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Research Article

A Mathematical Model of the Transmission Dynamics and Control of Bovine Brucellosis in Cattle

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Brucellosis is one of the most serious diseases that wreaks havoc on the production of livestock. Despite various efforts made to curb the spread of brucellosis, the disease remains a major health concern to both humans and animals. In this work, a deterministic model is developed to investigate the transmission dynamics and control of bovine brucellosis in a herd of cattle. The disease-free equilibrium point of the model is shown to be locally asymptotically stable whenever basic reproduction number $\mathscr{R}_0 \leq 1$ and unstable if $\mathscr{R}_0 > 1$. Also, the endemic equilibrium point of the model is shown to be locally asymptotically stable whenever $\mathscr{R}_0 > 1$ and unstable otherwise. Numerical simulations of the model suggest that vaccination is the most efficient single control intervention. Also, the most efficient pair of control interventions is vaccination and culling of seropositive cattle. However, the best way to control bovine brucellosis in cattle is the combination of the three control interventions (vaccination, culling of seropositive cattle, and observation of comprehensive biosecurity protocols).

1. Introduction

The number one Sustainable Development Goal (SDG) concerns ending poverty. Household income is identified as the major way by which extreme poverty can be reduced in developing countries. As a result, stakeholders and policy makers have turned their focus on livestock production as a means of raising income and improving the livelihood of rural dwellers. The livestock industry does not only supply manure for crop and vegetable growers but it also ensures the sustainability of food and nutrients and financial security, all of which contribute to raise the standard of living, particularly in rural areas. Animal production is beset by different kinds of diseases. The deleterious effect of brucellosis cannot be disregarded. According to international statistics, about 500,000 cases of the disease are reported each year around the world [1]. Also, Singh et al. ([2]) in a study revealed that the disease is accountable for an economic loss of US$3.4 billion in livestock production on average. This implies that the burden of the disease in developing countries cannot be underestimated.

Mathematical modelling is useful in helping us increase our understanding in the spread of infectious diseases. Over the years, several models have been proposed to study the dynamics of zoonosis. Specifically, Nyerere et al. [3] formulated a mathematical model to examine the impact of different control parameters on the transmission dynamics of brucellosis in human and animal populations and concluded that the prevention of human brucellosis depends solely on the prevention of domestic animal diseases. Nyerere et al. [4] proposed an optimal control problem for the control of brucellosis and observed that the combination of vaccination, gradual culling of cattle and small ruminants, environmental hygiene, and personal protection of humans is the most cost-effective combination of strategies for the control of brucellosis. Also, Nyerere et al. [5] proposed a mathematical

model to investigate the infectiology of brucellosis with some control strategies. Hobbs et al. [6] constructed a state-space model to examine the influence of brucellosis on Yellowstone bison population. The findings indicated that there is no need for implementing a park-wide vaccination programme. Nepomuceno et al. [7] presented an individual-based model to investigate the dynamics and control of bovine brucellosis. The model focused on heterogeneous populations and spatial aspects, such as migration among herds. It also placed emphasis on pulse interventions. The findings indicated further that pulse vaccination is an effective way to eradicate the disease.

Tumwiine and Robert [8] developed a mathematical model for treatment of bovine brucellosis in cattle population. The model dwelled on isolation and treatment as the only intervention strategies. They stated in their findings that massive awareness campaigns should be conducted in order to sensitise farmers on regular testing of aborted animals and be provided with the necessary treatment from veterinary officers. Lolika et al. [9] analysed the effects of seasonality on brucellosis infections. This model highlighted the differences between autonomous and periodic models. Li et al. [10] proposed a mathematical model to evaluate strategies to control brucellosis in China. They concluded that in order to ensure cost-effective control of brucellosis, there is a need to combine animal vaccination, environment disinfection, and elimination of infected animals. Savini et al. [11] developed a mathematical forecasting model to study the spread of brucellosis in Italian cattle trade network in order to codify field interventions. The model focused on the utilisation of computer knowledge to investigate the transmission dynamics of brucellosis and to implement control strategies. The results of the model highlighted that there was improvement in terms of efficacy and efficiency of the tracing activities as compared to the previously adopted one used by veterinary service to control brucellosis in Italy. Their general assessment has shown that SIR models are most suitable for the practical needs of veterinary works because of its shortest time for computation. Tasiame et al. [12] investigated the prevalence of brucellosis in cattle and their handlers in North Tongu District of the Volta Region, Ghana. They confirmed seroprevalence of bovine brucellosis in cattle to be 20.9% against 10.1% for human brucellosis. The findings of the study revealed that the predisposing factor for human brucellosis was to get into closed contact with the infected cattle. Abatih et al. [13] developed a mathematical model to investigate the transmission dynamics of brucellosis among bison. The results of the model highlighted the idea that direct transmission of brucellosis plays less significant role on the dynamics of bison as compared to indirect transmission. They concluded that culling is very expensive; hence, other control measures such as vaccination and good herd management should be considered.

Ebinger et al. [14] presented an epidemiological and individual-based model to study the efficacies of control interventions such as sterilisation, vaccination, and test-and-remove. The model was characterised with epidemiological data from bison in Yellowstone National Park, USA. The findings of the study captured sterilisation and test-and-remove as the most successful control interventions when targeting young seropositive animals.

