Research Article

Lyapunov Stability Analysis of a Delayed Foot-and-Mouth Disease Model with Animal Vaccination

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Foot-and-mouth disease virus remains one of the most important livestock diseases in sub-Saharan Africa and several Southeast Asian countries. Vaccination of livestock has been recognized as an important tool for the control of foot-and-mouth disease virus. However, this intervention strategy has some limitations. Generally, vaccine production is a complex multistep process which involves development, manufacturing, and delivery processes, and through this extensive process, some challenges such as poor vaccine storage often arise. More often, these challenges alter the validity of the vaccination. Foot-and-mouth disease virus epidemic dynamics have been extensively explored, but understanding the role of vaccination validity on virus endemicity is lacking. We present a time-delayed foot-and-mouth disease model that incorporates relevant biological and ecological factors, vaccination effects, and disease carriers. We determined the basic reproduction number and demonstrated that it is an important metric for persistence and extinction of the disease in the community. Numerical illustrations were utilised to support some of the analytical results.

1. Introduction

Foot-and-mouth disease (FMD) is one of the most important livestock diseases in sub-Saharan Africa and several Southeast Asian countries. It affects cloven-hoofed animals and is caused by an RNA virus commonly known as foot-and-mouth disease virus (FMDV). In many developed nations, the disease often occurs as epidemic (outbreak followed by extinction), whereas in many developing nations, such as Zimbabwe and Zambia and several Southeast Asian countries including Cambodia, Lao PDR, Malaysia, Myanmar, Thailand, and Vietnam, it is epidemic (persistent disease's presence) [1]. Epidemic or endemicity of the disease negatively affects agricultural economic world [2].

Among several other control strategies such as movement restrictions, public education, and culling, vaccination of animals has been recognized as the most important strategy to control the spread of the disease [3]. However, there are many limitations that affect vaccination validity

period. For instance, cultivation of FMDV in the manufacturing units poses a risk of escape from production sites. Furthermore, vaccines may sometimes contain traces of FMD viral nonstructural proteins (NSPs), therefore, interfering with the NSP-based serological differentiation of infected from vaccinated animals [4]. In addition, vaccine production is a complex multistep process which involves development, manufacturing, and delivery processes, and through this extensive process, some challenges such as poor vaccine storage often arise. More often, these challenges alter the validity of the vaccination. For example, a study carried out in one Cambodian province recorded that more than half of cattle vaccinated with donated FMD vaccines are subsequently becoming infected with FMD virus and showing clinical signs of FMD indicating possible vaccine failure [1, 5]. Moreover, most vaccine production plants belong to companies, usually driven by profit rather than disease control or eradication; hence, most of the farmers in FMD endemic countries cannot afford the cost of these high-

quality vaccines leading them to rely on donated or cheap vaccines obtained from unregistered suppliers, thereby compromising the outcome of vaccination programs [6, 7].

Since the 2001 FMD outbreak in UK, several mathematical models have been proposed to study the transmission and control of FMD (see, e.g., [6, 8–21]). Dexter [8] utilised stochastic epidemic models to explore the dynamics of FMD among feral pigs in the Australian semiarid rangelands. The author concluded that any control program designed to suppress FMD outbreak in feral pigs in the semiarid rangelands of Australia should take account of the prevailing environmental conditions. Using an SIR (susceptible-infectious-recovered) epidemic model, Bravo de Rueda et al. [9] demonstrated that both direct and indirect disease transmission pathways play a crucial role in FMD transmission. Utilising a nonautonomous mathematical model, Mushayabasa et al. [17] showed that seasonal variations may alter the dynamics of FMD. Recently, Zhang et al. [21] developed a dynamical switching model for FMD that incorporated three prevalent serotypes of the virus. The model was used to assess the spread of FMD in mainland China. Among several other important outcomes, their study showed that, under certain conditions, some of the FMD serotypes persist while others may disappear.

Despite all these efforts, however, mathematical models that aim to explore the role of vaccine waning in FMD endemic regions are still lacking. Therefore, in this study, we developed a time-delayed FMD model to explore the effects of vaccine waning on the dynamics of the disease. The proposed model incorporates all the relevant biological and ecological factors, vaccination, and disease carriers. We are aware that the role of FMD carriers in disease transmission remains a debatable issue [17, 22] and as such we have explored the outcomes of the model in two scenarios: (i) no transmission by carriers and (ii) when carriers are transmitting the disease. Time delay plays an important role in modeling the dynamics of infectious diseases, and the dynamical behaviour of an epidemic model with time delay(s) is known to be complex and difficult to comprehend [23]. In the proposed framework, the time delay represents the validity of the vaccination period.

We organize this paper as follows. In Section 2, we formulate and analyze the time-delayed FMD model. In particular, we computed the basic reproduction number and demonstrated that it is an important metric for the existence and global stability of the model steady states. In addition, we also explored the model numerically to support the analytical results. In the last section, we discuss the insightful implications of our findings on the role of vaccination validity on FMD transmission and control.

2. Methods and Results

In this section, we propose and analyze a time-delayed foot-and-mouth disease model incorporating direct and indirect disease transmission pathways, vaccination effects, and virus excreting carriers. We will investigate the qualitative behaviours of the proposed framework through studying the stability of the model steady states.

