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MATHEMATICAL MODELING AND PREDICTION OF ONCHOCERCIASIS TRANSMISSION DYNAMICS TOWARD ELIMINATION IN TARABA STATE, NIGERIA

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ABSTRACT

Onchocerciasis, commonly known as river blindness, is a neglected tropical disease caused by the filarial nematode Onchocerca volvulus and transmitted through bites of Simulium blackflies. A SEIR-SEI model was developed to simulate the bidirectional transmission dynamics between human and blackfly populations. The model incorporated key epidemiological parameters including transmission probabilities (human: 0.0005-0.001 per bite; vector: 0.001-0.0015 per bite), biting rate (0.3-0.7 bites/vector/day), incubation periods (human: 10-20 days; vector: 7-12 days), recovery rate (0.001-0.05 per day), and mortality rates (human: 0.000038 per day; vector: 0.05-0.1 per day). Seasonal variation was incorporated through sinusoidal functions with peaks at day 180. The basic reproduction number was calculated using the next-generation matrix approach. Results demonstrated that the calculated R_0 ranged seasonally from 0.004 to 0.013, with a baseline of 0.008 ($R_0 < 1$), indicating a projected gradual decline in transmission. The model predicted zero cases per 100,000 population by the fifth year, with disease prevalence stabilizing at very low levels as immunity accumulates. Seasonal oscillations were observed, with peak transmission occurring around day 180 (June-July), corresponding to periods of high vector abundance. The findings suggest that onchocerciasis in the studied LGAs of Taraba State is transitioning toward hypo-endemicity and eventual elimination. Targeted interventions, sustained vector control measures, scaled-up treatment programs, and continued epidemiological surveillance are recommended to accelerate disease elimination. These results align with Nigeria's goal of eliminating onchocerciasis by 2030 and provide evidence-based guidance for targeted intervention strategies in endemic communities.

Keywords: Onchocerciasis, River Blindness, Mathematical Modeling, SEIR Model, Disease Elimination

INTRODUCTION

Onchocerciasis, commonly known as river blindness, is a significant tropical neglected illness prevalent in Nigeria, impacting both socioeconomic conditions and public health. It is primarily caused by the filarial nematode Onchocerca volvulus, which is transmitted through bites from Simulium blackflies, predominantly found in swift, oxygen-rich waters. The disease predominantly affects rural populations, particularly those who are migratory, such as travelers, missionaries, and fishermen in riverine communities, exposing them to blackfly bites in endemic areas (Ahmed et al., 2024).

This parasitic infection leads to severe consequences, including blindness and skin disorders, drastically hindering the economic development of affected regions. For instance, the presence of visual impairment was estimated to be around 500,000 individuals, with approximately 270,000 blind people, positioning onchocerciasis as the second leading preventable cause of blindness in sub-Saharan Africa, following trachoma (Onwubuya et al., 2023). A total of 37 countries worldwide harbor the disease, with 30 situated in Africa.

In Nigeria, it is estimated that about seven million people are currently infected with onchocerciasis, and an additional 42 million are at risk, indicating a broader distribution than previously thought, particularly in central and northern regions such as Abuja, Borno, and Taraba states (Akogun, 1992). Despite ongoing treatment initiatives using ivermectin since 1995, a significant portion of the population 27% have missed treatments due to fears over drug safety, misconceptions about its efficacy, or absence during distribution events. Such gaps in treatment undermine progress toward controlling the disease, as untreated individuals remain reservoirs for the parasite, maintaining active transmission in communities where blackflies are found.

To counter these challenges, Nigeria aimed for the elimination of onchocerciasis by 2025 as set by the World Health Organization (WHO), but this target has since been extended to 2030 due to the complexities surrounding treatment gaps and prevalence rates. There is a pressing need for ongoing studies and follow-ups in endemic regions to better tackle the ongoing transmission of onchocerciasis and support efforts toward its eventual eradication.

MATERIALS AND METHODS

Study Area and Population

The study employed a purposive sampling method to sample five Local Government Areas (LGAs) of Taraba State. These LGAs are Bali, Gashaka, Ibbi, Jalingo, and Wukari, respectively. These LGAs were purposively sampled because they have a long-standing history of the disease. Their cumulative population of 1,191,200, based on the 2022 National Population Projections, was used as the base year.

