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RESEARCH ARTICLE

SIR-Based Modeling of Viral Infectious Diseases in Farm Animals

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Abstract

Throughout history, epidemic diseases have had profound impacts on societies, causing serious problems in public health as well as adverse effects on food security and animal health. When real-time data are processed through mathematical and statistical models, it becomes possible to evaluate the course and effects of an outbreak. In this study, the progression of a disease was simulated using the SIR (Susceptible-Infectious-Recovered/Removed) mathematical model, which is one of the most widely used models for epidemic analysis, by incorporating transmission and recovery rates. For this purpose, three different simulations were performed on a herd consisting of N=1000 animals over a 10-day period, and the expected numbers of susceptible, infected, and recovered animals were obtained. Evaluation of the different simulation rates revealed that when the contact rate and recovery rate were reduced, the number of susceptible animals remained constant, while the number of infected animals increased and the number of recovered animals decreased after 10 days. This model provides a valuable preliminary assessment and decision-support tool for epidemic management and control strategies. Furthermore, the development of such models is crucial for early detection and effective intervention in future outbreaks.

Keywords: Epidemic Diseases, Herd, SIR model, Viral diseases

INTRODUCTION

Epidemics have historically affected societies significantly, causing major health issues. Various strategies have been used to comprehend, manage, and avert outbreaks, with mathematical and statistical modeling offering crucial insights into the dynamics, effects, and control methods for infectious diseases [1,2]. The agriculture and livestock sector is of critical importance in both economic and social terms. Viral infectious diseases in animals pose significant challenges to this sector. The economic impacts of viral infectious diseases include mortality rates, reduced product quality, treatment costs and mandatory measures such as culling [3]. It is particularly important to closely monitor diseases such as anthrax, bluetongue and avian influenza. In their study, Govindaraj et al.[4] detailed the financial costs of outbreaks on farms, demonstrating that mass culling measures-such as those implemented during avian influenza outbreaks-result in significant financial losses for farm owners. Bovine viral diarrhoea (BVD), on the other hand, suppresses the immune system of cattle, leading to secondary infections. The study by Walz et al.[5] comprehensively examined the spread of BVD and its effects on health. Therefore, epidemiological analyses of such diseases are important for developing preventive and therapeutic strategies.

Interest in the dynamics of infectious diseases dates back a long way. The first known mathematical model was used by the renowned mathematician Bernoulli in 1760 to analyse a smallpox outbreak [6]. In the years that followed, the collection of statistical data on epidemic diseases led to studies covering different time periods and geographical regions, as well as the development of empirical mathematical models [7]. The control of viral diseases involves four stages: identifying risk factors, developing vaccination strategies, establishing early warning systems, and modeling disease spread. Initially, at-risk animals and regions are identified. Next, vaccination timing and target populations are defined, with control measures activated upon outbreak signs. Finally, intervention plans are created by predicting disease spread through epidemiological models. Mathematical and statistical models are essential in understanding disease transmission and shaping public health strategies [8]. They analyze the spread mechanisms, with models like SIR predicting outbreak progression and identifying key parameters such as the basic reproduction number (R_0).

The aim of this study is to provide a basic introduction to the dynamics of the SIR (Susceptible, Infected, Recovered/Removed) mathematical model, the most commonly used model for modelling infectious diseases, and to illustrate the course of the disease through a simulation using transmission and recovery rates.

MATERIAL AND METHODS

Ethical Statement

This study did not involve any experimental procedures on animals or humans. The analyses were based on open-access data and simulation-based modelling; therefore, approval from an ethics committee was not required.

Study Material and Simulation Design

In this study, a simulation-based modelling approach based on the Susceptible-Infected-Recovered (SIR) epidemic model was used to predict the course of viral infectious diseases and recovery dynamics in livestock populations. The model was developed to estimate the number of animals expected to recover within a 10-day period in a herd of 1000 animals under different transmission and recovery rate scenarios.

The dynamics of the disease within the herd were analyzed by considering various combinations of infection transmission rates *()* and recovery rates *()* specified by the researcher. Using these parameters, temporal changes in the numbers of susceptible, infected, and recovered animals were estimated. Analyses were conducted on different epidemiological scenarios created by varying the and parameters to examine their effects on the disease transmission process. The basic reproduction number was calculated as = /, and the potential for an outbreak was assessed.