2.1. Model Framework. Let the variables $S(t)$, $E(t)$, $I(t)$, $A(t)$, and $R(t)$ represent the densities of susceptible, exposed (latently infected), clinical infectious, carrier, and recovered cattle at time t , respectively, such that the total population of cattle at any given time is $N(t) = S(t) + E(t) + I(t) + A(t) + R(t)$. In addition, let the variable $P(t)$ denote the density of the FMDV excreted into the environment by clinically infected and carrier animals. The proposed model is as follows:

$$\begin{cases} S'(t) = \Pi - \beta_1 I(t)S(t) - \beta_1 \varepsilon A(t)S(t) - \beta_2 P(t)S(t) \\ \quad - (\mu + p)S(t) + p e^{-\mu\tau} S(t - \tau), \\ E'(t) = \beta_1 I(t)S(t) + \beta_1 \varepsilon A(t)S(t) + \beta_2 P(t)S(t) - (\mu + \gamma)E(t), \\ I'(t) = \gamma E(t) - (\mu + \phi)I(t), \\ A'(t) = f\phi I(t) - (\mu + \sigma)A(t), \\ P'(t) = \eta I(t) + \kappa\eta A(t) - \delta P(t), \end{cases} \quad (1)$$

$$R'(t) = (1 - f)\phi I(t) + \sigma A(t) - \mu R(t), \quad (2)$$

subject to the initial functions as follows:

$$\begin{cases} S(0) = \psi_1(\theta), \\ E(0) = \psi_2(\theta), \\ I(0) = \psi_3(\theta), \\ A(0) = \psi_4(\theta), \\ P(0) = \psi_5(\theta), \\ R(0) = \psi_6(\theta), \end{cases} \quad (3)$$

where

$$\psi_i(\theta) \geq 0, \quad \theta \in [-\tau, 0], \quad i = 1, 2, 3, 4, 5, 6, \quad (4)$$

are continuous on $[-\tau, 0]$.

All model parameters are assumed to be positive and are defined as follows: Π denotes the constant recruitment rate of animals through birth and they are assumed to be susceptible to infection. All animals are assumed to have a life span of $1/\mu$ days, despite the epidemiological status of the animal. Susceptible animals are assumed to acquire infection either directly through contact with clinically infected animals or carriers at rate, β_1 , or indirectly when they inhale the virus excreted into the environment by the aforementioned infectious animals; at rate β_2 , ε accounts for differential infectivity between clinically infected animals and carriers. Thus, $\varepsilon < 1$ implies that clinically infected animals are assumed to be more infectious than carriers, and the reverse will be true, for $\varepsilon > 1$. Model parameter p is the proportion of vaccinated animals, the term $S(t - \tau)e^{-\mu\tau}$ represents the vaccinated animals, and τ is the validity period of the vaccination. Animals exposed to FMDV incubate the disease for a period ranging between 2 and 14 days [6, 16–18]. Here, $1/\gamma$ represents the average incubation period.

FMD is rarely fatal and infected cattle generally clear the systemic infection within 8–15 days [22]. However, unlike pigs which usually clear FMDV within 3 weeks following infection and do not become carriers [22, 24–26], up to 50%

of FMD-recovered ruminants become persistently infected [22]. Hence, we have assumed that, after an average infectious period of $1/\phi$ days, a fraction f of clinically infected animals becomes carriers and the remainder $(1-f)$ successfully clear the infection. Furthermore, compared to pigs, ruminants like cattle are highly susceptible to FMDV infection via the inhalation route [22, 27]. Clinically infected and carrier animals shed the virus in the environment at rates η and $\kappa\eta$, respectively, where κ is a dimensionless parameter that accounts for the difference in pathogen shedding rate between animals from the aforementioned infectious classes. We assume that it takes $1/\delta$ days for the pathogen in the environment to clear the infection. Furthermore, carriers are assumed to clear the infection after a duration of $1/\sigma$ days. In this study, FMD carriers are animals from which the virus can be recovered more than 28 days after infection.

2.2. Properties of the Solutions. The following theorem shows that the model proposed in this study is biologically meaningful. Precisely, the theorem demonstrates that all the solutions of the proposed model are nonnegative and bounded for all $t > 0$. Since the five equations of model (1) do not depend on (2), it suffices to study the dynamical behaviour of the disease without this equation.

Theorem 1. *There exists a unique solution for the FMD model (1). Furthermore, the solution is nonnegative for all $t > 0$ and lies in the set*

$$\Omega = \left\{ (S(t), E(t), I(t), A(t), P(t)) \in \mathbb{R}_+^5 : S(t) + E(t) + I(t) + A(t) \leq \frac{\Pi}{\mu}, P(t) \leq \frac{\eta\Pi}{\delta\mu}(\kappa + 1) \right\}. \quad (5)$$

Proof. In order to demonstrate that the solutions of model (1) are nonnegative, we will investigate the direction of the vector field given by the right-hand side of (1) on each space and note whether the vector field points to the interior of $\mathbb{R}_+^5$ or is tangent to the coordinate space. Since

$$\begin{cases} S'(t)|_{S=0} = \Pi \geq 0, \\ E'(t)|_{E=0} = \beta_1 I(t)S(t) + \beta_1 \epsilon A(t)S(t) + \beta_2 P(t)S(t) \geq 0, \\ I'(t)|_{I=0} = \gamma E(t) \geq 0, \\ A'(t)|_{A=0} = f\phi I(t) \geq 0, \\ P'(t)|_{P=0} = \eta I(t) + \kappa\eta A(t) \geq 0, \end{cases} \quad (6)$$

it follows that the vector field given by the right-hand side of (1) on each coordinate plane either is tangent to the coordinate plane or points to the interior of $\mathbb{R}_+^5$. Hence, the domain $\mathbb{R}_+^5$ is a positively invariant region. Moreover, if the initial conditions $\psi_i \geq 0$ are nonnegative, then it follows that the corresponding solutions of model (1) are nonnegative.

