Technical University of Denmark



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Borck Høg, Birgitte; Sommer, Helle Mølgaard; Williams, N.; Merga, Y.; Cerda Cuellar, M.; Dolz, R.; Wieczorek, K; Osek, J; David, B.; Hofshagen, M.; Wagenaar, J. ; Bolder, N. M.; Rosenquist, Hanne

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FARM SPECIFIC RISK FACTORS FOR CAMPYLOBACTER **COLONIZATION OF BROILERS IN SIX EUROPEAN COUNTRIES**

B. Borck Høg, H.M. Sommer, N. Williams, Y. Merga, M. Cerdà-Cuéllar, R. Dolz, K. Wieczorek, J. Osek, B. David, M. Hofshagen, J. Wagenaar, N. Bolder, H. Rosenquist.

INTRODUCTION

What:

RESULTS

Several models were explored by applying different strategies for categorizing the explanatory variables and for selecting and eliminating variables for the final model.

This study, part of the EU financed CamCon project, presents the results from a multi-national risk factor study, where farm data were collected through a standardised questionnaire survey carried out in six EU countries: Denmark, Norway, the Netherlands, Poland, Spain and the UK.

Why:

To identify common and country-specific, on-farm risk factors that can be used to identify the most efficient on-farm measures for preventing broiler flocks from becoming colonized with Campylobacter (See presentation by H.M. Sommer, Wednesday morning

How:

By applying a variance model that handles the explanatory variables in the generalized linear model using backward elimination and forward selection

CONCLUSIONS

- > The results overlap with observations from other Campylobacter risk factor studies, however new observations were also made. Many of the risk factors were related to inadequate biosecurity
- The risk was clearly affected by country and by temperature

The observed *Campylobacter* prevalences are shown in Figure 1. A clear seasonal distribution, with low prevalences during the winter months was seen in DK, NO and the NL. In ES, PL and the UK, the prevalence never went below 26%, 59% and 29%, respectively.

Figure 1. Observed Campylobacter prevalence in DK, ES, NL, NO, PL and the UK



Table 1. Significant risk factors

Variable	Effect on prevalence
Country	Campylobacter positive flocks, in descending order: PL, ES, UK, NL, DK and NO
Temperature	Increasing temperature increasing number of positive flocks
Age of house	Newest house Jower prevalence
Biosecurity (anteroom + barrier)	Anteroom + barrier i lower prevalence
Biosecurity (designated tools)	Designated tools 🔿 lower prevalence
Downtime	Low downtime
Drinkers (bells, nipples with cups, nipples without cups)	Nipples without cups 📥 lower prevalence

- Many similar risk factors were found in all countries, but country- specific risk factors were also identified
- Strict biosecurity is essential, particularly in newer houses
- > Some of the risk factors cannot easily be targeted by an intervention strategy

METHOD

We obtained Campylobacter data through existing Campylobacter surveillance programmes in DK and NO and through a two-year survey of flocks on 20 selected farms in ES, NL, PL and UK. The study included *Campylobacter* status data from more than 6000 flocks and 44 explanatory variables.

The data was analysed using a generalized linear model with a logit link function.

$$logit(p_{i,j,k,...}) = log\left(\frac{p_{i,j,k,...}}{1 - p_{i,j,k,...}}\right) = \beta_0 + \beta_1 X_i + \dots + \beta_{4,k} + \dots$$

where, $p_{i,j,k,...}$ is the prevalence value, $\beta_1 X_i$ express a regression term with temperature, $\beta_{4,k}$ express a categorical term. The number index for the betas (1, 2, ...etc.) refers to the question number in the questionnaire (Høg et al. 2013).

Figure 2. Significant risk factors, LS means and logit values



The probability of broiler flocks becoming colonized with *Campylobacter* was clearly affected by country. In descending order; broiler flocks were more likely to be colonized in Poland, the UK, Spain, the Netherlands, Denmark and Norway due to country specific factors that could not be explained by the management and climate variables that we explored in the models.

The seasonality in the prevalence of Campylobacter was described nicely by temperature, i.e. the *Campylobacter* prevalence increased with increasing outside temperatures. The age of broiler houses, presence of anterooms and barriers in all houses, designated tools for each house as well as length of downtime and the type of drinker systems were found to significantly affect the probability of the broiler flocks becoming colonized by Campylobacter, Table 1 and Figure 2.

The analyses was carried out by using PROC GENMOD in SAS (version 9.4, SAS Institute Inc.). The unit of analysis was the number of positive flocks out of the total number of flocks per farm. Significant risk factors were found by backward elimination and stepwise forward selection (Sommer et al, 2013).

Contact information: Birgitte Borck Høg: bibo@food.dtu.dk, Helle Mølgaard Sommer: hems@dtu.dk



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