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MATHEMATICAL MODEL FOR BRUCELLOSIS TRANSMISSION DYNAMICS IN LIVESTOCK AND HUMAN POPULATIONS

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Abstract. Brucellosis is a contagious zoonotic infection caused by bacteria of genus *brucella* which affects humans and animals. The disease is of veterinary importance, public health concern and economic significance in both developed and developing countries. It is transmitted through direct or indirect contact with infected animals or their contaminated products. In this paper we formulate and analyze a deterministic mathematical model for the transmission dynamics of brucellosis. The model formulated incorporates contaminated environment to human, infected livestock to human, and human to human modes of transmission. The impacts of human treatment in controlling the spread of brucellosis in the human population is investigated. Both analytical and numerical solutions reveal that prolonged human treatment has a significant impact in reducing the spread of Brucellosis in human population only while elimination of the disease in domestic ruminants has promising results to both human and ruminants. Thus, brucellosis control strategies should always focus on elimination of the disease in domestic ruminants.

Keywords: brucellosis; mathematical model; human to human transmission.
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1. INTRODUCTION

Brucellosis is a contagious zoonotic infection caused by Gram-negative bacteria of genus brucella that includes; *B. abortus* primarly from cattle, *B. melitensis* from small ruminants, *B. suis* from swine, and *B. canis* from dogs [1, 2, 3, 4]. It is considered by the international organizations like Food and Agriculture Organization (FAO), the World Health Organization (WHO) and World Organization for Animal Health (Office International des Epizooties (OIE)) as one of the most widespread zoonoses in the world alongside bovine tuberculosis and rabies [5]. The disease is an ancient one that was described more than 2000 years ago by the Romans [6] and has been known by various names, including Mediterranean fever, Malta fever, gastric remittent fever, bang's disease, crimean fever, gibraltar fever, rock fever, lazybones disease and undulant fever [7].

Brucella bacteria was first isolated in 1887 from an infected individual's blood by a British military medical officer David Bruce and by that reason the disease was named brucellosis to honor his contribution [8]. Furthermore, in 1905 Zamitt carried out an experiment on goats to investigate the origin of human brucellosis, and found that, human brucellosis originates from goats [9]. To date, eight species of brucella have been identified and named primarily for the source animal or features of infection. Of these, the following four have moderate-to-significant human pathogenicity: *Brucella melitensis* (highest pathogenicity), *Brucella suis* (high pathogenicity), *Brucella abortus* (moderate pathogenicity), *Brucella canis* (moderate pathogenicity) [10, 11, 12].

Brucellosis causes devastating losses to the livestock industry especially small-scale livestock holders, thereby limiting economic growth and hindering access to international markets [13]. The economic importance of the disease is based on the fact that it causes financial losses through abortions, sterility, decreased milk production, veterinary fees and animal replacement costs. In animals, brucellosis is transmitted when a susceptible animal ingest contaminated materials by licking discharges from infected animals and suckling milk from infected dams. In humans the bacteria is transmitted through ingestion of contaminated raw blood and meat, unpasteurized milk or other dairy products. Furthermore, direct contact with aborted fetuses, vaginal discharges and occupational accidents through needle injection during mass vaccination

and during laboratory manipulation may be possible route of brucellosis transmission. In view of this, farmers, laboratory personnels, abattoir workers and veterinarians are at high risk of contracting the disease. According to Ducrotoy *et al.* [14], there are epidemiological situations in which *B. melitensis* is absent but infections of small ruminants by *B. abortus* occur in areas where they are in contact with cattle.

Infected animals exhibit clinical signs that are of economic significance to stakeholders, such as reduced fertility, late term abortion, poor weight gain, lost draught power, and a substantial decline in milk production [13, 15]. However, symptoms in human includes; continuous or intermittent fever, headache, weakness, profuse sweats, chills, joint pains, aches, weight loss as well as devastating complications that leads to miscarriage that occurs within the early trimester in pregnant women [16]. Infection may develop into chronic forms that characterised by neurological complications, endocarditis and testicular or bone abscess formation [17, 18]. The infection can also affect the liver and spleen, and may last for longer terms if not timely treated. Furthermore, the clinical signs of brucellosis in human presents diagnostic challenges because they overlap with other febrile conditions such as typhoid fever, malaria, rheumatic fever, joint diseases and relapsing fever. Since human brucellosis is debilitating disease, it requires prolonged treatment with combination of antibiotics [19].

The global burden of human brucellosis remains high and causes more than 500,000 new human cases per year worldwide. The annual number of reported cases in United States has dropped significantly to about 100 cases per year due to stringent animal vaccination programs and milk pasteurization. Most United States cases are now due to the consumption of illegally imported unpasteurized dairy products from Mexico and approximately 60% of human brucellosis cases occur in California and Texas [20].

In Africa, livestock brucellosis exists throughout sub-Saharan Africa, but the prevalence is unclear and poorly understood with varying reports from country to country, geographical regions as well as animal factors [21]. Most African countries have poor socioeconomic status, with people living with and by their livestock, while health networks, surveillance and vaccination programs are virtually non-existent [20]. Livestock brucellosis is a highly prevalent disease in many areas of Tanzania with limited data available regarding its distribution, affected

host species and impact. The first outbreak of brucellosis was reported in Arusha in 1927 [22]. Previous surveys in Tanzania have demonstrated the occurrence of the disease in cattle in various production systems, regions and zones with individual animal level seroprevalence varying from 1 to 30% while the average prevalence in humans varies from 1 to 5% [23]. A recent study by [24] shows that brucellosis incidence is moderate in northern Tanzania and suggests that the disease is endemic and an important human health problem in this area. Moreover, human cases had been reported in areas of northern, eastern, lake and western zones of Tanzania with seroprevalence varying from 0.7 to 20.5% [25, 26]. Despite the WHO, FAO, OIE efforts and interventions are available, brucellosis continues to pose great economic threat on livelihood and food security in both developed and developing countries from generation to generation. Thus, there is a need to assess the current control strategies and their effectiveness if we are to control or eradicate the disease. So far few studies [10, 27, 28, 29, 30, 31, 32], have been developed to analyze dynamics and spread of brucellosis in a homogeneous/heterogeneous populations. However, none of these studies had considered the mathematical approach to assess the impact of human to human transmission in reducing or eradicating the disease. In this paper, the dynamics and effectiveness of the control strategies for human brucellosis using mathematical models are rigorously studied.

2. Model Formulation

Human to human brucellosis transmission is possible as indicated in various studies including [16, 33, 34, 35, 36]. The possible modes of human to human brucellosis transmission are transplancental, breastfeeding, sexual, blood transfusion and organ transplantation [37]. In this section, we formulate a deterministic mathematical model for the transmission dynamics of brucellosis in domestic small ruminants, cattle and human populations. The model we formulate includes: direct transmission of brucellosis within the cattle, within small ruminants, within humans and from livestock to human, and from the environment to livestock and humans.

Furthermore, susceptible cattle and small ruminants are either vaccinated at some points (pulse vaccination) or remain susceptible. Based on the epidemiological status of individuals, the cattle population at any time t is divided into vaccinated $V_c(t)$, susceptible $S_c(t)$, and infectious $I_c(t)$ classes. Similarly, the small ruminant population at any time t is divided into

vaccinated $V_s(t)$, susceptible $S_s(t)$, and infectious $I_s(t)$ subpopulations while the total human population, $N_h(t)$ at any time t is divided into susceptible, $S_h(t)$, infected, $I_h(t)$ and recovered, $R_h(t)$ individuals. Susceptible cattle become infected through direct contact with infected cattle at the rate of β_c or through contact with the contaminated environment (indirect transmission) at the rate α_c while susceptible small ruminants become infected when they are in contact with infectious small ruminants at the rate of β_s or through contact with the contaminated environment at the rate α_s. The transmission to humans is expressed as additive contributions of transmissions from infective humans, cattle, small ruminants and contaminated environment. Appertaining to the fact that it is very difficult to determine the quantity of brucella in environment, we define the average number of brucella that is enough for a host to be infected with brucellosis as an infectious unit and let $B(t)$ to be the number of infectious units in the environment. The incubation period for brucellosis is hardly detected, but individuals at this period can infect the susceptible individuals at the same transmission rate as the infectious individual and discharge the same quantity of brucella into the environment per unit time as in [28]. It is against this background, we assume that individuals in the incubation period and post incubation period are hosted in the same population compartment called infectious class. The interaction within and between the four populations prompts that veterinary surgeons, laboratory assistants, and farmers are predominantly exposed to the brucella bacteria.

2.1. Model Assumptions. In formulation of the model we make the following assumptions:

i. The mixing of individuals in each population is homogeneous;
ii. There is no direct transmission between cattle and small ruminants;
iii. Infected animals shed brucella pathogens in the environment;
iv. Livestock seropositivity is life-long lasting;
v. Immunized individuals cannot be infected unless their resistance to infection wanes;
vi. There is constant natural mortality rate in each of the species;
vii. The birth rate for each population is greater than natural mortality rate.

