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RESEARCH ARTICLE

Lumpy Skin Disease: A Mathematical Model Application

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Abstract

Objectives: The purpose of the study is to decrease the value of reproduction number under the value of 1 for the purpose of eradicating Lumpy Skin Disease (LSD). **Method:** We provide three cases giving the basic reproduction numbers of few of the original systems' subsystems to calculate R_0 and provide a clearer grasp of its structure. **Finding:** The value of basic reproduction number for the Susceptible-Infected (S-I) epidemiological model is determined to establish the fundamental reproduction number by comparing it to the basic reproduction numbers of simplified subsystems in existing S-I models and present some intervention technique for the reduction of this value to control the transmission of the LSD. **Novelty:** LSD is not zoonotic; people can't get infected with it. Most of the epidemiological studies of LSD concentrate on curing the disease solely in cattle; however, they neglect to consider the possibility of human infection from contact with infected cattle. But we assume the infection on people through blood-feeding insects, certain species of flies and mosquitoes as well as through infected cattle that server of LSD Virus.

Keywords: Lumpy Skin Disease; Mathematical Modelling; Reproduction Number

1 Introduction

The lumpy skin disease virus (LSDV) is the cause of the infectious transboundary viral disease known as LSD in cattle. It is primarily spread indirectly by the bite of blood-feeding insects including ticks, flies, and mosquitoes[(1)]. Furthermore, fomites and, in certain cases, animals themselves can spread it. Clinically, the illness might range from a minor illness to a serious infection or even death. It was believed that LSDV was not zoonotic[(2)]. For the first time, a recent experimental investigation measured the variation in the likelihood of LSDV uptake by four attacking vector species (*A. aegypti*, *C. quinquefasciatus*, *C. nubeculosus*, and *S. calcitrans*) exposed to sub-clinical or clinically infected cattle. The likelihood that vectors would contract LSDV from asymptomatic animals was significantly lower than that of symptomatic animals. Vectors were 97% less likely to catch LSDV from feeding on an asymptomatic animal than from a symptomatic one, with estimated probabilities of spreading the disease from cattle to insect being 0.006 and 0.22, respectively.

It was discovered that there was no difference in this ratio of the chance of spreading among the four kinds of attacking vectors that were analysed. This study also showed that at the pre-symptomatic stage of the disease, when viremia is low and skin lesions had not yet developed, there was little chance of cattle to transmit the disease to vectors[3]. LSDV transmission between cattle in intensive commercial herds, which were separated from distinct herds, and mixed livestock herds, which were known to mix at shared pastures and watering points, was estimated in Ethiopia using a susceptible-infectious-recovered (SIR) epidemiological model and findings showed that the R_0 for these two forms of herds was comparable[4]. To calculate losses in productivity during an LSD epidemic, an epidemiological model referred to as susceptible-exposed-infectious-recovered (SEIR) was used to simulate LSDV transmission amongst cattle in Turkey. This study demonstrated how identifying LSD in cattle during the incubation phase may minimize the financial damage brought on by an LSD outbreak[5].

