CHAPTER I

INTRODUCTION

1.1 Background of the Study

Avian influenza, commonly known as bird flu, is a contagious viral disease that affects both domestic and wild birds. It can cause serious economic losses in the poultry industry and may also threaten public health. In particular, the H5N1 strain of bird flu remains highly infectious and often fatal in domestic birds [2]. Its persistence and rapid transmission, especially in densely populated poultry farms, continue to raise concern among researchers, veterinarians, and policymakers. For this reason, understanding the transmission dynamics of bird flu is essential for designing effective control and intervention strategies.

Bird flu viruses are generally classified into two groups: low pathogenic avian influenza (LPAI) and highly pathogenic avian influenza (HPAI) [3]. One group causes mild disease, while the other can cause severe outbreaks with high mortality in poultry [4]. The H5N1 strain, which is highly pathogenic, has spread widely across regions. It was first reported in Asia in 2003, then reached Europe in 2005, and later spread to the Middle East and Africa in 2006 [2]. Today, bird flu viruses continue to circulate among bird populations worldwide [3].

Although bird flu mainly infects birds, it can also infect humans. Human infection usually occurs through direct contact with infected birds, contact with contaminated secretions, or exposure to contaminated surfaces [5]. There is no scientific evidence of sustained human-to-human transmission, and no evidence that people have been infected by eating properly cooked poultry [4, 5]. The first major bird-to-human transmission was reported in Hong Kong in 1997, when 18 people were infected, and 6 died during a poultry outbreak [4, 6].

To better understand bird flu transmission, many researchers have developed mathematical models. For example, Iwami et al. [7] proposed a model to study transmission from birds to humans. In their bird population model, birds were divided into two compartments: susceptible birds, $X(t)$, and infected birds, $Y(t)$. Infected birds were assumed to remain infected until death, either from natural causes or disease-related mortality. More broadly, bird flu transmission is influenced by three main factors: the virus as the source of infection, poultry as the host, and the environment as the medium of transmission [8].

Bird flu has been especially difficult to control in Southeast Asia, where poultry farming is both a major source of income and an important source of protein. The rapid expansion of poultry production, increased demand for poultry products, and cross-border trade have all contributed to the spread of the disease. Governments and aid organizations have implemented control measures such as culling infected birds, vaccination, and improved biosecurity. However, outbreaks continue to occur, mainly because the virus can mutate and survive under farm conditions, making complete eradication difficult.

Mathematical models remain one of the most important tools for studying infectious disease transmission and control. Differential equation models, in particular, allow researchers to identify conditions under which a disease can invade, persist, or be eliminated. However, much of the existing bird flu literature focuses on complex multi-compartment models, such as SEIR-type systems (for example, SEIAVR), which are designed to capture broad epidemic patterns such as total outbreak size, multi-stage progression, or cross-species transmission between birds and humans [9, 10].

In contrast, less attention has been given to farm-level poultry dynamics, where a simpler model with a small number of key parameters can still provide important insights. Parameters such as recruitment rate (c), natural mortality rate (b), infection rate (ω), disease-induced mortality rate (m), and removal rate of infected birds (γ) are sufficient to derive equilibrium points and threshold conditions through the basic reproduction number (R_0). In addition, most bifurcation studies on bird flu have focused on extended control models, such as those including vaccination or culling, which often produce backward bifurcation or hysteresis behavior [11]. Other studies include delay effects or seasonal forcing, which may lead to Hopf bifurcations and oscillatory outbreaks [12]. While these approaches are useful for policy analysis, they can make it harder to identify the core bifurcation threshold that determines whether the infection dies out or persists at the farm level.

Based on this gap, the present study focuses on the mathematical modeling and analysis of bird flu transmission within a poultry farm. The proposed model describes the interaction between susceptible, infected, and removed birds, and includes key biological processes such as recruitment, natural mortality, disease-induced mortality, removal, and transmission. Unlike many previous studies that mainly discuss equilibrium existence and local stability, this study gives special attention to how vaccination changes the qualitative dynamics of transmission. In particular, it provides a comparative bifurcation analysis of models with and without vaccination at the farm level, which is still limited in the current literature.

To address this objective, the study develops a nonlinear system of ordinary differential equations to represent bird flu dynamics under two scenarios: without vaccination and with vaccination. The basic reproduction number and equilibrium points are derived, followed by a detailed local stability and bifurcation analysis. Numerical simulations are then used to support the analytical findings by illustrating time-dependent dynamics and phase portrait behavior. The results are expected to provide practical insights into how vaccination can influence disease control and improve decision-making in poultry farm management.

1.2 Problem Statement

1. How can the spread of bird flu within a poultry farm be described using a nonlinear system of differential equations under two conditions: without vaccination and with vaccination as a control strategy?

2. How does the basic reproduction number (R_0) act as a threshold parameter in determining whether the disease dies out or persists in the poultry

population?

3. Under what mathematical conditions does the disease-free equilibrium exist in the proposed models?
4. How can stability and bifurcation analysis, supported by numerical simulations, be used to explain changes in system dynamics and evaluate the impact of vaccination on disease control?

1.3 Aims and Objectives

This study aims to extend an existing SI-type nonlinear mathematical model of bird flu by including a removed compartment and a vaccination strategy. This extension allows for a clear comparison of disease dynamics with and without vaccination. It also supports a more detailed analysis of equilibrium behavior, threshold conditions, stability, and bifurcation dynamics. The specific objectives of this study are as follows:

1. To formulate and analyze two nonlinear models of bird flu transmission, with and without vaccination, in order to evaluate the impact of vaccination on disease spread and control.
2. To derive the basic reproduction number (R_0) for each model and examine its role as a threshold that determines whether the disease dies out or persists.
3. To determine the disease-free and endemic equilibrium points and establish the conditions required for their existence.

4. To analyze the stability of the equilibrium points and investigate possible bifurcation behavior, supported by numerical simulations to validate the analytical results.

1.4 Project Organization

This research is organized into five chapters. Chapter One introduces the background of the study, outlines the problem statement, states the research objectives, and presents the overall structure of the work. Chapter Two reviews relevant theoretical concepts and existing literature on mathematical modeling of bird flu. Chapter Three focuses on the formulation of the model and its qualitative analysis, including equilibrium points, reproduction numbers, stability, and bifurcation analysis. Chapter Four presents numerical simulations using biologically realistic parameter values to support and illustrate the analytical results. Finally, Chapter Five summarizes the main findings of the study and provides recommendations for future research.