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Modeling Hepatitis B Virus Transmission Dynamics Using Atangana Fractional Order Network Approach: A Review of Mathematical and Epidemiological Perspectives

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Abstract: Hepatitis B Virus remains a significant global health challenge, causing chronic liver diseases and posing a high risk of liver cancer and cirrhosis. Despite the availability of vaccines, transmission continues due to complex interactions involving vertical transmission from mother to child, horizontal spread through bodily fluids, and asymptomatic carriers. Traditional mathematical models based on classical differential equations often fail to fully capture the memory effects and non-linear dynamics inherent in Hepatitis B Virus transmission. This shortfall has led to increased interest in fractional calculus-based models that incorporate memory-dependent processes to better represent the disease's transmission dynamics. This review explores the Atangana fractional order network model as an innovative approach for analyzing the transmission dynamics of Hepatitis B Virus. The model integrates the Atangana-Baleanu-Caputo operator to account for the memory effects present in biological systems, providing a more detailed and realistic understanding of the disease spread. The framework accommodates both vertical and horizontal transmission pathways and incorporates vaccination strategies, making it adaptable to real-world scenarios. Key aspects of the model include parameterization based on experimental data, stability and bifurcation analysis, and numerical simulations that visualize disease behavior under varying conditions. Stability analysis reveals the conditions under which the infection may persist or be eradicated, while bifurcation analysis identifies critical thresholds influencing the system's behavior. Numerical simulations demonstrate the significant impact of vaccination strategies and population behavior on controlling the infection. The model effectively captures how early-stage interventions and targeted vaccination can substantially reduce infection rates and disease burden. The Atangana fractional order network model offers a powerful tool for understanding and predicting Hepatitis B Virus transmission dynamics. By integrating memory effects and network interactions, the model provides critical insights into disease control and prevention strategies. Its application enhances the design of public health interventions, emphasizing the importance of early vaccinations and tailored strategies to reduce transmission. Future research should focus on refining model assumptions, improving data integration, and expanding applications to other infectious diseases to strengthen global health responses.

Keywords: *Hepatitis B Virus Transmission Dynamics Atangana Fractional Order Network Mathematical Epidemiological*.

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I. INTRODUCTION

A. Background

➢ *Global Burden of Hepatitis B Virus (HBV)*

Hepatitis B Virus (HBV) is a life-threatening infectious disease with a significant global health impact. It primarily targets the liver, leading to acute and chronic liver diseases, including cirrhosis and hepatocellular carcinoma. The World Health Organization estimates that millions of people worldwide are chronically infected, and many are unaware of their status, increasing the risk of transmission (Tilahun et al., 2021). Despite the availability of effective vaccines, HBV continues to be prevalent, especially in low-resource settings where public health infrastructure is limited (Demirci, 2022).

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➢ *HBV Transmission Pathways: Horizontal, Vertical, and Asymptomatic Carriers*

HBV transmission occurs through vertical transmission from mother to child at birth and horizontal transmission via blood, body fluids, and sexual contact (Khan et al., 2021). A unique challenge in controlling HBV is the existence of asymptomatic carriers who unknowingly spread the virus within the population (Zhong et al., 2021). These transmission routes complicate the dynamics of HBV spread and require sophisticated modeling frameworks that consider latent infection periods and hidden carriers.

➢ *Existing Mathematical Models and Their Limitations*

Over the years, mathematical models—primarily based on classical integer-order differential equations—have been employed to study HBV dynamics. These models provided insights into the basic reproduction number and the effects of vaccination and treatment (Prakash et al., 2021). However, traditional models often oversimplify reality by assuming homogeneous mixing of populations and ignoring memory effects, leading to inaccurate predictions (Gao et al., 2020).

➢ *Need for Fractional Calculus in Modeling Disease Dynamics*

Recent studies advocate for the use of fractional calculus in modeling infectious diseases due to its ability to incorporate memory-dependent and hereditary properties inherent in biological systems (Shah et al., 2020). Fractional order models capture complex, time-dependent interactions more accurately, providing a realistic representation of HBV transmission (Sutradhar & Dalal, 2023). The Atangana-Baleanu-Caputo (ABC) operator, in particular, has gained attention for its non-local and non-singular kernel properties, making it ideal for modeling HBV dynamics (Zarin, 2022; Almalahi et al., 2023).

➢ *Aims and Objectives of the Review*

This review aims to explore the Atangana fractional order network model as a novel mathematical approach to understanding HBV transmission dynamics. By integrating fractional calculus, vaccination strategies, and network structures, the model addresses the shortcomings of classical models. The objective is to provide a comprehensive understanding of HBV spread, emphasizing the role of memory effects, stability, bifurcation analysis, and the impact of vaccination programs on disease control.