In order to better understand the dynamics of LSD transmission, several kinds of modelling studies have used information collected from epidemics and included in their consideration for the incubation rate, recruitment rate, vital dynamics (birth and natural death), and vaccination rate[6]. Humans are incapable of spreading LSD. There is no risk of human infection from cattle, and cow's milk is safe to consume[7,8]. The biological mechanism of the disease appears to be similar to that of LSD in cattle, although the extent of medical interventions determines the disease's phases and progression. But human biology is completely distinct from cattle[9]. The distinctive symptoms of lumpy skin disease in cattle (the primary host) include cutaneous lumps, fever, lymphadenopathy, emaciation, high morbidity, and an illness that can last for months in animals. Young animals have a high mortality rate, and all age groups have mortality rates, particularly in herds that were new to the area. Man, LSD infections are quite similar to the pathophysiology of bovine diseases. Ignored cases in humans might result in difficulties since systemic infections are likely to occur and are expected in those with weakened immune systems. Future research on human disease would be tremendous[10]. To determine the transmissibility of a disease, the basic reproduction number, or R_0, is estimated. Sensitivity analysis is used to determine the important factors affecting R_0. The effectiveness of vaccination and quarantine-based optimal control measures is developed and evaluated statistically. Three distinct situations are compared: vaccination alone, quarantine alone, and the combination of the two approaches. The results show that the best method for reducing the spread of disease is a combination of vaccination and quarantine[11]. To evaluate the suggested model for local and global stability at disease-free and endemic equilibrium points, as well as to determine how contagious a disease is, the study calculates the reproduction number R_0 [12]. The basic reproduction number R_0 of the model was derived and the disease-free equilibrium points was shown to be locally asymptotically stable when $R_0 < 1$. Sensitivity analysis to identify the most sensitive parameters was conducted and the vaccination parameter was varied using matplotlib module in Python to check the effect of vaccination on both vaccinated and infectious cow. Increase in the vaccination parameter cause the number of vaccinated cows to increase and hence leads to reduction in the number of infected cows[13].

In conclusion, cattle populations continue to be seriously threatened by Lumpy Skin Disease (LSD), which is mostly spread via fomites, blood-feeding insects, and animal-to-animal contact. According to the results, although if LSD is not zoonotic, the disease pathogenesis in humans may be similar to that in cattle, and the course of the illness may differ depending on the extent of healthcare treatment. In order to reduce LSD outbreaks and minimize financial losses in cattle populations, the study also highlights the significance of early diagnosis and treatment techniques including vaccination and quarantine. According to the sensitivity analysis and modelling simulations, the combination of vaccination and quarantine is the most successful method for preventing the spread of disease. The necessity for more research on the human interaction with LSD is generally highlighted by the previous research, as it could produce important information for next public health initiatives and disease prevention strategies. Hence, this literature offers a distinctive addition, to investigate the possible human interface with LSD—an area that has not yet been thoroughly investigated. Beyond its effects on cattle, this new study on human infection brings up new possibilities for studying the disease.

2 Methodology

This study focuses on the S-I epidemics model[14]. According to the S-I model, there are two categories in the population: susceptible people who could get the disease and infected people who could infect other susceptible people. The size of the susceptible class decreases as the infected class grows as a result of the susceptible moving into the infected group after becoming infected. Each member of the susceptible population has an equal chance of contracting the disease from contact with an infected person, according to the S-I model. Once infected, an individual cannot get better; they are always in the I class. Furthermore, death is not a factor because we assume that the disease outbreak will end quickly in comparison to the average lifespan of a person. Thus, this model can be used for illnesses that have a relatively rapid rate of spread and for which patients never fully recover. The mathematical modelling of lumpy skin disease in humans and animals has been examined by us. This modelling has allowed us to talk about the problems of understanding the dynamics of an LSD outbreak. The cattle population

should be divided into a variety of subpopulations as a means of disease prevention. The equation for reproduction number $(R_0)$is also demonstrated in this study.

2.1 Mathematical Modelling

The following theories such as the infection of healthy cattle and humans by poxviruses are the foundation of mathematical modelling. Capri poxvirus is present in the nearby livestock. The virus spreads in two ways: by reproduction and by feeding on blood from insects such as ticks, some types of flies, and mosquitoes. The movement of cattle is often associated with the long-distance spread of LSDV. An example of the LSDV transmission summary is shown in Figure 1. As carriers' movements might still contribute to the disease's transmission, the Panel on Animal Health and Welfare (AHAW) of the European Food Safety Authority (EFSA) suggested that quarantine by itself might not be sufficient to limit the spread of LSD. The transmission paths are shown in [Figure 1].

