# Dynamics Analysis and Optimal Control for an Avian Influenza Model among Multi-Populations*

Yantao Luo[1,2†], Jianhua Huang[1], Xiao Wang[1†], Tingting Zheng[3] and Zhidong Teng[2]

**Abstract** In this paper, a compartment model is formulated to study the transmission dynamics of avian influenza virus among birds, poultry and human population. Due to the strong coupling of the system caused by the transmission route, there are some mathematical challenges to obtain the existence of the endemic equilibrium and its global asymptotic stability. Firstly, we give the well-posedness of the model and then discuss the threshold dynamics for three sub-models. Next, we give the threshold dynamics for the whole system: the disease-free equilibrium is locally asymptotically stable with $R_0 < 1$, and the other conditions are required for the global asymptotic stability of the disease-free equilibrium. The endemic-equilibrium is globally attractive when $R_0 > 1$. Furthermore, the sensitivity analysis and an optimal control problem are discussed. Finally, some numerical simulations are carried out to illustrate our theoretical results and visualize the impact of various parameters on model dynamics, which suggest that decreasing the recruitment rate and increasing the death rate of poultry, can only control the disease by simultaneously cutting off the transmission from birds to poultry and humans even if the ultimate scale of the disease can be effectively controlled. In addition, enhancing public awareness of prevention to reduce the transmission from birds and poultry to humans is also effective in controlling the final scale of disease.

**Keywords** Avian influenza, bird-poultry, coexistence equilibrium, existence and stability

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[†]the corresponding author.
Email address: luoyantaoxj@163.com (Y.Luo), jhhuang32@nudt.edu.cn (J.Huang), wxiao_98@nudt.edu.cn (X.Wang), ztt0711@163.com (T.Zheng) zhidong_teng@sina.com(Z.Teng)
[1]College of Science, National University of Defense Technology, Changsha, 410073, P.R. China
[2]College of Mathematics and Systems Science, Xinjiang University, Urumqi 830017, P.R. China
[3]College of Medical Engineering and Technology, Xinjiang Medical University, Urumqi 830017, P.R. China

# 1. Introduction

Avian influenza(AI) is an animal infection caused by an avian influenza virus (AIV), a type of influenza A virus, which normally does not infect humans [1]. However, since human infection with avian influenza (highly pathogenic A (H5N1)) was discovered in Hong Kong in 1997, the disease has become a zoonotic disease and has been of great concern to WHO worldwide [2]. From 2003 to July 14, 2023, 878 confirmed human cases of H5N1 virus infection have been reported to WHO including 458 deaths [3]. In addition, in the biological sense, there is a gap between the host types of different types of avian influenza viruses, and there are many subtypes of influenza viruses which can infect humans, such as, H1N1, H5N6, H7N9, and H9N2 [4], which belong to zoonotic virus AIV. The outbreak and epidemic of AI has had a serious impact on the aquaculture, catering, international trade and the ecological environment [5]. Therefore, it is necessary and meaningful to study influenza dynamics and design control strategies by understanding of the transmission mechanism of pathogenic AIV among birds, poultry and humans.

In recent years, it has been well-recognized that mathematical models are one of the most powerful tools for studying the dynamics of infectious disease because they can provide some useful epidemiological characteristics and effective prevention and control measures for relevant departments [6–10]. In particular, a number of sophisticated mathematical models for the spread of AI have been previously developed, see e.g. [11–20]. In particular, Liu et al. [19] introduced two different laws for the avian population into an AI bird-to-human model and analyzed their dynamical behavior. Bourouiba et al. [20] used the patch-type delay model to characterize the transmission mechanism migratory birds and non-migratory poultry, and further studied the role of migratory birds in the spread of H5N1 avian influenza. In addition, considering the effect of seasonal temperature and spatial heterogeneity environment on AI, Zheng et al. [14] proposed a time-spatial heterogeneity reaction-diffusion AI model. And Calvin et al. [12] formulated an avian–human influenza epidemic model with diffusion, nonlocal delay and spatial homogeneous environment to describe the transmission of avian influenza among poultry, humans and environment. However, there are many noises in the real world that affect the spread of diseases in different degrees [24,25]. Mate et al. [17] proposed a stochastic AI model with Ornstein–Uhlenbeck (O-U) process to investigate the relative contribution of direct and environmental transmission routes in the recurrence of AI epidemics. Zhou et al. [9] examined a stochastic avian influenza model with a nonlinear incidence rate within avian populations and the psychological effect within the human population, and they obtained the threshold dynamics of AI and the probability density function.

Although many avian influenza dynamics models, such as ODE, PDE, DDE, and SDE, have been discussed above, most of these models are only related to two compartments: birds and poultry, birds and humans. In fact, the spread of avian influenza often involves three groups: birds, poultry and humans. And the transmission path is also relatively complex, for example, wild birds and poultry can infect each other, and the wild birds can infect humans and even humans can be infected by poultry. Hence, it is meaningful and reasonable to incorporate the complex transmission routes among wild birds, poultry and humans. Nevertheless, it poses significant challenges to the dynamic analysis of the system, especially the existence and global stability of endemic equilibrium. In addition, although there