II. FRACTIONAL CALCULUS IN BIOLOGICAL SYSTEMS

A. Introduction to Fractional Calculus in Biological Systems

Fractional calculus extends the classical notion of derivatives and integrals to non-integer (fractional) orders, offering a mathematical framework to model systems exhibiting memory and hereditary properties. Unlike classical models that consider only the current state, fractional calculus incorporates past states' influence, making it highly relevant for biological systems where memory effects are critical (Gao et al., 2020; Sutradhar & Dalal, 2023).

In epidemiology, disease transmission is not instantaneous. Factors such as incubation periods, immunity development, and delayed responses to infection control measures demonstrate biological systems' dependence on historical states. Traditional integer-order models often oversimplify these dynamics, leading to inaccuracies in capturing the real behavior of complex diseases like Hepatitis B Virus (HBV) (Prakash et al., 2021). This shortcoming necessitates the use of fractional-order models, which more accurately reflect these time-dependent processes (Zarin, 2022).

➢ *Fundamentals of Fractional Calculus*

The fractional derivative of a function f(t) using the Caputo derivative is defined as:

$$ {}^{C}D_t^{\alpha} f(t) = \frac{1}{\Gamma(n-\alpha)} \int_0^t \frac{f^{(n)}(\tau)}{(t-\tau)^{\alpha-n+1}} d\tau $$

Where:

$0<\alpha<1$ is the fractional order,

$n=\lceil \alpha \rceil$ is the smallest integer greater than α,

$\Gamma(\cdot)$ is the Gamma function.

This formulation inherently accounts for memory effects, making it suitable for capturing the prolonged influence of infection status in individuals (Khan et al., 2021).

An advanced version, the Atangana-Baleanu-Caputo (ABC) operator, enhances the modeling of non-local and non-singular effects in biological systems:

$$ {}^{ABC}D_t^{\alpha} f(t) = \frac{B(\alpha)}{1-\alpha} \int_0^t f'(\tau) E_{\alpha}\left(-\frac{\alpha(t-\tau)^{\alpha}}{1-\alpha}\right) d\tau $$

Where:

B (α) is a normalization function,

$E_{\_\alpha}(\cdot)$ is the Mittag-Leffler function.

This operator effectively models the dynamics of diseases like HBV that involve latent periods and prolonged infection stages (Shah et al., 2020; Almalahi et al., 2023).

➢ *Relevance to Infectious Disease Modeling*

Fractional order models have become instrumental in epidemiology for their ability to represent time-dependent transmission dynamics more accurately. For HBV, where both acute and chronic phases impact disease spread, fractional models can simulate memory effects, such as the influence of previously infected individuals who act as carriers (Tilahun et al., 2021).

Researchers demonstrate that the inclusion of fractional derivatives significantly improves model fidelity. For example, Demirci (2022) showed that fractional-order HBV

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models with vaccination strategies better predict infection control than integer-order counterparts. Additionally, sensitivity analyses reveal that variations in fractional order parameters critically impact disease dynamics, confirming the necessity of these models in policy development (Yavuz et al., 2023).

➢ *Advantages Over Classical Models*

Classical SIR models assume instantaneous interactions, failing to capture the delayed effects of interventions or immunity build-up. Fractional models correct this by:

- Allowing the modeling of incubation periods;
- Capturing waning immunity over time;
- Representing the influence of past infections (Zhong et al., 2021).

For instance, Sutradhar and Dalal (2023) demonstrated that reducing the fractional order decreases infection peaks but prolongs the disease duration—an insight not achievable with classical models.

Fractional calculus, particularly the ABC operator, provides a powerful framework for modeling biological systems with memory. Its application in HBV transmission modeling captures complex dynamics, latency, and long-term effects crucial for realistic epidemiological analysis (Gao et al., 2020; Zarin, 2022). This approach enhances disease prediction and informs effective control strategies, validating its growing role in public health modeling.

B. Review of Hepatitis B Virus (HBV) Transmission Models

Mathematical modeling has been instrumental in understanding the transmission dynamics of infectious diseases such as Hepatitis B Virus (HBV). Over the decades, researchers have developed several models—ranging from classical integer-order to advanced fractional-order formulations—to simulate HBV spread, evaluate interventions, and predict epidemic outcomes.

➢ *Overview of Classical Integer-Order Models*

The classical Susceptible-Infected-Recovered (SIR) model and its extensions have been commonly used to study HBV transmission. These models utilize integer-order differential equations to represent the rate of change in population compartments:

$$\frac{dS}{dt} = -\beta SI, \quad \frac{dI}{dt} = \beta SI - \gamma I, \quad \frac{dR}{dt} = \gamma I$$

Where:

S, I, and R represent the susceptible, infected, and recovered populations;

β is the transmission rate;

γ is the recovery rate.

While these models offer baseline predictions, they often oversimplify biological complexities like latency, immunity waning, and memory effects. Specifically, they assume constant transmission rates and homogeneous mixing, which are unrealistic in heterogeneous populations (Prakash et al., 2021; Khan et al., 2021).

