Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries

Antimicrobial resistance (AMR) in bacteria and associated human morbidity and mortality is increasing. The use of antimicrobials in livestock selects for AMR that can subsequently be transferred to humans. This flow of AMR between reservoirs demands surveillance in livestock and in humans. We quantified and characterized the acquired resistance gene pools (resistomes) of 181 pig and 178 poultry farms from nine European countries, sequencing more than 5,000 Gb of DNA using shotgun metagenomics. We quantified acquired AMR using the ResFinder database and a second database constructed for this study, consisting of AMR genes identified through screening environmental DNA. The pig and poultry resistomes were very different in abundance and composition. There was a significant country effect on the resistomes, more so in pigs than in poultry. We found higher AMR loads in pigs, whereas poultry resistomes were more diverse. We detected several recently described, critical AMR genes, including mcr-1 and optrA, the abundance of which differed both between host species and between countries. We found that the total acquired AMR level was associated with the overall country-specific antimicrobial usage in livestock and that countries with comparable usage patterns had similar resistomes. However, functionally determined AMR genes were not associated with total drug use.
Validation of the register-based lifetime antimicrobial usage measurement for finisher batches based on comparison with recorded antimicrobial usage at farm level

Assessing the relationship between antimicrobial usage (AMU) and antimicrobial resistance (AMR) requires the accurate and precise utilisation of register data. Therefore, validation of register-based data is essential for evaluating the quality and, subsequently, the internal validity of studies based on the data. In this study, different smoothing methods for Veterinary Medicine Statistic Program database (VetStat)-records were validated by comparing these with farm-records. Comparison between measurements included accuracy as; completeness and correctness, and precision as; a relative difference of the error, correlation with Fisher’s z transformation and reliability coefficient. The most valid methods of those examined were then used in re-analyses of the abundance of AMR genes in 10 finisher batches from a previous study. Improved accuracy was found when detailed smoothing methods were applied. Although the precision also increased, the effect was not as pronounced, as the usage estimate of all smoothing methods deviated moderately compared with the farm-registrations. Applying the most valid methods to the 10 finisher batches increased estimates of statistical model fit for aminoglycosides, lincosamides, tetracyclines and decreased estimates of statistical model fit for macrolides. The estimates of statistical model fit for sulfonamides and broad-spectrum penicillins remained the same. Through refined data transformation, VetStat-records can be used to calculate a daily amount of AMU per pig reflecting the true usage accurately and moderately precisely, which is the foundation for calculating lifetime AMU.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Dalhoff Andersen, V. (Intern), Munk, P. (Intern), de Knegt, L. (Intern), Stengaard Jensen, M. (Intern), Aarestrup, F. M. (Intern), Vigre, H. (Intern)
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
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Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 1.305 SNIP 1.016 CiteScore 2.19
Web of Science (2014): Indexed yes
Computational algorithm for lifetime exposure to antimicrobials in pigs using register data – the LEA algorithm

Accurate and detailed data on antimicrobial exposure in pig production are essential when studying the association between antimicrobial exposure and antimicrobial resistance. Due to difficulties in obtaining primary data on antimicrobial exposure in a large number of farms, there is a need for a robust and valid method to estimate the exposure using register data. An approach that estimates the antimicrobial exposure in every rearing period during the lifetime of a pig using register data was developed into a computational algorithm. In this approach data from national registers on antimicrobial purchases, movements of pigs and farm demographics registered at farm level are used. The algorithm traces batches of pigs retrospectively from slaughter to the farm(s) that housed the pigs during their finisher, weaner, and piglet period. Subsequently, the algorithm estimates the antimicrobial exposure as the number of Animal Defined Daily Doses for treatment of one kg pig in each of the rearing periods. Thus, the antimicrobial purchase data at farm level are translated into antimicrobial exposure estimates at batch level. A batch of pigs is defined here as pigs sent to slaughter at the same day from the same farm. In this study we present, validate, and optimise a computational algorithm that calculate the...
lifetime exposure of antimicrobials for slaughter pigs. The algorithm was evaluated by comparing the computed estimates
to data on antimicrobial usage from farm records in 15 farm units. We found a good positive correlation between the two
estimates. The algorithm was run for Danish slaughter pigs sent to slaughter in January to March 2015 from farms with
more than 200 finishers to estimate the proportion of farms that it was applicable for. In the final process, the algorithm
was successfully run for batches of pigs originating from 3,026 farms with finisher units (77% of the initial population). This
number can be increased if more accurate register data can be obtained. The algorithm provides a systematic and
repeatable approach to estimating the antimicrobial exposure throughout the rearing period, independent of rearing site for
finisher batches, as a lifetime exposure measurement.

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Authors: Birkegård, A. C. (Intern), Dalhoff Andersen, V. (Intern), Hisham Beshara Halasa, T. (Intern), Jensen, V. F. (Intern),
Toft, N. (Intern), Vigre, H. (Intern)
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Spatial patterns of antimicrobial resistance genes in a cross-sectional sample of pig farms with indoor non-organic production of finishers

Antimicrobial resistance (AMR) in pig populations is a public health concern. There is a lack of information of spatial distributions of AMR genes in pig populations at large scales. The objective of the study was to describe the spatial pattern of AMR genes in faecal samples from pig farms and to test if the AMR genes were spatially randomly distributed with respect to the geographic distribution of the pig farm population at risk. Faecal samples from 687 Danish pig farms were collected in February and March 2015. DNA was extracted and the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)) were quantified on a high-throughput real-time PCR array. Spatial differences for the levels of the AMR genes measured as relative quantities were evaluated by spatial cluster analysis and creating of risk maps using kriging analysis and kernel density estimation. Significant spatial clusters were identified for ermB, ermF, sulI, sulII and tet(W). The broad spatial trends in AMR resistance evident in the risk maps were in agreement with the results of the cluster analysis. However, they also showed that there were only small scale spatial differences in the gene levels. We conclude that the geographical location of a pig farm is not a major determinant of the presence or high levels of AMR genes assessed in this study.
Animal Husbandry, Animals, Anti-Bacterial Agents, Bacteria, Bacterial Infections, Bacterial Proteins, Cross-Sectional Studies, Denmark, Drug Resistance, Bacterial, Feces, High-Throughput Nucleotide Sequencing, Microbial Sensitivity Tests, Polymerase Chain Reaction, Swine, Swine Diseases, Antimicrobial resistance genes, pig farms, spatial patterns
TEACH FOOD – Developing a teacher’s community of practice

The National Food Institute (DTU FOOD) at DTU teaches and educates engineers for the food sector, the public authorities and the research communities. To meet these objectives faculty needs to be at the forefront of food science as well as in teaching and continuously develop the approach to how to teach. Learning environments with suitable student challenges requires devoted and involved faculty members, who continuously develop their competences in teaching. At DTU FOOD the faculty consists of scientist in a broad range of disciplines and cultures. TEACH FOOD was established to promote and enhance the development of community of practice, i.e. a Professional Learning Community (PLC) focusing on optimizing the learning outcome of the students. To achieve this, a 1½ residential seminar for all teachers was arranged. In the first seminar 76% of the teachers and the head of institute participated. Five core activities were identified and a series of half years seminars were started focusing on challenges in every day teaching experiences. The participation of DTU FOOD faculty members in the internal DTU conferences about teaching and learning has increased from 3 to 11 since the start of TEACH FOOD. These activities illustrate the extended willingness to discuss teaching and learning as well as share experiences from teaching at DTU FOOD exemplifying the growing PLC.

The association between measurements of antimicrobial use and resistance in the faeces microbiota of finisher batches

The objectives were to present three approaches for calculating antimicrobial (AM) use in pigs that take into account the rearing period and rearing site, and to study the association between these measurements and phenotypical resistance and abundance of resistance genes in faeces samples from 10 finisher batches. The AM use was calculated relative to the rearing period of the batches as (i) ‘Finisher Unit Exposure’ at unit level, (ii) ‘Lifetime Exposure’ at batch level and (iii) ‘Herd Exposure’ at herd level. A significant effect on the occurrence of tetracycline resistance measured by cultivation was identified for Lifetime Exposure for the AM class: tetracycline. Furthermore, for Lifetime Exposure for the AM classes: macrolide, broad-spectrum penicillin, sulfonamide and tetracycline use as well as Herd Unit Exposure for the AM classes: aminoglycoside, lincosamide and tetracycline use, a significant effect was observed on the occurrence of genes coding for the AM resistance classes: aminoglycoside, lincosamide, macrolide, β-lactam, sulfonamide and tetracycline. No effect was observed for Finisher Unit Exposure. Overall, the study shows that Lifetime Exposure is an efficient measurement of AM use in finisher batches, and has a significant effect on the occurrence of resistance, measured either by cultivation or metagenomics.
A decision support system for the control of Campylobacter in chickens at farm level using data from Denmark

The control of Campylobacter in poultry is considered a public health priority and some intervention strategies have been implemented in Denmark. Nonetheless, Campylobacter infection in poultry can still be considerable particularly during the summer when the most promising Campylobacter control strategy seems to be the use of fly screens. The use of cost-effective vaccines against Campylobacter is also desirable. In order to control Campylobacter, poultry producers need to make crucial decisions under conditions of uncertainty. With the aim of assisting poultry producers in decision making regarding Campylobacter control strategies, the objective of the present study was to produce a decision support system that integrated knowledge and used a Bayesian approach to handle uncertainty. This decision support system integrated epidemiological data, microbiological considerations, financial information and potential control strategies (the use of fly screens and hypothetical vaccines). In conclusion, results from model and sensitivity analyses indicated that the financial variables (cost–benefit functions) and the effectiveness of the different control strategies drove the results.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Technical University of Denmark, Aalborg University
Authors: Garcia, A. B. (Ekstern), Madsen, A. L. (Ekstern), Vigre, H. (Intern)
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BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.547 SNIP 1.063 CiteScore 1.4
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.579 SNIP 0.911 CiteScore 1.26
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.627 SNIP 1.013 CiteScore 1.57
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.822 SNIP 1.458 CiteScore 2.05
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.857 SNIP 1.337 CiteScore 1.79
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.697 SNIP 1.108 CiteScore 1.41
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.727 SNIP 0.98
An Approach to Cluster EU Member States into Groups According to Pathways of Salmonella in the Farm-to-Consumption Chain for Pork Products

The aim of the project as the cluster analysis was to in part to develop a generic structured quantitative microbiological risk assessment (QMRA) model of human salmonellosis due to pork consumption in EU member states (MSs), and the objective of the cluster analysis was to group the EU MSs according to the relative contribution of different pathways of Salmonella in the farm-to-consumption chain of pork products. In the development of the model, by selecting a case study MS from each cluster the model was developed to represent different aspects of pig production, pork production, and consumption of pork products across EU states. The objective of the cluster analysis was to aggregate MSs into groups of countries with similar importance of different pathways of Salmonella in the farm-to-consumption chain using available, and where possible, universal register data related to the pork production and consumption in each country. Based on MS-specific information about distribution of (i) small and large farms, (ii) small and large slaughterhouses, (iii) amount of pork meat consumed, and (iv) amount of sausages consumed we used nonhierarchical and hierarchical cluster analysis to group the MSs. The cluster solutions were validated internally using statistic measures and externally by comparing the clustered MSs with an estimated human incidence of salmonellosis due to pork products in the MSs. Finally, each cluster was characterized qualitatively using the centroids of the clusters.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: Vigre, H. (Intern), Coutinho Calado Domingues, A. R. (Intern), Pedersen, U. B. (Intern), Hald, T. (Intern)
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BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.381 SJR 1.01 CiteScore 2.43
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
A Quantitative Microbiological Risk Assessment for Salmonella in Pigs for the European Union

A farm-to-consumption quantitative microbiological risk assessment (QMRA) for Salmonella in pigs in the European Union has been developed for the European Food Safety Authority. The primary aim of the QMRA was to assess the impact of hypothetical reductions of slaughter-pig prevalence and the impact of control measures on the risk of human Salmonella infection. A key consideration during the QMRA development was the characterization of variability between E.U. Member States (MSs), and therefore a generic MS model was developed that accounts for differences in pig production, slaughterhouse practices, and consumption patterns. To demonstrate the parameterization of the model, four case study MSs were selected that illustrate the variability in production of pork meat and products across MSs. For the case study MSs the average probability of illness was estimated to be between 1 in 100,000 and 1 in 10 million servings given consumption of one of the three product types considered (pork cuts, minced meat, and fermented ready-to-eat sausages). Further analyses of the farm-to-consumption QMRA suggest that the vast majority of human risk derives from infected pigs with a high concentration of Salmonella in their feces (≥10⁴ CFU/g). Therefore, it is concluded that interventions should be focused on either decreasing the level of Salmonella in the feces of infected pigs, the introduction
of a control step at the abattoir to reduce the transfer of feces to the exterior of the pig, or a control step to reduce the level of Salmonella on the carcass post-evisceration.

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Scopus rating (2017): SNIP 1.381 SJR 1.01 CiteScore 2.43
Web of Science (2017): Indexed yes
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Scopus rating (2016): CiteScore 2.21 SJR 1.12 SNIP 1.485
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.334 SNIP 1.495 CiteScore 2.51
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.331 SNIP 1.588 CiteScore 2.2
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.067 SNIP 1.595 CiteScore 2.1
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.76 SNIP 1.593 CiteScore 2.12
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.735 SNIP 1.693 CiteScore 2.15
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.739 SNIP 1.51
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.639 SNIP 1.401
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.671 SNIP 1.429
Scopus rating (2007): SJR 0.914 SNIP 1.469
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.826 SNIP 1.441
Scopus rating (2005): SJR 0.736 SNIP 1.489
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.762 SNIP 1.359
Web of Science (2004): Indexed yes
A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds

Objectives
Reliable methods for monitoring antimicrobial resistance (AMR) in livestock and other reservoirs are essential to understand the trends, transmission and importance of agricultural resistance. Quantification of AMR is mostly done using culture-based techniques, but metagenomic read mapping shows promise for quantitative resistance monitoring.

Methods
We evaluated the ability of: (i) MIC determination for Escherichia coli; (ii) cfu counting of E. coli; (iii) cfu counting of aerobic bacteria; and (iv) metagenomic shotgun sequencing to predict expected tetracycline resistance based on known antimicrobial consumption in 10 Danish integrated slaughter pig herds. In addition, we evaluated whether fresh or manure floor samples constitute suitable proxies for intestinal sampling, using cfu counting, qPCR and metagenomic shotgun sequencing.

Results
Metagenomic read-mapping outperformed cultivation-based techniques in terms of predicting expected tetracycline resistance based on antimicrobial consumption. Our metagenomic approach had sufficient resolution to detect antimicrobial-induced changes to individual resistance gene abundances. Pen floor manure samples were found to represent rectal samples well when analysed using metagenomics, as they contain the same DNA with the exception of a few contaminating taxa that proliferate in the extraintestinal environment.

Conclusions
We present a workflow, from sampling to interpretation, showing how resistance monitoring can be carried out in swine herds using a metagenomic approach. We propose metagenomic sequencing should be part of routine livestock resistance monitoring programmes and potentially of integrated One Health monitoring in all reservoirs.

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Characterization of the Human Risk of Salmonellosis Related to Consumption of Pork Products in Different E.U. Countries Based on a QMRA

In response to the European Food Safety Authority's wish to assess the reduction of human cases of salmonellosis by implementing control measures at different points in the farm-to-consumption chain for pork products, a quantitative microbiological risk assessment (QMRA) was developed. The model simulated the occurrence of Salmonella from the...
farm to consumption of pork cuts, minced meat, and fermented ready-to-eat sausage, respectively, and a dose-response model was used to estimate the probability of illness at consumption. The QMRA has a generic structure with a defined set of variables, whose values are changed according to the E.U. member state (MS) of interest. In this article we demonstrate the use of the QMRA in four MSs, representing different types of countries. The predicted probability of illness from the QMRA was between 1 in 100,000 and 1 in 10 million per serving across all three product types. Fermented ready-to-eat sausage imposed the highest probability of illness per serving in all countries, whereas the risks per serving of minced meat and pork chops were similar within each MS. For each of the products, the risk varied by a factor of 100 between the four MSs. The influence of lack of information for different variables was assessed by rerunning the model with alternative, more extreme, values. Out of the large number of uncertain variables, only a few of them have a strong influence on the probability of illness, in particular those describing the preparation at home and consumption.
Explanation and Elaboration Document for the STROBE-Vet Statement: Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary Extension

The STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement was first published in 2007 and again in 2014. The purpose of the original STROBE was to provide guidance for authors, reviewers and editors to improve the comprehensiveness of reporting; however, STROBE has a unique focus on observational studies. Although much of the guidance provided by the original STROBE document is directly applicable, it was deemed useful to map those statements to veterinary concepts, provide veterinary examples and highlight unique aspects of reporting in veterinary observational studies. Here, we present the examples and explanations for the checklist items included in the STROBE-Vet Statement. Thus, this is a companion document to the STROBE-Vet Statement Methods and process document, which describes the checklist and how it was developed.

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BFI (2017): BFI-level 2
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.3 SJR 1.119 SNIP 0.988
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.263 SNIP 1.095 CiteScore 2.27
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Explanation and Elaboration Document for the STROBE-Vet Statement: Strengthening the Reporting of Observational Studies in Epidemiology-Veterinary Extension

The STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement was first published in 2007 and again in 2014. The purpose of the original STROBE was to provide guidance for authors, reviewers, and editors to improve the comprehensiveness of reporting; however, STROBE has a unique focus on observational studies. Although much of the guidance provided by the original STROBE document is directly applicable, it was deemed useful to map those statements to veterinary concepts, provide veterinary examples, and highlight unique aspects of reporting in veterinary observational studies. Here, we present the examples and explanations for the checklist items included in the STROBE-Vet statement methods and process document (JVIM_14575 "Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology—Veterinary (STROBE-Vet) Statement" undergoing proofing), which describes the checklist and how it was developed.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology
Authors: O’Connor, A. (Ekstern), Sargeant, J. (Ekstern), Dohoo, I. (Ekstern), Erb, H. (Ekstern), Cevallos, M. (Ekstern), Egger, M. (Ekstern), Erbsbøll, A. K. (Ekstern), Martin, S. (Ekstern), Nielsen, L. (Ekstern), Pearl, D. (Ekstern), Pfeiffer, D.
Methods and processes of developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) statement

Background: Reporting of observational studies in veterinary research presents challenges that often are not addressed in published reporting guidelines. Objective: To develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to health, production, welfare, and food safety. Design: Consensus meeting of experts. Setting: Mississauga, Canada. Participants: Seventeen experts from North America, Europe, and Australia. Methods: Experts completed a pre-meeting survey about whether items in the STROBE statement should be added to or modified to address unique issues related to observational studies in animal species with health, production, welfare, or food safety outcomes. During the meeting, each STROBE item was discussed to determine whether or not rewording was recommended and whether additions were warranted. Anonymous voting was used to determine consensus. Results: Six items required no modifications or additions. Modifications or additions were made to the STROBE items 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources-measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations), and 22 (funding). Conclusion: The methods and processes used were similar to those used for other extensions of the STROBE statement. The use of this STROBE statement extension should improve reporting of observational studies in veterinary research by recognizing unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture, and wildlife.

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BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.681 SJR 0.341 CiteScore 0.45
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.515 SNIP 0.807 CiteScore 0.57
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.453 SNIP 0.636 CiteScore 0.43
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.457 SNIP 1.006 CiteScore 0.46
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.366 SNIP 0.714 CiteScore 0.44
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.263 SNIP 0.588 CiteScore 0.27
Methods and processes of developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) statement

Background: The reporting of observational studies in veterinary research presents many challenges that often are not adequately addressed in published reporting guidelines. Objective: To develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to animal health, animal production, animal welfare, and food safety. Design: A consensus meeting of experts was organized to develop an extension of the STROBE statement to address observational studies in veterinary medicine with respect to animal health, animal production, animal welfare, and food safety outcomes. Setting: Consensus meeting May 11–13, 2014 in Mississauga, Ontario, Canada. Participants: Seventeen experts from North America, Europe, and Australia attended the meeting. The experts were epidemiologists and biostatisticians, many of whom hold or have held editorial positions with relevant journals. Methods: Prior to the meeting, 19 experts completed a survey about whether they felt any of the 22 items of the STROBE statement should be modified and if items should be added to address unique issues related to observational studies in animal species with health, production, welfare, or food safety outcomes. At the meeting, the participants were provided with the survey responses and relevant literature concerning the reporting of veterinary observational studies. During the meeting, each STROBE item was discussed to determine whether or not re-wording was recommended, and whether additions were warranted. Anonymous voting was used to determine whether there was consensus for each item change or addition.