Furthermore, let $M(t) = S(t) + E(t) + I(t) + A(t)$ and it follows that

$$\begin{aligned} M'(t) &= S'(t) + E'(t) + I'(t) + A'(t) \\ &= \Pi - \mu M(t) - \phi I(t) - \sigma A(t) \\ &\leq \Pi - \mu M(t). \end{aligned} \quad (7)$$

Since $M'(t) \leq \Pi - \mu M(t)$, it follows by applying the standard comparison [28] that $M(t) \leq M(0)e^{-\mu t} + (\Pi/\mu)(1 - e^{-\mu t})$. In particular, we $M(t) \leq \Pi/\mu$ if $M(0) \leq \Pi/\mu$. Hence we can conclude that the animal population is bounded. From the last equation of system (1),

$$\begin{aligned} P'(t) &= \eta[I(t) + \kappa A(t)] - \delta P(t) \\ &\leq \frac{\eta(\kappa + 1)\Pi}{\mu} - \delta P(t). \end{aligned} \quad (8)$$

Similarly, by the standard comparison theorem [28], we have $P(t) \leq P(0)e^{-\delta t} + (\eta\Pi/\delta\mu)(\kappa + 1)(1 - e^{-\delta t})$. Therefore, $P(t) \leq (\eta\Pi/\delta\mu)(\kappa + 1)$, if $P(0) \leq (\eta\Pi/\delta\mu)(\kappa + 1)$ and this implies that the pathogen population is also bounded. Hence, all solutions in $\mathbb{R}_+^5$ eventually enter Ω . $\square$

2.3. Stability and Bifurcation Analysis. In this section, we investigate the qualitative behaviours of the delay differential model (1). In particular, we will determine the basic reproduction number, existence, and global stability of the model steady states. Through direct calculations, one can easily note that model (1) admits two equilibrium points, namely, the disease-free $\mathcal{E}^0$ and the endemic $\mathcal{E}^*$ defined by

$$\begin{aligned} \mathcal{E}^0 : (S^0, E^0, I^0, A^0, P^0) &= \left(\frac{\mu}{\mu + p(1 - e^{-\mu\tau})}, 0, 0, 0, 0 \right), \\ \mathcal{E}^* &= (S^*, I^*, A^*, P^*), \end{aligned} \quad (9)$$

with

$$\begin{cases} S^* = \frac{\mu}{[\mu + p(1 - e^{-\mu\tau})]\mathcal{R}_0}, \\ E^* = \frac{\delta m_2 m_3 [\mu + p(1 - e^{-\mu\tau})][\mathcal{R}_0 - 1]}{\beta_1 \gamma \delta [f\phi\epsilon + m_3] + \beta\eta[\kappa f\phi + m_3]}, \\ I^* = \frac{\delta m_3 [\mu + p(1 - e^{-\mu\tau})][\mathcal{R}_0 - 1]}{\beta_1 \delta [f\phi\epsilon + m_3] + \beta\eta[\kappa f\phi + m_3]}, \\ A^* = \frac{f\phi\delta [\mu + p(1 - e^{-\mu\tau})][\mathcal{R}_0 - 1]}{\beta_1 \delta [f\phi\epsilon + m_3] + \beta\eta[\kappa f\phi + m_3]}, \\ P^* = \frac{\eta[\kappa f\phi + m_3][\mu + p(1 - e^{-\mu\tau})][\mathcal{R}_0 - 1]}{\beta_1 \delta [f\phi\epsilon + m_3] + \beta\eta[\kappa f\phi + m_3]}, \end{cases} \quad (10)$$

where $\mathcal{R}_0$, the basic reproduction number which is given by (1), is

$$\begin{aligned}\mathcal{R}_0 &= \mathcal{R}_1 + \mathcal{R}_2 \\ &= \frac{\beta_1 \gamma (f \phi \epsilon + m_3) \mu}{(\mu + p(1 - e^{-\mu \tau_1}) m_1 m_2 m_3)} + \frac{\beta_2 \eta \gamma (\kappa f \phi + m_3) \mu}{\delta m_1 m_2 m_3 (\mu + p(1 - e^{-\mu \tau_1}))},\end{aligned}\quad (11)$$

with

$$\begin{aligned}m_1 &= (\mu + \gamma), \\ m_2 &= (\mu + \phi), \\ m_3 &= (\mu + \sigma).\end{aligned}\quad (12)$$

The threshold quantity $\mathcal{R}_0$ is defined as the average number of secondary foot-and-mouth disease cases generated by a typical infected animal throughout its entire course of infection in a completely susceptible population in the presence of animal vaccination. The quantities $\mathcal{R}_1$ and $\mathcal{R}_2$ represent the basic reproduction number associated with direct and indirect disease transmission pathways, respectively. The basic reproduction number is an important metric for infectious disease models; it demonstrates the power of the disease to invade the population. From (17), we can observe that the disease persists if and only if $\mathcal{R}_0 > 1$ and it dies out for $\mathcal{R}_0 < 1$.