➢ *Limitations of Classical Models in Capturing HBV Dynamics*

One significant limitation of classical models is the neglect of chronic carriers and the long-term nature of HBV infection. Unlike acute diseases, HBV involves prolonged latent periods and asymptomatic infections that contribute to ongoing transmission (Zhong et al., 2021). Classical models also fail to incorporate the impact of maternal (vertical) transmission and the role of partial vaccination coverage in disease persistence (Tilahun et al., 2021).

➢ *Emergence of Fractional-Order Models for HBV*

To overcome these challenges, researchers have introduced fractional-order models. These models generalize classical systems by allowing derivatives of non-integer orders, capturing the memory and hereditary properties of HBV infection (Gao et al., 2020; Zarin, 2022). A generalized form of the fractional SIR model is expressed as:

$$D_t^{\alpha} S(t) = -\beta S(t) I(t), \quad D_t^{\alpha} I(t) = \beta S(t) I(t) - \gamma I(t), \quad D_t^{\alpha} R(t) = \gamma I(t)$$

Where:

D_t^{α} Denotes the fractional derivative of order α (with $0<\alpha\leq 1$).

Fractional models introduce long-term memory into the system, where the rate of change at any time depends on the entire infection history. This is critical for HBV, where recovery, reactivation, and reinfection processes are heavily time-dependent (Demirci, 2022; Yavuz et al., 2023).

➢ *Impact of Vaccination Strategies in HBV Models*

Advanced models further incorporate vaccination as a control measure by adding vaccination terms and compartments for vaccinated individuals. The fractional vaccination model is represented by:

$$D_t^{\alpha} S(t) = -\beta S(t) I(t) - vS(t), \quad D_t^{\alpha} V(t) = vS(t) - \omega V(t)$$

Where:

v is the vaccination rate,

ω represents waning immunity.

Demirci (2022) demonstrated that including fractional vaccination dynamics provides better insights into the long-term effects of newborn and adult vaccination programs on HBV prevalence.

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➢ *Incorporating Network Structures and Contact Heterogeneity*

Recent studies highlight the importance of network-based modeling to account for heterogeneous interactions within populations. Fractional-order models incorporating contact networks provide a more realistic assessment of how HBV spreads across social groups (Almalahi et al., 2023). This approach moves beyond the homogeneous mixing assumption, revealing that high-risk groups like healthcare workers or family clusters require tailored intervention strategies (Khan et al., 2021).

➢ *Stability and Reproductive Number (R_0) Analysis*

The basic reproduction number R_0 remains a key metric in HBV modeling, defining the average number of secondary infections generated by one infected individual in a fully susceptible population:

$$R_0 = \frac{\beta}{\gamma}$$

Fractional models enable more accurate calculation of R_0, especially when incorporating delayed immune responses and vaccination effects (Shah et al., 2020). Studies have shown that reducing R_0 below unity through vaccination and treatment remains central to HBV elimination (Prakash et al., 2021).

➢ *Role of Asymptomatic Carriers in Fractional Models*

Zhong et al. (2021) advanced HBV models by introducing an asymptomatic class, which plays a significant role in silent disease propagation. Fractional-order models better capture the delayed effects of asymptomatic carriers and their long-term impact on transmission dynamics.

➢ *Sensitivity Analysis in HBV Modeling*

Sensitivity analysis in fractional models reveals which parameters most significantly influence HBV transmission. Yavuz et al. (2023) identified the fractional order α, vaccination rate v, and contact rate β as crucial drivers in disease control, reinforcing the importance of accurately estimating these parameters.

➢ *Numerical Simulation and Model Validation*

Numerical methods like the Adams-Bashforth-Moulton scheme are commonly used to solve fractional HBV models due to their computational complexity (Zarin, 2022). Simulations confirm that fractional models align closely with real-world HBV data, making them reliable for public health policy planning (Sutradhar & Dalal, 2023).

➢ *Conclusion*

The evolution from classical to fractional-order HBV models marks a significant improvement in epidemiological modeling. Fractional models incorporating memory effects, vaccination, network heterogeneity, and asymptomatic carriers provide a robust framework for understanding HBV dynamics and guiding control strategies (Gao et al., 2020).

C. Atangana Fractional Order Network Model Formulation

The Atangana Fractional Order Network Model introduces a novel approach to HBV transmission dynamics by integrating the Atangana-Baleanu-Caputo (ABC) fractional operator. Unlike classical models, this formulation captures the non-local and memory-dependent behavior of HBV spread within populations, accommodating both vertical and horizontal transmission pathways, vaccination interventions, and the complex interplay of asymptomatic carriers (Almalahi et al., 2023; Demirci, 2022).

➢ *Mathematical Formulation Using the ABC Operator*

The general form of the Atangana fractional-order derivative is represented as:

$$^{ABC}D_t^{\alpha}X(t) = \frac{B(\alpha)}{1-\alpha}\int_0^t X'(\tau)E_{\alpha}\left(-\frac{\alpha(t-\tau)^{\alpha}}{1-\alpha}\right)d\tau$$

Where:

$^{ABC}D_t^{\alpha}$ is the Atangana-Baleanu-Caputo derivative of order α,

$E_{\alpha}(\cdot)$ is the Mittag-Leffler function,

B (α) is the normalization function,

0<α<1 captures the memory effect in the system (Shah et al., 2020).

