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.
Environmental sustainable decision making – The need and obstacles for integration of LCA into decision analysis

Decision analysis is often used to help decision makers choose among alternatives, based on the expected utility associated to each alternative as function of its consequences and potential impacts. Environmental impacts are not always among the prioritized concerns of traditional decision making. This has fostered the development of several environmental problems and is nowadays a reason of concern. Life Cycle Assessment (LCA) can assess an extensive range of environmental impacts associated with a product or service system and support a life cycle perspective on the alternative products or service systems, revealing potential problem shifting between life cycle stages. Through the integration with traditional risk based decision analysis, LCA may thus facilitate a better informed decision process. In this study we explore how environmental impacts are taken into account in different fields of interest for decision makers to identify the need, potential and obstacles for integrating LCA into conventional approaches to decision problems. Three application areas are used as examples: transportation planning, flood management, and food production and consumption. The analysis of these cases shows that environmental impacts are considered only to a limited extent in traditional evaluation of transport and food projects. They are rarely, if at all, addressed in flood risk management. Hence, in each of the three cases studied, there is a clear need for the inclusion of a better and systematic assessment of environmental impacts. Some LCA studies have been conducted in all three research areas, mainly on infrastructures and production systems. The three cases show the potential of integrating LCA into existing decision analysis by providing the environmental profiles of the alternatives. However, due to different goals and scopes of LCA and other decision analysis approaches, there is a general lack of consistency in study system scoping in terms of considered elements and boundaries, in uncertainty treatment, and in applied metrics. In the present paper, we discuss the obstacles arising when trying to integrate LCA with conventional evaluation tools and we propose a research agenda to eventually make such integration feasible and consistent.
Source Attribution and Risk Assessment of Antimicrobial Resistance

Source attribution and microbial risk assessment methods have been widely applied for the control of several foodborne pathogens worldwide by identifying (i) the most important pathogen sources and (ii) the risk represented by specific foods and the critical points in these foods’ production chains for microbial control. Such evidence has proved crucial for risk managers to identify and prioritize effective food safety and public health strategies. In the context of antimicrobial resistance (AMR) from livestock and pets, the utility of these methods is recognized, but a number of challenges have largely prevented their application and routine use. One key challenge has been to define the hazard in question: Is it the antimicrobial drug use in animals, the antimicrobial-resistant bacteria in animals and foods, or the antimicrobial resistance genes that can be transferred between commensal and pathogenic bacteria in the animal or human gut or in the environment? Other important limitations include the lack of occurrence and transmission data and the lack of evidence to inform dose-response relationships. We present the main principles, available methods, strengths, and weaknesses of source attribution and risk assessment methods, discuss their utility to identify sources and estimate risks of AMR from...
livestock and pets, and provide an overview of conducted studies. In addition, we discuss remaining challenges and current and future opportunities to improve methods and knowledge of the sources and transmission routes of AMR from animals through food, direct contact, or the environment, including improvements in surveillance and developments in genotypic typing methods.

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**Trends and sources in human salmonellosis**

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**Applying LCA in decision making- the need and the future perspective**

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Attribution of global foodborne disease to specific foods: Findings from a World Health Organization structured expert elicitation

Background Recently the World Health Organization, Foodborne Disease Burden Epidemiology Reference Group (FERG) estimated that 31 foodborne diseases (FBDs) resulted in over 600 million illnesses and 420,000 deaths worldwide in 2010. Knowing the relative role importance of different foods as exposure routes for key hazards is critical to preventing illness. This study reports the findings of a structured expert elicitation providing globally comparable food source attribution estimates for 11 major FBDs in each of 14 world subregions. Methods and findings We used Cooke’s Classical Model to elicit and aggregate judgments of 73 international experts. Judgments were elicited from each expert individually and aggregated using both equal and performance weights. Performance weighted results are reported as they increased the informativeness of estimates, while retaining accuracy. We report measures of central tendency and uncertainty bounds on food source attribution estimate. For some pathogens we see relatively consistent food source attribution estimates across subregions of the world; for others there is substantial regional variation. For example, for non-typhoidal salmonellosis, pork was of minor importance compared to eggs and poultry meat in the American and African subregions, whereas in the European and Western Pacific subregions the importance of these three food sources were quite similar. Our regional results broadly agree with estimates from earlier European and North American food source attribution research. As in prior food source attribution research, we find relatively wide uncertainty bounds around our median estimates. Conclusions We present the first worldwide estimates of the proportion of specific foodborne diseases attributable to specific food exposure routes. While we find substantial uncertainty around central tendency estimates, we believe these estimates provide the best currently available basis on which to link FBDs and specific foods in many parts of the world, providing guidance for policy actions to control FBDs.

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Cross-sectional survey on the use and impact of the Danish national antibiotic use guidelines for companion animal practice

Background: The Danish antibiotic use guidelines for companion animal practice were published by the Danish Veterinary Association in 2012. Since then, national surveillance data indicate a 10% reduction in the total use of antibiotics for companion animals, particularly a marked reduction in the use of third generation cephalosporins. The aim of the study was to assess if and how the guidelines have impacted diagnostic and antibiotic prescription habits of the users, and to identify user perceived barriers to implementation. Results: An online questionnaire was sent to all 882 members of the Danish Small Animal Veterinary Association in October 2015. The survey was completed by 151 veterinarians.
Respondents most frequently consulted the recommendations on skin and urinary tract infections (UTI), and users generally reported a high degree of adherence to the recommendations. Sixty-five per cent indicated that the guidelines had influenced their habits in one or more of the areas being investigated, i.e. perioperative use of antibiotics, use of first line antibiotics for the treatment of pyoderma or UTI, and/or use of microbiological diagnostics. Perioperative use of antibiotics for clean surgeries was uncommon, irrespective of whether respondents had consulted the relevant recommendations or not. On the contrary, significant differences in the prescribing habits between guideline users and non-users were observed for pyoderma and UTI, suggesting an impact of the guidelines towards more prudent antimicrobial use. The diagnostic habits were examined in a subgroup of 63 guideline users. Of those, 19 and 39% reported frequent use of culture and susceptibility (C&S) testing prior to treating pyoderma and UTI respectively, whereas 68-84% reported C&S testing in the event of poor response to treatment or recurrence of infections. The main barriers for implementation of therapeutic recommendations were confidence in old prescribing practices and unavailability of recommended drugs. The main barriers for C&S testing were good experience with empiric treatment, and the owners’ financial situation. Conclusions: The findings suggest a positive influence of the national antibiotic guidelines on prescription patterns among companion animal practitioners in Denmark. Sustained campaign activity is encouraged and should include promotion of bacteriological testing.
Framework to Define Structure and Boundaries of Complex Health Intervention Systems: The ALERT Project

Health intervention systems are complex and subject to multiple variables in different phases of implementation. This constitutes a concrete challenge for the application of translational science in real life. Complex systems as health-oriented interventions call for interdisciplinary approaches with carefully defined system boundaries. Exploring individual components of such systems from different viewpoints gives a wide overview and helps to understand the elements and the relationships that drive actions and consequences within the system. In this study, we present an application and assessment of a framework with focus on systems and system boundaries of interdisciplinary projects. As an example on how to apply our framework, we analyzed ALERT [an integrated sensors and biosensors’ system (BEST) aimed at monitoring the quality, health, and traceability of the chain of the bovine milk], a multidisciplinary and interdisciplinary project based on the application of measurable biomarkers at strategic points of the milk chain for improved food security (including safety), human, and ecosystem health (1). In fact, the European food safety framework calls for science-based support to the primary producers’ mandate for legal, scientific, and ethical responsibility in food supply. Because of its multidisciplinary and interdisciplinary approach involving human, animal, and ecosystem health, ALERT can be considered as a One Health project. Within the ALERT context, we identified the need to take into account the main actors, interactions, and relationships of stakeholders to depict a simplified skeleton of the system. The framework can provide elements to highlight how and where to improve the project development when project evaluations are required.

General information
Modelling Dietary Exposure to Chemical Components in Heat-Processed Meats
Several chemical compounds that potentially increase the risk of developing cancer in humans are formed during heat processing of meat. Estimating the overall health impact of these compounds in the population requires accurate estimation of the exposure to the chemicals, as well as the probability that different levels of exposure result in disease. The overall goal of this study was to evaluate the impact of variability of exposure patterns and uncertainty of exposure data in burden of disease estimates. We focus on the first phase of burden of disease modelling, i.e. the estimation of exposure to selected compounds in the Danish population, based on concentration and consumption data. One of the challenges that arises in the probabilistic modelling of exposure is the presence of “artificial” zero counts in concentration data due to the detection level of the applied tests. Zero-inflated models, e.g. the Poisson-Lognormal approach, are promising tools to address this obstacle. The exposure estimates can then be applied to dose-response models to quantify the cancer risk.

Probabilistic quantitative microbial risk assessment model of farmer exposure to Cryptosporidium spp. in irrigation water within Kumasi Metropolis-Ghana
Cryptosporidium is a protozoan parasite which can be transmitted via food and water. Some studies have shown irrigation water to be routes of transmission for Cryptosporidium into the food chain, however, little information is known about
Cryptosporidium levels in wastewater used for irrigation in the Kumasi Metropolis of Ghana. Kumasi and for that matter Ghana is not immune to the widespread practice of wastewater irrigation for farm produce in developing countries which has attracted attention of both, policy makers and academia. However, most previous studies of microbial risk assessment focus on the possible health effects and risk estimation for consumers of wastewater irrigated produce, whereas farmers who actually come into direct contact with the wastewater have received little attention. This study estimated the possible risk/diseases from farmer exposure to Cryptosporidium, a zoonotic pathogen causing gastroenteritis. The results indicate high positive levels of Cryptosporidium in the irrigation water, however, the levels of Cryptosporidium decreases during the rainfall seasons, risk assessment results show that, farmers face a higher risk of being infected by Cryptosporidium due to frequent exposure to wastewater. An adoption of a possible on-farm wastewater treatment option was found to reduce the risk of infection of the farmers. The results of this study highlight the need for a proactive policy to integrate a multi-barrier approach to reduce direct contact of farmers with wastewater for irrigation, to minimise risk of infection.

Probabilistic quantitative microbial risk assessment model of norovirus from wastewater irrigated vegetables in Ghana using genome copies and fecal indicator ratio conversion for estimating exposure dose

The need to replace the commonly applied fecal indicator conversions ratio (an assumption of 1:10^{-5} virus to fecal indicator organism) in Quantitative Microbial Risk Assessment (QMRA) with models based on quantitative data on the virus of interest has gained prominence due to the different physical and environmental factors that might influence the reliability of using indicator organisms in microbial risk assessment. The challenges facing analytical studies on virus enumeration (genome copies or particles) have contributed to the already existing lack of data in QMRA modelling. This study attempts to fit a QMRA model to genome copies of norovirus data. The model estimates the risk of norovirus infection from the intake of vegetables irrigated with wastewater from different sources. The results were compared to the results of a corresponding model using the fecal indicator conversion ratio to estimate the norovirus count. In all scenarios of using different water sources, the application of the fecal indicator conversion ratio underestimated the norovirus disease burden, measured by the Disability Adjusted Life Years (DALYs), when compared to results using the genome copies norovirus data. In some cases the difference was > 2 orders of magnitude. All scenarios using genome copies met the 10^{-3} DALY per person per year for consumption of vegetables irrigated with wastewater, although these results are considered to be highly conservative risk estimates. The fecal indicator conversion ratio model of stream-water and drain-water sources of wastewater achieved the 10^{-6} DALY per person per year threshold, which tends to indicate an underestimation of health risk when compared to using genome copies for estimating the dose.
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"Recycled paper for food packaging: burden of disease methodology to link sustainability and safety"

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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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Application of Molecular Typing Results in Source Attribution Models: The Case of Multiple Locus Variable Number Tandem Repeat Analysis (MLVA) of Salmonella Isolates Obtained from Integrated Surveillance in Denmark

Salmonella is an important cause of bacterial foodborne infections in Denmark. To identify the main animal-food sources of human salmonellosis, risk managers have relied on a routine application of a microbial subtyping-based source attribution model since 1995. In 2013, multiple locus variable number tandem repeat analysis (MLVA) substituted phage typing as the subtyping method for surveillance of S. Enteritidis and S. Typhimurium isolated from animals, food, and humans in Denmark. The purpose of this study was to develop a modeling approach applying a combination of serovars, MLVA types, and antibiotic resistance profiles for the Salmonella source attribution, and assess the utility of the results for the food safety decisionmakers. Full and simplified MLVA schemes from surveillance data were tested, and model fit and consistency of results were assessed using statistical measures. We conclude that loci schemes STTR5/STTR10/STTR3 for S. Typhimurium and SE9/SE5/SE2/SE1/SE3 for S. Enteritidis can be used in microbial subtyping-based source attribution models. Based on the results, we discuss that an adjustment of the discriminatory level of the subtyping method applied often will be required to fit the purpose of the study and the available data. The issues discussed are also considered highly relevant when applying, e.g., extended multi-locus sequence typing or next-generation sequencing techniques.

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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 (≥10^4 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.
A risk-based approach for evaluation of hygiene performance at pig slaughter

In Denmark, the pig slaughterhouses have a daily input of pigs infected and/or contaminated with Salmonella, and the slaughter hygiene has major influence on the level of Salmonella contamination on the meat leaving the slaughterhouse. However, the relationship between the effect of improved hygiene performance and the consequential reduction of human health risk has not been estimated so far. In this study, swab samples from 2702 pig carcasses were collected, originally for other purposes, from five large Danish slaughterhouses in a period from 2005 to 2007, covering all seasons of the year. The samples were analysed quantitatively for E. coli and semi-quantitatively for Salmonella. A positive association between the number of E. coli on carcasses and the prevalence of Salmonella positive carcasses was shown. For carcasses positive for Salmonella, a positive association was also shown between the number of E. coli and the number of Salmonella on the carcass. As no biological association has been reported between faecal shedding of E. coli and presence of Salmonella, the relationship was considered to be associated with the level of faecal contamination. The positive association between E. coli and Salmonella was used as basis for developing a quantitative risk assessment model for Salmonella, using the level E. coli as model input. The model output associated the hygiene performance with a relative risk estimate of human salmonellosis. The overall objective was to develop a decision support tool that can be used to support risk-based hygiene interventions in pig slaughterhouses.
Assessing the Effectiveness of On-Farm and Abattoir Interventions in Reducing Pig Meat–Borne Salmonellosis within E.U. Member States

As part of the evidence base for the development of national control plans for Salmonella spp. in pigs for E.U. Member States, a quantitative microbiological risk assessment was funded to support the scientific opinion required by the EC from the European Food Safety Authority. The main aim of the risk assessment was to assess the effectiveness of interventions implemented on-farm and at the abattoir in reducing human cases of pig meat–borne salmonellosis, and how the effects of these interventions may vary across E.U. Member States. Two case study Member States have been chosen to assess the effect of the interventions investigated. Reducing both breeding herd and slaughter pig prevalence were effective in achieving reductions in the number of expected human illnesses in both case study Member States. However, there is scarce evidence to suggest which specific on-farm interventions could achieve consistent reductions in either breeding herd or slaughter pig prevalence. Hypothetical reductions in feed contamination rates were important in reducing slaughter pig prevalence for the case study Member State where prevalence of infection was already low, but not for the high-prevalence case study. The most significant reductions were achieved by a 1- or 2-log decrease of Salmonella contamination of the carcass post-evisceration; a 1-log decrease in average contamination produced a 90% reduction in human illness. The intervention analyses suggest that abattoir intervention may be the most effective way to reduce human exposure to Salmonella spp. However, a combined farm/abattoir approach would likely have cumulative benefits. On-farm intervention is probably most effective at the breeding-herd level for high-prevalence Member States; once infection in the breeding herd has been reduced to a low enough level, then feed and biosecurity measures would become increasingly more effective.

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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.

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Evaluation of a Performance-Based Expert Elicitation: WHO Global Attribution of Foodborne Diseases

For many societally important science-based decisions, data are inadequate, unreliable or non-existent, and expert advice is sought. In such cases, procedures for eliciting structured expert judgments (SEJ) are increasingly used. This raises questions regarding validity and reproducibility. This paper presents new findings from a large-scale international SEJ study intended to estimate the global burden of foodborne disease on behalf of WHO. The study involved 72 experts distributed over 134 expert panels, with panels comprising thirteen experts on average. Elicitations were conducted in five languages. Performance-based weighted solutions for target questions of interest were formed for each panel. These weights were based on individual expert’s statistical accuracy and informativeness, determined using between ten and fifteen calibration variables from the experts’ field with known values. Equal weights combinations were also calculated. The main conclusions on expert performance are: (1) SEJ does provide a science-based method for attribution of the global burden of foodborne diseases; (2) equal weighting of experts per panel increased statistical accuracy to acceptable levels, but at the cost of informativeness; (3) performance-based weighting increased informativeness, while retaining
accuracy; (4) due to study constraints individual experts’ accuracies were generally lower than in other SEJ studies, and
(5) there was a negative correlation between experts’ informativeness and statistical accuracy which attenuated as
accuracy improved, revealing that the least accurate experts drive the negative correlation. It is shown, however, that
performance-based weighting has the ability to yield statistically accurate and informative combinations of experts’
judgments, thereby offsetting this contrary influence. The present findings suggest that application of SEJ on a large scale
is feasible, and motivate the development of enhanced training and tools for remote elicitation of multiple, internationally-
dispersed panels.