According to Kang et al. [15], the utilisation of a system-based approach to studying the dynamics of infectious disease is very important. They added that mathematical models allow for much better comprehension, analysis, and improvement of control strategies at population level. Although several researches have indicated strategies to combat the spread of brucellosis and reduce its impact using mathematics modelling, recent investigations have revealed that bovine brucellosis continues to wreak havoc on cattle production. However, the incorporation of vaccination, culling of seropositive cattle, and comprehensive biosecurity protocols in mathematical models to examine the dynamics of bovine brucellosis in cattle has not been attended to the best of our knowledge. This research is intended to propose and analyse an ODE model that incorporates these controls. The rest of the paper is arranged as follows. The next section presents the assumptions and formulation of the model formulation under consideration. Section 3 presents qualitative analysis and properties of the model. Numerical simulation of the model is conducted in Section 4. Section 5 presents discussion of results, and finally, the conclusions and recommendations from the findings of the research are presented in Section 6.

2. Model Formulation

A deterministic model is proposed to study the influence of multifaceted interventions on the spread of bovine brucellosis. The cattle population is subdivided into five (5) compartments, namely, susceptible compartment (S), infected compartment (I), recovered compartment (R), vaccinated compartment (V), and biosecured compartment (B). The susceptible class represents cattle that are likely to contract brucellosis and are not immuned. The infected class (I) represents cattle that have contracted the disease and could transmit the disease to other animals. The recovered class (R) represents cattle that have recovered from bovine brucellosis infections. The biosecured class (B) represents cattle that can never contract bovine brucellosis due to the observation of comprehensive biosecurity protocols. The vaccinated class (V) represents cattle that are vaccinated with temporary immunity vaccines. The proportions of cattle in compartment S, I, R, B, and V at time (t) are denoted by $\mathrm{S}(t)$, $\mathrm{I}(t)$, $\mathrm{R}(t)$, $\mathrm{B}(t)$, and $\mathrm{V}(t)$, respectively. To mathematically formulate the model, it is assumed that cattle are recruited into the susceptibles at a rate (ω), and they are vaccinated at a rate, γS. The vaccinated cattle lose immunity at a rate of τV and move back to the susceptible compartment. Cattle are transited from the susceptible compartment to the biosecured compartment due to the observation of comprehensive biosecurity protocols at a rate, ϵS. Infected cattle transmit bovine brucellosis to the susceptibles at a rate, β. The infected cattle recover from the disease and then move into the recovered compartment at a rate, αI. Also, the infected individuals are culled at a rate, χI. The recovered cattle lose natural immunity and then move to rejoin the susceptibles at a rate, κR. μ and ψ are considered as the

natural death and disease-induced death rates, respectively. The transmission dynamics in general are depicted in Figure 1.

The above descriptions are represented in Figure 1, and the model under discussion is represented by the following set of ordinary differential equations.

$$\left.\begin{aligned}
\frac{dS}{dt} &= \omega - \beta SI - (\mu + \gamma + \epsilon)S + \kappa R + \tau V;\\
\frac{dI}{dt} &= \beta SI - (\mu + \psi + \alpha + \chi)I;\\
\frac{dR}{dt} &= \alpha I - (\mu + \kappa)R;\\
\frac{dB}{dt} &= \epsilon S - \mu B;\\
\frac{dV}{dt} &= \gamma S - (\mu + \tau)V.
\end{aligned}\right\} \quad (1)$$

The model parameters are summarised in Table 1.

3. Qualitative Properties

Some basic analytical properties of the model are present in this section. The following result concerns the epidemiological feasibility of the model.

Theorem 1. *If the initial conditions of the model equations (1) are nonnegative, so are future solutions.*

Proof. From the first equation of (1), we have

$$\frac{dS}{dt} = \omega + \kappa R + \tau V - (\mu + \gamma + \epsilon + \beta I)S. \quad (2)$$

This implies that

$$\frac{dS}{dt} \geq -(\mu + \gamma + \epsilon + \beta I)S. \quad (3)$$

Integrating equation (3) gives

$$S(t) \geq S(0)e^{-(\mu+\gamma+\epsilon+\beta I)t}, \quad (4)$$

which implies that $S(t) \geq 0$.

Similarly, it can be shown that $I(t) \geq 0$, $R(t) \geq 0$, $B(t) \geq 0$, and $V(t) \geq 0$ for all $t > 0$. From the analysis above, it is obvious that if the initial conditions are nonnegatives, then the future solutions are also nonnegatives. The proof is completed. □

The set containing the reasonable solutions of the model is known as the feasible region. The model predictions are shown to be bounded within the region defined in the following theorem.

Theorem 2. *For all $t \geq 0$, all solutions of the model equations (1) are uniformly bounded and contained in the feasible region defined by $\xi = \{(S(t), I(t), R(t), B(t), V(t)) \in \mathbb{R}_+^5 | 0 \leq N(t) \leq \omega/\mu\}$.*

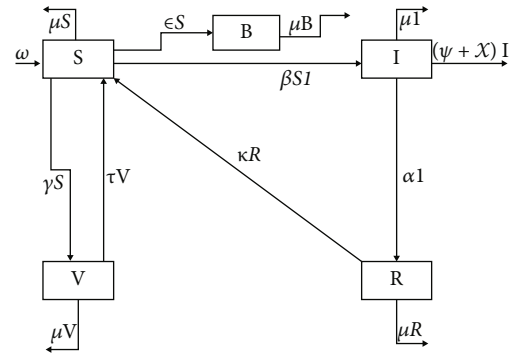


Figure 1: Schematic diagram of the transmission dynamics of bovine brucellosis in cattle with biosecurity.