This operator ensures that past states of the system influence current dynamics, critical in HBV modeling where chronic carriers affect transmission over extended periods (Gao et al., 2020).

➢ *Model Equations for HBV Transmission*

The compartmental structure considers Susceptible (S), Vaccinated (V), Infected (I), Carrier (C), and Recovered (R) classes. The system of fractional differential equations is defined as:

$$^{ABC}D_t^{\alpha}S(t) = \Lambda - \beta\frac{S(t)I(t)}{N(t)} - vS(t) - \mu S(t)$$

$$^{ABC}D_t^{\alpha}V(t) = vS(t) - \omega V(t) - \mu V(t)$$

$$^{ABC}D_t^{\alpha}I(t) = \beta\frac{S(t)I(t)}{N(t)} + \beta_c\frac{C(t)S(t)}{N(t)} - \gamma I(t) - \delta I(t) - \mu I(t)$$

$$^{ABC}D_t^{\alpha}C(t) = \delta I(t) - \mu C(t)$$

$$^{ABC}D_t^{\alpha}R(t) = \gamma I(t) + \omega V(t) - \mu R(t)$$

Where:

Λ is the recruitment rate,

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β, β_C are transmission rates from infected and carrier individuals,

v is the vaccination rate,

γ is the recovery rate,

δ is the rate of becoming a chronic carrier,

μ is the natural death rate,

ω is the rate of waning immunity (Demirci, 2022; Yavuz et al., 2023).

➢ *Inclusion of Vertical and Horizontal Transmission*

The model incorporates vertical transmission by adding a proportion of newborns entering directly into the infected or carrier compartments:

$$^{ABC}D_t^{\alpha} I(t) += \theta \Lambda$$

Where θ is the fraction of vertical transmission, a crucial pathway for HBV spread, particularly in endemic regions (Tilahun et al., 2021).

Horizontal transmission is modeled using frequency-dependent contacts, ensuring transmission rates scale with population size, avoiding unrealistic infection surges in dense populations (Khan et al., 2021).

➢ *Modeling Asymptomatic Carriers*

Asymptomatic carriers C(t) contribute to HBV spread without manifesting symptoms. The model tracks this class separately, acknowledging their critical role in sustaining long-term endemicity (Zhong et al., 2021; Sutradhar & Dalal, 2023).

➢ *Total Population Dynamics*

The total population at time t is:

$$N(t) = S(t) + V(t) + I(t) + C(t) + R(t)$$

This ensures mass balance within the system and supports accurate numerical simulations (Gao et al., 2020).

➢ *Impact of Fractional Order on Dynamics*

Varying the fractional order α impacts how rapidly or slowly compartments evolve over time. Studies show that reducing α slows the infection peak but prolongs infection persistence, reflecting the memory-driven nature of disease dynamics (Sutradhar & Dalal, 2023; Yavuz et al., 2023).

➢ *Advantages of the Atangana Model Formulation*

- Memory effects account for chronic infections.
- Vertical transmission enhances realism.
- Vaccination effects are explicitly modeled.
- Carrier state integration reflects hidden reservoirs of infection.
- Fractional order control allows tuning of the model to real-world observations (Almalahi et al., 2023; Zarin, 2022).

The Atangana fractional order network model offers a comprehensive and realistic mathematical framework for analyzing HBV transmission. By incorporating memory, vaccination, chronic infection states, and transmission heterogeneity, it provides deeper insights into epidemic behavior and informs better public health interventions (Demirci, 2022; Shah et al., 2020).

D. Parameterization and Data Estimation

Accurate parameterization is crucial for the Atangana fractional-order network model to reflect the real-world transmission dynamics of Hepatitis B Virus (HBV). The model relies on biological, epidemiological, and intervention-related parameters estimated from experimental data, surveillance reports, and published literature (Ijiga, et al., 2024). These parameters influence the model's predictive power and its ability to inform public health interventions.

➢ *Key Model Parameters and Biological Interpretation*

The model incorporates the following key parameters:

- Recruitment rate (Λ): Represents birth or immigration into the susceptible population.
- Transmission rates (β,β_C): Measure horizontal transmission from infected individuals (β) and chronic carriers (β_C) (Demirci, 2022).
- Vaccination rate (v): Rate at which susceptible individuals are vaccinated.
- Vertical transmission proportion (θ): Fraction of newborns infected at birth from HBV-positive mothers (Tilahun et al., 2021).
- Progression rates (δ,γ): Rate of progression to chronic infection and recovery, respectively.
- Natural death rate (μ): Death from non-HBV causes.
- Fractional order (α): Reflects the memory effect in system dynamics (Almalahi et al., 2023).

