A Fractional-Order Within-Host Model of Swine Flu Infection with Autophagy Effects: Qualitative and Stability Analysis

Abstract

Swine influenza (H1N1) is a rapidly replicating respiratory virus characterized by complex within-host interactions between epithelial target cells, infected cells, and immune-mediated intracellular processes. In this study, we develop and analyze a fractional-order mathematical model describing the within-host dynamics of H1N1 infection, explicitly incorporating autophagy as a key intracellular antiviral mechanism. The model is formulated using Caputo fractional derivatives to account for memory effects associated with delayed viral replication, immune activation, and persistence of infection observed in influenza pathogenesis. We establish fundamental qualitative properties of the model, including positivity, boundedness, and the existence of a biologically feasible invariant region. The disease-free equilibrium and was derived, and the basic reproduction number R_0 is obtained using the next-generation matrix. This represents the threshold for viral establishment within the host. The stability analysis conducted showed that the infection was cleared when $R_0 < 1$. Sustained viral replication occurs when $R_0 > 1$, consistent with known influenza infection behavior. The results of the study demonstrates that autophagy does not influence the initial infection threshold. It although reduces viral load significantly and impede infected cell burden during the progression phase of H1N1 infection. The fractional-order model analysis further reveals that memory effects slow down infection dynamics. This reflects clinically observed delays in viral peak and immune response activation. The findings of this study provides a more realistic mathematical representation of swine flu infection kinetics. It also highlights the potential of targeting autophagy pathways as a therapeutic strategy for controlling influenza severity.

Keywords: Swine flu, H1N1, Influenza infections, Influenza virus, Mathematical modeling, Autophagy, Stability Analysis.

1 Introduction

Swine influenza (H1N1) is a highly infectious respiratory disease caused by influenza A viruses. The disease has a significant global health implications due to its rapid transmission and pandemic potential. During the 2009–2010 flu season, a novel H1N1 strain emerged and began infecting humans. This strain resulted from a reassortment of influenza viruses originating from pigs, birds, and humans. The 2009 H1N1 outbreak highlighted the relevance of understanding the population-level and within-host dynamics of influenza infections [1, 2, 6, 4]. These viruses have high mutation rates and complex host interactions. In 2009, the World Health Organization (WHO) declared the outbreak a global pandemic, which led to an estimated 284,400 deaths worldwide. By August 2010, the pandemic was officially declared over. However, the H1N1 strain persisted and became one of the viruses responsible for seasonal influenza. It has been recorded that many individuals have recovered without medical treatment, it is also possible that severe complications can arise among high-risk populations. There are some seasonal influenza vaccines that can provide protection against H1N1 and other strains.

The epithelial cells lining the throat, nose, and lungs are the primary targets of the H1N1 Influenza viruses. When an infected individual sneezes, coughs, talks, or breathes, airborne droplets released can

carry this viruses and become the sorce of transmission. Inhaling these droplets can cause infection.. Mere touching of contaminated surfaces and subsequently contacting the eyes, nose, or mouth can also lead to infection. It is worth noting that swine flu cannot be contracted through the consumption of pork. Infected individuals become contagious within one day before symptom onset to about four days afterward. It is believed that individuals weak immunes, and children may remain infectious for a longer duration.

The Centers for Disease Control and Prevention (CDC) recommends annual influenza vaccination for all individuals aged six months and older. The H1N1 strain is included in the seasonal influenza vaccine, which reduces both the risk of infection and the severity of illness. Each years vaccine is formulated to protect against the three or four influenza strains most likely to circulate during the season. Vaccination is particularly important because influenza and COVID-19 present with similar clinical symptoms and may co-circulate. Immunization helps reduce diagnostic confusion, lowers the incidence of severe illness and complications, and decreases hospitalization rates.

Classical integer-order differential equation models, such as SIR and SEIR systems, are widely used to describe infectious disease transmission [3, 5]. However, these models assume no memories and do not account for hereditary effects associated to biological systems. Practically, viral replication, immune responses, and the outcome of treatments are dependent on both current and past states. This limitation has motivated the use of fractional calculus in epidemiological modeling.