The study employed a compartmental epidemiological approach using a coupled SEIR-SEI model that simultaneously simulates disease dynamics in human and vector populations. We adopted a deterministic mathematical model with separate compartments for humans and blackflies, respectively. This dual population framework captures the bidirectional transmission dynamics of vector-borne diseases, where vectors transmit infection to humans, and infected humans transmit back to susceptible vectors. The model is parameterized for a specific epidemiological context with a human population of 1,191,200 individuals (based on 2022 national population projections). The vector population is

scaled proportionally to the human population at a ratio of 5-10 times, yielding a vector population range of approximately 5.96-11.91 million blackflies. This vector-to-human ratio is estimated based on ecological and entomological field observations.

The core transmission mechanism incorporates several key epidemiological parameters, such as the transmission Probabilities. The model uses human transmission probability of 0.0005-0.001 per bite and vector transmission probability of 0.001-0.0015 per bite. These values reflect the probabilistic nature of vector transmission during blood meals and represent estimated parameters based on vector competence studies. Also, the biting rate ranges from 0.3-0.7 bites per vector per day. This parameter is made dynamic through seasonal variation, following a sinusoidal function that peaks at a specific day of the year (day 180) with an amplitude of ±0.15 bites per day. This captures the well-documented seasonal patterns in vector abundance and behaviour (see Table 4).

The intrinsic incubation period is parameterized as 0.05-0.1 per day, corresponding to a 10–20-day incubation period in humans, while the intrinsic incubation period of blackflies is set at 0.08-0.15 per day, representing a 7-12-day incubation in vectors, the period required for pathogen development before vectors become infectious. The recovery/treatment rate (γ) ranges from 0.001-0.05 per day, based on Akindele (2024), allowing the model to simulate intervention effectiveness through improved treatment outcomes. Natural mortality (μ_h) is set at 0.000038 per day, consistent with a standard life expectancy of approximately 70 years. Consequently, vector mortality (μ_v) ranges from 0.05-0.1 per day, reflecting typical blackfly lifespans of 10-20 days. The data were analyzed using Java scripts.

Model Description

The study employed a deterministic model with two populations: the human and the blackfly populations. Furthermore, the human population at time, t, is subdivided into four (4) compartments: the susceptible$S_h(t)$, the exposed$E_h(t)$, the Infected, $I_h(t)$ and the recovered $R_h(t)$ human compartments at any given time t. while the blackfly population consists of three (3) compartments: the susceptible$S_h(t)$, the exposed, $E_b(t)$ and the infected $I_b(t)$ at any given time, t. The dynamic of the human population is through birth, and it is denoted by$\wedge_h$. However, the susceptible human becomes infected when bitten by infected blackflies at a rate of $\lambda_h$and the force of infection is given by the formula:

$$\lambda_h = \frac{\beta_h b I_v}{N_h} \quad (1)$$

Where; $b$is the biting rate of a blackfly while $\beta_h$is the human transmission rate. After some time, the exposed human progresses to the infected human compartment at a rate ofδ_h. As time goes on, the infected humans recovered from onchocerciasis at a rate of γ_h.

The natural mortality of the human population takes place at a rate ofμ_h. However, the blackflies population recruitment rate is given by $\wedge_v$that occurs through birth in the population. Furthermore, the rate of the vector incubation period is given δ_v . The probability that the disease is being transmitted from the infected vector blackfly population is given by β_v and the rate of the force of infections is $\lambda_v$which is governed by the formula:

$$\lambda_v = \frac{\beta_v b I_h}{N_h} \quad (2)$$

Where $b$is the biting rate of a blackfly, β_v is the blackfly's transmission rate from the infected humans $I_h(t)$ at any given time t. The exposed vector population $E_v(t)$ decreases at the rate of δ_v and becomes an infected blackfly $I_v(t)$.