General information

State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology
Number of pages: 9
Pages: 188–196
Publication date: 2016
Main Research Area: Technical/natural sciences
Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) Statement

Background: The reporting of observational studies in veterinary research presents many challenges that often are not adequately addressed in published reporting guidelines. Objective: To develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to health, production, welfare, and food safety. Design: A consensus meeting of experts was organized to develop an extension of the STROBE statement to address observational studies in veterinary medicine with respect to animal health, animal production, animal welfare, and food safety outcomes. Setting: Consensus meeting May 11–13, 2014 in Mississauga, Ontario, Canada. Participants: Seventeen experts from North America, Europe, and Australia attended the meeting. The experts were epidemiologists and biostatisticians, many of whom hold or have held editorial positions with relevant journals. Methods: Prior to the meeting, 19 experts completed a survey about whether they felt any of the 22 items of the STROBE statement should be modified and if items should be added to address unique issues related to observational studies in animal species with health, production, welfare, or food safety outcomes. At the meeting, the participants were provided with the survey responses and relevant literature concerning the reporting of veterinary observational studies. During the meeting, each STROBE item was discussed to determine whether or not re-wording was recommended, and whether additions were warranted. Anonymous voting was used to determine whether there was consensus for each item change or addition. Results: The consensus was that six items needed no modifications or additions. Modifications or additions were made to the STROBE items numbered: 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources/measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations), and 22 (funding). Limitation: Published literature was not always available to support modification to, or inclusion of, an item. Conclusion: The methods and processes used in the development of this statement were similar to those used for other extensions of the STROBE statement. The use of this extension to the STROBE statement should improve the reporting of observational studies in veterinary research related to animal health, production, welfare, or food safety outcomes by recognizing the unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture, and wildlife.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Ontario Veterinary College, Iowa State University, University of Prince Edward Island, Cornell University, University of Bern, University of Southern Denmark, University of Copenhagen, Royal Veterinary College, Center for Food Safety and Applied Nutrition, University of Saskatchewan, University of Sydney
Number of pages: 9
Pages: 1887-1895
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Veterinary Internal Medicine
Volume: 30
Issue number: 6
ISSN (Print): 0891-6640
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.787 SJR 1.481 CiteScore 2.38
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.35 SNIP 1.286 CiteScore 2.06
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.217 SNIP 1.233 CiteScore 2.09
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.273 SNIP 1.495 CiteScore 2.08
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.541 SNIP 1.674 CiteScore 2.24
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.301 SNIP 1.522 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.604 SNIP 1.499 CiteScore 1.98
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.626 SNIP 1.691
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.502 SNIP 1.578
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.373 SNIP 1.306
Scopus rating (2007): SJR 1.531 SNIP 1.66
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.111 SNIP 1.509
Scopus rating (2005): SJR 1.184 SNIP 1.674
Scopus rating (2004): SJR 0.962 SNIP 1.386
Scopus rating (2003): SJR 1.306 SNIP 2.032
Scopus rating (2002): SJR 1.279 SNIP 1.419
Scopus rating (2001): SJR 1.181
Scopus rating (2000): SJR 0.689
Scopus rating (1999): SJR 0.759 SNIP 2.26
Original language: English
Animal Health, Animal Welfare, Food Safety, Observational Studies, Production, Animal Reporting Guidelines
Electronic versions:
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Source-ID: 2348739530
Publication: Research - peer-review › Journal article – Annual report year: 2016

Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) Statement
The reporting of observational studies in veterinary research presents many challenges that often are not adequately addressed in published reporting guidelines. A consensus meeting of experts was organized to develop an extension of the STROBE statement to address observational studies in veterinary medicine with respect to animal health, animal production, animal welfare and food safety outcomes. The consensus meeting was held 11-13 May 2014 in Mississauga, Ontario, Canada. Seventeen experts from North America, Europe and Australia attended the meeting. The experts were epidemiologists and biostatisticians, many of whom hold or have held editorial positions with relevant journals. Prior to the meeting, 19 experts completed a survey about whether they felt any of the 22 items of the STROBE statement should be modified and whether items should be added to address unique issues related to observational studies in animal species with health, production, welfare or food safety outcomes. At the meeting, the participants were provided with the survey responses and relevant literature concerning the reporting of veterinary observational studies. During the meeting, each STROBE item was discussed to determine whether or not re-wording was recommended, and whether additions were warranted. Anonymous voting was used to determine whether there was consensus for each item change or addition. The consensus was that six items needed no modifications or additions. Modifications or additions were made to the STROBE items numbered as follows: 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources/measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations) and 22 (funding). Published literature was not always available to support modification to, or inclusion of, an item. The methods and processes used in the development of this statement were similar to those used for other extensions of the STROBE statement. The use of this extension to the STROBE statement should improve the reporting of observational studies in veterinary research related to animal health, production, welfare or food safety outcomes by recognizing the unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture and wildlife.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology, University of Guelph, Iowa State University, University of Prince Edward Island, Cornell University, University of Bern, University of Southern Denmark, Ontario Veterinary College, Royal Veterinary College, Center for Food Safety and Applied Nutrition, University of Saskatchewan, University of Sydney, University of Copenhagen
Number of pages: 11
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Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
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Volume: 63
Issue number: 8
ISSN (Print): 1863-1959
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.59 SJR 1.248 SNIP 1.074
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.3 SJR 1.119 SNIP 0.988
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.263 SNIP 1.095 CiteScore 2.27
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.036 SNIP 0.955 CiteScore 1.97
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.948 SNIP 1.041 CiteScore 2.24
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.052 SNIP 1.223 CiteScore 2.35
Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology—Veterinary (STROBE-Vet) Statement

Reporting of observational studies in veterinary research presents challenges that often are not addressed in published reporting guidelines. Our objective was to develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to health, production, welfare, and food safety. We conducted a consensus meeting with 17 experts in Mississauga, Canada. Experts completed a premeeting survey about whether items in the STROBE statement should be modified or added to address unique issues related to observational studies involving food-producing and companion animals, products of animal origin, aquaculture, and wildlife.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology, University of Guelph, Iowa State University, University of Prince Edward Island, Cornell University, University of Bern, University of Southern Denmark, University of Copenhagen, University of London, United States Food and Drug Administration, University of Saskatchewan, University of Sydney
Spatial patterns of Antimicrobial Resistance Genes in Danish Pig Farms

Samples from 687 Danish pig farms were collected at five finisher slaughterhouses in February and March 2015. Faecal samples from five pigs per farm were collected randomly at the slaughter line and pooled into one sample per farm. DNA was extracted from the pooled samples and the level of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W), was quantified by a high-throughput qPCR. It was evaluated whether the sample method resulted in a study population representative of Danish pig farms with finishers where it was found that the study population was biased towards farms having more finisher and a higher productivity. Spatial cluster analyses were performed in SaTScan®. The results showed significant spatial clusters for ermF, ermB, sulII and tet(W) whereas no significant clusters were found for sulI, tet(M) and tet(O).

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Number of pages: 10
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Publication date: 2016

Host publication information
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Main Research Area: Technical/natural sciences
Conference: SVEPM, Elsinore, Denmark, 16/03/2016 - 16/03/2016

Relations
Activities:

The impact of farmers' participation in field trials in creating awareness and stimulating compliance with the World Health Organization's farm-based multiple-barrier approach

The results of a study aimed as assessing the extent to which urban vegetable farmers’ participation in field trials can impact on their awareness and engender compliance with the World Health Organization’s farm-based multiple-barrier approach are presented in this paper. Both qualitative and quantitative approaches have been used in this paper. One hundred vegetable farmers and four vegetable farmers’ associations in the Kumasi Metropolis in Ghana were covered. The individual farmers were grouped into two, namely: (1) participants and (2) non-participants of the farm-based multiple-barrier approach field trials. The results of the study show that participation in the field trials has statistically significant effects on farmers’ awareness of the farm-based multiple-barrier approach. Compliance has, however, been undermined by the farmers’ perception that the cost of compliance is more than the benefits. Policy tools that can address these constraints have been recommended in the paper.
The policy implications of urban open space commercial vegetable farmers' willingness and ability to pay for reclaimed water for irrigation in Kumasi, Ghana

The acute waste management problems, coupled with the proliferation of small scale industries in many developing countries, make low quality water treatment before use inevitable in the long run. These industries have the potential to discharge effluent containing chemicals and heavy metals into the environment. The indiscriminative use of pharmaceutical products by households in many of these countries is another source of health concern. Low quality water treatment in these countries has however been hampered by the high cost of infrastructure provision and maintenance. Cost-sharing among stakeholders appears to be a promising strategy to finance and maintain the wastewater treatment infrastructure. In this study therefore, the willingness and ability of urban open space commercial vegetable farmers to pay for reclaimed water for irrigation purposes has been assessed. One hundred open space commercial vegetable farmers and four vegetable farmers' associations were selected and interviewed in Kumasi in Ghana using semi-structured interview schedules and interview guides respectively. The results of the study show that approximately three out of every five vegetable farmers were willing to pay for reclaimed water for irrigation. The results further show that the probability of being willing to pay by farmers who agreed that the current water they used for irrigation was harmful is approximately 5.3 times greater than that of those who did not. The analysis of the farmers' ability to pay revealed that all the farmers would be capable of paying for reclaimed water at a price of US$0.11/m³. This has implications for land tenure security and vegetable consumers' willingness to pay higher prices for the produce.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology, DHI Hørsholm, Kwame Nkrumah University of Science and Technology
Authors: Amponsah, O. (Ekstern), Vigre, H. (Intern), Braimah, I. (Ekstern), Schou, T. W. (Ekstern), Abaidoo, R. C. (Ekstern)
Number of pages: 38
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Journal: Heliyon
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ISSN (Print): 2405-8440
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Agricultural economics, Agriculture, Development
Electronic versions:
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Assessing low quality water use policy framework: Case study from Ghana
We bought to understand the factors that have undermined the effective implementation of the low quality water reuse provision in Ghana's Irrigation Policy. Two Strategic Environmental Assessment tools (i.e. compatibility matrix and sustainability test) were used for the policy analyses. The analyses identified neither conflicts nor sustainability issues which could undermine the effective implementation of the policy in Ghana. Rather, its effective implementation was found to be the result of the lack of supportive legislation, regulations and guidelines. Furthermore, most of the institutions, which have been identified as key stakeholders for the policy implementation, not only lack the commitment to implement the policy but also perceive low quality water reuse as a practice that can endanger public health. We conclude that effective implementation of the low quality water reuse policy requires an integration of the policy into the broader water resources management context supported with legislation and regulations which spell out clearly institutional responsibilities, and rewards and punishments for compliance or otherwise. (C) 2015 Elsevier B.V. All rights reserved.
Intestinal colonization of broiler chickens by Campylobacter spp. in an experimental infection study

Consumption of poultry meat is considered as one of the main sources of human campylobacteriosis, and there is clearly a need for new surveillance and control measures based on quantitative data on Campylobacter spp. colonization dynamics in broiler chickens. We conducted four experimental infection trials, using four isolators during each infection trial to evaluate colonization of individual broiler chickens by Campylobacter jejuni over time. Individual and pooled faecal samples were obtained at days 4, 7 and 12 post-inoculation (p.i.) and caecal samples at day 12 p.i. There were large differences between broiler chickens in the number of C. jejuni in caecal and faecal material. Faecal samples of C. jejuni ranged from 4·0 to 9·4 log c.f.u./g and from 4·8 to 9·3 log c.f.u./g in the caeca. Faecal c.f.u./g decreased with time p.i. Most variation in c.f.u. for faecal and caecal samples was attributed to broiler chickens and a minor part to isolators, whereas infection trials did not affect the total variance. The results showed that pooled samples within isolators had lower c.f.u./g compared to the arithmetic mean of the individual samples. There was a significant correlation between faecal c.f.u./g at days 4 and 7 p.i., days 7 and 12 p.i. and for caecal and faecal c.f.u./g at day 12 p.i.

General information

State: Published
Organisations: National Food Institute, Division of Food Microbiology, Division of Epidemiology and Microbial Genomics, National Veterinary Institute, Section for Immunology and Vaccinology, Dianova
Authors: Bahrndorff, S. (Intern), Garcia Clavero, A. B. (Intern), Vigre, H. (Intern), Nauta, M. (Intern), Heegaard, P. M. H. (Intern), Madsen, M. (Ekstern), Hoorfar, J. (Intern), Hald, B. (Intern)
Number of pages: 9
Pages: 2381-2389
Publication date: 2015
Main Research Area: Technical/natural sciences
The use of third and fourth generation cephalosporins affects the occurrence of extended-spectrum cephalosporinase-producing Escherichia coli in Danish pig herds

Extended-spectrum cephalosporinase resistance is currently the fastest emerging antimicrobial resistance problem worldwide; however, evidence documenting the effect of potential risk factors is limited. The main objective of this study was to investigate the effect of using third and fourth generation cephalosporins on the occurrence of extended-spectrum cephalosporinase-producing Escherichia coli (ESC-Ec) in Danish pig herds. Conventional, integrated, medium to large herds were selected based on information from the Danish Central Husbandry Register and two groups were formed based on the use of third and fourth generation cephalosporins within a specified period, namely, 20 herds with no cephalosporin use (non-exposed) and 19 herds with frequent use (exposed). Data on prescribed antimicrobials were obtained from the National database (VetStat). Management data were obtained through a questionnaire. At the herd level, three pooled faecal samples were collected from sows with their piglets (farrowing pens), weaners, and finishers. ESC-Ec were then identified using selective enrichment. Because several of the herds only had a low number of weaners and/or finishers, analysis was only performed on samples from the farrowing pens. Logistic regression showed a significant
effect of using cephalosporins-III/IV on the occurrence of ESC-Ec in the farrowing pens, even when adjusted for use of other antimicrobials 1 year prior to sampling. No confounding effect was identified in relation to management data. The relative risk ESC-Ec in exposed compared to non-exposed was 4.7 (95% confidence interval 2.0–11.5), confirming that regular use of cephalosporins-III/IV was a significant risk factor for the occurrence of ESC-Ec.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Division of Epidemiology and Microbial Genomics, Danish Agriculture and Food Council
Authors: Dalhoff Andersen, V. (Intern), Jensen, V. F. (Intern), Vigre, H. (Intern), Andreasen, M. (Ekstern), Agersø, Y. (Intern)
Number of pages: 6
Pages: 345-350
Publication date: 2015
Main Research Area: Technical/natural sciences

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Journal: Veterinary Journal
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Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 1.87 SJR 0.979 SNIP 1.22
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.78 SJR 1.059 SNIP 1.14
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.968 SNIP 1.042 CiteScore 1.61
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.943 SNIP 1.118 CiteScore 1.7
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.064 SNIP 1.318 CiteScore 1.91
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.059 SNIP 1.64 CiteScore 2.09
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.104 SNIP 1.418 CiteScore 2
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.111 SNIP 1.486
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.994 SNIP 1.401
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.7 SNIP 1.066
Scopus rating (2007): SJR 0.749 SNIP 1.312
Scopus rating (2006): SJR 0.663 SNIP 1.168
Scopus rating (2005): SJR 0.752 SNIP 1.257
Towards the production of reliable quantitative microbiological data for risk assessment: Direct quantification of Campylobacter in naturally infected chicken fecal samples using selective culture and real-time PCR

Poultry has been identified as a significant source for human campylobacteriosis which constitutes an important zoonosis and public health problem in many areas of the world. Rapid, direct and accurate quantification of Campylobacter in poultry is essential for the assessment of public health risks and for the evaluation of control strategies implemented in poultry production. The aim of this study was to compare estimates of the numbers of Campylobacter spp. in naturally infected chicken fecal samples obtained using direct quantification by selective culture and by real-time PCR. Absolute quantification of Campylobacter by real-time PCR was performed using standard curves designed for two different DNA extraction methods: Easy-DNA™ Kit from Invitrogen (Easy-DNA) and NucliSENS® MiniMAG® from bioMérieux (MiniMAG). Results indicated that the estimation of the numbers of Campylobacter present in chicken fecal samples was partly dependent on the methodologies used. In general, the numbers of Campylobacter obtained by real-time PCR when extracting DNA using the MiniMAG method were in most cases higher than the numbers of Campylobacter obtained by selective culture and by real-time PCR when using the Easy-DNA method. Although there were differences in terms of estimates of Campylobacter numbers between the methods and samples, the differences between culture and real-time PCR were not statistically significant for most of the samples used in this study.

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Division of Food Microbiology
Authors: Garcia Clavero, A. B. (Intern), Vigre, H. (Intern), Josefsen, M. H. (Intern)
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Publication date: 2015
Main Research Area: Technical/natural sciences

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Journal: Food Control
Volume: 55
ISSN (Print): 0956-7135
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.06 SJR 1.502 SNIP 1.69
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.86 SJR 1.492 SNIP 1.709
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.498 SNIP 1.73 CiteScore 3.65
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.38 SNIP 1.717 CiteScore 3.27
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.278 SNIP 1.728 CiteScore 3.14
Comparison of air samples, nasal swabs, ear-skin swabs and environmental dust samples for detection of Methicillin Resistant Staphylococcus aureus (MRSA) in pig herds

To identify a cost-effective and practical method for detection of methicillin-resistant Staphylococcus aureus (MRSA) in pig herds, the relative sensitivity of four sample types: nasal swabs, ear-skin (skin behind the ears) swabs, environmental dust swabs and air was compared. Moreover, dependency of sensitivity on within-herd prevalence was estimated. spa-typing was applied in order to study strain diversity. The sensitivity of one air sample was equal to the sensitivity of ten pools of five nasal swabs and relatively independent of within-herd prevalence [predicted to be nearly perfect (99%) for within-herd prevalence 25%]. The results indicate that taking swabs of skin behind the ears (ten pools of five) was even more sensitive than taking nasal swabs (ten pools of five) at the herd level and detected significantly more positive samples. spa types t011, t034 and t4208 were observed. In conclusion, MRSA detection by air sampling is easy to perform, reduces costs and analytical time compared to existing methods, and is recommended for initial testing of herds. Ear-skin swab sampling may be more sensitive for MRSA detection than air sampling or nasal swab sampling.

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Division of Food Microbiology
Authors: Agersø, Y. (Intern), Vigre, H. (Intern), Cavaco, L. (Intern), Josefsen, M. H. (Intern)
Pages: 1727-1736
Publication date: 2014
Main Research Area: Technical/natural sciences

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Volume: 142
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.88 SJR 1.128 SNIP 0.807
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.98 SJR 1.18 SNIP 0.866
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.349 SNIP 1.052 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.305 SNIP 1.016 CiteScore 2.19
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.337 SNIP 1.113 CiteScore 2.57
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.437 SNIP 1.17 CiteScore 2.69
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.326 SNIP 1.214 CiteScore 2.71
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.066 SNIP 1.042
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.065 SNIP 1.197
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.082 SNIP 1.031
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.958 SNIP 1.047
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.218
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.862 SNIP 0.948
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.944 SNIP 1.176
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.901 SNIP 1.184
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.926 SNIP 1.088
Web of Science (2002): Indexed yes
Effect of subinhibitory concentrations of four commonly used biocides on the conjugative transfer of Tn916 in Bacillus subtilis

Objectives: Large amounts of biocides are used to reduce and control bacterial growth in the healthcare sector, food production and agriculture. This work explores the effect of subinhibitory concentrations of four commonly used biocides (ethanol, hydrogen peroxide, chlorhexidine digluconate and sodium hypochlorite) on the conjugative transposition of the mobile genetic element Tn916.

Methods: Conjugation assays were carried out between Bacillus subtilis strains. The donor containing Tn916 was pre-exposed to subinhibitory concentrations of each biocide for a defined length of time, which was determined by an analysis of the transcriptional response of the promoter upstream of tet(M) using β-glucuronidase reporter assays.

Results: Ethanol significantly (P = 0.01) increased the transfer of Tn916 by 5-fold, whereas hydrogen peroxide, chlorhexidine digluconate and sodium hypochlorite did not significantly affect the transfer frequency.