Next, we investigate the global stability of the disease-free equilibrium, using a Lyapunov functional. We define a continuous and differentiable function $F: \mathbb{R}_{>0} \rightarrow \mathbb{R}_{\geq 0}$ as

$$F(z) = z - 1 - \ln z. \quad (13)$$

We note that $F(z) \geq 0$ for any $z > 0$ and has the global minimum 0 at $z = 1$.

Theorem 2. *Let $\psi \subset \Omega$ be a closed and bounded positively invariant set with respect to system (1) [29]. Let*

$\mathcal{V}_0(t): \mathbb{R}_+^5 \rightarrow \mathbb{R}_+$ be continuous and differentiable function such that $\mathcal{V}_0(t) > 0$ and $\mathcal{V}_0'(t) \leq 0$ in ψ for $x(t)$ solutions of system (1). Let $E = \{x \in \Omega \mid \mathcal{V}_0'(t) = 0\}$. Let $\mathcal{M}$ be the largest invariant set in E ; then every bounded solution starting in Ω approaches $\mathcal{M}$ as $t \rightarrow \infty$. Particularly, when $\mathcal{M} = x^* = \mathcal{E}^0$, then $x \rightarrow x^*$, as $t \rightarrow \infty$.

Theorem 3. *For system (1), when $\mathcal{R}_0 < 1$, the disease-free equilibrium point is globally asymptotically stable.*

Proof. To establish the global stability of the DFE, we consider the following Lyapunov functional:

$$\begin{aligned}\mathcal{V}_0(t) &= a_1 \left(S(t) - S^0 - S^0 \ln \frac{S(t)}{S^0} \right) \\ &\quad + a_1 p e^{-\mu \tau} \int_{t-\tau}^t \left(S(u) - S^0 - S^0 \ln \frac{S(u)}{S^0} \right) du \quad (14) \\ &\quad + a_1 E(t) + a_2 I(t) + a_3 A(t) + a_4 P(t),\end{aligned}$$

where

$$\begin{cases} a_1 = \frac{\beta_1 \gamma (f \phi \epsilon + m_3)}{m_1 m_2 m_3} + \frac{\beta_2 \eta \gamma (\kappa f \phi + m_3)}{\delta m_1 m_2 m_3}, & a_3 = \frac{\beta_1 \epsilon \delta + \beta_2 \kappa \eta}{\delta m_3}, \\ a_2 = \frac{\beta_1 (f \phi \epsilon + m_3)}{m_2 m_3} + \frac{\beta_2 \eta (\kappa f \phi + m_3)}{\delta m_2 m_3}, & a_4 = \frac{\beta_2}{\delta}. \end{cases} \quad (15)$$

Taking the derivative of $\mathcal{V}_0(t)$ along the solutions of system (1) leads to

$$\begin{aligned}\mathcal{V}_0'(t) &= a_1 \left(1 - \frac{S^0}{S(t)} \right) S'(t) + a_1 p e^{-\mu \tau} \left(S(t) - S(t-\tau) + S^0 \ln \frac{S(t-\tau)}{S(t)} \right) \\ &\quad + a_1 E'(t) + a_2 I'(t) + a_3 A'(t) + a_4 P'(t) \\ &= a_1 \left(1 - \frac{S^0}{S(t)} \right) [\Pi - (\beta_1 I(t) + \beta_1 \epsilon A(t) + \beta_2 P(t)) S(t) - (\mu + p) S(t) + a_1 p e^{-\mu \tau} S(t-\tau)] \\ &\quad + a_1 p e^{-\mu \tau} \left(S(t) - S(t-\tau) + S^0 \ln \frac{S(t-\tau)}{S(t)} \right) \\ &\quad + a_1 [\beta_1 I(t) S(t) + \beta_1 \epsilon A(t) S(t) + \beta_2 P(t) S(t) - m_1 E(t)] \\ &\quad + a_2 [\gamma E(t) - m_2 I(t)] + a_3 [f \phi I(t) - m_3 A(t)] + a_4 [\eta I(t) + \kappa \eta A(t) - \delta P(t)].\end{aligned}\quad (16)$$

At disease-free equilibrium, we have the identity $\Pi = (\mu + p) S^0 - p e^{-\mu \tau} S^0$. Using this identity and simplifying, one obtains