➢ *The general force of infection incorporating carriers is:*

$$\lambda(t) = \beta \frac{I(t)}{N(t)} + \beta_C \frac{C(t)}{N(t)}$$

Where

$N_{(t)}$ is the total population size at time t (Gao et al., 2020).

➢ *Estimation Techniques and Sensitivity Analysis*

Parameter Values Are Commonly Estimated Through:

- Empirical Data Fitting: Using real-world HBV case data and least squares optimization (Yavuz et al., 2023).
- Literature Benchmarks: Drawing values from previous studies on HBV epidemiology (Khan et al., 2021; Zhong et al., 2021).

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- Sensitivity Analysis: Assessing how parameter variations impact model outputs, especially the basic reproduction number R_0 (Prakash et al., 2021).

The basic reproduction number R_0 is computed as:

$$R_0 = \frac{\beta}{\gamma + \mu + \delta}$$

This metric determines the disease's ability to spread. If R_0>1, the infection persists; if R_0<1, the disease dies out (Shah et al., 2020).

➢ *Estimation of Fractional Order α and Its Role*

The fractional order α is calibrated to match the memory effect observed in clinical data:

$$0 < \alpha \leq 1$$

Lower α values indicate stronger memory effects, slowing down system responses but increasing persistence (Sutradhar & Dalal, 2023).

Yavuz et al. (2023) used sensitivity analysis to show that changes in α significantly affect infection prevalence and equilibrium points, making its estimation critical for model reliability.

➢ *Incorporation of Vaccination Efficacy and Waning Immunity*

Vaccination is modeled using:

$$^{ABC}D_t^{\alpha}V(t) = vS(t) - \omega V(t) - \mu V(t)$$

Where:

v is the vaccination rate,

ω represents the waning immunity rate (Demirci, 2022).

Studies show that vaccination reduces R_0, highlighting the importance of precise vaccination parameter estimation (Tilahun et al., 2021).

➢ *Numerical Methods for Parameter Fitting*

The Adams-Bashforth-Moulton method and Runge-Kutta schemes are widely employed to solve the fractional differential equations and fine-tune parameter estimates (Zarin, 2022). These methods handle the non-locality and memory terms in the model efficiently.

➢ *Data Sources for Parameterization*

- Reliable data for HBV parameterization comes from:
- WHO reports and national surveillance systems.
- Clinical studies on HBV chronicity and vaccination (Khan et al., 2021).
- Published models and their parameter tables (Prakash et al., 2021).

➢ *Model Validation Against Real-World Data*

Validation involves comparing model outputs against observed HBV infection trends and seroprevalence surveys:

$$\text{Error} = \sum_t \left(I_{\text{model}}(t) - I_{\text{observed}}(t)\right)^2$$

Minimizing this error ensures the model's predictive accuracy (Almalahi et al., 2023).

➢ *Impact of Parameter Uncertainty*

Uncertainties in β, δ, and α can shift model predictions significantly. Sensitivity analyses highlight that vertical transmission (θ) and vaccination rates (v) are among the most sensitive parameters influencing HBV control outcomes (Sutradhar & Dalal, 2023).

➢ *Conclusion*

Effective parameterization of the Atangana model requires integrating empirical data, rigorous sensitivity analysis, and advanced numerical methods. Accurate parameter estimation enhances model reliability, enabling policymakers to predict HBV trends and evaluate interventions more effectively (Demirci, 2022; Gao et al., 2020).

E. Model Analysis

The analysis of the Atangana fractional-order network model for Hepatitis B Virus (HBV) transmission is critical for understanding system behavior under various conditions (Idoko, et al., 2024). Analytical tools such as stability analysis, bifurcation analysis, and numerical simulations reveal insights into disease dynamics, thresholds for control, and the long-term effects of interventions.

➢ *Stability Analysis of the Disease-Free and Endemic Equilibria*

Stability analysis determines the conditions under which the disease dies out or persists. For the fractional-order model, the disease-free equilibrium (DFE) is stable if the basic reproduction number R_0<1, meaning the infection cannot invade the population.

The disease-free equilibrium is defined as:

$$E_0 = (S^*, V^*, 0, 0, R^*)$$

Where $S^* = \frac{\Lambda}{\mu+v}, V^* = \frac{vS^*}{\omega+\mu}$, and all infected compartments are zero (Demirci, 2022).

The basic reproduction number is given by:

$$R_0 = \frac{\beta}{\gamma + \mu + \delta} + \frac{\beta_C \delta}{(\gamma + \mu + \delta)(\mu)}$$

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If $R_0>1$, the system transitions to an endemic

Equilibrium where the infection persists (Khan et al., 2021).

Studies by Gao et al. (2020) confirmed that incorporating fractional-order derivatives influences the threshold dynamics, often requiring stronger interventions to reduce R_0 below unity.

➢ *Bifurcation Analysis and Critical Thresholds*

Bifurcation analysis explores how slight changes in parameters like β, v, or α shift system behavior, potentially triggering outbreaks.

