Open Access

Check for updates

Research Article

Journal of Veterinary and Animal Sciences
ISSN (Print): 0971-0701, (Online): 2582-0605
https://doi.org/10.51966/jvas.2025.56.1.45-52

Analysing the dynamics of Foot-and-Mouth Disease transmission: A model-based approach#

P.A. Aparna[1], K. Justin Davis[1*], Kaniyamattam Karun[2], P.V. Tresamol[1], K. Vinodkumar[1] and Deepa Jolly[3]

[1]Department of Veterinary Epidemiology and Preventive Medicine, [3]Department of Veterinary Public Health, College of Veterinary and Animal Sciences, Mannuthy, Thrissur-680 651, [2]Department of Animal Sciences and AgriLife Research, Texas A & M University, USA, Kerala Veterinary and Animal Sciences University, Pookode, Wayanad, Kerala

Citation: Aparna, P.A., Davis, J.K., Kaniyamattam, K., Tresamol, P.V., Vinodkumar, K., and Jolly, D. 2025. Analyzing the dynamics of Foot-and-Mouth Disease transmission: A model-based approach.
J. Vet. Anim. Sci. **56** (1):45-52

Received: 24.09.2024 Accepted: 26.12.2024 Published: 31.03.2025

Abstract

Foot-and-mouth disease (FMD) is a highly contagious viral infection affecting cloven-footed animals, including cattle, sheep, goats, pigs, and wildlife. This study developed a system dynamics compartmental model to elucidate the transmission dynamics of FMD in cattle. Key parameters influencing disease spread such as the basic reproduction number (R_0), duration of infectivity, and immunisation coverage were identified through a thorough literature review and integrated into the model, which comprised Susceptible (S), Infectious (I), and Recovered (R) compartments. The analysis focused on the effects of varying R_0 values, infectivity durations, and vaccination rates on disease transmission. Findings highlighted the critical role of reducing R_0 and increasing vaccination coverage to mitigate FMD outbreaks and enhance control measures.

Keywords: *Foot and mouth disease, models, simulation, transmission dynamics, basic reproduction number*

The cattle population in India experienced a growth of 0.8 percent when comparing the most recent livestock censuses (DAHD, 2019). Among the number of diseases which affect cattle population, foot and mouth disease is a major transboundary disease known for its high contagiousness among cloven footed animals (Edo and Bekele, 2019). The etiology behind the disease is foot and mouth disease virus (FMDV) within the genus aphthovirus of picornaviridae family (Azeem *et al*., 2020). Seven immunologically distinct serotypes have been identified for the disease namely O, A, C, Asia 1, SAT1, SAT2 and SAT3. Most of the outbreaks are commonly due to serotype O, whereas serotype A and Asia1 are associated with sporadic occurrence only (Subramaniam *et al*., 2013). Despite their low mortality rate, FMD affects a large number of animals across multiple species each time (James and Rushton, 2002). Understanding FMD dynamics is essential for developing effective prevention and control strategies. Epidemiological models play an important role in predicting outbreaks, assessing intervention strategies and formulating policy decisions (Keeling, 2005). Models help us understand complex systems, often using mathematics to define and analyze ideas. These models can be simulated on computers to forecast broader outcomes; however, they are simplified representations of reality. Consequently, the results they produce should be interpreted as estimates. For FMD spread, current knowledge is insufficient to create a fully accurate model, highlighting the need for further research to develop effective epidemiological models (Woolhouse,

Part of MVSc thesis submitted to Kerala Veterinary and Animal Sciences University, Pookode, Wayanad, Kerala
**Corresponding author: justinpm@kvasu.ac.in, Ph. 94467 97772*

2003). The present study aimed to develop a simulated SIR model to represent the transmission dynamics of FMD. The SIR model, with its three-compartment structure, offers a simplified framework that enhances understanding of disease dynamics, particularly for non-specialist readers, compared to more complex models like SEIR or SEIRC. Additionally, the developed SIR model is adaptable, allowing the incorporation of diverse field parameter values.