Within the scope of the analysis, two main scenarios were examined over a 10-day simulation period. In the first scenario, while the infection transmission rate β was fixed at 0.004, recovery rates of = 0.1 and = 0.5 were evaluated. In the second scenario, the infection transmission rate was set at β = 0.007, and the recovery rate was taken as = 0.3. For each scenario, the expected numbers of susceptible, infected, and recovered animals were calculated over the simulation period and presented graphically to assess the progression of the disease and recovery patterns within the herd.

Software and Numerical Analysis

All simulations and numerical solutions were carried out using the "deSolve" package in the R programming environment. This package was used to solve the system of differential equations forming the basis of the SIR model and to generate the relevant epidemic curves. By adjusting the selected model parameters, the proposed framework enables the prediction of disease transmission dynamics and recovery processes for flocks of different sizes and under varying epidemiological conditions.

Model Compartments and Transition Structure

The SIR model divides the herd population into three epidemiological groups: susceptible animals (S), infected animals (I), and recovered animals (R). The sum of these three groups yields the total population constant N. Susceptible animals are animals that have not yet been exposed to the disease but are capable of becoming infected. Infected animals are those that are actively infected and capable of transmitting the disease, and recovered animals are those that have recovered from the disease and gained immunity.

The model mathematically defines the rates at which animals move between these three categories and is used to analyse the progression of an epidemic over time. The way in which individuals transition between states in the model depends on various factors. Transition from the susceptible state to the infected state requires transmission of the disease, and this transition depends on the rate and prevalence of transmission. Transition from the infected compartment to the recovered compartment depends on the recovery rate of the infection. These transitions are summarised in *Fig. 1*.

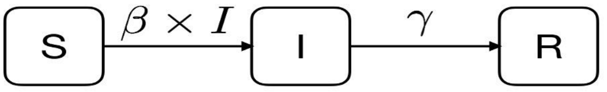

Fig 1. Structure of the SIR Model

Equations

Differential equations were used to mathematically define the SIR model. The equations represent the rate of change over time of the number of individuals in each compartment at any given time. The SIR model is defined by the following system of differential equations:

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$

$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

In these equations, $N=S+I+R$ represents the total population size, β is the effective transmission coefficient, and is the recovery rate. In this formulation, the infection term is normalized by the total population size (N), allowing the transmission process to be represented independently of population magnitude and ensuring biologically realistic epidemic dynamics.

Transmission and Recovery Parameters

The model assumes that a transmission rate (p) applies to each contact. The value, generally referred to as the effective contact rate and denoted by β, is calculated as the product of the number of contacts (σ) and the transmission rate. Accordingly, the transmission rate, defined as the number of susceptible individuals moving from compartment S to compartment I during the time interval t, is expressed as:

$$\frac{\beta \times S \times I}{N}$$

where the parameter β represents the effective contact rate between susceptible and infected individuals. The recovery process is assumed to occur at a constant per capita rate γ, such that infected individuals move to the recovered compartment at a rate of:

$$\gamma \times \mathrm{I}$$

where $\gamma = 1/D$, and D denotes the average infectious period [9].

Basic Reproduction Number

The basic reproduction number is an important measure of the strength of an infectious disease outbreak (R_0). In the normalized SIR framework, the basic reproduction number is commonly defined as:

$$R_0 = \frac{\beta}{\gamma}$$

which represents the average number of secondary infections generated by a single infected individual in a fully susceptible population. It is measured by counting the number of secondary cases following the introduction of the infection into a fully susceptible population [10]. In other words, it is the number of new infectious animals that an infected animal will produce during its infectious period when introduced into a fully susceptible herd. If $R_0 > 1$ in the population, the conditions are conducive to an outbreak, as each primary infection leads to more than one secondary infection. Conversely, if $R_0 < 1$, as an average primary infection does not lead to an additional secondary infection, the conditions for an outbreak to emerge do not arise. The level of herd immunity can be measured by the magnitude of the decrease in the R value [11].

Statistical Analysis

The expected numbers of susceptible, infected, and recovered animals were calculated for each parameter combination over the 10-day simulation period. The effects of different infection transmission and recovery rates on epidemic progression were evaluated by comparing the temporal changes in the SIR compartments across the selected scenarios. The results were presented graphically to assess disease progression and recovery patterns within the herd.

RESULTS

Examples of SIR model applications in an epidemic can be given as follows.