$$\begin{aligned}
\mathcal{V}'_0(t) &= (\mu + p(1 - e^{-\mu\tau}))S^0 \left(\frac{\beta_1\gamma(f\phi\epsilon + m_3)}{m_1m_2m_3} + \frac{\beta_2\eta\gamma(\kappa f\phi + m_3)}{\delta m_1m_2m_3} \right) \left(2 - \frac{S(t)}{S^0} - \frac{S^0}{S(t)} \right) \\
&\quad + pe^{-\mu\tau}S^0 \left(\frac{\beta_1\gamma(f\phi\epsilon + m_3)}{m_1m_2m_3} + \frac{\beta_2\eta\gamma(\kappa f\phi + m_3)}{\delta m_1m_2m_3} \right) \left(1 - \frac{S(t-\tau)}{S(t)} + \ln \frac{S(t-\tau)}{S(t)} \right) \\
&\quad + \left(\left[\frac{\beta_1\gamma(f\phi\epsilon + m_3)}{m_1m_2m_3} + \frac{\beta_2\eta\gamma(\kappa f\phi + m_3)}{\delta m_1m_2m_3} \right] S - 1 \right) (\beta_1I + \beta_1\epsilon A + \beta_2P) \\
&\leq \left(\left[\frac{\beta_1\gamma(f\phi\epsilon + m_3)}{m_1m_2m_3} + \frac{\beta_2\eta\gamma(\kappa f\phi + m_3)}{\delta m_1m_2m_3} \right] S^0 - 1 \right) (\beta_1I + \beta_1\epsilon A + \beta_2P) \\
&= (\mu + p(1 - e^{-\mu\tau}))S^0 \left(\frac{\beta_1\gamma(f\phi\epsilon + m_3)}{m_1m_2m_3} + \frac{\beta_2\eta\gamma(\kappa f\phi + m_3)}{\delta m_1m_2m_3} \right) \left(2 - \frac{S(t)}{S^0} - \frac{S^0}{S(t)} \right) \\
&\quad + pe^{-\mu\tau}S^0 \left(\frac{\beta_1\gamma(f\phi\epsilon + m_3)}{m_1m_2m_3} + \frac{\beta_2\eta\gamma(\kappa f\phi + m_3)}{\delta m_1m_2m_3} \right) \left(1 - \frac{S(t-\tau)}{S(t)} + \ln \frac{S(t-\tau)}{S(t)} \right) \\
&\quad + (\mathcal{R}_0 - 1)(\beta_1I + \beta_1\epsilon A + \beta_2P).
\end{aligned} \tag{17}$$

Since the arithmetic mean is greater than or equal to the geometric mean, we have

$$\frac{S(t)}{S^0} + \frac{S^0}{S(t)} \geq 2\sqrt{\frac{S(t)}{S^0} \cdot \frac{S^0}{S(t)}} = 2, \tag{18}$$

and it follows that

$$\left(2 - \frac{S(t)}{S^0} - \frac{S^0}{S(t)} \right) \leq 0. \tag{19}$$

Furthermore, we define a continuous and differentiable function $\Phi(x) = 1 - x + \ln x$, for $x > 0$. It follows that $\Phi(x) \leq 0$, with the equality satisfied if and only if $x = 1$. Thus, we can note that

$$1 - \frac{S(t-\tau)}{S(t)} + \ln \frac{S(t-\tau)}{S(t)} = \Phi\left(\frac{S(t-\tau)}{S(t)}\right). \tag{20}$$

From the earlier discussion on initial conditions (3) as well as the properties of solutions of model system (1), we can have $S(0) = \psi_1(\theta) \geq 0$ for $\theta \in [-\tau, 0]$ and this implies that $S(t-\tau) \geq 0$, $\forall t \geq 0$. Hence, it follows that $\Phi((S(t-\tau))/S(t)) \leq 0$.

Hence, if $\mathcal{R}_0 \leq 1$, we have $\mathcal{V}'_0(t) \leq 0$. Furthermore, let $\mathcal{M}$ be the largest invariant subset of the set $\Omega = \{(S(t), E(t), I(t), A(t), P(t)) \mid \mathcal{V}'_0(t) = 0\}$. We now claim that $\mathcal{M} = \{\mathcal{E}^0\}$. In fact, when $\mathcal{R}_0 < 1$, it follows from (17) that $\Omega = \{(S(t), E(t), I(t), A(t), P(t)) \mid S(t) = S^0, E(t) = 0, I(t) = 0, A(t) = 0, P(t) = 0\}$, which leads to $\mathcal{M} = \{\mathcal{E}^0\}$. If $\mathcal{R}_0 < 1$ and

$\Omega = \{(S(t), E(t), I(t), A(t), P(t)) \mid S(t) = S^0, E(t) = 0, I(t) = 0, A(t) = 0, P(t) = 0\}$ from the first and second equations of system (1), we have $S(t) = S^0$. Again, we have $\mathcal{M} = \{\mathcal{E}^0\}$. Noting that $\mathcal{M}$ is invariant, by Lasalle's invariance principle [30], the disease-free equilibrium is globally asymptotically stable whenever $\mathcal{R}_0 \leq 1$.

In what follows, we shall investigate the global stability of the endemic equilibrium $\mathcal{E}^*$ (we have shown that it exists whenever $\mathcal{R}_0 > 1$, i.e., $S^* > 0, E^*, I^*, A^* > 0$, and $P^* > 0$ if and only if $\mathcal{R}_0 > 1$) by using the Lyapunov direct method. The construction of the Lyapunov functional is also based on the function $F(z) = z - 1 - \ln z$, by which we have already observed that it satisfies $F(z) \geq 0$ for any $z > 0$ and has the global minimum 0 at $z = 1$. $\square$

Theorem 4. Let $\psi_1 \subset \Omega$ be a closed and bounded positively invariant set with respect to system (1) [29]. Let $\mathcal{V}_1(t): \mathbb{R}_+^5 \rightarrow \mathbb{R}_+$ be continuous and differentiable function such that $\mathcal{V}_1(t) > 0$ and $\mathcal{V}'_1(t) \leq 0$ in ψ_1 for $x(t)$ solutions of system (1). Let $E^* = \{x \in \Omega \mid \mathcal{V}'_1(t) = 0\}$. Let $\mathcal{M}_1$ be the largest invariant set in E^* ; then every bounded solution starting in Ω for $\mathcal{R}_0 > 1$ approaches $\mathcal{M}_1$ as $t \rightarrow \infty$. Particularly, when $\mathcal{M}_1 = x^{**} = \mathcal{E}^*$, then $x \rightarrow x^{**}$, as $t \rightarrow \infty$.