Conclusions: These results suggest that exposure to subinhibitory concentrations of ethanol may induce the transfer of Tn916-like elements and any resistance genes they contain.

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Three pre-PCR processing strategies for the detection and/or quantification of Salmonella in naturally contaminated soya bean meal were evaluated. Methods included: (i) flotation-qPCR [enumeration of intact Salmonella cells prior to quantitative PCR (qPCR)], (ii) MPN-PCR (modified most probable number method combined with qPCR) and (iii) qualitative culture enrichment PCR. The limit of quantification was 1.8 × 10^2 CFU g⁻¹ (flotation-qPCR) and 0.02 MPN g⁻¹ (MPN-PCR). Fifteen naturally contaminated Salmonella positive soya bean meal samples from one lot were analysed in parallel with the three methods, using 2.5, 50 and 25 g of feed, respectively, resulting in detection of Salmonella in 6, 15 and 9 bags. Enumeration resulted in 1.8 × 10^2–7.8 × 10^3 CFU g⁻¹ (flotation-qPCR) and 0.024 to >5.2 MPN g⁻¹ (MPN-PCR). Except for differences in methodology, results obtained with the three techniques could be due to the presence of nonculturable Salmonella and/or a heterogeneous distribution of Salmonella in the material. The evaluated methods provide different possibilities to assess the prevalence of Salmonella in feed, together with the numbers of culturable, as well as nonculturable cells, and can be applied to generate data to allow more accurate quantitative microbial risk assessment for Salmonella in the feed chain.
Relative human risk of Salmonella Enteritidis in table eggs

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Campylobacter vaccination of poultry: Clinical trials, quantitative microbiological methods and decision support tools for the control of Campylobacter in poultry

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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, National Veterinary Institute, Aalborg University
Authors: Garcia Clavero, A. B. (Intern), Vigre, H. (Intern), Læsø Madsen, A. (Ekstern), Christensen, L. S. (Intern)
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Direct Quantification of Campylobacter jejuni in Chicken Fecal Samples Using Real-Time PCR: Evaluation of Six Rapid DNA Extraction Methods

Direct and accurate quantification of Campylobacter in poultry is crucial for the assessment of public health risks and the evaluation of the effectiveness of control measures against Campylobacter in poultry. The aim of this study was to assess several rapid DNA extraction methods for their effectiveness for the direct quantification (without enrichment) of Campylobacter jejuni in chicken fecal samples using real-time PCR. The presence of inhibitory substances in chicken fecal samples may reduce or even completely impede the PCR amplification process making quantification very difficult. Six rapid DNA extraction methods were compared based on their limit of detection, efficiency, reproducibility, and
precision. Standard curves were designed for all the methods tested in order to assess their performance on the direct quantification of C. jejuni in chicken fecal samples. As a result of this study, the Easy-DNA (Invitrogen) method generated lower Ct values, the best amplification efficiency (AE = 93.2 %) and good precision (R squared = 0.996). The method NucleoSpin® Tissue was able to detect samples spiked with the lowest Campylobacter concentration level (10 CFU/ml) but the amplification efficiency was not optimal (AE = 139.5 %). DNA extraction methods Easy-DNA Invitrogen, MiniMAG® and NucleoSpin® Tissue produced good real-time PCR reproducibility generating standard deviations from 0.3 to 0.8 between replicates.

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Evaluation of pre-PCR processing approaches for enumeration of Salmonella enterica in naturally contaminated animal feed

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Evaluating pre-PCR processing approaches for enumeration of Salmonella enterica in naturally contaminated animal feed

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In silico and in vitro evaluation of PCR-based assays for the detection of Bacillus anthracis chromosomal signature sequences

Bacillus anthracis, the causative agent of anthrax, is a zoonotic pathogen that is relatively common throughout the world and may cause life threatening diseases in animals and humans. There are many PCR-based assays in use for the detection of B. anthracis. While most of the developed assays rely on unique markers present on virulence plasmids pXO1 and pXO2, relatively few assays incorporate chromosomal DNA markers due to the close relatedness of B. anthracis to the B. cereus group strains. For the detection of chromosomal DNA, different genes have been used, such as BA813, rpoB, gyrA, plcR, S-layer, and prophage-lambda. Following a review of the literature, an in silico analysis of all signature sequences reported for identification of B. anthracis was conducted. Published primer and probe sequences were compared for specificity against 134 available Bacillus spp. genomes. Although many of the chromosomal targets evaluated are claimed to be specific to B. anthracis, cross-reactions with closely related B. cereus and B. thuringiensis strains were often observed. Of the 35 investigated PCR assays, only 4 were 100% specific for the B. anthracis chromosome. An interlaboratory ring trial among five European laboratories was then performed to evaluate six assays, including the WHO recommended procedures, using a collection of 90 Bacillus strains. Three assays performed adequately, yielding no false positive or negative results. All three assays target chromosomal markers located within the lambdaBa03 prophage region (PL3, BA5345, and BA5357). Detection limit was further assessed for one of these highly specific assays.

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Organisations: National Food Institute, Division of Food Microbiology, Division of Epidemiology and Microbial Genomics, Lund University, National Institute of Public Health and the Environment, Wageningen IMARES, Universite Paris-Est, National Veterinary Institute
Integration of Epidemiological Evidence in a Decision Support Model for the Control of Campylobacter in Poultry Production

The control of human Campylobacteriosis is a priority in public health agendas all over the world. Poultry is considered a significant risk factor for human infections with Campylobacter and risk assessment models indicate that the successful implementation of Campylobacter control strategies in poultry will translate on a reduction of human Campylobacteriosis cases. Efficient control strategies implemented during primary production will reduce the risk of Campylobacter introduction in chicken houses and/or decrease Campylobacter concentration in infected chickens and their products. Consequently, poultry producers need to make difficult decisions under conditions of uncertainty regarding the implementation of Campylobacter control strategies. This manuscript presents the development of probabilistic graphical models to support decision making in order to control Campylobacter in poultry. The decision support systems are constructed as probabilistic graphical models (PGMs) which integrate knowledge and use Bayesian methods to deal with
uncertainty. This paper presents a specific model designed to integrate epidemiological knowledge from the United Kingdom (UK model) in order to assist poultry managers in specific decisions related to vaccination of commercial broilers for the control of Campylobacter. Epidemiological considerations and other crucial aspects including challenges associated with the quantitative part of the models are discussed in this manuscript. The outcome of the PGMs will depend on the qualitative and quantitative data included in the models. Results from the UK model and sensitivity analyses indicated that the financial variables (cost/reward functions) and the effectiveness of the control strategies considered in the UK model were driving the results. In fact, there were no or only small financial gains when using a hypothetical vaccine B (able to decrease Campylobacter numbers from two to six logs in 20% of the chickens with a cost of 0.025 £/chicken) and reward system 1 (based on similar gross profits in relation to Campylobacter levels) under the specific assumptions considered in the UK model. In contrast, significant reductions in expected Campylobacter numbers and substantial associated expected financial gains were obtained from this model when considering the reward system 2 (based on quite different gross profits in relation to Campylobacter levels) and the use of a hypothetical cost-effective vaccine C (able to reduce the level of Campylobacter from two to six logs in 90% of the chickens with a cost of 0.03 £/chicken). The flexibility of probabilistic graphical models allows for the inclusion of more than one Campylobacter vaccination strategy and more than one reward system and consequently, diverse potential solutions for the control of Campylobacter may be considered. Cost-effective Campylobacter control strategies that can significantly reduce the probability of Campylobacter introduction into a flock and/or the numbers of Campylobacter in already infected chickens, and translate to an attractive cost-reward balance will be preferred by poultry producers.

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Molecular diagnostics of foodborne pathogens
Illness caused by foodborne pathogens represents an important economic and public health burden worldwide. In order to minimize the occurrence of foodborne pathogens in the food production chain and thereby increase the food safety, better detection methods and knowledge about the behavior of pathogens are needed. The introduction of the molecular diagnostics methods based on detection of the organisms nucleic acids have made detection, identification and characterization of foodborne pathogens faster and with greater specificity and sensitivity. The objectives of research in this thesis were to investigate the use of different nucleic acid based methods for molecular diagnostics of foodborne pathogens focusing on Salmonella and Bacillus cereus with respect to improve food safety. The
work represents two parts of molecular diagnostics; the characterization Salmonellafor better understanding of its behavior in pork processing environments, and detection of B. cereusin food, feed and water samples without prior cultivation. The persistence of Salmonellain food production chains has been suggested to be a result of bacterial attachment and surface colonization. It was found that the physiological state of Salmonellahas an impact on the ability of Salmonellato attach to a pork meat surface and subsequently the possibility of contributing to cross contamination in the slaughter-line. Cells that were grown immobilized prior application on a pork meat surface were found to be more easily removed. In the pork processing, Salmonellamight appear in an immobilized state on the pork surfaces where low attachment ability might pose a risk for cross contamination. A stronger attachment to a surface makes on the other hand decontamination steps more difficult. The attachment ability of Salmonellacould to some extend be connected to specific genes. Deletion of either of the operons prgor flhDin S. Typhimurium resulted in lower attachment ability to the pork meat surface. In addition, was it found that a S. Rissen isolate with low attachment ability after immobilized growth lacked two fimbriae genes, safC and lpfD, important for the adhesion and biofilm formation. It was further found that S. Typhimurium exposed to a heat shock was more resistance to heat and acid inactivation conditions, which might make later decontamination steps more difficult and subsequently lead to a higher risk of contamination of food products. Deliberate or accidental contamination of food, feed and water supplies pose a threat to human health worldwide and the need for generic detection methods that can screen for many pathogens at the time are highly desirable. A metagenomics based direct 16S rDNA sequencing approach was evaluated as a diagnostic tool for screening of unknown bacteria in bottled water without prior cultivation. B. cereusartificially inoculated in bottled water was used as a model. The results revealed that the method was able to detect B. cereusat levels of $10^7$-$10^8$ CFU/L, a detection level low enough for detection in outbreaks situations. Consequently, the method was found to be a good candidate as a method for detection of B. cereusand for screening of other bacterial contaminants in water samples. The capability of the method was further evaluated on a variety of food and feed model samples. Before the method could be adapted to these types of samples, an optimization of the total DNA extraction step was applied. Five different commercial available DNA extraction kits were evaluated and the MasterPure DNA Purification Kit was found to be suitable for the food and feed samples. The detection of B. cereusin food and feed samples was found to be more complicated and for the method to be used for this type of samples, additional optimizations have to be conducted. In conclusion, the work present in this thesis contributes to the better understanding of the behavior of Salmonellain the pork processing and which factors that might influence the persistence and adaption. The information can be used for control of Salmonella by contributing to developments of more specific control measures and treatments within the food production chain thereby improve the food safety. In addition, the method for direct detection of B. cereusin different biological matrices was found promising with the potential to be adapted for screening of bacterial contamination. This makes the method useful in outbreaks situations where the causing agent might be unknown.
The interpretation of quantitative microbial data: meeting the demands of quantitative microbiological risk assessment

Foodborne diseases carry important social, health, political and economic consequences. Quantitative microbiological risk assessment (QMRA) is a science based tool used to estimate the risk that foodborne pathogens pose to human health, i.e. it estimates the number of cases of human foodborne infection or disease due to ingestion of a specific pathogenic microorganism conveyed by specific food products; it is also used to assess the effect of different control measures. In their role of risk managers, public authorities base their policies on the outcome of risk assessment studies. Therefore, they need to be transparent and affected by minimum imprecision.

The potential exposure to and infection by foodborne microorganisms depend, among other factors, on the microbial concentrations in food and on the microbial behaviour (growth, survival and transfer) along the food chain. Both factors are therefore important inputs in QMRA.

Since microbial concentrations vary among different samples of a food lot, probability distributions are used to describe these concentrations in QMRA. As microbial behaviour varies with food storage conditions (because it depends on intrinsic properties of food and extrinsic environmental variables), predictive models of bacterial growth and survival that account for those factors are used in QMRA, to describe expected changes in bacterial concentrations.

Both probability distributions and predictive models may contribute to the imprecision of QMRA: on one hand, there are several distribution alternatives available to describe concentrations and several methods to fit distributions to bacterial data; on the other hand predictive models are built based on controlled laboratory experiments of microbial behaviour, and may not be appropriate to apply in the context of real food. Hence, these models need to be validated with independent data for conditions of real food before use in QMRA.

The overall goal of the work presented in this thesis is to study different factors related to quantitative microbial data that may have an impact on the outcome of QMRA, in order to find appropriate solutions that limit the imprecision of risk estimates. A new method of fitting a distribution to microbial data is developed that estimates both prevalence and distribution of concentrations (manuscript I). Different probability distributions are used to describe concentrations in a simple QMRA model and the risk estimates obtained are compared (manuscript II). The predictive accuracy of a microbial growth model against different literature datasets are compared in order to identify different factors related to experimental data collection with a relevant impact on the model evaluation process (manuscript III).

In manuscript I ("Fitting a distribution to microbial counts: making sense of zeroes") it is hypothesised that when "artificial" zero microbial counts, which originate by chance from contaminated food products, are not separated from "true" zeroes originating from uncontaminated products, the estimates of prevalence and concentration may be inaccurate. Such inaccuracy may have an especially relevant impact in QMRA in situations where highly pathogenic microorganisms are involved and where growth can occur along the food pathway. Hence, a method is developed that provides accurate estimates of concentration parameters and differentiates between artificial and true zeroes, thus also accurately estimating prevalence. It is demonstrated that depending on the original distribution of concentrations and the limit of quantification (LOQ) of microbial enumeration, it may be incorrect to treat artificial zeroes as censored below a quantification threshold. The method that is presented estimates the prevalence of contamination within a food lot and the parameters (mean and standard deviation) characterizing the within-lot distribution of concentrations, without assuming a LOQ, and using raw plate count data as input. Counts resulting both from contaminated and uncontaminated sample units are analysed together, which allows estimating the proportion of artificial zeroes among the total of zero counts.

The method yields good estimates of mean, standard deviation and prevalence, especially at low prevalence levels and low expected standard deviation. This study shows that one of the keys to an accurate characterization of the overall microbial contamination is the correct identification and separation of true and artificial zeroes, and that estimation of prevalence and estimation of the distribution of concentrations are interrelated and therefore should be done simultaneously.

In manuscript II ("Impact of microbial count distribution on human health risk estimates") the impact of fitting microbial distributions on risk estimates is investigated at two different concentration scenarios and at a range of prevalence levels. Four different parametric distributions are used to investigate the importance of accounting for the randomness in counts, the difference between treating true zeroes as such or as censored below a LOQ and the importance of making the correct assumption about the underlying distribution of concentrations. By running a simulation experiment it is possible to assess the difference between expected risk and the risk estimated with using a lognormal, a zero-inflated lognormal, a Poisson-gamma and a zero-inflated Poisson-lognormal distribution. The method developed in manuscript I is used in this study to fit the latter.

The results show that the impact of the choice of different probability distributions to describe concentrations at retail on risk estimates depends both on the concentration and prevalence levels, but that in general it is larger at high levels of microbial contamination (high prevalence and high concentration). Also, a zero-inflation tends to improve the accuracy of the risk estimates.

In manuscript III ("Variability and uncertainty in the evaluation of predictive models with literature data – consequences to..."
quantitative microbiological risk assessment") it is assessed how different growth settings inherent to literature datasets affect the performance of a growth model compared to its performance with the data used to generate it. The effect of the number of observations, the ranges of temperature, water activity and pH under which observations were made, the presence or absence of lactic acid in the growth environment, the use of a pathogenic or non-pathogenic strain and the type of growth environment on model performance are analysed. Model performance is measured in terms of DifAf- the difference between the accuracy factor (Af) of the model with the data used to generate it and the Af with an independent dataset. The study is performed using a square root-type model for the growth rate of Escherichia coli in response to four environmental factors and literature data that have been previously used to evaluate this model. It is hypothesised that the Af of the model with the data used to generate it reflects the model’s best possible performance, and hence DifAf smaller and less variant when the conditions of an independent dataset are closer to the data that originated the model. The distributions of DifAf values obtained with different datasets are compared graphically and statistically. The results suggest that if predictive models developed under controlled experimental conditions are validated against independent datasets collected from published literature, these datasets must contain a high number of observations and be based on a similar experimental growth media in order to reduce the variation of model performance. By reducing this variation, the contribution of the predictive model with uncertainty and variability sources in QMRA also decreases, which affects positively the precision of the risk estimates.

To conclude, this thesis contributes to the clarification of the impact that the analysis of microbial data may have in QMRA, provides a new accurate method of fitting a distribution to microbial data, and suggests guidelines for the selection of appropriate published datasets for the validation of predictive models of microbial behaviour, before their use in QMRA. Perspectives of future work include the validation of the method developed in manuscript I with real data, and its presentation as a tool made available to the scientific community by developing, for example, a working package for the statistical software R. Also, the author expects that a standardized way of reporting microbial counts that clearly specifies the steps taken during data collection should be adopted in the future. Extending the work presented on manuscript II will allow obtaining more sound conclusions about the general impact of different frequency distributions on risk estimates. Following manuscript III, a simulation study could help to investigate to what level QMRA-targeted development and validation of predictive models are necessary for the accurate estimation of risk. Future needs in food microbiology and QMRA include the development of appropriate statistical methods to summarize novel data obtained from different “omics” technologies, adaptation of the current structure of QMRA studies to allow them to make the use of such data, and the assessment of the variability and uncertainty attending those data.
Diagnostic herd sensitivity using environmental samples

Due to logistic and economic benefits, the animal industry has an increased interest in using environmental samples to classify herds free of infections. For a valid interpretation of results obtained from environmental samples, the performance of the diagnostic method using these samples must be assessed. In this abstract we present an approach to evaluate the sensitivity of environmental samples used for herd classification. This is illustrated using results from samples for isolation of meticillin resistant Staphylococcus aureus (MRSA) in 48 pig herds that had previously been tested positive either at farm or slaughter. Three sample matrices were collected; dust samples (5 environmental swabs), nasal swabs (10 pools with 5 animals per pool) and air samples (1 filter). Based on the assumption that MRSA occurred in all 48 herds the overall herd sensitivity was 58% for nasal swabs, 33% for dust samples and 63% for air samples. However, we assumed that the sensitivity of environmental samples varies between herds due to variation in the amount of the analyte. This assumption can be tested by analyzing the association between animal prevalence and the result obtained using environmental
samples. In our example, the prevalence of infected pigs in each herd was estimated from the pooled samples of nasal swabs. Logistic regression was used to estimate the effect of animal prevalence on the probability to detect MRSA in the dust and air samples at herd level. The results show a significant increase in the probability of isolating MRSA in the environmental samples by increasing within-herd prevalence. This relationship was strongest for dust where the sensitivity increased from 25% at 1% infected pigs, to 35% at a 25% infected pigs. The air sampling was more sensitive to detect infected herds irrespectively of the within herd prevalence, and performed almost perfectly at a prevalence of 25% infected pigs (sensitivity=99%). In general, the dependence of within herd prevalence should be considered in designing surveillance programs based on environmental samples.

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Enumeration of Salmonella enterica in naturally contaminated animal feed samples by flotation prior to real-time quantitative PCR

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Enumeration of Salmonella enterica in naturally contaminated animal feed samples by flotation prior to real-time quantitative PCR

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Estimation of the variation that can be attributed to different levels in a clinical trial of a vaccine

This presentation is focusing on the interaction between the experimental design of a vaccination trial and appropriate data analysis using a trial of a vaccine against Campylobacter in broilers as an example. This study was designed using four rotations with eight isolators per rotation (10 chickens per isolator). Treatment was administered at isolator level on day 14 (vaccine or placebo). The broilers were inoculated with Campylobacter jejuni at day 31 and slaughtered at day 42. The numbers of Campylobacter (cfu/g) were obtained in the laboratory using selective cultivation methods and log transformed to obtain a Gaussian distribution. Initially, the effect of the vaccine was analyzed using all data in a t-test. Subsequently, the t-test was stratified by rotation. Finally, mixed linear models were used, taking into account the physical hierarchical setup of the trial. Results from the t-test indicate an effect of the vaccine, whereas the result obtained from the complex model indicated high variability between birds and isolators but not significant vaccine effect. The apparent observed differences between vaccinated and placebo groups in the t-tests could be attributed to the variation between incubators. Broilers in the same isolator had more equal numbers of C. jejuni compared to chickens in other incubators. It is possible that chickens in the same isolator re-infect each other with Campylobacter. In this study, the design effect was considerable, reducing the effective sample size (67 animals instead of the 290 animals included). The clustered design used in this trial was trying to emulate the clustering effect found in broiler flocks and farms.