The variables and parameters used in this model are respectively summarized in TABLE 1 and TABLE 2.

TABLE 1. Model Variables

Variable	Description
$S_h(t)$	Number of susceptible humans at time t
$I_h(t)$	Number of infected human at time t
$R_h(t)$	Number of recovered humans at time t
$S_c(t)$	Number of susceptible cattle at time t
$I_c(t)$	Number of infected cattle at time t
$V_c(t)$	Number of vaccinated cattle at time t
$S_s(t)$	Number of susceptible small ruminants at time t
$I_s(t)$	Number of infected small ruminants at time t
$V_s(t)$	Number of vaccinated small ruminants at time t
$B(t)$	Number of *brucella* bacteria load per unit volume in the environment at time t

2.2. Compartmental Flow Diagram for the Disease Dynamics. The interactions between the human, cattle, small ruminants populations and the brucella in the environment are illustrated in FIGURE 1.

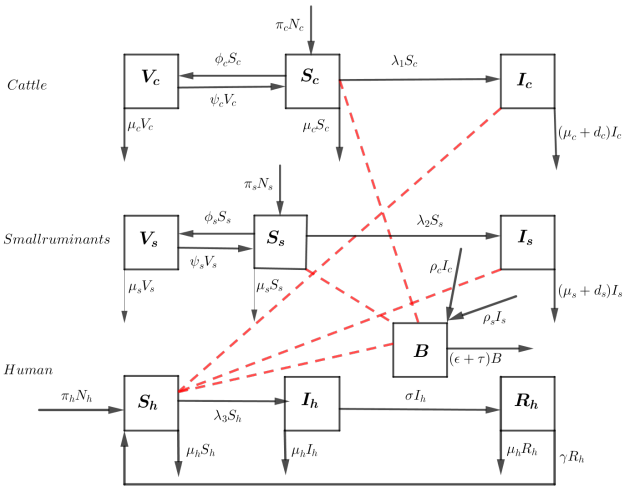


FIGURE 1. A schematic diagram for direct and indirect transmission of brucellosis in cattle, small ruminants and human populations. Solid arrows represent transfer of individuals from one subpopulation to another while dotted lines represent interactions leading to infections.

TABLE 2. Model Parameters used in the model and their description

Parameter	Description
π_c	Per capita cattle birth rate
ϕ_c	Cattle vaccination rate
π_h	Per capita human birth rate
σ	Human recovery rate
μ_h	Per capita human natural death rate
ψ_c	Cattle vaccine efficacy waning rate
β_c	Within cattle transmission rate
d_c	Culling rate of seropositive cattle
μ_c	Per capita cattle natural death rate
α_c	*Brucella* from the environment to cattle transmission rate
α_s	*Brucella* from the environment to small ruminants transmission rate
α_h	*Brucella* from the environment to human transmission rate
ρ_c	*Brucella* shedding rate by infected cattle
ρ_s	*Brucella* shedding rate by infected small ruminants
β_{ch}	Cattle to human transmission rate
β_{sh}	small ruminants to human transmission rate
ε	Decaying rate of brucella in the environment
τ	Environmental hygiene and sanitation rate
π_s	Small ruminants per capita birth rate
ϕ_s	Vaccination rate of small ruminants
ψ_s	Small ruminant vaccine efficacy waning rate
β_s	Within small ruminants transmission rate
d_s	Culling rate of seropositive small ruminants
μ_s	Per capita small ruminants natural death rate

2.3. Model Equations. Based on the assumptions and the inter-relations between the variables and the parameters shown in FIGURE 1, the transmission dynamics of Brucellosis can be described by the following ordinary differential equations:

$$
\begin{aligned}
\frac{dV_c}{dt} &= \phi_c S_c - (\psi_c + \mu_c)V_c \\
\frac{dS_c}{dt} &= \pi_c N_c + \psi_c V_c - (\lambda_1 + \phi_c + \mu_c)S_c \\
\frac{dI_c}{dt} &= \lambda_1 S_c - (\mu_c + d_c)I_c \\
\frac{dV_s}{dt} &= \phi_s S_s - (\mu_s + \psi_s)V_s \\
\frac{dS_s}{dt} &= \pi_s N_s + \psi_s V_s - (\lambda_2 + \phi_s + \mu_s)S_s \\
\frac{dI_s}{dt} &= \lambda_2 S_s - (\mu_s + d_s)I_s \\
\frac{dS_h}{dt} &= \pi_h N_h + \gamma R_h - (\lambda_3 + \mu_h)S_h \\
\frac{dI_h}{dt} &= \lambda_3 S_h - (\sigma + \mu_h + d_h)I_h \\
\frac{dR_h}{dt} &= \sigma I_h - (\gamma + \mu_h)R_h \\
\frac{dB}{dt} &= \rho_c I_c + \rho_s I_s - (\varepsilon + \tau)B
\end{aligned} \tag{1}
$$

where,

$$\lambda_1 = \beta_c I_c + \alpha_c B. \tag{2}$$

$$\lambda_2 = \beta_s I_s + \alpha_s B. \tag{3}$$

$$\lambda_3 = \beta_{hc} I_c + \beta_{hh} I_h + \beta_{hs} I_s + \alpha_h B. \tag{4}$$

3. Model Properties

3.1. Invariant Region. In this subsection we assess the well-posedness of the model by investigating the existence and feasibility of its solution. In other words, we investigate whether the solutions are epidemiologically (variables have biological interpretation) and mathematically (a unique bounded solution exists for all the time) well-posed. That is solutions of model system

(1) with nonnegative initial data remain nonnegative for all time $t \geq 0$. The model system (1) can be expressed in the compact form as:

$$\frac{dX}{dt} = AX + F$$

where,

$$A = \begin{bmatrix}
-(\mu_c+\psi_c) & \phi_c & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\psi_c & -d_0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \lambda_1 & -(\mu_c+d_c) & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & -(\mu_s+\psi_s) & \phi_s & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & \psi_s & -d_1 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \lambda_2 & -(\mu_s+d_s) & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & -d_2 & 0 & \gamma & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \lambda_3 & -d_3 & 0 & 0 \\
0 & 0 & \rho_c & 0 & 0 & 0 & 0 & \sigma & -(\gamma+\mu_h) & 0 \\
0 & 0 & \rho_c & 0 & 0 & \rho_s & 0 & 0 & 0 & -(\varepsilon+\tau)
\end{bmatrix}$$

with,

$$d_0 = (\lambda_1 + \phi_c + \mu_c),\ d_1 = (\lambda_2 + \phi_s + \mu_s),$$

$$d_2 = (\lambda_3 + \mu_h),\ d_3 = (\sigma + \mu_h + d_h),$$

$$X = (V_c, S_c, I_c, V_s, S_s, I_s, S_h, I_h, R_h, B),$$

and F is a column vector given by

$$F = (0, \pi_c N_c^0, 0, 0, \pi_s N_s^0, 0, \pi_h N_h^0, 0, 0, 0)^T.$$

It can be noticed that AX is Meltzer matrix since all of its off diagonal entries are non negative, for all $X \in \mathbb{R}_+^{10}$. Therefore, using the fact that $F > 0$, the model system (1) is positively invariant in $\mathbb{R}_+^{10}$, which means that an arbitrary trajectory of the system starting in $\mathbb{R}_+^{10}$ remains in $\mathbb{R}_+^{10}$ forever. In addition, the right hand F is Lipschitz continuous. Thus, a unique maximal solution exists and so:

$$\Omega = \{(V_c, S_c, I_c, V_s, S_s, I_s, S_h, I_h, R_h, B) \geq 0\} \in \mathbb{R}_+^{10}.$$

is the feasible region for the model (1). Thus, the model (1) is epidemiologically and mathematically well-posed in the region Ω.