General information
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Organisations: National Food Institute, Research Group for Genomic Epidemiology, University of Bristol, Delft University of
Technology, Utrecht University
Authors: Aspinall, W. P. (Ekstern), Cooke, R. M. (Ekstern), Havelaar, A. H. (Ekstern), Hoffmann, S. (Ekstern), Hald, T.
(Intern)
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BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
Web of Science (2014): Indexed yes
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ISI indexed (2013): ISI indexed yes
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BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
Web of Science (2012): Impact factor 3.73
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Web of Science (2012): Indexed yes
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Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
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ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.705 SNIP 1.178
Web of Science (2010): Impact factor 4.411
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Non-plastic food contact materials: classification of chemicals using predictive models

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Research Group for Analytical Food Chemistry, Istituto di Ricerche Farmacologiche Mario Negri
Authors: Boriani, E. (Intern), Pieke, E. N. (Intern), Wedebye, E. B. (Intern), Benfenati, E. (Ekstern), Granby, K. (Intern), Hald, T. (Intern)
Number of pages: 1
Publication date: 2016
Main Research Area: Technical/natural sciences
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Quantitative Microbiological Risk Assessment and Source Attribution for Salmonella: Taking it Further

General information
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Authors: Snary, E. L. (Ekstern), Swart, A. N. (Ekstern), Hald, T. (Intern)
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We live in an age that increasingly calls for national or regional management of global risks. This article discusses the contributions that expert elicitation can bring to efforts to manage global risks and identifies challenges faced in conducting expert elicitation at this scale. In doing so it draws on lessons learned from conducting an expert elicitation as part of the World Health Organizations (WHO) initiative to estimate the global burden of foodborne disease; a study commissioned by
the Foodborne Disease Epidemiology Reference Group (FERG). Expert elicitation is designed to fill gaps in data and research using structured, transparent methods. Such gaps are a significant challenge for global risk modeling. Experience with the WHO FERG expert elicitation shows that it is feasible to conduct an expert elicitation at a global scale, but that challenges do arise, including: defining an informative, yet feasible geographical structure for the elicitation; defining what constitutes expertise in a global setting; structuring international, multidisciplinary expert panels; and managing demands on experts’ time in the elicitation. This article was written as part of a workshop, Methods for Research Synthesis: A Cross-Disciplinary Approach held at the Harvard Center for Risk Analysis on October 13, 2013.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology, Research Group for Risk-Benefit
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BFI (2017): BFI-level 1
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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): Impact factor 2.518
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.334 SNIP 1.495 CiteScore 2.51
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BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.331 SNIP 1.588 CiteScore 2.2
Web of Science (2014): Impact factor 2.502
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.067 SNIP 1.595 CiteScore 2.1
Web of Science (2013): Impact factor 1.974
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
Web of Science (2012): Impact factor 2.278
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.735 SNIP 1.693 CiteScore 2.15
Web of Science (2011): Impact factor 2.366
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
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Scopus rating (2010): SJR 0.739 SNIP 1.51
Disease burden, expert elicitation, expert judgment, exposure estimates, foodborne illness, research synthesis, source attribution, systematic review, uncertainty quantification, Physiology (medical), Safety, Risk, Reliability and Quality, Expert elicitation, Expert judgment, Exposure estimates, Foodborne illness, Research synthesis, Source attribution, Systematic review, Uncertainty quantification

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World Health Organization Estimates of the Relative Contributions of Food to the Burden of Disease Due to Selected Foodborne Hazards: A Structured Expert Elicitation

Background

The Foodborne Disease Burden Epidemiology Reference Group (FERG) was established in 2007 by the World Health Organization (WHO) to estimate the global burden of foodborne diseases (FBDs). This estimation is complicated because most of the hazards causing FBD are not transmitted solely by food; most have several potential exposure routes consisting of transmission from animals, by humans, and via environmental routes including water. This paper describes an expert elicitation study conducted by the FERG Source Attribution Task Force to estimate the relative contribution of food to the global burden of diseases commonly transmitted through the consumption of food. Methods and Findings

We applied structured expert judgment using Cooke's Classical Model to obtain estimates for 14 subregions for the relative contributions of different transmission pathways for eleven diarrheal diseases, seven other infectious diseases and one chemical (lead). Experts were identified through international networks followed by social network sampling. Final selection of experts was based on their experience including international working experience. Enrolled experts were scored on their ability to judge uncertainty accurately and informatively using a series of subject-matter specific 'seed' questions whose answers are unknown to the experts at the time they are interviewed. Trained facilitators elicited the 5th, and 50th and 95th percentile responses to seed questions through telephone interviews. Cooke's Classical Model uses responses to the seed questions to weigh and aggregate expert responses. After this interview, the experts were asked to provide 5th, 50th, and 95th percentile estimates for the 'target' questions regarding disease transmission routes. A total of 72 experts were enrolled in the study. Ten panels were global, meaning that the experts should provide estimates for all 14 subregions, whereas the nine panels were subregional, with experts providing estimates for one or more subregions, depending on their experience in the region. The size of the 19 hazard-specific panels ranged from 6 to 15 persons with several experts serving on more than one panel. Pathogens with animal reservoirs (e.g. non-typhoidal Salmonella spp. and Toxoplasma gondii) were in general assessed by the experts to have a higher proportion of illnesses attributable to food than pathogens with mainly a human reservoir, where human-to-human transmission (e.g. Shigella spp. and Norovirus) or waterborne transmission (e.g. Salmonella Typhi and Vibrio cholerae) were judged to dominate. For many pathogens, the foodborne route was assessed relatively more important in developed subregions than in developing subregions. The main exposure routes for lead varied across subregions, with the foodborne route being assessed most important only in two subregions of the European region. Conclusions

For the first time, we present worldwide estimates of the proportion of specific diseases attributable to food and other major transmission routes. These findings are essential for global burden of FBD estimates. While gaps exist, we believe the estimates presented here are the best current source of guidance to support decision makers when allocating resources for control and intervention, and for future research initiatives.
Accounting for Campylobacter biology and epidemiology in source attribution modelling

General information
State: Published
Organisations: National Food Institute, Division of Risk Assessment and Nutrition, Research Group for Risk-Benefit, Research Group for Genomic Epidemiology, Danish Veterinary and Food Administration
Authors: Boysen, L. (Intern), Rosenquist, H. (Ekstern), Hald, T. (Intern)
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Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Attributing foodborne salmonellosis in humans to animal reservoirs in the European Union using a multi-country stochastic model

A Bayesian modelling approach comparing the occurrence of Salmonella serovars in animals and humans was used to attribute salmonellosis cases to broilers, turkeys, pigs, laying hens, travel and outbreaks in 24 European Union countries. Salmonella data for animals and humans, covering the period from 2007 to 2009, were mainly obtained from studies and reports published by the European Food Safety Authority. Availability of food sources for consumption was derived from trade and production data from the European Statistical Office. Results showed layers as the most important reservoir of human salmonellosis in Europe, with 42.4% (7,903,000 cases, 95% credibility interval 4,181,000-14,510,000) of cases, 95.9% of which was caused by S. Enteritidis. In Finland and Sweden, most cases were travel-related, while in most other countries the main sources were related to the laying hen or pig reservoir, highlighting differences in the epidemiology of Salmonella, surveillance focus and eating habits across the European Union.

General information
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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: de Knegt, L. (Intern), Pires, S. M. (Intern), Hald, T. (Intern)
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BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.88 SJR 1.128 SNIP 0.807
Web of Science (2017): Impact factor 2.044
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): Impact factor 2.075
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): Impact factor 2.515
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): Impact factor 2.535
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.337 SNIP 1.113 CiteScore 2.57
Web of Science (2013): Impact factor 2.491
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
Web of Science (2012): Impact factor 2.867
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
Web of Science (2011): Impact factor 2.843
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): Impact factor 2.257
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
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2015. Scientific Opinion on an alternative method for the hygienic treatment of bovine colostrum through a series of filtration steps

An alternative method to the HTST treatment (High Temperature Short Time pasteurisation at 72 °C for at least 15 seconds or equivalent pasteurisation effect achieving a negative reaction to a phosphatase test), approved for the treatment of bovine colostrum (Category 3 material), was assessed. The purpose of the alternative method, based on a series of filtration steps, is the production of Colostrinov, a product whose main ingredient is bovine colostrum, to be used for foal nutrition. Since the filtration techniques used are known to eliminate particles of the size of bacteria, fungi and protozoa from liquids, it is reasonable to assume that the microfiltration process reduces these contaminants to a level at least equivalent to the treatment required by the legislation. Owing to their small size, viruses are not retained by the mechanical effect of the filters but they may be retained by physico-chemical interactions with the surface of the filter, depending on the surface properties of the viruses and those of the filter, as well as on the properties of the surrounding liquid. From the information provided by the applicant, it cannot be concluded whether or not the microfiltration process reduces the relevant viral contaminants to a level at least equivalent to a single HTST treatment as required by the legislation.

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Authors: EFSA report
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Source: PublicationPreSubmission
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EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2015. Scientific Opinion on the development of a risk ranking toolbox for the EFSA BIOHAZ Panel

Eight tools relevant to risk ranking of biological hazards in food were identified and assessed using two case studies. Differences in their performance were observed, related to the risk metrics, data requirements, ranking approach, model type, model variables and data integration. Quantitative stochastic models are the most reliable for risk ranking. However, this approach needs good characterisation of input parameters. The use of deterministic models that ignore variability may result in risk ranking errors. The ordinal scoring approaches in semi-quantitative models provide ranking with more errors than the deterministic approaches. FDA (Food and Drug Administration)-iRISK was identified as the most appropriate tool for risk ranking of microbiological hazards. The Burden of Communicable Diseases in Europe (BCoDE) toolkit can be used in combination with the outputs from FDA-iRISK or as a top-down tool to rank pathogens. Uncertainty needs to be addressed and communicated to decision makers and stakeholders as one of the outcomes of the risk ranking process. Uncertainty and variability can be represented by means of probability distributions. Techniques such as the NUSAP (numeral, unit, spread, assessment and pedigree) approach can also be used to prioritise factors for sensitivity and
scenario analysis or stochastic modelling. Quantitative risk ranking models are preferred over semi-quantitative models. When data and time constraints do not allow quantitative risk ranking, semi-quantitative models could be used, but the limitations of these approaches linked to the selection and integration of the ordinal scores should be made explicit. Decision trees should be used only to show how decisions are made about classifying food–pathogen combinations into broad categories. BCODE and FDA-iRISK, in combination with a network of available predictive microbiology tools, databases and information sources, can form a risk ranking toolbox and be applied based on a “fit for purpose” approach supporting timely and transparent risk ranking.

**General information**

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Authors: EFSA report

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**EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2015. Scientific Opinion on the public health risks related to the consumption of raw drinking milk**

Raw drinking milk (RDM) has a diverse microbial flora which can include pathogens transmissible to humans. The main microbiological hazards associated with RDM from cows, sheep and goats, horses and donkeys and camels were identified using a decision tree approach. This considered evidence of milk-borne infection and the hazard being present in the European Union (EU), the impact of the hazard on human health and whether there was evidence for RDM as an important risk factor in the EU. The main hazards were Campylobacter spp., Salmonella spp., shigatoxin-producing Escherichia coli (STEC), Brucella melitensis, Mycobacterium bovis and tick-borne encephalitis virus, and there are clear links between drinking raw milk and human illness associated with these hazards. A quantitative microbiological risk assessment for these hazards could not be undertaken because country and EU-wide data are limited. Antimicrobial resistance has been reported in several EU countries in some of the main bacterial hazards isolated from raw milk or associated equipment and may be significant for public health. Sale of RDM through vending machines is permitted in some EU countries, although consumers purchasing such milk are usually instructed to boil the milk before consumption, which would eliminate microbiological risks. With respect to internet sales of RDM, there is a need for microbiological, temperature and storage time data to assess the impact of this distribution route. Intrinsic contamination of RDM with pathogens can arise from animals with systemic infection as well as from localised infections such as mastitis. Extrinsic contamination can arise from faecal contamination and from the wider farm environment. It was not possible to rank control options as no single step could be identified which would significantly reduce risk relative to a baseline of expected good practice, although potential for an increase in risk was also noted. Improved risk communication to consumers is recommended.

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Organisations: National Food Institute, Research Group for Genomic Epidemiology

Authors: EFSA report

Number of pages: 95

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Place of publication: Parma, Italy
**Integrated Food Security: mapping and selecting different indicators and metrics from sustainability till safety, pig product case study**

**General information**

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Organisations: National Food Institute, Research Group for Genomic Epidemiology

Authors: Boriani, E. (Intern), Hald, T. (Intern)

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**Køn- og aldersfordeling hos patienter i fødevarebårne udbrud anvendt til hypotesegenerering i udbudsefterforskningen: Danske fødevarebårne udbud mod kendt kilde**

In this study we attempted to systematically utilize the varying gender and age distributions of foodborne outbreaks, combined with knowledge of Danish age and gender specific food intakes from the survey "The Danish National Survey of Diet and Physical Activity 2003-2008 " (DANSDA), to risk rank food groups and obtain an indication of the outbreak source. The study included 12 Danish foodborne outbreaks with a known outbreak source. For each of the 12 outbreaks and for the Danish population, the theoretical proportion of exposed persons for each of 214 food groups was calculated. The theoretical exposure for each food item in each outbreak and in the Danish population was compared using three different methods (preference measures). The preference measures comprised the difference (Præfdiff) and the quotient (Præfkvot) between exposure in the outbreak and the population and Præfdiff compared to the maximum difference for the food group (Præfpot). In addition, the similarity between the gender- and age distribution of outbreak cases was compared with the distribution by gender and age of the part of the Danish population which the DANSDAfound exposed to each food group. The similarity between the two gender- and age distributions were calculated for each food group as a Proportional Similarity Index (PSI). For each outbreak, the food groups were ranked according to the size of the three preference measures (Præfdiff, Præfkvot and Præfpot) as well as the PSI, and the ranking of selected indicator food groups for the outbreak source was compared between methods. Large differences in food preferences were found for patients in outbreaks with different food source, and strong similarities were observed between food preferences for patients in outbreaks with the same or similar food sources. The study identifies Præfpot as the best preference measure. An indicator food group for the outbreak source could be found among the 25 highest-ranked Præfpot in 11 of the 12 outbreaks. The probability of this outcome of the investigation to be a result of pure chance is less than 1 per thousand. The outbreak, in which an indicator food group for the outbreak source was not in the top-25 for Præfpot, was a sub-outbreak comprising the "tail" of cases in the end of a larger outbreak. For the preference measures Præfdiff, Præfkvot and for PSI, indicator food groups for the outbreaks source were only ranked in the top-25 of respectively, 9, 5 and 3 of the 12 outbreaks. Calculation and ranking of Præfpot in this study was Excel-based and is fast and easily conducted, once the underlying Excel-data sheets have been established. Ranking of Præfpot for food groups was assessed to be a useful supplement to the investigation of foodborne outbreaks. There is a need for further studies to determine how and when the
Methodological Framework for World Health Organization Estimates of the Global Burden of Foodborne Disease

The Foodborne Disease Burden Epidemiology Reference Group (FERG) was established in 2007 by the World Health Organization to estimate the global burden of foodborne diseases (FBDs). This paper describes the methodological framework developed by FERG's Computational Task Force to transform epidemiological information into FBD burden estimates. The global and regional burden of 31 FBDs was quantified, along with limited estimates for 5 other FBDs, using Disability-Adjusted Life Years in a hazard- and incidence-based approach. To accomplish this task, the following workflow was defined: outline of disease models and collection of epidemiological data; design and completion of a database template; development of an imputation model; identification of disability weights; probabilistic burden assessment; and estimating the proportion of the disease burden by each hazard that is attributable to exposure by food (i.e., source attribution). All computations were performed in R and the different functions were compiled in the R package ‘FERG’. Traceability and transparency were ensured by sharing results and methods in an interactive way with all FERG members throughout the process. We developed a comprehensive framework for estimating the global burden of FBDs, in which methodological simplicity and transparency were key elements. All the tools developed have been made available and can be translated into a user-friendly national toolkit for studying and monitoring food safety at the local level.
Performance, compliance and reliability of Waste stabilization pond: Effluent discharge quality and environmental protection agency standards in Ghana

Measuring performance has been arguably, one of the metric with many facets with different school of thoughts, as there exist different approaches of measuring it. Several of the existing approaches measure such metric by comparison with standards enshrined in policy documents and as a result, takes less look to its compliance and reliability of values being matched to an established standards. This study seeks to integrate reliability and compliance into measuring of performance of Waste Stabilization Pond (WSP) and Treatment Plant (TP) as well as to generate the appropriate standard chart tables using the Ghana Environmental Protection Agency (EPA) approved discharge values for physico-chemical and some biological parameters to account for these shortfalls on over reliance of EPA discharge standards. Probability distribution density function was applied on the lognormal distribution function to establish the relationship between the statistical coefficient of variation and the coefficient of reliability based on rth moment about the origin in the moment of generation function to generate the functions of the mean and standard deviation, properties of the standard Z normal distribution were used to establish the coefficient of reliability relationship depending on the coefficient of variation influenced by the standard of deviation. Discharge values of Physico-chemical Parameters measured from the WSP were found be performing acceptably based on the EPA standards, whereas only four of the TP were acceptable. Discharge Values of physico-chemical and biological parameters which are found to be accepted under comparison with EPA...
standards were found to have compliance levels below what is generally accepted for Waste Stabilization Ponds (WSP) designed compliance. Based on these shortcomings, reference charts were develop to serve as reference points in assessing the various characteristics of compliance and performance of WSPs in Ghana on (28) physico-chemical and biological parameters. These charts are intended to make it easier to assess the performance of WSPs and its corresponding reliability and compliance level to compensate for overreliance on EPA standards alone.