Proof. Let $(\xi) = \{(S(t), I(t), R(t), B(t), V(t))\} \in \mathbb{R}_+^5$ be the solutions of the model equations (1) with nonnegative initial conditions and let $N = S + I + R + B + V$ be the total cattle population. Then

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dB}{dt} + \frac{dV}{dt} = \omega - \mu N - (\psi + \chi)I \leq \omega - \mu N. \quad (5)$$

Therefore

$$N(t) \leq \frac{\omega}{\mu} + \left(N_0 - \frac{\omega}{\mu}\right)e^{-\mu t}. \quad (6)$$

Hence

$$\lim_{t \longrightarrow \infty} N(t) \leq \frac{\omega}{\mu}. \quad (7)$$

Thus, the solutions of the model are uniformly bounded and contained in the feasible set $\xi = \{(S(t), I(t), R(t), B(t), V(t)) \in \mathbb{R}_+^5 | 0 \leq N(t) \leq \omega/\mu\}$. □

3.1. Equilibrium Points of the Model. The model has two equilibria, the disease-free equilibrium $\mathscr{E}_0$ and an endemic equilibrium $\mathscr{E}^*$. The disease-free equilibrium is given by $\mathscr{E}_0 = ((\omega(\mu + \tau)/\eta), 0, 0, (\epsilon\omega(\mu + \tau)/\mu\eta), (\omega\gamma/\eta))$, where $\eta = \mu(\mu + \gamma + \tau) + \epsilon(\mu + \tau)$.

The basic reproduction number refers to the average number of secondary cases that occurs when a single infectious individual is introduced into a completely susceptible population [16]. According to Van den Driessche and Watmough [16], the spectral radius of the matrix FV^{-1} is the reproduction number of system, where V and F are the transition and transmission matrices, respectively. The matrices of the model are given by $F = \beta S$ and $V = (\mu + \psi + \alpha + \chi)$.

The basic reproduction number is expressed as $\mathscr{R}_0 = \rho(FV^{-1}) = \beta\omega(\mu + \tau)/(\mu + \psi + \alpha + \chi)\eta$.

Table 1: Description of the model parameters.

Parameter	Description
β	The rate at which infected cattle transmit Brucella infections
ω	The rate at which cattle are recruited into the susceptible class
μ	The rate at which cattle die naturally in each compartment
γ	The rate at which susceptible cattle are vaccinated
τ	The rate at which vaccinated cattle lose temporal immunity
ψ	The rate at which cattle die as a result of Brucella infections
χ	The rate at which infected cattle are culled
α	The rate at which cattle recover from Brucella infections
κ	The rate of waning of recovery-derived immunity
ϵ	The rate at which susceptibles enter the biosecured compartment

Table 2: Sensitivity indices of R_0 parameters.

Description	Parameter	Index
The rate at which infected cattle transmit Brucella infections	β	+1.0000
The rate at which cattle are recruited into the susceptible class	ω	+1.0000
The rate at which vaccinated cattle lose temporal immunity	τ	+0.4904
The rate at which cattle die naturally in each compartment	μ	-0.5218
The rate at which susceptible cattle are vaccinated	γ	-0.7355
The rate at which cattle recover from Brucella infections	α	-0.0293
The rate at which cattle die as a result of Brucella infections	ψ	-0.5574
The rate at which susceptibles enter the biosecured compartment	ϵ	-0.2425
The rate at which infected cattle are culled	χ	-0.4107

Table 3: The parameter values.

Para.	Description	Value	Source
ω	The rate at which cattle are recruited into the susceptible class	200/year	[18]
β	The rate at which infected cattle transmit Brucella infections	0.0001/year	[18]
μ	The rate at which cattle die naturally in each compartment	0.001/year	[18]
ϵ	The rate at which susceptibles enter the biosecured compartment	0.011/year	Assumed
γ	The rate at which susceptible cattle are vaccinated	0.1/year	[18]
ψ	The rate at which cattle die as a result of Brucella infections	0.19/year	Assumed
κ	The rate at which recovered cattle lose natural immunity	0.02/year	[18]
τ	The rate at which vaccinated cattle lose temporal immunity	0.002/year	Assumed
χ	The rate at which infected cattle are culled	0.14/year	Assumed
α	The rate at which cattle recover from Brucella infections	0.01/year	[18]

Table 4: Combination of control measures and the ranks of their basic reproduction numbers.

