Modelling transmission dynamics of Campylobacter in Dutch broiler flocks

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Campylobacter

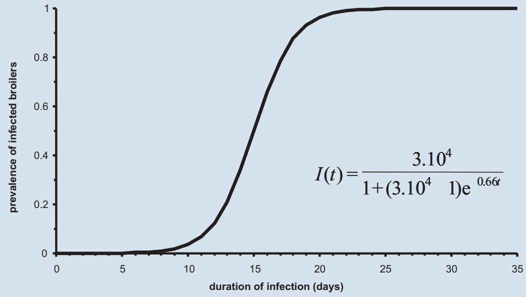
a motile spiral shaped Gram-negative bacterium, is an important cause of bacterial gastro-enteritis in human. Contaminated poultry meat is the culprit of a substantial part of human Campylobacter infections.
Hence a compulsory control and surveillance program is in effect in The Netherlands since 1998. In spite of all extensive and strict control measures taken, over 30% of all retail chicken still appear to be contaminated. Since Campylobacter multiplies only during the live stage of broilers, control strategies are most profitable if applied at farms. Given the complexity to assess the efficacy of strategies in the field, we formulated a model (base scenario) on the transmission dynamics of Campylobacter in and between broiler flocks.

The base scenario

incorporates the transmission between broilers (Box 1) and the transmission between flocks (Box 2) within a production cycle and between production cycles. Combining both models we are able to calculate the probability for a random flock to be infected. The model predicts that 44% of all Dutch flocks are Campylobacter infected, of which 38% is detectible by current methods. These percentages are in the same range as has been estimated from the surveillance data. The probability to detect an infected flock within 10 days after infection is less then 20 %.

Box 1.
Experimental data were fitted to a logistic growth curve $I(t)=\frac{NI_0}{I_0+(N-I_0)e^{-rt}}$

N total number of broilers, I_0 initial number of colonised broilers, I_t number of colonised broilers at time (*t*) , *r* growth rate of colonised broilers (estimate of *r*= 066). The course of infection is visualised in Figure 1



$$I(t)=\frac{3.10^4}{1+(3.10^4\quad 1)e^{\ 0.66t}}$$

Figure 1. Model of Campylobacter prevalence over time when a flock (*N* = 30 000 broilers) has become infected (I_0= 0).

Box 2.
To estimate the probability for a flock to get infected (*p*), field data were assessed with a Generalized Linear model applying a logit-link and assuming a binomial distribution of the data.
The following model is applied: $p=\frac{1}{1+e^{\left(a\frac{I(t)}{N}+bI(t-1)+c\right)}}$. This includes three possible infection routes for a flock to become infected, i.e. introduction from other flocks in the present production cycle (*a*), introduction from the previous cycle (*b*) and all other sources of introduction (*c*). Note that *p* depends on the number of flocks in a farm.
To calculate the overall prevalence of infected flocks first the equilibrium probability of infected flocks (pr_n) on a farm with n flocks was calculated, next pr_n was multiplied the with the Dutch farm size frequency of broiler farms.

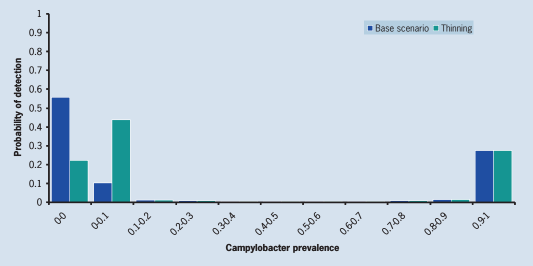


Figure 2. Probability distribution of Campylobacter prevalence in a random flock at the end of a complete production cycle. Estimates are derived from the base scenario and the thinning scenario.

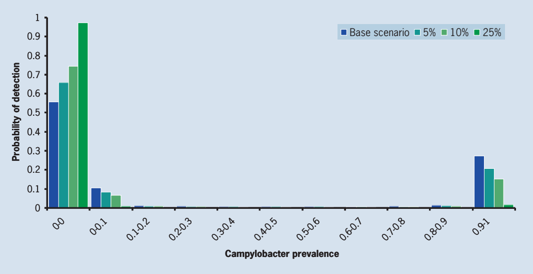


Figure 3. The effect of improving hygiene on a farm by reducing transmission parameters of the various possible transmission routes.

Possible intervention scenarios

Thinning,

early removal of some part of the broilers from a house, is applied for economical reasons. It allows a farmer to start flocks with a higher number of broilers per square meter. We assumed that 60 % of all Dutch flocks are thinned and that all other flocks become infected at time of thinning (1 colonised broiler per house). Thinning leads to an increase of the probability that a flock is infected (80% versus 44% base scenario) but the prevalence of infected broilers in flocks infected at thinning remains low within the time span of only 1 week between thinning and final slaughter (Figure 2).

Other livestock on the premises,

possibly leads to an increased risk of Campylobacter infections in flocks. To assess this risk we assumed that mixed farms with only 1 flock will close the broiler house. Farms with 2 or more flocks will quit producing the other livestock and, to compensate income losses, expand with 1 house. We found an increased risk of 4% (to 48%) when changing into mono-species farming. This is probably explained by the increased farm size, also an important risk factor.

Improvement of hygiene

has proven its value over years in reducing the prevalence of bacterial infections, but despite these efforts the prevalence of Campylobacter-infected flocks is still high. The effect of hygiene was assessed on the basis of a sensitivity analysis, because it is impossibility to connect hygiene and Campylobacter prevalence unambiguously. Parameters *a*, *b* and *c* in the model (between flock transmission) were reduced wit 5%, 10% and 25% respectively (Figure 3). A 25% reduction of the chance introducing an infection seems to be sufficient to control Campylobacter. However it is not clear what measures are needed to achieve such a reduction.

This model is built as part of the Campylobacter Risk Management and Assessment (CARMA) project. For more information on this project see www.rivm.nl/carma

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