For a herd of 1000 head over a 10-day period, with a contact rate (β) of 0.004 and a recovery rate (γ) of 0.5, the numbers

Table 1. *Contact rate (β) = 0.004, recovery rate gamma (γ) = 0.5 for a herd of 1000 animals over a 10-day period, showing the number of suspected, infected and recovered animals in relation to the epidemic situation*

Day	Susceptible	Infected	Recovered
0	999.0000000	1.00000	0.000000
1	963.7055761	31.79830	4.496125
2	461.5687749	441.91575	96.515480
3	46.1563480	569.50418	384.339476
4	7.0358807	373.49831	619.465807
5	2.1489407	230.12934	767.721720
6	1.0390927	140.41085	858.550058
7	0.6674074	85.44479	913.887801
8	0.5098627	51.94498	947.545162
9	0.4328913	31.56515	968.001960
10	0.3919173	19.17668	980.431400

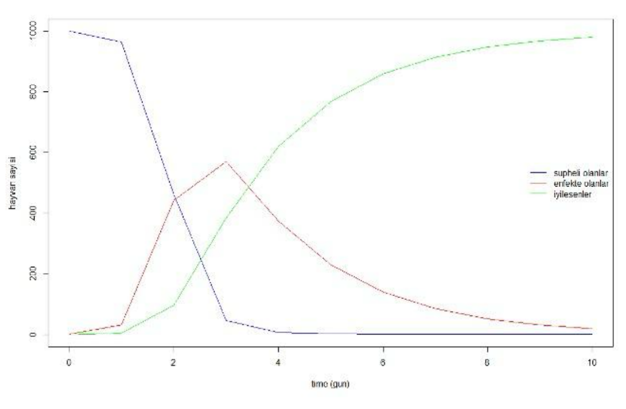

Fig 2. Graphical illustration of the SIR model with β = 0.004 and γ = 0.5 parameters

of suspected, infected and recovered animals during the outbreak are given in *Table 1* and shown in *Fig. 2*.

Here, the basic reproduction number (R_0) is calculated as beta/gamma × 1000 (N) = 8. The number of infected animals in the herd peaked at 569 on the third day following the onset of the outbreak, then declined, falling to 19 by the tenth day, whilst the number of recovered animals rose to 980.

The results of calculating the number of suspected, infected and recovered animals over a 10-day period for a herd of 1000 head, assuming a contact rate (β) of 0.007 and a recovery rate (γ) of 0.3, are presented in *Table 2*, and the values shown in *Fig. 3* were obtained.

***Table 2.** Contact rate (β) = 0.007, recovery rate gamma (γ) = 0.3. Results when calculating the number of suspected, infected and recovered animals over a 10-day period for a herd of 1000 head in relation to an outbreak situation*

Day	Susceptible	Infected	Recovered
0	9.990000e+02	1.00000	0.00000
1	5.447443e+02	429.26553	25.99019
2	2.947830e+00	747.37983	249.67234
3	3.163976e-02	555.96434	444.00402
4	1.096517e-03	411.89289	588.10601
5	9.078179e-05	305.13857	694.86134
6	1.434115e-05	226.05226	773.94773
7	3.653873e-06	167.46361	832.53638
8	1.362408e-06	124.06015	875.93985
9	6.179429e-07	91.90604	908.09396
10	3.523122e-07	68.08570	931.91430

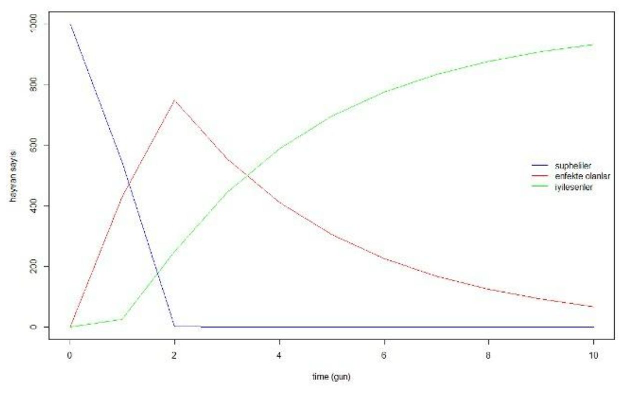

Fig 3. Graphical illustration of the SIR model with β = 0.007 and γ = 0.3 parameters

Here, the basic reproduction number (R_0) is calculated as beta/gamma × 1000 = 23. As the basic reproduction number in the herd increased, the number of infected animals in the herd peaked at 747 on the second day; by the tenth day, this number had fallen to 68, whilst the number of recovered animals had risen to 931.