Vaccination (γ)	Biosecurity protocols (ϵ)	Culling of seropositive cattle (χ)	$\mathscr{R}_0$	Rank
0.1	0.011	0	2.1948	R3
0.1	0	0.14	1.7083	R2
0	0.011	0.14	4.8076	R4
0.1	0.011	0.14	1.2938	R1

The model can be shown to have an endemic equilibrium $\mathscr{E}^* = (S^*, I^*, R^*, B^*, V^*)$ where:

$$\left.\begin{aligned} S^* &= \frac{(\mu+\tau)}{\mu+\kappa}\left[\frac{\omega(\mu+\kappa)+\alpha\kappa I^*}{\beta I^*(\mu+\tau)+\eta}\right];\\ I^* &= \left(\frac{\omega(\mu+\kappa)}{(\mu+\psi+\alpha+\chi+\kappa)\mu+\kappa\psi}\right)\left(1-\frac{1}{\mathscr{R}_0}\right);\\ R^* &= \left(\frac{\omega\alpha}{(\mu+\psi+\alpha+\chi+\kappa)\mu+\kappa\psi}\right)\left(1-\frac{1}{\mathscr{R}_0}\right);\\ B^* &= \frac{\epsilon(\mu+\tau)}{\mu(\mu+\kappa)}\left[\frac{\omega(\mu+\kappa)+\alpha\kappa I^*}{\beta I^*(\mu+\tau)+\eta}\right];\\ V^* &= \frac{\gamma}{\mu+\kappa}\left[\frac{\omega(\mu+\kappa)+\alpha\kappa I^*}{\beta I^*(\mu+\tau)+\eta}\right]. \end{aligned}\right\} \quad (8)$$

The following result holds about the equilibria of the model (1).

Lemma 3. *The model exhibits a unique disease-free equilibrium ($\mathscr{E}_0$) whenever $\mathscr{R}_0 \le 1$ and a unique endemic equilibrium ($\mathscr{E}^*$) whenever $\mathscr{R}_0 > 1$.*

Proof. When $\mathscr{R}_0 > 1$, then $1-(1/\mathscr{R}_0) > 0$, making $I^* > 0$ guaranteeing the existence of $\mathscr{E}^*$. When $\mathscr{R}_0 = 1$, then $I^* = 0$ which corresponds to $\mathscr{E}_0$. Furthermore, if $\mathscr{R}_0 < 1$, then $1-(1/\mathscr{R}_0) < 0$ making $I^* < 0$ which is epidemiologically unreasonable. This completes the proof. □

The following result follows from Routh-Hurwitz criteria.

3.2. Local Stability of Equilibria. The results on stability of the equilibria of the model are presented in Theorems 4 and 5.

Theorem 4. *The disease-free equilibrium point ($\mathscr{E}_0$) is locally asymptotically stable if $\mathscr{R}_0 \le 1$ and unstable if $\mathscr{R}_0 > 1$.*

Proof. The Jacobian matrix of the model at ($\mathscr{E}_0$) is given by

$$J(\mathscr{E}_0) = \begin{bmatrix} -(\mu+\epsilon+\gamma) & -(\mu+\psi+\alpha+\chi)\mathscr{R}_0 & \kappa & 0 & \tau \\ 0 & (\mu+\psi+\alpha+\chi)(\mathscr{R}_0-1) & 0 & 0 & 0 \\ 0 & \alpha & -(\mu+\kappa) & 0 & 0 \\ \epsilon & 0 & 0 & -\mu & 0 \\ \gamma & 0 & 0 & 0 & -(\mu+\tau) \end{bmatrix}. \quad (9)$$

Clearly, $\lambda_1 = (\mu+\psi+\alpha+\chi)(\mathscr{R}_0-1)$, $\lambda_2 = -(\mu+\kappa)$, and $\lambda_3 = -\mu$ are eigenvalues of $J(\mathscr{E}_0)$, which are all negative whenever $\mathscr{R}_0 < 1$, and the remaining eigenvalues are those of the following submatrix:

$$J^1(\mathscr{E}_0) = \begin{bmatrix} -(\mu+\epsilon+\gamma) & \tau \\ \gamma & -(\mu+\tau) \end{bmatrix}, \quad (10)$$

whose characteristic polynomial is given by

$$\lambda^2 + (2\mu+\epsilon+\tau+\gamma)\lambda + \left(\mu^2+\mu\gamma+\mu\tau+\mu\epsilon+\epsilon\tau\right) = 0. \quad (11)$$

Since all the coefficients of equation (3) are positive, the Routh–Hurwitz criterion shows that all zeros of (3) have negative real parts.

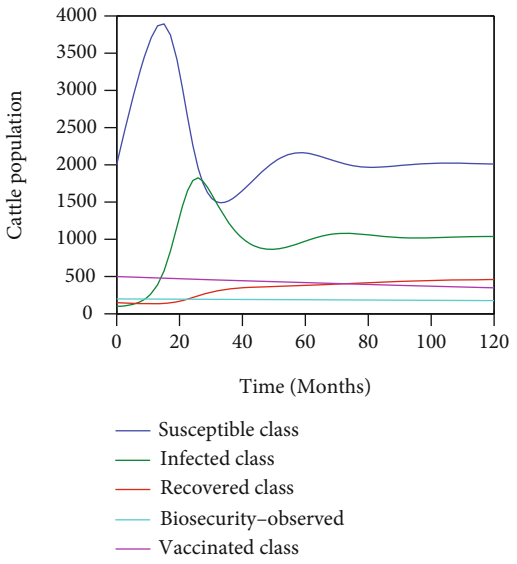
Therefore, the disease-free equilibrium point ($\mathscr{E}_0$) is locally asymptotically stable if $\mathscr{R}_0 \le 1$ and unstable if $\mathscr{R}_0 > 1$.