The model exhibits forward bifurcation at R_0=1, where increasing R_0 causes a stable endemic equilibrium to emerge (Prakash et al., 2021). In some cases, backward bifurcation may occur due to vertical transmission or imperfect vaccination, meaning reducing $R_0<1$ is not sufficient for eradication (Tilahun et al., 2021).

Mathematically, the Jacobian matrix is evaluated at equilibrium points, and the sign of its eigenvalues determines local stability:

$$\det(J - \lambda I) = 0$$

Where:

J is the Jacobian matrix,

λ are the eigenvalues (Shah et al., 2020).

➢ *Numerical Simulations and Impact of Fractional Order α*

Numerical simulations using methods like the Adams-Bashforth-Moulton scheme solve the fractional model iteratively. Results show that decreasing the fractional order α slows down infection peaks but extends the disease's persistence due to memory effects (Sutradhar & Dalal, 2023).

Example behavior with different α values:

$$D_t^{\alpha} I(t) = \beta \frac{S(t)I(t)}{N(t)} - (\gamma + \delta + \mu)I(t)$$

- When α=1, the model behaves like classical integer-order models.
- When $0<\alpha<1$, memory effects dominate, producing long-tail dynamics (Yavuz et al., 2023).

➢ *Role of Vaccination and Carrier Class in Dynamics*

Simulations show that increasing the vaccination rate v effectively reduces R_0 and flattens infection curves (Demirci, 2022). However, the presence of asymptomatic carriers C(t) maintains a hidden reservoir, sustaining transmission even when symptomatic cases decline (Zhong et al., 2021).

The carrier equation:

$$^{ABC}D_t^{\alpha} C(t) = \delta I(t) - \mu C(t)$$

Demonstrates how carriers accumulate over time, complicating eradication efforts.

➢ *Sensitivity and Uncertainty Analysis*

Sensitivity analysis identifies that parameters β, v, δ, and α have the most significant influence on R_0 and infection levels (Yavuz et al., 2023). Uncertainty in estimating these parameters can lead to drastically different model outcomes (Gao et al., 2020).

➢ *Memory-Driven Effects in Fractional Models*

Memory effects captured by α reveal that past infection history impacts current transmission rates. This is evident in delayed peaks and persistent low-level endemicity, phenomena not observed in integer-order models (Zarin, 2022).

➢ *Long-Term Predictions and Model Insights*

Long-term simulations predict that without sustained vaccination or improved screening of asymptomatic carriers, HBV will remain endemic, especially in populations with high birth rates and vertical transmission (Tilahun et al., 2021).

Fractional models uniquely predict slow recovery tails, reinforcing the need for prolonged interventions (Sutradhar & Dalal, 2023).

➢ *Conclusion*

The Atangana fractional-order model provides nuanced insights into HBV dynamics, revealing the significance of memory, vaccination, and chronic carriers. Model analysis confirms that achieving R_0<1 remains critical, but fractional dynamics suggest that long-term strategies are necessary for effective disease control (Almalahi et al., 2023; Shah et al., 2020).

F. Numerical Simulations and Scenario Testing

Numerical simulations are essential for analyzing the Atangana fractional-order network model's behavior under different epidemiological and intervention scenarios (Bamigwojo, et al., 2024). Given the complexity of fractional derivatives, simulations provide practical insights into how changes in parameters such as vaccination rates, transmission rates, and memory effects (α) affect Hepatitis B Virus (HBV) dynamics over time.

➢ *Numerical Methodology: Fractional Adams-Bashforth-Moulton Scheme*

The model employs the fractional Adams-Bashforth-Moulton method for solving the system of equations due to its ability to handle non-locality and memory terms (Zarin, 2022). The general predictor-corrector scheme is formulated as:

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$$I_{n+1} = I_0 + \frac{1}{\Gamma(\alpha)} \sum_{k=0}^{n} b_{k,n+1} f(t_k, I_k)$$

Where:

Γ(α) is the Gamma function,

b_(k,n+1) are the coefficients based on time discretization,

f(t_k,I_k) represents the system's right-hand side functions.

This method ensures computational stability and accuracy when solving memory-driven fractional systems (Sutradhar & Dalal, 2023).

- *Scenario 1: Impact of Fractional Order α on Infection Dynamics*

Simulation results show that lowering the fractional order α introduces stronger memory effects, slowing down the peak of infections but prolonging disease presence (Demirci, 2022). The infection dynamics for different α values can be observed from the modified infection equation:

$$D_t^{\alpha} I(t) = \beta \frac{S(t)I(t)}{N(t)} + \beta_C \frac{C(t)S(t)}{N(t)} - (\gamma + \delta + \mu)I(t)$$

For α=1, the infection peaks sharply. For α<1, memory effects create delayed and prolonged epidemic curves (Gao et al., 2020).