Fractional-order differential equations have extended classical derivatives to non-integer orders. This has allowed the inclusion of memory and long-range temporal dependence [7, 8, 9]. Result from recent studies have shown that such models better align with epidemiological data. This is particularly evident in its capturing of delay responses and the dynamics of persistent infections [11, 12, 13]. A better representation of biological processes where past states influence system behavior have been improved by this approach.

Beyond memory effects, host immune response plays a key role in infection dynamics. Autophagy, a conserved intracellular degradation process, has a dual function in viral infections. It aids viral clearance by degrading pathogens and enhancing immune signaling, but can also be exploited by viruses to support replication [14, 15]. In influenza, autophagy influences both viral replication and immune regulation, making it relevant for within-host models.

Recent work on fractional epidemiological models includes immune response dynamics and control strategies such as optimal control and sensitivity analysis [16, 17, 10]. Fractional influenza models have established results on existence, reproduction numbers, and stability [11, 13, 6, 4]. However, integrating fractional dynamics with autophagy mechanisms in swine flu models remains limited.

In this study, we develop a fractional-order within-host model of swine flu incorporating autophagy. The model describes interactions among target cells, infected cells, virus particles, and autophagy using Caputo fractional derivatives. We analyze key properties including positivity, boundedness, equilibria, and stability of disease-free and endemic states. This work combines fractional dynamics with autophagy to provide a more realistic framework for influenza modeling.

2 Model Formulation

Let:

- $T(t)$: Healthy epithelial cells
- $I(t)$: Infected cells
- $V(t)$: Free virus particles
- $A(t)$: Autophagy level

We define the Caputo fractional derivative of order $\alpha \in (0, 1]$.

The model is given by:

$$
\begin{aligned}
{}^{C}D_t^{\alpha} T &= \lambda - d_T T - \beta T V, && (1)\\
{}^{C}D_t^{\alpha} I &= \beta T V - d_I I - \kappa A I, && (2)\\
{}^{C}D_t^{\alpha} V &= pI - cV - \eta A V, && (3)\\
{}^{C}D_t^{\alpha} A &= sI - d_A A. && (4)
\end{aligned}
$$

where:

- λ: production rate of target cells
- d_T: natural death rate of healthy cells
- β: infection rate
- d_I: death rate of infected cells
- κ: autophagy-induced clearance of infected cells
- p: viral production rate
- c: viral clearance rate
- η: autophagy-mediated viral inhibition
- s: autophagy stimulation rate
- d_A: decay rate of autophagy

3 Qualitative Analysis of the Model

3.1 Positivity of Solutions

Theorem 1. *Given non-negative initial conditions*

$$T(0) \geq 0, \quad I(0) \geq 0, \quad V(0) \geq 0, \quad A(0) \geq 0,$$

the solutions $T(t), I(t), V(t), A(t)$ of the fractional-order swine flu model remain non-negative for all $t > 0$.

Proof. We prove that the non-negative orthant $\mathbb{R}^4_+$ is positively invariant.

Let $x(t)$ be continuous with Caputo derivative ${}^C D_t^\alpha x(t)$, $\alpha \in (0, 1]$. If $x(t)$ attains a (local) minimum at $t_0 > 0$, then

$${}^C D_t^\alpha x(t_0) \geq 0.$$

This fact is standard in fractional calculus and underpins comparison principles.

Let us consider the First-exit (contradiction) argument

Assume, for contradiction, that at least one component becomes negative. Let $t_0 > 0$ be the *first time* such that one component hits zero and attempts to cross into negative values. Then for all $t \in [0, t_0)$, we have

$$T(t) \geq 0, \quad I(t) \geq 0, \quad V(t) \geq 0, \quad A(t) \geq 0,$$

and at $t = t_0$ at least one component equals zero while the others are non-negative.

We check each equation at such a boundary point.

Let us inspect the behavior of $T(t)$ at $T = 0$.

If $T(t_0) = 0$, then from

$${}^C D_t^\alpha T = \lambda - d_T T - \beta T V,$$

we obtain

$${}^C D_t^\alpha T(t_0) = \lambda > 0.$$

Thus $T(t)$ is increasing at t_0 and cannot cross into negative values.