At the endemic equilibrium point, the characteristic polynomial of the Jacobian matrix of the model is given by

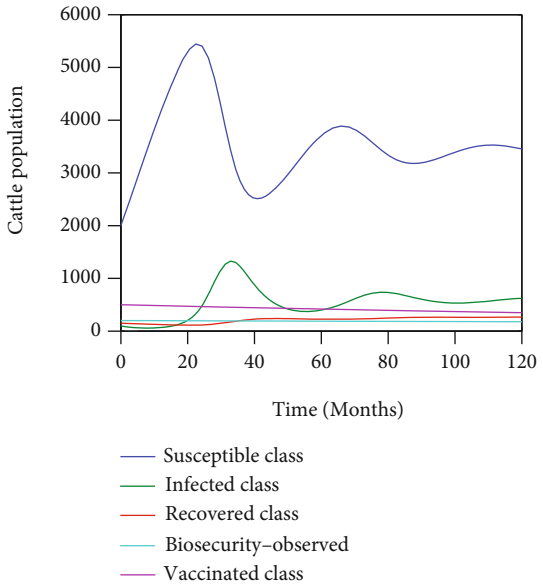
$$\mathscr{P}_2(\lambda) = (\lambda+\mu)\left(\lambda^4 + \mathscr{K}_3\lambda^3 + \mathscr{K}_2\lambda^2 + \mathscr{K}_1\lambda + \mathscr{K}_0\right), \quad (12)$$

where

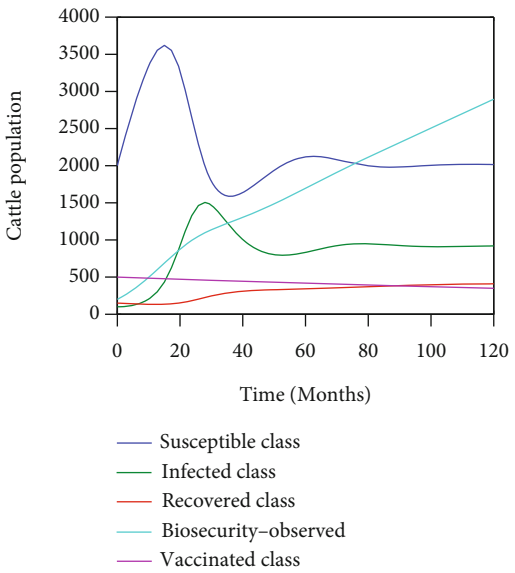
$$\begin{aligned} \mathscr{K}_3 &= \eta_1^* + \eta_2^* + \eta_3^* + \eta_4^* - \beta(S^* + I^*),\\ \mathscr{K}_2 &= 2\beta^2 I^* S^* - \beta(\eta_1^* S^* + \eta_2^* I^*) - (\eta_3^* + \eta_4^*)(\beta(S^* + I^*) - \eta_1^* - \eta_2^*) - \gamma\tau + \eta_1^*\eta_2^* + \eta_3^*\eta_4^*,\\ \mathscr{K}_1 &= \beta(\eta_3^* + \eta_4^*)(2I^*S^*\beta - I^*\eta_2^* - \eta_1^* S^*) + \beta(\gamma\tau S^* - I^*\alpha\kappa) - \beta\eta_3^*\eta_4^*(S^* + I^*) - (\eta_2^* + \eta_3^*)(\gamma\tau - \eta_1^*\eta_4^*) + \eta_2^*\eta_3^*(\eta_1^* + \eta_4^*),\\ \mathscr{K}_0 &= \eta_3^*\left[\eta_4^*\left(2\beta^2 S^* I^* - (\eta_2^* I^* + \eta_1^* S^*)\beta + \eta_1^*\eta_2^*\right) + \tau\gamma(\beta S^* - \eta_2^*)\right] - \alpha\beta\kappa\eta_4^* I^*,\\ \eta_1^* &= \gamma + \epsilon + \mu, \eta_2^* = \alpha + \mu + \psi + \chi, \eta_3^* = \mu + \kappa, \eta_4^* = \mu + \tau. \end{aligned} \quad (13)$$



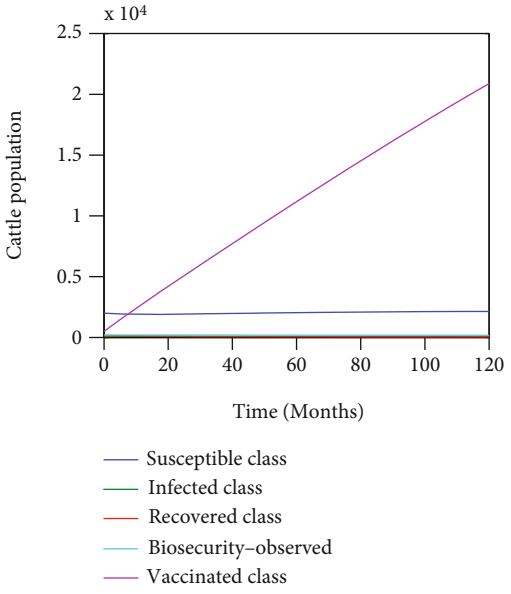
(a) Trajectories of model solution without vaccination, comprehensive biosecurity protocols, and culling of seropositive cattle