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Infectious risk factors for individual postweaning multisystemic wasting syndrome (PMWS) development in pigs from affected farms in Spain and Denmark

Two prospective longitudinal studies in 13 postweaning multisystemic wasting syndrome (PMWS)-affected farms from Spain (n = 3) and Denmark (n = 10) were performed. Blood samples from pigs were longitudinally collected from 1st week until the occurrence of the PMWS outbreak. Wasted and healthy age-matched pigs were euthanized, necropsied and histopathologically characterised. PMWS diagnosis was confirmed by means of lymphoid lesions and detection of porcine circovirus type 2 (PCV2) in these tissues by in situ hybridization or immunohistochemistry. Serological analyses were performed in longitudinally collected serum samples to detect antibodies against PCV2, porcine reproductive and respiratory syndrome virus (PRRSV), porcine parvovirus (PPV), swine influenza virus (SIV) and Lawsonia intracellularis (law), Mycoplasma hyopneumoniae, Aujeszky's disease virus (ADV) and Salmonella spp. A Cox proportional hazards model was used to investigate the simultaneous effects of seroconversion and maternal immunity against the studied pathogens. Results showed that high levels of maternal immunity against PCV2 had a protecting effect in farms from both countries. Moreover, for the Danish dataset, seroconversion against law had an overall protecting effect, but for animals with very low levels of maternal antibody levels against this pathogen, the effect appeared neutral or aggravating. Otherwise, for the Spanish dataset, maternal immunity against PPV and PRRSV gave protective and aggravating effects, respectively. In conclusion, the present study reflects the complex interaction among different pathogens and their effects in order to trigger PMWS in PCV2 infected pigs.
Porcine circovirus type 2 (PCV2), Postweaning multisystemic wasting syndrome (PMWS), Infectious risk factors, Survival analysis

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Quantitative microbiological data analysis of a Campylobacter vaccination trial

Campylobacter jejuni is considered the main pathogen causing human campylobacteriosis and poultry has been identified as one of the main risk factors. Strategies that aim to control Campylobacter in poultry such as vaccination strategies could reduce the incidence of human campylobacteriosis. The objective of the present trial was to assess whether or not a vaccine candidate could give a 2 logs reduction of the numbers of Campylobacter in broilers. Sample size calculations indicated the use of 400 animals (200 vaccinated and 200 controls). The experiment was conducted in four different rotations using 8 incubators per rotation with 10 chickens in each incubator. The vaccination treatment was randomly assigned at incubator level. Broilers were challenged with C. jejuni at day 31 and faecal/caecum samples were collected at slaughter at day 42 and processed in the laboratory. To illustrate the importance of analysing the data in accordance with the setup of the study, the data was analysed both without and with taking the nested design into account. Initially, the effect of the vaccine was analyzed using all data in a t-test. Subsequently, the t-test was stratified by rotation. Finally, mixed linear models were used, taking into account the physical hierarchical setup of the trial. Results from the t-test indicate an effect of the vaccine, whereas the result obtained from mixed linear models indicated high variability between birds and isolators but not significant vaccine effect. The apparent observed differences between vaccinated and placebo
groups in the t-tests could be attributed to the variation between incubators. Broilers in the same isolator had more equal numbers of C. jejuni compared to chickens in other incubators. It is possible that chickens in the same isolator re-infect each other with Campylobacter.

**General information**
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, National Veterinary Institute
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Publication date: 2012
Main Research Area: Technical/natural sciences

**Relations**

**Bibliographical note**
Poster presentation

**Project**
Quantitative microbiological data analysis of a Campylobacter vaccination trial
Source: dtu
Source-ID: u::6165
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2012

**The effect of cephalosporin usage on the occurrence of ESCs producing E. coli in pig herds**
An increased occurrence of bacterial strains producing extended-spectrum cephalosporinases (ESCs) has been observed and it is now the fastest emerging antimicrobial resistance problems worldwide. The usage of 3rd- and 4th-generation cephalosporins (ceph.) in livestock is believed to be significant for the development and spread of ESCs resistance. Generic antimicrobials usage is assumed to have an impact on the spread of ESCs resistance as well. The objective of this study was to assess the effect of prescribed ceph. in pig herds on the occurrence of ESCs producing Escherichia coli. The study was conducted in 19 pig herds which have had five to fourteen prescriptions of ceph. and 20 pig herds without prescribed ceph. in a previous 12 month period. The 39 herds were all integrated and represent typical Danish pig farms. The occurrence of ESCs producing E. coli in the herds were tested in a total of 9 pooled samples per herd. A pig herd was considered positive if one or more of the nine samples contained ESCs producing E. coli. Initially, the association between usages of ceph. and occurrence of ESCs producing E. coli in the pig herds was analyzed using logistic regression, and the effect was adjusted for potential confounding effect due to purchase of pigs, number of sows, and use of disinfectant. The change of OR for ceph. usages, when the potential confounders were added were less than 20%, which indicated no confounding effect of these risk factors. Therefore, the effect of ceph. usage on occurrence of ESCs producing E. coli was estimated as risk ratio (RR). The results showed that consumption of ceph. increased the risk of occurrence of ESCs producing E. coli significantly with a RR of 5 (95% CI: 2-11). This demonstrates that ceph. usage significant affect the occurrence of ESCs resistance, and in order to limit further emerging and spread, considerations of ceph. use in livestock should be taken into account. The next phase will be to consider occurrence of ESCs due to co-selection from generic antimicrobial usage.

**General information**
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: Dalhoff Andersen, V. (Intern), Jensen, V. F. (Intern), Agersø, Y. (Intern), Vigre, H. (Intern)
Publication date: 2012
Main Research Area: Technical/natural sciences
Source: dtu
Source-ID: u::6161
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2012

**The use of probabilistic graphical models (PGMs) to develop a cost-effective vaccination strategy against Campylobacter in poultry**
Human campylobacteriosis represents an important economic and public health problem. Campylobacter originating from feces of infected chickens will contaminate chicken meat posing a risk to the consumer. Vaccination against Campylobacter in broilers is one probable measure to reduce consumers’ exposure to Campylobacter. In this presentation we focus on the development of a computerized decision support system to aid management decisions on Campylobacter vaccination of commercial broilers. Broilers should be vaccinated against Campylobacter in the first 2 weeks of age. Therefore, the decision about vaccination needs to be made usually before Campylobacter is introduced in the flock. In fact, there is uncertainty regarding the introduction of Campylobacter into the flock that needs to be taken into account in the decision making process. Probabilistic Graphical Models (PGMs) integrate knowledge from diverse sources and can be used as decision support systems under conditions of uncertainty. The relationships between different entities in
model can be designed and conditional probability distributions are used to define the strength of these relationships. Important microbiological, epidemiological and economic factors (cost-reward functions) have been included in the models. The final outcome of the models is presented in probabilities of expected level of Campylobacter and financial terms influenced by the decision on vaccination. For example, if the best decision seems to be to vaccinate, the outcome will be expressed as the most probable number of Campylobacter in broilers and a cost-profit balance. There are other factors that could be considered increasing the complexity of the models, but we need to balance model efficiency with simplicity and usefulness for poultry managers to run the model as a tool for decision making on vaccination.

**General information**

State: Published  
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Aalborg University  
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Projects:  
The use of probabilistic graphical models (PGMs) to develop a cost-effective vaccination strategy against Campylobacter in poultry  
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2012

**Microarray-based genotyping of Salmonella: Inter-laboratory evaluation of reproducibility and standardization potential**

Bacterial food-borne infections in humans caused by Salmonella spp. are considered a crucial food safety issue. Therefore, it is important for the risk assessments of Salmonella to consider the genomic variation among different isolates in order to control pathogen-induced infections. Microarray technology is a promising diagnostic tool that provides genomic information on many genes simultaneously. However, standardization of DNA microarray analysis is needed before it can be used as a routine method for characterizing Salmonella isolates across borders and laboratories. A comparative study was designed in which the agreement of data from a DNA microarray assay used for typing Salmonella spp. between two different labs was assessed. The study was expected to reveal the possibility of obtaining the same results in different labs using different equipment in order to evaluate the reproducibility of the microarray technique as a first step towards standardization. The low-density array contains 281 57–60-mer oligonucleotide probes for detecting a wide range of specific genomic marker genes associated with antibiotic resistance, cell envelope structures, mobile genetic elements and pathogenicity. Several critical methodology parameters that differed between the two labs were identified. These related to printing facilities, choice of hybridization buffer, wash buffers used following the hybridization and choice of procedure for purifying genomic DNA. Critical parameters were randomized in a four-factorial experiment and statistical measures of inter-lab consistency and agreement were performed based on the kappa coefficient. A high level of agreement (kappa=0.7–1.0) in microarray results was obtained even when employing different printing and hybridization facilities, different procedures for purifying genomic DNA and different wash buffers. However, less agreement (Kappa=0.2–0.6) between microarray results were observed when using different hybridization buffers, indicating this parameter as being highly critical when transferring a standard microarray assay between laboratories. In conclusion, this study indicates that DNA microarray assays can be reproduced in at least two different facilities, which is a pre-requisite for the development of standard guidelines.

**General information**

State: Published  
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Federal Institute for Risk Assessment, Lund University, NOFIMA  
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BFI (2018): BFI-level 2
A novel strategy to obtain quantitative data for modelling: Combined enrichment and real-time PCR for enumeration of salmonellae from pig carcasses

Salmonella is a major zoonotic pathogen which causes outbreaks and sporadic cases of gastroenteritis in humans worldwide. The primary sources for Salmonella are food-producing animals such as pigs and poultry. For risk assessment and hazard analysis and critical control point (HACCP) concepts, it is essential to produce large amounts of quantitative data, which is currently not achievable with the standard cultural based methods for enumeration of Salmonella. This study presents the development of a novel strategy to enumerate low numbers of Salmonella in cork borer samples taken from pig carcasses as a first concept and proof of principle for a new sensitive and rapid quantification method based on combined enrichment and real-time PCR. The novelty of the approach is in the short pre-enrichment step, where for most bacteria, growth is in the log phase. The method consists of an 8-h pre-enrichment of the cork borer sample diluted 1:10 in non-selective buffered peptone water, followed by DNA extraction, and Salmonella detection and quantification by real-time PCR. The limit of quantification was 1.4 colony forming units (CFU)/20 cm² (approximately 10 g) of artificially contaminated sample with 95% confidence interval of ± 0.7 log CFU/sample. The precision was similar to the standard reference most probable number (MPN) method. A screening of 200 potentially naturally contaminated cork borer samples obtained over seven weeks in a slaughterhouse resulted in 25 Salmonella-positive samples. The analysis of salmonellae within these samples showed that the PCR method had a higher sensitivity for samples with a low contamination level (<6.7 CFU/sample), where 15 of the samples negative with the MPN method was detected with the PCR method and 5 were found to be negative by both methods. For the samples with a higher contamination level (6.7-310 CFU/sample) a good agreement between the results obtained with the PCR and MPN methods was obtained. The quantitative real-time PCR method can easily be applied to other food and environmental matrices by adaptation of the pre-enrichment time and media.

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Federal Institute for Risk Assessment
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Scopus rating (2015): SJR 1.614 SNIP 1.683 CiteScore 4.02
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Scopus rating (2014): SJR 1.493 SNIP 1.695 CiteScore 3.62
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ISI indexed (2013): ISI indexed yes
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A novel strategy to obtain quantitative data for modelling: Combined enrichment and real-time PCR for enumeration of salmonellae from pig carcasses

The primary sources for the major zoonotic pathogen Salmonella are food-producing animals such as pigs and poultry. For risk assessment and hazard analysis and critical control point (HACCP) concepts, it is essential to produce large amounts of quantitative data, which is currently not achievable with the standard cultural based methods for enumeration of Salmonella. As part of the European research project BIOTRACER, this study presents the development of a novel strategy to enumerate low numbers of Salmonella in cork borer samples taken from pig carcasses as a first concept and proof of principle for a new sensitive and rapid quantification method based on combined enrichment and real-time PCR. The novelty of the approach is in the short pre-enrichment step, where for most bacteria, growth is in the log phase. The method consists of an 8-h pre-enrichment of the cork borer sample diluted 1:10 in non-selective buffered peptone water, followed by DNA extraction, and Salmonella detection and quantification by real-time PCR. The limit of quantification was 1.4 colony forming units (CFU)/20 cm² (approximately 10 g) of artificially contaminated sample with 95% confidence interval of ± 0.7 log CFU/sample. The precision was similar to the standard reference most probable number (MPN) method. A screening of 200 potentially naturally contaminated cork borer samples obtained over seven weeks in a
slaughterhouse resulted in 25 Salmonella-positive samples. The analysis of salmonellae within these samples showed that the PCR method had a higher sensitivity for samples with a low contamination level (<6.7 CFU/sample), where 15 of the samples negative with the MPN method was detected with the PCR method and 5 were found to be negative by both methods. For the samples with a higher contamination level (6.7-310 CFU/sample) a good agreement between the results obtained with the PCR and MPN methods was obtained.

A novel strategy to obtain quantitative data for modelling: Combined enrichment and real-time PCR for enumeration of salmonellae from pig carcasses

To facilitate quantitative risk assessment in the meat production chain, there is a need for culture-independent quantification methods. The aim of this study was to evaluate the use of flotation, a non-destructive sample preparation method based on traditional buoyant density centrifugation, for culture-independent quantification of intact Salmonella in pig carcass gauze swabs (100 cm²) prior to quantitative PCR (qPCR). A novel approach was investigated, excluding the homogenization step prior to flotation, to improve the detection limit and speed up the quantification procedure. The buoyant density of two Salmonella strains in different growth conditions was determined to be 1.065 – 1.092 g/ml. Based on these data, an optimal discontinuous flotation with three different density layers, 1.200, 1.102 and 1.055 g/ml, was designed for extracting intact Salmonella cells from pig carcass swabs. The method allowed accurate quantification from 4.4 × 102 to at least 2.2 × 10⁷ CFU Salmonella per swab sample using qPCR (without preceding DNA extraction) or selective plating on xylose lysine deoxycholate agar. Samples with 50 CFU could be detected occasionally but fell outside the linear range of the standard curve. The swab samples showed a broad biological diversity; for seven samples not inoculated with Salmonella, the microbial background flora (BGF) was determined to 5.0 ± 2.2 log CFU/ml sample withdrawn after flotation. It was determined that the proceeding PCR step was inhibited by BGF concentrations of ≥ 6.1 ×
108 CFU/swab sample, but not by concentrations ≤ 6.1 × 106 CFU/swab sample. By using the gauze swabs directly in the flotation procedure, the homogenization step normally used for preparation of food-related samples could be excluded, which simplified the culture independent quantification method considerably.

**Main Research Area:** Technical/natural sciences
Endemic gastrointestinal (GI) diseases have a substantial negative impact on pig production, because, when present, they reduce animal welfare, productivity and generate high antimicrobial (AM) demand. In Danish legislation, AM can be prescribed only for therapeutic purposes. The objective of the study was to estimate the association between herd-level risk factors and the amount of AM use (AMU) in connection with GI diseases in finisher herds. We conducted a register-based cross-sectional study with repeated measurements from 2004 to 2007. Data were extracted from databases in the Danish Register of Veterinary Medicine, the Central Husbandry Register and the Danish Agriculture and Food Council. In total, 3192 pig herds with 26,973 records (quarters with prescriptions) were included. The outcome was presented as average AM use (measured as Animal Daily Dosage) for GI diseases per finishing pig per quarter per herd. Three potential herd-level risk factors were evaluated: herd size (number of finishers delivered for slaughter); herd health status (herds in the Specific Pathogen Free (SPF) System, conventional herds); and herd type (herds including only finishers, integrated herds). Data were analyzed using general linear mixed models with repeated measurements. Smaller herds had a larger AMU per finisher than larger herds. Integrated herds had lower AMU as compared with herds with only finishers. Herds within the SPF System had a larger decrease in AMU with increasing herd size compared to conventional herds. Significant regional differences in AMU were seen. Additionally, the results showed that other herd factors and veterinarians were more influential than the investigated herd risk factors. This illustrates the difficulties of characterising AM-demanding GI diseases in herds by the use of register data only.
Seasonal influence on the prevalence of thermotolerant Campylobacter in retail broiler meat in Denmark

In Denmark, the incidence of human campylobacteriosis cases, as well as the Campylobacter prevalence in broiler flocks, is strongly influenced by season with a summer peak in July–August. Therefore, it was considered that the prevalence of Campylobacter in broiler meat sold at retail in Denmark might also be influenced by season. A retrospective survey analysis was performed on 2001–2007 national surveillance data of the prevalence of thermotolerant Campylobacter in all conventional broiler flocks at slaughter, and in randomly sampled broiler meat at retail. There was a significant effect of season on the occurrence of Campylobacter in meat at retail; the largest effect was found for domestic chilled meat. Thus, the Campylobacter prevalence in Danish broiler flocks, which fluctuated with season, was found to be a strong predictor for the occurrence of Campylobacter in fresh, chilled, Danish broiler meat. However, besides flock prevalence, there was also a direct effect of season on the occurrence of Campylobacter in Danish broiler meat at retail.
Seasonality, Campylobacter, Retail, Broiler meat, Prevalence

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Statistical Data Analysis of Results Based on Alternative Detection and Enumeration Methods

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
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Source: orbit
Source-ID: 283007
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Strongyle egg counts in Standardbred trotters: Are they associated with race performance?
Reasons for performing study: Strongyle worm burdens are assumed to subclinically affect equine performance. This assumption appears to be particularly pronounced in the equine racing industry. Hypothesis: Race results of Standardbred trotters are negatively affected by high strongyle faecal egg count levels. Methods: Faecal samples were obtained from 213 racing Standardbred trotters, aged ≥2 years, and stabled at training facilities of 21 professional trainers with license at racecourses in Denmark. Strongyle egg counts were generated using a McMaster technique. Race results were recorded as the finishing position of the horse (position 1-3 vs. finishing lower) and winning purse. The effect of strongyle egg counts on performance was assessed using regression analyses. Results: Strongyle egg counts ranged from 0-3500 with a mean of 319 and a median of 150 eggs/g. Finishing in positions 1-3 was significantly associated with higher egg counts. Conclusions: Race performance of the population of professionally trained Danish Standardbred trotters was not
negatively affected by higher strongyle faecal egg count levels. Potential relevance: The traditional frequent anthelmintic treatments of racehorses may be inordinate.
Culture-independent quantification of Salmonella enterica in carcass gauze swabs by flotation prior to real-time PCR

To facilitate quantitative risk assessment in the meat production chain, there is a need for culture-independent quantification methods. The aim of this study was to evaluate the use of flotation, a non-destructive sample preparation method based on traditional buoyant density centrifugation, for culture-independent quantification of intact Salmonella in pig carcass gauze swabs (100 cm²) prior to quantitative PCR (qPCR). A novel approach was investigated, excluding the homogenization step prior to flotation, to improve the detection limit and speed up the quantification procedure. The buoyant density of two Salmonella strains in different growth conditions was determined to be 1.065 – 1.092 g/ml. Based on these data, an optimal discontinuous flotation with three different density layers, ~1.200, 1.102 and 1.055 g/ml, was designed for extracting intact Salmonella cells from pig carcass swabs. The method allowed accurate quantification from 4.4×10² to at least 2.2×10⁷ CFU Salmonella per swab sample using qPCR (without preceding DNA extraction) or selective plating on xylose lysine deoxycholate agar. Samples with 50 CFU could be detected occasionally but fell outside the linear range of the standard curve. The swab samples showed a broad biological diversity; for seven samples not inoculated with Salmonella, the microbial background flora (BGF) was determined to 5.0 ± 2.2 log CFU/ml sample withdrawn after flotation. It was determined that the proceeding PCR step was inhibited by BGF concentrations of ≥ 6.1×10⁸ CFU/swab sample, but not by concentrations ≤ 6.1×10⁶ CFU/swab sample. By using the gauze swabs directly in the flotation procedure, the homogenization step normally used for preparation of food-related samples could be excluded, which simplified the culture independent quantification method considerably.

