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Transmission dynamics of a brucellosis model: Basic reproduction number and global analysis

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ABSTRACT

Brucellosis is a major problem worldwide in public health and existing work mainly focused on severity estimation based on the real data. However, global analysis on brucellosis transmission model is not well understood. In this paper, we presented a dynamical model of brucellosis transmission coupled with sheep and human populations and global analysis is shown based on Lyapunov functions. We found that the global dynamics of brucellosis model is determined by basic reproduction number R_0: if $R_0 < 1$, then the disease-free equilibrium is globally asymptotically stable; otherwise, the endemic equilibrium is globally asymptotically stable. We hope that our study may provide theoretical basis for the further work on brucellosis control.

1. Introduction

Brucellosis is one of the contagious bacterial diseases which is caused by various species of the genus brucella [1,2]. It can spread between animals and from animals to humans by directed contact with infected animals or indirect transmission by brucella in the environment [3]. Brucellosis was first reported in the Fifth Plague of Egypt and the bacteria of the genus brucella has six species [4]. The main source of infection is sheep and next are cattle and pig. There is incubation period during infection process and the period is 14–180 days [5]. It is classified as Class B animal epidemics by the World Organization for Animal Health (OIE) and Class II as one of the notifiable diseases by the Law on Prevention and Control of Infectious Diseases of the People's Republic of China [6]. As a result, investigations on mechanisms on transmission dynamics of brucellosis are received more and more attentions.

Dynamical models are useful tools in finding out the transmission rules of brucellosis [7]. Sun and Zhang showed the influence of immigration on brucellosis transmission and found that elimination, vaccination and disinfection were the useful control strategies [7]. Li et al. presented a multi-group brucellosis model with mixed cross infection in public farm and found that removing mixed cross infection may eliminate the brucellosis [8]. Nie et al. proposed an Susceptible-Exposed-Infected-Virus dynamical model with outside transferred amount to describe the transmission of brucellosis amongst dairy cattle in Jilin province, China [9]. Li et al. estimated that the control reproduction number for the brucellosis transmission in Hinggan League and compare the effect of existing mixed cross infection between basic ewes and other sheep or not for newly infected human brucellosis cases [4]. Zhang et al. revealed that the external input of dairy cows from northern areas may lead to high fluctuation of the number of the infectious cows in Zhejiang province which can reach several hundreds [10]. In one word, previous work focused on estimating basic reproduction number and finding out the most effective control measures on brucellosis. However, global analysis on these transmission model is still lack.

Due to that the infected sheep have symptoms including abortion during the last third of pregnancy, retained afterbirth, and weak calves at birth, infections in sheep is highly contagious [7]. In this study, we want to investigate the global dynamics of a brucellosis model coupled with sheep and human populations. The paper is organized as follows. In section II, we construct a mathematical model of brucellosis transmission based on twelve equations. In section III, we obtain the basic reproduction number. In section IV, global stability of both disease-free and endemic equilibrium is proved. Finally, we give some discussion.

2. Dynamical model

In this paper, we consider a dynamical model of brucellosis transmission coupled with sheep and human populations. And the flock of sheep is divided into basic ewes and other sheep [4]. Some

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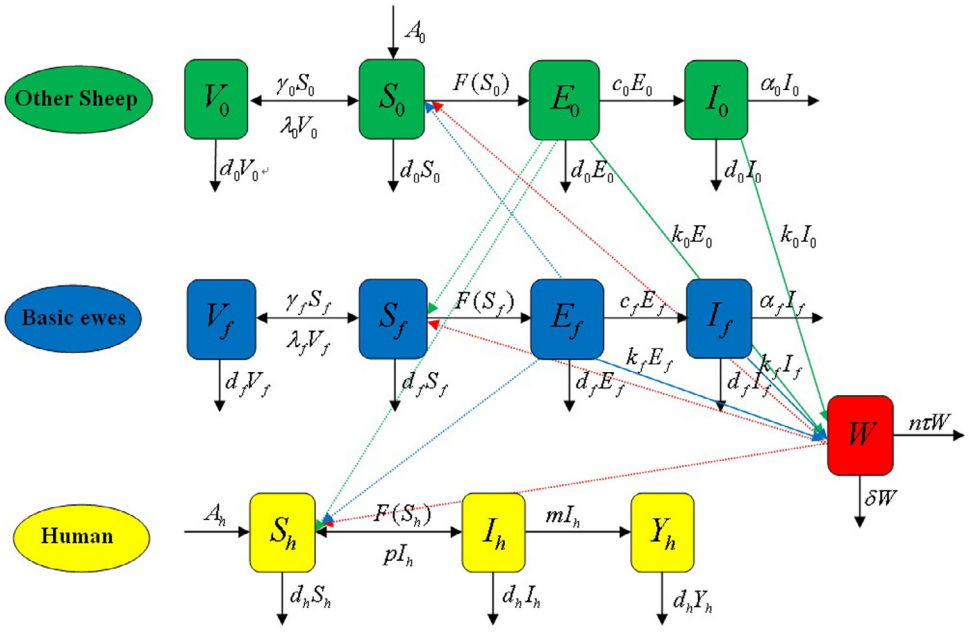

Fig. 1. Rules of brucellosis transmission among sheep and from sheep to humans. $F(S_0) = (\beta_{oo}E_o + \beta_{of}E_f + \beta_o \frac{W}{W+k})S_o$, $F(S_f) = (\beta_{ff}E_f + \beta_{fo}E_o + \beta_f \frac{W}{W+k})S_f$ and $F(S_h) = (\beta_{ho}E_o + \beta_{hf}E_f + \beta_h \frac{W}{W+k})S_h$.

related data can be found in [11,12]. Firstly, we give four main assumptions:

(i) The sheep population comprises four subgroups: susceptible (S_o or S_f), recessive infected (E_o or E_f), quarantined seropositive infected (I_o or I_f) and vaccinated (V_o or V_f). Here, subscript f and o are corresponding to basic ewes and other sheep.
(ii) The human population comprises three subgroups: susceptible individuals (S_h), acute infections (I_h), chronic infections (Y_h).
(iii) If recessive infected sheep is detected as seropositive, then it will enter into quarantined seropositive infected individuals compartment.
(iv) The susceptible sheep and human can be infected by recessive infected sheep and polluted environment.