The variables and the parameters are depicted in Table 1 below:

Table 1: Model Variables

Variable	Meaning
$S_h(t)$	Susceptible human population
$E_h(t)$	Exposed human population
$I_h(t)$	Infected human population
$R_h(t)$	Recovered human population
$S_v(t)$	Susceptible blackfly population
$E_v(t)$	Exposed blackfly population
$I_v(t)$	Infected blackfly population

Table 2: Model Parameters

Parameter	Meaning
Λ_h	Recruitment rate of the human population through birth/immigration
λ_h	The rate of force of human infection when bitten by a blackfly
β_h	Transmission rate of a human population
δ_h	Transmission rate of an infected human population
R_0.	Recovery rate of the human population
μ_h	Natural mortality rate of a human population
ε	Public health and human education
Λ_v	Recruitment rate of the blackfly population via birth/immigration
β_v	Blackfly transmission rate
b	Biting rate of a blackfly
λ_v	Rate of Force of infections of blackfly

Table 3: Assumptions of the Model

Assumption	Description
Homogeneous mixing	All individuals have equal contact rates
Constant population sizes	Birth rate equals death rate
No vertical transmission	Disease is only transmitted through vector bites
Permanent immunity	Not assumed (recovery can lead back to susceptibility)
Vector lifecycle	Simplified (no explicit aquatic stages)
Seasonal effect	Not included (can be added with periodic functions)
Spatial heterogeneity	Not explicitly modeled

The schematic model diagram of the disease dynamics is depicted in Figure 1 below.

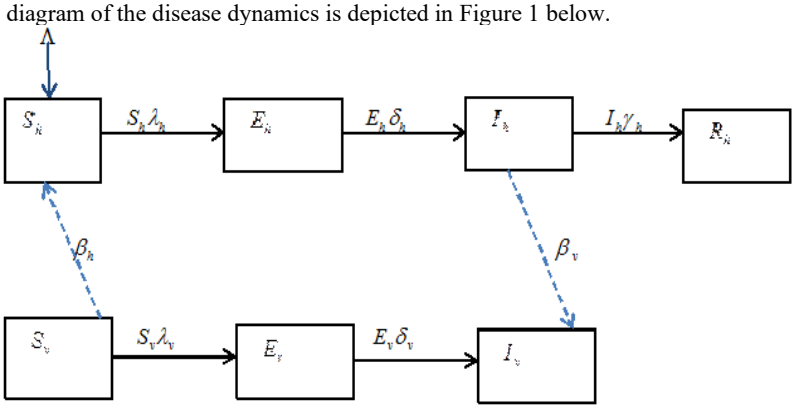

Figure 1: Compartmental model involving the interaction between the human host and blackfly with *Onchocercid Volvulus*

From the definition, the total population for the human compartments is given by:

$$N_h = S_h(t) + E_h(t) + I_h(t) + R_h(t) \quad (3)$$

While the total population for the blackfly is given by:

$$N_v = S_v(t) + E_v(t) + I_v(t) \quad (4)$$

From the schematic transmission diagram, we can obtain the model equations as seen below:

$$\frac{dS_h}{dt} = \Lambda_h - \lambda_h S_h - \mu_h S_h \quad (5)$$

$$\frac{dE_h}{dt} = \lambda_h S_h - \delta_h E_h - \mu_h E_h \quad (6)$$

$$\frac{dI_h}{dt} = \delta_h E_h - \gamma_h I_h - (\mu_h + \delta_h) I_h \quad (7)$$

$$\frac{dR_h}{dt} = \gamma_h I_h - \mu_h R_h \quad (8)$$

$$\frac{dS_v}{dt} = \Lambda_v - \lambda_v S_v - \mu_v S_v \quad (9)$$

$$\frac{dE_v}{dt} = \lambda_v S_v - \delta_v E_v - \mu_v E_v \quad (10)$$

$$\frac{dI_v}{dt} = \delta_v E_v - \mu_v I_h \quad (11)$$

Where the two forces of infections for the human and blackfly have the initial data solution as:

$$S_h(0) = S_{h0}, E_h(0) = E_{h0}, I_h(0) = I_{h0}, R_h(0) = R_{h0}, S_v(0) = S_{v0}, E_v(0) = E_{v0}, I_v(0) = I_{v0}$$

$$\frac{dN_h(t)}{dt} = \Lambda_h - \mu_h N_h(t) \quad (12)$$

$$\frac{dN_v(t)}{dt} = \lambda_v(\quad) \quad (13)$$

The model equations were as follows:

Positivity Solution

It is established that all system Equations 5 to 11 with non-negative initial data are non-negative for all t > 0. This postulates the theorem that if the initial data of the above Equations 5 to 11 are non-negative, then the solutions $\{S_h(t), E_h(t), I_h(t), R_h(t), S_b(t), E_b(t), I_b(t)\}$ remain non-negative for all time $t \geq 0$.

Proof: from equation 5: $\frac{\partial S_h}{\partial t} = \Lambda_h - \gamma R_h - \lambda_h S_h - \mu_h S_h$

We have:

$$S_h(t) \geq S_h(0)\, exp\left\{\int_0^t -(\lambda_h + \mu_h)dt\right\} \geq 0 \quad (14)$$

It can be shown that $S_h(t) \geq 0, forall, t \geq 0$.

This same idea can be used to show the positivity of other state variables for all $t > 0$. Hence, the solution of Equations 5 to 11 remains positive for all $t \geq 0$ since they are exponential functions.

***Lemma 1*:** Given the solution of S_h, E_h, I_h, R_h, S_v, E_v, I_v of equations 5 to 11 with a positive initial condition, the region can be given by the set:

$$\Omega = \Omega_h X \Omega_b \Omega_h = \left\{S_h, E_h, I_h, R_h \leq \varepsilon {R_+}^4 : N_h \leq \frac{\Lambda_h}{\mu}\right\}$$

$$\Omega_b = \left\{(S_v, E_v I_v) \varepsilon R_+^3 : N_v \leq \frac{\Lambda_v b I_v}{N_v}\right\} \quad (15)$$

is a positive invariant for the system of Equations 5 to 11. Also, from Equations 12 and 13, it can be shown that:

$$limsup\, N_h \leq \frac{\Lambda_h}{\mu_h} t \to \infty \quad \text{and} \quad limsup\, N_v \leq \frac{\Lambda_v}{\mu_v} t \to \infty$$

Therefore, the set is positive invariant, that is, all solutions in Ω remain in Ω for all t >0.

Disease Free Equilibrium (DFE)

The disease-free equilibrium implies that at equilibrium, all the equations from 5 to 11 do not change; they remain constant. Taking the derivative of the above equations and equating it to zero, solving it simultaneously to obtain the disease-free equilibrium. For instance, when the exposed human beings $E_h = 0$, then we have:

$$E_v = \left(S_h^0, E_h^0, I_h^0, R_h^0, S_b^0, E_b^0, I_b^0\right) \quad (16)$$

$$E_v = \left(\frac{\Lambda_h}{\mu_0} 0 \quad 0 \quad 0 \quad \right) \quad (17)$$

$$N_h^0 = S_h^0 = \frac{\Lambda_h}{\mu_h} \quad (18)$$

The Basic Reproduction Number

The basic reproduction number is very significant in modeling infectious diseases. It measures the threshold of infectious disease maximum reproduction potentials, denoted by R_0

There are three ways of measuring the basic reproduction number. However, this study considered the next generation matrix approach to derive and find the spectral radius matrix FV^{-1}

Where F is the appearance of the new infection's matrix and V^{-1} is the matrix of infections transferred by other means. These matrices are Jacobian matrices of column vectors and are represented by:

$$F_i = \begin{pmatrix} \beta_h S_h^0 I_v \\ 0 \\ \beta_v S_v^0 I_v \\ 0 \end{pmatrix} \quad (19)$$

The Jacobian Matrix F of Equation (19) above at the Disease-Free Equilibrium (DFE) is :

$$F = \begin{bmatrix} 0 & 0 & 0 & \beta_h N_h \\ 0 & 0 & 0 & 0 \\ 0 & \beta_v N_v & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (20)$$