Materials and methods

Prior to model development, it is crucial to define the population under study. Given their significant role in FMD transmission, cattle were selected as the primary focus. The model incorporates specific assumptions to address unavoidable complexities and ensure feasibility and those were listed below

- Model assumed to contain one million homogenous cattle population
- The disease progression was categorised into discrete stages: susceptible, infected, and recovered
- Animals were assumed to recover at a constant rate and acquire immunity, making them resistant to reinfection for a certain period
- Birth and death rates were considered to be equal, with no new animals entering or leaving during the study period
- No significant variations in factors like climate and geography were assumed to exist within the study area
- Rare events, such as unlikely virus mutations and unusual pathways of transmission, were disregarded

Model parameterisation and description

Literature review was conducted to identify different parameters affecting FMD transmission (Table 1). A system dynamics compartmental model was created, consisting of stocks, flows, and auxiliary variables which were organized into compartments that represent different disease states of the cattle population concerning FMD. Vensim®Personal Learning Edition was used to construct the model. The model included the following stages: susceptible, infectious and recovered, as described by McLachlan *et al*. (2019). The elements of the model, including stocks, flows, and the parameters designated as stocks, flows, and auxiliary variables, are outlined below. After selecting the variables, the model was initially conceptualized and subsequently transformed into a dynamic framework through simulation.

Stocks, also known as levels or accumulations, represented the quantities or resources that built up within the system over time. They essentially served as the disease state variables of the system. The key stock variables were,

- Susceptible (S): Cattle that were vulnerable of getting infected
- Infected (I): Cattle that were currently infectious
- Recovered (R): Cattle that had recovered from the infection

Flows, which captured the transitions between different states were influenced by processes such as infection, recovery, death and other dynamics. The main flows considered were,

- Infection rate (β): The rate at which susceptible cattle became infected
- Recovery rate (γ): The rate at which infected cattle recovered and transitioned into the recovered state

Auxiliary variables that were considered included the following:-

- Total Population (N): The total number of cattle within the study area
- Basic Reproduction Number (R0): The average number of secondary infections caused by one infected individual in a fully susceptible population. It's a number so it doesn't have units
- Transmission Rate (ω): The rate at which the disease spread from infected cattle to susceptible cattle
- Proportion of animals immunized (ι): The percentage of the total cattle population that had been vaccinated
- Infectivity duration (d): The average time an individual remained infectious before recovering
- Fraction susceptible (χ): The proportion of the total population at risk of contracting the disease
- Movement control reduction fraction (κ): The fraction or percentage by which animal movement was reduced due to control measures, indicating the effectiveness of movement restrictions in limiting disease spread
- Movement control start time (ϕ): The point in time when movement restrictions were first introduced to curb the spread of the disease
- Movement control duration (ν): The duration for which movement restrictions were enforced

Model conceptualization

The model conceptualisation of FMD in cattle was done in Vensim®PLE, a software used to create disease models. The key components, including stocks for susceptible, infected and recovered states, along with various flows that governed the transitions between these stages. Auxiliary variables were used to establish the relationships between these compartments. Disease

Table. 1. Parameters identified through literature review

Sl. No.	Parameter	Value	References
1	Basic reproduction number (R_0)	3.5-4.5 (Great Britain) 2.5 (Netherlands) 1.27(Amhara, Ethiopia) 1.68 (Ethiopia) 1.27 (India) 4(2-6) (Africa)	(Ferguson *et al*., 2001) (De Rueda *et al*., 2015) (Belayneh *et al*., 2020) (Tadesse *et al*., 2019) (Krishnamoorthy *et al*., 2020) (Mclachlan *et al*., 2019)
2	Transmission rate (β)	0.27 per day 0.26 per day	(Belayneh *et al*., 2020) (Tadesse *et al*., 2019)
3	Recovery rate	0.2222 per day	(Mardones *et al*., 2010)
4	Duration of subclinical period	2.0 days	
5	Duration of infectious period	4.0 days	
6	Duration of clinical period	7.5 days	
7	Incubation phase	3.6 days (2.7–4.8)	
8	Subclinical infectious phase	2.2 days (1.5–3.5)	(Yadav *et al*., 2019)
9	Clinical infectious phase	8.5 days (6.2–11.6)	
10	Total infectious phase	10.8 days (8.2–14.2)	
11	Latent period	4.6 days	
12	Probability of becoming a carrier	0.5	(Mclachlan *et al*., 2019)
13	Infectious period	1.7 days	
14	Pre-clinical infectious animals	0.99	
15	Latent	4.8 days	
16	Pre-clinical infectious period	2.8 days	
17	Clinically infectious period	0.8 days	
18	Vaccine protectiveness	0.88 %	(Hayer *et al*., 2018)
19	Effective reproductive number- R (number of number of secondary infections caused by one infected individual in a fully partially susceptible population	8.04	

transmission was primarily driven by the transmission rate and the basic reproduction number, determining how susceptible cattle became infected after contact with infected animals. Once exposed, cattle moved into the infected stock, where they either recovered or gained temporary immunity. The model also incorporated intervention measures like vaccination and movement control, which helped to reduce the number of susceptible animals and limit the spread of FMD.