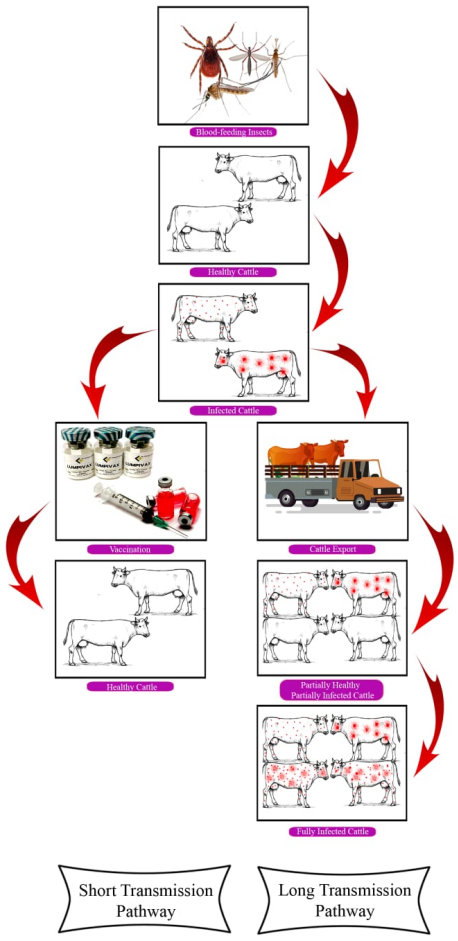

Fig 1. Transmission Routes

By using ordinary differential equation, we will introduce the mathematical model.

$$\dot{S}_C = -(X_1 I_C + X_2 V) S_C + \theta_2 T_C - \eta S_C \tag{1}$$

$$\dot{I}_C = (X_1 I_C + X_2 V) S_C - \eta I_C \tag{2}$$

$$\dot{S}_P = -(X_3 I_C + X_4 V) S_P + \theta_1 I_P \tag{3}$$

$$\dot{I}_P = (X_3 I_C + X_4 V) S_P - \theta_1 I_P \tag{4}$$

$$V = (X_P I_C + X_C I_C) - mV \tag{5}$$

Where, S_C , I_C , S_P & I_P indicate the number of susceptible cattle, infected cattle, susceptible people and infected people respectively. V represents population of virus. X_i for $i = 1,2,3,4.$ are the rates of infection in the group of various cattle, although X_P is the infection rate through virus in people and X_C is the infection rate through virus in cattle to the surrounding. θ_1 is the recovery rate of people whereas θ_2 is the recovery rate of cattle in which births should be involve. η is the susceptible or infected cattle removal rate. T_C & T_P are the total population of cattle and people respectively which is suppose to have constant. $m \geq 0$ is the inverse of time of habitation of virus in surrounding.

By using above mentioned hypotheses, we will obtain new model, which is given as below;

$$\dot{I}_C = (X_1 I_C + X_2 V)(T_C - I_C) - \theta_2 I_C \tag{6}$$

$$\dot{I}_P = (X_C I_C + X_4 V)(T_P - I_P) - \theta_1 I_P \tag{7}$$

$$V = (X_P I_C + X_C I_C) - mV$$

[Figure 2] presents pattern of infection in the group of infected cattle, people and virus.

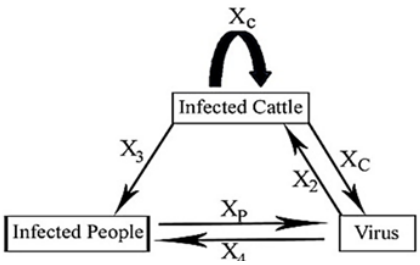

Fig 2. Pattern of infection in infected cattle, people and virus

Under the below mentioned hypothesis, the framework is roughly calculated as:

- The rate of infection,
- The production rate of virus and
- The rate of removal: $\frac{1}{\theta_1}$, $\frac{1}{\theta_2}$, $\frac{1}{m}$.