The V, which represents the transfer of individuals out of infected compartments through progression or death, is given by the matrix below:

$$V = \begin{bmatrix} \delta_h + \mu_h & 0 & 0 & \beta_h N_h \\ -\delta_h & \gamma_h + \mu_h & 0 & 0 \\ 0 & 0 & \delta_v + \mu_v & 0 \\ 0 & 0 & -\delta_v & \mu_v \end{bmatrix} \quad (21)$$

From the matrix of equation (21), the inverse of the matrix is given by:

$$V^{-1} = \begin{bmatrix} \frac{1}{\delta_h + \mu_h} & 0 & 0 & 0 \\ \frac{\delta_h}{(\delta_h + \mu_h)(\gamma_h + \mu_h)} & \frac{1}{\gamma_h + \mu_h} & 0 & 0 \\ 0 & 0_v & \frac{1}{\delta_v + \mu_v} & 0 \\ 0 & 0 & \frac{\delta_v}{(\delta_v + \mu_v)\mu_v} & \frac{1}{\mu_v} \end{bmatrix} \quad (22)$$

The reproduction number R_0, which is always obtained by FV^{-1}, yields the matrix K below:

$$K = \begin{bmatrix} 0 & 0 & 0 & \frac{\beta_h N_h}{\mu_v} \\ 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_v N_v \delta_h}{(\delta_h + \mu_h)(\gamma_h + \mu_h)} & 0 & 0 \\ 0 & 0 & 0_v & 0 \end{bmatrix} \quad (23)$$

In the matrix of Equation (23), we see that the characteristic equation shows that the eigenvalues are zero except those that come from the non-zero entries, which yields:

$$R_0^2 = \left(\frac{\beta_h N_h}{\mu_v}\right) X \left(\frac{\beta_v N_v \delta_h}{(\delta_h + \mu_h)(\gamma_h + \mu_h)}\right) \quad (24)$$

This yields our basic reproduction number R_0 as in Equation (25) below:

$$R_0 = \sqrt{\frac{\beta_h \beta_{\ v} N_v N_v \delta_h}{\mu_v (\delta_h + \mu_h)(\gamma_h + \mu_h)}} \quad (25)$$

Table 4: Parameter Definitions, Description, Values, Unit, and Source

Parameter	Description	Value	Unit	Source
β_h	Probability of human transmission rate	0.0005-0.001	Per bite	Estimated
β_v	Probability of a vector transmission rate	0.001-0.0015	Per bite	Estimate
b	Biting rate	0.3-0.7	Bites/vector/day	Estimated
δ_h	Human incubation rate	0.05-0.1	Per day (10-20 days)	Estimated
δ_v	Vector incubation rate	0.08-0.15	Per day (7-12 days)	Estimated
γ_h	Recovery/treatment rate	0.05-0.001	Per day	Akindele (2024)
μ_h	Human natural mortality	0.000038	Per day (≈ 70 years)	Standard estimate of age of death
μ_v	Mortality rate of a vector	0.05-0.1	Per day (10-20 days)	Estimated
N_h	Human population	1,191,200	Per year, five local government areas	National population 2022 projection
N_v	Vector population	5-10 X N_h	vectors	Estimated

RESULTS AND DISCUSSION

The results obtained were depicted in the table and figures as seen below:

Table 5: All Variables and Parameters obtained from the Analysis

Parameter/Variable	Value Obtained	Meaning
$\boldsymbol{R_0}$	0.008 < 1	Disease will die off in the long run
$\boldsymbol{\beta_h}$	0.00075 < 1	The transmission rate is slow, confirming $\boldsymbol{R_0}$
$\boldsymbol{\beta_v}$	0.00125 < 1	The transmission rate is very slow
b	0.5 < 1	The biting rate is not high
$\boldsymbol{\delta_h}$	0.075 (1/day)	Insignificant
$\boldsymbol{\delta_v}$	0.115 (1/day)	Insignificant
$\boldsymbol{\gamma_h}$	0.0255 (1/day)	Insignificant
$\boldsymbol{\mu_v}$	0.075	insignificant

Table 5 shows that the onchocerciasis disease is going to die out in the long run. This is evident as all the parametric values confirmed the result of $\boldsymbol{R_0}$.

