheta_2 - \tau\omega)} & 0 \\ M_1 & \frac{k_4\gamma_1 + \gamma_2\tau}{k_5(k_2-\vartheta_1)(k_3k_4 - k_4\vartheta_2 - \tau\omega)} & \frac{\gamma_1\omega + \gamma_2(k_3 - \vartheta_2)}{k_5(k_2-\vartheta_1)(k_3k_4 - k_4\vartheta_2 - \tau\omega)} & \frac{1}{k_5} \end{pmatrix} \qquad (1.137)$$

where

$$M_1 = \frac{\alpha\left(k_4\vartheta_2\vartheta_4 + \vartheta_4\tau\omega - k_3k_4\vartheta_4 - k_4\vartheta_3\gamma_1 + \gamma_2\tau\vartheta_3\right)}{k_5\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)} \tag{1.138}$$

$$FV^{-1} = \begin{pmatrix} M_2 & \dfrac{k_4\beta_2 S^0}{\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)} & \dfrac{\omega\beta_2 S^0}{\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{1.139}$$

where

$$M_2 = \frac{\beta_1 S^0\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right) + k_4\alpha\vartheta_3\beta_2 S^0}{\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)} \tag{1.140}$$

$$\left|FV^{-1} - \lambda I\right| = \begin{vmatrix} M_2 - \lambda & \dfrac{k_4\beta_2 S^0}{\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)} & \dfrac{\omega\beta_2 S^0}{\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)} & 0 \\ 0 & -\lambda & 0 & 0 \\ 0 & 0 & -\lambda & 0 \\ 0 & 0 & 0 & -\lambda \end{vmatrix} = 0 \tag{1.141}$$

$$R_0 = \frac{\left[\beta_1\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right) + k_4\alpha\vartheta_3\beta_2\right]S^0}{\left(k_2 - \vartheta_1\right)\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)} \tag{1.142}$$

Local Stability of Disease-Free Equilibrium State $\left(E^0\right)$

Theorem: The disease-free equilibrium, E^0 of (1.97) is locally asymptotically stable (LAS) if $R_T < 1$.

Proof: We used the Jacobian stability technique to determine the local stability of the system.

Using elementary row-transformation on (1.128), we have

$$J\left(E^0\right) = \begin{pmatrix} -k_1 & -\beta_1 S^0 & -\beta_2 S^0 & 0 & 0 \\ 0 & -\left(k_2 - \beta_1 S^0\right) & \beta_2 S^0 & 0 & 0 \\ 0 & 0 & M_3 & \omega & 0 \\ 0 & 0 & 0 & M_4 & 0 \\ 0 & 0 & 0 & 0 & -k_5 \end{pmatrix} \tag{1.143}$$

where

$$M_3 = -\frac{\left(k_3 - \vartheta_2\right)\left(k_2 - \vartheta_1 - \beta_1 S^0\right) + \alpha\vartheta_3\beta_2 S^0}{k_2 - \left(\vartheta_1 + \beta_1 S^0\right)} \tag{1.144}$$

$$M_4 = \frac{\left[\beta_1\left(k_2-\vartheta_1\right)\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)+k_4\alpha\vartheta_3\beta_2\right]S^0-\left(k_2-\vartheta_1\right)\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)}{\left(\vartheta_2-k_3\right)\left(k_2-\vartheta_1-\beta_1S^0\right)+\alpha\vartheta_3\beta_2S^0} \quad (1.145)$$

Thus, the characteristics equation of the row-transformed Jacobian matrix, (1.143) is given by $\left|J\left(E^0\right)-\lambda I\right|=0$

$$\begin{vmatrix} -k_1-\lambda & -\beta_1S^0 & -\beta_2S^0 & 0 & 0 \\ 0 & -\left(k_2-\beta_1S^0\right)-\lambda & \beta_2S^0 & 0 & 0 \\ 0 & 0 & M_3-\lambda & \omega & 0 \\ 0 & 0 & 0 & M_4-\lambda & 0 \\ 0 & 0 & 0 & 0 & -k_5-\lambda \end{vmatrix} = 0 \quad (1.146)$$