Let us also inspect the behavior of $I(t)$ at $I = 0$.

If $I(t_0) = 0$, then

$${}^C D_t^\alpha I = \beta T V - d_I I - \kappa A I,$$

so

$${}^C D_t^\alpha I(t_0) = \beta T(t_0) V(t_0) \geq 0.$$

Hence $I(t)$ cannot decrease below zero.

We inspect the behavior of $V(t)$ at $V = 0$.

If $V(t_0) = 0$, then

$${}^C D_t^\alpha V = pI - cV - \eta A V,$$

so

$${}^C D_t^\alpha V(t_0) = pI(t_0) \geq 0.$$

Thus $V(t)$ cannot become negative.

Inspecting the behavior of $A(t)$ at $A = 0$.
If $A(t_0) = 0$, then

$$^{C}D_t^{\alpha} A = sI - d_A A,$$

so

$$^{C}D_t^{\alpha} A(t_0) = sI(t_0) \geq 0.$$

Thus $A(t)$ cannot become negative.

Thus, at any boundary point where a component equals zero, its fractional derivative is non-negative. We conclude that no component can cross from non-negative to negative values.
This contradicts the assumption of a first exit time t_0.

Therefore,

$$T(t),\ I(t),\ V(t),\ A(t) \geq 0 \quad \forall t > 0.$$

□

3.2 Boundedness via Fractional Grönwall Inequality

We establish boundedness of solutions using the fractional Grönwall inequality.
Let us construct a suitable Lyapunov-type function.
Define the total population functional

$$N(t) = T(t) + I(t) + \frac{p}{c} V(t) + \frac{\kappa}{d_A} A(t).$$

Taking the Caputo fractional derivative of order $\alpha \in (0, 1]$,

$$^{C}D_t^{\alpha} N(t) = {}^{C}D_t^{\alpha} T + {}^{C}D_t^{\alpha} I + \frac{p}{c} {}^{C}D_t^{\alpha} V + \frac{\kappa}{d_A} {}^{C}D_t^{\alpha} A.$$

Substituting the model equations:

$$\begin{aligned} ^{C}D_t^{\alpha} N(t) = \lambda &- d_T T - \beta TV \\ &+ \beta TV - d_I I - \kappa AI \\ &+ \frac{p}{c}(pI - cV - \eta AV) \\ &+ \frac{\kappa}{d_A}(sI - d_A A). \end{aligned}$$

We cancel βTV terms to have:

$$\begin{aligned} ^{C}D_t^{\alpha} N(t) = \lambda &- d_T T - d_I I - \kappa AI \\ &+ \frac{p^2}{c} I - pV - \frac{p\eta}{c} AV \\ &+ \frac{\kappa s}{d_A} I - \kappa A. \end{aligned}$$

We discard negative terms to obtain an upper bound:

$$^{C}D_t^{\alpha} N(t) \leq \lambda + \left(\frac{p^2}{c} + \frac{\kappa s}{d_A} \right) I.$$

Using $I(t) \leq N(t)$, we obtain

$$^{C}D_t^{\alpha} N(t) \leq \lambda + \gamma N(t),$$

where

$$\gamma = \frac{p^2}{c} + \frac{\kappa s}{d_A}.$$

We apply fractional Grönwall inequality.

Lemma 1 (Fractional Grönwall Inequality)**.** *Let $u(t)$ satisfy*

$$^{C}D_t^{\alpha}u(t) \leq a + bu(t),$$

then

$$u(t) \leq \left(u(0) + \frac{a}{b}\right) E_{\alpha}(bt^{\alpha}) - \frac{a}{b},$$

where $E_{\alpha}(\cdot)$ is the Mittag–Leffler function.

Applying this with $u(t) = N(t)$, $a = \lambda$, $b = \gamma$, we obtain

$$N(t) \leq \left(N(0) + \frac{\lambda}{\gamma}\right) E_{\alpha}(\gamma t^{\alpha}) - \frac{\lambda}{\gamma}.$$

Since the Mittag-Leffler function satisfies

$$E_{\alpha}(\gamma t^{\alpha}) \leq Ce^{\gamma t},$$

for some constant $C > 0$, it follows that

$$N(t) \leq C_1, \quad \forall t \geq 0,$$

for some constant $C_1 > 0$.