General information
State: Published
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Publication date: 2010

Host publication information
Title of host publication: BIOTRACER EC Review Meeting and 4th General Meeting : Meeting Booklet
Place of publication: Copenhagen, Denmark
Main Research Area: Technical/natural sciences
Detection of Lawsonia intracellularis in formalin-fixed Porcine Intestinal Tissue Samples: Comparison of Immunofluorescence and In-situ Hybridization, and Evaluation of the Effect of Controlled Autolysis

Two methods, an immunofluorescence assay (IFA; with a Lawsonia intracellularis-specific monoclonal antibody) and fluorescent in-situ hybridization (FISH; with a specific oligonucleotide probe targeting 16S ribosomal RNA of the bacterium), were compared for their ability to detect L. intracellularis (the cause of porcine proliferative enteritis [PE]) in formalin-fixed samples of intestinal tissue. Of 69 intestinal samples with gross lesions of PE, 63 were positive by both FISH and IFA, but six were positive only by IFA. This indicated that the sensitivity of FISH was 91% that of IFA. However, both methods had a specificity of 100%. Fifty normal porcine intestines were negative by both tests. IFA was much less susceptible than FISH to the effects of autolysis. Thus, three of nine samples from pigs with PE were FISH-negative after being kept at 20°C for 4 days, and seven were FISH negative after 2 weeks; after 4 weeks at this temperature, however, six of the nine samples were still IFA positive. After being kept at 4°C for 12 weeks, the majority of samples (≥66%) were positive by both methods.
From event of disease in pigs to recording of data in Vetstat

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hybschmann, G. (Ekstern), Houe, H. (Ekstern), Ersbøll, A. (Ekstern), Vigre, H. (Intern)
Publication date: 2010
Event: Poster session presented at 24th NKVet Symposium, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
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Infectious risk factors for postweaning multisystemic wasting syndrome (PMWS) development

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Organisations: National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics, Virology, Centre de Recerca en Sanitat Animal, Danish Agriculture and Food Council
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Quantitative Microbiological Risk Assessment on Salmonella in Slaughter and Breeder pigs: Final Report
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SCIENTIFIC REPORT submitted to EFSA prepared by VLA in consortium with DTU and RIVM.

Risk factors for antimicrobial demanding gastrointestinal diseases in Danish finisher herds using register data

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hybschmann, G. (Ekstern), Ersbøll, A. (Ekstern), Vigre, H. (Intern), Houe, H. (Ekstern)
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Towards standardization of microarray-based genotyping of Salmonella

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Federal Institute for Risk Assessment, Lund University, NOFIMA
Authors: Löfström, C. (Intern), Granlund, H. A. (Intern), Riber, L. (Intern), Vigre, H. (Intern), Folling, L. (Intern), Huehn, S. (Ekstern), Malorny, B. (Ekstern), Rådström, P. (Ekstern), Rudi, K. (Ekstern), Hoorfar, J. (Intern)
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Main Research Area: Technical/natural sciences

Links:
http://www.biotracer.org
Towards standardization of microarray-based genotyping of Salmonella

Genotyping is becoming an increasingly important tool to improve risk assessments of Salmonella. DNA microarray technology is a promising diagnostic tool that can provide high resolution genomic profile of many genes simultaneously. However, standardization of DNA microarray analysis is needed before it can be used as a tool in source attribution models for comparable characterization of isolates across laboratories and countries. The reproducibility of data was evaluated for a simple and single-dye DNA microarray (Huehn et al., Appl Environ Microbiol, 2009, 75:1011-1020) for genotyping of Salmonella at two different laboratories. The low-density array contained 281 of 57-60-mer oligonucleotide probes for detecting a wide range of specific genomic markers associated with antibiotic resistance, cell envelope structures, mobile genetic elements and pathogenicity. Several test parameters that differed between the two labs were identified: printing facilities and equipment, choice of hybridization buffer, wash buffers used following hybridization and the choice of procedure for purifying genomic DNA. These critical parameters were randomized in a four-factorial experiment and statistical measures of inter-lab consistency and agreement were performed based on the kappa coefficient. A high level of agreement (kappa = 0.7-1.0) was obtained even when using different printing and hybridization facilities, different procedures for purifying genomic DNA and different wash buffers. However, less agreement (Kappa = 0.2-0.6) between microarray results were observed when using different hybridization buffers, indicating this as the most critical factor for standardization between laboratories. In conclusion, this study indicates that it is possible to set up an international standard for a decentralized and simple-to-implement DNA microarray as part of a pan-European source-attribution model for risk assessment of Salmonella.
Using Outbreak Data for Source Attribution of Human Salmonellosis and Campylobacteriosis in Europe

Salmonella and Campylobacter are the most important bacterial causes of foodborne illness in Europe. To identify and prioritize food safety interventions, it is important to quantify the burden of human foodborne illness attributable to specific sources. Data from outbreak investigations are observed at the public health endpoint and can therefore be a direct measure of attribution at the point of exposure. An analysis or summary of outbreak investigations is useful for attributing illnesses to foods, but often the implicated foods in reported outbreaks are complex foods, containing several food items, many of which could be the specific source of the infection. We describe a method that is able to attribute human cases to specific food items contained in complex foods. The model is based on data from investigations of Salmonella and Campylobacter outbreaks in the European Union in 2005 and 2006. The reporting of the causative vehicles for the outbreaks was not harmonized between and within countries. Consequently, we organized the implicated foods in mutually exclusive food categories. We estimated that the most important food sources for salmonellosis cases were eggs (32%) and meat and poultry-meat (15%), and that the majority of the cases of campylobacteriosis were attributed to chicken (10%). For both pathogens, a large proportion of cases could not be linked to any source. Among illnesses that could be attributed to a source, 58% of salmonellosis cases were attributed to eggs, and 29% of campylobacteriosis cases were attributed to chicken. Results also revealed regional differences in the relative importance of specific sources. We assessed the method to be of limited value to attribute human campylobacteriosis due to the limited number of outbreaks. Nevertheless, the presented source attribution approach can be applied to other foodborne pathogens, and is easily adaptable to countries having an appropriate number of reported outbreaks.
Induction of porcine post-weaning multisystemic wasting syndrome (PMWS) in pigs from PMWS unaffected herds following mingling with pigs from PMWS-affected herds

In this paper we present the results from two experimental studies (I and II) investigating whether post-weaning multisystemic wasting syndrome (PMWS) can be induced in pigs from PMWS unaffected herds by mingling with pigs from PMWS-affected herds and to observe whether transportation and/or mingling of healthy pigs from unaffected herds could induce PMWS. The studies comprised pigs from 12 different herds. Eight herds had PMWS while four were unaffected. All 12 herds were found to be infected with PCV2. Pigs from PMWS-affected herds were mingled with pigs from unaffected herds in four separate compartments in both study I and study II. In addition, in study II, four groups of pigs from unaffected herds were included. Two groups with pigs transported and mingled from unaffected herds and two groups with pigs which were only transported. The PMWS diagnoses on the individual pigs were based on lymphoid depletion, histiocytic proliferation and the presence of giant cells or inclusion bodies together with the demonstration of PCV2 in lymphoid tissue. Healthy pigs, in both studies, developed PMWS 4–5 weeks after mingling with pigs clinically affected with PMWS. None of the pigs from unaffected herds which had no contact with pigs from PMWS-affected herds developed clinical signs of PMWS. Transportation and mingling of pigs from PMWS unaffected herds in combination or alone was insufficient to provoke PMWS.

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology, Danish Pig Production
Authors: Kristensen, C. S. (Ekstern), Bækbo, P. (Ekstern), Bille-Hansen, V. (Intern), Bøtner, A. (Intern), Vígræ, H. (Intern), Enøe, C. (Intern), Larsen, L. E. (Intern)
Pages: 244-250
Publication date: 2009
Main Research Area: Technical/natural sciences
Temporal trend in antimicrobial requiring gastrointestinal diseases in Danish finisher herds, 2002-07

General information
State: Published
Organisations: National Veterinary Institute, Department of Informatics and Mathematical Modeling, Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2009
Event: Poster session presented at The Society for Veterinary Epidemiology and Preventive Medicine (SVEPM).
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 265718
Publication: Research - peer-review › Poster – Annual report year: 2009

The effect of production type and antimicrobial usage on the occurrence of tetracycline resistant E. coli in Danish slaughter pig farms

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: Struve, T. (Intern), Vigre, H. (Intern), Wingstrand, A. (Intern), Sørensen, A. I. V. (Intern), Lundsby, K. L. (Intern), Emborg, H. (Intern)
Number of pages: 1
Publication date: 2009
Event: Poster session presented at 12th Conference of the International Society for Veterinary Epidemiology and Economics, Durban, South Africa.
Main Research Area: Technical/natural sciences
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Source: PublicationPreSubmission
Source-ID: 93044370
Publication: Research - peer-review › Poster – Annual report year: 2009

The effect of production type and antimicrobial usage on the occurrence of tetracycline resistant E. coli in Danish slaughter pig farms

The Qualysafe project was initiated in 2007 to support and strengthen the sustainable production systems in Danish food production. One of the objectives of the epidemiological investigation was to find new methods to improve food safety in conventional as well as in alternative pig production systems. At nine different slaughterhouses 1500 ceacum samples were collected from slaughter pigs originating from 226 farms. One thousand samples were analyzed and one E. coli isolate per sample was susceptibility tested to Tetracycline. Data on management practice and health status at farm level was collected through telephone interviews. Data on antimicrobial consumption at farm level was collected from the Danish surveillance program VetStat. In total, 99 farms used Tetracycline and participated in the interview and from these farms, 411 isolates were available. We assumed that production type (organic, free range and conventional farms) was a risk factor for occurrence of antimicrobial resistance and Tetracycline usage was regarded as an intervening factor between production type and occurrence of antimicrobial resistance. Therefore, the effect of production type and Tetracycline usage was estimated in two separate models using logistic regression, taking into account the correlation of results obtained from the same farm. Among the 411 isolates, 129 was found resistant to Tetracycline (Organic: 10%, Free Range: 27 % Conventional: 39 %). Differences was seen in the consumption pattern among the farm types, with the Organic having the lowest consumption (0.14 doses /annually produced slaughter pig) while Free Range had the highest consumption (0.85 doses/annually produced slaughter pig) and Conventional farms was in between (0.67 doses/annually produced slaughter pig). The effect of Tetracycline usage was estimated using a quadratic polynomial. This showed a significant effect of Tetracycline consumption on the occurrence of Tetracycline resistance, where the occurrence of resistance increased by increased antimicrobial usage. Production type had significant effect on the occurrence of antimicrobial resistance, with the lowest occurrence in Organic production and the highest in Conventional production.
When analyzing the effect of production type and usage of antimicrobials on occurrence of resistance in the same model, the usage of antimicrobials was not found to have an effect. This lack of effect can be explained by the fact that Tetracycline, at least partly, is an intervening factor between production type and the consumption. The results from our analysis showed the importance of correctly classifying different risk factors as causal and intervening factors before analyzing the effect of potential risk factors on the occurrence of antimicrobial resistance in animal production.

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: Struve, T. (Intern), Vigre, H. (Intern), Wingstrand, A. (Intern), Sørensen, A. I. V. (Intern), Lundsby, K. L. (Intern), Emborg, H. (Intern)
Number of pages: 1
Publication date: 2009
Event: Abstract from 12th Conference of the International Society for Veterinary Epidemiology and Economics, Durban, South Africa.
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2009

Animal health in Denmark 2006

General information
State: Published
Organisations: National Veterinary Institute, Management, National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: Mousing, J. (Intern), Møller, K. (Intern), Vigre, H. (Intern)
Number of pages: 54
Publication date: Sep 2008

Publication information
Publisher: Danish Veterinary and Food Administration
Edition: 1
ISBN (Print): 978-87-92109-76-7
Original language: English
Main Research Area: Technical/natural sciences
Publication: Research › Report – Annual report year: 2008

Postweaning multisystematic wasting syndrome in Danish pig herds: productivity, clinical signs and pathology
A case-control study of 74 herds with postweaning multisystematic wasting syndrome (PMWS) and 74 matched control herds was carried out. In the case herds the mortality rates of weaner and finisher pigs were 11.2 and 5.2 per cent respectively, compared with 3.1 and 3.2 per cent in the control herds. In most case herds, PMWS developed within the first four weeks after weaning. Wasting, diarrhoea and respiratory signs were observed in 10 per cent of the weaner pigs (7 to 30 kg) in the case herds compared with 7 per cent in the control herds. The average daily gains of the weaner pigs and finisher pigs were 36 g and 52 g less in the case herds than in the control herds. By examining three weaner pigs from each herd the PMWS diagnosis was confirmed by histopathology and immunohistochemistry in 78 per cent of the case herds, but at least one PMWS-positive weaner pig was found in 19 of the control herds. The prevalence of PMWS-positive pigs among illthriven weaner pigs was 45 per cent (101/222) in the case herds, and 12 per cent (27/222) in the control herds. Specific gross pathological findings were associated with a positive PMWS diagnosis; pigs with heavy, rubber-like lungs, atonic intestines, and enlarged bronchial and inguinal lymph nodes, had a 0.7 probability of having PMWS diagnosis by laboratory examinations. However, for illthriven pigs, this probability of having PMWS was equal in the case herds and the control herds.

General information
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Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Section of Swine fever etc., Division of Virology, Danish Pig Production, Danske Slagterier
Authors: Okholm Nielsen, E. (Ekstern), Enæe, C. (Intern), Jorsal, S. E. L. (Intern), Barfod, K. (Ekstern), Svensmark, B. (Ekstern), Bille-Hansen, V. (Intern), Vigne, H. (Intern), Bøtner, A. (Intern), Baekbo, P. (Ekstern)
Pages: 505-508
Publication date: 2008
Main Research Area: Technical/natural sciences
Post-weaning multisystemic wasting syndrome (PMWS) in Danish pig herds: productivity, clinical symptoms, and pathology

A case-control study of 74 herds with postweaning multisystemic wasting syndrome (PMWS) and 74 matched control herds was carried out. In the case herds the mortality rates of weaner and finisher pigs were 11·2 and 5·2 per cent respectively, compared with 3·1 and 3·2 per cent in the control herds. In most case herds, PMWS developed within the first four weeks after weaning. Wasting, diarrhoea and respiratory signs were observed in 10 per cent of the weaner pigs (7 to 30 kg) in the case herds compared with 7 per cent in the control herds. The average daily gains of the weaner pigs and finisher pigs were 36 g and 52 g less in the case herds than in the control herds. By examining three weaner pigs from each herd the PMWS diagnosis was confirmed by histopathology and immunohistochemistry in 78 per cent of the case herds, but at least one PMWS-positive weaner pig was found in 19 of the control herds. The prevalence of PMWS-positive pigs among illthriven weaner pigs was 45 per cent (101/222) in the case herds, and 12 per cent (27/222) in the control herds. Specific gross pathological findings were associated with a positive PMWS diagnosis; pigs with heavy, rubber-like lungs, atonic intestines, and enlarged bronchial and inguinal lymph nodes, had a 0·7 probability of a positive PMWS diagnosis by laboratory examinations. However, for illthriven pigs, this probability of having PMWS was equal in the case herds and the control herds.

General information

State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Nielsen, E. O. (Ekstern), Enøe, C. (Intern), Jorsal, S. E. L. (Intern), Barfod, K. (Ekstern), Svensmark, B. (Ekstern), Bille-Hansen, V. (Intern), Vigre, H. (Intern), Bøtner, A. (Intern), Bækbo, P. (Ekstern)
Pages: 505-508
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BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.858 SJR 0.464 CiteScore 0.39
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.482 SNIP 0.745 CiteScore 0.3
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.521 SNIP 0.796 CiteScore 0.39
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.489 SNIP 0.844 CiteScore 0.41
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.506 SNIP 0.821 CiteScore 0.5
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.505 SNIP 0.878 CiteScore 0.52
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Seneste udvikling antibiotikaforbruget til dyr i Danmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Vigre, H. (Intern), Jensen, V. F. (Intern)
Pages: 10 - 14
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 91
Issue number: 3
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: English
Source: orbit
Source-ID: 224083
Publication: Research - peer-review › Journal article – Annual report year: 2008
The effect of discontinued use of antimicrobial growth promoters on the risk of therapeutic antibiotic treatment in Danish farrow-to-finish pig farms

This study estimated the effect of discontinued use of antimicrobial growth promoters (duAGPs) on the risk of antibiotic treatment for diarrhoea, arthritis, pneumonia, unthriving and miscellaneous disorders in Danish pig farms. The estimation was done in a case-crossover study comparing: (1) the proportion of days per farm where treatment was performed (PDT) and (2) the proportion of pigs treated per day per farm at days where treatment was performed (PPT) before and after duAGPs at 68 farrow-to-finish farms. The farms were selected using a two-stage (veterinarian/farm) convenience sampling. On average, during the first year after duAGPs there was a significant increase in the risk of antibiotic treatment for diarrhoea (PDT: OR 2.5, 95% CI 1.7-3.8; PPT: OR 1.6, 95% CI 1.1-2.2). However, the effect varied among farms - some farms experienced substantial problems, while others experienced few problems after duAGPs. No effect was identified for the risk of treatment for other diseases.

General information
State: Published
Organisations: National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Technical University of Denmark
Authors: Vigre, H. (Intern), Larsen, P. (Ekstern), Andreasen, M. (Intern), Christensen, J. (Intern), Jorsal, S. E. L. (Intern)
Pages: 92-107
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Epidemiology and Infection
Volume: 136
Issue number: 1
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Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.88 SJR 1.128 SNIP 0.807
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.98 SJR 1.18 SNIP 0.866
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.349 SNIP 1.052 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.305 SNIP 1.016 CiteScore 2.19
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.337 SNIP 1.113 CiteScore 2.57
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.437 SNIP 1.17 CiteScore 2.69
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.326 SNIP 1.214 CiteScore 2.71
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.066 SNIP 1.042
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.065 SNIP 1.197
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.082 SNIP 1.031
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.958 SNIP 1.047
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.218
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.862 SNIP 0.948
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.944 SNIP 1.176
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.901 SNIP 1.184
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.926 SNIP 1.088
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.853 SNIP 1.08
Scopus rating (2000): SJR 0.824 SNIP 1.317
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.866 SNIP 1.331
Original language: English
DOIs:
10.1017/S095026880700814X
Source: orbit
Source-ID: 237546
Publication: Research - peer-review › Journal article – Annual report year: 2008

Dynamics in PMWS positive herds

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Microbial Ecology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2007
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241481
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2007

Molecular and phylogenetic characterization of Cryptosporidium and Giardia from pigs and cattle in Denmark

The genetic diversity of Cryptosporidium spp. and Giardia duodenalis from dairy cattle and pigs in Denmark was determined in the present study. Faecal samples from 1237 pigs and 1150 cattle originating from 50 sow herds and 50 dairy herds, respectively, were analysed for the presence of the two parasites by immunofluorescence microscopy. A large proportion of the (oo)cyst containing samples were selected for molecular characterization. Sequencing and phylogenetic analysis of the 18S rDNA locus and/or the HSP70 gene of 183 pig and 154 cattle isolates of Cryptosporidium revealed the presence of C. suis, pig genotype II, C. parvum (cattle genotype), C. bovis, Cryptosporidium deer-like genotype and a novel C. suis-like genotype. For both cattle and pigs, a host age-related change in distribution of species/genotypes was observed. The zoonotic C. parvum (cattle genotype) was most prevalent in young calves. For Giardia, 82 and 145 isolates from pigs and cattle, respectively, were analysed at the 18S rDNA locus and/or the gdh gene. Giardia isolates belonging to the zoonotic Assemblage A was found in both young and older calves, as well as in weaners and piglets, whereas cows seemed to be infected purely by isolates of the livestock group, Assemblage E.