Where,

$\frac{1}{\theta_1}$ is average duration it takes for a person to become infected,
$\frac{1}{\theta_2}$ is average duration of the life expectancy of various cattle of virus,
$\frac{1}{m}$ is virus life expectancy in temperature, rainfall, etc. like natural conditions.
[Table 1] represents the range of approximate values involved in our research.

Table 1. Approximate Values

Sr. No.	Symbols	Specification	Values
1	$\frac{1}{\theta_1}$	Average duration of infected people	7 to 30 days
2	$\frac{1}{\theta_2}$	Life expectancy of cattle	365 to 7300 days
3	$\frac{1}{m}$	Life expectancy of virus	18 to 35 days
4	T_p	Total population of people	$(T_P \geq 0)$
5	T_c	Total population of cattle	$(T_C \geq 0)$
6	X_1	Rate of infection in cattle	0.068 to 0.085 per day
7	X_2	Rate of infection between cattle & virus	0.068 to 0.076 per day
8	X_3	Rate of infection between people & cattle	0.0003 to 0.0007 per day
9	X_4	Rate of infection between people & virus	0.00009 to 0.0004 per day
10	X_P	Virus contribution to the environment by people	0.008 to 0.014 per day
11	X_c	Virus contribution to the environment by cattle	0.2 to 0.5 per day

Source: Fictitious data, for illustration purposes only.

2.2 Estimation of Basic Reproduction Number (R_0)

From the Equations (5), (6) and (7), it is clearly defined that the coordinate (I_{C_1}, I_{P_1}, V_1)=(0,0,0) is a balanced resolution which describe the LSD free state.

$$\theta_1 m X_1 T_C + \theta_1 X_2 X_P T_C + X_2 X_3 X_C T_C T_P + \theta_2 X_4 X_C T_P > \theta_1 \theta_2 m + X_1 X_4 X_C T_C T_P \tag{8}$$

Equation (8) is both essential and appropriate for a non-trivial equilibrium solution with (I_{C_2}, I_{P_2}, V_2) as a positive coordinate and which suggest the presence of endemic problem.

It is important to specify that the mathematical representation of the basic reproduction number is absent from the mathematical form for the presence of non-trivial balanced condition. (I_{C_3}, I_{P_3}, V_3) is universal asymptotically stable which when detected in the group

$$I_C \in [0, T_C], \; T_P \in [0, T_P], \; V \in \left[0, \frac{X_P T_C}{m} + \frac{X_C T_P}{m}\right]$$

and it could be probable to demonstrate, obviously this group is not stated. To prove the stability of the non-trivial equilibrium, it is important that, the trajectories of the solution propose the non-trivial equilibrium, if the surfaces that make up the nullclines connect, separate the group into eight areas; consequently, having initial condition individually of them and by determining the vector field's orientation in every area separately, it can be examined.

Case 1: Let X_1 is the autoinfection rate and X_3 is the rate of infection from cattle to people, considered as zero and the basic reproduction number is,

$$R_{4C} = \left({R_4}^2 + {R_C}^2\right)^{\frac{1}{2}}$$

In this methodology, R_4 & R_C are the basic reproduction numbers of independent pattern. From these above-mentioned observations showed that basic reproduction numbers from two junctions pattern behave in similar manner mathematically shown in [Figure 3].

Case 2: Now, we consider and eliminated group of people entirely from this methodology, means, X_3 , X_4 *and* X_P are considered as zero. Then, the reproduction number of this methodology is:

$$R_{1C} = \frac{R_1}{2} + \left(\frac{{R_1}^2}{4} + {R_C}^2\right)^{\frac{1}{2}}$$

From this above-mentioned observation showed that the autoinfection (R_1) behaves independently and behaves with (R_C) shown in [Figure 4].