Hence, $N(t)$ is uniformly bounded.

For the boundedness of individual variables, we say, since

$$T(t), I(t), V(t), A(t) \leq N(t),$$

it follows that all state variables are bounded.

Theorem 2. *All solutions of the fractional-order swine flu model remain in a positively invariant and bounded region*

$$\Omega = \{(T, I, V, A) \in \mathbb{R}_+^4 : N(t) \leq C_1\}.$$

Proof. The proof follows directly from the above estimates and the fractional Grönwall inequality. □

4 Equilibrium Points

4.1 Disease-Free Equilibrium (DFE)

Setting $I = V = A = 0$, we obtain:

$$E_0 = \left(\frac{\lambda}{d_T}, 0, 0, 0\right).$$

4.2 Derivation of the Basic Reproduction Number

We derive the basic reproduction number R_0 using the next-generation matrix approach.

We identify the infected compartments from the model

$$^{C}D_t^{\alpha}I = \beta TV - d_I I - \kappa AI,$$
$$^{C}D_t^{\alpha}V = pI - cV - \eta AV,$$

the infected compartments are:

$$x = (I, V)^T.$$

We decompose into new infection and transition terms by writing the system in the form

$$^{C}D_t^{\alpha}x = \mathcal{F}(x) - \mathcal{V}(x),$$

where:

- $\mathcal{F}(x)$ = new infection terms
- $\mathcal{V}(x)$ = transfer (transition and removal) terms

New infection terms:

$$\mathcal{F}(x) = \begin{pmatrix} \beta TV \\ 0 \end{pmatrix}.$$

Transition terms:

$$\mathcal{V}(x) = \begin{pmatrix} d_I I + \kappa AI \\ cV - pI + \eta AV \end{pmatrix}.$$

We evaluate at the Disease-Free Equilibrium (DFE):

$$E_0 = (T^*, I^*, V^*, A^*) = \left(\frac{\lambda}{d_T}, 0, 0, 0\right).$$

Thus:

$$T = T^* = \frac{\lambda}{d_T}, \quad A = 0.$$

We compute the Jacobian matrices F and V. Therefore, the Jacobian of $\mathcal{F}$ with respect to (I, V) is:

$$F = \begin{pmatrix} \frac{\partial(\beta TV)}{\partial I} & \frac{\partial(\beta TV)}{\partial V} \\ 0 & 0 \end{pmatrix}.$$

At DFE:

$$F = \begin{pmatrix} 0 & \beta T^* \\ 0 & 0 \end{pmatrix} = \begin{pmatrix} 0 & \frac{\beta\lambda}{d_T} \\ 0 & 0 \end{pmatrix}.$$

The Jacobian of $\mathcal{V}$ is:

$$V = \begin{pmatrix} \frac{\partial(d_I I + \kappa AI)}{\partial I} & \frac{\partial(\cdot)}{\partial V} \\ \frac{\partial(cV - pI + \eta AV)}{\partial I} & \frac{\partial(\cdot)}{\partial V} \end{pmatrix}.$$

At DFE ($A = 0$):

$$V = \begin{pmatrix} d_I & 0 \\ -p & c \end{pmatrix}.$$

We compute V^{-1}.

$$V^{-1} = \frac{1}{d_I c} \begin{pmatrix} c & 0 \\ p & d_I \end{pmatrix}.$$

We compute the next-generation matrix $K = FV^{-1}$.

$$K = \begin{pmatrix} 0 & \frac{\beta\lambda}{d_T} \\ 0 & 0 \end{pmatrix} \cdot \frac{1}{d_I c} \begin{pmatrix} c & 0 \\ p & d_I \end{pmatrix}.$$

Multiplying:

$$K = \frac{1}{d_I c} \begin{pmatrix} \frac{\beta\lambda}{d_T} \cdot p & \frac{\beta\lambda}{d_T} \cdot d_I \\ 0 & 0 \end{pmatrix}.$$

Thus,

$$K = \begin{pmatrix} \frac{\beta\lambda p}{d_T d_I c} & \frac{\beta\lambda}{d_T c} \\ 0 & 0 \end{pmatrix}.$$

We compute eigenvalues of K.

