



Review

Using quantitative disease dynamics as a tool for guiding response to avian influenza in poultry in the United States of America



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ABSTRACT

Wild birds are the primary source of genetic diversity for influenza A viruses that eventually emerge in poultry and humans. Much progress has been made in the descriptive ecology of avian influenza viruses (AIVs), but contributions are less evident from quantitative studies (e.g., those including disease dynamic models). Transmission between host species, individuals and flocks has not been measured with sufficient accuracy to allow robust quantitative evaluation of alternate control protocols. We focused on the United States

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of America (USA) as a case study for determining the state of our quantitative knowledge of potential AIV emergence processes from wild hosts to poultry. We identified priorities for quantitative research that would build on existing tools for responding to AIV in poultry and concluded that the following knowledge gaps can be addressed with current empirical data: (1) quantification of the spatio-temporal relationships between AIV prevalence in wild hosts and poultry populations, (2) understanding how the structure of different poultry sectors impacts within-flock transmission, (3) determining mechanisms and rates of between-farm spread, and (4) validating current policy-decision tools with data. The modeling studies we recommend will improve our mechanistic understanding of potential AIV transmission patterns in USA poultry, leading to improved measures of accuracy and reduced uncertainty when evaluating alternative control strategies.

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1. Introduction

Emergence of avian influenza viruses (AIVs) in poultry remains a global problem that can cost hundreds of millions of US dollars (Halvorson, 2009; Lupiani and Reddy, 2009). In the USA, even low-pathogenic avian influenza viruses (LPAIVs) can cost millions of dollars to control once detected in commercial poultry (Davison et al., 1999; Halvorson, 2009). Major goals of the USA national plan (Foreign Animal Diseases Preparedness and Response Plan) for minimizing losses due to AIVs are: (1) to prevent the introduction of AIVs into poultry, (2) to identify infected flocks as quickly as possible, and (3) to eliminate the virus as quickly as possible once it is detected (USDA, 2012). These goals are achieved through biosecurity (management procedures that minimize introduction or dissemination of infectious diseases), diagnostics and surveillance (detection of AIVs), depopulation and controlled slaughter, education of flock owners/workers and public outreach, all of which occur in a planned, coordinated manner (USDA, 2012).

In developing and implementing specific prevention and response activities, multiple biological, political and economic factors are considered, such as virus pathotype (either highly pathogenic avian influenza virus: HPAIV, or LPAIV), the poultry commodity or commodities affected, the type of operation (i.e., commercial, backyard or live-bird market), the density of poultry in a geographic area, the demands of export markets, federal versus state regulatory authority, availability of financial compensation, public perception and potential for zoonotic transmission of the virus. Thus, the numerous response activities that occur depend on scenario-specific circumstances. The success of any strategy is dependent on trust, co-operation and interaction between industry and government (Swayne and Akey, 2005). Consequently, it can be challenging to assimilate all of the necessary information during an emergency. Sound quantitative tools are essential for preparedness and response planning.

Preparedness and response modeling are two complementary quantitative approaches for informing policy-based decisions made during an AIV event. During preparedness modeling, there is more time for model formulation, evaluation and “situational analysis”, but appropriate data from previous outbreaks may be unavailable or irrelevant. In response modeling, appropriate quantitative data are likely being collected and analyzed

as the outbreak unfolds, but time for detailed evaluation of quantitative methods is very limited. Because preparedness and response modeling involve similar methods and data, preparedness modeling can and does facilitate response modeling. The development, detailed investigation, and validation of several sound quantitative approaches prior to an event are important for performing response analyses with high confidence in a short period of time.

Disease-dynamic models are useful for informing control policies (Anderson and May, 1992) because they incorporate a quantitative description of how transmission changes during the course of an epidemic (Fig. 1). Adding additional components, such as age-structure or life-history stage, to simple disease-stage models (i.e., models with different disease states such as susceptible, infectious or recovered; Fig. 1) allows determination of how alternative control strategies, implemented at different stages of the transmission process, will impact epidemic dynamics. Disease-dynamic models are characterized by the presence of a force of infection (rate at which a susceptible individual acquires disease) term that defines precisely how the infection hazard experienced by a susceptible individual (or farm) depends on the current number of infectious individuals (or farms), their proximity and their type. A key parameter that can usually be derived using the force of infection term is the basic reproductive number, R_0 , defined as the expected number of secondary infections generated by one infectious individual (or farm) in an otherwise susceptible population. R_0 is used to assess the required proportion of a population that must be rendered non-transmissible for an outbreak to be controlled (Heesterbeek and Roberts, 2007) and is predictive of the impact of interventions in reducing the attack rate, even when full control is not achieved (Wu et al., 2006). Sometimes, models are too complex in their assumptions about the population or the pathogen for the derivation of R_0 to be tractable (e.g., individual-based spatial simulations).

Below, we outline some of the key policy decisions related to minimizing AIV emergence in poultry, for which quantitative disease-dynamic models could be of service. The article is organized in three sections to reflect the stages of emergence: (1) wildlife reservoir dynamics and spillover to poultry, (2) transmission within poultry flocks and (3) transmission between poultry flocks (Fig. 2). For each stage of emergence, we highlight key quantitative data that are

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