

Comparison of the transmission characteristics of high and low pathogenicity avian influenza (H5N2, H7N1 and H7N7)

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Summary

In this paper we compare the transmission characteristics of various combinations of low and high pathogenicity avian influenza strains under experimental conditions (H5N2, H7N1 and H7N7). In particular, we perform so-called ‘transmission experiments’ in which a number of inoculated individuals is put into a stable with a number of susceptible ‘contact’ individuals, and the transmission chain is monitored by virus isolation (PCR and egg culture) and serology (HI test). The data are analysed by ‘final size’ methods and a Generalized Linear Model based on a stochastic SIR model. We discuss the implications of our results for the transmission dynamics of avian influenza strains of the H5 and H7 type in poultry, as well as the implications for control measures.

Introduction

Low pathogenicity avian influenza A strains (LPAI) of the H5 and H7 type are noted for their ability to transform into highly pathogenic counterparts (HPAI). At least 20 outbreaks of HPAI have been recorded in poultry since 1959 (Alexander 2000, Capua *et al.* 2000), the most recent being the outbreak of H7N7 in the Netherlands in 2003. The outbreak has led to the culling of more than 25 million chickens and has cost the community well over 500 million euros.

Characterization of the virus under conditions met during outbreaks is very difficult if not impossible, as population structure, control measures, and surveillance usually change considerably over the time course of an outbreak. Nevertheless, for the design of optimal control strategies it is of great importance to have reliable estimates of the basic epidemiological characteristics of the host-pathogen interaction (duration of the infectious period, transmission rate parameter, pathogen induced mortality). To determine these parameters, we here report on experimental transmission studies with various combinations of low and high pathogenicity avian influenza A strains (H5N2 A/Chicken/Pennsylvania/83, H7N1 A/Turkey/Italy/99 and H7N7 H7N7/Chicken/Netherlands/03).

Methods

In the transmission experiments, a number of inoculated animals are placed in one cage with a number contact animals, and the infection chain is monitored by taking blood samples, and samples from the trachea and cloaca. The analysis of the data is based on a stochastic susceptible-infected-removed (SIR) model, making it possible to ascribe differences between strains to biologically interpretable parameters. Specifically, the data are analyzed by (1) final size methods and (2) generalized linear models. For details of the method, we refer to Ball (1986) and van der Goot *et al.* (2003).

Results and conclusions

Overall, our results show that HPAI viruses are more infectious than the corresponding LPAI viruses. In addition, in case of the H5N2 strain the infectious period of HPAI is also longer than the infectious period of the corresponding LPAI. In fact, in all experiments fully susceptible contact animals are almost invariably infected and die within six days after infection. Animals previously infected with LPAI virus, on the other hand, always survive an infection with HPAI virus or escape infection altogether. This implies that previous infection with LPAI virus effectively reduces susceptibility of the host to infection and decreases transmission of HPAI virus. We will speculate on the implications of the observed differences between H5 and H7 strains, and we will discuss the results in the light of the epidemiology and control of avian influenza viruses in poultry.

References

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