Since K is upper triangular, eigenvalues are:

$$\lambda_1 = \frac{\beta\lambda p}{d_T d_I c}, \quad \lambda_2 = 0.$$

We define R_0.

The basic reproduction number is the spectral radius:

$$R_0 = \rho(K) = \max\{|\lambda_1|, |\lambda_2|\}.$$

Hence,

$$R_0 = \frac{\beta\lambda p}{d_T d_I c}.$$

We note that:

- β: infection rate
- $\frac{\lambda}{d_T}$: available target cells
- p: viral production
- d_I: infected cell death
- c: viral clearance

$$R_0 = \frac{\text{infection} \times \text{production}}{\text{removal}}.$$

Autophagy parameters κ and η do not appear in R_0 because:

$$A^* = 0 \quad \text{at the DFE.}$$

Thus, autophagy does not influence the initial invasion threshold but affects the endemic dynamics.

5 Endemic Equilibrium

Let $E^* = (T^*, I^*, V^*, A^*)$.

Solving:

$$\begin{aligned} T^* &= \frac{cd_I}{\beta p}, \\ I^* &= \frac{c}{p}V^*, \\ A^* &= \frac{s}{d_A}I^*, \\ V^* &= \frac{d_T}{\beta}(R_0 - 1). \end{aligned}$$

5.1 Stability of Endemic Equilibrium

Theorem 3. *The endemic equilibrium $E^* = (T^*, I^*, V^*, A^*)$ of the fractional-order swine flu model is locally asymptotically stable if $R_0 > 1$ and the Routh–Hurwitz conditions for the associated characteristic polynomial are satisfied.*

Proof. Linearization around the endemic equilibrium.

Let the system be

$$\begin{aligned} {}^C D_t^\alpha T &= \lambda - d_T T - \beta TV, \\ {}^C D_t^\alpha I &= \beta TV - d_I I - \kappa AI, \\ {}^C D_t^\alpha V &= pI - cV - \eta AV, \\ {}^C D_t^\alpha A &= sI - d_A A. \end{aligned}$$

We linearize the system at $E^* = (T^*, I^*, V^*, A^*)$.

The Jacobian matrix is

$$J(E^*) = \begin{pmatrix} -d_T - \beta V^* & 0 & -\beta T^* & 0 \\ \beta V^* & -d_I - \kappa A^* & \beta T^* & -\kappa I^* \\ 0 & p & -c - \eta A^* & -\eta V^* \\ 0 & s & 0 & -d_A \end{pmatrix}.$$

Next is the characteristic polynomial:
The eigenvalues λ satisfy

$$\det(\lambda I - J(E^*)) = 0.$$

This yields a fourth-degree polynomial of the form

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0,$$

where the coefficients a_i depend on the model parameters and equilibrium values.

Let us consider the positivity of coefficients under $R_0 > 1$.
At the endemic equilibrium, all state variables satisfy

$$T^* > 0, \quad I^* > 0, \quad V^* > 0, \quad A^* > 0,$$

which occurs only when $R_0 > 1$.

From the structure of $J(E^*)$, all diagonal entries are negative and interaction terms are bounded. Direct expansion shows that:

$$a_1 = -\text{trace}(J(E^*)) > 0,$$
$$a_4 = \det(J(E^*)) > 0,$$

and similarly $a_2 > 0$, $a_3 > 0$ under biologically feasible parameter values.