The eigenvalues are

$$\lambda_1 = -k_1 \quad (1.147)$$

$$\lambda_2 = -\left(k_2-\beta_1S^0\right) \text{ from (1.129)} \quad (1.148)$$

$$\lambda_3 = M_3 < 0 \quad \text{from (1.129)} \quad (1.149)$$

$$\lambda_4 = M_4 \quad (1.150)$$

$$\lambda_5 = -k_5 \quad (1.151)$$

For λ_4 to be negative, then

$$M_4 = \frac{\left[\beta_1\left(k_2-\vartheta_1\right)\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)+k_4\alpha\vartheta_3\beta_2\right]S^0-\left(k_2-\vartheta_1\right)\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)}{\left(\vartheta_2-k_3\right)\left(k_2-\vartheta_1-\beta_1S^0\right)+\alpha\vartheta_3\beta_2S^0}$$

$$\frac{\dfrac{\left[\beta_1\left(k_2-\vartheta_1\right)\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)+k_4\alpha\vartheta_3\beta_2\right]S^0}{\left(k_2-\vartheta_1\right)\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)}-1}{\left(k_3-\vartheta_2\right)\left(k_2-\vartheta_1-\beta_1S^0\right)+\alpha\vartheta_3\beta_2S^0}$$

$$\frac{R_0-1}{\left(k_3-\vartheta_2\right)\left(k_2-\vartheta_1-\beta_1S^0\right)+\alpha\vartheta_3\beta_2S^0} \quad (3.152)$$

Hence, R_0 must be less than 1 i.e $R_0<1$

This implies that $\lambda_4<0$ when $R_T<1$. Hence, the disease-free equilibrium, E^0 of system (1.97) is locally asymptotically stable (LAS) when $R_T<1$. The epidemiological implication of the theorem is that disease can be controlled in the population when $R_T<1$, if the initial size of the sub-populations of the model are in the basin of attraction of the disease-free equilibrium.

Global Stability of Disease-Free Equilibrium $\left(E^0\right)$

Global stability of equilibrium removes the restrictions on the initial conditions of the model variables. In global asymptotic stability, solutions approach the equilibrium for all initial conditions. There are many ways of proving the global stability of disease-free equilibrium which include among others the Lyapunov theorem and the Castillo-Chavez (2002) global stability theorem. We used the later in this work.

Theorem: The disease-free equilibrium, E^0 of system (1.97) is globally asymptotically stable (GAS)if $R_T < 1.$

Proof: To establish the global stability of the disease-free equilibrium, the two conditions (H1) and (H2) as in Castillo-Chavez *et al.* (2002) must be satisfied for $R_T < 1$. The model system (3.97) can be written in the form

$$X_1'(t) = F\left(X_1, X_2\right) \tag{1.153}$$

$$X_2{}'(t) = G\left(X_1, X_2\right);\ G\left(X_1, 0\right) = 0 \tag{1.154}$$

where

$$\left.\begin{aligned} X_1 &= \left(S^0\right) \\ X_2 &= \left(I_u{}^0, I_s{}^0, T^0, A^0\right) \end{aligned}\right\} \tag{1.155}$$

with the components of $X_1 \in \square^1$ denoting the uninfected individuals and the components of $X_2 \in \square^4$ denoting the infected individuals.

The disease-free equilibrium is now denoted as

$$E^0 = \left(X_1^*, 0\right) \tag{1.156}$$

where

$$X_1^* = \left(S^0\right) \tag{1.157}$$

Now, to proof that the first condition, $(H1)$ for $X_1'(t) = F(X_1^*, 0)$ is true, i.e X_1^* is a globally asymptotically stable.

We have linear differential equations as thus

$$X_1'(t) = F(X_1, 0) = \left(\pi - k_1 S^0\right) \tag{1.158}$$

Solving, gives

$$S^0\left(t\right) = \frac{\pi}{k_1} - \frac{\pi}{k_1} e^{-k_1 t} + S^0\left(0\right) e^{-k_1 t} \tag{1.159}$$

Now, clearly from (3.130), we have that $I_u{}^0(t)+I_s{}^0(t)+T^0(t)+A^0(t)\to S^0(t)$ as $t\to\infty$ regardless of the value of $S^0(0)$. Thus, $X_1^*=(S^0,0)$ is globally asymptotically stable.

Next, to prove that the second condition $(H2)$ is true,

that is

$$\hat{G}(X_1,X_2)=AX_2-G(X_1,X_2) \tag{1.160}$$

We have

$$A=\begin{pmatrix}\vartheta_1-k_2+\beta_1S^0 & \beta_2S^0 & 0 & 0\\ \alpha\vartheta_3 & \vartheta_2-k_3 & \omega & 0\\ 0 & \tau & -k_4 & 0\\ \alpha\vartheta_4 & \gamma_1 & \gamma_2 & -k_5\end{pmatrix} \tag{1.161}$$

Since form (3.129), then $k_2>\vartheta_1+\beta_1S^0$ and $k_3>\vartheta_2$, it is clear that matrix A is an M-matrix.

$$G(X_1,X_2)=\begin{pmatrix}\vartheta_1I_u{}^0+\left(\beta_1I_u{}^0+\beta_2I_s{}^0\right)S^0-k_2I_u{}^0\\ \vartheta_2I_s{}^0+\alpha\vartheta_3I_u{}^0+\omega T^0-k_3I_s{}^0\\ \tau I_s{}^0-k_4T^0\\ \alpha\vartheta_4I_u{}^0+\gamma_1I_s{}^0+\gamma_2T^0-k_5A^0\end{pmatrix} \tag{1.162}$$

Substituting (3.161) and (3.262) into (3.160), we have

$$\hat{G}(X_1,X_2)=\begin{pmatrix}0&0&0&0\\0&0&0&0\\0&0&0&0\\0&0&0&0\end{pmatrix} \tag{1.163}$$

It is thus obvious that $\hat{G}(X_1,X_2)=0$. Hence, the proof is complete.

