1051-92-55   **Joseph Lucchetti** (`jbl@math.ufl.edu`), Department of Mathematics, University of Florida, Gainesville, FL 32611, **Manojit Roy** (`roym@ufl.edu`), Department of Biology, University of Florida, Gainesville, FL 32611, and **Maia Martcheva*** (`maia@math.ufl.edu`), Department of Mathematics, 358 Little Hall, University of Florida, Gainesville, FL 32611. *Avian Influenza: Modeling, Analysis, and Data Fitting.*

Low Pathogenic Avian Influenza (LPAI) virus, which circulates in wild bird populations in mostly benign form, is suspected to have mutated into a highly pathogenic (HPAI) strain after transmission to the domestic birds. HPAI has recently garnered worldwide attention because of the "spillover" infection of this strain from domestic birds to humans - primarily those in poultry industry - causing significant human fatality and thus creating potentially favorable conditions for another flu pandemic. We use an ordinary differential equation model to describe this complex dynamics of the HPAI virus, which epidemiologically links a number of species in a multi-species community. We include the wild bird population as a periodic source feeding infection to the coupled domestic bird-human system. We also account for mutation between the low and high pathogenic strains. We fit our model to the actual number of human avian influenza cases obtained from WHO, and estimate the relevant reproduction numbers and invasion reproduction numbers. We discuss outcomes of the competition of LPAI and HPAI. (Received August 08, 2009)