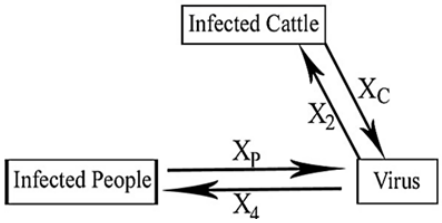

Fig 3. Methodology of Equations (5), (6) and (7) with two patterns of two junctions

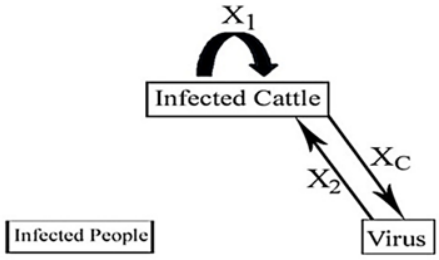

Fig 4. Methodology with autoinfection and two junctions' pattern

Case 3: Now, we assume that there is no autoinfection means, X_1 is considered as zero then we get the reproduction number,

$$R_{4C} = \left[\frac{R^3}{2} + \sqrt{\left(\frac{R^3}{2}\right)^2 - \left(\frac{R_4^2 + R_C^2}{3}\right)^3}\right]^{\frac{1}{3}} + \frac{\left(\frac{R_4^2+R_C^2}{3}\right)}{\left[\frac{R^3}{2} + \sqrt{\left(\frac{R^3}{2}\right)^2 - \left(\frac{R_4^2+R_C^2}{3}\right)^3}\right]^{\frac{1}{3}}}$$

We will derive the reproduction number R_0 for the complex system, for the purpose to realize the situation of system and which is demonstrated by the largest eigenvalue in the measure of the next generation matrix stated as:

$$A = \begin{bmatrix} \frac{X_1 T_C}{\theta_2} & 0 & \frac{X_2 T_C}{m} \\ \frac{X_3 T_P}{\theta_2} & 0 & \frac{X_4 T_P}{m} \\ \frac{X_P}{\theta_2} & \frac{X_C}{\theta_1} & 0 \end{bmatrix} \tag{9}$$

$$F(\mu) = -\mu^3 + R_1\mu^2 + (R_4 + R_C^2)\mu + \overline{R}^3 - R_1 R_4^2 \tag{10}$$

Equation (10) is the characteristic polynomial of A, where,

$$R_1 = \frac{X_1 T_C}{\theta_2} \qquad R_4 = \sqrt{\frac{X_4 X_C T_P}{\theta_1 m}}$$

$$R_C = \sqrt{\frac{X_2 X_P T_C}{\theta_2 m}} \qquad \overline{R} = \sqrt[3]{\frac{X_2 X_3 X_C T_C T_P}{\theta_1 \theta_2 m}} \tag{11}$$

For every subsystem, these are its fundamental reproduction numbers. which are found by separating the cycle of infection of original system R_2, R_3, R_P do not develop because these will be utilize in a generalization of the modeling.

We will analyze that R_0 established by the simpler subsystems of R_0's depending upon the below mentioned results. And by this result, we will propose to show the techniques which are decrease the reproduction number for the purpose to eradicate the lumpy skin disease.

$$R_0 = \frac{1}{3}R_1 + \sqrt[3]{Y} + \frac{|Y|\frac{2}{3}}{\sqrt[3]{Y}} \tag{12}$$

Where,

$Y = \frac{\overline{R}^3}{2} + \frac{R_1^3}{27} + \frac{R_1 R_C^2}{6} - \frac{R_1 R_4^2}{3} + \frac{1}{18}(81\overline{R}^6 + 12R_1^3\overline{R}^3 - 108R_1R_4^2\overline{R}^3 + 54R_1R_C^2\overline{R}^3$
$-12R_1^4R_4^2 + 24R_1^2R_4^2 - 60R_1^2R_4^2R_C^2 - 3R_1^2R_C^4 - 12R_4^6 - 36R_4^4R_C^2 - 36R_4^2R_C^4 - 12R_C^6)^{\frac{1}{2}}$

Equation (12) is the basic reproduction number of lumpy skin disease for the modeling.