4. Model Analysis

4.1. Disease Free Equilibrium. The Brucellosis free equilibrium point is obtained by setting the right hand side of equations in model system (1) to zero, that is:

$$\frac{dV_c}{dt} = \frac{dS_c}{dt} = \frac{dI_c}{dt} = \frac{dV_s}{dt} = \frac{dS_s}{dt} = \frac{dI_s}{dt} = \frac{dS_h}{dt} = \frac{dI_h}{dt} = \frac{dR_h}{dt} = \frac{dB}{dt} = 0.$$

Let the disease free equilibrium point of Brucellosis model be E^0. In case there is no disease $I_c = I_s = I_h = B = 0$ that is, the sum of susceptible and vaccinated populations is equal to total population. There exists a disease free equilibrium $E^0 = (V_c^0, S_c^0, 0, V_s^0, S_s^0, 0, S_h^0, 0, 0, 0)$ for model system (1) where:

$$V_c^0 = \frac{\phi_c \pi_c N_c^0}{\mu_c(\phi_c + \psi_c + \mu_c)}, S_c^0 = \frac{(\mu_c + \psi_c)\pi_c N_c^0}{\mu_c(\phi_c + \psi_c + \mu_c)}, V_s^0 = \frac{\phi_s \pi_s N_s^0}{\mu_s(\phi_s + \psi_s + \mu_s)}, \; S_s^0 = \frac{(\mu_s + \psi_s)\pi_s N_s^0}{\mu_s(\phi_s + \psi_s + \mu_s)},$$

and

$$S_h^0 = \frac{\pi_h N_h^0}{\mu_h}.$$

4.2. The Effective Reproduction Number. In this subsection, we compute the effective reproduction number for model system (1) using the standard method of the next generation matrix developed in [38, 39]. The effective reproduction number, R_e is defined as the measure of average number of infections caused by a single infectious individual introduced in a community in which intervention strategies are administered [40]. The magnitude of the effective reproduction number is used to indicate both the risk of an epidemic and effort required to control an infection. When there are no interventions or controls, the number of secondary infections caused by typical infected individual during his entire period of infectiousness is called basic reproduction number, R_0. Moreover, due to the natural history of some infections, transmissibility is better quantified by the effective reproduction number rather than the basic

reproduction number [42]. Considering the system for the infective variables:

$$\begin{aligned}
\frac{dI_c}{dt} &= (\beta_c I_c + \alpha_c B)S_c - (\mu_c + d_c)I_c \\
\frac{dI_s}{dt} &= (\beta_s I_s + \alpha_s B)S_s - (\mu_s + d_s)I_s \\
\frac{dI_h}{dt} &= (\beta_{hc} I_c + \beta_{hs} I_s + \beta_{hh} I_h + \alpha_h B)S_h - (\mu_h + d_h)I_h \\
\frac{dB}{dt} &= \rho_c I_c + \rho_s I_s - (\varepsilon + \tau)B
\end{aligned} \tag{5}$$

The effective reproduction number is obtained by taking the spectral radius of the next generation matrix:

$$FV^{-1} = \left[\frac{\partial \mathscr{F}_i(E^0)}{\partial t}\right]\left[\frac{\partial \mathscr{V}_i(E^0)}{\partial t}\right]^{-1}$$

where E^0 is the brucellosis-free equilibrium point while $\mathscr{F}_i$ and $\mathscr{V}_i$ are vectors representing respectively, the rate of appearance of new infection in compartment i and the transfer of infections from compartment i to another, such that:

$$\mathscr{F}_i = \begin{bmatrix} (\beta_c I_c + \alpha_c B)S_c \\ (\beta_s I_s + \alpha_s B)S_s \\ (\beta_{hc} I_c + \beta_{hs} I_s + \beta_{hh} I_h + \alpha_h B)S_h \\ 0 \end{bmatrix}$$

$$\mathscr{V}_i = \begin{bmatrix} (\mu_c + d_c)I_c \\ (\mu_s + d_s)I_s \\ (\sigma + \mu_h + d_h)I_h \\ -\rho_c I_c - \rho_s I_s + (\varepsilon + \tau)B \end{bmatrix}$$

It is important to note that $\mathscr{V}_i$ is a resultant vector of the two vectors: $\mathscr{V}_i^+$, defined as the rate of transfer of individuals into compartment i by all other means(e.g births and immigration); and $\mathscr{V}_i^-$, which is the rate of transfer of individuals out of compartment i (e.g deaths, recovery and emigration). In particular:

$$\mathscr{V}_i = \mathscr{V}_i^- - \mathscr{V}_i^+, i = \{1,2,3,4\}$$

The Jacobian matrices F of $\mathscr{F}_i$ and V of $\mathscr{V}_i$ evaluated at E^0 are respectively:

$$F = \begin{bmatrix} \beta_c S_c^0 & 0 & 0 & \alpha_c S_c^0 \\ 0 & \beta_s S_s^0 & 0 & \alpha_s S_s^0 \\ \beta_{hc} S_h & \beta_{hs} S_h & \beta_{hh} S_h & \alpha_h B \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

and

$$V = \begin{bmatrix} \mu_c + d_c & 0 & 0 & 0 \\ 0 & \mu_s + d_s & 0 & 0 \\ 0 & 0 & \sigma + \mu_h + d_h & 0 \\ -\rho_c & -\rho_s & 0 & (\varepsilon + \tau) \end{bmatrix}$$

Referring to the infected states with indices i and j, for $i, j \in [1,2,3,4]$, the entry F_{ij} is the rate at which individuals in infected state j give rise or produce new infections to individuals in infected state i, in the linearized system. Thus, when there is no new cases produced in infected state i by an individual in infected state j immediately after infection, we have $F_{ij} = 0$. The inverse of V is found to be:

$$V^{-1} = \begin{bmatrix} \frac{1}{\mu_c + d_c} & 0 & 0 & 0 \\ 0 & \frac{1}{\mu_s + d_s} & 0 & 0 \\ 0 & 0 & \frac{1}{\sigma + \mu_h + d_h} & 0 \\ \frac{\rho_c}{(\mu_c + d_c)(\varepsilon + \tau)} & \frac{\rho_s}{(\mu_s + d_s)(\varepsilon + \tau)} & 0 & \frac{1}{\varepsilon + \tau} \end{bmatrix}$$

The entry $\left(V^{-1}\right)_{ij}$ is the average length of time an infected individual spends in compartment j during its lifetime when introduced into the compartment i of disease free equilibrium, assuming that the population remains near the disease free equilibrium and barring reinfection. In particular, $\frac{1}{\mu_c + d_c}$, $\frac{1}{\mu_s + d_s}$, $\frac{1}{\sigma + \mu_h + d_h}$ are respectively the average times an infectious cattle, small ruminant, human spend in the state of being infective, and $\frac{1}{\varepsilon + \tau}$ is the average time *brucella* bacteria spend in the environment. Furthermore, *brucella* from cattle will spend $\frac{\rho_c}{\mu_c + d_c} \times \frac{1}{\varepsilon + \tau}$ time in the environment where, $\frac{\rho_c}{\mu_c + d_c}$ is the probability that an infective cattle will shed *brucella* into the environment. On the other hand, *brucella* shed by small ruminants will spend $\frac{\rho_s}{\mu_s + d_s} \times \frac{1}{\varepsilon + \tau}$ time in the environment where $\frac{\rho_s}{\mu_s + d_s}$ is the probability that an infected small ruminant will shed *brucella* into the environment. Moreover, the Next Generation

Matrix is calculated to be:

$$FV^{-1} = \begin{bmatrix} R_{11} & R_{12} & 0 & \frac{\alpha_c S_c^0}{\varepsilon+\tau} \\ R_{21} & R_{22} & 0 & \frac{\alpha_s S_s^0}{\varepsilon+\tau} \\ R_{31} & R_{32} & R_{33} & \frac{\alpha_h S_h^0}{\varepsilon+\tau} \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{6}$$

where,

$$\begin{aligned} R_{11} &= \frac{\beta_c S_c^0}{\mu_c + d_c} + \frac{\alpha_c \rho_c S_c^0}{(\mu_c + d_c)(\varepsilon+\tau)}, \\ R_{12} &= \frac{\alpha_c \rho_s S_c^0}{(\mu_s + d_s)(\varepsilon+\tau)}, \\ R_{21} &= \frac{\alpha_s \rho_c S_s^0}{(\mu_c + d_c)(\varepsilon+\tau)}, \\ R_{22} &= \frac{\beta_s S_s^0}{\mu_s + d_s} + \frac{\alpha_s \rho_s S_s^0}{(\mu_s + d_s)(\varepsilon+\tau)}, \\ R_{31} &= \frac{\beta_{hc} S_h^0}{\mu_c + d_c} + \frac{\alpha_h \rho_c S_h^0}{(\mu_c + d_c)(\varepsilon+\tau)}, \\ R_{32} &= \frac{\beta_{hs} S_h^0}{\mu_s + d_s} + \frac{\alpha_h \rho_s S_h^0}{(\mu_c + d_c)(\varepsilon+\tau)}, \\ R_{33} &= \frac{\beta_{hh} S_h^0}{(\sigma + \mu_h + d_h)}. \end{aligned}$$