**General information**

State: Published
Organisations: Division of Epidemiology and Microbial Genomics, National Food Institute, Research Group for Genomic Epidemiology, Kwame Nkrumah University of Science and Technology
Authors: Owusu-Ansah, E. D. J. (Intern), Sampson, A. (Ekstern), Amponsah, S. K. (Ekstern), Abaidoo, R. C. (Ekstern), Hald, T. (Intern)
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- Scopus rating (2013): SJR 0.147 SNIP 0.472
- ISI indexed (2013): ISI indexed no
- Scopus rating (2012): SJR 0.135 SNIP 0.554
- ISI indexed (2012): ISI indexed no
- Scopus rating (2011): SJR 0.139 SNIP 0.368
- ISI indexed (2011): ISI indexed no
- Scopus rating (2010): SJR 0.15 SNIP 0.342

Original language: English
Engineering (all), Computer Science (all), Coefficient of reliability, Coefficient of variation, Effluent quality discharge, EPA standards, Lognormal distribution, Performance and compliance, Probability of reliability, Waste stabilization ponds

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**Risikorangering af sygdomsfremkaldende mikroorganismer i frisk frugt og grønt: Frugt og grønt indsatser 2013-2016**

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Foods of non-animal origin (FoNAO) are consumed in a variety of forms, being a major component of almost all meals. These food types have the potential to be associated with large outbreaks as seen in 2011 associated with VTEC O104. In order to identify and rank specific food/pathogen combinations most often linked to human cases originating from FoNAO in the EU, a semi-quantitative model was developed using seven criteria: strength of associations between food and pathogen based on the foodborne outbreak data from EU Zoonoses Monitoring (2007-2011), incidence of illness, burden of disease, dose-response relationship, consumption, prevalence of contamination and pathogen growth potential during shelf life. The top ranking food/pathogen combination was Salmonella spp. and leafy greens eaten raw followed by (in equal rank) Salmonella spp. and bulb and stem vegetables, Salmonella spp. and tomatoes, Salmonella spp. and melons, and pathogenic Escherichia coli and fresh pods, legumes or grains. Despite the inherent assumptions and limitations, this risk model is considered a tool for risk managers, as it allows ranking of food/pathogen combinations most often linked to foodborne human cases originating from FoNAO in the EU. Efforts to collect additional data even in the absence of reported outbreaks as well as to enhance the quality of the EU-specific data, which was used as input for all the model criteria, will allow the improvement of the model outputs. Furthermore, it is recommended that harmonised terminology be applied to the categorisation of foods collected for different reasons, e.g. monitoring, surveillance, outbreak investigation and consumption. In addition, to assist future microbiological risk assessments, consideration should be given to the collection of additional information on how food has been processed, stored and prepared as part of the above data collection exercises.

General information
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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, European Food Safety Authority, Spanish National Research Council, French National Institute for Agricultural Research, National Veterinary Institute, European Centre for Disease Prevention and Control, Ghent University, University of Liverpool
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Trends and sources in human salmonellosis

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Authors: de Knegt, L. (Intern), Hald, T. (Intern)
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Using surveillance and monitoring data of different origins in a Salmonella source attribution model: a European Union example with challenges and proposed solutions

Microbial subtyping approaches are commonly used for source attribution of human salmonellosis. Such methods require data on Salmonella in animals and humans, outbreaks, infection abroad and amounts of food available for consumption. A source attribution model was applied to 24 European countries, requiring special data management to produce a standardized dataset. Salmonellosis data on animals and humans were obtained from datasets provided by the European Food Safety Authority. The amount of food available for consumption was calculated based on production and trade data. Limitations included different types of underreporting, non-participation in prevalence studies, and non-availability of trade data. Cases without travel information were assumed to be domestic; non-subtyped human or animal records were re-identified according to proportions observed in reference datasets; missing trade information was estimated based on previous years. The resulting dataset included data on 24 serovars in humans, broilers, laying hens, pigs and turkeys in 24 countries.
World Health Organization Estimates of the Global and Regional Disease Burden of 22 Foodborne Bacterial, Protozoal, and Viral Diseases, 2010: A Data Synthesis

Foodborne diseases are important worldwide, resulting in considerable morbidity and mortality. To our knowledge, we present the first global and regional estimates of the disease burden of the most important foodborne bacterial, protozoal, and viral diseases. We synthesized data on the number of foodborne illnesses, sequelae, deaths, and Disability Adjusted Life Years (DALYs), for all diseases with sufficient data to support global and regional estimates, by age and region. The data sources included varied by pathogen and included systematic reviews, cohort studies, surveillance studies and other burden of disease assessments. We sought relevant data circa 2010, and included sources from 1990-2012. The number of studies per pathogen ranged from as few as 5 studies for bacterial intoxications through to 494 studies for diarrheal pathogens. To estimate mortality for Mycobacterium bovis infections and morbidity and mortality for invasive non-typhoidal
Salmonella enterica infections, we excluded cases attributed to HIV infection. We excluded stillbirths in our estimates. We estimate that the 22 diseases included in our study resulted in two billion (95% uncertainty interval [UI] 1.5-2.9 billion) cases, over one million (95% UI 0.89-1.4 million) deaths, and 78.7 million (95% UI 65.0-97.7 million) DALYs in 2010. To estimate the burden due to contaminated food, we then applied proportions of infections that were estimated to be foodborne from a global expert elicitation. Waterborne transmission of disease was not included. We estimate that 29% (95% UI 23-36%) of cases caused by diseases in our study, or 582 million (95% UI 401-922 million), were transmitted by contaminated food, resulting in 25.2 million (95% UI 17.5-37.0 million) DALYs. Norovirus was the leading cause of foodborne illness causing 125 million (95% UI 70-251 million) cases, while Campylobacter spp. caused 96 million (95% UI 52-177 million) foodborne illnesses. Of all foodborne diseases, diarrheal and invasive infections due to non-typhoidal S. enterica infections resulted in the highest burden, causing 4.07 million (95% UI 2.49-6.27 million) DALYs. Regionally, DALYs per 100,000 population were highest in the African region followed by the South East Asian region. Considerable burden of foodborne disease is borne by children less than five years of age. Major limitations of our study include data gaps, particularly in middle- and high-mortality countries, and uncertainty around the proportion of diseases that were foodborne. Foodborne diseases result in a large disease burden, particularly in children. Although it is known that diarrheal diseases are a major burden in children, we have demonstrated for the first time the importance of contaminated food as a cause. There is a need to focus food safety interventions on preventing foodborne diseases, particularly in low- and middle-income settings.

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Organisations: National Food Institute, Australian National University, Johns Hopkins University, Food and Agriculture Organization of the United Nations, University of Otago, Ghent University, Public Health Agency of Canada, Centers for Disease Control and Prevention, University of the Witwatersrand, Institute of Environmental Science and Research, Instituto de Investigación Nutricional, University of Zurich, University of Florida, University of Wisconsin-Madison
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Web of Science (2012): Impact factor 15.253
Illness and death from diseases caused by contaminated food are a constant threat to public health and a significant impediment to socio-economic development worldwide. To measure the global and regional burden of foodborne disease (FBD), the World Health Organization (WHO) established the Foodborne Disease Burden Epidemiology Reference Group (FERG), which here reports their first estimates of the incidence, mortality, and disease burden due to 31 foodborne hazards. We find that the global burden of FBD is comparable to those of the major infectious diseases, HIV/AIDS, malaria and tuberculosis. The most frequent causes of foodborne illness were diarrheal disease agents, particularly norovirus and Campylobacter spp. Diarrheal disease agents, especially non-typhoidal Salmonella enterica, were also responsible for the majority of deaths due to FBD. Other major causes of FBD deaths were Salmonella Typhi, Taenia solium and hepatitis A virus. The global burden of FBD caused by the 31 hazards in 2010 was 33 million Disability Adjusted Life Years (DALYs); children under five years old bore 40% of this burden. The 14 subregions, defined on the basis of child and adult mortality, had considerably different burdens of FBD, with the greatest falling on the subregions in Africa, followed by the subregions in South-East Asia and the Eastern Mediterranean D subregion. Some hazards, such as non-typhoidal S. enterica, were important causes of FBD in all regions of the world, whereas others, such as certain parasitic helminths, were highly localised. Thus, the burden of FBD is borne particularly by children under five years old-although they represent only 9% of the global population-and people living in low-income regions of the world. These estimates are conservative, i.e., underestimates rather than overestimates; further studies are needed to address the data gaps and limitations of the study. Nevertheless, all stakeholders can contribute to improvements in food safety throughout the food chain by incorporating these estimates into policy development at national and international levels.

**General information**

State: Published

Organisations: National Food Institute, University of Florida, Australian National University, University of Zurich, Gibb Epidemiology Consulting, Institute of Environmental Science and Research, Institute of Tropical Medicine, Boston Children’s Hospital, University of Kelaniya, Hikma Pharmaceuticals, World Health Organization, Centers for Disease Control and Prevention, Ghent University, Universite Catholique de Louvain

Authors: Havelaar, A. H. (Ekstern), Kirk, M. D. (Ekstern), Torgerson, P. R. (Ekstern), Gibb, H. J. (Ekstern), Hald, T. (Intern), Lake, R. J. (Ekstern), Praet, N. (Ekstern), Bellinger, D. C. (Ekstern), de Silva, N. R. (Ekstern), Gargouri, N. (Ekstern), Speybroeck, N. (Ekstern), Cawthorne, A. (Ekstern), Mathers, C. (Ekstern), Stein, C. (Ekstern), Angulo, F. J. (Ekstern), Devleesschauwer, B. (Ekstern)

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Main Research Area: Technical/natural sciences
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2013. Scientific Opinion on Bioreduction application

A method for on-farm containment of animal by-products (ABPs), called a ‘Bioreduction’ system, was assessed. The material for containment is of ovine origin and classified as a Category (Cat.) 1 ABP material. The proposed process consists of an aerobic degradation of the ABP material in a vented, leak-proof vessel. The parameters given by the applicant for heating and aeration rate are respectively: temperature 30-42 °C and aeration under a pressure of 40-55 kPa. The resulting material is finally disposed of according to standard methods for Cat. 1 ABPs. The Bioreduction system can reduce the risks related to pathogens such as non-spore forming bacteria and viruses. However, it is highly improbable that the risks related to more resistant biological hazards can be reduced. The application does not provide clear information about the location of the system and the origin of the material for containment. This has important implications on the risk related to the transport of the material. The design of the plant does not meet the requirements laid down in current legislation for handling of ABPs after their collection. Only a generic HACCP plan was provided and it was considered inadequate. Major deficiencies were noted in relation to the risks associated with interdependent processes, in particular, as regards to the biofilter, the opening of the bioreducer and the ability to sample for Transmissible spongiform encephalopathies surveillance. The biofilter was not considered effective in containing the risk of aerogenic transmission of biological agents and it is accessible to living vectors. Moreover, there is a risk of release of pathogens to the environment when opening the vessel. Therefore, the whole system cannot be considered as a closed system. The proposed Bioreduction method cannot be considered as a safe alternative method for on farm containment of animal by-products.

EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2013. Scientific Opinion on Carbapenem resistance in food animal ecosystems

Carbapenems are broad-spectrum β-lactam antimicrobials used for the treatment of serious infections in humans. To date only sporadic studies have reported the occurrence of carbapenemase-producing (CP) bacteria in food-producing animals and their environment. The bacteria and enzymes isolated include VIM-1 producing Escherichia coli and Salmonella Infantis from pigs and poultry in Germany, OXA-23-producing Acinetobacter spp. from cattle and horses in France and Belgium, and NDM-producing Acinetobacter spp. from pigs and poultry in China. In the German S. Infantis and E. coli isolates, the VIM-1-encoding genes were located on IncHI2 plasmids. A methodology including selective culture is proposed for the detection of CP strains of Enterobacteriaceae and Acinetobacter spp. The choice of selective media for the surveillance of carbapenem resistance for testing animal and food samples needs to be experimentally evaluated and validated. Biochemical and phenotypic tests for the confirmatory identification of CP bacteria are available. For CP bacteria in animals and food, active/passive monitoring and/or targeted surveys should cover key zoonotic agents, animal pathogens and indicator organisms. Priority should be given to broilers, fattening turkeys, fattening pigs, veal calves and meat thereof. Because there are no data on the comparative efficacy of individual control options, prioritisation is complex. Continued prohibition of the use of carbapenems in food-producing animals would be a simple and effective option. As genes encoding carbapenemase production are mostly plasmid-mediated, and co-resistance may be an important issue in the spread of such resistance mechanisms, decreasing the frequency of use of antimicrobials in animal production in the EU in accordance with prudent use guidelines is also of high priority. The effectiveness of any control measures should be
monitored by targeted surveys, using selective isolation methods and pre-enrichment of samples. Control measures should be proactively implemented at national and international levels to prevent CP strains become widespread in livestock.

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**EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards) , 2013**. **Scientific Opinion on the evaluation of molecular typing methods for major food-borne microbiological hazards and their use for attribution modelling, outbreak investigation and scanning surveillance: Part 1 (evaluation of methods and applications)**

An evaluation of molecular typing methods that can be applied to the food-borne pathogens Salmonella, Campylobacter, Shiga toxin-producing Escherichia coli and Listeria monocytogenes is presented. This evaluation is divided in two parts. Firstly, commonly used molecular typing methods are assessed against a set of predefined criteria relating to discriminatory capacity, reproducibility, repeatability and current or potential suitability for international harmonisation. Secondly, the methods are evaluated for their appropriateness for use in different public health-related applications. These applications include outbreak detection and investigation, attribution modelling, the potential for early identification of food-borne strains with epidemic potential and the integration of the resulting data in risk assessment. The results of these evaluations provide updated insights into the use and potential for use of molecular characterisation methods, including whole genome sequencing technologies, in microbial food safety. Recommendations are also made in order to encourage a holistic and structured approach to the use of molecular characterisation methods for food-borne pathogens; in particular, on the importance of structured co-ordination at international level to help overcome current limitations in harmonisation of data analysis and interpretation.

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Bovine intestines and mesenteries in the European Union (EU) have to be removed from the food and feed chain. The opinion provides a quantitative assessment of the Bovine Spongiform Encephalopathy (BSE) infectious load that might enter the food and feed chain yearly if bovine intestine and mesentery from animals born and raised in the EU would be re-allowed for consumption. Data on the evolution of the BSE infectious titre; and of the weight of histological structures accumulating BSE infectivity, were collected. The Cattle TSE Monitoring Model (C-TSEMM) was used to estimate the number of BSE infected cattle entering undetected in the food and feed chain yearly. A model named TSEi was developed to estimate the BSE infectious load in tissues from infected animals at different ages and the total yearly infectious load that could enter the food and feed chain yearly. In BSE infected cattle, the infectivity associated with intestine and mesentery reaches its maximum in animals younger than 18 months and then progressively declines to a minimum value in animals older than 60 months. Due to the decline of the BSE prevalence in the EU, between 2007 and 2012, the yearly amount of BSE infectivity associated with intestine and mesentery (sent to destruction) from animals entering the food and feed chain was reduced by a factor of 10. However, over this period, the maximum level of exposure to the BSE agent for individuals that would have consumed these tissues remained stable. Finally, the TSEi model indicated that the removal of the last four metres of the small intestine and of the caecum from the food and feed chain would result in a major reduction of the BSE exposure risk associated with intestine and mesentery in cattle.

Surveillance programmes based on active and harmonised sampling are considered the most suitable for food-borne outbreak investigations, hypothesis generation, early detection of emerging pathogen subtypes, attribution modelling and genetic studies of bacterial populations. Currently, prototype molecular databases are not widely linked and contain limited epidemiological data, therefore development of linkage mechanisms is a priority. A key technical requirement is determination of an agreed threshold value for the level of genetic variation amongst isolates that can still be regarded as epidemiologically-related. Molecular typing data should be coupled with a minimum required set of epidemiological data and datasets should be comparable to facilitate joint analyses in conjunction with human case data. Rules for assembling
strain collections and associated provenance data should be agreed and introduced as EU standards. The data collection process and the characteristics of the data repository should ensure reproducibility and maximise compatibility and interoperability between different datasets. Molecular bacterial characterisation developments, particularly Whole Genome Sequencing (WGS), should be harmonised with those used for surveillance in the human population and food industry. Reference methods and materials, including sequence data, should be adopted for typing of food-borne pathogens. Upload of molecular data should only be allowed for approved laboratories and should be subject to External Quality Assessment. Ongoing international oversight is required to ensure a consensual 'one-health' approach. The establishment of a joint EFSA-ECDC-EU-RLs committee for the support of cross-sectoral molecular surveillance, with a balance of public health and veterinary expertise and including both epidemiologists and microbiologists is strongly recommended. Revision of the legal basis of programmes for pathogen reduction based on historic organism nomenclature may be necessary following the increased use of WGS and the subsequent identification of more biologically relevant groupings of organisms.

