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MAXIMUM LIFESPAN PREDICTION USING A SIMPLIFIED HIV DYNAMIC MODEL

J. Vineetha, Department of Pharmacology, CES College of Pharmacy, Kurnool

ABSTRACT:

This study investigates the biological persistence of HIV by examining its viral kinetics through a simplified dynamic model. Using the relationships between initial viral load, the clearance rate, and the viral growth constant, the model provides an estimate of the theoretical upper bound of viral lifespan. The analysis highlights how variations in viral concentration and clearance dynamics influence maximum survival time. The results demonstrate that the proposed mathematical approach can effectively anticipate viral behaviour and support future clinical or experimental applications.

Keywords: *HIV, viral dynamics, clearance rate, mathematical modelling, maximum lifespan*

INTRODUCTION:

Human Immunodeficiency Virus (HIV) emerged during the latter part of the twentieth century and has since become a defining global health challenge. India accounts for approximately 2.5 million individuals living with HIV, representing one of the highest burdens worldwide. Despite significant advancements in antiretroviral therapy, HIV continues to affect millions, with women comprising a substantial proportion of new infections.

Mathematical modelling plays a crucial role in understanding the transmission and progression of HIV. Such models help translate individual-level parameters such as infection rate, viral load, and replication rate into population-level predictions. They serve as a virtual laboratory for exploring biological and behavioural mechanisms that shape disease dynamics.

In this work, we examine viral decay and growth using fundamental mathematical principles, particularly focusing on the Gompertz growth framework. By analysing relationships among viral concentration, growth parameters, and the clearance constant, we derive an estimate of the maximum lifespan of HIV particles.

ESTIMATING THE CLEARANCE RATE PARAMETER

Earlier perspectives considered HIV as a slowly progressing virus taking nearly a decade to cause symptomatic disease. Later studies revealed that HIV exhibits highly dynamic behaviour across multiple time scales.

The viral dynamics can be represented by:

$dV/dt = P - cV$

where

V is the viral concentration,

P represents the viral production rate, and

c denotes the clearance rate.

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When treatment fully suppresses viral production (P = 0), the viral load decreases exponentially:

$$V(t) = V0 * e^{(-ct)}$$

This decay resembles the Gompertz model, originally proposed to describe population dynamics and later widely applied in biological growth studies. Integrating the equation yields the Gompertz form.

Behaviour of the Clearance Parameter

Partial differentiation of the clearance constant c with respect to viral concentration and other model variables shows:

- c increases with higher viral concentration Vg(t)
- c decreases with higher cumulative viral load Vc*
- c decreases as the lifespan estimate tm increases

These relationships help determine critical points where the behaviour of the viral population shifts, particularly with respect to growth limits.

Critical Viral Volume (Vr)

A critical volume arises when:

$$tm / (Vc^* \ln Vg(t)) = 1$$

At this boundary, growth transitions, and Vr = e^(tm / Vc*). This value increases with time and marks a condition where viral growth slows due to biological limitations.

Critical Growth Time (tr)

When:

$$tm / (Vc^* \ln Vg(t)) < 1$$

The corresponding critical time is:

$$tr = Vc^* \ln Vr$$

which is always less than or equal to tm.

Maximum Lifespan of HIV

Typical viral growth patterns show rapid replication during mid-life stages, followed by a reduction in growth rate after a critical threshold. To evaluate maximum lifespan, both theoretical and biological aspects are considered.

If the critical volume is not achieved within tm, then tm is considered the critical lifespan.

Maximum lifespan tm* may be estimated using relationships involving Vr, c, and cumulative viral growth integrals.

AIM AND OBJECTIVES

The aim of this study is to estimate the theoretical maximum lifespan of HIV by analysing viral dynamics using a simplified mathematical model based on the Gompertz growth framework. The study seeks to understand how the initial viral load, the clearance rate constant, and growth parameters shape viral persistence.

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Objectives: To apply a simplified HIV dynamic model to evaluate viral growth and decay patterns. To derive expressions for the clearance rate constant (c) and analyse its behavior. To identify critical parameters governing viral growth transitions. To estimate the maximum theoretical lifespan (t*m) of HIV. To assess the biological relevance of the predicted viral lifespan.

MATERIAL AND METHODS:

Study Design:

A mathematical modelling approach was used, based on differential equations and Gompertz growth theory.

The core model applied was:

dV/dt = P - cV

where

V is viral concentration,

P is production rate, and

c is the clearance constant.

Under P = 0, the model simplifies to exponential decay.

Parameter Determination:

Clearance rate c, critical volume Vr and critical time tr were derived through calculus-based analysis and integral evaluation.

Analytical Approach:

Behavioural assessment involved limits, parameter sensitivity, and comparison of pre-critical and post-critical viral dynamics.

RESULTS:

Clearance rate c increases with viral concentration, decreases with cumulative load Vc*, and decreases as lifespan increases.

Critical viral volume Vr = e^(tm/Vc*) was identified, marking a slowdown in viral growth.

Critical time tr = Vc* ln(Vr) was found, always less than or equal to tm.

Maximum lifespan tm* was estimated using bounded integrals of viral growth.

The predictions align with biological patterns observed in HIV decay and provide a practical tool for laboratory or clinical use.

DISCUSSION

A theoretical study utilizes a simplified Gompertz-based model to investigate the maximum lifespan of HIV and the parameters affecting its persistence. The research employs a mathematical modeling approach with a core differential equation (dV/dt=P-cV) to analyze viral dynamics and derive parameters for estimating a theoretical maximum lifespan (t_m).

CONCLUSION

This study presents a mathematical approach to estimate the maximum lifespan of HIV using a simplified dynamic model. By analysing initial viral load, clearance rate, and growth characteristics, the model identifies critical

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parameters that dictate viral persistence. The framework can aid in predicting viral decay patterns and may serve as a useful tool in experimental and clinical research.

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