Modeling the within-host co-infection of influenza A virus and pneumococcus

Author links open overlay panelFulgensia KamugishaMbabazi[a]J.Y.T.Mugisha[ab]M.Kimathi[c]

[a] Pan African University Institute of Basic Sciences Technology and Innovation, Nairobi P.O. Box 62000–00200, Kenya

[b] Department of Mathematics, Makerere University, Kampala P.O. Box 7062, Uganda

[c] Department of Mathematics, Statistics and Actuarial Sciences, Machakos University, Machakos P.O. Box, 136–90100, Kenya

Abstract

In this paper a nonlinear mathematical model for a within-host co-infection of influenza A virus and pneumococcus is investigated. Conditions that explain the relations amid R_{IP} and its relationship to the global asymptotic stability of the infection-free steady state are discussed. A graph-theoretic method shows that; the unique endemic steady state is globally asymptotically stable. The sensitivity analysis show that, the pathogen fitness for pneumococcus and influenza A virus are most sensitive to maximum number of bacteria an alveolar macrophage can catch, phagocytosis rate, number of infectious IAV and pneumococcus particles liberated from lysis of infected cells and infection rates of influenza A virus and pneumococcal. Numerical results of the model show that, there exists a biologically important steady state where the two infectious pathogens of unequal strength co-exist and replace each other in the epithelial cell population (with pneumococcus leading) when the pathogen fitness for each infection exceeds unity, and we find that this endemic steady state is globally asymptotically stable. Further, the impact of influenza A virus on pneumococcus and vice-visa leads to a bifurcation state.

Keywords