For the Routh–Hurwitz conditions, let us consider the fourth-degree polynomial

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0,$$

the Routh–Hurwitz conditions are:

$$\begin{aligned}
&a_1 > 0,\\
&a_2 > 0,\\
&a_3 > 0,\\
&a_4 > 0,\\
&a_1a_2 > a_3,\\
&a_1a_2a_3 > a_1^2a_4 + a_3^2.
\end{aligned}$$

If these conditions hold, then all eigenvalues satisfy

$$\text{Re}(\lambda_i) < 0.$$

For the fractional-order stability criterion, let us consider a fractional-order system of order $\alpha \in (0, 1]$, the equilibrium is locally asymptotically stable if all eigenvalues λ_i satisfy

$$|\arg(\lambda_i)| > \frac{\alpha\pi}{2}.$$

Let us verify the fractional condition.
If the Routh–Hurwitz conditions are satisfied, then

$$\text{Re}(\lambda_i) < 0 \quad \forall i.$$

Thus, all eigenvalues lie strictly in the left-half complex plane. Hence,

$$|\arg(\lambda_i)| > \frac{\pi}{2}.$$

Since $\alpha \in (0, 1]$, we have

$$\frac{\alpha\pi}{2} \leq \frac{\pi}{2}.$$

Therefore,

$$|\arg(\lambda_i)| > \frac{\alpha\pi}{2},$$

and the fractional stability condition is satisfied.

To conclude, when $R_0 > 1$ and the Routh-Hurwitz conditions hold, all eigenvalues lie in the fractional stability region, implying that the endemic equilibrium E^* is locally asymptotically stable.

□

5.2 Global Stability Analysis of the Endemic Equilibrium

We establish global asymptotic stability of the endemic equilibrium using a Lyapunov functional approach adapted to fractional-order systems.

Theorem 4. *Let $R_0 > 1$. Then the endemic equilibrium $E^* = (T^*, I^*, V^*, A^*)$ of the fractional-order swine flu model is globally asymptotically stable in the feasible region Ω.*

Proof. We construct the Lyapunov function:

$$L = \left(T - T^* - T^* \ln \frac{T}{T^*}\right) + \left(I - I^* - I^* \ln \frac{I}{I^*}\right)$$
$$+\frac{c}{p}\left(V - V^* - V^* \ln \frac{V}{V^*}\right) + \frac{\kappa}{s}\left(A - A^* - A^* \ln \frac{A}{A^*}\right).$$

For the positivity of Lyapunov function using the inequality

$$x - x^* - x^* \ln \frac{x}{x^*} \geq 0,$$

for all $x > 0$, we have:

$$L \geq 0, \quad \text{and} \quad L = 0 \iff (T, I, V, A) = E^*.$$

Using properties of Caputo derivatives and standard inequalities (see fractional Lyapunov theory), we obtain:

$${}^C D_t^\alpha L \leq \left(1 - \frac{T^*}{T}\right) {}^C D_t^\alpha T + \left(1 - \frac{I^*}{I}\right) {}^C D_t^\alpha I$$
$$+\frac{c}{p}\left(1 - \frac{V^*}{V}\right) {}^C D_t^\alpha V + \frac{\kappa}{s}\left(1 - \frac{A^*}{A}\right) {}^C D_t^\alpha A.$$

Substituting the system:

$$\begin{aligned}
{}^C D_t^\alpha T &= \lambda - d_T T - \beta T V, \\
{}^C D_t^\alpha I &= \beta T V - d_I I - \kappa A I, \\
{}^C D_t^\alpha V &= pI - cV - \eta A V, \\
{}^C D_t^\alpha A &= sI - d_A A,
\end{aligned}$$

and using equilibrium identities:

$$\begin{aligned}
\lambda &= d_T T^* + \beta T^* V^*, \\
\beta T^* V^* &= d_I I^* + \kappa A^* I^*, \\
pI^* &= cV^* + \eta A^* V^*, \\
sI^* &= d_A A^*,
\end{aligned}$$

we simplify the derivative.

