

A MATHEMATICAL MODEL FOR THE SPREAD OF HIGHLY PATHOGENIC AVIAN INFLUENZA H5N2 IN YUNLIN COUNTY, TAIWAN IN 2015 IN DOMESTIC GEESE

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Avian influenza (AI), more commonly known as "bird flu", is a viral disease that commonly infects poultry and wild birds, as well as mammals and humans. The virus is able to spread to infected individuals either by contact with infected hosts, or by acquiring the virus from the environment in areas where infected birds have shed virus particles due to the capability of viral particles to survive in the environment outside of a host for certain period of time [1]. During an outbreak, the usual mitigation strategy various countries employ is culling, the elimination of a group or a subgroup of infected and susceptible poultry [2]. In this work, a model for avian influenza is adapted to investigate the spread of AI virus for domestic geese that incorporates two transmission routes [1] and two culling mechanisms [2]. Each individual is classified into one of three compartments: susceptible (S), infected but not reported (I), or reported (R), due to the fact that AI is declared at least a few days after a farm reports a possible case. We also take into account the virus population in the environment (V). In addition, we perform parameter estimation for some key parameters on data acquired from the 2015 Highly Pathogenic AI H5N2 outbreak among domestic geese in Yunlin County, Taiwan [?].

REFERENCES

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