The model is a system of twelve ordinary differential equations (transmission flowchart is in Fig. 1):

$$\begin{cases}
\frac{dS_o}{dt} = A_o - (\beta_{oo}E_o + \beta_{of}E_f + \beta_o \frac{W}{W+k})S_o + \lambda_o V_o - (\gamma_o + d_o)S_o, \\
\frac{dE_o}{dt} = (\beta_{oo}E_o + \beta_{of}E_f + \beta_o \frac{W}{W+k})S_o - (c_o + d_o)E_o, \\
\frac{dI_o}{dt} = c_o E_o - (\alpha_o + d_o)I_o, \\
\frac{dV_o}{dt} = \gamma_o S_o - (\lambda_o + d_o)V_o, \\
\frac{dS_f}{dt} = A_f - (\beta_{ff}E_f + \beta_{fo}E_o + \beta_f \frac{W}{W+k})S_f + \lambda_f V_f - (\gamma_f + d_f)S_f, \\
\frac{dE_f}{dt} = (\beta_{ff}E_f + \beta_{fo}E_o + \beta_f \frac{W}{W+k})S_f - (c_f + d_f)E_f, \\
\frac{dI_f}{dt} = c_f E_f - (\alpha_f + d_f)I_f, \\
\frac{dV_f}{dt} = \gamma_f S_f - (\lambda_f + d_f)V_f, \\
\frac{dW}{dt} = k_o(E_o + I_o) + k_f(E_f + I_f) - (\delta + n\tau)W, \\
\frac{dS_h}{dt} = A_h - (\beta_{ho}E_o + \beta_{hf}E_f + \beta_h \frac{W}{W+k})S_h - d_h S_h + pI_h, \\
\frac{dI_h}{dt} = (\beta_{ho}E_o + \beta_{hf}E_f + \beta_h \frac{W}{W+k})S_h - (m + d_h + p)I_h, \\
\frac{dY_h}{dt} = mI_h - d_h Y_h,
\end{cases} \tag{1}$$

where A_o (A_f) represents recruitment rate of other sheep (basic ewes). $(\beta_{oo}E_o + \beta_{of}E_f + \beta_o \frac{W}{W+k})S_o$ is transmission term, where β_{oo} represents other sheep-to-other sheep transmission rate, β_{of} represents basic ewes-to-other sheep transmission rate, and β_o represents brucella-to-other sheep transmission rate. Parameter λ_o (λ_f) represents losing immunity rate of other sheep (basic ewes), γ_o (γ_f) represents efficient vaccination rate of other sheep (basic ewes), d_o (d_f) represents removed rate of other sheep (basic ewes), c_o (c_f) represents seropositive detection rate of other sheep (basic ewes), α_o (α_f) represents disease-related elimination rate of other sheep (basic ewes). $(\beta_{ff}E_f + \beta_{fo}E_o + \beta_f \frac{W}{W+k})S_f$ is transmission term, where β_{ff} represents basic ewes-to-basic ewes transmission rate, β_{fo} represents other sheep-to-basic ewes transmission rate, and β_f represents brucella-to-basic ewes transmission rate. k_o (k_f) represents brucella shedding rate by infected other sheep (basic ewes), δ represents decaying rate of brucella in the environment, n represents disinfection times, τ represents effective disinfection rate, A_h represents annual birth rate of human. $(\beta_{ho}E_o + \beta_{hf}E_f + \beta_h \frac{W}{W+k})S_h$ is transmission term, where β_{ho} represents other sheep-to-human transmission rate, β_{hf} represents basic ewes-to-human transmission rate, and β_h represents brucella-to-human transmission rate. d_h represents natural mortality rate of human, p represents transfer rate from acute infections to susceptible individuals, and m represents transfer rate from acute infections to chronic infections. More details for the biological meanings of the parameters in system (1) can be found in Table 1.

3. Basic reproduction number

By calculations, we have the disease-free equilibrium of system (1): $(\frac{A_o(\lambda_o+d_o)}{d_o(\gamma_o+\lambda_o+d_o)}, 0, 0, \frac{A_o\gamma_o}{d_o(\gamma_o+\lambda_o+d_o)}, \frac{A_f(\lambda_f+d_f)}{d_f(\gamma_f+\lambda_f+d_f)}, 0, 0, \frac{A_f\gamma_f}{d_f(\gamma_f+\lambda_f+d_f)}, 0, \frac{A_h}{d_h}, 0, 0)$, which is denoted as $(S_o^0, E_o^0, I_o^0, V_o^0, S_f^0, E_f^0, I_f^0, V_f^0, W^0, S_h^0, I_h^0, Y_h^0)$.

According to the methods in Refs. [13–15], we can first order the infected variables by rewriting the vector on the right hand side of Eq. (1) into $y = (E_0, I_0, E_f, I_f, W, I_h)$. Then, we have the fol-