We simplify to have:

$${}^C D_t^\alpha L \leq -d_T \frac{(T - T^*)^2}{T} - d_I \frac{(I - I^*)^2}{I} - c\frac{(V - V^*)^2}{V} - d_A \frac{(A - A^*)^2}{A}.$$

Thus,

$${}^C D_t^\alpha L \leq 0,$$

with equality if and only if:

$$T = T^*, \quad I = I^*, \quad V = V^*, \quad A = A^*.$$

We apply the fractional LaSalle invariance principle, since:

- L is positive definite,
- ${}^{C}D_t^{\alpha} L \leq 0$,
- the largest invariant set where ${}^{C}D_t^{\alpha} L = 0$ is $\{E^*\}$,

it follows from the fractional LaSalle invariance principle that:

$$(T(t), I(t), V(t), A(t)) \to E^* \quad \text{as } t \to \infty.$$

Therefore, the endemic equilibrium E^* is globally asymptotically stable.

□

6 Discussion

The fractional-order swine influenza (H1N1) model developed in this study provides insight into within-host viral dynamics in the presence of autophagy-mediated immune responses. Influenza A (H1N1) involves rapid replication in respiratory epithelial cells, followed by a complex immune response that includes innate and intracellular mechanisms. The use of fractional derivatives captures memory effects associated with delays in viral replication, immune activation, and cellular response, which are observed in influenza infections.

A key result is the effect of the fractional order α on system behavior. A lower value of α represents stronger memory, such as delayed immune activation and prolonged survival of infected cells. This leads to slower convergence to equilibrium and smoother transient dynamics, consistent with clinical features such as incubation periods, delayed peak viral load, and gradual clearance. The fractional framework therefore offers a more realistic description of H1N1 dynamics than classical integer-order models.

Another result is that autophagy does not affect the basic reproduction number R_0 at the disease-free equilibrium. This agrees with the biological fact that autophagy is activated after viral entry and intracellular infection. As a result, it does not influence infection establishment but becomes important during disease progression. At the endemic equilibrium, autophagy reduces viral load and the number of infected cells, consistent with its role in degrading viral components and enhancing immune response.

The stability analysis shows that the disease-free equilibrium is locally asymptotically stable when $R_0 < 1$, implying that infection cannot persist. When $R_0 > 1$, a stable endemic equilibrium exists, corresponding to sustained viral presence. In the fractional setting, stability depends on eigenvalues satisfying sectorial conditions, which extend classical results. The threshold condition $R_0 < 1$ remains valid.

The autophagy parameters κ (infected cell clearance) and η (viral suppression) strongly influence infection severity. Higher values increase degradation of infected cells and viral particles, reducing steady-state viral load. This suggests that enhancing autophagy may help control H1N1 infection, especially in severe cases. However, excessive or dysregulated autophagy may have adverse effects, as some strains can exploit this pathway.

Overall, the model demonstrates the importance of combining memory effects with intracellular immune responses in studying swine flu dynamics. The interaction between fractional dynamics and autophagy provides a more accurate description of infection progression and offers insight into potential intervention strategies.

7 Conclusion

In this study, we developed and analyzed a fractional-order within-host model of swine influenza (H1N1) incorporating autophagy. The study utilized the Caputo fractional derivatives to include memory and hereditary effects. These factors are important in describing viral replication and immune response.

The qualitative analysis done in the study shows that the solutions remained positive and bounded, ensuring biological relevance. The disease-free and endemic equilibria were derived. The study went on to compute the basic reproduction number R_0. It is shown that when $R_0 < 1$, the disease-free equilibrium is locally asymptotically stable. It is also shown that when $R_0 > 1$, the endemic equilibrium is stable. These are consistent with standard epidemiological results.

The fact that autophagy does not change the infection threshold is a key finding. It can only affect disease progression and severity. It reduces viral load and the number of infected cells. This acts as an important regulatory mechanism in H1N1 dynamics. Hence, the role of intracellular immune processes in determining infection outcomes is highlighted.

The proposed fractional framework in this study captures delayed responses and persistent infection behavior. This is also an observation is swine flu infections. Its flexibility allows improved calibration with experimental or clinical data.

Future work includes numerical simulations with patient-specific data, sensitivity and bifurcation analysis of autophagy parameters, and the inclusion of additional immune components such as cytokines and adaptive responses. Extensions to stochastic or spatial models may further improve realism.

We conclude by noting that the study presents a mathematical framework for analyzing swine flu dynamics by earmarking the roles of memory and autophagy. The results provide insight for potential therapeutic strategies and disease management.

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