3 Result & Discussion

The current study has shown that the LSD virus can infect humans as a zoonotic illness, causing skin conditions that resemble those seen in cattle. People who come into contact with sick cattle might quickly become infected with LSD virus. We will be aware that human in places where LSD virus epidemics are occurring will not consume any beef or seafood because dead cattle are dumped into waterways. Accuracy of the value of reproduction number to every parameter might be resolved by estimating the related partial differentiation. To effectively minimize or eliminate the disease, one must identify the modifiable parameters and determine their relative efficiency in achieving a disease-free state, assuming all other costs remain constant. The main objective of the study is to lower R_0 below 1, which is necessary to prevent the spread of disease. In the result, we have developed and examined a model for the investigation of lumpy skin disease in people as well as cattle. We have also been able to tackle the issue of interpreting the dynamics of an epidemic of lumpy skin disease due to our model. The cattle population should be divided into as many subpopulations as feasible as a preventative strategy [Figure 5]. Groups of the same size are suggested if possible. The detailed formulation for R_0 can be expressed in terms of R_0 s for simpler sub cycles, which provides some understanding into the overall framework of the entire study.

$R_{1_a} = \frac{X_1 T_{C_a}}{\theta_2}$, $R_{1_b} = \frac{X_1 T_{C_b}}{\theta_2}$, $R_{C_a} = \left[\frac{X_2 X_P T_{C_a}}{\theta_2 m}\right]^{\frac{1}{2}}$ and $R_{C_b} = \left[\frac{X_2 X_P T_{C_b}}{\theta_2 m}\right]^{\frac{1}{2}}$

$$T_{C_a} + T_{C_a} = T_C$$

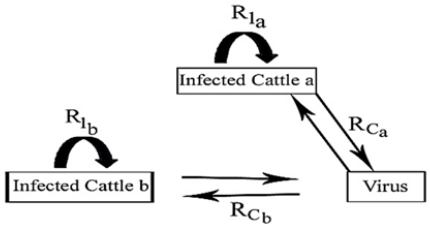

Fig 5. Methodology formed by partitioning the population of cattle into two subgroups

4 Conclusion

The study aimed to decrease the value of reproduction number under the value of 1. The value of to each variable can be calculated by estimating the equivalent partial differentiation. The straightforward formula for R_0 recognizes to indicate simple intervention. This study provides mathematical modeling of lumpy skin disease in cattle and people. The LSD virus can infect humans and cause skin nodules. If the infection spreads to other parts of the body or affects internal organs, it can be fatal. This modeling has permitted us to discuss the problem of realizing the dynamics of LSD outbreak. As an approach for prevention of disease, it can be suggested to separate the population of cattle into numerous subpopulations. This study also be interpreted that by demonstrating the equation for reproduction number R_0 concerning with simpler sub cycle's R_0's. And by using the general structure of the modeling can be achieved certain understanding.

Nomenclature

1. $S_P - No.\ of\ susceptible\ people$
2. $S_C - No.\ of\ susceptible\ cattle$
3. $I_P - No.\ of\ Infected\ people$
4. $I_C - No.\ of\ Infected\ cattle$
5. $V -\ Population\ \ of\ virus\ count$
6. $X_i - Rate\ of\ Infection\ by\ various\ classes$
7. $X_P - Rate\ of\ Infection\ of\ people$
8. $X_C - Rate\ of\ Infection\ of\ cattle$
9. $T_P - Total\ population\ of\ people$
10. $T_C - Total\ population\ of cattle$
11. $\theta_1 - Recovery\ rate\ of\ people$
12. $\theta_2 - Recovery\ rate\ of\ cattle$
13. $\eta - Removal\ rate\ of\ cattle,\ even\ if,\ it\ can\ be\ included\ in\ susceptible\ or\ inflected\ area$
14. $m - Inverse\ duration\ of\ virus\ on\ environment$

Data availablity

Not Applicable.

Details of Ethical clearance

Not applicable.

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