The matrix FV^{-1} can be written as: The (i,k) entry of the Next Generation Matrix FV^{-1} is the expected number of secondary infections in compartment i produced by individuals initially in compartment k assuming that the environment of an infective individual remains homogeneous for the duration of its infection [41, 42, 43]. In particular; R_{11} is the expected number of infected cattle produced by one infectious cattle, R_{12} is the expected number of infected cattle produced by one infectious small ruminant via consumption of brucella from the environment, R_{21} is the expected number of infected small ruminant as a result of one infected cattle, R_{22} is the expected number of infected small ruminant as a result of effective contact with one infected small ruminant, R_{31} is the expected number of infected people caused by one infectious cattle,R_{32} is the expected number of infected people caused as a result of contact with brucella from small ruminants, R_{33} is the expected number of infected people caused by one infectious

person, and R_{34} is the expected number of infected people as a result of contact of brucella from the environment. It can further be noticed that, matrix FV^{-1} is non-negative and therefore, has a nonnegative eigenvalue. The non-negative eigenvalue is associated with a non-negative eigenvector which represents the distribution of infected individuals that produces the greatest number R_e of secondary infections per generation [44]. Thus, the spectral radius for our Next Generation Matrix is:

$$\rho(FV^{-1}) = R_e = max\left\{\frac{R_{11}+R_{22}+\sqrt{(R_{22}-R_{11})^2+4R_{12}R_{21}}}{2}, \frac{\beta_{hh}\pi_h N_h^0}{\mu_h(\sigma+\mu_h+d_h)}\right\} \tag{7}$$

where,

$$\begin{aligned}
R_{11} =& \frac{(\beta_c(\varepsilon+\tau)+\alpha_c\rho_c)(\psi_c+\mu_c)\pi_c N_c^0}{\mu_c(\mu_c+d_c)(\varepsilon+\tau)(\phi_c+\psi_c+\mu_c)},\\
R_{12} =& \frac{(\psi_c+\mu_c)\alpha_c\rho_s\pi_c N_c^0}{\mu_c(\mu_s+d_s)(\varepsilon+\tau)(\phi_c+\psi_c+\mu_c)},\\
R_{22} =& \frac{(\beta_s(\varepsilon+\tau)+\alpha_s\rho_s)(\psi_s+\mu_s)\pi_s N_s^0}{\mu_s(\mu_s+d_s)(\varepsilon+\tau)(\phi_s+\psi_s+\mu_s)},\\
R_{21} =& \frac{(\psi_s+\mu_s)\alpha_s\rho_c\pi_s N_s^0}{\mu_s(\mu_c+d_c)(\varepsilon+\tau)(\phi_s+\psi_s+\mu_s)}.
\end{aligned}$$

The first and the second expressions of equation (7) represents respectively the effective reproduction numbers in the livestock and human populations. It can further be noticed that, the first expression which is independent of the human population represents the threshold transmission dynamics of brucellosis in the cattle and small ruminants populations that was analyzed and discussed in [45]. The fact that human brucellosis significantly reduces work performance of individuals calls for a special interest of investigating the transmission dynamics and controls of human brucellosis. Thus, we focus on brucellosis transmission dynamics within the human population. The effective reproduction number within the human population is found to be:

$$R_{eh} = \frac{\beta_{hh}\pi_h N_h^0}{\mu_h(\sigma+\mu_h+d_h)}.$$

When there is no treatment, $\sigma = 0$, we have the within human basic reproduction number which is given by:

$$R_{0h} = \frac{\beta_{hh}\pi_h N_h^0}{\mu_h(\mu_h+d_h)}.$$

Besides, brucellosis is a zoonosis; it is transmitted to human from animals, referring to our particular case in the next generation matrix (6) the cattle to human effective reproduction number is intuitively given by:

$$R_{hc} = R_{31} = \frac{(\beta_{hc}(\varepsilon+\tau)+\alpha_h\rho_c)\pi_h N_h^0}{(\mu_c+d_c)(\varepsilon+\tau)}.$$

On the other hand, the small ruminants to human effective reproduction number is given by:

$$R_{hs} = R_{32} = \frac{(\beta_{hs}(\varepsilon+\tau)+\alpha_h\rho_s)\pi_h N_h^0}{(\mu_s+d_s)(\varepsilon+\tau)}.$$

Moreover, equation (4) indicates that, the transmission of brucellosis in the human population results from human to human transmission, small ruminants to human transmission, cattle to human transmission and environment to human transmission. Thus, if it happens one infected cattle, one infected small ruminant and one infected human are simultaneously introduced in the human population, then the effective human reproduction number is intuitively given by:

$$R_h = \frac{\beta_{hh}\pi_h N_h^0}{\mu_h(\sigma+\mu_h+d_h)} + \frac{(\beta_{hc}(\varepsilon+\tau)+\alpha_h\rho_c)\pi_h N_h^0}{(\mu_c+d_c)(\varepsilon+\tau)} + \frac{(\beta_{hs}(\varepsilon+\tau)+\alpha_h\rho_s)\pi_h N_h^0}{(\mu_s+d_s)(\varepsilon+\tau)}. \tag{8}$$

4.3. Local Stability of the Disease Free Equilibrium. In this subsection we use the trace-determinant method to investigate the local stability of the brucellosis free equilibrium point.

Theorem 4.1. *The disease free equilibrium for the brucellosis model system(1) is locally asymptotically stable if* $R_0 < 1$ *and unstable if* $R_0 > 1$.

Proof. We show that, variational matrix $J(E_0)$ of the brucellosis model at DFE has a negative trace and positive determinant. The Jacobian matrix for system (1) is given by:

$$J(E_0) = \begin{bmatrix} -a_1 & \phi_c & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \psi_c & -a_2 & a_3 & 0 & 0 & 0 & 0 & 0 & 0 & -\alpha_c S_c^0 \\ 0 & 0 & a & 0 & 0 & 0 & 0 & 0 & 0 & \alpha_c S_c^0 \\ 0 & 0 & 0 & -b_1 & \phi_s & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \psi_s & b_2 & b_3 & 0 & 0 & 0 & -\alpha_s S_s^0 \\ 0 & 0 & 0 & 0 & 0 & b & 0 & 0 & 0 & \alpha_s S_s^0 \\ 0 & 0 & -\beta_{hc} S_h & 0 & 0 & -\beta_{hs} S_h & -\mu_h & -c_1 & \gamma & -\alpha_h S_h^0 \\ 0 & 0 & \beta_{hc} S_h & 0 & 0 & \beta_{hs} S_h & 0 & c & 0 & \alpha_h S_h^0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma & -(\gamma+\mu_h) & 0 \\ 0 & 0 & \rho_c & 0 & 0 & \rho_s & 0 & 0 & 0 & -(\varepsilon+\tau) \end{bmatrix}$$

where,

$$a_1 = \mu_c + \psi_c,\ a_2 = (\phi_c + \mu_c)\ , a_3 = -\beta_c S_c^0,$$

$$b_1 = \mu_s + \psi_s,\ b_2 = -(\phi_s + \mu_s)\ , b_3 = -\beta_s S_s^0,$$

$$c_1 = \beta_{hh} S_h^0,\ , c = \beta_{hh} S_h^0 - (\sigma + \mu_h + d_h),$$

$$a = \beta_c S_c^0 - (\mu_c + d_c),$$

and

$$b = \beta_s S_s^0 - (\mu_s + d_s).$$

The trace of the Jacobian matrix $J(E_0)$is given by:

$$\begin{aligned} Tr(J(E_0)) = &-(\mu_c + d_c)\left(1 - \frac{\beta_c S_c^0}{\mu_c + d_c}\right) - (\mu_s + d_s)\left(1 - \frac{\beta_s S_s^0}{\mu_s + d_s}\right) \\ &-(\sigma + \mu_h + d_h)\left(1 - \frac{\beta_{hh} S_h^0}{\sigma + \mu_h + d_h}\right) - (\phi_c + \psi_c + 2\mu_c) \\ &-(\phi_s + \psi_s + 2\mu_s) - (\gamma + 2\mu_h) - (\varepsilon + \tau) \end{aligned}$$

Thus, the trace of the Jocobian matrix is the less than zero, that is $Tr(J(E_0)) < 0$ if:

$$\frac{\beta_c S_c^0}{\mu_c + d_c} < 1,\ \frac{\beta_s S_s^0}{\mu_c + d_s} < 1 \text{ and } \frac{\beta_{hh} S_h^0}{\sigma + \mu_h + d_h} < 1.$$

Furthermore, the determinant of matrix $J(E_0)$ is computed using Maple 16 Software and is found to be:

$$Det(J(E_0)) = a_0\,(1-R_h)\left((1-R_c)\,(1-R_{ec}) - \frac{\rho_c\alpha_c S_c^0}{(\mu_c+d_c)(\varepsilon+\tau)}\,(1-R_s)\right).$$

where,

$$R_h = \frac{\beta_{hh}S_h^0}{\sigma+\mu_h+d_h},\ R_s = \frac{\beta_s S_s^0}{\mu_s+d_s},\ R_c = \frac{\beta_c S_c^0}{\mu_c+d_c},\ R_{es} = \frac{(\varepsilon+\tau)\beta_s S_s^0}{(\varepsilon+\tau)(\mu_s+d_s)},$$

and

$$a_0 = (\phi_c+\psi_c+\mu_c)(\phi_s+\psi_s+\mu_s)(\gamma+\mu_h)(\sigma+\mu_h+d_h)(\mu_c+d_c)(\mu_s+d_s)(\varepsilon+\tau)\mu_c\mu_s\mu_h.$$