(b) Trajectories of model solution with only culling of seropositive cattle by slaughter



(c) Trajectories of model solution with only comprehensive biosecurity protocols



(d) Trajectories of model solution with only vaccination

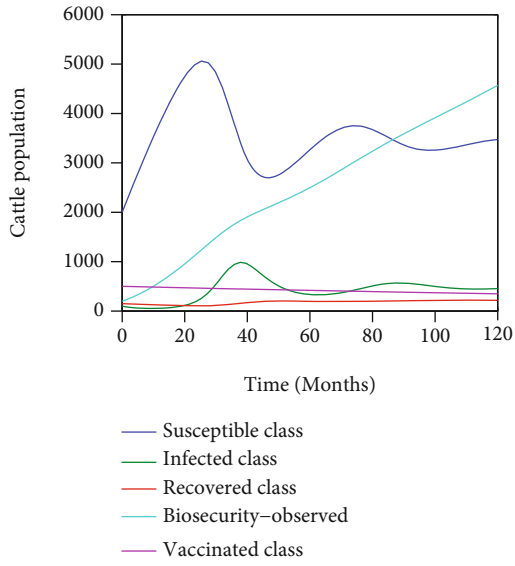
Figure 2: Trajectories of model solutions without any intervention and the implementation of single control measure.

Theorem 5. *The endemic equilibrium is locally asymptotically stable if the following conditions hold:*

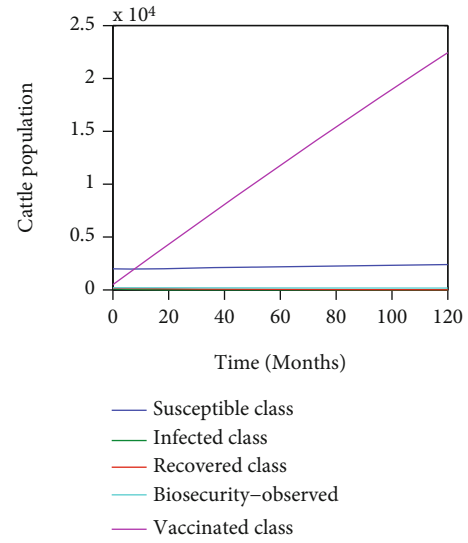
$$\mathcal{K}_0 > 0,\ \mathcal{K}_3 > 0,\ \frac{\mathcal{K}_2\mathcal{K}_3 - \mathcal{K}_1}{\mathcal{K}_3} > 0,$$
$$\frac{\mathcal{K}_3^2\mathcal{K}_0 - \mathcal{K}_1\mathcal{K}_2\mathcal{K}_3 + \mathcal{K}_1^2}{\mathcal{K}_1 - \mathcal{K}_2\mathcal{K}_3} > 0. \tag{14}$$

3.3. Sensitivity Analysis of $\mathcal{R}_0$. Sensitivity analysis refers to the examination of how uncertainty in model output can be apportioned to various sources of uncertainty in the model input [17]. The incidence and prevalence of bovine brucellosis can be reduced or controlled if the significant impact of each parameter in the dynamics of the disease is taken into consideration. Here, the impact of each parameter on the basic reproduction number ($\mathcal{R}_0$) is investigated. Using the normalised forward sensitivity index method (NFSIM), the sensitivity index of the infection rate β is given as

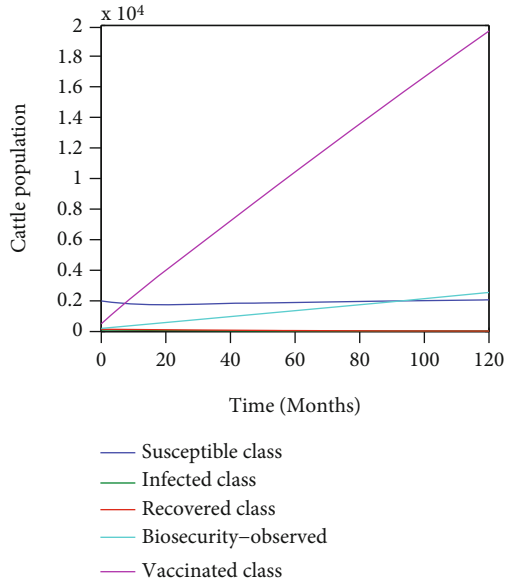
$$\Sigma_\beta^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial \beta} \times \frac{\beta}{\mathcal{R}_0}. \tag{15}$$