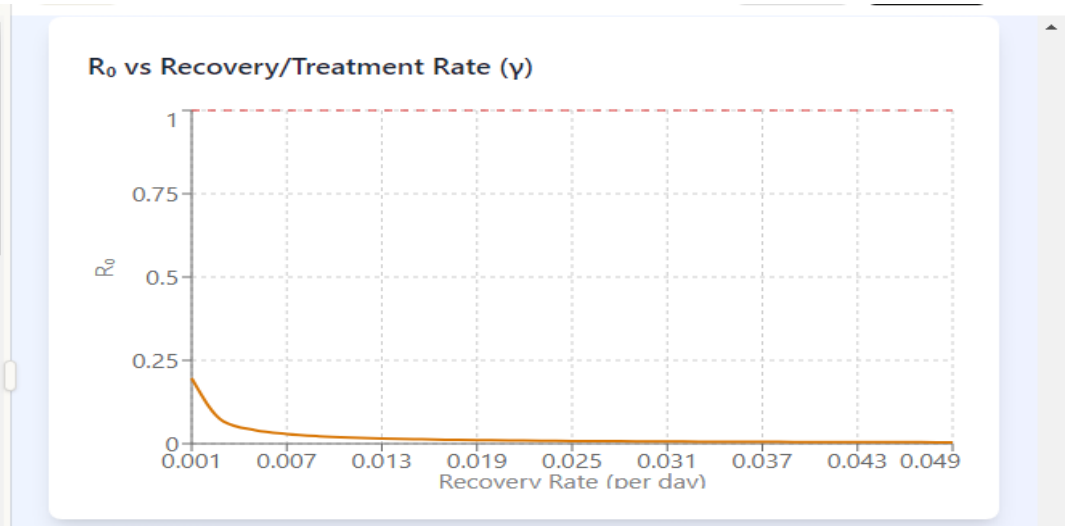

Figure 2: The graph of the reproduction number against the recovery rate

Figure 2 shows that as the disease spread diminishes over time, the recovery rate becomes significantly faster. This implies that in the future, the endemic community will be free of the disease.

Table 6: Average Prevalence, Maximum Prevalence, New Cases, and Average Reproduction Number Predicted for Five Years

Year	Avg. prevalence	Maximum prevalence	New cases	Avg. R_0
1	0.15	0.84	0	0.005
2	0.00	0.00	0	0.008
3	0.00	0.00	0	0.008
4	0.00	0.00	0	0.006
5	-	∞	-	-

Table 6 shows that the model predicts zero (0) cases per 100,000 in the fifth year, with a maximum prevalence of Infinity per 100,000 during peak seasons. The prevalence typically rises sharply in the first 1-2 years as the disease spreads through the susceptible population, then stabilizes as immunity accumulates. Indicating that the disease prevalence is not high and may decline quickly.

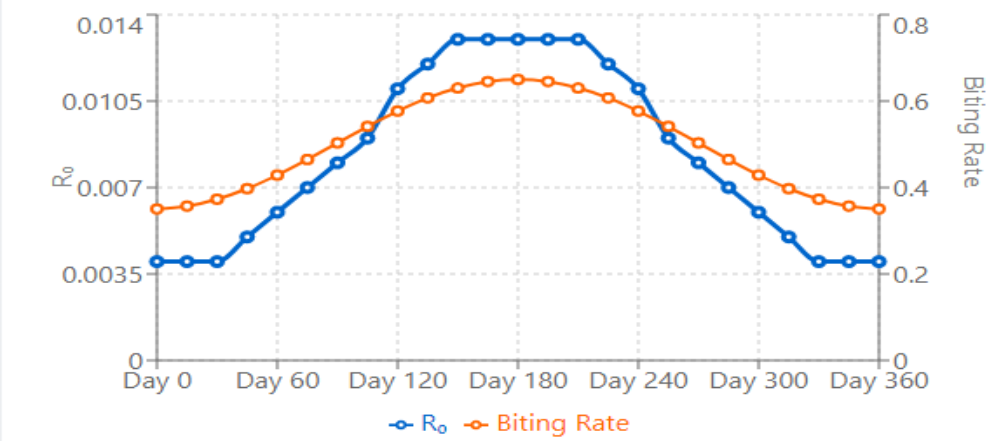

Figure 3: Showing the R_0 and the biting rate of the blackfly

The study models the prevalence of onchocerciasis in five local governments of Taraba State. Data were collected from the National Population Commission, while others, like the disease biting rate, disease lifespans, and incubation rate, were estimated. These were analyzed using Java.