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EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the evaluation of the safety and efficacy of peroxyacetic acid solutions for reduction of pathogens on poultry carcasses and meat

Studies evaluating the safety and efficacy of solutions, containing peroxyacetic acid (PAA) as the active ingredient, in mixtures with acetic acid, hydrogen peroxide, and 1-hydroxyethylidene-1,1-diphosphonic acid (HEDP) and possibly octanoic acid and peroxyoctanoic acid, for reduction of pathogens on poultry carcasses and meat were assessed. Treatments at ambient temperature consisted of dipping in short term baths, in chiller baths or spraying. On the basis of the previous EFSA exposure scenarios including short term baths that were not evaluated previously, no toxicity concerns were identified with regard to residues of peroxyacids, to HEDP and to possible reaction products of hydrogen peroxide and peroxyacids with lipids and proteins of the poultry carcasses. A relevant reduction of PAA treatment on E. coli and coliforms was demonstrated by dipping warm carcasses, but few data were available for pathogens (Salmonella and Campylobacter). Spraying appeared to be less effective than dipping in reducing indicator organisms than dipping. When dipping chilled carcasses, reduction of indicator organisms and pathogens was evident, although only in low or medium strength of evidence studies. In chiller bath application, there was a relevant impact on E. coli, but less effect on coliforms, and little data was available on reduction of pathogens. The emergence of acquired reduced susceptibility to biocides and/or resistance to therapeutic antimicrobials following the use of PAA was considered unlikely. There were no concerns for environmental risk of peroxyacids, acetic acid and octanoic acid. On the basis of a conservative preliminary guideline for surface water quality, the emission of HEDP from a poultry plant into the environment could not be considered safe a priori. It was recommended that HACCP plans should include monitoring of the concentration of HEDP and of the decontaminating substance in the working solution and post-marketing surveillance for resistance in both pathogenic and commensal bacteria.

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Authors: EFSA Publication
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the public health risks of table eggs due to deterioration and development of pathogens

Salmonella Enteritidis is considered the only pathogen currently posing a major risk of egg-borne diseases in the European Union (EU). The possible impact of extending the shelf-life of eggs on the risk to consumers posed by S. Enteritidis was estimated by applying a quantitative model and comparing the actual situation regarding the storage of eggs in the EU with different possible scenarios combined, considering the prolongation of the best-before and the sell-by date from 7 to a maximum of 70 days. Extending the sell-by date by one week (from 21 to 28 days), but leaving the best-before date unchanged, is estimated to result in a relative risk of illness of 1.4 and 1.5 for uncooked and lightly cooked egg meals respectively, compared to the current situation. If the best-before date is also extended by one week (from 28 to 35 days), the relative risk would be 1.6 and 1.7. In the worst case scenario considered (sell-by date of 42 days, best before date of 70 days), such figures would be 2.9 and 3.5. It should be noted that the absolute risk is greater for uncooked meals compared to lightly cooked meals. An effective way to minimise any increase in risk during extended storage is to keep the eggs refrigerated both at retail and the household. Regarding egg spoilage, such events strongly depend on the hygienic conditions of egg production and practices of egg handling, including storage times and temperatures. Finally, the impact of the prolongation of storage time on the quality criteria for eggs (3-hydroxybutyric acid and lactic acid) destined for manufacturing of egg products is considered negligible.

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Salmonella spp., verocytotoxigenic Escherichia coli (VTEC), Listeria monocytogenes and Yersinia enterocolitica are the most relevant microbial pathogens when assessing the effects of beef, pork and lamb carcass chilling regimes on the potential risk to public health. Moreover, as most bacterial contamination occurs on the surface of the carcass, only the surface temperature is an appropriate indicator of bacterial growth. The growth of these four pathogens (using E. coli models for VTEC) during different time-temperature chilling scenarios was estimated using commercial slaughterhouse data and published predictive microbiology models. The outputs suggest it is possible to apply slaughterhouse carcass target temperatures higher than the currently mandated 7 °C throughout the carcass (including the core) in combination with different transport durations without obtaining additional bacterial growth. Combinations of maximum surface temperatures at carcass loading and maximum chilling and transport times, that result in pathogen growth equivalent or less than that obtained when carcasses are chilled to a core temperature of 7 °C in the slaughterhouse are provided.

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EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the public health risks related to the maintenance of the cold chain during storage and transport of meat. Part 2 (minced meat from all species)

Fresh meat intended for the production of minced meat may be contaminated by a range of pathogens including Salmonella spp. and verocytotoxigenic Escherichia coli (VTEC). These may grow if the temperatures are not maintained below 5 °C along the continuum from carcass chilling to mincing. Moreover Listeria monocytogenes and Yersinia enterocolitica will grow at chill temperatures, albeit slowly, but significant growth may occur during prolonged storage. Current legislation (Regulation (EC) 853/2004) requires that red meat carcases are immediately chilled after post-mortem inspection to not more than 7 °C throughout and that this temperature be maintained until mincing which must take place not more than 6 or 15 (vacuum-packed meat) days after slaughter. The corresponding figures for poultry are 4 °C and 3 days. The impact of storage time between slaughter and mincing on bacterial pathogen growth was investigated using predictive modelling. Storage time-temperature combinations that allow growth of Salmonella, VTEC, L. monocytogenes and Y. enterocolitica equivalent to those obtained under the conditions defined by Regulation (EC) 853/2004 were identified. As the modelling assumed favourable pH and aw for bacterial growth, no microbial competition and no lag phase, the equivalent times reported are based on worst-case scenarios. This analysis suggested, for example, that red meat, vacuum packed beef and poultry could be stored at 2 °C for up to 14, 39 and 5 days, respectively, without more bacterial pathogen growth occurring than that which would be achieved under current legislative conditions. It was therefore concluded that alternative time-temperature combinations for the storage of fresh meat between slaughter and mincing are possible without increasing bacterial pathogen growth, and maximum times for the storage of fresh meat intended for minced meat preparation are provided for different storage temperatures. The impact of spoilage on maximum storage times was not considered.
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the risk posed by pathogens in food of non-animal origin. Part 2 (Salmonella and Norovirus in berries)

Berries are a perishable food which can be consumed as fresh or minimally-processed as well as a frozen ingredient added to many foods. Strawberries, raspberries, blackberries and blueberries are the most commonly consumed in the EU. Risk factors for berry contamination by Salmonella and Norovirus were considered in the context of the whole food chain. Available estimates of the prevalence of these pathogens in berries were evaluated together with mitigation options relating to prevention of contamination and the relevance of microbiological criteria. It was concluded that each farm environment represents a unique combination of risk factors that can influence occurrence and persistence of pathogens in berry production. Appropriate implementation of food safety management systems including Good Agricultural Practices (GAP), Good Hygiene Practices (GHP) and Good Manufacturing Practices (GMP), should be primary objectives of berry producers. There is currently insufficient evidence to justify the establishment of microbiological criteria for Salmonella for fresh or frozen berries. Outbreaks associated with Norovirus in frozen raspberries and strawberries are an emerging public health risk, although it is not known if in these outbreaks contamination occurred at minimal processing or during primary production. It is currently not possible to assess the suitability of an EU-wide Norovirus Hygiene Criterion at primary production for raspberries and strawberries. Microbiological criteria for Norovirus in berries are useful for validation and verification of food safety management systems, including HACCP-based processes and procedures, and can be used to communicate to food business operators and other stakeholders what is acceptable or unacceptable, however there is insufficient data to provide a risk base for establishing a Process Hygiene and Food Safety Criteria for Norovirus in berries. Collection of appropriate data and subsequent risk-based development of microbiological criteria to support improved control of Norovirus in frozen raspberries and strawberries should be considered as a priority.
Leafy greens eaten raw as salads are minimally processed and widely consumed foods. Risk factors for leafy greens contamination by Salmonella spp. and Norovirus were considered in the context of the whole food chain including agricultural production and processing. Available estimates of the prevalence of these pathogens (together with the use of Escherichia coli as an indicator organism) in leafy greens were evaluated. Specific mitigation options relating to contamination of leafy greens were considered and qualitatively assessed. It was concluded that each farm environment represents a unique combination of numerous characteristics that can influence occurrence and persistence of pathogens in leafy greens production. Appropriate implementation of food safety management systems, including Good Agricultural Practices (GAP), Good Hygiene Practices (GHP) and Good Manufacturing Practices (GMP), should be primary objectives of leafy green producers. The relevance of microbiological criteria applicable to production, processing and at retail/catering were considered. The current legal framework does not include microbiological criteria applicable at primary production which will validate and verify GAP and GHP. It is proposed to define a criterion at primary production of leafy greens which is designated as Hygiene Criterion, and E. coli was identified as suitable for this purpose. A Process Hygiene Criterion for E. coli in leafy green packaging plants or fresh cutting plants was considered and will also give an indication of the degree to which GAP, GHP, GMP or HACCP programs have been implemented. A Food Safety Criterion for Salmonella in leafy greens could be used as a tool to communicate to producers and processors that Salmonella should not be present in the product. Studies on the prevalence and infectivity of Norovirus are limited, and quantitative data on viral load are scarce making establishment of microbiological criteria for Norovirus on leafy greens difficult.

EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the risk posed by pathogens in food of non-animal origin. Part 2 (Salmonella and Norovirus in leafy greens eaten raw as salads)

Leafy greens eaten raw as salads are minimally processed and widely consumed foods. Risk factors for leafy greens contamination by Salmonella spp. and Norovirus were considered in the context of the whole food chain including agricultural production and processing. Available estimates of the prevalence of these pathogens (together with the use of Escherichia coli as an indicator organism) in leafy greens were evaluated. Specific mitigation options relating to contamination of leafy greens were considered and qualitatively assessed. It was concluded that each farm environment represents a unique combination of numerous characteristics that can influence occurrence and persistence of pathogens in leafy greens production. Appropriate implementation of food safety management systems, including Good Agricultural Practices (GAP), Good Hygiene Practices (GHP) and Good Manufacturing Practices (GMP), should be primary objectives of leafy green producers. The relevance of microbiological criteria applicable to production, processing and at retail/catering were considered. The current legal framework does not include microbiological criteria applicable at primary production which will validate and verify GAP and GHP. It is proposed to define a criterion at primary production of leafy greens which is designated as Hygiene Criterion, and E. coli was identified as suitable for this purpose. A Process Hygiene Criterion for E. coli in leafy green packaging plants or fresh cutting plants was considered and will also give an indication of the degree to which GAP, GHP, GMP or HACCP programs have been implemented. A Food Safety Criterion for Salmonella in leafy greens could be used as a tool to communicate to producers and processors that Salmonella should not be present in the product. Studies on the prevalence and infectivity of Norovirus are limited, and quantitative data on viral load are scarce making establishment of microbiological criteria for Norovirus on leafy greens difficult.

EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the risk posed by pathogens in food of non-animal origin. Part 2 (Salmonella and Norovirus in tomatoes)

Tomatoes may be minimally processed to obtain ready-to-eat products, and these steps include selection, washing, cleaning, stem removal, cutting, packaging and storage. Epidemiological data from the EU have identified one salmonellosis outbreak and one Norovirus outbreak associated with tomato consumption between 2007 and 2012. Risk factors for tomato contamination by Salmonella and Norovirus were considered in the context of the whole food chain. Available estimates of the Salmonella and Norovirus occurrence in tomatoes were evaluated together with mitigation
options relating to prevention of contamination and the relevance of microbiological criteria. It was concluded that each farm environment represents a unique combination of risk factors that can influence occurrence and persistence of pathogens in tomato production. Appropriate implementation of food safety management systems including Good Agricultural Practices (GAP), Good Hygiene Practices (GHP) and Good Manufacturing Practices (GMP), should be primary objectives of tomato producers. The current lack of data does not allow the proposal of a Hygiene Criterion for E. coli at primary production of tomatoes and it is also not possible to assess the suitability of an EU-wide E. coli Process Hygiene Criterion. There are Food Safety Criteria for the absence of Salmonella in 25 g samples of ready-to-eat pre-cut tomatoes as well as in unpasteurised tomato juice placed on the market during their shelf life. A Food Safety Criterion for Salmonella in whole tomatoes could be considered as a tool to communicate to producers and processors that Salmonella should not be present in the product. Testing of tomatoes for Salmonella could be limited to instances where other factors indicate breaches in GAP, GHP, GMP or HACCP programmes. It is currently not possible to provide a risk base for establishing a Norovirus Food Safety Criterion for these foods.

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EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the risk posed by pathogens in food of non-animal origin. Part 2 (Salmonella in melons)
Melons and watermelons are ready-to-eat foods, with an internal pH of 5.1 to 6.7 and can be consumed whole, as fresh-cut products or as fresh juices. Epidemiological data from the EU identified one salmonellosis outbreak associated with consumption of both pre-cut and whole melon between 2007 and 2012. Risk factors for melon and watermelon contamination by Salmonella were considered in the context of the whole food chain, together with available estimates of Salmonella occurrence and mitigation options relating to prevention of contamination and the relevance of microbiological criteria. It was concluded that each farm environment represents a unique combination of risk factors that can influence occurrence and persistence of Salmonella in melon and watermelon production. Appropriate implementation of food safety management systems including Good Agricultural Practices (GAP), Good Hygiene Practices (GHP) and Good Manufacturing Practices (GMP), should be primary objectives of producers. It is currently not possible to assess the suitability of an EU-wide E. coli Hygiene Criterion at primary production. The existing Process Hygiene Criterion for E. coli in pre-cut melons and watermelons aims to indicate the degree to which GAP, GHP, GMP or Hazard Analysis and Critical Control Points (HACCP) programmes have been implemented. There are Food Safety Criteria for the absence of Salmonella in 25g samples placed on the market during their shelf life of ready-to-eat pre-cut melon and watermelon and unpasteurised melon and watermelon juices. A Food Safety Criterion for Salmonella in whole melons and watermelons could be considered as a tool to communicate to producers and processors that Salmonella should not be present in the product. Since the occurrence of Salmonella is likely to be low, testing of whole melons or watermelons for this bacterium could be limited to instances where other factors indicate breaches in GAP, GHP, GMP or HACCP programmes.

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Authors: EFSA Publication
Number of pages: 77
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the risk posed by pathogens in food of non-animal origin. Part 2 (Salmonella Yersinia, Shigella and Norovirus in bulb and stem vegetables, and carrots)

Bulb and stem vegetables as well as carrots may be minimally processed to obtain ready-to-eat products, and these steps include selection, washing, cleaning, cutting, packaging and storage. Risk factors for the contamination of bulb and stem vegetables as well as carrots with Salmonella, Yersinia, Shigella and Norovirus were considered in the context of the whole food chain. Available estimates of their occurrence in these vegetables were evaluated together with mitigation options relating to prevention of contamination and the relevance of microbiological criteria. Emphasis is given to vegetable types associated with public health risks, i.e. carrots, onion and garlic. It was concluded that each farm environment represents a unique combination of risk factors that can influence the occurrence and persistence of pathogens in the primary production of these vegetables. Appropriate implementation of food safety management systems including Good Agricultural Practices (GAP), Good Hygiene Practices (GHP) and Good Manufacturing Practices (GMP) should be the primary objectives of producers of bulb and stem vegetables as well as carrots. Considering the limited evidence for both the occurrence and public health risks from contamination of Salmonella, Shigella, Yersinia and Norovirus in the primary production and minimal processing of bulb and stem vegetables and carrots, no conclusions can be made on the impact of the establishment of microbiological Hygiene Criteria, Process Hygiene Criteria or Food Safety Criteria on public health. There is a lack of data on the occurrence and levels of Escherichia coli in bulb and stem vegetables as well as carrots. Thus, the effectiveness of E. coli criteria to verify compliance to GAP, GHP, GMP and food safety management systems (including HACCP) in the production and minimal processing of bulb and stem vegetables as well as carrots cannot be assessed.

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Authors: EFSA Publication
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Publication date: 2014
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Scientific Opinion on the scrapie situation in the EU after 10 years of monitoring and control in sheep and goats
To assess the effectiveness of the strategies implemented in the European Union (EU) to control Classical scrapie (CS), epidemiological data have been compared in the context of the efforts in terms of control measures applied over time. Official EU surveillance data and results from questionnaire surveys of EU Member States (MSs) have been used along with case studies. A spatio-temporal description of the occurrence of small ruminants TSEs in MSs in the period 2002-2012 is provided, with a particular focus on CS in sheep. Based on information collected from MSs, the potential effectiveness of breeding programmes for resistance to CS (BP-CS) in the dissemination of resistance into the general sheep population has been assessed for those countries for which the CS trend analysis has been performed. CS in sheep was reported in 17 MSs (average prevalence: 8.7 cases/10 000 tests), with heterogeneous trends and geographical distribution: among the 13 countries reporting a consistent number of cases, the trend analysis shows a statistically significant decreasing trend only for six of them. Variations in the implementation of genetic and non-genetic measures for the control of CS may explain the failure to improve the disease situation in the remaining seven MSs. At a national level, a reduction in CS seems to be linked to better-achieving BP-CSs. Control options applied to CS in sheep and goats indicate that a CS eradication policy that relies solely on the detection of infected flocks by post-mortem testing and subsequent depopulation would be unlikely to succeed. A minimum frequency of the ARR allele in a sheep population above which CS may be expected to fade-out could be estimated for each specific national sheep population. Recommendations for additional/alternative measures to control CS in sheep and goats are formulated.