General information
State: Published
Pathology and diagnosis of PMWS in a Danish case – control study

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Ekstotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy
Authors: Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Nielsen, E. O. (Ekstern), Svensmark, B. (Ekstern), Holm, G. (Ekstern), Barfod, K. (Intern), Vigre, H. (Intern), Bøtner, A. (Intern), Enæe, C. (Intern), Bækbo, P. (Ekstern)
Publication date: 2007
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241483
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2007

Pathology and Diagnosis of PMWS in a Danish Case-Control Study

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Ekstotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy
Authors: Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Nielsen, E. O. (Ekstern), Svensmark, B. (Ekstern), Holm, G. (Ekstern), Barfod, K. (Ekstern), Vigre, H. (Intern), Bøtner, A. (Intern), Enæe, C. (Intern), Bækbo, P. (Ekstern)
Publication date: 2007
Event: Poster session presented at 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241778
Publication: Research › Poster – Annual report year: 2007

PCV2 dynamics in PMWS positive Herds

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Microbial Ecology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2007
Event: Paper presented at 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240510
Publication: Research - peer-review › Paper – Annual report year: 2007

Seneste udvikling i forbruget af antibiotika til dyr i Danmark
Seological testing for Porcine circovirus type 2 in Danish pig herds with and without PMWS

Spatial pattern of high pathogenic H5N1 Avian Influenza infection in dead wild birds in Denmark 2006
Tetracycline consumption and occurrence of tetracycline resistance in Salmonella typhimurium phage types from Danish pigs

The aims of the present study were to investigate at the farm-owner level the effect of prescribed tetracycline consumption in pigs and different Salmonella Typhimurium phage types on the probability that the S. Typhimurium was resistant to tetracycline. In this study, 1,307 isolates were included, originating from 877 farm owners, and data were analyzed using logistic regression. The analysis showed that both the S. Typhimurium phage type (p <0.0001) and an increase in tetracycline consumption (p = 0.0007) were significantly associated with tetracycline resistance. In particular, the phage type was strongly associated with tetracycline resistance. A further analysis of data from the Danish Integrated Antimicrobial Resistance Monitoring and Research Programme (DANMAP) indicates that the tetracycline-susceptible phage types only slowly become tetracycline resistant, although tetracycline consumption more than doubled at the national level from 12,000-13,000 kg of active compound in 1996-1998 to 29,000 kg of active compound in 2004. Instead, tetracycline-resistant S. Typhimurium phage types became more prevalent. This suggests that the spread of already established or new resistant clones, rather than conversion of "old" well-established susceptible clones to resistant clones by uptake of resistance genes, explains most of the increased levels of tetracycline resistance in S. Typhimurium in Danish swine production in response to increased tetracycline consumption.
A Danish case-control study on risk factors for PMWS – bio security in the herd

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Diagnostics
Authors: Enøe, C. (Intern), Vigre, H. (Intern), Nielsen, E. O. (Ekstern), Larsen, P. (Ekstern), Bøtner, A. (Intern), Bille-Hansen, V. (Intern), Jorsal, S. E. L. (Intern), Bækbo, P. (Ekstern)
Number of pages: 163
Publication date: 2006

Host publication information
Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
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Conference: The 19th International Pig Veterinary Congress, Copenhagen, Denmark, 16/07/2006 - 16/07/2006
Source: orbit
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Publication: Research › Article in proceedings – Annual report year: 2006

A Danish case-control study on risk factors for PMWS-biosecurity in the herd

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Diagnostics
Antimicrobial use in pig herds with and without Post-weaning Multisystemic Wasting Syndrome

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Jensen, V. F. (Intern), Enøe, C. (Intern), Wachman, H. (Ekstern), Nielsen, E. (Ekstern), Vigre, H. (Intern), Larsen, P. (Ekstern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241478
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2006

Association between PMWS and PRRSV

General information
State: Published
Organisations: National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Diagnostics
Authors: Vigre, H. (Intern), Enøe, C. (Intern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Baekbo, P. (Ekstern), Okholm, E. (Ekstern)
Number of pages: 174
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
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Publication: Research › Conference abstract for conference – Annual report year: 2006

Avian Influenza in wild birds: Evaluation of the risk of transmission to swine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Paisley, L. (Ekstern), Vigre, H. (Intern), Bøtner, A. (Intern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241739
Publication: Research › Article in proceedings – Annual report year: 2006

Cryptosporidium and Giardia in Danish cattle and pigs: prevalence of different species and genotypes
Cryptosporidium and Giardia in Danish dairy herds: prevalence, typing and risk factors

General information
State: Published
Organisations: National Veterinary Institute, Department of Systems Biology, Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Maddox-Hyttel, C. (Intern), Langkjær, R. B. (Intern), Enemark, H. L. (Intern), Vigre, H. (Intern)
Publication date: 2006
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241256
Publication: Research › Conference abstract for conference – Annual report year: 2006

Cryptosporidium and Giardia in different age groups of cattle and pigs in Denmark – prevalence, genotypes and risk factors

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Department of Systems Biology, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Enemark, H. L. (Intern), Maddox-Hyttel, C. (Intern), Langkjær, R. B. (Intern), Vigre, H. (Intern)
Publication date: 2006
Event: Abstract from 24th World Buiatrics Congress, Nice, France.
Main Research Area: Technical/natural sciences
Source: orbit
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Publication: Research › Conference abstract for conference – Annual report year: 2006

Cryptosporidium and Giardia in different age groups of cattle and pigs in Denmark – prevalence, genotypes and risk factors

General information
State: Published
Organisations: National Veterinary Institute, Department of Systems Biology, Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Maddox-Hyttel, C. (Intern), Langkjær, R. B. (Intern), Enemark, H. L. (Intern), Vigre, H. (Intern)
Pages: 24-29
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 89 (23)
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Chinese
Source: orbit
Source-ID: 241085
Publication: Research › Journal article – Annual report year: 2006
Cryptosporidium and Giardia in different age groups of Danish cattle and pigs - Occurrence and management associated risk factors

To obtain information both about the prevalence of Giardia and Cryptosporidium in Danish cattle and pigs as well as the possible influence of different management systems on the occurrence and intensity of infection, we conducted an epidemiological survey comprising 50 randomly selected dairy and sow herds, respectively. Each herd was visited once for the collection of faecal samples and registration of basic management parameters. Faecal samples were collected from three different age groups of animals, i.e. 5 sows/cows, 10 nursing piglets/calves less than 1 month, and 10 weaner pigs 8-45 kg/calves 1-12 months. The faecal samples were purified and the number of (oo)cysts quantified. The study revealed an age-specific herd prevalence of Cryptosporidium of 16, 31 and 100% for sows, piglets and weaners, respectively, and of 14, 96 and 84% for cows, young calves and older calves, respectively. For Giardia the age-specific herd prevalence was 18, 22 and 84% for the sows, piglets and weaners, while for cattle herds the prevalence was 60, 82 and 100% for cows, young calves and older calves, correspondingly. The (oo)cyst excretion levels varied considerably both within and between herds for all age groups. Risk factors were evaluated by using proportional odds models with (oo)cyst excretion levels divided into four categories as response. Among the numerous risk factors examined, only a few were demonstrated to have a statistically significant influence, e.g. the use of an empty period in the calf pen between introduction of calves for both parasites had a protective effect in young calves. For weaners, use of straw in the pen and high pressure cleaning between batches of weaners had a preventive effect against higher Cryptosporidium oocyst excretion levels.

General information
State: Published
Organisations: National Veterinary Institute, Department of Systems Biology, Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Maddox-Hyttel, C. (Intern), Langkjær, R. B. (Intern), Enemark, H. L. (Intern), Vigre, H. (Intern)
Pages: 48-59
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Parasitology
Volume: 141
Issue number: 1-2
ISSN (Print): 0304-4017
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.215 SJR 1.275 CiteScore 2.55
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.49 SJR 1.228 SNIP 1.218
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.21 SNIP 1.309 CiteScore 2.46
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.324 SNIP 1.42 CiteScore 2.53
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.262 SNIP 1.437 CiteScore 2.63
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.163 SNIP 1.439 CiteScore 2.6
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.233 SNIP 1.429 CiteScore 2.61
Cryptosporidium and Giardia infections are widespread in weaner pigs in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute, Department of Systems Biology, Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research
Authors: Vigre, H. (Intern), Maddox-Hyttel, C. (Intern), Langkjær, R. B. (Intern), Enemark, H. L. (Intern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 230030
Publication: Research - peer-review › Journal article – Annual report year: 2006

Cryptosporidium og Giardia I forskellige aldersgrupper af kvæg og svin I Danmark: forekomst, genotyper og risikofaktorer

General information
State: Published
Organisations: National Veterinary Institute, Division of Microbiology and Risk Assessment
Authors: Maddox-Hyttel, C. (Intern), Enemark, H. L. (Intern), Vigre, H. (Intern), Langkjær, R. B. (Ekstern)
Pages: 24-29
Publication date: 2006
Main Research Area: Technical/natural sciences
Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 89
Distinction between porcine circovirus type 2 enteritis and porcine proliferative enteropathy caused by Lawsonia intracellularis

The presence of porcine circovirus type 2 (PCV2) was studied immunohistochemically in formalin-fixed, paraffin wax-embedded samples of intestinal tissue from 80 pigs with a clinical history suggestive of Lawsonia intracellularis-associated diarrhoea. Histopathologically, enteritis of varying intensity was diagnosed in 64 of the pigs. Of these 64 animals, 34 (18%) were infected with both PCV2 and L. intracellularis. Of the remaining 30 cases of enteritis, 23 (77%) were attributed to PCV2 infection alone. The PCV2-associated enteritis cases showed necrotizing ileitis and colitis, indistinguishable macroscopically from proliferative enteritis (PE) due to L. intracellularis. Histopathologically, L. intracellularis-positive intestines showed adenomatous proliferation of crypt enterocytes, whereas PCV2 enteritis was characterized by histiocytosis of varying intensity, with PCV2-positive cells in the submucosa, lamina propria and crypt epithelium, as well as in the lymphoid tissue of the ileum and colon. Multinucleated giant cells, however, were seen in both infections. PCV2 was about three times more likely to be detected in L. intracellularis-negative than in L. intracellularis-positive samples (P <0.001). There was no association between PCV2 and other intestinal bacterial pathogens. The Study demonstrated that PCV2 enteritis should be borne in mind in the differential diagnosis of L. intracellularis infection in pigs aged 2-4 months with a clinical history of diarrhoea. (c) 2006 Elsevier Ltd. All rights reserved.

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Jensen, T. K. (Intern), Vigre, H. (Intern), Svensmark, B. (Ekstern), Bille-Hansen, V. (Intern)
Pages: 176-182
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Comparative Pathology
Volume: 135
Issue number: 4
ISSN (Print): 0021-9975
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.828 SJR 0.594 CiteScore 1.36
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.17 SJR 0.671 SNIP 0.697
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.698 SNIP 0.868 CiteScore 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.562 SNIP 0.773 CiteScore 1.17
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.635 SNIP 0.896 CiteScore 1.32
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.728 SNIP 1.047 CiteScore 1.57
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Effect of PMWS pig serum and PCV2 specific serum on mortality and weight gain in PMWS affected herds

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hassing, A. (Ekstern), Wachman, H. (Ekstern), Bækbo, P. (Ekstern), Bøtner, A. (Intern), Nielsen, J. (Ekstern), Vigre, H. (Intern), Feenstra, A. (Ekstern)
Number of pages: 157
Publication date: 2006

Host publication information
Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 19th International Pig Veterinary Congress, Copenhagen, Denmark, 16/07/2006 - 16/07/2006
Source: orbit
Source-ID: 241736
Publication: Research › Article in proceedings – Annual report year: 2006

Estimation of the national prevalence of PMWS using two different data sources

General information
State: Published
Organisations: National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research
Authors: Vigre, H. (Intern), Bækbo, P. (Ekstern), Jorsal, S. E. L. (Intern)
Publication date: 2006
Evaluation of a nested PCR test and bacterial culture of swabs from the nasal passages and from abscesses in relation to diagnosis of Streptococcus equi infection (strangles)

Reasons for performing study: Streptococcus equi is the cause of strangles in horses. To improve diagnostic sensitivity, development and evaluation of DNA-based methods are necessary. Objectives: To evaluate diagnostic methods and observe the pattern of bacterial shedding during natural outbreaks. Methods: Two herds with natural outbreaks of strangles were visited over a period of 15 weeks and 323 samples originating from 35 horses investigated. The diagnostic use of a nested PCR test was evaluated using a collection of 165 isolates of Lancefield group C streptococci (species specificity) and swabs from nasal passages or from abscesses from horses infected with S. equi (diagnostic sensitivity). Results: All 45 S. equi isolates tested positive in the nested PCR, whereas no amplicon was formed when testing the other 120 Lancefield group C isolates. A total of 43 samples were collected from 11 horses showing clinical signs of strangles during the study period. The diagnostic sensitivity for PCR test was 45% and 80% for samples from the nasal passages and abscesses, respectively; the corresponding diagnostic sensitivity for cultivation was 18% and 20%. The diagnostic sensitivity was significantly higher for PCR than for bacterial cultivation. Furthermore, the shedding of S. equi in 2 infected horse populations was evaluated. An intermittent shedding period of S. equi of up to 15 weeks was recorded in this part of the study. It was also shown that shedding of S. equi occurred both from horses with and without clinical signs.

Conclusions and potential relevance: The nested PCR test represents a species-specific and -sensitive method for diagnosis of S. equi from clinical samples. It may, however, be desirable in future to develop detection methods with high diagnostic sensitivity and specificity without the potential problems inherent in nested PCR.
Evaluation of the risk of spread of Echinococcus multilocularis from Denmark to Sweden: DFVF Risk Assessment Report

General information
State: Published
Organisations: National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Authors: Maddox-Hyttel, C. (Intern), Vigre, H. (Intern), Bødker, R. (Intern)
Publication date: 2006

Publication information
Volume: 55017-0005
Original language: English
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240703
Publication: Research › Report – Annual report year: 2006

Histopathologic findings in a case control study of PMWS in Danish pig herds

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Authors: Bille-Hansen, V. (Intern), Jorsal, S. E. L. (Intern), Vigre, H. (Intern), Larsen, L. E. (Intern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240803
Publication: Research › Conference abstract for conference – Annual report year: 2006
New swine influenza A H1N2 re-assortment found in Danish swine

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240801
Publication: Research › Conference abstract for conference – Annual report year: 2006

New swine influenza A H1N2 reassortment found in Danish swine

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2006
Event: Paper presented at 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240512
Publication: Research - peer-review › Paper – Annual report year: 2006

New swine influenza A H1N2 reassortment found in Danish swine

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Division of Microbiology and Risk Assessment, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Number of pages: 265
Publication date: 2006

Host publication information
Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 19th International Pig Veterinary Congress, Copenhagen, Denmark, 16/07/2006 - 16/07/2006
Source: orbit
Source-ID: 241727
Publication: Research › Article in proceedings – Annual report year: 2006

PMWS in Denmark: Epidemiology, diagnosis and control

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Virology, Section for Veterinary Epidemiology and public sector consultancy
Authors: Bøtner, A. (Intern), Vigre, H. (Intern), Jorsal, S. E. L. (Intern), Nielsen, J. (Intern), Lohse, L. (Intern), Bille-Hansen, V. (Intern), Larsen, L. E. (Intern), Baekbo, P. (Ekstern), Kristensen, C. S. (Ekstern), Nielsen, E. O. (Ekstern), Enøe, C. (Intern)
Publication date: 2006
PMWS in Denmark: Epidemiology, Diagnosis and Control: Merial White Book

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research
Authors: Bøtner, A. (Intern), Vigre, H. (Intern), Jorsal, S. E. L. (Intern), Nielsen, J. (Ekstern), Lohse, L. (Ekstern), Bille-Hansen, V. (Intern), Larsen, L. E. (Ekstern), Bækbo, P. (Ekstern)
Pages: 9-22
Publication date: 2006

PMWS - Laboratory Diagnosis on Herd and Pig Level in a Danish Case-Control Study

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy
Authors: Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Vigre, H. (Intern), Larsen, P. (Ekstern), Bøtner, A. (Intern), Nielsen, E. O. (Ekstern), Enøe, C. (Intern), Bækbo, P. (Ekstern)
Number of pages: 270
Publication date: 2006

PMWS-laboratory diagnosis on herd and pig level in a Danish case-study

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy
Authors: Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Vigre, H. (Intern), Larsen, P. B. (Ekstern), Bøtner, A. (Intern), Nielsen, E. O. (Ekstern), Enøe, C. (Intern), Bækbo, P. (Ekstern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241477
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2006
Risikovurdering gennemført af Danmarks Fødevareforskning vedr. effekten af at fjerne loftet på 500 dyreenheder pr. landbrugsejendom

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section of Poultry Diseases, Division of Poultry, Fish and Fur Animals, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Publication date: 2006

Publication information
Publisher: Danmarks Fødevareforskning
Original language: Danish
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240707
Publication: Research › Report – Annual report year: 2006

Sammenhæng mellem besætningsforhold og PMWS sygdomsudbrud – foreløbige resultater

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Okholm Nielsen, E. (Ekstern), Enøe, C. (Intern), Bækbo, P. (Ekstern), Vigre, H. (Intern), Jorsal, S. E. L. (Intern), Bøtner, A. (Intern)
Pages: 726
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Månedsbladet Svin
Original language: Danish
Source: orbit
Source-ID: 242217
Publication: Research › Journal article – Annual report year: 2006

Tetracycline consumption and occurrence of tetracycline resistance in Salmonella Typhimurium from Danish pigs

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Number of pages: 284
Publication date: 2006

Host publication information
Title of host publication: Proceedings of the 11th Symposium of the International Society for Veterinary Epidemiology and Economics, Cairns, Australia: ISVEE 11
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 238745
Publication: Research › Article in proceedings – Annual report year: 2006
Transmission of PMWS between pen mates

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy, Virology
Authors: Kristensen, C. (Ekstern), Bille-Hansen, V. (Intern), Vigre, H. (Intern), Betnser, A. (Intern), Bækbo, P. (Ekstern), Enøe, C. (Intern), Larsen, L. E. (Intern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240802
Publication: Research › Conference abstract for conference – Annual report year: 2006

Cryptosporidium and cryptosporidiosis in Denmark: current status

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Enemark, H. L. (Intern), Langkjaer, R. B. (Ekstern), Vigre, H. (Intern), Maddox-Hyttel, C. (Intern), Andersen, J. S. (Ekstern), Petersen, R. F. (Ekstern)
Pages: 193-198
Publication date: 2005
Main Research Area: Technical/natural sciences
Publication information
Journal: Parassitologia
Volume: 47
ISSN (Print): 0048-2951
Ratings:
Web of Science (2017): Indexed yes
Scopus rating (2013): SJR 0.111
ISI indexed (2013): ISI indexed no
Scopus rating (2012): SJR 0.142
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.357
ISI indexed (2011): ISI indexed no
Scopus rating (2010): SJR 0.314 SNIP 0.489
Scopus rating (2009): SJR 0.321 SNIP 0.553
Scopus rating (2008): SJR 0.341 SNIP 0.563
Scopus rating (2007): SJR 0.312 SNIP 0.56
Scopus rating (2006): SJR 0.318 SNIP 0.567
Scopus rating (2005): SJR 0.195 SNIP 0.316
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.288 SNIP 0.681
Scopus rating (2003): SJR 0.261 SNIP 0.521
Scopus rating (2002): SJR 0.811 SNIP 0.55
Scopus rating (2001): SJR 0.467 SNIP 0.371
Scopus rating (2000): SJR 0.12 SNIP 0.488
Scopus rating (1999): SJR 0.192 SNIP 0.635
Original language: English
Source: orbit
Source-ID: 239911
Publication: Research - peer-review › Journal article – Annual report year: 2005

Naturally acquired Lawsonia intracellularis infection in pigs studied from weaning to slaughter by indirect immunofluorescence antibody test and polymerase chain reaction on faeces
The course of naturally acquired Lawsonia intracellularis infection was studied in 41 pigs by testing blood and faeces samples collected four to seven times from before weaning to slaughter 5 months old. At slaughter, a sample of ileum was taken for histopathology. In the first sampling when the pigs were 2-4 weeks old maternally derived IgG against L. intracellularis was demonstrated by immunofluorescence antibody test in nine pigs whereas the bacterium was detected by PCR in faeces from six pigs. The maternally derived antibodies did not prevent pigs from becoming infected as seven pigs later on shed and/or were seropositive for L. intracellularis. The lowest prevalence of L. intracellularis was observed in 6-13 weeks old pigs and it seemed as though L. intracellularis in early infected pigs only activates a minor antibody response. At slaughter 66% of the pigs were found positive by immunofluorescence antibody test compared to 24% by immunohistochemistry on ileal samples. Thus, applied at the time of slaughter the antibody test appeared to be a highly sensitive ante-mortem diagnostic tool for identifying L. intracellularis exposed pigs with or without current proliferative enteropathy. (c) 2004 Elsevier Ltd. All rights reserved.