Theorem 5. If $\mathcal{R}_0 > 1$, then the endemic equilibrium of model system (1) exists and is globally asymptotically stable.

Proof. We consider a Lyapunov functional $\mathcal{V}_1(t)$ as follows:

$$\begin{aligned}
\mathcal{V}_1(t) &= \left(S(t) - S^* - S^* \ln \frac{S(t)}{S^*} \right) + \left(E(t) - E^* - E^* \ln \frac{E(t)}{E^*} \right) \\
&\quad + b_1 \left(I(t) - I^* - I^* \ln \frac{I(t)}{I^*} \right) + b_2 \left(A(t) - A^* - A^* \ln \frac{A(t)}{A^*} \right) \\
&\quad + b_3 \left(P(t) - P^* - P^* \ln \frac{P(t)}{P^*} \right) + pe^{-\mu\tau} \int_{t-\tau}^t \left(S(u) - S^* - S^* \ln \frac{S(u)}{S^*} \right) du,
\end{aligned} \tag{21}$$

where

$$\begin{aligned} b_1 &= \frac{g_1(I^*, A^*, P^*)S^*}{\gamma E^*}, \\ b_2 &= \frac{g_1(I^*, A^*, P^*)S^*}{f\phi I^*}, \\ b_3 &= \frac{g_1(I^*, A^*, P^*)S^*}{g_2(I^*, A^*)}, \end{aligned} \quad (22)$$

with

$$\begin{aligned} g_1(I(t), A(t), P(t))S(t) &= \beta_1 I(t)S(t) + \beta_1 \epsilon A(t)S(t) \\ &\quad + \beta_2 P(t)S(t), \\ g_2(I(t), A(t)) &= \eta I(t) + \kappa \eta A(t). \end{aligned} \quad (23)$$

From Section 2.2, properties of solutions of model system (1), $\mathcal{V}_1(t)$ is well defined and $\mathcal{V}_1(t) \geq 0, \forall t \geq 0$. The

equality holds if and only if $S(t) = S^*, E(t) = E^*, I(t) = I^*, A(t) = A^*$, and $P(t) = P^*$.

Taking the derivative of $\mathcal{V}_1(t)$ along the solutions of system (1), one obtains

$$\begin{aligned} \mathcal{V}_1'(t) &= \left(1 - \frac{S^*}{S(t)}\right)S'(t) + \left(1 - \frac{E^*}{E(t)}\right)E'(t) \\ &\quad + b_1 \left(1 - \frac{I^*}{I(t)}\right)I'(t) + b_2 \left(1 - \frac{A^*}{A(t)}\right)A'(t) \\ &\quad + b_3 \left(1 - \frac{P^*}{P(t)}\right)P'(t) \\ &\quad + pe^{-\mu\tau} \left(S(t) - S(t-\tau) + S^* \ln \frac{S(t-\tau)}{S(t)} \right). \end{aligned} \quad (24)$$

At the endemic equilibrium of model system (1), we have the following identities:

$$\begin{cases} \Pi = g_1(I^*, A^*, P^*)S^* + (p(1 - e^{-\mu\tau}) + \mu)S^*, \\ m_1 E^* = g_1(I^*, A^*, P^*)S^*, \\ m_2 I^* = \gamma E^*, \\ m_3 A^* = f\phi I^*, \\ \delta P^* = g_2(I^*, A^*). \end{cases} \quad (25)$$

Utilising the identities leads to

$$\begin{aligned} \mathcal{V}_1'(t) &= (p(1 - e^{-\mu\tau}) + \mu)S^* \left(2 - \frac{S(t)}{S^*} - \frac{S^*}{S(t)} \right) + pe^{-\mu\tau} S^* \left(1 - \frac{S(t-\tau)}{S(t)} + \ln \frac{S(t-\tau)}{S(t)} \right) \\ &\quad + g_1(I^*, A^*, P^*)S^* \left(1 - \frac{P}{P^*} - \frac{P^* g_2(I, A)}{P g_2(I^*, A^*)} + \frac{g_2(I, A)}{g_2(I^*, A^*)} \right) \\ &\quad + g_1(I^*, A^*, P^*)S^* \left(4 - \frac{S^*}{S} - \frac{SE^*}{S^*E} \frac{g_1(I, A, P)}{g_1(I^*, A^*, P^*)} + \frac{g_1(I, A, P)}{g_1(I^*, A^*, P^*)} - \frac{EI^*}{E^*I} - \frac{IA^*}{I^*A} - \frac{A}{A^*} \right). \end{aligned} \quad (26)$$

Once again, since the arithmetic mean is greater than or equal to the geometric mean, we have

$$\frac{S(t)}{S^*} + \frac{S^*}{S(t)} \geq 2 \sqrt{\frac{S(t)}{S^*} \cdot \frac{S^*}{S(t)}} = 2, \quad (27)$$

and it follows that

$$\left(2 - \frac{S(t)}{S^*} - \frac{S^*}{S(t)} \right) \leq 0. \quad (28)$$

Furthermore, as already illustrated on demonstrating the global stability of the disease-free equilibrium,

$$1 - \frac{S(t-\tau)}{S(t)} + \ln \frac{S(t-\tau)}{S(t)} \leq 0. \quad (29)$$

Moreover, using the function $\Phi(x)$, defined earlier, we have

TABLE 1: Model parameters and their interpretations.