The R_0 is highly significant in epidemiological modeling. For instance, when $R_0 > 1$, it shows that there will be a high prevalence and incidence rate of the disease in an endemic community; when $R_0 = 1$, the disease is in a steady state, that is, though it is going to spread, but at a very slow rate, or there is going to be a forward bifurcation. On the other hand, when $R_0 < 1$, the disease transmission will gradually decline. The results showed that the calculated R_0 varies seasonally from 0.004 to 0.013, with a baseline of 0.008. This seasonal variation reflects the dynamics of vector populations and biting behaviour, which peak at certain times of year, suggesting that the disease will die out.

The model predicts zero (0) cases per 100,000 in the fifth year, with maximum prevalence of Infinity per 100,000 during peak seasons (see Table 6). The prevalence typically rises sharply in the first 1-2 years as the disease spreads through the susceptible population, then stabilizes as

immunity accumulates. Indicating that the disease prevalence is not high and can die out in no distant time.

The combined SEIR visualization shows the four population states evolving. Initially, susceptible individuals decline as they become exposed and infected. Compartmental peaks occur when the effective reproduction number falls below 1, signaling the start of epidemic decline. By the fifth (5^{th}) year, a significant proportion has recovered, which suppresses new transmission.

Both R_0 and prevalence show pronounced seasonal oscillations. Peak transmission occurs around day 180 (see Table 5) of each year, probably around June or July, corresponding to high vector abundance. These predictable patterns suggest that public health interventions can be strategically timed to occur before seasonal peaks.

The cumulative attack rate represents the total proportion of the population that experiences infection over the 5 years. This metric is crucial for estimating healthcare burden, disability-adjusted life years, and mortality impacts. These results are in line with the study of Akindele *et al.* (2024) whose results show that comprehensive onchocerciasis vector management is crucial in eliminating the disease. Based on these results, we recommend that early interventions before the peaks will maximize effectiveness, preparation for mitigating the disease seasonally, and resource allocation should be the central focus. Scaling up treatment can significantly reduce disease burden. Vector control measures during the high season period are highly recommended, and surveillance during the endemic phase should be sustained to prevent resurgence. Consequently, further research is needed to capture the entire state.

CONCLUSION

This study presented a deterministic SEIR–SEI compartmental model to describe and predict the dynamics of onchocerciasis transmission in five endemic Local Government Areas of Taraba State, Nigeria. The model incorporated key epidemiological and ecological parameters governing human–vector interactions, including the biting rate, transmission probabilities, incubation periods, and recovery rates, to simulate bidirectional infection processes between human and blackfly populations. Analysis of the model indicated that the basic reproduction number (R_0) ranged seasonally between 0.004 and 0.013, with a baseline value of 0.008 ($R_0 < 1$), suggesting that the disease is unlikely to sustain transmission in the long term under current control measures. The simulation results further predicted a progressive decline in disease prevalence, approaching zero within five years, consistent with the transition of onchocerciasis toward hypoendemicity and eventual elimination in the study area.

The model's outcomes highlight the continuing significance of integrated control strategies (particularly sustained vector control, community-directed mass drug administration MDA with ivermectin, and enhanced health education) to consolidate existing gains and prevent disease resurgence. The observed seasonal oscillations, with transmission peaks around mid-year (June–July), emphasize the importance of synchronizing intervention activities with periods of high vector abundance to maximize impact.