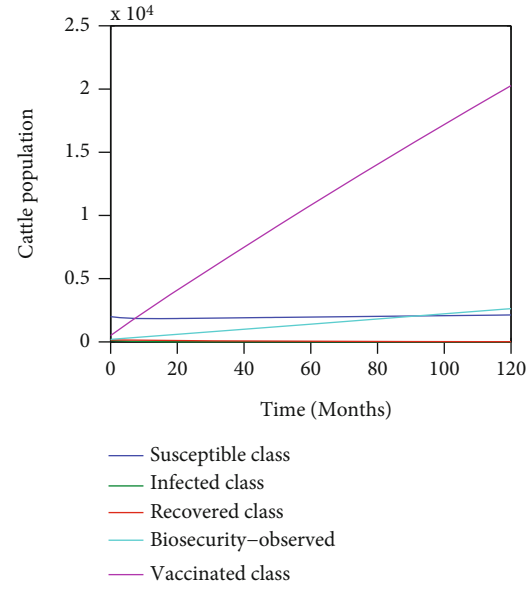
(a) Trajectories of model solution with the implementation of comprehensive biosecurity protocols and culling of seropositive cattle



(b) Trajectories of model solution with vaccination and culling of seropositive cattle by slaughter



(c) Trajectories of model solution with vaccination and comprehensive biosecurity protocols



(d) Trajectories of model solution with vaccination, comprehensive biosecurity protocols, and culling of seropositive cattle by slaughter

FIGURE 3: Trajectories of model solutions with various combination of control interventions.

This implies that

$$\Sigma_{\beta}^{\mathcal{R}_0} = \frac{\omega(\mu+\tau)}{(\mu+\psi+\alpha+\chi)\eta} \times \frac{\beta}{\mathcal{R}_0},$$
$$\Sigma_{\beta}^{R_0} = \frac{0.6}{0.00004676} \times \frac{0.0001}{1.2938} = 0.99998 \approx 1.0000. \quad (16)$$

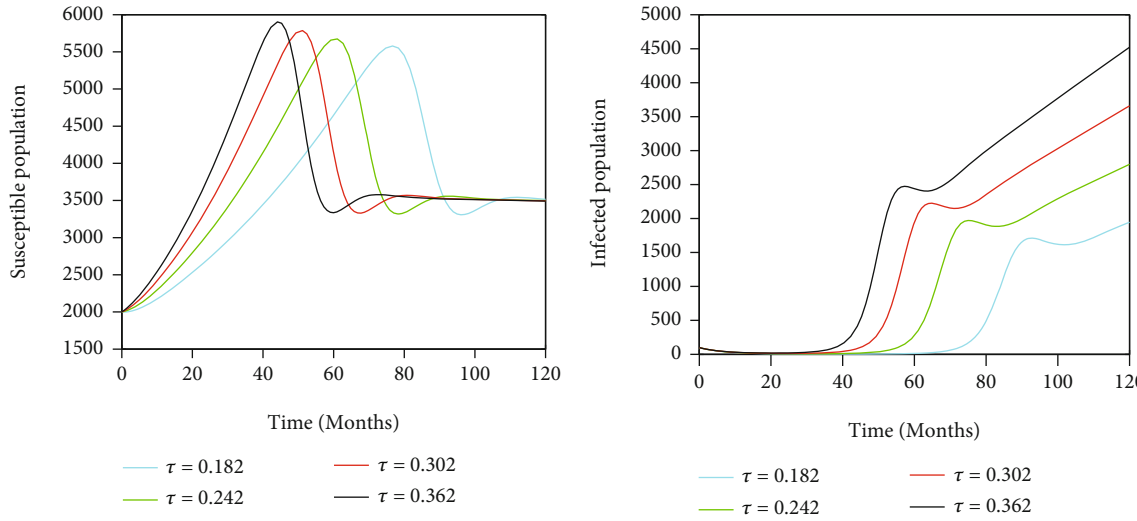
Therefore, the sensitivity index of the infection rate (β) = 1.0000.

Similarly, the rest of the sensitivity indices are computed and tabulated in Table 2.

4. Numerical Simulation

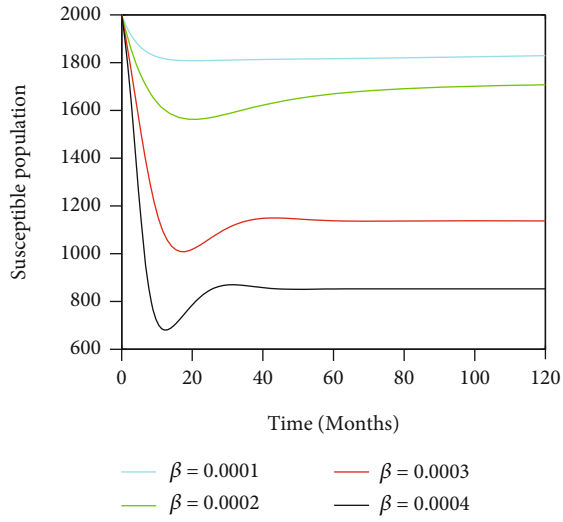
The parameter values used in the simulation of the model are presented in Table 3.