Symbol	Definition	Baseline value	Units	Source
γ	Rate of progression from latent to infectious	0.25	day ⁻¹	Reference [17]
δ	Environmental pathogen decay rate	0.07	day ⁻¹	Reference [27]
β_2	Indirect disease transmission rate	10^{-10}	Pathogen ⁻¹ day ⁻¹	
β_1	Direct disease transmission rate	10^{-6}	day ⁻¹	
f	Proportion of infectious animals which progress to carrier population	0.5	Dimensionless	Reference [17]
κ, ϵ	Modification factor	Varied	Dimensionless	
p	Proportion of vaccinated animals	0.01	Dimensionless	
ϕ^{-1}	Average infectious period of clinically infected animals	7	Days	Reference [17]
σ	Recovery rate of FMD carriers	Varied	Days	
η	Pathogen shedding rate	10^4	Pathogen animal ⁻¹ day ⁻¹	Reference [27]
μ	Natural mortality rate	0.001	day ⁻¹	Reference [17]

$$\begin{aligned}
1 - \frac{P}{P^*} - \frac{P^* g_2(I, A)}{P g_2(I^*, A^*)} + \frac{g_2(I, A)}{g_2(I^*, A^*)} &= \Phi\left(\frac{P^* g_2(I, A)}{P g_2(I^*, A^*)}\right) - \ln\left(\frac{P^* g_2(I, A)}{P g_2(I^*, A^*)}\right) - \frac{P}{P^*} + \frac{g_2(I, A)}{g_2(I^*, A^*)} \\
&\leq \ln\left(\frac{P}{P^*}\right) - \frac{P}{P^*} - \ln\left(\frac{g_2(I, A)}{g_2(I^*, A^*)}\right) + \frac{g_2(I, A)}{g_2(I^*, A^*)} \\
&\leq 0.
\end{aligned} \tag{30}$$

Furthermore,

$$\begin{aligned}
4 - \frac{S^*}{S} - \frac{SE^*}{S^*E} \frac{g_1(I, A, P)}{g_1(I^*, A^*, P^*)} + \frac{g_1(I, A, P)}{g_1(I^*, A^*, P^*)} - \frac{EI^*}{E^*I} - \frac{IA^*}{I^*A} - \frac{A}{A^*} \\
= \Phi\left(\frac{S^*}{S}\right) + \Phi\left(\frac{EI^*}{E^*I}\right) + \Phi\left(\frac{IA^*}{I^*A}\right) + \Phi\left(\frac{SE^*}{S^*E} \frac{g_1(I, A, P)}{g_1(I^*, A^*, P^*)}\right) \\
+ \frac{g_1(I, A, P)}{g_1(I^*, A^*, P^*)} - \frac{A}{A^*} - \ln\left(\frac{A^* g_1(I, A, P)}{A g_1(I^*, A^*, P^*)}\right) \\
\leq \ln\left(\frac{A}{A^*}\right) - \frac{A}{A^*} + \frac{g_1(I, A, P)}{g_1(I^*, A^*, P^*)} - \ln\left(\frac{g_1(I, A, P)}{g_1(I^*, A^*, P^*)}\right) \\
\leq 0.
\end{aligned} \tag{31}$$

Hence, from the illustrations (28)–(31), if $\mathcal{R}_0 > 1$, we have $\mathcal{V}'_1(t) \leq 0$. By Theorem 5.3.1 in [31], solutions are limited to $\mathcal{M}$, the largest invariant subset of $\{\mathcal{V}'_1(t) = 0\}$. Therefore, for all $(S(t), E(t), I(t), A(t), P(t)) \geq 0$ provided that S^*, E^*, I^*, A^*, P^* are nonnegative, it follows by Lasalle's invariance principle [30] that the endemic equilibrium point is globally asymptotically stable whenever $\mathcal{R}_0 > 1$. $\square$

2.4. Numerical Results. To explore the behaviour of system (1) and illustrate the stability of equilibria solutions, we utilised dde23 [32] based on Runge-Kutta methods. The baseline values for the model parameters are in Table 1, and the

initial population levels were assumed as follows: $S(0) = 10^4$, $E(0) = 200$, $I(0) = 50$, $A(0) = 0$, and $P(0) = 10^3$.

Simulation results in Figures 1–3 illustrate the dynamical solutions of model (1) under the assumption that FMD carriers are noninfectious; that is, $\kappa = \epsilon = 0$. In all the cases, we can note the existence of periodic oscillations for a certain period, before stability at endemic point is attained. We can also note that the intensity and amplitude of oscillations decrease as the vaccination validity period increases, implying that if the vaccine waning period is “reasonably longer,” then the possibility of having periodic oscillations on the solutions of system (1) decreases.

