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Stability and Persistence of an Age Structured Epidemic Model with Mutation and Vaccination

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Abstract. In this paper, we propose an age-structured epidemic model with strain mutation and age-based vaccination. We define the reproduction numbers of both the original and mutant strains (R_0^1 and R_0^2). If the reproduction number $R_0<1$, the disease-free steady state is locally asymptotically stable. If the reproduction number $R_0^2>1$, there exists a dominant steady state of the mutant strain. Conditions for local stability of this dominant steady state are also obtained. If both reproduction numbers R_0^1 and R_0^2 are greater than 1, a coexistence steady state may occur. Finally, the uniform persistence of the disease described by our age structured model is strictly proved when the reproduction number $R_0^1>1$. By using the data of the COVID-19 epidemic in Wuhan and the theoretical results obtained in this paper, some numerical calculations are carried out to prove the effect of the age-based vaccination strategy.

AMS subject classifications: 92B05, 92D25, 92D30

Key words: Age structured epidemic model, mutation, vaccination, basic reproduction number, local stability, uniform persistence.

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1 Introduction

Age structured epidemic models are used to study disease transmission when the characteristics of the disease, such as transmission rate, depend on age. In 1974, Hoppensteadt [6] proposed and studied an age structured epidemic model. It is shown that age structure of a population affects the dynamics of disease transmission. In recent

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decades, there are many research articles investigating age structured epidemic models [2, 4, 8, 9, 11, 13, 14, 16, 20, 21]. Most of the age structured epidemic models are partial differential equation systems.

Threshold dynamics analysis of age structured epidemic models has attracted the attention of many authors. Zou *et al.* [21] studied an age structured model for hepatitis B transmission, established the basic reproduction number, and analyzed the existence and stability of the disease-free steady state and the endemic steady state. Liu *et al.* [14] discussed the global stability of an age-structured SIR epidemic model under pulsed vaccination. Castillo-Chavez and Feng [2] studied the stability of an age structured TB model and obtained the optimal vaccination strategies. Ai and Wang [1] proved the global stability of disease free steady state of an age-structured epidemic model with latent and asymptomatically infectious, and then studied vaccination strategies to achieve the optimal vaccination results based on the real data. One can refer to the articles [1,2,7,14,16,21] as well as the references therein for more information about the threshold dynamics of age structured models.

Establishing uniform persistence for an age-structured epidemic model is necessary to determine the long-term presence of disease [5, 16, 17, 19]. Qiu *et. al.* [17] proposed and studied a two strain age-structured epidemic model and proved existence of a coexistence equilibrium of two competing strains using the theory of uniform persistence of infinite dimensional dynamical systems. Wu *et. al.* [19] studied the uniform persistence of an age structured syphilis model applying the theory of uniform persistence. Okuwa *et. al.* [16] proposed an SIRS epidemic model with chronological age structure in a demographic steady state. The authors strictly proved the threshold dynamics of the model and uniform persistence of the disease [16].

With globalization and increased population mobility, virus mutation has a significant impact on the transmission, pathogenicity and immune escape ability of a disease microorganism. Wang *et. al.* [18] proposed a two-strain epidemic model with age structure and mutation to study the effect of the mutation on the disease spread. The authors investigated the stability of equilibria of the age-structured epidemic model under certain conditions. The dynamics of a two-strain epidemic model with differential susceptibility and virus mutation has been fully established in [10]. An age-structured two-strain epidemic model with super-infection was formulated and its dynamics including competitive exclusion and coexistence of the two strains were strictly proved by using invasion reproduction numbers and a fixed point theorem [12].

Vaccination can significantly reduce the spread of a virus. Reasonable vaccination strategies can improve the efficacy of vaccines [1, 2, 7, 14, 21]. In this paper, we formulate an age-structured epidemic model with virus mutation and vaccination to study the effect of the age-based vaccination on the spread of a disease with pathogen mutation. In order to predict epidemic trend and determine efficient control strategies we study thoroughly the dynamics of the pathogen. Age-structured epidemic models are always mathematically complex and their dynamic analysis is quite challenging. In this paper, we will examine the dynamic behavior of the proposed model, including the existence