4.1. The Impact of Combining Controls Using the Basic Reproduction Number ($\mathcal{R}_0$) of the Model. Table 4 shows the implementation of different control measures at the same time with the ranks of their basic reproduction numbers. It is shown that the implementation of all the three control measures (vaccination, culling of seropositive cattle, and comprehensive biosecurity protocols) is ranked as the first and the best option in the model to minimise the spread

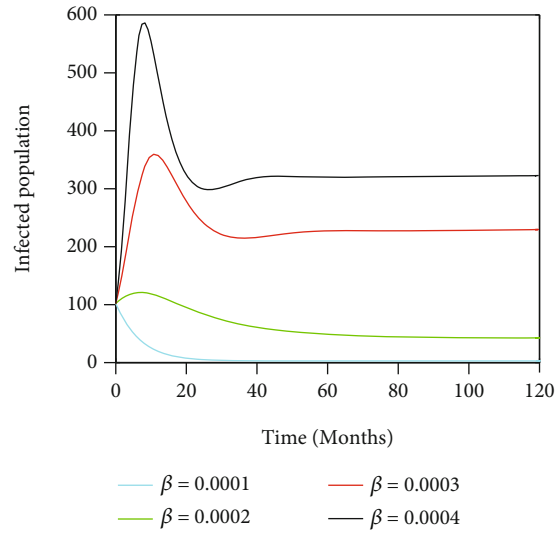


(a) Trajectories of model solution for varying vaccine immunity loss rate in the susceptible population

(b) Trajectories of model solution for varying vaccine immunity loss rate in the infected population



(c) Trajectories of model solution for varying rates of transmission in the susceptible population



(d) Trajectories of model solution for varying rates of transmission in the infected population

Figure 4: Trajectories of model solution for varying rates of vaccine-induced immunity loss and transmission.

of bovine brucellosis, and this is indicated in 4th row, 4th column represented by R1. In addition, when double control measures are implemented at the same time, the combination of vaccination and culling of seropositive cattle is ranked as the second best option in the model to reduce the spread of the disease in a herd of cattle, and this is seen in 2nd row, 4th column represented by R2. Also, the combination of vaccination and biosecurity protocols is ranked third, and it is captured in 1st row, 4th column represented by R3. Finally, the last option in the model to control the spread of bovine brucellosis is the combination of culling of seropositive cattle and biosecurity protocols, and this is indicated in 3rd row, 4th column represented by R4.

4.2. Simulations. In this section, MATLAB Ode45 is considered for the numerical simulations of the model. Table 3 contains the parameter values used for the various simulations.

The numerical simulations of different combination of control measures (vaccination, culling of seropositive cattle, and comprehensive biosecurity protocols) 185 are performed on the cattle population, see Figures 2 and 3.

The impact of the various parameters on the subpopulations is also investigated, see Figure 4.

5. Discussion of Results

It is indicated in Table 2 that the parameters with positive sensitivity index such as the recruitment rate (ω), the transmission rate (β), and the vaccine-induced immunity loss rate (τ) are directly related to the basic reproduction number $(\mathcal{R}_0)$. Also, the parameters with negative sensitivity index such as the vaccination rate (γ), disease-induced death rate (ψ), natural death rate (μ), and culling of seropositive cattle (χ) are inversely related to the basic reproduction

number ($\mathscr{R}_0$). So, in order to curb the spread of bovine brucellosis in cattle, the most sensitive positive parameters should be reduced while the parameters that are inversely related to the basic reproduction number ($\mathscr{R}_0$) should be increased.

It is established in Figures 4(c) and 4(d) that whenever the transmission rate (β) is increased, the number of susceptibles decreased while the number of infectives increased and vice visa. This means that there is a need to minimise the rate of contact between the susceptibles and the infectives in order to reduce transmission of bovine brucellosis in cattle.

It is observed in Figure 2 that the most efficient single control measure is vaccination. Also, it is observed from Table 4 and Figure 3 that the most efficient pair of control measures is vaccination and culling of seropositive cattle by slaughter. However, it is found in Table 4 and Figure 3(d) that the best way to control bovine brucellosis in the cattle is the combination of the three interventions (vaccination, culling of seropositive cattle, and comprehensive biosecurity protocols).

6. Conclusions and Recommendations

6.1. Conclusions. In this paper, a mathematical model is developed to investigate the transmission dynamics of bovine brucellosis in cattle. The basic reproduction number which measures the transmission potential of the disease in the dynamics of the system was computed. Both the disease free equilibrium and the endemic equilibrium points were proven to be asymptotically stable whenever $\mathscr{R}_0 \leq 1$ and $\mathscr{R}_0 > 1$, respectively. The sensitivity analysis conducted as well as the numerical simulations confirms that the most sensitive positive parameters should be reduced, and the parameters that are inversely related to the basic reproduction number ($\mathscr{R}_0$) should be increased in order to minimise the spread of bovine brucellosis. The study of implementing multifaceted control measures revealed that vaccination is the most efficient single control measure. In addition, the most efficient pair of control measures is vaccination and culling of seropositive cattle. However, the overall best option in the model to minimise the spread of bovine brucellosis is the implementation of all the three control measures (vaccination, culling of seropositive cattle, and comprehensive biosecurity protocols).

6.2. Recommendations. To curb the spread of bovine brucellosis in cattle, it is recommended that

(1) Constant vaccination of the susceptible cattle should be encouraged to ensure that the cattle are protected against Brucella infections at all times

(2) Comprehensive biosecurity protocols should be observed across all cattle farms to prevent the disease from invading farms

(3) Cattle movement should be restricted to prevent them from coming into contact with other animals in order to reduce the spread of bovine brucellosis

Data Availability

The data used to support the findings of the study are included within the article.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

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