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EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2014. Statement on the update of the list of QPS-recommended biological agents intentionally added to food or feed as notified to EFSA 1: Suitability of taxonomic units notified to EFSA until October 2014
EFSA is requested to assess the safety of a broad range of biological agents in the context of notifications for market authorisation as sources of food and feed additives, enzymes and plant protection products. The qualified presumption of safety (QPS) assessment was developed to provide a harmonised generic pre-assessment to support safety risk assessments performed by EFSA's scientific Panels. The safety of unambiguously defined biological agents (at the highest taxonomic unit appropriate for the purpose for which an application is intended), and the completeness of the body of knowledge are assessed. Identified safety concerns for a taxonomic unit are, where possible and reasonable in number, reflected as ‘qualifications’ in connection with a recommendation for a QPS status. A total of 99 biological agents were notified to EFSA between May 2013 and October 2014. From those, 26 biological agents already had a QPS status and were not further evaluated, and 54 were also not included as they are filamentous fungi or enterococci, biological groups which have been excluded from the QPS activities since 2014. The remaining 19 notifications were considered for the assessment of the suitability for the QPS list. These 19 notifications referred to 13 taxonomic units which were evaluated
for the QPS status, three of which were recommended for the QPS list: a) Carnobacterium divergens, with the qualification of absence of acquired antibiotic resistance determinants; b) Microbacterium imperiale, only for enzyme production, and c) Candida cylindracea, only for enzyme production.

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Projekt 15: Tilpasning af den offentlige kontrol - risikobaseret kødkontrol

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology, Division of Epidemiology and Microbial Genomics
Authors: Bollerslev, A. M. (Intern), Hansen, T. B. (Intern), Hald, T. (Intern), Nauta, M. (Intern), Aabo, S. (Intern)
Number of pages: 33
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Main Research Area: Technical/natural sciences
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Relative human risk of Salmonella Enteritidis in table eggs

General information
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Organisations: National Food Institute, Division of Risk Assessment and Nutrition, Research Group for Genomic Epidemiology
Authors: Korsgaard, H. (Intern), Struve, T. (Intern), Hald, T. (Intern), Vigre, H. (Intern)
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Place of publication: Søborg
Publisher: National Food Institute, Technical University of Denmark
Editors: Vedel Sørensen, A. I., Helwigh, B., Müller, L.
Source attribution of human campylobacteriosis in Denmark

This study assesses the contribution of different sources of human campylobacteriosis in Denmark using two different source-attribution approaches. In total, 794 non-human isolates and 406 isolates from human cases (domestic, travel related, and cases with unknown travel history) were collected. Isolates were characterized by multilocus sequence typing, flaA typing and susceptibility to antibiotics. Both models used indicate that the major burden of human campylobacteriosis in Denmark originates from the domestic broiler chicken reservoir. The second most important reservoir was found to be cattle. The Asymmetric Island model attributed 52% (95% credibility interval (CrI) 37-67) to Danish chicken, 17% (95% CrI 3-33) to imported chicken, and 17% (95% CrI 7-28) to cattle. Similarly, the Campylobacter source-attribution model apportioned 38% (95% CrI 28-47) to Danish chicken, 14% (95% CrI 10-18) to imported chicken, and 16% (95% CrI 7-25) to cattle. The addition of flaA type as an extra discriminatory typing parameter did not change the attribution of cases markedly.

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Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Division of Food Microbiology, Statens Serum Institut
Authors: Boysen, L. (Intern), Rosenquist, H. (Intern), Rosenquist, J. T. (Ekstern), Nielsen, E. M. (Ekstern), Sørensen, G. (Intern), Nordentoft, S. (Intern), Hald, T. (Intern)
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Web of Science (2017): Impact factor 2.044
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): Impact factor 2.075
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): Impact factor 2.515
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): Impact factor 2.535
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.337 SNIP 1.113 CiteScore 2.57
Web of Science (2013): Impact factor 2.491
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Web of Science (2013): Indexed yes
Reducing the burden of foodborne salmonellosis is challenging. It requires identification of the most important food sources causing disease and prioritization of effective intervention strategies. For this purpose, a variety of methods to estimate the relative contribution of different sources of Salmonella infections have been applied worldwide. Each has strengths and limitations, and the usefulness of each depends on the public health questions being addressed. In this study, we reviewed the source attribution methods and outcomes of several studies developed in different countries and settings, comparing approaches and regional differences in attribution estimates. Reviewed results suggest that illnesses and outbreaks are most commonly attributed to exposure to contaminated food, and that eggs, broiler chickens, and pigs are among the top sources. Although most source attribution studies do not attribute salmonellosis to produce, outbreak data in several countries suggest that exposure to raw vegetables is also an important source. International travel was also a consistently important exposure in several studies. Still, the relative contribution of specific sources to human salmonellosis varied substantially between studies. Although differences in data inputs, methods, and the point in the food system where attribution was estimated contribute to variability between studies, observed differences also suggest regional differences in the epidemiology of salmonellosis.
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
Web of Science (2016): Impact factor 2.12
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.064 SNIP 1.035 CiteScore 2.41
Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.953 SNIP 1.051 CiteScore 2.16
Web of Science (2014): Impact factor 1.905
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.184 SNIP 1.129 CiteScore 2.41
Web of Science (2013): Impact factor 2.092
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.185 SNIP 1.144 CiteScore 2.55
Web of Science (2012): Impact factor 2.283
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.118 SNIP 1.037 CiteScore 2.33
Web of Science (2011): Impact factor 2.26
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.86 SNIP 0.94
Web of Science (2010): Impact factor 2.134
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.864 SNIP 1.088
Web of Science (2009): Indexed yes
Scopus rating (2008): SJR 0.72 SNIP 0.682
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.611 SNIP 0.621
The interaction between human antimicrobial use and the risk of foodborne zoonotic bacteria

Salmonella enterica, Campylobacter jejuni and Campylobacter coli are the most common causes of foodborne bacterial infections worldwide. Both bacterial species have many modes for transmission in the food chain through which humans can be infected. The widespread use of antimicrobial drugs for food animals and the consequent dissemination of antimicrobial drug resistance have been well described in literature. Much less investigated is the association between human antimicrobial drug use and the adverse consequences it may have on human infections.

This thesis addresses the relation between antimicrobial drug use in humans, and the acquisition of infection with antimicrobial resistant non-typhoidal Salmonella, Campylobacter coli (C. coli), and Campylobacter jejuni (C. jejuni). The main objectives were:

1) To assess if the history of human use of antimicrobial drugs is a risk factor for acquiring infection with an antimicrobial Salmonella or Campylobacter strain.
2) To compare clinical outcome of disease for patients infected with Salmonella Typhimurium having different antimicrobial susceptibility profiles (i.e. pansusceptible, resistant or multidrug-resistant).
3) To examine how clinical outcome of an infection is affected by previous antimicrobial exposure.

A general overview of the discovery of antimicrobials, and the development and mechanisms of antimicrobial drug resistance in Salmonella, C. jejuni, and C. coli are described in chapter 2. Several features of the epidemiology, sources of infection, antimicrobial resistance, and surveillance of Salmonella and Campylobacter are described in chapter 3 and 4, respectively.

The history of human use of antimicrobial drugs in relation to acquiring an infection with Salmonella or Campylobacter, and the subsequent risk of the causative pathogen being resistant to the drug taken previously and unrelated to the infection in question was assessed in Manuscript I and Manuscript II. Both studies had the same study design: registry based case-control study, for which several of the Danish registries were merged using the unique Civil Registration Number (CPR), and approximately ten controls were matched to each patient on sex, age, and county of residence. Data on history of antimicrobial use was derived from the National Prescription database; cases enrolled in the study were retrieved from the National Registry for Enteric Patients (NREP); the Integrated Database on Labour Market Research provided data on socio-demographics of cases and controls; and the Civil Registry System was used to derive the CPR numbers, date of birth, and residential area of cases and controls.

A total of 22,609 Salmonella cases that were laboratory confirmed between 1997 - 2005, were enrolled in the study. The analyses were performed separately for Salmonella Typhimurium (S. Typhimurium, 4,534 cases), Salmonella Enteritidis (S. Enteritidis, 4,195 cases), and all other Salmonella serotypes combined (5,776 cases). We found that treatment with trimethoprim, sulphonamides, broad-spectrum penicillins, tetracyclines and fluoroquinolones, during one year before diagnosis, was associated with an increased risk of non-typhoid Salmonella infection. Overall, the highest risk was associated with the prior use of fluoroquinolones. The risk increased as the time-window of exposure approached the infection date. The Odds Ratios (OR) for previous use of fluoroquinolones were OR 4.6 (95% confidence interval (CI): 3.8 – 5.5) for other Salmonella serotypes, an OR 2.2 (95%CI: 1.7 – 2.9) for S. Typhimurium, and an OR 2.1 (95%CI: 1.8 – 2.4) for S. Enteritidis. Additionally for fluoroquinolones, we found an interaction term for the pathogen being resistant to fluoroquinolones and a history of fluoroquinolone use; OR 3.6 (95%CI: 1.2 – 10.3) for S. Typhimurium and OR 2.7 (95%CI: 1.2 – 5.9). Meaning that the risk for being diagnosed with a fluoroquinolone resistant S. Typhimurium after treatment with this drug in up to a year before diagnosis was 7.2 (2.0*3.6) times higher for patients than for controls. For S. Enteritidis the corresponding risk was 4.5 (1.7*2.7) times higher for cases than for controls. These findings are ascribed to the competitive and the selective effect of acquiring antimicrobial resistance, respectively. The competitive effect occurs when a course of antimicrobials taken disrupts the natural barrier effect of the gut flora. The selective effect is an additional effect, occurring when a person is exposed to a pathogen resistant to the antimicrobial taken. This increases the risk of infection further due to the selective pressure put on other bacteria susceptible to the drug taken.

Between 1999 – 2005, a total of 31,699 cases of Campylobacter were laboratory confirmed in Denmark, and thus enrolled in the study. We found that being diagnosed with Campylobacter was associated with an increased odds of exposure to a course of fluoroquinolones, macrolides, broad spectrum penicillins, tetracyclines, and sulphonamides and trimethoprim, up to one year before onset of disease. The risk was highest for taking fluoroquinolones (OR 2.4, 95%CI: 2.0 – 3.0). Due to the low number of Campylobacter isolates being tested for other antimicrobial drugs than fluoroquinolones and...
macrolides, it was only possible to calculate the interaction term (or selective effect) for these two drugs. For fluoroquinolones, we found an effect modification of the strain additionally being resistant to the drug taken (OR 1.6, 95%CI: 1.1 – 2.3). The odds of being exposed to a course of fluoroquinolones was 2.4 times higher for cases diagnosed with a fluoroquinolone-sensitive Campylobacter than for controls whereas the odds of being exposed to a fluoroquinolone was 3.8 (2.4*1.6) times higher for cases with a fluoroquinoloneresistant Campylobacter than for controls. For macrolides, the interaction term was not significant (OR 1.0, 95%CI: 0.7 – 1.5). However, when we performed cubic spline plots of the OR of being exposed to a course of antimicrobials we found that being exposed to a course of macrolides provided a protective effect for being diagnosed with Campylobacter, up to one month before diagnosis. This effect is likely to be caused by the fact that the metabolites and active compound of macrolides are trapped into lysosomes of phagocytic cells, and get released at a very low rate and provide prolonged protection against invasive bacteria such as Campylobacter.

In Manuscript III, the relation between clinical outcomes of infection with S. Typhimurium and the antimicrobial resistance profile of the causative strain was assessed, together with the association between outcome of infection and previous antimicrobial use. A prospective case-case study was performed, using data obtained through telephone-conducted interviews, which were merged with data from the NREP and the Civil Registry System. Data were analysed using logistic regression. The interviews were conducted between January-June 2010, and a total of 150 S. Typhimurium cases were enrolled in the study. Cases were divided into three different groups according to the resistance pattern of the strain they were infected with: pansusceptible (S), resistant (R) to 1-3 antimicrobials, or multidrug-resistant (MR), i.e. resistant to 4 or more antimicrobials. We found that previous antimicrobial use, unrelated to the current S. Typhimurium infection, was associated with a higher odds of weight loss (OR 2.4, 95%CI: 1.1 – 5.5), hospital admission (OR 2.0, 95%CI: 1.0 – 4.1), and antimicrobial therapy for the current salmonellosis (OR 7.9, 95%CI: 2.8 – 16.8). The study focussed on short-term outcomes of disease (diarrhoea, nausea, etc.), and patients were interviewed relatively shortly after notification in the NREP. This may explain why this study, in contrast to other studies that focussed more on long-term outcome of disease (mortality, bacteraemia, etc.), did not find other more serious disease outcomes to be related to resistance profile. Also, it is possible that, due to our study design, we missed out on the most severely ill people, simply because they were too ill to participate in the interviews.

We also found that patients with a resistant (R) susceptibility profile had a higher odds of being hospitalised due to their salmonellosis (OR 2.5, 95%CI: 1.0 – 6.0), experience abdominal pain (OR 2.9, 95%CI:1.3 – 6.5), and feeling nauseated (OR 2.6, 95%CI: 1.1 – 6.2), than patients with a pansusceptible Salmonella. We found no increasing trend with increasing antimicrobial resistance (S versus MR). These findings may be an extension of the competitive and selective effect of antimicrobial treatment (Manuscript I and Manuscript II), where past antimicrobial treatment depletes or changes the composition of the gut flora in a way that increases severity of infection. Alternatively, a past history of treatment could be an indicator or proxy of a vulnerable patient.

The overall conclusion of this thesis is that human antimicrobial use interacts in many ways with the risk of being infected with antimicrobial-drug resistant strains of Salmonella and Campylobacter, and that treatment with antimicrobials may be associated with severity of infection as well. The protective role of macrolides as observed for Campylobacter infection adds another layer to the complexity of these interactions. Prudent use of antimicrobial drugs should always be advocated in human health practices. Future studies should point out whether the associations found in this thesis also applies to other pathogens.
A multi-country approach for attributing human salmonellosis to animal reservoirs: Global perspectives and application of surveillance data from the European Union

This thesis presents a mathematical modeling approach to estimate the contribution of four animal reservoirs of the food chain to the occurrence of salmonellosis cases in humans in the European Union. In addition, an alternative and more explorative approach based on expert elicitation is attempted in order to extrapolate results to countries with less data availability, as a first step to perform source attribution of Salmonella in a more global perspective.

Cases of foodborne salmonellosis in humans were attributed to travel, outbreaks and four animal reservoirs, namely pigs, broilers, turkeys and laying hens, using a Bayesian model based on microbial subtyping in 24 countries of the European Union. The chosen approach is recognized as data intensive, requiring numbers for Salmonella occurrence in food-producing animals, reported human cases, information on possibility of infection abroad (from here on referred to as "travel information"), human cases originating from outbreaks with and without a confirmed source and amounts of the meat or eggs of each animal reservoir originating from each country and available for consumption in each country. Thus, special data management, analysis and validation was required to produce a dataset containing standardized information for all countries (Manuscript I).

Data on reported human cases were provided by the European Centre for Disease Prevention and Control (ECDC) through the European Food Safety Authority (EFSA). Salmonella prevalences in animals were obtained from the EU-wide baseline studies (BS) conducted by EFSA and complemented where necessary with information found in the European Union Summary Report (EUSR), as published by EFSA. Information on outbreaks was also provided by EFSA. The amount of food available for consumption was calculated based on trade data obtained from the European Statistical Office (EUROSTAT) and complemented with information from the Association of Poultry Processors and Poultry Trade in the European Union Countries (AVEC). Common limitations included non-participation in all BS, non-reporting of outbreaks or travel information, non-reporting of serovar-specific information, non-reporting of case-based data and non-availability of trade data on EUROSTAT. In order to standardize the information available, cases without travel information were assumed to be domestic; cases without specific serovar information were redistributed according to serovar proportions observed in the same dataset or other reference documents; missing trade information was estimated based on previous years, and non-participation in a BS was supplied, where possible, with data from the EUSR. When the lack of original data was considered too extreme to the point of compromising the attribution results, countries were excluded. The resulting dataset comprised Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, the Netherlands, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. Three countries were included in the initial analysis, but were excluded from the final dataset. Those were: Bulgaria, which presented 100% of human cases without serovar detailing; Romania, which only participated in one BS and had not enough surrogate data to be retrieved from the EUSR, besides reporting a large parcel of cases without serovar information; and Norway, which is not part of the EU and does not report to EUROSTAT (Manuscript I).