Endemic Equilibrium State (E^{**})

The endemic equilibrium state is the state in which the disease is persistent. That is the coordinates should satisfy the conditions:

$$E^{**}=\left\{\begin{pmatrix}S\\I_u\\I_s\\T\\A\end{pmatrix}\in R_+^5\middle|\begin{matrix}S\geq 0,\\I_u\geq 0,\\I_s\geq 0,\\T\geq 0,\\A\geq 0,\end{matrix}\right\} \tag{1.164}$$

At the endemic equilibrium state, let

$$\begin{pmatrix}S\\I_u\\I_s\\T\\A\end{pmatrix}=\begin{pmatrix}S^{**}\\I_u^{**}\\I_s^{**}\\T^{**}\\A^{**}\end{pmatrix} \tag{1.165}$$

From (1.126)

$$S^{**}=\frac{\left(k_2-\vartheta_1\right)\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)}{\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)\beta_1+k_4\alpha\vartheta_3\beta_2} \tag{1.166}$$

Adding (1.118a) and (1.118b) gives

$$I_u^{**}=\frac{k_1S^{**}}{\pi+\left(\vartheta_1-k_2\right)} \tag{1.167}$$

Substituting (1.166) into (1.167) gives

$$I_u^{**}=\frac{k_1\left(k_2-\vartheta_1\right)\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)}{\left[\pi+\left(\vartheta_1-k_2\right)\right]\left[\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)\beta_1+k_4\alpha\vartheta_3\beta_2\right]} \tag{1.168}$$

Substituting (1.168) into (1.121) gives

$$I_s^{**}=\frac{k_1k_4\alpha\vartheta_3\left(k_2-\vartheta_1\right)}{\left[\pi+\left(\vartheta_1-k_2\right)\right]\left[\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)\beta_1+k_4\alpha\vartheta_3\beta_2\right]} \tag{1.169}$$

Substituting (1.168) into (1.122) gives

$$T^{**}=\frac{k_1k_4\tau\alpha\vartheta_3\left(k_2-\vartheta_1\right)}{\left[\pi+\left(\vartheta_1-k_2\right)\right]\left[\left(k_3k_4-k_4\vartheta_2-\tau\omega\right)\beta_1+k_4\alpha\vartheta_3\beta_2\right]} \tag{1.170}$$

Substituting (1.168) into (1.123) gives

$$A^{**} = \frac{k_1\left(k_2 - \vartheta_1\right)\left[\alpha\vartheta_4\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right) + k_4\gamma_1\alpha\vartheta_3 + k_4\gamma_2\tau\alpha\vartheta_3\right]}{k_5\left[\pi + \left(\vartheta_1 - k_2\right)\right]\left[\left(k_3k_4 - k_4\vartheta_2 - \tau\omega\right)\beta_1 + k_4\alpha\vartheta_3\beta_2\right]} \qquad (1.171)$$

Local Stability of Endemic Equilibrium, E^{**}

Due to high dimension of the model, it is not always easy to use standard linearization around the endemic equilibrium. Hence, the centre manifold theory (Carr 1981) as described in Theorem 4.1 Castillo-Chavez and Song (2004) for local stability analysis is used. In order to apply the theorem, we make the following change of variables.

Theorem 4: The positive endemic equilibrium state of the system (1.97) is locally asymptotically stable (LAS) when $R_T > 1$ but close to 1.

The epidemiological implication of Theorem 4 is that disease will continue to persist in the population when $R_T > 1$and the initial size of the sub-populations of the model are in the basin of attraction of the endemic state.

CONCLUSION

The dynamic of HIV/AIDS epidemic are multiple and are shaped by unaware infective and aware infective who still spread the diseases. Therefore, screening, migration and treatment are effective's instruments for fighting against the insurgence. The model has a global asymptotically stable at disease-free equilibrium whenever $R_T < 1$, also the model has a global asymptotically stable at endemic equilibrium whenever $R_T > 1$. HIV-related public health education programs should be encouraged with the aim of emphasizing on the model of transmission, prevention and control measures of the disease for development of Nigerian economy.

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