**General information**

State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Secretariat, Management
Authors: Jensen, T. K. (Intern), Vigre, H. (Intern), Sørensen, V. (Intern), Møller, K. (Intern)
Pages: 93-98
Publication date: 2005
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Research in Veterinary Science
Volume: 79
Issue number: 2
ISSN (Print): 0034-5288
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 1.82 SJR 0.593 SNIP 0.941
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 0.646 SNIP 0.779 CiteScore 1.46
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.774 SNIP 0.933 CiteScore 1.57
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.687 SNIP 0.887 CiteScore 1.58
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.691 SNIP 0.945 CiteScore 1.62
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.633 SNIP 1.067 CiteScore 1.63
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.726 SNIP 1.054 CiteScore 1.65
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.631 SNIP 0.98
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.609 SNIP 1.009
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.569 SNIP 0.941
Porcine Circovirus Type 2 Enteritis is an Important Differential Diagnosis to Porcine Proliferative Enteropathy caused by Lawsonia Intracellularis

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Virology
Authors: Jensen, T. K. (Intern), Vigre, H. (Intern), Svensmark, B. (Ekstern), Larsen, L. E. (Intern), Bille-Hansen, V. (Intern)
Publication date: 2005
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241475
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2005

Revideret PMWS diagnostik

General information
State: Published
Organisations: National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Authors: Larsen, P. B. (Ekstern), Vigre, H. (Intern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Hassing, A. (Ekstern), Enøe, C. (Intern)
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: DVT
Volume: 8
Original language: Danish
Source: orbit
Source-ID: 241775
Publication: Research › Journal article – Annual report year: 2005

Sammenhæng mellem besætningsforhold og PMWS sygdomsudbrud – foreløbige resultater

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Sektion for Eksotiske Virussygdomme, Division of Virology
Spatial and temporal patterns of pig herds diagnosed with Postweaning Multisystemic Wasting Syndrome (PMWS) during the first two years of its occurrence in Denmark

The clinical syndrome Postweaning Multisystemic Wasting Syndrome (PMWS) in pigs has emerged globally during the last decade. In October 2001, the first pig herd diagnosed with PMWS was reported in Denmark, and since then the number of herds diagnosed with PMWS has increased markedly. The etiology of PMWS is not well understood, but increased knowledge of the causal factors is prerequisite for applying preventive interventions. In this study we described the temporal (time of diagnosis), spatial (location of herds) and spatio-temporal pattern of Danish pig herds diagnosed with PMWS during the first two years after the first herd was diagnosed, and we tested for spatial and spatio-temporal clustering using scan statistics. The study population consisted of pig herds that during the study period (October 2001 - September 2003) performed diagnostic submissions to the two major veterinary diagnostic laboratories in Denmark (6724 herds). Of these, 277 herds were diagnosed with PMWS. Two statistically significant spatial clusters of herds diagnosed with PMWS were identified. These clusters included 11% and 8% of the study herds, respectively. Within these two clusters the relative risk for a herd to be diagnosed with PMWS was twice as high as expected. One statistically significant spatio-temporal cluster was identified between February and May 2002. We discuss different hypotheses that could explain why pig herds diagnosed with PMWS were clustered both spatially and spatio-temporally, and conclude that the results support the hypothesis that PMWS is caused by introduction of a new, unidentified, pathogen into the Danish pig production. (c) 2005 Elsevier B.V. All rights reserved.
Behandling med serum i PMWS besætninger

**General information**

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hassing, A. (Ekstern), Bækbo, P. (Ekstern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Wachmann, H. (Ekstern), Vigre, H. (Intern)
Publication date: 2004
Main Research Area: Technical/natural sciences
Behandling med serum i PMWS besætninger

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hassing, A. (Ekstern), Bækbo, P. (Ekstern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Wachmann, H. (Ekstern), Vigre, H. (Intern)
Pages: 675
Publication date: 2004

Diarrhoea, enteritis and unthrifty pigs: Lawsonia Intracellularis or porcine circovirus type 2 infection

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Jensen, T. K. (Intern), Vigre, H. (Intern), Svensmark, B. (Ekstern), Bille-Hansen, V. (Intern)
Number of pages: 326
Publication date: 2004

Host publication information
Title of host publication: Proceedings 18th IPVS Congress
Place of publication: Hamburg
Main Research Area: Technical/natural sciences
Conference: 18th International Pig Veterinary Society Congress, Hamburg, Germany, 27/06/2004 - 27/06/2004
Source: orbit
Source-ID: 240681
Publication: Research › Article in proceedings – Annual report year: 2004

Effects of the termination of antibiotic growth promoters use on antimicrobial resistance in pig farms: Macrolide-resistance among enterococci in finishers

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Vigre, H. (Intern)
Number of pages: 199
Pages: 29-34
Publication date: 2004

Host publication information
Title of host publication: DIAS report : Working papers from the international symposium: Beyond Antimicrobial Growth Promoters in Food Animal Production
Publisher: Ministry of Food, Agriculture and Fisheries, Danish Institute of Agricultural Sciences
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 244200
Intra-unit correlations in seroconversion to Actinobacillus pleuropneumoniae and Mycoplasma hyopneumoniae at different levels in Danish multi-site pig production facilities

In this paper, multilevel logistic models which take into account the multilevel structure of multi-site pig production were used to estimate the variances between pigs produced in Danish multi-site pig production facilities regarding seroconversion to Actinobacillus pleuropneumoniae serotype 2 (Ap2) and Mycoplasma hyopneumoniae (Mh). Based on the estimated variances, three newly described computational methods (model linearisation, simulation and linear modelling) and the standard method (latent-variable approach) were used to estimate the correlations (intra-class correlation components, ICCs) between pigs in the same production unit regarding seroconversion. Substantially different values of ICCs were obtained from the four methods. However, ICCs obtained by the simulation and the model linearisation were quite consistent. Data used for estimation were collected from 1161 pigs from 429 litters reared in 36 batches at six Danish multi-site farms chronically infected with the agents. At the farms, weaning age was 3-4.5 weeks, after which batches of pigs were reared using all-in/all-out management by room. Blood samples were collected shortly before: weaning, transfer from weaning-site to finishing-site, and sending the first pigs in the batch for slaughter (third sampling). Few pigs seroconverted at the weaning-sites, whereas considerable variation in seroconversion was observed at the finishing-sites. Multilevel logistic models (initially including four levels: farm, batch, litter, pig) were used to decompose the variation in seroconversion at the finishing-site. However, there was essentially no clustering at the litter level-leading to the use of three-level models. In the case of Ap2, clustering within batch was so high that the data eventually were reduced to two levels (farm, batch). For seroconversion to Ap2, ICC between pigs within batches was similar to90%, whereas the ICC between pigs within batches for Mh was similar to40%. This indicates that the possibility for Mh to spread between pigs within batches is lower than for Ap2. The diversity in seroconversion between batches within the same farm was large for Ap2 (ICC similar to 10%), whereas there was a relative strongly ICC (similar to50%) between batches for Mh. This indicates that the transmission of Mh is more consistent within a farm, whereas the presence of Ap2 varies between batches within a farm.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Vigre, H. (Intern), Dohoo, I. (Ekstern), Stryhn, H. (Ekstern), Busch, M. (Ekstern)
Pages: 9-28
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 63
Issue number: 1-2
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.26 SJR 1.144 SNIP 1.31
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
Molecular typing of Cryptosporidium and Giardia in Danish cattle and pig herds

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Department of Systems Biology, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Enemark, H. L. (Intern), Langkjær, R. B. (Intern), Vigre, H. (Intern), Maddox-Hyttel, C. (Intern)
Publication date: 2004
Event: Abstract from The 1st International Giardia and Cryptosporidium Conference, Amsterdam, Netherlands.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 229624
Publication: Research › Conference abstract for conference – Annual report year: 2004
Cryptosporidium parvum: infectivity and pathogenicity of the 'porcine' genotype

Genetic studies have demonstrated profound differences between the 'porcine' genotype of Cryptosporidium parvum, versus 'human' and 'bovine' genotypes. The study analysed infectivity and pathogenicity of the 'porcine' genotype (CPP-13 isolate) of C. parvum, and compared the results with published data on the 'bovine' genotype (CPB-0 isolate). This was investigated in calves and piglets from commercial herds. Piglets were mildly affected by the CPP-13 isolate, contrary to piglets infected with the CPB-0 isolate, which caused diarrhoea of a mean duration of 3.5 days. CPP-13 produced no or very mild clinical signs in piglets despite the excretion of high numbers of oocysts. Concomitant infection with rotavirus, however, caused a dramatic aggravation of the clinical signs, and 5 of 6 experimentally infected piglets died. CPP-13 appeared to be adapted to porcine hosts as illustrated by the lack of infectivity to 1 experimentally inoculated calf, and the absence of clinical signs, the long pre-patent period (15 days), and the excretion of very low numbers of oocysts following experimental infection of another calf. Thus, in accordance with other molecular studies, our results support the genetic evidence for the existence of a new species of Cryptosporidium adapted to pigs.
Decay of acquired colostral antibodies to Actinobacillus pleuropneumoniae in pigs

The main objective of this study was to estimate the decay of acquired colostral antibodies to Actinobacillus pleuropneumoniae serotype 2 in pigs. Data were obtained from pigs in an isolated cohort of 47 pigs born to five sows seropositive to A. pleuropneumoniae serotype 2. The pigs were examined serologically at 18 different times from birth until an age of about 22 weeks, using an A. pleuropneumoniae serotype 2-specific blocking enzyme-linked immunosorbent assay. Antibody concentration was expressed as an OD% derived from the optical density of the sample and the median from eight wells without serum on the same plate. A non-linear mixed model assuming a constant rate of decay (half-life)
was specified and fitted to the serological data. To estimate the between-pig variability of different components, between-pig random effects of each component of the model were estimated. The estimated average half-life of acquired colostral antibodies was approximately 2 weeks, but there was a considerable variation between pigs (half-life ranged from 1-3 weeks). The duration until acquired colostral antibodies were no longer detectable ranged from 2 weeks to 2 months postpartum among the pigs in the study, mainly depending on the initial level of acquired colostral antibodies to A. pleuropneumoniae serotype 2.

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Secretariat, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Department of Informatics and Mathematical Modeling
Authors: Vigre, H. (Intern), Sørensen, V. (Intern), Ersbøll, A. K. (Intern)
Pages: 430-435
Publication date: 2003
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Journal of Veterinary Medicine Series B-Infectious Diseases and Veterinary Public Health
Volume: 50
Issue number: 9
ISSN (Print): 0931-1793
Ratings: BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Original language: English
DOIs: 10.1046/j.0931-1793.2003.00700.x
Source: orbit
Source-ID: 229705
Publication: Research - peer-review › Journal article – Annual report year: 2003

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Pathogenicity of Cryptosporidium parvum - evaluation of an animal infection model
With the intention of developing a standardised method for assessment of pathogenicity of Cryptosporidium parvum, the CPB-0 isolate was studied by propagation in 1-day-old calves followed by inoculation into specific pathogen free (SPF) piglets. The experiment was repeated. Diarrhoea and shedding of oocysts were seen in all animals infected with the CPB-0 isolate. Clinical signs included depression, inappetence, vomiting (exclusively in the piglets), and death. Histological examination at 17 and 19 days post-infection revealed parasitic stages and microscopic changes primarily restricted to colon and rectum. The unintended presence of rotavirus in some of the experimental animals revealed an additive or
synergistic effect between rotavirus and C. parvum as indicated by prolonged diarrhoea, increased oocyst shedding, decreased weight gain and elevated levels of serum haptoglobin and serum amyloid A (SAA) in piglets infected simultaneously with both pathogens. The difference in daily weight gain between infected and control animals was significant only for piglets co-infected with rotavirus. The acute phase response of haptoglobin and SAA was characterised by a large individual variation. In piglets, co-infected with rotavirus, the levels of serum haptoglobin were 3.5 and 4.6 times higher in the infected versus the controls 6 and 9 dpi, respectively (mean values: 2411 mug/ml +/- S.D. 2023 and 1840 mug/ml +/- S.D. 1697). In the controls infected with rotavirus, peak haptoglobin concentration was seen 3 dpi (mean: 1022 mug/ml +/- S.D. 425). Elevated levels of SAA were seen in 1 of 6 piglets infected with C. parvum, and in 5 of 6 piglets co-infected with rotavirus. Tumour necrosis factor alpha (TNFalpha) was undetectable in all serum samples from piglets. The obvious advantages of the SPF pig model are the naturally acquired intestinal microflora, the development of distinct clinical signs similar to cryptosporidiosis in humans and calves, the size of the animals, and the accessibility of individuals born within a short time span. This makes the model ideal for dose-response studies, evaluation of therapeutic agents as well as for assessment of differences in the clinical response to isolates of diverse genetic background. In conclusion, it was shown that the CPB-0 isolate was pathogenic to calves and piglets at a dose of 2.5 x 10^5 oocysts, and that the clinical signs could be replicated during separate experiments. Moreover, diarrhoea, oocyst shedding, body weight changes, histological alterations, and the acute phase response of haptoglobin and SAA were identified as useful parameters for discrimination of isolate-specific differences of pathogenicity.

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Section for Veterinary Epidemiology and public sector consultancy, Innate Immunology
Authors: Enemark, H. L. (Intern), Bille-Hansen, V. (Intern), Lind, P. (Intern), Heegaard, P. M. H. (Intern), Vigre, H. (Intern), Ahrens, P. (Intern), Thamsborg, S. (Ekstern)
Pages: 35-57
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Parasitology
Volume: 113
Issue number: 1
ISSN (Print): 0304-4017
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.215 SJR 1.275 CiteScore 2.55
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.49 SJR 1.228 SNIP 1.218
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.21 SNIP 1.309 CiteScore 2.46
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.324 SNIP 1.42 CiteScore 2.53
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.262 SNIP 1.437 CiteScore 2.63
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.163 SNIP 1.439 CiteScore 2.6
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.233 SNIP 1.429 CiteScore 2.61
ISI indexed (2011): ISI indexed yes
Sundhed og produktion hos svin i multisitesystemer

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Secretariat, Division of Veterinary Diagnostics and Research
Authors: Busch, M. E. (Ekstern), Vigre, H. (Intern), Lohse, L. (Intern), Jensen, T. (Ekstern), Bækbo, P. (Ekstern), Bøtner, A. (Intern), Nielsen, J. (Intern), Nielsen, J. P. (Ekstern), Sørensen, V. (Intern)
Pages: 28-34
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 86
Issue number: 13
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
Crypto Infektion med Eimeria-arter hos kalve: Vurdering af risikofaktorer og sammenhæng mellem diarré og oocysteudskillelse

General information
State: Published
Organisations: National Veterinary Institute
Authors: Autzen, S. (Ekstern), Maddox-Hyttele, C. (Intern), Vigre, H. (Intern), Monrad, J. (Ekstern)
Pages: 6-10
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 85
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 240271
Publication: Research - peer-review › Journal article – Annual report year: 2003

Frequency of health problems in Danish Standardbred trotters and identification of time-dependent and time-independent covariates associated with the occurrence of lameness

General information
State: Published
Organisations: National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Vigre, H. (Intern), Chriél, M. (Intern), Hesselholt, M. (Ekstern), Falk-Rønne, J. (Ekstern), Kjær-Ersbøll, A. (Ekstern)
Pages: 105-117
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 56
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.26 SJR 1.144 SNIP 1.31
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Risk factors for the hazard of lameness in Danish Standardbred trotters

A follow-up study focusing on health problems interfering with optimal training of Danish Standardbred trotters was conducted with the participation of seven professional trainers. Our aim was to estimate the incidence of health problems that cause interruptions of optimal training, and to identify associations between the hazard of lameness and selected risk factors. The study population was dynamic and contained data of 265 Standardbred trotters monitored during 5 months in
The horses were greater than or equal to 2 years old. Optimal training was defined as when the horse followed scheduled training including fast-speed trotting. Interruption of optimal training could only be caused by health problems and castration. A total of 123 new events of interruption of optimal training caused by health problems were reported. Lameness (injury located to joints and tendons) was the most-frequent cause of interruption of optimal training: 84 events in 69 horses (0.09 events per horse-month). Respiratory diseases (16 events) and muscular problems (seven events) were the second and third most-frequent causes of interrupted training. The effects of trainer, gender, age-group, time with a trainer, participation in races and current month on the hazard of lameness were estimated in a multivariable Cox proportional-hazard model. The effects of trainer, gender and age-group were modelled as time-independent. The effects of time with a trainer, participation in races and the current month were modelled as time-dependent variables. Trainer affected the hazard of lameness. Geldings had higher hazard than mares, as did 3-year olds (compared to >4-year olds). Compared to the period where horses had been trained by the same trainer for >3 months, horses in the period 1.5-2.5 months after they had entered the training regime had higher risk of lameness (hazard ratio: 3.2; 95% CI: 1.1-9.9). Participation in races increased the hazard of lameness significantly in the 5 days after a races. 

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Vigre, H. (Intern), Chriel, M. (Ekstern), Hesselholt, M. (Ekstern), Falk-Ronne, J. (Ekstern), Ersboll, A. K. (Ekstern)
Pages: 105-117
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 56
Issue number: 2
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.26 SJR 1.144 SNIP 1.31
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Transmission of Actinobacillus pleuropneumoniae in pigs under field-like conditions: emphasis on tonsillar colonisation and passively acquired colostral antibodies

The objectives of this study were to elucidate at which age tonsillar colonisation by Actinobacillus pleuropneumoniae occurs in pigs and relate this occurrence to the presence of colostral antibodies to A. pleuropneumoniae. The infection patterns were studied in an isolated cohort of pigs, which consisted of the offspring from five sows originating from a conventional pig herd. The sows were transferred to isolated research facilities before farrowing. A. pleuropneumoniae was detected on the tonsils of all sows. After a nursing period of 3 weeks, the pigs were weaned and reared isolated from other pigs until slaughter. The pigs were examined repeatedly for the presence of A. pleuropneumoniae on the tonsils and for antibodies to A. pleuropneumoniae using bacteriological and serological techniques, respectively. A. pleuropneumoniae was detected in the tonsils of one pig as early as 11 days after birth, showing that A. pleuropneumoniae can be transmitted from sow to offspring during a 3-week nursing period. The cumulative proportion of pigs carrying A. pleuropneumoniae in their tonsils increased significantly between the age of 4-12 weeks. This age period corresponded to the age at which the proportion of pigs with detectable levels of colostral antibodies to the different serotypes of A. pleuropneumoniae was declining. Since these two events take place in the same age period, we expect a possible biological association between the level of the passive immunity and the degree of tonsillar colonisation. The median duration of tonsillar colonisation was estimated to approximately 7-8 weeks. (C) 2002 Elsevier Science B.V All rights reserved.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Vigre, H. (Intern), Angen, Ø. (Intern), Barfod, K. (Ekstern), Lavritsen, D. T. (Ekstern), Sørensen, V. (Ekstern)
Pages: 151-159
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 89
Issue number: 2-3
ISSN (Print): 0378-1135
Ratings:
Transmission of infection with Actinobacillus pleuropneumoniae and Mycoplasma hyopneumoniae in Danish multi-site pig production

General information
State: Published
Organisations: University of Copenhagen
Authors: Vigre, H. (Intern)
Publication date: 2002

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 243328
Publication: Research › Ph.D. thesis – Annual report year: 2002

Respiratory diseases in Danish multi-site systems

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Veterinary Institute
Authors: Busch, M. (Ekstern), Bækbo, P. (Ekstern), Pedersen, B. K. (Ekstern), Sørensen, V. (Ekstern), Vigre, H. (Intern)
Publication date: 2000

Host publication information
Title of host publication: 16th. Congress of the International Pig Veterinary Society
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 244202
Publication: Research › Article in proceedings – Annual report year: 2000

Respiratory diseases in Danish multi-site systems

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Secretariat, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Busch, M. E. (Ekstern), Bækbo, P. (Ekstern), Pedersen, B. K. (Ekstern), Vigre, H. (Intern), Sørensen, V. (Intern)
Publication date: 2000

Host publication information
Title of host publication: Proceedings of the 16th International Pig Veterinary Society Congress
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240235
Publication: Research - peer-review › Article in proceedings – Annual report year: 2000