The determinant of the Jacobian matrix is positive (i.e. $J(E_0)>0$) if:

$$R_c<1,\ R_s<1,\ R_{es}<1, \text{ and } (1-R_c)\,(1-R_{ec}) > \frac{\rho_c\alpha_c S_c^0}{(\mu_c+d_c)(\varepsilon+\tau)}\,(1-R_s).$$

Furthermore, R_h, R_s, R_c, and R_{es} are respectively the average number of secondary human infections as a result of direct contact between susceptible and infected humans, susceptible and infected small ruminants, susceptible and infected cattle, and the average number of secondary infections caused directly or indirectly by one infected small ruminant in the susceptible ruminant population. Thus, the brucellosis free equilibrium for each population is locally asymptotically stable if $R_e<1$. A similar result is found on Theorem 2 of [41] and Theorem 6.13 of [46]. □

4.4. Global Stability of the Disease-Free Equilibrium. In this section, we analyze the global stability of the disease-free equilibrium point by applying the [47] approach. We write model system (1) in the form:

$$\begin{cases} \dfrac{dX_s}{dt} = A(X_s - X_{DFE,S}) + A_1X_i \\ \dfrac{dX_i}{dt} = A_2X_i \end{cases} \tag{9}$$

where X_s is the vector representing the non-transmitting compartments and X_i is the vector representing the transmitting components. The DFE is globally asymptotically stable if A has

real negative eigenvalues and A_2 is a Metzler matrix (i.e. the off-diagonal elements of A_2 are non-negative). From model system (1) we have:

$$X_i = (I_c, I_s, I_h, B)^T, X_s = (V_c, S_c, V_s, S_s, S_h, R_h)^T,$$

$$X_s - X_{DFE,s} = \begin{bmatrix} V_c - \dfrac{\phi_c \pi_c N_c^0}{\mu_c(\psi_c + \phi_c + \mu_c)} \\ S_c - \dfrac{(\phi_c + \mu_c)\pi_c N_c^0}{\mu_c(\psi_c + \phi_c + \mu_c)} \\ V_s - \dfrac{\phi_s \pi_s N_s^0}{\mu_s(\psi_s + \phi_s + \mu_s)} \\ S_s - \dfrac{(\phi_s + \mu_s)\pi_s N_s^0}{\mu_s(\psi_s + \phi_s + \mu_s)} \\ S_h - \dfrac{\pi_h N_h^0}{\mu_h} \\ R_h \end{bmatrix}$$

and

$$A_1 = \begin{bmatrix} 0 & 0 & 0 & 0 \\ -\beta_c S_c & 0 & 0 & -\alpha_c S_c \\ 0 & 0 & 0 & 0 \\ 0 & -\beta_s S_s & 0 & -\alpha_s S_s \\ -\beta_{hc} S_h & -\beta_{hs} S_h & -\beta_{hc} S_h & -\alpha_h S_h \\ 0 & 0 & \sigma & 0 \end{bmatrix}$$

We need to check whether a matrix A for the non-transmitting compartments has real negative eigenvalues and that A_2 is a Metzler matrix. From the equation for non-transmitting compartments in (1) we have:

$$A = \begin{bmatrix} -(\psi_c+\mu_c) & \phi_c & 0 & 0 & 0 & 0 \\ \psi_c & -(\phi_c+\mu_c) & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\psi_s+\mu_s) & \phi_s & 0 & 0 \\ 0 & 0 & \psi_s & -(\phi_s+\mu_s) & 0 & 0 \\ 0 & 0 & 0 & 0 & -\mu_h & \gamma \\ 0 & 0 & 0 & 0 & 0 & -(\gamma+\mu_h) \end{bmatrix}$$

with eigenvalues $\lambda_1 = -\mu_s, \lambda_2 = -(\psi_s+\phi_s+\mu_s), \lambda_3 = -\mu_c, \lambda_4 = -(\psi_c+\phi_c+\mu_c)$; and

$$A_2 = \begin{bmatrix} \beta_c S_c^0 - (\mu_c+d_c) & 0 & 0 & \alpha_c S_c^0 \\ 0 & \beta_s S_s^0 - (\mu_s+d_s) & 0 & \alpha_s S_s^0 \\ \beta_{hc} S_h & \beta_{hs} S_h^0 & \beta_{hh} S_h - (\mu_h+d_h) & \alpha_h S_h^0 \\ \rho_c & \rho_s & 0 & -(\varepsilon+\tau) \end{bmatrix}$$

Appertaining the fact that all model parameters and variables are non-negative, it is evident that A_2 is a Metzler matrix and A, have real negative eigenvalues. This implies that the disease free equilibrium for the model system (1) is globally asymptotically stable.

4.5. Global Stability of Endemic Equilibrium. The local stability of the disease free equilibrium suggests local stability of the endemic equilibrium for the reverse condition. In this subsection we study the global behaviour of the endemic equilibrium, E^* for the model system (1).

Theorem 4.2. *The endemic equilibrium point for the brucellosis model system (1) is globally asymptotically stable on* Ω *if* $R_0 > 1$.

Proof. We construction an explicit Lyapunov function for model system (1) using [48, 49, 50, 51, 52] approach as it is useful to most of the sophisticated compartmental epidemiological models. In this approach, we construct Lyapunov functions of the form:

$$V = \sum a_i (x_i - x_i^* \ln x)$$

where a_i is a properly selected positive constant, x_i is the population of the i^{th} compartment and x_i^* is the equilibrium level. We define the Lyapunov function candidate V for model system (1) as:

$$\begin{aligned} L =&(S_c - S_c^* \ln S_c) + A_1(V_c - V_c^* \ln V_c) + A_2(I_c - I_c^* \ln I_c) + (S_s - S_s^* \ln S_s) \\ &+ A_3(V_s - V_s^* \ln V_s) + A_4(I_s - I_s^* \ln I_s) + (S_h - S_h^* \ln S_h) + A_5(I_h - I_h^* \ln I_h) \\ &+ A_6(R_h - R_h^* + A_7(B - B^* \ln B)). \end{aligned} \tag{10}$$

where $A_1, A_2, A_3, A_4, A_5, A_6$ and A_7 are positive constants. The time derivative of the Lyapunov function L is given by:

$$\begin{aligned} \frac{dL}{dt} =& \left(1 - \frac{S_c^*}{S_c}\right)\frac{dS_c}{dt} + A_1\left(1 - \frac{V_c^*}{V_c}\right)\frac{dV_c}{dt} + A_2\left(1 - \frac{I_c^*}{I_c}\right)\frac{dI_c}{dt} + \left(1 - \frac{S_s^*}{S_s}\right)\frac{dS_s}{dt} \\ &+ A_3\left(1 - \frac{V_s^*}{V_s}\right)\frac{dV_s}{dt} + A_4\left(1 - \frac{I_s^*}{I_s}\right)\frac{dI_s}{dt} + \left(1 - \frac{S_h^*}{S_h}\right)\frac{dS_h}{dt} + A_5\left(1 - \frac{I_h^*}{I_h}\right)\frac{dI_h}{dt} \\ &A_6\left(1 - \frac{R_h^*}{R_h}\right)\frac{dR_h}{dt} + A_7\left(1 - \frac{B^*}{B}\right)\frac{dB}{dt}. \end{aligned} \tag{11}$$