Model simulation

SIR model with both immunisation and movement control:

Susceptible-Infected-Recovered (SIR) model had key parameters such as transmission rate, infection duration, basic reproduction number (R_0), and the proportion of animals vaccinated was used in the study. Movement control measures, such as the start time, duration, and reduction fraction, were also integrated into the model. Susceptible individuals transitioned to the infected state based on the transmission rate and current number of infected individuals, with the fraction susceptible influenced by the total population and vaccination rates. Infected individuals recovered over a specified duration, moving to the recovered compartment. The reproduction ratio, reflecting the actual number of secondary infections per infected individual, was impacted by movement control measures and vaccination. This model effectively simulated disease spread and evaluated the impact of interventions such as vaccination and movement restrictions. All simulations were carried out for a time step of one day, initial time of zero day and final time of 365 days.

A set of experiments were carried to evaluate the impact of key parameters and control measures for the spread of FMD. During the literature review, basic reproduction number (R_0) found to range from 1-8. Hence the simulations were carried out at an R_0 of 2, 4 and 8. Yadav *et al*. (2019) reported that different serotypes are having different infectivity periods, accordingly to which in this study simulations were carried out. Also the effect of

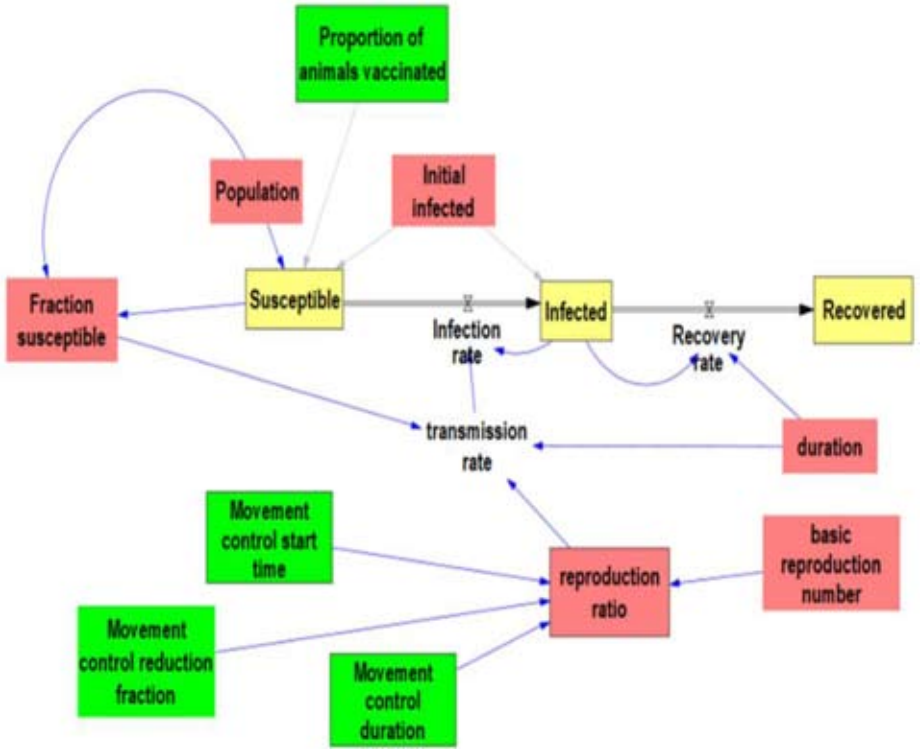

Fig.1. Conceptual SIR model for FMD

different proportions of population immunised were also assessed by the model simulations.

Results and discussion

The SIR model was simulated by systematically varying key parameter values, including R_0, vaccination rates, and the duration of the infectious period. The effects of these changes were observed and recorded to analyse their influence on the disease dynamics and outcomes.