Sundhed i multisite-systemer

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Busch, M. E. (Ekstern), Vigre, H. (Intern), Lohse, L. (Intern)
Publication date: 2000
Survival analysis of time-dependent covariates associated with the occurrence of lameness among Danish Standardbreed trotters

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Veterinary Institute, National Food Institute
Authors: Vigre, H. (Intern), Chriél, M. (Intern), Hesselholt, M. (Ekstern), Falk-Rønne, J. (Ekstern), Ersbøll, A. (Ekstern)
Publication date: 2000

Host publication information
Title of host publication: 9th Symposium of the International Society for Veterinary Epidemiology and Economics
Main Research Area: Technical/natural sciences
Conference: 9th Symposium of the International Society for Veterinary Epidemiology and Economics, Breckenridge, CO, United States, 06/08/2000 - 06/08/2000
Source: orbit
Source-ID: 244201
Publication: Research › Article in proceedings – Annual report year: 2000

Transfer of pathogens from sows to offspring

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Management, Secretariat
Authors: Lavritsen, D. T. (Ekstern), Angen, Ø. (Intern), Barfod, K. (Intern), Bøtner, A. (Intern), Lohse, L. (Intern), Møller, K. (Intern), Nielsen, J. (Intern), Sørensen, V. (Intern), Vigre, H. (Intern)
Publication date: 2000

Host publication information
Title of host publication: Proceedings of the 16th International Pig Veterinary Society Congress
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240230
Publication: Research - peer-review › Article in proceedings – Annual report year: 2000

Transfer of pathogens from sows to offspring

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Secretariat
Authors: Lavritsen, D. T. (Ekstern), Angen, Ø. (Intern), Barfod, K. (Intern), Bøtner, A. (Intern), Lohse, L. (Intern), Møller, K. (Ekstern), Nielsen, J. (Ekstern), Sørensen, V. (Intern), Vigre, H. (Intern)
Publication date: 2000
Event: Abstract from 16th International Pig Veterinary Society Congress, Melbourne, Australia.
Projects:

**Air-sampling: A Low-Cost Screening Tool in Biosecured Broiler Production**

National Food Institute  
Period: 01/01/2018 → 31/12/2020  
Number of participants: 3  
Phd Student: Christensen, Julia (Intern)  
Supervisor: Vigre, Håkan (Intern)  
Main Supervisor: Hoorfar, Jeffrey (Intern)

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Anden EU-finansiering  
Project: PhD

**Evaluate and Establish Surveillance program of Salmonella in Imported and domestic Poultry Meat in Jordan**

National Food Institute  
Period: 15/02/2017 → 14/02/2020  
Number of participants: 3  
Phd Student: Hantash, Tariq (Ekstern)  
Supervisor: Alali, Walid (Ekstern)  
Main Supervisor: Vigre, Håkan (Intern)

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Ansat eksternt  
Project: PhD

**Evaluate and Establish Surveillance program of Salmonella in Imported and domestic Poultry Meat in Jordan**

National Food Institute  
Period: 15/02/2017 → 14/05/2019  
Number of participants: 3  
Phd Student: Hantash, Tariq (Ekstern)  
Supervisor: Alali, Walid (Ekstern)  
Main Supervisor: Vigre, Håkan (Intern)

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Ansat eksternt  
Project: PhD

**Generic open science data platform for surveillance, exposure assessment and risk analysis**

National Food Institute
Period: 01/12/2016 → 10/02/2020
Number of participants: 5
Phd Student:
Backhaus, Liv Louise Victoria (Intern)
Supervisor:
Lund, Ole (Intern)
Pamp, Sünje Johanna (Intern)
Vigre, Håkan (Intern)
Main Supervisor:
Aarestrup, Frank Møller (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD

Ecology and Epidemiology of Pathogens and Antimicrobial Resistance
National Food Institute
Period: 01/11/2015 → 31/03/2018
Number of participants: 4
Phd Student:
Wimmer, Bettina (Intern)
Supervisor:
Aarestrup, Frank Møller (Intern)
Pamp, Sünje Johanna (Intern)
Main Supervisor:
Vigre, Håkan (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD

Veterinary Epidemiology - biological models of vector borne diseases
National Veterinary Institute
Period: 15/02/2015 → 13/08/2018
Number of participants: 7
Phd Student:
Haider, Najmul (Intern)
Supervisor:
Kjær, Lene Jung (Intern)
Toft, Nils (Intern)
Main Supervisor:
Bødker, Rene (Intern)
Examiner:
Vigre, Håkan (Intern)
Lindström, Anders (Ekstern)
Mortensen, Sten (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Offentlig finansiering
Project: PhD

Genomic antimicrobial resistance, prediction of functionality, resistance gene mobility and zoonotic relevance
National Food Institute
Period: 15/12/2013 → 16/05/2018
Number of participants: 7
The epidemiology of zoonotic antimicrobial resistance in animal production

National Food Institute
Period: 15/10/2013 → 15/08/2018
Number of participants: 7
Phd Student:
Dalhoff Andersen, Vibe (Intern)
Supervisor:
Agerse, Yvonne (Intern)
de Knecht, Leonardo (Intern)
Main Supervisor:
Vigre, Håkan (Intern)
Examiner:
Hald, Tine (Intern)
Dalsgaard, Anders (Ekstern)
Emanuelson, Ulf (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD

Pathogen detection: On-site diagnostics with focus on pre-analytical engineering

National Food Institute
Period: 01/03/2012 → 15/12/2015
Number of participants: 8
Phd Student:
Fachmann, Mette Sofie Rousing (Intern)
Supervisor:
Josefsen, Mathilde Hasseldam (Intern)
Löfström, Charlotta (Intern)
Pedersen, Karl (Intern)
Main Supervisor:
Hoorfar, Jeffrey (Intern)
Examiner:
Vigre, Håkan (Intern)
Knutsson, Rickard (Ekstern)
Mathiasen, Thomas Erik (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Development of a decision tool for vaccination against Campylobacter in poultry

National Food Institute
Period: 15/08/2010 → 29/01/2014
Number of participants: 7
Phd Student: Garcia Clavero, Ana Belén (Intern)
Supervisor: Christensen, Laurids Siig (Intern)
Madsen, Anders Læsø (Ekstern)
Main Supervisor: Vigre, Håkan (Intern)
Examiner: Pedersen, Karl (Intern)
Pielaat, Annemarie (Ekstern)
Rådström, Gunde Peter (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Forskningsrådsfinansiering
Project: PhD

Molecular Diagnostics of Foodborne Pathogens

National Food Institute
Period: 01/05/2010 → 18/09/2013
Number of participants: 8
Phd Student: Hansen, Trine (Intern)
Supervisor: Löfström, Charlotta (Intern)
Riber, Leise (Intern)
Vigre, Håkan (Intern)
Main Supervisor: Hoorfar, Jeffrey (Intern)
Examiner: Pedersen, Karl (Intern)
Rudi, Knut (Ekstern)
Schelin, Jenny Regina (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Anden EU-finansiering
Project: PhD

CamVac: Campylobacter vaccination of poultry
The main objective of this project is to develop a cost-effective vaccination strategy for the poultry production, hereby reducing the colonization of Campylobacter in both parental and broiler flocks. Vaccination is one of the few measures that can be applied to reduce the colonization of Campylobacter in free range organic poultry. The project aims to identify a vaccination strategy based on reduction, since risk assessment studies have shown that a 2 log reduction of colonization in poultry can reduce the risk of human infection by 30 times.

National Food Institute
Division of Food Microbiology
Division of Epidemiology and Microbial Genomics
National Veterinary Institute
TD Vaccines

University of Copenhagen

Utrecht University

University of Arizona

Hugin Expert

**Period:** 01/03/2010 → 31/12/2014

**Number of participants:** 18

Campylobacter, vaccination

**Acronym:** CamVac

**Project participant:**

- Bang-Berthelsen, Iben (Intern)
- Christensen, Laurids Siig (Intern)
- Josefsen, Mathilde Hasseldam (Intern)
- Vigre, Hákan (Intern)
- Garcia Clavero, Ana Belén (Intern)
- Saunders, Ingelise (Ekstern)
- Darsley, Mike (Ekstern)
- Lund, Mogens (Ekstern)
- Sandøe, Peter (Ekstern)
- Cooper, Kerry (Ekstern)
- Madsen, Anders (Ekstern)
- Hald, Birthe (Intern)
- Bahndorff, Simon (Intern)
- Heegaard, Peter Mikael Helweg (Intern)

**Project Manager, organisational:**

- Madsen, Mogens (Ekstern)
- Wagenaar, Jaap (Ekstern)
- Joens, Lynn (Ekstern)

**Project Coordinator:**

- Hoorfar, Jeffrey (Intern)

**Relations**

**Related projects:**

CamCon: Campylobactoer control - Novel approaches in primary poultry production

Publications:

- Low-cost monitoring of campylobacter in poultry houses by air sampling and quantitative PCR.
- Design and data analysis of experimental trials to test vaccine candidates against zoonotic pathogens in animals: the case of a clinical trial against campylobacter in broilers
- Intestinal colonization of broiler chickens by Campylobacter spp. in an experimental infection study
- Direct Quantification of Campylobacter jejuni in Chicken Fecal Samples Using Real-Time PCR: Evaluation of Six Rapid DNA Extraction Methods
- Integration of Epidemiological Evidence in a Decision Support Model for the Control of Campylobacter in Poultry Production
- Towards a best practice for Campylobacter prevention at farm and house level
- The use of probabilistic graphical models (PGMs) to develop a cost-effective vaccination strategy against Campylobacter in poultry
- Quantitative microbiological data analysis of a Campylobacter vaccination trial
- Campylobacter vaccination of poultry: Clinical trials, quantitative microbiological methods and decision support tools for the control of Campylobacter in poultry
- Estimation of the variation that can be attributed to different levels in a clinical trial of a vaccine against Campylobacter in broilers
- Estimation of the variation that can be attributed to different levels in a clinical trial of a vaccine
The interpretation of quantitative microbiology data: meeting the demands of quantitative microbiological risk assessment

National Food Institute
Period: 01/03/2010 → 18/09/2013
Number of participants: 7
Phd Student: Ribeiro Duarte, Ana Sofia (Intern)
Supervisor: Aabo, Søren (Intern)
Vigre, Håkan (Intern)
Main Supervisor: Nauta, Maarten (Intern)
Examiner: Dalggaard, Paw (Intern)
Evers, Eric (Ekstern)
Nørung, Birgit (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: 1/3 FUU, 1/3 inst 1/3 Andet
Project: PhD

Dyrevelfærd i husdyrbesætninger: Et samspil mellem husdyrbruger og myndigheder

Section for Veterinary Epidemiology and public sector consultancy
Division of Veterinary Diagnostics and Research
National Veterinary Institute
FoodDTU
Aarhus University
University of Copenhagen
Period: 01/01/2009 → 31/12/2012
Number of participants: 13
Project ID: 22377
Project participant: Vaarst, Mette (Ekstern)
Nielsen, Tine Rousing (Ekstern)
Bonde, Marianne (Ekstern)
Thomsen, Peter T. (Ekstern)
Ersbøll, Annette Kjær (Ekstern)
Christensen, Tove (Ekstern)
Jensen, Karsten Klint (Ekstern)
Mørkbak, Morten (Ekstern)
Vigre, Håkan (Intern)
Project Manager, organisational: Sørensen, Jan Tind (Ekstern)
Houe, Hans (Ekstern)
Sandøe, Peter (Ekstern)
Enæe, Claes (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 1,051,000.00 Danish Kroner
Project
The interaction between drug use and the risk of infection with foodborne zoonotic bacteria

National Food Institute
Period: 01/01/2009 → 26/02/2014
Number of participants: 6
Phd Student:
Koningstein, Maike (Intern)
Supervisor:
Mølbak, Kåre (Ekstern)
Main Supervisor:
Hald, Tine (Intern)
Examiner:
Vigre, Håkan (Intern)
Emborg, Hanne-Dorthe (Intern)
Engberg, Jørgen H. (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Ansat eksternt
Project: PhD

Evaluation and optimisation of surveillance programmes for antimicrobial resistance and drug use
The overall objective of the project is to provide a quantitative risk assessment of the relationship between consumption of antimicrobials in food animals and the occurrence of antimicrobial resistant bacteria in animals and foods including their potential adverse health effects in humans. The assessment is expected to provide the scientific basis for future recommendations, partly in order to optimize the existing surveillance for antibiotic resistance (DANMAP), and partly in order to develop guidelines regarding antimicrobial consumption and management of specific risk factors in the primary production. The project focuses on the development of resistance to antimicrobial (cephalosporins, macrolides and quinolones), which is critically important for human therapy, for example, persons having a foodborne infection with Salmonella or Campylobacter. The project is a pilot study of transfer of resistance determinants through the food-production chain.

Division of Microbiology and Risk Assessment
National Food Institute
Period: 01/10/2008 → 30/11/2011
Number of participants: 5
Project participant:
Struve, Tina (Intern)
Aarestrup, Frank Møller (Intern)
Emborg, Hanne-Dorthe (Intern)
Vigre, Håkan (Intern)
Project Manager, organisational:
Hald, Tine (Intern)

Evaluation and optimisation of surveillance programmes for antimicrobial resistance and drug use
The overall objective of the project is to provide a quantitative risk assessment of the relationship between consumption of antimicrobials in food animals and the occurrence of antimicrobial resistant bacteria in animals and foods including their potential adverse health effects in humans. The assessment is expected to provide the scientific basis for future recommendations, partly in order to optimize the existing surveillance for antibiotic resistance (DANMAP), and partly in order to develop guidelines regarding antimicrobial consumption and management of specific risk factors in the primary production. The project focuses on the development of resistance to antimicrobial (cephalosporins, macrolides and quinolones), which is critically important for human therapy, for example, persons having a foodborne infection with Salmonella or Campylobacter. The project is a pilot study of transfer of resistance determinants through the food-production chain.

Division of Microbiology and Risk Assessment
National Food Institute
EFSA Quantitative Microbiological Risk Assessment on Salmonella in Slaughter and Breeder pigs
In this project we developed a generic Quantitative Microbiological Risk Assessment (QMRA) on Salmonella in slaughter and breeder pigs that could be used in all EU states. The aims of the QMRA were to assess the expected reduction of Salmonella cases in humans in EU countries by different interventions at different points of the food chain. In order to facilitate the investigation of interventions at different points of the food chain, a farm-to-consumption framework was adopted, so that we could model the prevalence of infection / contamination and the microbial load from the farm to the point of consumption of different pork products. The probability of illness could then be estimated by applying a dose-response model using the estimated amount of Salmonella bacteria ingested at consumption as an input.
Division of Microbiology and Risk Assessment
National Food Institute
Veterinary Laboratories Agency
National Institute of Public Health and the Environment
Period: 01/01/2008 → 02/03/2010
Number of participants: 10
Project participant:
Nauta, Maarten (Intern)
Coutinho Calado Domingues, Ana Rita (Intern)
Vigre, Håkan (Intern)
Hill, Andrew (Ekstern)
Simons, Robin (Ekstern)
Tanton, Jane (Ekstern)
Denman, Sarah (Ekstern)
Swart, Arno (Ekstern)
Evers, Eric (Ekstern)
Project Manager, organisational:
Hald, Tine (Intern)
Project

Activities:

TEACH FOOD - Developing a teacher's community of practice
Period: 23 May 2017 → 24 May 2017
Lene Duedahl-Olesen (Speaker)
Håkan Vigre (Other)
Lars Bøge Jensen (Other)
Pernille Hammar Andersson (Other)
National Food Institute
Research Group for Analytical Food Chemistry
Research Group for Genomic Epidemiology
Research Group for Microbial Food Safety
Office for Study Programmes and Student Affairs
Description
Oral Presentation and paper
Degree of recognition: International

Documents:
TEACH FOOD abstract

Related event

ETALEE 2017: Exploring Teaching for Active Learning in Engineering Education 2017
23/05/2017 → 24/05/2017
Odense, Denmark
Activity: Talks and presentations › Conference presentations

Owusu Amponsah
Start date: 1 Apr 2016 → 21 Jun 2016
Håkan Vigre (Host)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Activity: Hosting a guest lecturer

TEACH FOOD seminars
Period: Mar 2016 → …
Lene Duedahl-Olesen (Organizer)
Lars Bogø Jensen (Organizer)
Håkan Vigre (Organizer)
National Food Institute
Research Group for Analytical Food Chemistry
Research Group for Microbial Food Safety
Research Group for Genomic Epidemiology

Description
Workshops on Teaching and Learning for teachers every March and September at DTU FOOD
Degree of recognition: Local

Related event

TEACH FOOD seminars: biannual workshops on Teaching and Learning
18/03/2016 → …
Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Head of assessment committee
Period: 3 Dec 2015
Håkan Vigre (Internal examiner)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Activity: Examinations and supervision › Internal examination

TEACH FOOD seminar
Lene Duedahl-Olesen (Organizer)
Lars Bogø Jensen (Organizer)
Håkan Vigre (Organizer)
Pernille Hammar Andersson (Organizer)
Sofie Katrine Lorentzen (Organizer)
National Food Institute
Research Group for Analytical Food Chemistry
Research Group for Microbial Food Safety
Research Group for Genomic Epidemiology
Office for Study Programmes and Student Affairs
Office for HR
Office for Finance and Accounting

Description
Seminar for teachers at DTU FOOD
Degree of recognition: Local

Related event

TEACH FOOD seminar: seminar for DTU FOOD teachers
29/10/2015 → 30/10/2015
Hvalsø, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Hvordan bruger vi risikovurdering i forskellige sammenhæng?
Period: 4 Sep 2015
Håkan Vigre (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
Presentation at Dyrlægerens Dag - Mikrobiologisk Risiko Analyse

Related event

Dyrlægernes Dag 2015: Dyrlægen i risikosamfundet
04/09/2015 → 04/09/2015
Activity: Talks and presentations › Conference presentations

Owusu Amponsah
Start date: 19 Jun 2015 → 19 Dec 2015
Håkan Vigre (Host)
National Food Institute
Research Group for Genomic Epidemiology

Description
Hosting Phd student Owusu Amponsah from Department of Planning, Kwame Nkrumah University of Science and Technology, Ghana. Research project SAWAFO
Degree of recognition: International
Activity: Hosting a guest lecturer

Better Training Safer Food
Håkan Vigre (Organizer)
National Food Institute
Research Group for Genomic Epidemiology
Better Training for Safer Food - Mikrobiological Risk Assessment

One week training course in the EU program better training for safer food.
Training coordinator
Degree of recognition: International

Related event

Better Training Safer Food
04/05/2015 → 08/05/2015
Tallinn, Estonia
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Lecturing in the education "Master i Fødevarekvalitet og -sikkerhed" at Copenhagen University
Period: 2 Feb 2015 → 24 Mar 2015
Håkan Vigre (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
Lecturing in the course Mikrobiologisk og Kemisk fødevaresikkerhed
Degree of recognition: National

Related external organisation

University of Copenhagen
Thorvaldssenväj 40, DK-1871 Frederiksberg C, 1871 , Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Molekylære metoder til Salmonella og Campylobacter
Period: 28 Sep 2011
Håkan Vigre (Participant)
Division of Microbiology and Risk Assessment
National Food Institute

Description
Course lecturer
Documents:
Invitation_WS_molekylaere_metoder.pdf

Related event

Molekylære metoder til Salmonella og Campylobacter
DTU, Lyngby
Activity: Other

Lecture and workshop in microbiological food risk assessment
Håkan Vigre (Lecturer)
Division of Microbiology and Risk Assessment
National Food Institute
Activity: Other

Lecture and workshop in microbiological food risk assessment
Period: 1 Apr 2011 → 6 Apr 2011
Håkan Vigre (Lecturer)
DTU's workshop on climate changes and animal health and food safety; 39397
Period: 3 Sep 2009
Håkan Vigre (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Frederiksberg, Denmark

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Tetracycline consumption and occurrence of tetracycline resistance in Salmonella Typhimurium from Danish pigs
Håkan Vigre (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: The 11th Symposium of the International Society for Veterinary Epidemiology and Economics, Cairns, Australia

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Unknown
Period: 1 Jan 2006 → 2 Jan 2006
Håkan Vigre (Participant)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Antimicrobial use in pig herds with and without Post-weaning Multisystemic Wasting Syndrome
Place: Copenhagen
Degree of recognition: National

Related event
Unknown
Period: 01/01/2006 → …
Activity: Attending an event › Participating in or organising a conference