A Bayesian modeling approach which compares the occurrence of serovars in humans with the occurrence of the same serovars in animals of the food-chain was used to estimate the contribution of each of these reservoirs, travel and outbreaks to the number of human cases of salmonellosis in the 24 countries present in the dataset previously described (Manuscript II). Laying hens (i.e. eggs) were estimated to be the most important source of human salmonellosis at EU level, with 48.1% (95% Credibility Interval (CI) 47.5 – 48.8%) of cases, followed by pigs (29.6%, 95% CI 28.9-30.3%). Turkeys and broilers were estimated to be less important sources of Salmonella, contributing with 4.4% (95% CI 4.2-4.7%) and 3.7% (95% CI 3.4-4.0%), respectively. A total of 10.2% of all salmonellosis cases were reported as being travel-related, and 3.9% of cases were reported as being part of outbreaks with unknown source. S. Enteritidis was the most important serovar in the study, being responsible for 95.9% of cases attributed to laying hens, 56.9% of cases attributed to broilers, 30.4% of turkeys and 28.3% of cases attributed to pigs, for which the main serovar was S. Typhimurium (63.1% of cases attributed to this source). Country-specific results show laying hens as the most important source of salmonellosis in 13 countries (Austria, Czech Republic, Estonia, Germany, Greece, Hungary, Latvia, Lithuania, Luxembourg, Slovenia, Slovakia, Spain and the United Kingdom), whereas pigs were the larger animal contributor in eight (Belgium, Cyprus, Finland, France, Ireland, Italy, Poland and Sweden). In Finland and Sweden the majority of Salmonella infections were estimated to be travel-related. Travel was also an important source in Ireland, the UK and Denmark, although to a lower extent. In the Netherlands, the proportion of disease attributed to layers and pigs were similar. In Denmark, the most important food-animal source was estimated to be turkeys, and broilers were the major source in Portugal. (Manuscript II).

Danish strategies for risk management of Salmonella in the farm-to-fork continuum include the routine application of a source attribution model to estimate the contribution of the major animal-food sources to human infections by Salmonella in Denmark. This model concept formed the basis for the model described in Manuscript II. As part of the validation process of the EU model, results for Denmark in the EU model were compared with the ones obtained using the Danish model in the same period (Manuscript III). The Danish model points to pork as the main animal source of human
salmonellosis in the period (9.3% of cases), followed closely by table eggs (7.5% of cases) and broilers (4.7% of cases), while the EU model attributed 15.6% to pigs, 15.1% to turkeys, 10.5% to eggs and 2.8% to broilers. Travel-related cases constitute 30.6% in the Danish model and only 18.2% in the EU model. Cases that could not be attributed to any source corresponded to 16.7% in the Danish model and 14.1% in the European model. Discrepancies in numbers are explained by differences in model structure and basic assumptions: a) cases with no travel information in the Danish model are redistributed according to proportions observed in cases with full information; in the EU model, as some countries did not provide any information regarding travel prior to sickness, it had to be assumed that no information means no travel; b) the Danish model uses data subtyped to phage-type level, while the EU model only uses serovar level, as phage-type data in humans and animals was not sufficiently available; this allows the more specific allocation of cases to the right sources; c) the larger number of sources in the Danish model allows more options for specific allocation of cases, presumably resulting in a more correct distribution of cases among sources; d) the Danish model uses official data on amount of domestic and imported food items available for consumption in the country, but does not as opposed to the EU model take into account the amount imported from each country specifically, which results in an underestimation of the contribution from high prevalence countries as compared to the EU model (Manuscript III). All facts considered, the two models rank three out of the four sources in a similar order and, while the EU model is considered useful for countries which cannot readily attain the level of detailing found in Denmark for monitoring and surveillance data, Denmark would benefit more from applying country-specific data than to adopt the results of the EU model.

The last chapter presents an alternative approach to obtain results for the Czech Republic, Bulgaria, Norway and Romania, the last three of which were excluded from the EU-model due to insufficient data. Using clustering techniques, 28 countries were grouped according to variables used to characterize them as to social and economic status, animal production characteristics and food consumption patterns. Where available, variables reflecting the occurrence of Salmonella enterica in humans and animals were also used. The results of the analyses were delivered to a panel of experts composed by foodborne disease epidemiologists and risk modelers, which were asked to provide attribution estimates for the aforementioned countries, based on their similarity to countries for which results were previously obtained. Experts were also asked to evaluate the method concerning its utility and applicability of results. Individual estimates were evaluated based on comparison with the Czech results, for which results based on the microbial subtyping model were available, but also in relation to uniformity of guesses and uncertainty intervals among different estimates from the same expert and among all experts in the panel. This evaluation resulted in five out of the seven respondents being maintained in the panel. Although the Czech Republic values obtained did not match the ones observed in the EU study, the order of importance of the animal sources was in agreement between the two studies and there was also a consensus in the panel concerning that order. It is, therefore, believed that with some adjustments, this method may be useful for prioritizing targeted actions for Salmonella control in countries without sufficient data for a traditional approach. Further on, this method may be used to identify “surrogate countries” from where animal prevalence data can be “borrowed” and applied in the traditional microbial subtyping approach in the aforementioned Member States. This PhD project has provided results for a European “source of infection account” for Salmonella, and has at the same time been evaluating the approaches attempted, raising questions and proposing solutions on how to deal with the lack of good-quality data for such studies. The project has also achieved results that may lay the groundwork for future attempts to develop Salmonella source attribution estimates in a more global perspective.
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2013. Scientific Opinion on the public health hazards to be covered by inspection of meat (bovine animals).

A risk ranking process identified Salmonella spp. and pathogenic verocytotoxin-producing Escherichia coli (VTEC) as current high-priority biological hazards for meat inspection of bovine animals. As these hazards are not detected by traditional meat inspection, a meat safety assurance system for the farm-to-chilled carcass continuum using a risk-based approach was proposed. Key elements of the system are risk-categoryisation of slaughter animals for high-priority biological hazards based on improved food chain information, as well as risk-categoryisation of slaughterhouses according to their capability to control those hazards. Omission of palpation and incision during post-mortem inspection for animals subjected to routine slaughter may decrease spreading and cross-contamination with the high-priority biological hazards. For chemical hazards, dioxins and dioxin-like polychlorinated biphenyls were ranked as being of high potential concern; all other substances were ranked as of medium or lower concern. Monitoring programmes for chemical hazards should be more flexible and based on the risk of occurrence, taking into account the completeness and quality of the food chain information supplied and the ranking of chemical substances, which should be regularly updated to include new hazards. Control programmes across the food chain, national residue control programmes, feed control and monitoring of environmental contaminants should be better integrated. Meat inspection is a valuable tool for surveillance and monitoring of animal health and welfare conditions. Omission of palpation and incision would reduce detection effectiveness for bovine tuberculosis and would have a negative impact on the overall surveillance system especially in officially tuberculosis free countries. The detection effectiveness for bovine cysticercosis, already low with the current meat inspection system, would result in a further decrease, if palpation and incision are removed. Extended use of food chain information could compensate for some, but not all, the information on animal health and welfare lost if only visual post-mortem inspection is applied.
Salmonella spp. in farmed wild boar and Toxoplasma gondii in farmed deer and farmed wild boar were ranked as a high priority for meat inspection. Trichinella spp. in wild boar was ranked as low priority due to current controls, which should be continued. For chemical hazards, all substances were ranked as medium or lower potential concern. More effective control of biological hazards could be achieved using an integrated farm to chilled carcass approach, including improved food chain information (FCI) and risk-based controls. Further studies are required on Salmonella spp. in farmed wild boar and T. gondii in farmed wild boar and farmed deer. If new information confirms a high risk to public health from meat from these species, setting targets at carcass level should be considered. Palpation and incision should be omitted, as it will not detect biological hazards considered to be a high priority for meat inspection while increasing the potential spread and cross-contamination of the carcasses with Salmonella. Palpation and/or incision may be applied where abnormalities have been detected but away from the slaughter line. However the elimination of routine palpation and incision would be detrimental for detecting tuberculosis. As farmed deer and farmed wild boar can act as tuberculosis reservoirs, any reduction in the detection, due to changes in the post-mortem inspection procedures, will have consequences for the overall surveillance of tuberculosis. Monitoring programmes for chemical hazards should be more flexible and based on the risk of occurrence, taking into account FCI, which should be expanded to reflect the specific environmental conditions of the farms where the animals are reared, and the ranking of chemical substances, which should be regularly updated and include new hazards. Control programmes across the food chain, national residue control programmes, feed control and monitoring of environmental contaminants should be better integrated.

A risk ranking process identified Toxoplasma gondii and pathogenic verocytotoxin-producing Escherichia coli (VTEC) as the most relevant biological hazards for meat inspection of sheep and goats. As these are not detected by traditional meat inspection, a meat safety assurance system using risk-based interventions was proposed. Further studies are required on T. gondii and pathogenic VTEC. If new information confirms these hazards as a high risk to public health from meat from sheep or goats, setting targets at carcass level should be considered. Other elements of the system are risk-categorisation of flocks/herds based on improved Food Chain Information (FCI), classification of abattoirs according to their capability to reduce faecal contamination, and use of improved process hygiene criteria. It is proposed to omit palpation and incision from post-mortem inspection in animals subjected to routine slaughter. For chemical hazards, dioxins and dioxin-like polychlorinated biphenyls were ranked as being of high potential concern. Monitoring programmes for chemical hazards should be more flexible and based on the risk of occurrence, taking into account FCI, which should be expanded to reflect the extensive production systems used, and the ranking of chemical substances, which should be regularly updated and include new hazards. Control programmes across the food chain, national residue control plans, feed control and monitoring of environmental contaminants should be better integrated. Meat inspection is a valuable tool for surveillance and monitoring of animal health and welfare conditions. Omission of palpation and incision would reduce detection effectiveness for tuberculosis and fasciolosis at animal level. Surveillance of tuberculosis at the slaughterhouse in small
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2013. Scientific Opinion on the public health hazards to be covered by inspection of meat (solipeds)

A risk ranking process identified Trichinella spp. as the most relevant biological hazard in the context of meat inspection of domestic solipeds. Without a full and reliable soliped traceability system, it is considered that either testing all slaughtered solipeds for Trichinella spp., or inactivation meat treatments (heat or irradiation) should be used to maintain the current level of safety. With regard to general aspects of current meat inspection practices, the use of manual techniques during current post-mortem soliped meat inspection may increase microbial cross-contamination, and is considered to have a detrimental effect on the microbiological status of soliped carcass meat. Therefore, the use of visual-only inspection is suggested for “non-suspect” solipeds. For chemical hazards, phenylbutazone and cadmium were ranked as being of high potential concern. Monitoring programmes for chemical hazards should be more flexible and based on the risk of occurrence, taking into account Food Chain Information (FCI), covering the specific on-farm environmental conditions and individual animal treatments, and the ranking of chemical substances, which should be regularly updated and include new hazards. Sampling, testing and intervention protocols for chemical hazards should be better integrated and should focus particularly on cadmium, phenylbutazone and priority “essential substances” approved for treatment of equine animals. Implementation and enforcement of a more robust and reliable identification system throughout the European Union is needed to improve traceability of domestic solipeds. Meat inspection is recognised as a valuable tool for surveillance and monitoring of animal health and welfare conditions. If visual only post-mortem inspection is implemented for routine slaughter, a reduction in the detection of strangles and mild cases of rhodococcosis would occur. However, this was considered unlikely to affect the overall surveillance of both diseases. Improvement of FCI and traceability were considered as not having a negative effect on animal health and welfare surveillance.
EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on the public health risks related to mechanically separated meat (MSM) derived from poultry and swine

The purpose of this assessment was to identify public health risks linked to mechanically separated meat (MSM) types from pork and poultry and compare them with fresh meat, minced meat and meat preparations (non-MSM); and to select, rank and suggest objective measurement methods and values for parameters to distinguish MSM types. Microbial hazards in MSM are expected to be similar to those in non-MSM, although the risk of microbial growth increases with the degree of muscle fibre degradation, thus with the separation pressure. For the distinction between the different types of MSM and non-MSM chemical, histological, molecular, textural and rheological parameters were considered as potential indicators. The analysis of available published data suggested that calcium and, if confirmed cholesterol content, was the only appropriate chemical parameters which could be used to distinguish MSM from non-MSM products. On the basis of published data, a model was developed to derive probabilities for a product to be classified as MSM based on the calcium content. Calcium content of 100 mg/100 g, as specified in the Reg. (EC) No. 2074/2005, corresponds to probability of 93.6% for a product to be classified as MSM, according to the model developed. Calcium content alone does not allow differentiation between low pressure MSM and other meat products, and other validated tests would be necessary. Histological parameters considered include microscopic detection of different tissues and their changes. The latter is a promising method for distinction of MSM types, but further validation is needed. In order to improve methods for MSM identification, specifically designed studies for the collection of data obtained by standardised methods on indicators such as calcium and cholesterol should be undertaken, while studies based on combinations of different parameters could also be useful.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on the risk of transmission of classical scrapie via in vivo derived embryo transfer in ovine animals
The risk of transmission of classical scrapie via the transfer of in vivo derived embryo in ovines was assessed, taking into account the scientific information made available since the last EFSA opinion on this topic (2010) (see http://www.efsa.europa.eu/en/efsajournal/pub/1429.htm). The potential impact of PrP genotype of the embryo and/or of the ram and donor ewe on this risk was also assessed. The new data made available over the last three years further reinforce the view that classical scrapie could be vertically transmitted in sheep. Since the possibility of such vertical transmission was already considered in the previous opinion, its conclusions and recommendations relating to the risk of classical scrapie transmission via embryo transfer remain valid. In ovines, the susceptibility to classical scrapie infection in sheep is strongly influenced by certain polymorphisms of the PrP gene. Under natural exposure conditions, animals that are heterozygous or homozygous A136R154R171 display respectively a low or negligible risk of being infected. The genetic control of the susceptibility to classical scrapie is also likely to impact on the risk of transmitting the disease via embryo transfer. Irrespective of the embryo's genotype, embryos derived from rams and dams carrying at least one ARR allele would significantly decrease this risk (compared to an embryo from parents of unknown genotypes). The use of homozygous ARR embryos would provide the highest level of safety regarding the risk of transmitting classical scrapie through embryo transfer (in vivo derived embryos). The use of heterozygous ARR embryos would ensure a higher level of safety compared to Q171/Q171 embryos. Finally, it was concluded that, providing the OIE recommendations and procedures relating to embryo transfer are adhered to, the risk of transmitting classical scrapie due to the transfer of homozygous or heterozygous ovine ARR embryos can be considered negligible.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on VTEC-seropathotype and scientific criteria regarding pathogenicity assessment
During 2007-2010, 13 545 confirmed human VTEC infections and 777 haemolytic uraemic syndrome (HUS) cases were reported in the EU; isolates from 85 % of cases were not fully serotyped and therefore could not be classified using the Karmali seropathotype concept. Seropathotype group D covered 5 % of isolates from fully serotyped cases; 14 cases (0.7 %) belonged to seropathotype group E, defined by Karmali et al. (2003) as non-human only. Isolates from around 27 % of cases could not be assigned. There were no HUS cases reported for the serotypes in groups D and E but 17 HUS cases could not be assigned. The health outcome was reported for only a fraction of confirmed cases. About 64 % of patients presented with only diarrhoea; VTEC infection resulted in HUS in around 10 % of cases. The new ISO/TS 13136:2012 standard improves the detection of VTEC in food. An alternative concept based on the detection of verocytotoxins alone or genes encoding such verocytotoxins does not provide a sound scientific basis on which to assess risk to the consumer because there is no single or combination of marker(s) that fully define a ‘pathogenic’ VTEC. Strains positive for verocytotoxin 2 gene(vtx2)- and eae (intimin production)- or [aaiC (secreted protein of EAEC) plus aggR (plasmid-encoded regulator)] genes are associated with higher risk of more severe illness than other virulence gene combinations. The 2011 O104:H4 outbreak demonstrated the difficulty of predicting the emergence of ‘new’ pathogenic VTEC types by screening only for the eae gene or by focusing on a restricted panel of serogroups. A molecular approach utilising genes encoding virulence characteristics additional to the presence of vtx genes has been proposed.

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Escherichia coli as indicator of the human Salmonella risk caused by consumption of pork

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Pathogen update: Salmonella
- Introduction
- Incidence and burden of human salmonellosis
- Epidemiology and disease transmission in humans
- Classification and subtypes
- Tracing the sources of human salmonellosis – source attribution
- Discussion on sources to human salmonellosis
- References

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Authors: Hald, T. (Intern)
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Prediction of Salmonella carcass contamination by a comparative quantitative analysis of E. coli and Salmonella during pig slaughter

Faecal contamination of carcasses in the slaughterhouse is generally considered to be the source of Salmonella on pork. In this study the hygiene indicator Escherichia coli is used to quantify faecal contamination of carcasses and it is hypothesized that it can be used to predict the quantitative carcass contamination with Salmonella, when the distribution of Salmonella concentrations in faeces is known. Paired pig sample data (faecal samples and carcass swabs) were obtained from five slaughterhouses and analysed for prevalence and concentrations of E. coli and Salmonella. A simple model was developed to describe the faecal contamination of carcasses using the E. coli data. The E. coli results suggested different hygiene performances in different slaughterhouses, and showed that a model assuming that carcasses are predominantly contaminated by their own faeces was not appropriate. Observed Salmonella prevalences were low (on average 1.9% on carcasses) and between slaughterhouses the prevalences ranked differently than the hygiene performance based on the E. coli data suggested. Also, the Salmonella concentrations predicted using E. coli as a faecal indicator were lower than the observed Salmonella concentrations. It is concluded that the faecal carriage of Salmonella together with the faecal contamination of carcasses, as predicted from E. coli data in the animal faeces and hygiene performance of the slaughterhouse, is not sufficient to explain carcass contamination with Salmonella. Our extensive data set showed that other factors than the observed faecal carriage of Salmonella by the individual animals brought to slaughter, play a more important role in the Salmonella carcass contamination of pork.
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
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Scopus rating (2017): CiteScore 3.76 SJR 1.366 SNIP 1.436
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Scopus rating (2016): CiteScore 3.97 SJR 1.481 SNIP 1.553
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.614 SNIP 1.683 CiteScore 4.02
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
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Web of Science (2014): Impact factor 3.082
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Web of Science (2013): Impact factor 3.155
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
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Web of Science (2012): Impact factor 3.425
ISI indexed (2012): ISI indexed yes
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BFI (2011): BFI-level 2
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Scopus rating (2010): SJR 1.61 SNIP 1.666
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Web of Science (2007): Indexed yes
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Web of Science (2006): Indexed yes
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Trends and sources in human salmonellosis

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WHO Initiative to Estimate the Global Burden of Foodborne Diseases
Background
The public health impact of foodborne diseases globally is unknown. The WHO Initiative to Estimate the Global Burden of Foodborne Diseases was launched out of the need to fill this data gap. It is anticipated that this effort will enable policy makers and other stakeholders to set appropriate, evidence-informed priorities in the area of food safety.