Furthermore, this study demonstrates the utility of mathematical modeling as a cost-effective and predictive tool for guiding evidence-based public health planning. The modeling framework offers a basis for optimizing resource allocation, refining intervention timing, and assessing progress toward national and global elimination targets. Future research should extend this work by incorporating spatial heterogeneity, climatic variability, and stochastic effects to improve predictive accuracy and applicability across broader geographical scales. Such extensions would strengthen the capacity of epidemiological models to support decision-making in vector-borne disease management and contribute to achieving Nigeria's and the World Health Organization's goal of onchocerciasis elimination by 2030.

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REFERENCES

Ahmed, M. T., Adeyemi, F. O., Hassan, A. K., & Okafor, I. N. (2024). Prevalence of onchocerciasis in Adamawa State, North senatorial zone: A community-based survey. *Journal of Tropical Diseases and Public Health*, 12(3), 145-158.

Akindele, A. O., Ademola, I. O., Rychtář, J., & Taylor, D. (2024). A deterministic mathematical model for quantifiable prediction of antimalarials limiting the prevalence of multidrug-resistant malaria. *Healthcare Analytics*, *5*, 100333.

Akogun, O. B. (1992). The epidemiology and control of onchocerciasis in Nigeria. *Parasitology Today*, 8(1), 20-24.

Akogun, O. B., & Onwuliri, C. O. (1991). Onchocerciasis in Nigeria: Current status and control strategies. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, 85(4), 475-480.

Asha, M., & Nyimvua, S. (2020). Mathematical modeling of onchocerciasis transmission dynamics with treatment, education, and vector control interventions. *Computational and Mathematical Methods in Medicine*, 2020, 8547392. https://doi.org/10.1155/2020/8547392

Awadzi, K., Opoku, N. O., Attah, S. K., Lazdins-Helds, J. K., & Kuesel, A. C. (2004). A randomized, single-ascending-dose, ivermectin-controlled trial of moxidectin in onchocerciasis. *PLoS Medicine*, 1(3), e60. https://doi.org/10.1371/journal.pmed.0010060

Costa, M. I. S., Kodaka, F., & Fontanari, J. F. (2021). Mathematical modeling of infectious diseases: Deterministic and stochastic approaches. *Mathematical Biosciences and Engineering*, 18(4), 4197-4218. https://doi.org/10.3934/mbe.2021210

Cromwell, E. A., Oswald, P., & Hemingway, J. (2021). Environmental niche modeling for onchocerciasis in Africa: Implications for disease control and elimination. *Parasites & Vectors*, 14(1), 192. https://doi.org/10.1186/s13071-021-04692-6

Crosskey, R. W. (1990). The natural history of blackflies. *British Museum (Natural History) Publication*, 1, 1-711.

Idowu, E. T., Akinbo, F. O., Olaniyan, R. T., & Ogunniyi, T. A. (2013). Onchocerciasis in Taraba State, Nigeria: A follow-up study of disease status and treatment compliance. *East African Medical Journal*, 90(5), 178-185.

Onwubuya, C., Nwachukwu, K. U., & Okafor, P. N. (2023). Onchocerca volvulus infection as a leading cause of preventable blindness in sub-Saharan Africa: A systematic

review. *Journal of Global Health Reports*, 7, e2023010. https://doi.org/10.29392/joghR.7

Onwujekwe, O., Chima, R., & Okoronkwo, I. (2000). Willingness to pay for community-based ivermectin therapy in endemic onchocerciasis areas of Nigeria. *Tropical Medicine & International Health*, 5(7), 435-444. https://doi.org/10.1046/j.1365-3156.2000.00589.x

Schmidt, M. L., Ylönen, S., Moxon, S. A., & Trpis, M. (2022). Measuring onchocerciasis prevalence: Methods and applications in control programs. *The Lancet Infectious Diseases*, 22(2), e89-e97. https://doi.org/10.1016/S1473-3099(21)00705-6

Turner, H. C., Walker, M., Lustigman, S., Taylor, D. W., & Basáñez, M. G. (2024). Modeled Therapeutic efficacy of moxidectin for onchocerciasis elimination: Projections from the EPIONCHO-IBM model. *eLife*, 13, e92187. https://doi.org/10.7554/eLife.92187

World Health Organization. (2016). Guidelines for stopping mass drug administration and verifying elimination of human onchocerciasis: Criteria and procedures. WHO Press.