Effect of basic reproduction number (R_0) in FMD dynamics

Simulations were carried at different R_0's and the impacts were given below

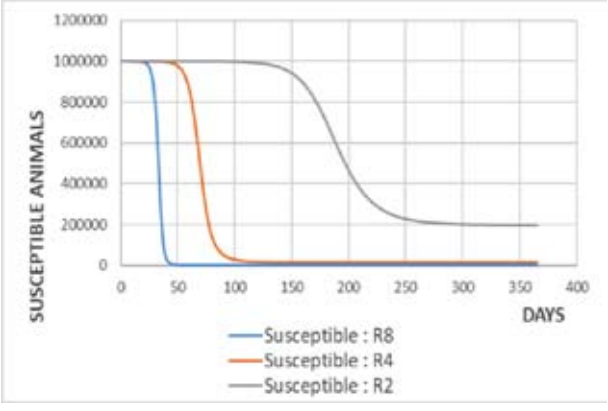

Fig. 2

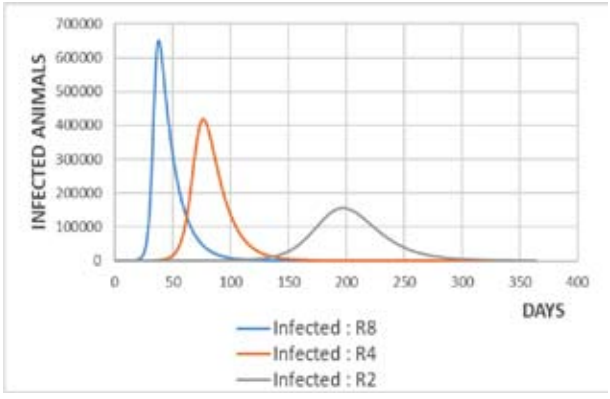

Fig. 3

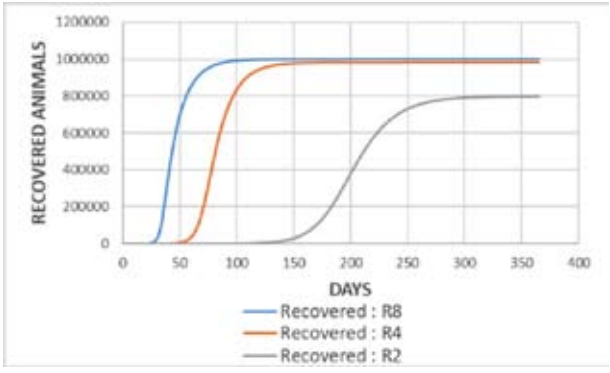

Fig. 4

Fig. 2, 3, 4. Graphs representing changes in SIR stock in accordance with change in R_0 of 2,4 and 8 at an infectivity period of 14 days and no control measures applied.

Table 2. Parameters and their values given as an input to the model

Parameter	Value	Unit
Transmission rate (ω)	R' / d * χ	fraction/day
Susceptible (S)	INTEG (-β , (N - I_0) * (1 - ι))	animals
Reproduction ratio (R')	R_0*(1-STEP(κ, ϕ)+ STEP(κ, ϕ + ν))	fraction
Recovering (γ)	I / d	animals/day
Recovered (R)	INTEG (γ, 0)	animals
Proportion of animals immunized (ι)	0	fraction
Population (N)	1e+06	animals
Movement control start time (ψ)	0	day
Movement control reduction fraction (κ)	0.5	fraction
Movement control duration (ν)	15	day
Initial infected (I_0)	1	animals
Infection rate (β)	I* ω	animals/day
Infected (I)	INTEG (β-γ , I_0)	animals
Fraction susceptible (χ)	S/N	fraction
Infectivity period (d)	14	day
Basic reproduction number (R_0)	4	dimensionless

Computational models enable us to turn observations into predictions, serving as a platform for testing ideas and to derive insights from data and explore system behaviors (Calder *et al*., 2018). Modeling plays a vital role in understanding and managing complex systems, particularly in epidemiology. Epidemiological models are essential tools for predicting disease outbreaks, evaluating intervention strategies, and guiding policy decisions. By utilizing mathematical frameworks, these models help simplify and analyze intricate dynamics, enabling a clearer understanding of disease spread and control. Computer simulations of these models allow for forecasting broader outcomes, providing valuable insights while recognizing that they are simplified representations of real-world scenarios (Keeling, 2005). System dynamics modeling enables the analysis of complex relationships over time by depicting causal connections among variables. It has been effectively used in various business and socio-economic areas to` understand issues and evaluate different policy interventions. System dynamics is a robust tool that can be applied successfully to a broad range of problems (Tang and Vijay, 2001). Numerous experiments can be done in Vensim® Personal Learning Edition software simulation language (Shamsuddoha and Nedelea, 2013).

According to Heffernan *et al*. (2005), the basic reproduction number (R_0) represents the average number of secondary infections caused by a single infected individual, reflecting the disease's contagiousness. Simulations were carried out at R_0 of 2,4 and 8 and found that higher R_0 was found to lead to higher infection peak.