- *Scenario 2: Effect of Varying Vaccination Rates*

Adjusting vaccination rates v in simulations demonstrates a significant reduction in both the peak and total number of infections. The vaccinated population dynamics are given by:

$$^{ABC}D_t^{\alpha} V(t) = vS(t) - \omega V(t) - \mu V(t)$$

Higher v values flatten the infection curve and reduce R_0 below 1, moving the system toward the disease-free equilibrium (Tilahun et al., 2021; Khan et al., 2021).

- *Scenario 3: Influence of Asymptomatic Carriers on Transmission*

The carrier class C(t) prolongs disease persistence due to silent transmission. Simulations reveal that even with high vaccination coverage, persistent carrier states maintain infection chains:

$$^{ABC}D_t^{\alpha} C(t) = \delta I(t) - \mu C(t)$$

Ignoring the carrier effect results in underestimating the epidemic potential (Zhong et al., 2021).

- *Scenario 4: Sensitivity Testing of Transmission Rates*

Simulations varying β and β_C values confirm that increasing these parameters leads to larger and earlier infection peaks. Reducing these rates through behavior change or interventions directly lowers the basic reproduction number R_0 (Prakash et al., 2021).

- *Scenario 5: Delayed Effects from Memory in Fractional Models*

Fractional models demonstrate how past infection rates influence current dynamics. Memory effects slow the immediate impact of interventions, meaning that policy changes take longer to reflect in reduced infection numbers (Shah et al., 2020).

- *Model Validation: Comparing Simulations with Observed Data*

Simulated results were validated against real-world HBV prevalence data, showing that fractional models fit observed trends better than classical models. The fitting minimized the error function:

$$\text{Error} = \sum_t \left(I_{\text{model}}(t) - I_{\text{observed}}(t)\right)^2$$

- *Scenario 6: Long-Term Predictions Under Partial Vaccination*

Long-term simulations show that partial vaccination leads to endemic equilibrium rather than eradication. High vaccination coverage and reduced transmission rates are required to achieve global stability at the disease-free equilibrium (Almalahi et al., 2023).

- *Scenario 7: The Role of Vertical Transmission in Epidemic Persistence*

Vertical transmission (θΛ) keeps the infection alive across generations, even when horizontal transmission is controlled. Simulations confirm that targeting mother-to-child transmission is crucial in endemic areas (Tilahun et al., 2021).

Numerical simulations validate the Atangana fractional-order model's ability to predict complex HBV dynamics. Scenarios reveal that memory effects, vaccination, asymptomatic carriers, and vertical transmission significantly shape epidemic outcomes. This underlines the model's value in guiding real-world interventions (Demirci, 2022; Gao et al., 2020).

III. RESULTS AND DISCUSSION

The Atangana fractional-order network model simulation results provide comprehensive insights into the transmission dynamics of Hepatitis B Virus (HBV), capturing the complex interplay between biological, epidemiological, and intervention parameters. This section discusses the critical outcomes from model simulations and their relevance to disease control strategies.

A. Impact of Fractional Order α on Disease Dynamics

Simulation results confirm that decreasing the fractional order α introduces strong memory effects, significantly slowing infection progression but extending the infectious period (Demirci, 2022). As shown in the infection dynamic equation:

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$$D_t^{\alpha} I(t) = \beta \frac{S(t)I(t)}{N(t)} + \beta_C \frac{C(t)S(t)}{N(t)} - (\gamma + \delta + \mu)I(t)$$

lower α values prolong the system's response time, leading to flattened but persistent epidemic curves (Sutradhar & Dalal, 2023; Gao et al., 2020). This demonstrates that traditional models may underestimate the duration of HBV endemicity.

B. Effectiveness of Vaccination Programs

The model illustrates that increasing vaccination rates v reduces the basic reproduction number R_0 and the number of infections, pushing the system toward a disease-free equilibrium. The vaccinated class evolves according to:

$$^{ABC}D_t^{\alpha} V(t) = vS(t) - \omega V(t) - \mu V(t)$$

High vaccination coverage (above 85%) is necessary to achieve substantial reductions in HBV prevalence (Tilahun et al., 2021; Khan et al., 2021). However, incomplete vaccination programs fail to eliminate the virus, especially with the presence of asymptomatic carriers.

C. The Role of Asymptomatic Carriers and Vertical Transmission

Carriers C(t) were shown to significantly influence the infection reservoir. Numerical results confirmed that even with reduced symptomatic cases, carriers sustain HBV in the population:

$$^{ABC}D_t^{\alpha} C(t) = \delta I(t) - \mu C(t)$$

(Zhong et al., 2021). Similarly, vertical transmission adds complexity, where infected mothers pass the virus to newborns, sustaining the endemic state despite control efforts (Prakash et al., 2021).

D. Stability and Bifurcation Outcomes

Analysis of the basic reproduction number:

$$R_0 = \frac{\beta}{\gamma + \mu + \delta} + \frac{\beta_C \delta}{(\gamma + \mu + \delta)(\mu)}$$

showed that stability of the disease-free equilibrium depends heavily on transmission and vaccination parameters. Simulations confirm that R_0>1 leads to endemicity, while R_0<1 results in disease eradication (Gao et al., 2020; Yavuz et al., 2023).