Considering (1) at the endemic equilibrium solution E^* we have:

$$\pi_h N_h = -\gamma R_h^* + (\beta_{hc} I_c^* + \beta_{hs} I_s^* + \beta_{hh} I_h^* + \alpha_h B^*) S_h^*,$$

$$\sigma + \mu_h + d_h = (\beta_{hc} I_c^* + \beta_{hs} I_s^* + \beta_{hh} I_h^* + \alpha_h B^*)\frac{S_h^*}{I_h^*},$$

$$\pi_s N_s = (\beta_s I_s^* + \alpha_s B^* + \phi_s + \mu_s) S_s^* - \psi_s V_s^*,$$

$$\pi_c N_c = (\beta_c I_c^* + \alpha_c B^* + \phi_c + \mu_c) S_c^* - \psi_c V_c^*,$$

$$\mu_c + d_c = \frac{(\beta_c I_c^* + \alpha_c B^*) S_c^*}{I_c^*},$$

$$\mu_s + d_s = \frac{(\beta_s I_s^* + \alpha_s B^*) S_s^*}{I_s^*},$$

$$(\varepsilon + \tau) = \frac{\rho_c I_c^* + \rho_s I_s^*}{B^*},$$

$$\phi_c = \frac{(\psi_c + \mu_c) V_c^*}{S_c^*},$$

$$\phi_s = \frac{(\psi_s + \mu_s) V_s^*}{S_s^*},$$

$$\sigma = \frac{(\gamma + \mu_h) R_h^*}{I_h^*}.$$

Then, equation (11) may be re-written as:

$$\begin{aligned}
\frac{dL}{dt} =& -(\phi_c+\mu_c)S_c\left(1-\frac{S_c^*}{S_c}\right)^2-(\phi_s+\mu_s)S_s\left(1-\frac{S_s^*}{S_s}\right)^2-\mu_h S_h\left(1-\frac{S_h^*}{S_h}\right)^2\\
&-\left(1-\frac{S_c^*}{S_c}\right)\left(\beta_c I_c S_c\left(1-\frac{I_c^*S_c^*}{I_cS_c}\right)+\alpha_c BS_c\left(1-\frac{B^*S_c^*}{BS_c}\right)+\psi_c V_c\left(\frac{V_c^*}{V_c}-1\right)\right)\\
&-\left(1-\frac{S_s^*}{S_s}\right)\left(\beta_s I_s S_s\left(1-\frac{I_s^*S_s^*}{I_sS_s}\right)+\alpha_s BS_s\left(1-\frac{B^*S_s^*}{BS_s}\right)+\psi_s V_s\left(\frac{V_s^*}{V_s}-1\right)\right)\\
&-a_1\left(1-\frac{V_c^*}{V_c}\right)\left(1-\frac{V_c^*S_c}{V_cS_c^*}\right)-(\psi_s+\mu_s)BV_sA_3\left(1-\frac{V_s^*}{V_s}\right)\left(1-\frac{V_s^*S_s}{V_sS_s^*}\right)\\
&+A_2\left(1-\frac{I_c^*}{I_c}\right)\left(\beta_c I_c S_c\left(1-\frac{S_c^*}{S_c}\right)+\alpha_c BS_c\left(1-\frac{B^*S_c^*I_c}{BS_cI_c^*}\right)\right)\\
&+A_4\left(1-\frac{I_s^*}{I_s}\right)\left(\beta_s I_s S_s\left(1-\frac{S_s^*}{S_s}\right)+\alpha_s BS_s\left(1-\frac{B^*S_s^*I_s}{BS_sI_s^*}\right)\right)\\
&-A_5\left(1-\frac{S_h^*}{S_h}\right)\left(a_2\left(\frac{R_h^*}{R_h}-1\right)+a\left(1-\frac{I_c^*S_h^*}{I_cS_h}\right)+b\left(1-\frac{I_s^*S_h^*}{I_sS_h}\right)+c\left(1-\frac{B^*S_h^*}{BS_h}\right)\right)\\
&+A_6\left(1-\frac{I_h^*}{I_h}\right)\left(\beta_{hc}I_cS_h\left(1-\frac{I_c^*S_h^*I_h}{I_cS_hI_h^*}\right)+\beta_{hs}I_sS_h\left(1-\frac{I_s^*S_h^*I_h}{I_sS_hI_h^*}\right)\right)\\
&+A_6\left(1-\frac{I_h^*}{I_h}\right)\left(\beta_{hh}I_hS_h\left(1-\frac{I_h^*S_h^*I_h}{I_hS_hI_h^*}\right)+\alpha_h BS_h\left(1-\frac{B^*S_h^*I_h}{BS_hI_h^*}\right)\right)\\
&-A_7(\gamma+\mu_h)R_h\left(1-\frac{R_h^*}{R_h}\right)\left(1-\frac{I_hR_h^*}{I_h^*R_h}\right)\\
&+A_8\left(1-\frac{B^*}{B}\right)\left(\rho_c I_c\left(1-\frac{BI_c^*}{B^*I_c}\right)+\rho_s I_s\left(1-\frac{BI_s^*}{B^*I_s}\right)\right). \qquad (12)
\end{aligned}$$

where,

$$a_1=(\psi_c+\mu_c)BV_cA_1,\ a_2=\gamma R_h,$$

$$a=\beta_{hc}I_cS_h,\ b=\beta_{hs}I_sS_h,\ c=\alpha_hBS_h.$$

Equation (12) can be written as:

$$\begin{aligned}
\frac{dL}{dt} =& -\left((\phi_c+\mu_c)S_c\left(1-\frac{S_c^*}{S_c}\right)^2+(\phi_s+\mu_s)S_s\left(1-\frac{S_s^*}{S_s}\right)^2+\mu_hS_h\left(1-\frac{S_h^*}{S_h}\right)^2\right)\\
&+F(S_c,V_c,I_c,S_s,V_s,I_s,B).
\end{aligned}$$

where, F is the balance of the right hand terms of equation (12). Following the approach of [29, 48, 49, 51, 50, 52], F is a non-positive function for $S_c,V_c,I_c,S_s,V_s,I_s,S_h,I_h,R_h,B\geq 0$. Thus, $\frac{dL}{dt}<0$ for $S_c,V_c,I_c,S_s,V_s,I_s,S_h,I_h,R_h,B\geq 0$ and is zero if $S_c=S_c^*,V_c=V_c^*,I_c=I_c^*,S_s=$

$S_s^*, V_s = V_s^*, I_s = I_s^*, S_h = S_h^*, I_h = I^*, R_h = R_h^*$, and $B = B^*$. Therefore, if $R_e > 1$, model system (1) has a unique endemic equilibrium point E^* which is globally asymptotically stable. □

5. NUMERICAL SIMULATIONS

This section presents numerical simulations of model system (1) for the purpose of verifying some of the analytical results. The parameter values used in our computations are mainly from [3], a literature similar to this work. The parameter values are in TABLE 3 and FIGURE 2 illustrates the variations in livestock, human and brucella subpopulations as time increases.

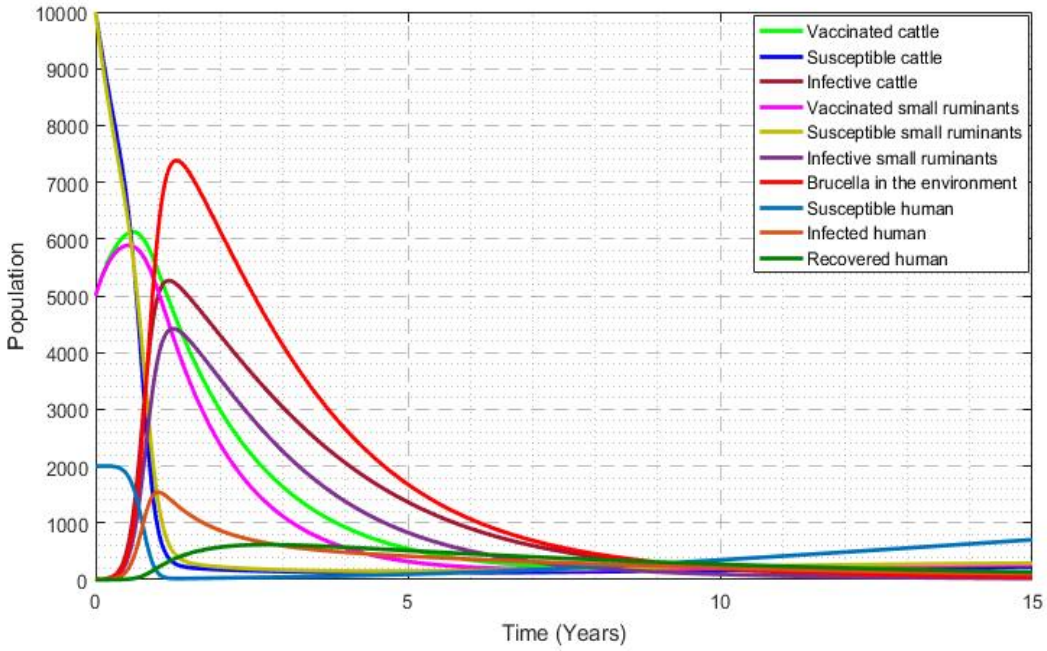


FIGURE 2. Time Series graph for Brucellosis

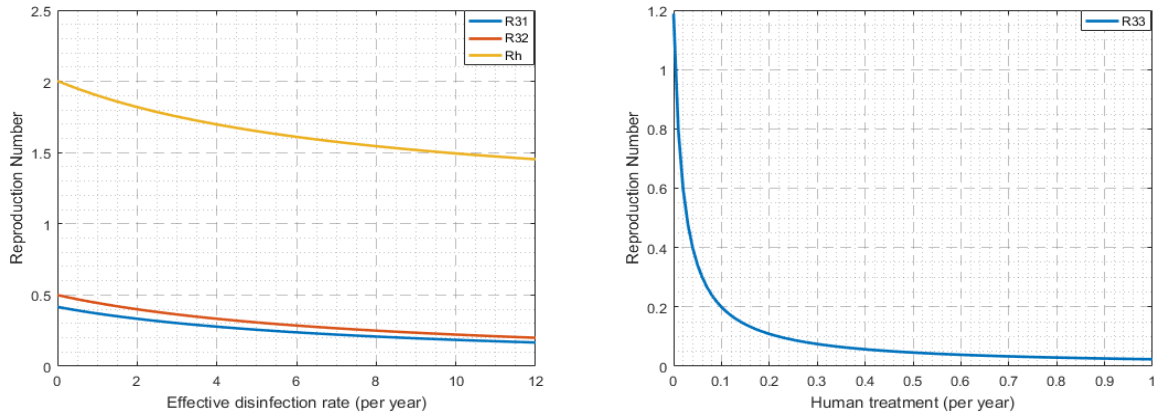
Furthermore, FIGURE 2 shows that susceptible human subpopulation decreases rapidly as time increases due to brucellosis infections and natural mortality rate. On the other hand, the number of infective humans initially increases with time due to large number of susceptible individuals that gets infected while its decrease is associated with the increase and decrease in effective treatment and susceptibility of individuals respectively. The recovered population increases as a result of increase in the effective treatment of infected humans.