In SIR model, at an R_0 of 8, the infection spreads rapidly and caused a sharp peak where the number of infected animals surged from just one to approximately 418037 within 76 days, followed by a swift decline back to one infected animal in 271 days. With an R_0 of 4, the outbreak was more moderate, reached a peak of 367914 infected animals after 89 days and returned to the initial state after 293 days. At the lowest R_0 of 2, the outbreak progressed much more slowly, peaking at 156,058 infected animals in 197 days. Initially, 99.9 per cent of the animal population was susceptible, irrespective of the R_0 value. After 365 days, the remaining number of susceptible animals for R_2, R_4, and R_8 were 199348, 30182 and 16671, respectively. The number of recovered animals in the population after 365 days for R_0 of 2, 4, and 8 were 800374, 969,817 and 983,329, respectively.

A higher R_0 led to a more rapid spread of the infection, with a sharper peak and faster transition of animals between compartments compared to scenarios with a lower R_0. Lower R_0 made the curve flattened with a lower infection peak (Van den Driessche and Watmough, 2008), as observed in this study too. So, all intervention strategies should aim to reduce the R_0 (Mushayabasa *et al*., 2011).

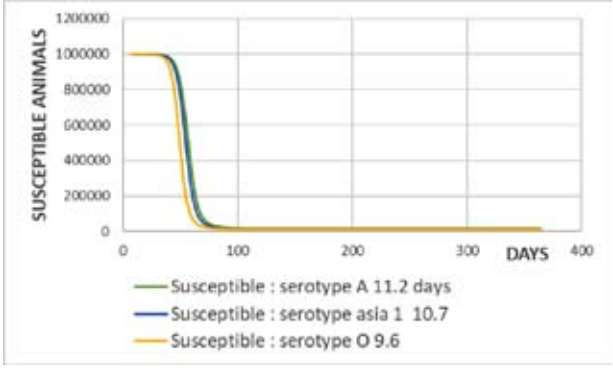

Fig. 5

Effect of infectivity period in infection dynamics

Simulations were conducted by varying the infectious period while keeping all other parameter values constant to isolate its effect. R_0 was fixed at 4, as the literature review indicated that both the basic and effective reproduction numbers ranged from 1 to 8, with an average value of 4 being chosen for all other scenarios.

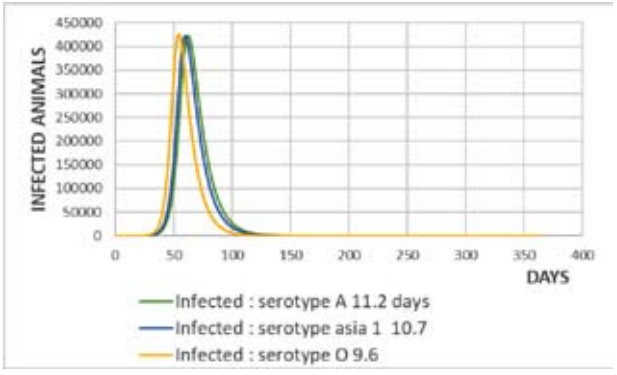

Fig. 6

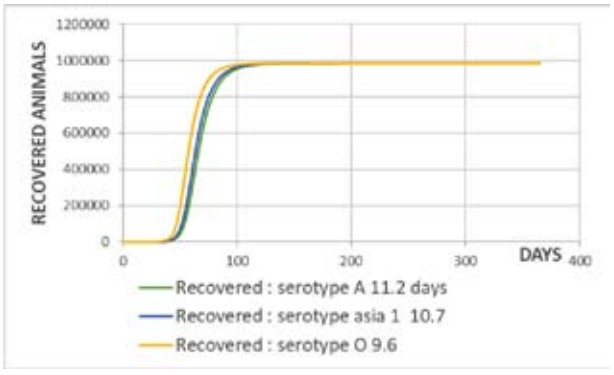

Fig. 7

Fig. 5, 6, 7. Graphs representing changes in SIR stock in accordance with change in infectivity period at an R_0 of 4 and no control measures applied

Simulations were carried out in SIR with a R_0 of 4 and the infectivity period of 9.6 days, 10.7 days, 11.2 days for serotype O, Asia 1 and A, respectively and it was observed that peak infection status of all the serotypes remained more or less same and it was seen that lesser duration of infectivity anticipated sudden onset of outbreak with exhibition of clinical signs. So serotype O would be associated with rapid manifestation of clinical signs. This is in accordance with Islam *et al*. (2017) who also reported that animals affected with serotype O will exhibits sudden occurrence of outbreak with clinical signs initially. Serotyping is essential in immunization as the vaccines do not offer cross-protection (Parida, 2009)

