A MATHEMATICAL MODEL FOR HIGH PATHOGENICITY AVIAN INFLUENZA VIRUSES EMERGING FROM OUTBREAKS WITH LOW PATHOGENICITY AVIAN INFLUENZA VIRUSES

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Abstract. In this article, we establish a mathematical model for a complexity phenomenon that emerges from epidemiology. After the low pathogenicity avian influenza (LPAI) A virus (H5N2) outbreaks, most of time the high pathogenicity avian influenza (HPAI) viruses will emerges. This superinfection property is a typical complexity emerging from a system. Our model is based on traditional mathematical epidemiology models, experimental and field evidences. It has several submodels which are traditional SEIR models or SIR models. We analyze our model and their submodels. We carry out comparisons between model predictions and experimental data, and answer several important biological questions with our model. In addition, the complexity property is not derived from bifurcation theory.

Keywords. epidemiology, influenza, emergence, H5N2, pathogenicity

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1   Introduction

Complexity is a common phenomenon in ecological systems. Most of mathematical descriptions for complexity use bifurcation theory where systems are described by differential equations. In disease ecology, particulary, in epidemiology, although it seems common that a new strain of infectious virus emerges from the spreading of other viral infection in the same population, a mathematical description seems lack. In this study, we establish a mathematical model for emergence of high pathogenicity avian influenza virus from outbreaks of low pathogenicity avian influenza viruses. There is a parameter designed for emerging of the complexity. When this parameter is zero, the system is for the spreading of low pathogenicity avian