For a herd of 1.000 head over a 10-day period, with a contact rate (β) of 0.004 and a recovery rate (γ) of 0.1, the numbers of suspected, infected and recovered animals during the outbreak are presented in *Table 3*, and the results shown in *Fig. 4* were obtained.

***Table 3.** Contact rate (β) = 0.004, recovery rate gamma (γ) = 0.1 for a herd of 1000 animals over a 10-day period, number of animals suspected, infected and recovered in relation to the epidemic situation*

Day	Susceptible	Infected	Recovered
0	9.990000e+02	1.0000	0.000000
1	9.517764e+02	47.0130	1.210619
2	2.901416e+02	678.9487	30.909671
3	1.007621e+01	875.0093	114.914523
4	3.505072e-01	800.7713	198.878178
5	1.661487e-02	724.8784	275.105032
6	1.052368e-03	655.9116	344.087394
7	8.667749e-05	593.4942	406.505696
8	9.087673e-06	537.0159	462.984137
9	1.163745e-06	485.9121	514.087924
10	1.811918e-07	439.6715	560.328496

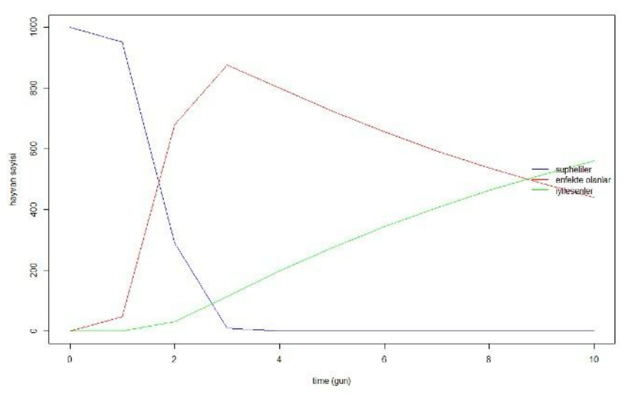

Fig 4. Graphical illustration of the SIR model with β = 0.004 and γ = 0.10 parameters

Here, the basic reproduction number (R_0) is calculated as beta/gamma × 1000 = 40. In a herd where the contact rate is 0.004 but the recovery rate is as low as 0.1, 47 animals were infected on the first day, rising to 678 on the second day; by the tenth day, the number of infected animals remained at 439, whilst the number of recovered animals was limited to 560.

A summary of the course of the disease on the tenth day, based on three different simulation rates, is presented in *Table 4*.

DISCUSSION

This study evaluated the role of the SIR model in the epidemiological analysis of infectious diseases within

Table 4. *Disease progression on the 10th day based on varying contact rates, recovery rates, and basic reproduction numbers*

Simulation	Contact Rate (β)	Recovery Rate (γ)	Reproduction Number (R_0)	Susceptible	Infected	Recovered
1	0.004	0.5	8	0.39	19.17	980.43
2	0.007	0.3	23	0.001	68.08	931.91
3	0.004	0.1	40	0.001	439.67	560.32

the framework of seroprevalence data on animal diseases in Türkiye and the broader mathematical modelling literature.

Examination of seroprevalence data concerning viral diseases in Türkiye reveals that these infections are widespread, yet exhibit pronounced regional variation. In a study encompassing 26 dairy cattle farms across different regions, BVDV seropositivity rates were found to range from 0.6% to 70.0% [12]. In the provinces of Ankara, Çorum, Kırıkkale, and Yozgat, this rate was determined to be 70.89% [13]. Similarly, IBR (Infectious Bovine Rhinotracheitis) seroprevalence demonstrated substantial variability, with seropositivity rates ranging from 14% to 81% [14]; in the North-Eastern Anatolia Region this figure ranged from 44.04% to 76.47% [15], while in the South-Eastern Anatolia Region it varied between 6.06% and 79.35% [16]. A comparable pattern was observed for bluetongue disease: seropositivity rates of 2.5% in Amasya and 10% in Sinop were detected in the Central Black Sea Region, whereas no seropositivity was identified in the provinces of Samsun, Ordu, and Giresun [17]. Seropositivity rates reached 65.2% in goats in Tokat and Samsun, while this rate was measured at 8.6% in sheep in Sivas [18]. These findings collectively demonstrate that the infections in question are widespread throughout Türkiye, yet seroprevalence varies considerably depending on geographical region, animal species, and local conditions.