Similarly, from FIGURE 3a we see that effective environmental hygiene and sanitation controls the transmission route of brucellosis from contaminated environment to human population.

TABLE 3. Model Parameter Values

Parameter	Value	Unit
π_c	0.3	$year^{-1}$
β_c	0.0011	$year^{-1}$
ϕ_c	0.7	$year^{-1}$
ψ_c	0.4	$year^{-1}$
μ_c	0.25	$year^{-1}$
d_c	0.35	$year^{-1}$
α_c	0.00035	$year^{-1}$
ρ_c	10	$year^{-1}$
ϕ_h	0.03	$year^{-1}$
β_h	0.0002	$year^{-1}$
σ_h	0.9	$year^{-1}$
μ_h	0.00005	$year^{-1}$
d_h	0.000002	$year^{-1}$
α_h	0.002	$year^{-1}$
β_{hc}	0.000158	$year^{-1}$
β_{hs}	0.000158	$year^{-1}$
γ	0.5	$year^{-1}$
ε	8	$year^{-1}$
τ	12	$year^{-1}$
π_s	0.4	$year^{-1}$
β_s	0.001	$year^{-1}$
ϕ_s	0.8	$year^{-1}$
ψ_s	0.5	$year^{-1}$
μ_s	0.35	$year^{-1}$
d_s	0.4	$year^{-1}$
α_s	0.00032	$year^{-1}$
ρ_s	15	$year^{-1}$

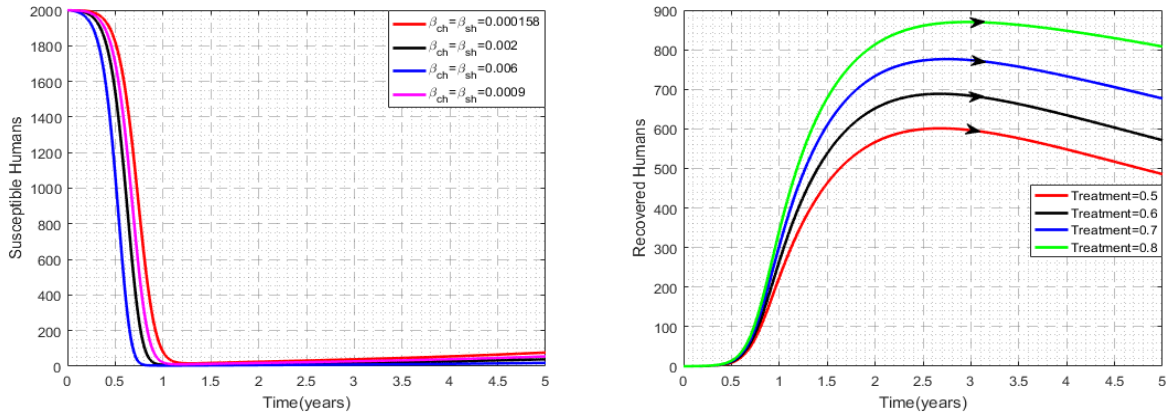
However, the ruminants to human effective reproduction number does not reduce to less than unit due to the fact that direct contact between infective cattle or small ruminants is not effectively controlled. In addition FIGURE 3b illustrates that, human treatment has a significant



(A) (B)

FIGURE 3. Variations in the effective reproduction number with respect to changes in environmental hygiene and human treatment

contribution in reduction or elimination of human to human brucellosis transmission. This is based on the fact that human treatment reduces the number of infective humans.



(A) (B)

FIGURE 4. The impact of transmission rates on susceptible humans and treatment rate on recovered human populations with respect to time.

Moreover, FIGURE 4a shows that both cattle to human and small ruminants to human transmission reduces the number of susceptible humans to almost zero in one year period of time. On the other hand, FIGURE 4b illustrates that, recovered humans increases with the increase in treatment rate. This implies that, in order to minimize or eliminate the prevalence of brucellosis

in the human population, measures should be taken to control the disease in animals as well as eliminating the disease in humans through treatment.

6. CONCLUSION

This paper aimed at formulating and analyzing a mathematical model to investigate the impacts of different control parameters to the transmission dynamics of brucellosis in the human and animal populations. We focused on livestock vaccination, gradual culling of ruminants through slaughter, environmental hygiene and sanitation, and human treatment. Analytical solutions as well as numerical simulations reveals that human brucellosis can be prevented or controlled only if the prevalence in both ruminants and humans can be controlled. Moreover, prevention of human brucellosis largely depends on prevention of the disease in domestic animals. In view of that, the effective control of brucellosis needs cooperation between public health and animal health sectors.

CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

REFERENCES

[1] WHO. Brucellosis in humans and animals, http://www.who.int/csr/resources/publications/Brucellosis.pdf. Accessed: 2018-11-08.

[2] F. P. Poester, L. E. Samartino, R. L. Santos. Pathogenesis and pathobiology of brucellosis in livestock, Rev. Sci. Tech. 32 (1) (2013), 105–115.

[3] M. Li, G. Sun, Y. Wu, J. Zhang, and Z. Jin. Transmission dynamics of a multi-group brucellosis model with mixed cross infection in public farm, Appl. Math. Comput. 237 (2014), 582–594.

[4] CFSPH. Brucellosis Brucella abortus, http://cfsph.iastate.edu/Factsheets/pdfs/brucellosis-abortus.pdf. Accessed 2018-11-07.

[5] E. Schelling, C. Diguimbaye, S. Daoud, J. Nicolet, P. Boerlin, M. Tanner, and J. Zinsstag. Brucellosis and Q-fever seroprevalences of nomadic pastoralists and their livestock in Chad, Prev. Vet. Med. 61 (4) (2003), 279–293.

[6] R. A. Greenfield, D. A. Drevets, L. J. Machado, G. W. Voskuhl, P. Cornea, and M. S. Bronze. Bacterial pathogens as biological weapons and agents of bioterrorism, Amer. J. Med. Sci. 323 (6) (2002), 299–315.

[7] J. Zhang, G. Sun, X. Sun, Q. Hou, M. Li, B. Huang, H. Wang, and Z. Jin. Prediction and control of brucellosis transmission of dairy cattle in Zhejiang Province, China, Plos one, 9 (11) (2014), e108592.

[8] F. Zhang, Z. Li, X. La, X. Ma, Y. Zhang, P. Ji, M. Jiang, J. Hu, Z. Zhang, X. Lu, and J. Ding. Multiple-locus variable-number tandem-repeat analysis of Brucella isolates from patients in Xinjiang China, Int. J. Clinic. Exp. Med. 8 (9) (2015), 15716–15723.

[9] B. Ainseba, C. Benosman, and P. Magal. A model for ovine brucellosis incorporating direct and indirect transmission, J. Biol. Dyn. 4 (1) (2010), 2–11.

[10] J. Zinsstag, and F. Roth, D. Orkhon, G. Chimed-Ochir, M. Nansalmaa, J. Kolar, and P. Vounatsou. A model of animal–human brucellosis transmission in Mongolia, Prev. Vet. Med. 69 (1–2) (2005), 77–95.

[11] M. N Xavier, T. A. Paixao, A. B. den Hartigh, R. M. Tsolis, and R. L. Santos. Pathogenesis of Brucella spp., Open Vet. Sci. J. 4 (1) (2010), 109–118.

[12] Medscape. Brucellosis Pathogenicity, https://emedicine.medscape.com/article/213430-overview, Accessed: 2018-11-07.

[13] K. A. Franc, R. C. Krecek, B. N. Häsler, and A. M. Arenas-Gamboa. Brucellosis remains a neglected disease in the developing world, BMC Public Health, 18 (1) (2018), 18-125.