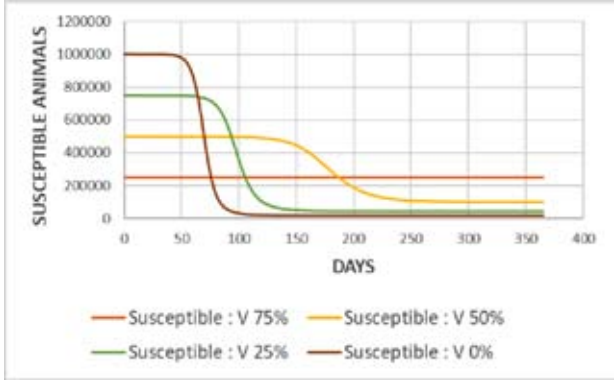

Fig. 8

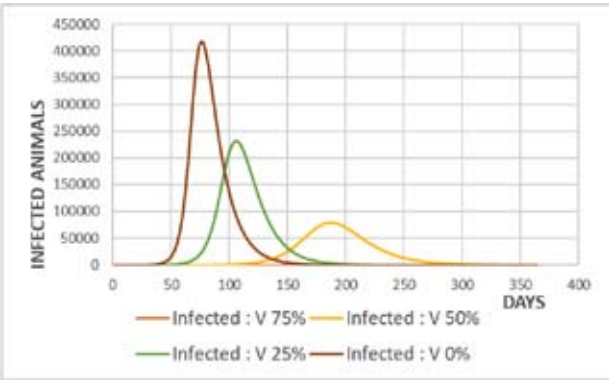

Fig. 9

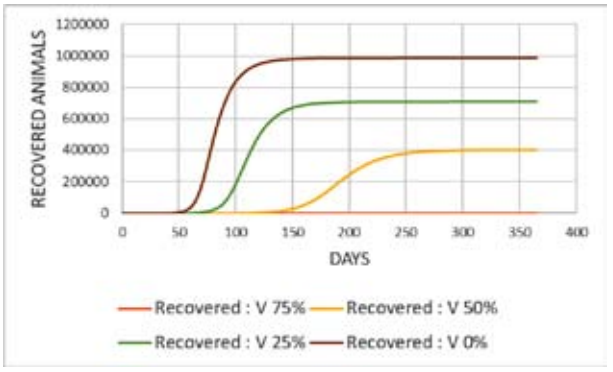

Fig. 10

Fig. 8, 9, 10. Graphs representing changes in SIR stock in accordance with change in proportion of population vaccinated at an infectivity period of 14 days and R_0 of 4.

Effect of immunisation in FMD dynamics

SIR model revealed that, when no animals were vaccinated, the peak infection reached 418037 animals on the 76th day. With 25 percent vaccination coverage, the highest infection level dropped to 231668 infected animals on the 106th day. When 50 percent of the population was immunized, the maximum infection observed occurred on the 187th day, with 78031 infected animals. Finally, vaccinating 75 percent of the population resulted in only one infected animal.

Vaccination is an important strategy adopted for controlling outbreaks (Orsel and Bouma, 2009). Simulation studies revealed that 75 per cent vaccination yielded very less numbers of infected animals at an R_0 of 4. This is in line with Gibson *et al*. (2021) who used an equation for calculating herd immunity threshold (HIT = 1-1/R_0). Sharma *et al*. (2017) stated that achieving herd

immunity threshold would prevent disease transmission as well as confer protection to even in animals who are not vaccinated. These findings align with those of Capon *et al*. (2021), who found that targeted interventions substantially reduced the duration of outbreaks. Similarly, Gunasekera *et al*. (2022) demonstrated that increased vaccination coverage and robust control measures significantly lowered outbreak risks, underscoring the importance of early and targeted actions in minimizing disease spread and economic losses.

The practical applications of this model are highlighted in its ability to guide policymakers in designing effective vaccination campaigns to reduce the basic reproduction number (R_0) of foot and mouth disease (FMD). For instance, the model demonstrated that vaccinating 75 per cent of the population significantly curtails disease transmission. This evidence provides policymakers with a scientific basis for setting vaccination coverage targets. Furthermore, the model emphasizes the importance of identifying the specific FMD serotype to tailor control measures effectively, thereby optimizing resource allocation. These insights enable stakeholders to proactively implement strategies that mitigate disease spread, avoiding the socio-economic impacts of a real outbreak.

This study is based on several assumptions that also highlight its limitations. It considers a homogeneous population of one million cattle, overlooking natural variations in factors such as age, breed, and individual susceptibility. Furthermore, it disregarded the effects of population turnover, livestock movement, environmental variations, and rare events like virus mutations, which could influence the FMD dynamics. While these assumptions simplify the model and enhance computational feasibility, they also impose constraints that may limit its applicability and the accuracy of its predictions in real-world scenarios.