These regional differences underscore the fact that disease dynamics cannot be addressed within a uniform framework, and that epidemiological models must be calibrated using local data. Indeed, herd health is critically important not only for protecting individual animal health, but also for preventing the spread of diseases at the population level [13,18]. In this context, control strategies -particularly vaccination- must be evaluated not merely from a clinical perspective, but also in terms of their epidemiological and economic dimensions [5,12].

Mathematical models have emerged as indispensable tools for understanding disease transmission mechanisms and designing control strategies. Basic epidemiological approaches such as the SIR model predict the course of an outbreak over time by examining the transitions of animals between different disease states within a population [10,19]. The basic reproduction number (R_0), a parameter that occupies a central role in determining the critical dynamics of an outbreak, is widely calculated using the SIR model [8]. The principal factors influencing R_0 include the ease with which the virus spreads among animals via shared resources such as air, water, and feed; the incubation period of the disease; the duration during which infected animals shed the virus; herd density and contact frequency; the age and immune status of animals; and temperature, humidity, and hygiene conditions [9,20]. The accuracy and reliability of the predictions yielded by the model are, moreover, largely contingent upon the known transmission rate and seroprevalence data of the disease [21,22].

Recent studies have clearly demonstrated that the SIR model is not confined to providing a theoretical framework, but is equally capable of generating practical policy outputs. Zhang et al.[23], employing the SIR model in an integrated epidemiological-economic model designed to control a PRRS outbreak in Vietnam, determined an R R_0 value of 1.3 and identified that the optimal vaccination rate should be approximately 26%, further reporting that the societal benefit of vaccination programmes was 2.3-4.5 times higher than the associated costs. These findings substantiate the capacity of SIR models to produce concrete economic outputs for livestock policy planning. Valdes-Donoso and Jarvis [24], in their analysis of intra-farm and inter-farm PRRS-transmission using an SIR model, demonstrated that vaccination programmes yield considerable economic benefits for both individual farms and regional production systems, placing particular emphasis on the decisive role of herd density, animal movements, and the distance between farms in transmission dynamics. In a study on Newcastle Disease Virus (NDV), Annapragada et al.[25], using an extended version of the classical SIR model to examine the effects of vaccination coverage on herd immunity, found that vaccination rates constitute a critical factor for the sustainability of poultry flocks, particularly in rural areas, and stated that a vaccination coverage of at least 40% is required to achieve a significant increase in flock population. These findings further highlight the importance of accounting for the dynamic nature of animal populations within mathematical models.

A review of the historical record reveals that epidemics have left deep impressions on societies and have given rise to serious public health problems [6]. This reality further reinforces the critical role of mathematical and statistical modelling in understanding, controlling, and preventing infectious diseases [7,8]. Modelling approaches provide valuable insights into disease spread, its impacts, and control strategies [10]; by simulating in advance the effects of interventions such as vaccination, quarantine, and social distancing, they enable the identification of the most effective measures [21,22]; and they serve as an indispensable instrument for planning healthcare system capacity. It is also noteworthy that whilst statistical indicators such as disease incidence rates and recovery rates have found an established place of application in medicine, the insufficiency of such data in the livestock sector constitutes a conspicuous gap and signals an urgent need in this domain.

When all these findings are considered in their entirety, it becomes evident that SIR-based models can be effectively utilised not only in epidemiological analyses, but also in economic planning, the optimisation of vaccination strategies, and the formulation of biosecurity policies. It is understood that clinical approaches alone are insufficient for bringing infectious diseases under control, and that mathematical modelling methods must be integrated into decision-making processes [4,14]. The increasing mobility of animals and the consequent rise in the rate of viral disease transmission further underscore the importance of epidemiological models. Accordingly, the integrated use of SIR models with real-time field data, artificial intelligence-supported forecasting methods, and economic analyses will contribute substantially to the more effective management of outbreaks.

DECLARATIONS

Availability of Data and Materials: All simulations and numerical solutions were carried out using the "deSolve" package in the R programming environment.

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Conflict of Interest: The authors declared that there is no conflict of interest.

Ethical Statement: The analyses were based on open-access data and simulation-based modelling; therefore, approval from an ethics committee was not required.

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