Reviewer Report on “2026JAMCS152206”

1. In Eq. (1), the term k should be clearly defined as the exponent of the infection rate, not a constant multiplier.
2. The right-hand side of Eq. (2) lacks dimensional consistency; verify units of δY and ρYZ.
3. In Eq. (3), the clearance term should be cZ, not cYZ—viral clearance is typically independent of infected cells.
4. The steady-state condition in Eq. (7) assumes $Y = 0$, but this is only valid for infection-free equilibrium.
5. The Jacobian matrix is missing explicit partial derivatives; write $\frac{\partial f_i}{\partial x_j}$ for clarity.
6. Eigenvalues in Tables 1–6 are listed without corresponding characteristic polynomial—include Eq. (11) explicitly.
7. In Eq. (15), the infection term should be βXZ^k, not βXZ, to match the model’s nonlinearity.
8. The next-generation matrix in Eq. (19) uses FV^{-1}, but F and V are not partitioned correctly for a 3D system.
9. The basic reproduction number $\mathcal{R}_0$ in Eq. (20) does not reduce to known forms when $k = 1$—verify derivation.
10. The term “cure factor” appears in text but is absent in Eqs. (1)–(3); include ρY consistently if it represents reversion.
11. In Eq. (8), $f_1 = s + pX(1 - X/X_{\max}) - dX - \beta XZ^k$ is implied but not stated—define all f_i.
12. The quadratic formula application after Eq. (6) is unclear—show discriminant and roots explicitly.
13. The eigenvalue condition “λ real if $\Delta \geq 0$” is omitted; add discriminant analysis for Eq. (11).
14. In Eq. (12), coefficients a, b, c of the characteristic polynomial are undefined—specify in terms of model parameters.
15. The stability claim “eigenvalues negative stable” holds only for linearized systems—clarify local asymptotic stability.
16. The infection-free equilibrium in Eq. (14) should satisfy $X^* = s/d + p(1 - X^*/X_{\max})/d$—current form ignores proliferation.
17. In Eq. (17), $F = (\beta XZ^k, 0, 0)^T$ is incorrect; only infected compartments belong in F.
18. The transition matrix V in Eq. (18) must be invertible—verify $\det(V) \neq 0$ before computing FV^{-1}.
19. The expression for $\mathcal{R}_0$ lacks dependence on k in denominator—re-derive carefully.
20. In Table 7, $\mathcal{R}_0$ values grow as k increases, but no analytical justification is given—add $\frac{d\mathcal{R}_0}{dk} > 0$.
21. The model assumes Z^k is differentiable at $Z = 0$, but for $k < 1$, $\frac{d}{dZ} Z^k \to \infty$—address regularity.
22. Eq. (1) uses t in days, but simulations are weekly—ensure time scaling consistency in numerical scheme.
23. The proliferation term $pX(1 - X/X_{\max})$ should vanish at $X = X_{\max}$, but Eq. (14) gives $X^* \neq X_{\max}$—check logic.
24. In eigenvalue tables, complex eigenvalues are reported as real—verify computation of $\mathrm{Im}(\lambda)$.
25. The Jacobian at endemic equilibrium is never computed—only IFE is analyzed.
26. The cure term ρY reduces infected cells but doesn’t increase X—mass balance is violated.

27. In Eq. (20), $\mathcal{R}_0 = \frac{\beta N X_0}{cd}$ is standard, but here X_0 depends on proliferation—justify modification.
28. The parameter N (virions per infected cell) is used in $\mathcal{R}_0$ but absent in Eqs. (1)–(3)—define or remove.
29. The exponent k applies to Z, but biologically, nonlinearity may involve X or Y—justify choice of Z^k.
30. In stability analysis, Routh-Hurwitz criteria are more appropriate than eigenvalue signs for 3D systems—consider using them.