[14] M. Ducrotoy, W. J. Bertu, G. Matope, S. Cadmus, R. Conde-Álvarez, A. M. Gusi, S. Welburn, R. Ocholi, J. M. Blasco, and I. Moriyón. Brucellosis in Sub-Saharan Africa: current challenges for management, diagnosis and control, Acta Tropica, 165 (2017), 179–193.

[15] M. Yilma, and G. Mamo, and B. Mammo. Review on Brucellosis Sero-prevalence and Ecology in Livestock and Human Population of Ethiopia, Ach. Life Sci. 10 (1) (2016), 80–86.

[16] M. J. Michael. Brucellosis in humans and animals, World Health Organization, 2006.

[17] A. S. Dean, L. Crump, H. Greter, E. Schelling, and J. Zinsstag. Global burden of human brucellosis: a systematic review of disease frequency, PLoS Negl. Trop. Dis. 6 (10) (2012), e1865.

[18] CDC. Brucellosis Signs and Symptoms, https://www.cdc.gov/brucellosis/symptoms/index.html. Accessed 2018-11-07.

[19] K. John, J. Fitzpatrick, N. French, R. Kazwala, D. Kambarage, G. S. Mfinanga, A. MacMillan, and S. Cleaveland. Quantifying risk factors for human brucellosis in rural northern Tanzania, PloS one, 5 (4) (2010), e9968.

[20] G. Pappas, P. Papadimitriou, N. Akritidis, L. Christou, and E. V. Tsianos. The new global map of human brucellosis, Lancet Infect. Dis. 6 (2) (2006), 91–99.

[21] G. Tumwine, E. Matovu, J. D. Kabasa, D. O. Owiny, and S. Majalija. Human brucellosis: sero-prevalence and associated risk factors in agro-pastoral communities of Kiboga District, Central Uganda, BMC Public Health, 15 (2015), 900.

[22] J. Kitaly. Bovine brucellosis in Government parastatal and Ujamaa village dairy farms in Central Zone of Tanzania: Assessment of Control measures in some farms In. In Proceedings of the 2 nd Tanzania Veterinary Association Scientific Conference (pp. 24-30), 1984.

[23] E. S. Swai, and L. Schoonman. Human brucellosis: seroprevalence and risk factors related to high risk occupational groups in Tanga Municipality, Tanzania, Zoonoses Public Health, 56 (4) (2009), 183–187.

[24] M. Carugati, H. M. Biggs, M. J. Maze, R. A. Stoddard, S. Cash-Goldwasser, J. T. Hertz, J. E. B. Halliday, W. Saganda, B. F. Lwezaula, R. R. Kazwala, S. Cleaveland, V. P. Maro, M. P. Rubach, and J. A. Crump. Incidence of human brucellosis in the Kilimanjaro Region of Tanzania in the periods 2007–2008 and 2012–2014, Trans. R. Soc. Trop. Med. Hyg. 112 (3) (2018), 136–143.

[25] G. M. Shirima. The epidemiology of brucellosis in animals and humans in Arusha and Manyara regions in Tanzania, PhD thesis. University of Glasgow, 2005.

[26] E. S. Swai, and L. Schoonman. A survey of zoonotic diseases in trade cattle slaughtered at Tanga city abattoir: a cause of public health concern, Asian Pac. J. Trop. Biomed. 2 (1) (2012), 55–60.

[27] A. G. Alhamada, I. Habib, A. Barnes, and I. Robertson. Risk factors associated with brucella seropositivity in sheep and goats in Duhok Province, Iraq, Vet Sci. 4 (4) (2017), 65.

[28] Q. Hou, X. Sun, J. Zhang, Y. Liu, Y. Wang, and Z. Jin. Modeling the transmission dynamics of sheep brucellosis in Inner Mongolia Autonomous Region, China, Math. Biosci. 242 (1) (2013), 51–58.

[29] C. Li, Z. Guo, and Z. Zhang. Transmission dynamics of a brucellosis model: Basic reproduction number and global analysis, Chaos Solitons Fractals, 104 (2017), 161–172.

[30] B. Nannyonga, G. G. Mwanga, and L.S. Luboobi. An optimal control problem for ovine brucellosis with culling, J. Biol. Dyn. 9 (1) (2015), 198–214.

[31] P. O. Lolika, C. Modnak, and S. Mushayabasa. On the dynamics of brucellosis infection in bison population with vertical transmission and culling, Math. Biosci. 305 (2018), 42–54.

[32] F. Roth, J. Zinsstag, D. Orkhon, G. Chimed-Ochir, G. Hutton, O. Cosivi, G. Carrin, and J. Otte. Human health benefits from livestock vaccination for brucellosis: case study, Bull. World Health Organ. 81 (2003), 867–876.

[33] A. Palanduz, S. Palanduz, K. Guler and N. Guler. Brucellosis in a mother and her young infant: probable transmission by breast milk, Int. J. Infect. Dis. 4 (1) (2000), 55–56.

[34] O. Mesner, K. Riesenberg, N. Biliar, E. Borstein, L. Bouhnik, N. Peled, and P. Yagupsky. The many faces of human-to-human transmission of brucellosis: congenital infection and outbreak of nosocomial disease related to an unrecognized clinical case, Clin. Infect. Dis. 45 (12) (2007), e135-e140, .

[35] E. Meltzer, Y. Sidi, G. Smolen, M. Banai, S. Bardenstein, and E. Schwartz. Sexually transmitted brucellosis in humans, Clin. Infect. Dis. 51 (2) (2010), e12–e15.

[36] A. El-Sayed and W. Awad. Brucellosis: Evolution and expected comeback, Int. J. Vet. Sci. Med. 6 (sup 1) (2018), S31-S35..

[37] F. F. Tuon, R. B. Gondolfo, and N. Cerchiari. Human-to-human transmission of Brucella–a systematic review, Trop. Med. Int. Health, 22 (5) (2017), 539–546.

[38] O. Diekmann, J. A. P. Heesterbeek, and J. A.J. Metz. On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations,J. Math. Biol. 28 (4) (1990), 365–382.

[39] O. Diekmann, J.A.P. Heesterbeek, and M.G. Roberts. The construction of next-generation matrices for compartmental epidemic models, J. R. Soc. Interface, 7 (47) (2010), 873–885.

[40] D. Okuonghae, and A. Korobeinikov. Dynamics of tuberculosis: the effect of direct observation therapy strategy (DOTS) in Nigeria, Math Model Nat Phenom. 2 (1) (2007), 113–128.

[41] P. van den Driessche, and J. Watmough. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci. 180 (1-2) (2002), 29–48.

[42] A. Cintrón-Arias, C. Castillo-Chávez, Luıs M.A. Bettencourt, A. L. Lloyd, and H.T. Banks. The estimation of the effective reproductive number from disease outbreak data, Math. Biosci. Eng. 6 (2) (2009), 261–282.

[43] P. van den Driessche. Reproduction numbers of infectious disease models, Infect. Dis. Model. 2 (3) (2017), 288–303.

[44] P. Padmanabhan, P. Seshaiyer, and C. C. Chavez. Mathematical modeling, analysis and simulation of the spread of Zika with influence of sexual transmission and preventive measures, Lett. Biomath. 4 (1) (2017), 148–166.

[45] N. Nyerere, L. S. Luboobi, S. C. Mpeshe, and G. M. Shirima. Mathematical Model for the Infectiology of Brucellosis with some Control Strategies, New Trends Math. Sci. 7 (4) (2019), 387–405.

[46] O. Diekmann and J.A.P. Heesterbeek. Mathematical epidemiology of infectious diseases: model building, analysis and interpretation; John Wiley & Sons, Vol. 5, 2000.

[47] C.C. Chavez, S. Blower, P. van den Driessche, D. Kirschner, and A. Yakubu. Mathematical approaches for emerging and reemerging infectious diseases: an introduction, Vol. 1. Springer Science & Business Media, 2002.

[48] A. Korobeinikov, and G. C. Wake. Lyapunov functions and global stability for SIR, SIRS, and SIS epidemiological models, Appl. Math. Lett. 15 (8) (2002), 955–960.

[49] A. Korobeinikov. Lyapunov functions and global properties for SEIR and SEIS epidemic models, Math. Med. Biol. 21 (2) (2004), 75–83.

[50] A. Korobeinikov. Global properties of infectious disease models with nonlinear incidence, Bull. Math. Biol. 69 (6) (2007), 1871–1886.

[51] C. C. McCluskey. Lyapunov functions for tuberculosis models with fast and slow progression, Math. Biosci. Eng. 3 (2006), 603614.

[52] S. Bowong, J. J. Tewa, and J. C. Kamgang. Stability analysis of the transmission dynamics of tuberculosis models, World J. Model. Simul. 7 (2) (2011), 83–100.