FIGURE 1: Numerical results of system (1) depicting the persistence of the disease of $\mathcal{R}_0 > 1$ when the vaccination validity τ is 15 days. Parameter values used to construct the simulations are in Table 1, with $p = 0.01$ and $\kappa = \epsilon = 0$, leading to $\mathcal{R}_0 = 6.7$.

FIGURE 2: Continued.

FIGURE 2: Numerical results of system (1) depicting the persistence of the disease of $\mathcal{R}_0 > 1$ when the vaccination validity τ is 30 days. Parameter values used to construct the simulations are in Table 1, with $p = 0.01$ and $\kappa = \epsilon = 0$, leading to $\mathcal{R}_0 = 5.9$.

FIGURE 3: Numerical results of system (1) depicting the persistence of the disease of $\mathcal{R}_0 > 1$ when the vaccination validity τ is 150 days. Parameter values used to construct the simulations are in Table 1, with $p = 0.01$ and $\kappa = \epsilon = 0$, leading to $\mathcal{R}_0 = 3.2$.

FIGURE 4: Numerical results of system (1) depicting the persistence of the disease of $\mathcal{R}_0 > 1$ when the vaccination validity τ is 30 days. Parameter values used to construct the simulations are in Table 1, with $f = 0.5$, $p = 0.01$, and $\kappa = \epsilon = 0.1$, leading to $\mathcal{R}_0 = 9.8$.

FIGURE 5: Continued.

FIGURE 5: Numerical results of system (1) depicting the persistence of the disease of $\mathcal{R}_0 > 1$ when the vaccination validity τ is 30 days. Parameter values used to construct the simulations are in Table 1, with $p = 0.01$, $\kappa = \epsilon = 0.1$, and $f = 0.01$, leading to $\mathcal{R}_0 = 6.0$.

FIGURE 6: Numerical results of system (1) depicting the persistence of the disease of $\mathcal{R}_0 > 1$ when the vaccination validity τ is 30 days. Parameter values used to construct the simulations are in Table 1, with $p = 0.01$, $\kappa = \epsilon = 1.05$, and $f = 0.01$, leading to $\mathcal{R}_0 = 6.7$.

Graphical results in Figures 4–6 demonstrate the potential impact of infecting FMD carriers on altering the dynamics of foot-and-mouth disease. The contribution of FMD carriers on the disease dynamics remains a debatable issue. Some researchers argue that these animals are

noninfectious, while others postulate that they are infectious [22]. However, a recent study [22] demonstrated that FMD carrier cattle are capable of shedding the virus into the environment. Thus, in Figures 4–6, we fixed the vaccination validity period to 30 days and explored the role of

FMD carrier cattle on the dynamics of the disease by varying model parameters associated with increasing or decreasing the infectivity of the FMD carriers. In Figure 4, we set $f = 0.5$, $p = 0.01$, and $\kappa = \epsilon = 0.1$, leading to $\mathcal{R}_0 = 9.8$. We observed that if the proportion of animals which become carriers, f , is large while the contribution of carriers to new infections (through transmission, ϵ , and pathogen shedding into the environment, κ) is less than that of clinically infected animals, then intensity and amplitude of periodic oscillation in the solutions of model system (1) decrease. However, results in Figures 5 and 6 suggest that if the proportion of animals that become carriers decreases, then the intensity and amplitude of periodic solutions increase despite irrespective of whether carriers are less or more infectious compared to clinically infected animals. Overall, the results demonstrate that understanding the contribution of carriers on FMD dynamics is an important issue that requires multidimensional research.

3. Concluding Remarks

Foot-and-mouth disease, a highly contagious, acute viral disease of cloven-hoofed domestic and wild ruminants including cattle, buffalo, swine, goats, and sheep, remains a major challenge in many developing nations in the sub-Saharan Africa, such as Zimbabwe and Zambia. Vaccination is regarded as the most effective means of foot-and-mouth disease mitigation. Nevertheless, this important intervention strategy has some limitations. Generally, vaccine production is a complex multistep process which involves development, manufacturing, and delivery processes, and through this extensive process, challenges such as poor vaccine storage often arise. Such challenges are known to affect the validity period of the vaccines. In this work, we proposed and analyzed a time-delayed foot-and-mouth disease model that incorporates vaccine waning and foot-and-mouth disease carriers. We are aware that the role of FMD carriers in disease transmission remains a debatable issue [17, 22] and as such we have explored the outcomes of the model in two scenarios: (i) no transmission by carriers and (ii) when carriers are transmitting the disease. We computed the basic reproduction number and demonstrated that it is an important threshold parameter for the existence and global stability of the model steady states. Utilising numerical illustrations, we demonstrated the impact of foot-and-mouth disease carriers on long- and short-term dynamics of the disease.

This work demonstrated that understanding the role of vaccine waning and FMD carriers is an important topic that requires multidimensional research. Nevertheless, this work is not exhaustive; it can be extended by adding diffusion terms to the proposed model so as to represent the movement and dispersal of the animals and the pathogen and by adding convection terms to represent the migration of animals.

Data Availability

The data used to support the findings of this study are included within the article.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

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