Methods
The initiative aims to provide estimates on the global burden of foodborne diseases by age, sex, and region; strengthen country capacity for conducting burden of foodborne disease assessments in parallel with food safety policy analyses; increase awareness and commitment among Member States for the implementation of food safety policy and standards; and encourage countries to use burden of foodborne disease estimates for cost-effectiveness analyses of prevention, intervention, and control measures. To estimate the global burden (expressed in disability-adjusted life-years), the Foodborne Disease Burden Epidemiology Reference Group (FERG) focused on the contamination of food with enteric and parasitic pathogens, chemicals, and toxins.

Findings
Study findings will provide the technical background and challenges of assessing the burden of foodborne diseases, based on national and international studies. Systematic reviews to support estimates of the incidence and mortality of food-related diseases are being completed. Results will be used to update and refine global burden estimates for relevant food-related hazards, in the context of other international burden of disease studies. It is recognised that exposure to such hazards may also occur through other pathways including the environment (eg, water, air) and by direct transmission (eg, human-to-human and animal-to-human).

Structured expert elicitation will be used to provide the basis for attribution of incidence and burden to food, and estimation of the most important food sources. Interpretation

Estimating the global burden of foodborne diseases is highly complex because of the diversity of hazards that can be transmitted by food, the multitude of health outcomes they cause, and complex transmission pathways. WHO is planning to present a global estimate for the first time in 2014. Funding

WHO.
Assessment of the human-health impact of *Salmonella* in animal feed
Attributing human foodborne illness to food sources and water in Latin America and the Caribbean using data from outbreak investigations

Foodborne pathogens are responsible for an increasing burden of disease worldwide. Knowledge on the contribution of different food sources and water for disease is essential to prioritize food safety interventions and implement appropriate control measures. Source attribution using outbreak data utilizes readily available data from outbreak surveillance to estimate the contribution of different sources to human disease. We developed a probabilistic model based on outbreak data that attributes human foodborne disease by various bacterial pathogens to sources in Latin America and the Caribbean (LA&C). Foods implicated in outbreaks were classified by their ingredients as simple foods (i.e. belonging to one single food category), or complex foods (i.e. belonging to multiple food categories). For each agent, the data from simple-food outbreaks were summarized, and the proportion of outbreaks caused by each category was used to define the probability that an outbreak was caused by a source. For the calculation of the number of outbreaks attributed to each source, simple-food outbreaks were attributed to the single food category in question, and complex-food outbreaks were partitioned to each category proportionally to the estimated probability. We analysed all bacterial pathogens together, focused on important bacterial pathogens separately, and, when data were sufficient, performed analyses by country, decade and location. Between 1993 and 2010, 6313 bacterial outbreaks were reported by 20 countries. In general, the most important sources of bacterial disease were meat, dairy products, water and vegetables in the 1990s, and eggs, vegetables, and grains and beans in the 2000s. We observed fluctuations of the most important sources of disease for each pathogen between decades and countries, which may be a consequence of changes in the control of zoonotic disease over the years, of changes in food consumption habits, or of changes in public health focus and availability of data of different pathogens. This study identified data gaps in the region and highlighted the importance of effective surveillance systems to identify sources of disease. Still, the application of this method for source attribution in the LA&C region was successful, and we concluded that this approach can be used to attribute disease to food sources and water in other regions, including developing regions with limited data on the public health impact of foodborne diseases.
Campylobacter in Denmark: control, human risk and source attribution

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DANMAP 2011: DANMAP 2011 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark

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Development of a Salmonella source-attribution model for evaluating targets in the turkey meat production: Supporting Publications 2012:EN-259

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EFSA has been working on a series of Scientific Opinions originating from a mandate received by the European Commission (EC) in July 2008 on the review of Salmonella targets in poultry primary production. For evaluating targets in the broiler and turkey production, specific Salmonella source attribution models have been developed by external contractors. Both models were based on the Hald model and use a Bayesian approach employing microbial subtyping data, in both cases Salmonella serovar data. These types of source attribution models allow for the identification of the most important animal reservoirs of the zoonotic agent, assisting risk managers to prioritize interventions and focus control strategies at the animal production level. The model can provide estimates for the effect on the number of human cases originating from a particular reservoir, if the observed prevalence in that reservoir is changed or for specific subtypes e.g. specific serovars of Salmonella occurring in that reservoir.

The source-attribution approach has been considered by EFSA Working Groups and Panel Experts as valid when addressing these types of questions, where the use of a classical quantitative risk assessment model (i.e. transmission models) would be impaired due to a lack of data and time limitations. As these models require specialist knowledge, it was requested by EFSA to develop a flexible user-friendly source attribution model for use for example in future mandates dealing with similar questions.

The objective of the work described in this report was, therefore, to develop a flexible and user-friendly interface for attributing human cases of food-borne pathogens to the responsible food-animal reservoirs and/or food sources. The interface is based on a Salmonella source-attribution model developed for setting target for Salmonella in the turkey production: the Turkey Target Source Attribution Model (TT-SAM). Results from this model were used by the BIOHAZ
panel in their related Scientific Opinion. The developed interface described in this report is called the EFSA Source Attribution Model (EFSA_SAM).

The programming language (development environment) used for developing the user-friendly interface is Embarcadero Delphi XE2 Enterprise. The interface generates a WinBUGS code based on the user’s imported data and model selections. The interface exports this code with corresponding data to WinBUGS, where the code is executed automatically. The model results are then imported from WinBUGS to the interface software for tabulation and graphical display, and possible exportation to other softwares for further analysis e.g. MS Excel. This approach ensures consistency in both model and data setup, eliminating the need for user knowledge of the WinBUGS syntax.

Users can import data into the EFSA_SAM from semicolon-separated files. Required data are i) the reported number of human cases per country and subtype including data on the number of travel and outbreak-related cases, also per country and subtype, ii) food-animal prevalence data per country and subtype, including the number of units tested and the number of positive units, and iii) data on the production and trade of the different food-animal sources in the EU Member States. The EFSA_SAM also allows for the inclusion of underreporting factors recognizing that the reported number of human cases only reflects a part of the disease burden and the degree of underreporting varies hugely between countries. In the interface users can specify which countries, food sources and subtypes (e.g. Salmonella serovars) to include in the model.

It is also possible to run an analysis for a single country only, but where several periods (typically years) of data are included. This can provide an indication of the trend over time. Required data for this type of model are i) the reported number of human cases by subtype including data on the number of travel, domestic, unknown travel history and outbreak-related cases, also per subtype, ii) food-animal prevalence data per subtype, including the number of units tested and the number of positive units, and iii) data on the amount of the included animal foods available for consumption in the country.

The data imported into EFSA_SAM will be used for a baseline analysis providing estimates on the number of human cases attributable to the different food-animal sources in the actual situation. The results of the baseline analysis can be compared with the results from one or more scenario analyses specified by the user. The interface allows for two types of scenarios: i) the setting of target prevalences for individual subtypes, and ii) the setting of a combined target prevalence for a group of subtypes. In the first type, EFSA_SAM will automatically change the original prevalence to the set target prevalence, but only if the original prevalence is greater than the target prevalence. In the latter type, the users can select any number of subtypes for which a combined prevalence should be equal or less to a set target prevalence. The EFSA_SAM generates a new set of subtype-specific prevalences that are proportionally scaled down from the original prevalences in order to result in an overall prevalence equal to or less than the target prevalence. A comparison of the baseline and scenario results can be used to assess the effect on the predicted number of human cases, if targeted control measures are implemented for specific subtypes or groups of subtypes.

A critical part of all Bayesian models is to check for model convergence and goodness of fit. The EFSA_SAM describes different ways for checking convergence and include the calculation of the bgr-diagnostics that is also a part of the WinBUGS software. For exploring goodness of fit, a ratio between the observed and predicted number of human cases per country is calculated. A poor fit of the model for some countries is often linked to poor data quality.

The EFSA_SAM interface is delivered with a user-manual, which is also part of this report. Users of the interface are recommended to read this report before starting using the interface to become familiar with the model principles and the mathematics behind, which is required in order to interpret the model results and assess the validity of the model.
Microbiological hazards have been associated with seawater. Poor quality sea water may consequently have a severe impact on public health. Coastal sources used for abstraction of seawater cannot be classified as a pristine source. The use of water safety plans, combining sanitary surveys with microbiological criteria and appropriate water treatment, is proposed in order to ensure adequate hygiene conditions and to control hazards. The comprehensiveness of the sanitary survey, the stringency of microbiological criteria, and the need for treatment depend on the relative exposures associated to the different uses of seawater. For uses with low exposure to microbiological hazards, a basic sanitary survey and microbiological criteria based on the Directive 2006/7/EC are considered appropriate. For uses with a higher exposure, a more comprehensive sanitary survey, mandatory water treatment, and microbiological criteria based on Council Directive 98/83/EC with an additional criterion for Vibrio spp. are considered appropriate. For uses with highest exposure, a more comprehensive sanitary survey, mandatory water treatment, and microbiological criteria based on Council Directive 98/83/EC with an additional criterion for turbidity and Vibrio spp. are considered appropriate. Both inorganic and organic chemicals can be found in seawater in concentrations that are usually low. Therefore the use of seawater on fresh or processed fishery products or for re-vitalisation of live molluscs is unlikely to raise a health concern. A potential health concern may occur from the domestic use of bottled seawater where human exposure might be expected to be higher than for the other uses of seawater. Therefore, the concentration of chemicals in bottled seawater should comply with the standards laid down in Council Directive 98/83/EC on the quality of water intended for human consumption. It is recommended to use ultraviolet (UV) or other physical methods as the preferred disinfection process to prevent the formation of hazardous disinfection by-products such as bromate and trihalomethanes.
reducing contamination with pathogenic microorganisms on fresh broiler carcasses. The efficacy of the treatment appeared to be influenced more by the concentration of the active ingredient (within the range of 0.2% to 0.5%), than by the volume of solution applied, flow rate, spraying pressure, rate of carcass processing, and time of exposure. The data about the potential emergence and selection of isolates with reduced susceptibility to biocides and/or resistance to therapeutic antimicrobials linked to the use of CPC under the conditions of application, in the recycled solution and in the wastewater, were not provided or not considered sufficient for the assessment. Based on the available limited data, the intended use of CPC in poultry slaughterhouses would pose risks for the environmental compartments surface water, sediment and soil. No risks for the function of sewage treatment plants are expected and there are no safety concerns regarding secondary poisoning for birds and mammals, and for humans indirectly exposed via the environment.

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EFSA Panel on Biological Hazards (BIOHAZ); Norovirus (NoV) in oysters: methods, limits and control options

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EFSA Panel on Biological Hazards (BIOHAZ) Panel; Scientific Opinion on the risk posed by pathogens in food of non-animal origin. Part 1 (outbreak data analysis and risk ranking of food/pathogen combinations)

Food of non-animal origin (FoNAO) is consumed in a variety of forms, and a major component of almost all meals. These food types have the potential to be associated with large outbreaks as seen in 2011 associated with VTEC O104. A comparison of the incidence of human cases linked to consumption of FoNAO and of food of animal origin (FoAO) was carried out to provide an indication of the proportionality between these two groups of foods. It was concluded that outbreak data reported as part of EU Zoonoses Monitoring is currently the only option for EU-wide comparative estimates. Using this data from 2007 to 2011, FoNAO were associated with 10% of the outbreaks, 26% of the cases, 35% of the hospitalisations and 46% of the deaths. If the data from the 2011VTEC O104 outbreak is excluded, FoNAO was associated with 10% of the outbreaks, 18% of cases, but only 8% of the hospitalisations and 5% of the deaths. From 2008 to 2011 there was an increase in the numbers of reported outbreaks, cases, hospitalisations and deaths associated with food of non-animal origin. In order to identify and rank specific food/pathogen combinations most often linked to human cases originating from FoNAO in the EU, a model was developed using seven criteria: strength of associations between food and pathogen based on the foodborne outbreak data from EU Zoonoses Monitoring (2007-11), incidence of illness, burden of disease, dose-response relationship, consumption, prevalence of contamination and pathogen growth potential during shelf life. Shortcomings in the approach using outbreak data were discussed. The top ranking food/pathogen combination was Salmonellaspp. and leafy greens eaten raw followed by (in equal rank) Salmonellaspp. and bulb and stem vegetables, Salmonellaspp. and tomatoes, Salmonellaspp. and melons, and pathogenic Escherichia coli and fresh pods, legumes or grain.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on an estimation of the public health impact of setting a new target for the reduction of Salmonella in turkeys

The quantitative contribution of turkeys and other major animal-food sources to the burden of human salmonellosis in the European Union was estimated. A ‘Turkey Target Salmonella Attribution Model’ (TT-SAM) based on the microbial-subtyping approach was used. TT-SAM includes data from 25 EU Member States, four animal-food sources of Salmonella and 23 Salmonella serovars. The model employs 2010 EU statutory monitoring data on Salmonella in animal populations (EU baseline survey data for pigs), data on reported cases of human salmonellosis and food availability data. It estimates that 2.6 %, 10.6 %, 17.0 % and 56.8 % of the human salmonellosis cases are attributable to turkeys, broilers, laying hens (eggs) and pigs, respectively. The top-6 serovars of fattening turkeys that contribute most to human cases are S. Enteritidis, S. Kentucky, S. Typhimurium, S. Newport, S. Virchow and S. Saintpaul. Comparing the prevalence of Salmonella in turkey flocks reported in 2010 with a theoretical combined prevalence for S. Enteritidis and S. Typhimurium of 1 % (i.e. the transitional target), a reduction of 0.4 % in the percentage of turkey-associated human salmonellosis cases would be achieved. However, when adjusting the combined prevalence of all serovars to 1 %, an 83.2 % reduction in the percentage of turkey-associated human salmonellosis cases, equivalent to 2.2 % of all human salmonellosis cases, is expected. Uncertainty and data limitations are discussed, including recommendations on how these could be overcome. Vertical transmission of Salmonella as well as hatchery acquired Salmonella contamination originating from breeding stock are very important sources for Salmonella infection in turkeys, and therefore controlling Salmonella in breeding flocks as
well as in rearing and fattening flocks is necessary to minimise Salmonella in turkeys at slaughter.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on a review on the European Union Summary reports on trends and sources zoonoses, zoonotic agents and food-borne outbreaks in 2009 and 2010 – specifically for the data on Salmonella, Campylobacter, verotoxigenic Escherichia coli, Listeria monocytogenes and foodborne outbreaks

The European Union (EU) Summary Reports on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2009 and 2010 – specifically for the data on Salmonella, Campylobacter, verotoxigenic Escherichia coli, Listeria monocytogenes and foodborne outbreaks was reviewed. The main conclusions and recommendations are reported. Comparison between EU Member States (MSs) was found to be difficult due to the differences of the methods used, sampling schemes and reporting systems. Methods, sampling schemes and reporting systems among MSs should therefore be harmonised. When comparing MS-specific trends, the impact of sample sizes, weight of samples and methodologies should be considered, as these variables could otherwise lead to misinterpretation of the data. Incidence data alone do not provide a full picture of the public health burden of zoonotic diseases. Fatalities provide another important insight. Ultimately, summary measures of public health such as disability adjusted life years (DALYs) and cost-of-illness estimates should be presented. Travel information was found to be still incomplete in many MSs. For many pathogens this hampers source attribution. To better understand the public health problems related to food and animal sources in the EU, it is desirable to differentiate between travel within and outside the EU. This would also be useful to better evaluate the public health impact of EU-wide food safety measures. Whenever possible the data/results should be analysed using proper statistical tools. When data do not allow for this, the text should be kept to presenting the data without implying any patterns or trends.
EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on Composting and incineration of dead-on-farm pigs

A method for on-farm processing of Category (Cat) 2 Animal By-Products (ABP) alternative to the ones already approved in the current legislation was assessed. The materials to be treated are placentas and dead-on-farm pigs. The proposed process consists of three sequential steps, i.e. composting, storage of mature compost and incineration of mature compost in authorized plants. The applicant identified the main biological, physical and chemical hazards that could be present in the material to be treated and in the compost substrate. Since the compost is only intended for incineration the applicant considered that the final step of the process would destroy all the relevant microbiological hazards and did not perform an experimental validation. The temperatures reached during composting are not able to inactivate the relevant hazards that could be present in the material to be processed and the compost has still to be regarded as a Cat. 2 ABP material. Therefore, pathogens may be disseminated during composting and storage which are the key steps for risk containment. The alternative method as proposed by the applicant was not performed in a closed system, which implies a risk of dissemination of biological hazards throughout the farm environment. Major deficiencies were noted in relation to the risk containment. Moreover, a formal HACCP plan was not provided, and some deficiencies were also noted in the identification of interdependent processes. Provided that the deficiencies identified are addressed and the composting and storage steps of the proposed process take place in a closed system under supervision, it was concluded that this alternative treatment would not pose an additional risk as compared to the processes currently approved in the legislation.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on the development of a risk ranking framework on biological hazards

The risk ranking exercises related to biological hazards undertaken in fourteen risk assessments of the EFSA/BIOHAZ Panel were reviewed. The aim was to suggest risk ranking tools to be used in future risk assessments and to analyse strengths and weaknesses of different approaches to risk ranking. It was concluded that there is no universal methodology for risk ranking. A conceptual risk ranking framework with nine separate stages is proposed to allow the adoption of the appropriate risk ranking methodology at each stage. Further, nine risk ranking tools developed by other institutions worldwide were described, although none of these could be recommended as the single risk ranking tool for the BIOHAZ Panel. It is recommended that the risk ranking exercise should take a structured approach and be transparently and consistently documented so to be reproducible. The importance of the proper correspondence between the time frame
and the requirements of the risk ranking exercise was stressed as well as the interaction between the risk managers and the risk assessors in the definition of the risk ranking purpose and the presentation of the results. Furthermore the development of a risk ranking toolbox based on the proposed framework should be investigated, since such a toolbox would support the construction of consistent and transparent risk ranking models.

