

Epidemiogenetic Modelling for Enhanced Coccidiosis Management in Poultry

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Coccidiosis is a prevalent disease in poultry, caused by protozoan parasites belonging to the genus *Eimeria*. It is widespread and endemic across the majority of European poultry farms, leading to significant economic losses. These losses stem from expenses associated with medication for prevention and treatment, as well as from mortality rates and the reduced feed efficiency and growth rates of chickens. The growing resistance of *Eimeria* species to coccidiostatic drugs, coupled with the high costs of vaccines, stress the need for alternative intervention strategies against coccidiosis. In this context, genetic selection could play an important role.

An individual's potential for transmitting the disease can be understood through several traits: (1) susceptibility, indicating the likelihood of infection upon contact with oocysts, (2) the intensity of oocyst shedding, and (3) the duration of shedding, influenced by the animal's immune response. Furthermore, the disease's impact on farm profitability also hinges on (4) an animal's tolerance to disease, defined as its capacity to maintain growth during infection, and (5) compensatory growth after infection. While much remains unknown about the genetic determinism of these five traits in poultry, existing knowledge regarding coccidiosis epidemiology enables us to model the effects of these traits on disease spread and impacts.

We propose an individual stochastic epidemiological model of coccidiosis, exploring the consequences of genetic selection on these traits. This epidemiogenetic approach has the potential to guide genetic selection strategies aimed at enhancing coccidiosis management within the poultry industry.