Conclusion

This study demonstrated the critical influence of the basic reproduction number (R_0) on the spread and severity of foot-and-mouth disease (FMD) outbreaks. Higher R_0 values led to more rapid and extensive disease transmission, while vaccination proved to be a highly effective strategy for reducing infection rates and delaying outbreak peaks. The simulations showed that as vaccination coverage increased, the number of infected animals and the speed of transmission significantly decreased, with 75 per cent vaccination nearly eradicating the outbreak. The model outputs were comparable against real-world scenarios, demonstrating that vaccination and movement control served as a robust defence mechanisms during outbreaks. Future directions for FMD research include adapting field data for model refinement, exploring agent-based modeling approaches, and investigating macro- and microclimatic effects on disease spread. Additionally, research should focus on heterogeneous population dynamics, intra- and inter-herd transmission patterns, and the role of other animals, such as sheep, goats, and pigs, in the epidemiology of FMD. These areas of investigation will help refine control strategies and improve our understanding of disease transmission in diverse environments.

Acknowledgements

The authors are thankful to the Department of Veterinary Epidemiology and Preventive Medicine, College of Veterinary and Animal Sciences, Mannuthy for providing the facilities necessary to carry out the study.

Conflict of interest

The authors declare that they have no conflict of interest.

References

Azeem, A., Rashid, I., Hassan, M.M., Asad, M., Kaukab, G., Tehseen, A. and Aamir, S. 2020. 10. A review on foot and mouth disease in dairy animals, etiology, pathogenesis and clinical findings. *Pure Appl. Biol.* **9**(1): 821-832.

Belayneh, N., Molla, W., Mesfine, M. and Jemberu, W.T. 2020. Modeling the transmission dynamics of foot and mouth disease in Amhara region, Ethiopia. *Prev. Vet. Med*. **181**: 104673. Available: https://doi.org/10.1016/j.prevetmed.2019.04.002 [Aug. 2020].

Calder, M., Craig, C., Culley, D., De Cani, R., Donnelly, C.A., Douglas, R., Edmonds, B., Gascoigne, J., Gilbert, N., Hargrove, C. and Hinds, D. 2018. Computational modelling for decision-making: where, why, what, who and how. *Royal Soc. Open Sci*. **5**(6): 172096. Available: https://doi.org/10.3389/frai.2022.750763 [Feb. 2022].

Capon, T.R., Garner, M.G., Tapsuwan, S., Roche, S., Breed, A.C., Liu, S., Miller, C., Bradhurst, R. and Hamilton, S. 2021. A simulation study of the use of vaccination to control foot-and-mouth disease outbreaks across Australia. *Front. Vet. Sci.* **8:** 648003. Available: https://doi.org/10.3389/fvets.2021.648003 [11 Aug. 2021]

DAHD. 2019. 20th Livestock Census. All India Report published by Department of Animal Husbandary and Dairying, Government of India. Available: https://dahd.nic.in/about-us/divisions/statistics

De Rueda, C.B., Dekker, A., Eble, P.L. and De Jong, M.C.M. 2015. Vaccination of cattle only is sufficient to stop FMDV transmission in mixed populations of sheep and cattle. *Epidemiol. Infect*. **143**(11): 2279-2286.

Edo, J.J. and Bekele, J.T. 2019. A review on trans-boundary animal diseases management. *Vet. Res*. **12**(1): 1-9.

Ferguson, N.M., Donnelly, C.A. and Anderson, R.M. 2001. The foot-and-mouth epidemic in Great Britain: pattern of spread and impact of interventions. *Sci.* **292**(5519): 1155-1160.

Gibson, A.J., Paton, D.J. and Werling, D. 2021. *Vaccination Strategies, Implementation, and Monitoring. Vet. Vaccines: Principles and Applications*. (1st Ed.). Wiley- Blackwell, United Kingdom, 442p.

Gunasekera, U., Biswal, J.K., Machado, G., Ranjan, R., Subramaniam, S., Rout, M., Mohapatra, J.K., Pattnaik, B., Singh, R.P., Arzt, J. and Perez, A. 2022. Impact of mass vaccination on the spatiotemporal dynamics of FMD outbreaks in India, 2008–2016. *Transbound. Emerg. Dis.* **69(**5): 1936-1950.

Hayer, S.S., Ranjan, R., Biswal, J.K., Subramaniam, S., Mohapatra, J.K., Sharma, G.K., Rout, M., Dash, B.B., Das, B., Prusty, B.R. and Sharma, A.K. 2018. Quantitative characteristics of the foot and mouth disease carrier state under natural conditions in India. *Transbound. Emerg. Dis*. **65**(1): 253-260.