Backward bifurcation is possible due to vaccination imperfections and vertical transmission, where lowering R_0 below 1 is insufficient for disease elimination (Shah et al., 2020).

E. Sensitivity Analysis of Critical Parameters

Sensitivity testing revealed that transmission rates (β,β_C), fractional order (α), and vaccination rate (v) are the most influential on infection dynamics. Small changes in these parameters led to significant variations in infection curves and equilibrium states (Yavuz et al., 2023; Almalahi et al., 2023).

F. Long-Term Predictions and Policy Implications

The model predicts that without sustained high vaccination coverage and carrier screening programs, HBV will persist. Memory-driven effects prolong epidemic tails, emphasizing that short-term interventions are insufficient (Sutradhar & Dalal, 2023).

- Policy implications include:
- Targeting vertical transmission with maternal screening.
- Scaling vaccination coverage beyond 90%.
- Incorporating carrier detection programs to break silent transmission chains.

G. Model Validation with Observational Data

Comparisons with real-world data showed a strong fit, especially when fractional dynamics were included. The model minimized the error:

$$\text{Error} = \sum_t \left(I_{\text{model}}(t) - I_{\text{observed}}(t)\right)^2$$

Validating its applicability in public health decision-making (Zarin, 2022).

H. Relevance of Fractional Memory Effects

Unlike integer-order models, the fractional model captures long-memory effects, explaining HBV's persistence and the delayed impact of interventions. This highlights the need for prolonged monitoring even after apparent reductions in cases (Gao et al., 2020; Shah et al., 2020).

The Atangana fractional-order network model offers a robust framework for understanding HBV dynamics. It underscores the critical roles of memory, vaccination, carriers, and vertical transmission. Results suggest that integrated, long-term control strategies targeting all infection pathways are essential for HBV elimination (Demirci, 2022; Almalahi et al., 2023).

IV. CONCLUSION

This study provides a comprehensive review and numerical analysis of the Atangana fractional-order network model applied to Hepatitis B Virus (HBV) transmission dynamics. The incorporation of fractional derivatives, particularly the Atangana-Baleanu-Caputo (ABC) operator, significantly enhances the model's ability to capture memory-dependent processes, long-term infection dynamics, and the impact of asymptomatic carriers.

The model results demonstrate that memory effects, represented by the fractional order parameter α, are critical in understanding the prolonged nature of HBV infections. Lower fractional orders slow the infection peak but extend the epidemic's duration, highlighting the inadequacy of classical integer-order models in capturing such long-tail behaviors (Gao et al., 2020; Sutradhar & Dalal, 2023). This emphasizes

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the importance of considering fractional dynamics in infectious disease modeling for more realistic predictions.

Furthermore, vaccination emerges as a pivotal control measure in reducing infection prevalence and pushing the system towards disease eradication. However, numerical simulations confirm that partial vaccination and the presence of chronic asymptomatic carriers sustain the infection, making HBV elimination challenging (Demirci, 2022; Khan et al., 2021). The impact of vertical transmission further complicates eradication efforts, reinforcing the necessity for maternal screening and comprehensive immunization strategies.

Sensitivity and bifurcation analyses reveal that transmission rates, fractional order, and vaccination rates are the most influential parameters affecting the basic reproduction number R_0 and the system's stability (Prakash et al., 2021; Yavuz et al., 2023). These findings underscore the importance of targeted interventions focusing on reducing transmission and increasing vaccination coverage.

In conclusion, the Atangana fractional-order network model offers a robust framework for analyzing HBV dynamics, integrating biological complexity and real-world intervention challenges. Its application provides valuable insights for public health strategies, emphasizing long-term monitoring, aggressive vaccination campaigns, and management of asymptomatic carriers to achieve effective disease control. Future research should focus on refining parameter estimations with more empirical data and expanding the model's application to other infectious diseases with similar chronic characteristics.

LIST OF ABBREVIATIONS

Abbreviation	Full Meaning
HBV	Hepatitis B Virus
ABC	Atangana- Baleanu- Caputo
DFE	Disease-Free Equilibrium
R_0	Basic Reproduction Number
SIR	Susceptible-Infected-Recovered Model
WHO	World Health Organization
α	Fractional Order Parameter
β	Transmission Rate from Infected Individuals
βc	Transmission Rate from Carriers
δ	Rate of Progression to Chronic Carrier State
γ	Recovery Rate
μ	Natural Death Rate
v	Vaccination Rate
ω	Waning Immunity Rate
θ	Proportion of Vertical Transmission
N(t)	Total Population at Time t
C(t)	Carrier Population at Time t
I(t)	Infected Population at Time t
S(t)	Susceptible Population at Time t
V(t)	Vaccinated Population at Time t
N(t)	Total Population at Time t
C(t)	Carrier Population at Time t

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