Heffernan, J.M., Smith, R.J. and Wahl, L.M. 2005. Perspectives on the basic reproductive ratio. *J. R. Soc. Interface*. **2**(4): 281-293.

Islam, M.S., Habib, M.A., Islam, M.R., Mahmud, M.S., Saha, P.C., Ruba, T., Das, P.M. and Khan, M.A. 2017. Clinicopathological investigation of foot and mouth disease and serotype identification of the viruses in cattle of Bangladesh. *Immunol. Infect. Dis*. **5**(2): 16-23.

James, A.D. and Rushton, J. 2002. The economics of foot and mouth disease. *Rev. Sci. Tech. - Off. Int. Epizoot.* **21**(3): 637-641.

Keeling, M.J. 2005. Models of foot-and-mouth disease. *Proc. R. Soc. B.* **272**(1569): 1195-1202.

Krishnamoorthy, P., Suresh, K.P., Dheeraj, R. and Roy, P. 2020. Basic reproduction number (R_0), an epidemiological tool for prioritizing livestock diseases' an example of Karnataka. *Indian J. Anim. Sci.* **90**(4): 510-514.

Mardones, F., Perez, A., Sanchez, J., Alkhamis, M. and Carpenter, T. 2010. Parameterization of the duration of infection stages of serotype O foot-and-mouth disease virus: an analytical review and meta-analysis with application to simulation models. *Vet. Res*. **41**(4): 45. Available: https://doi.org/10.1051%2Fvetres%2F2010017 [8 Mar. 2010].

McLachlan, I., Marion, G., McKendrick, I.J., Porphyre, T., Handel, I.G. and Bronsvoort, B.D. 2019. Endemic foot and mouth disease: pastoral in-herd disease dynamics in sub-Saharan Africa. *Sci. Rep*. **9**(1): 17349. Available: https://doi.org/10.1038/s41598-019-53658-5 [22 Nov. 2019].

Mushayabasa, S., Bhunu, C.P. and Dhlamini, M. 2011. Impact of vaccination and culling on controlling foot and mouth disease: a mathematical modelling approach. *Wld. J. Vaccines.* **1**:156-161.

Orsel, K. and Bouma, A. 2009. The effect of foot-and-mouth disease (FMD) vaccination on virus transmission and the significance for the field. *Can. Vet. J*. **50**(10): 1059–1063.

Parida, S. 2009. Vaccination against foot-and-mouth disease virus: strategies and effectiveness. *Expert Rev. Vaccines*. **8**(3): 347-365.

Shamsuddoha, M. and Nedelea, A.M. 2013. A Vensim based analysis for supply chain model. *Ecoforum.* **2**(2): 49-54.

Sharma, G.K., Mahajan, S., Matura, R., Biswal, J.K., Ranjan, R., Subramaniam, S., Misri, J., Bambal, R.G. and Pattnaik, B. 2017. Herd immunity against foot and mouth disease under different vaccination practices in India. *Transbound. Emerg. dis*. **64**(4): 1133-1147.

Subramaniam, S., Pattnaik, B., Sanyal, A., Mohapatra, J.K., Pawar, S.S., Sharma, G.K., Das, B. and Dash, B.B. 2013. Status of Foot and mouth Disease in India. *Transbound. Emerg. Dis*. **60**(3): 197-203.

Tadesse, B., Molla, W., Mengsitu, A. and Jemberu, W.T. 2019. Transmission dynamics of foot and mouth disease in selected outbreak areas of northwest Ethiopia. *Epidemiol. Infect*. **147**: 189.

Tang, V. and Vijay, S. 2001. System dynamics. Origins, development, and future prospects of a method. *Res. Seminar. Engineering. Syst.* **83**: 1-12.

Van den Driessche, P. and Watmough, J. 2008. Further notes on the basic reproduction number. *Math. Epidemiol*. **1**: 159-178.

Woolhouse, M.E. 2003. Foot and mouth disease in the UK: What should we do next time? *J. Appl. Microbiol.* **94**(s1): 126-130.

Yadav, S., Stenfeldt, C., Branan, M.A., Moreno-Torres, K.I., Holmstrom, L.K., Delgado, A.H. and Arzt, J. 2019. Parameterization of the durations of phases of foot-and-mouth disease in cattle. *Front. Vet. Sci*. **6**: 263. Available: https://doi.org/10.3389/fvets.2019.00263 [9 Aug. 2019]. ■