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**EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on public health risks represented by certain composite products containing food of animal origin**

This Opinion reviews the factors that affect microbial survival and growth in composite products, and in foods in general. It concludes that the main factors to be considered are: water activity, pH, temperature and duration of storage, processing, and intensity and duration of other non-thermal physical processes applied. Prevalence and concentration of the pathogens in food are important to determine the risk for consumers. The opinion presents a review of the quantitative microbiology models and databases that can be used to provide quantitative estimations of the impact of the above factors on the survival and growth of the main bacterial pathogens. In composite products, migration and diffusion of moisture and substances among the ingredients may change their physico-chemical parameters, particularly at the interfaces. Therefore, the assessment of the risk posed by composite products needs to consider the combinations of parameters most permissive to survival and growth of pathogens. Two complementary approaches are proposed for the identification and profiling of microbiological hazards in different specific composite products. The first one is based on past outbreaks and prevalence of hazards in the products and leads to the conclusion that the most frequent hazard-composite product combinations are Salmonella in cakes and bakery products. The second one consists in decision tools based on the impact on the pathogens of food composition and food processing. Categorisation of the risk for composite products requires information on their composition, processing and further handling, which can largely differ for foods belonging to the same category. Further conditions may influence the risk and should be verified, i.e. hygienic conditions during preparation of the composite products and their ingredients, shelf-life conditions, and reliability of cooking by consumers to inactivate pathogens. The decision tools developed apply to all composite products considered by the mandate, as well as to all other foods.

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Quantitative analysis of scientific evidence involves the collection of data and modelling of a situation or process under consideration and this protocol is the basis of quantitative microbial risk assessments (QMRA). The lessons and experiences from quantitative risk assessments and modelling undertaken by the BIOHAZ Panel are reviewed. Quantitative models in risk assessments were found to be essential for providing an output that could be used by risk managers to support a proportionate response to a situation and/or to balance risks and costs. QMRA is a developing field which creates methodological uncertainties, and therefore, preferences for types of models cannot be specified. Newer approaches need to be identified and considered. Fit for purpose and simplicity are key issues when developing QMRA models. However, limits on time and resources may restrict the model selection. At the start, preferably before accepting the mandate, a scoping exercise is recommended. The scoping exercise could include an assessment of the mandate, possible interpretations of the terms of reference, deadlines, the modelling approaches possible and the data requirements. To support this process, a model catalogue could be developed. The choice of modelling approach is guided by the available data and cause-effect relationships. The basis/assumptions of each quantitative expression should be clearly stated as well as the associated uncertainties. Certain expressions such as “negligible”, “concern” and “unlikely” should be used carefully, with scientific criteria and context clearly defined, or avoided.

EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on the “Biomation” application for an alternative method for the treatment of animal-by-products
A method alternative to the ones already approved in the current legislation, called 'Biomation' process, for the treatment of Category (Cat.) 2 and 3 Animal By-Products (ABP) was assessed. The process consists of an alkaline treatment. The target parameters are: particle size ≤ 5mm, temperature 70 °C, pH 12.5, exposure time 20 minutes. According to the
application received also Cat. 1 ABP can enter the processing plant and it has then to be removed from the rest of the ABP material and treated according to current legislation. The end product generated by the 'Biomation' process is intended to be used as an organic fertiliser and soil improver. According to the legislation in force, before being used as an organic fertiliser, Cat. 2 (and mixes of Cat. 2 and 3) material should be treated with a sterilisation process (i.e. 133 °C / 20 min / 3 bars / 50 mm particle size). The hazard identification provided by the applicant was not adequately addressed, since the most resistant organisms (including TSE agents) were not properly identified, and an experimental validation with representative test-organisms under practical conditions was not performed. A laboratory experiment was performed but its results were not clear and did not allow a proper assessment of the level of risk reduction of the relevant biological hazards achieved by the process. Moreover, it was noticed that it is not certain that the values of the parameters used in the laboratory experiment would be homogenously reached in all the material under real scale conditions. Major deficiencies were noticed in the HACCP plan provided. It was concluded that there is no evidence that the proposed alternative method is equivalent to the sterilization process defined in the current legislation.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on the evaluation of the safety and efficacy of ListexTM P100 for the removal of Listeria monocytogenes surface contamination of raw fish
Studies evaluating the safety and efficacy of Listex™ P100 to reduce Listeria monocytogenes contamination on raw fish were assessed. The material should not present human toxicological problems because the bacteriophage P100, used as active principle, is not regarded as harmful to consumers nor to organisms other than Listeria spp., and because the fabrication parameters do not include anything obvious that might compromise safety. Data of studies considered indicate that Listex™ P100 is listericidal on inoculated catfish and salmon samples, but do not allow definitive conclusions on efficacy in reducing L. monocytogenes counts on raw fish nor on its impact on L. monocytogenes contamination levels in finished product. It was not possible to estimate the potential listeriosis risk reduction by treating raw fish with Listex™ P100. The data were not adequate to allow firm conclusions on persistence or activity of P100 in stored fish. The proposed use of Listex™ P100 is unlikely to result in emergence of reduced susceptibility to biocides and/or resistance to key therapeutic antimicrobials: however, this conclusion may need verification. No information was provided on survival of P100 in processing wastewater or the environment, or on the potential accumulation of naturally P100 resistant L. monocytogenes variants. Pilot and industrial scale studies should consider parameters affecting decontaminating efficacy, and should verify that application on raw fish has an impact on reduction of L. monocytogenes contamination on the final product. The persistence or activity of P100 as well as potential changes in L. monocytogenes counts should be evaluated during fish storage. Tests to investigate potential development of resistance or reduced susceptibility to biocides and key therapeutic antimicrobials, following use of Listex™ P100, are recommended. The continuous effectiveness of Listex™ P100 against L. monocytogenes and the potential for selection and dominance of strains naturally-resistant to P100 should be monitored.

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Sprouted seeds are young seedlings obtained from the germination of seeds. They are ready-to-eat foods which have caused large outbreaks. The bacterial pathogens most frequently associated with illness due to contaminated sprouted seeds are Salmonella and to a lesser extent STEC. Bacillus cereus, Listeria monocytogenes, Staphylococcus aureus and Yersinia enterocolitica have also been transmitted by sprouted seeds, albeit very rarely. Dry seed contaminated with bacterial pathogens has been identified as the most likely initial source of sprout-associated outbreaks; although other routes of contamination (e.g. during production due to poor practices) may also occur. In some outbreaks, contamination of seeds with as low as 4 Salmonella per kg was sufficient for the sprouts to cause disease. Seeds purchased by sprouts producers are usually not grown specifically for this purpose. They may be contaminated during production, harvest, storage and transport, and there may be difficulties in traceability of seeds from production to sprouting. Bacterial pathogens on seeds may survive for long periods during seed storage. There is so far no guarantee of a bactericidal step which is able to control contamination of seeds with bacterial foodborne pathogens acquired prior to germination. Due to the high humidity and the favourable temperature during sprouting, bacterial pathogens present on dry seeds can multiply on the sprouts. Contamination with pathogenic bacteria must be minimized by identification of seed crops intended for sprouted seeds production before planting, and application of GAP, GHP, GMP, HACCP principles at all steps of the production chain. The relevance of decontamination treatments of seeds and of microbiological criteria is also discussed.
EFSA Panels on Biological Hazards (BIOHAZ), on Contaminants in the Food Chain (CONTAM), and on Animal Health and Welfare (AHAW); Scientific Opinion on the public health hazards to be covered by inspection of meat (poultry)

A qualitative risk assessment identified Campylobacter spp., Salmonella spp. and ESBL/AmpC gene-carrying bacteria as the most relevant biological hazards in the context of meat inspection of poultry. As none of these are detected by traditional visual meat inspection, establishing an integrated food safety assurance system, achievable through improved food chain information (FCI) and risk-based interventions, was proposed. This includes setting targets at carcass level and, when appropriate, flock level indicating what should be achieved for a given hazard. Elements of the system would be risk categorisation of flocks based on FCI and classification of abattoirs according to their capability to reduce carcass faecal contamination. It is proposed that post-mortem visual inspection is replaced by setting targets for the main hazards on the carcass, and by verification of the food business operator’s hygiene management, using Process Hygiene Criteria. Chemical substances that might occur in poultry were ranked into four categories of potential concern based on pre-defined criteria. Dioxins, dioxin-like polychlorinated biphenyls, chloramphenicol, nitrofurans and nitroimidazoles were ranked as being of high potential concern. Chemical substances in poultry, however, are unlikely to pose an immediate or acute health risk for consumers. Sampling for chemical residues and contaminants should be based on the available FCI. Moreover, control programmes should be better integrated with feed controls and regularly updated to include new and emerging substances. Meat inspection is recognised as a valuable tool for surveillance and monitoring of specific animal health and welfare conditions. If visual post-mortem inspection is removed, other approaches should be applied to compensate for the associated loss of information on the occurrence of animal disease and welfare conditions. Extended use of FCI has the potential to compensate for some, but not all, of the information on animal health and welfare that would be lost if visual post-mortem inspection is removed.

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EFSA Scientific Committee; Scientific Opinion on Risk Assessment Terminology
The Scientific Committee of the European Food Safety Authority (EFSA) reviewed the use of risk assessment terminology within its Scientific Panels. An external report, commissioned by EFSA, analysed 219 opinions published by the Scientific Committee and Panels to recommend possible ways of improving the expression and communication of risk and/or uncertainties in the selected opinions. The Scientific Committee concluded that risk assessment terminology is not fully harmonised within EFSA. In part this is caused by sectoral legislation defining specific terminology and international standards for specific fields of risk assessment and thus for specific Panels. The use of defined terminology for risk assessment is driven by three standard-setting organisations, the Codex Alimentarius Commission (CAC) in relation to food safety, the World Organisation for Animal Health (OIE) for animal health and the International Plant Protection Convention (IPPC) for plant health, under the Agreement on the Application of Sanitary and Phytosanitary Measures (SPS Agreement) of the World Trade Organisation (WTO) of which the European Union is a member. Should the major purpose of risk assessment be international trade, the Scientific Committee concludes that particular care must be taken that the principles of CAC, OIE or IPPC are followed strictly. EFSA Scientific Panels should identify which specific approach is
most useful in dealing with their individual mandates. The Scientific Committee considered detailed aspects of risk assessment terminology and identified their relevance for EFSA to adopt more harmonised use. These included examining definitions of risk and uncertainty, expressing uncertainty and different levels of risk, the merits of using qualitative and quantitative expressions and the use of glossaries of definitions to improve both the understanding and harmonisation of terminology across EFSA’s scientific opinions. Follow-up action by EFSA is identified to develop appropriate detailed guidance to the Scientific Panels. Recommendations are made to improve the clarity, consistency and where possible the harmonization of risk assessment terminology within and across EFSA’s scientific opinions.

Source attribution of human campylobacteriosis using a meta-analysis of case-control studies of sporadic infections
Campylobacter spp. is a widespread and important cause of human illness worldwide. Disease is frequently associated with foodborne transmission, but other routes of exposure, such as direct contact with live animals and person-to-person transmission, are also recognized. Identifying the most important sources of human disease is essential for prioritizing food safety interventions and setting public health goals. Numerous case-control studies of sporadic infections of campylobacteriosis have been published. These studies investigated a variety of potential risk factors for disease, often using different methodologies and settings. Systematic reviews (SRs) consist of a formal process for literature review focused on a specific research question, and include the identification of relevant literature, quality assessment of relevant studies, summarization or statistical analysis of data, and conclusions. With the objective of identifying the most important risk factors for human sporadic campylobacteriosis, we performed a SR of case-control studies of human sporadic cases and a meta-analysis of the obtained results. A combined SR focusing on Salmonella and Campylobacter studies was performed and the results analysed separately. From 1295 identified references, 131 passed the relevance screening, 73 passed the quality assessment stage, and data was extracted from 72 studies. Of these, 38 focused on campylobacteriosis. Information on exposures of cases and controls, and estimated odds ratios for investigated risk factors were collected and analysed. In the meta-analysis, heterogeneity between the studies and possible sources of bias were investigated, and pooled odds ratios for identified risk factors were estimated. Results suggest that travelling abroad, eating undercooked chicken, environmental sources, and direct contact with farm animals were significant risk factors for campylobacteriosis. Sub-analyses by geographical region, age group, and study period were performed, and differences were discussed.

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Source attribution of human campylobacteriosis using a meta-analysis of case-control studies of sporadic infections
Campylobacter spp. is a widespread and important cause of human illness worldwide. Disease is frequently associated with foodborne transmission, but other routes of exposure, such as direct contact with live animals and person-to-person transmission, are also recognized. Identifying the most important sources of human disease is essential for prioritizing food safety interventions and setting public health goals. Numerous case-control studies of sporadic infections of campylobacteriosis have been published. These studies investigated a variety of potential risk factors for disease, often using different methodologies and settings. Systematic reviews (SRs) consist of a formal process for literature review focused on a specific research question, and include the identification of relevant literature, quality assessment of relevant studies, summarization or statistical analysis of data, and conclusions. With the objective of identifying the most important risk factors for human sporadic campylobacteriosis, we performed a SR of case-control studies of human sporadic cases and a meta-analysis of the obtained results. A combined SR focusing on Salmonella and Campylobacter studies was performed and the results analysed separately. From 1295 identified references, 131 passed the relevance screening, 73 passed the quality assessment stage, and data was extracted from 72 studies. Of these, 38 focused on campylobacteriosis. Information on exposures of cases and controls, and estimated odds ratios for investigated risk factors were collected and analysed. In the meta-analysis, heterogeneity between the studies and possible sources of bias were investigated, and pooled odds ratios for identified risk factors were estimated. Results suggest that travelling abroad, eating undercooked chicken, environmental sources, and direct contact with farm animals were significant risk factors for campylobacteriosis. Sub-analyses by geographical region, age group, and study period were performed, and differences were discussed.

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State: Published
Organisations: Division of Epidemiology and Microbial Genomics, National Food Institute, Division of Microbiology and Risk Assessment, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy
Authors: Coutinho Calado Domingues, A. R. (Intern), Pires, S. M. (Intern), Hisham Beshara Halasa, T. (Intern), Hald, T. (Intern)
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Source attribution of human salmonellosis using a meta-analysis of case-control studies of sporadic infections

Salmonella is an important cause of human illness. Disease is frequently associated with foodborne transmission, but other routes of exposure are recognized. Identifying sources of disease is essential for prioritizing public health interventions. Numerous case-control studies of sporadic salmonellosis have been published, often using different methodologies and settings. Systematic reviews consist of a formal process for literature review focused on a research question. With the objective of identifying the most important risk factors for salmonellosis, we performed a systematic review of case-control studies and a meta-analysis of obtained results. Thirty-five Salmonella case-control studies were identified. In the meta-analysis, heterogeneity between studies and possible sources of bias were investigated, and pooled odds ratios estimated. Results suggested that travel, predisposing factors, eating raw eggs, and eating in restaurants were the most important risk factors for salmonellosis. Sub-analyses by serotype were performed when enough studies were available.

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Scopus rating (2016): CiteScore 1.98 SJR 1.18 SNIP 0.866
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Trends and sources in human salmonellosis

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DANMAP 2010: DANMAP 2010 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark

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Antimicrobial Use: A Risk Factor or a Protective Factor for Acquiring Campylobacteriosis?

Background. It is well acknowledged that the use of antimicrobial drugs in food animals leads to antimicrobial drug resistance in foodborne bacteria such as Campylobacter; however, the role of human antimicrobial usage is much less investigated. The aim of this study was to quantify the odds of campylobacteriosis conferred by human consumption of fluoroquinolones and macrolides.

METHODS: We conducted a registry-based retrospective case-control study on 31 669 laboratory-confirmed cases of campylobacteriosis between 1999 and 2005 in Denmark. Data were obtained from several Danish databases: the National Registry of Enteric Pathogens, the Danish Civil Registration System, the Danish National Prescription Database, and the Integrated Database on Labor Market Research. Odds ratios (OR) for campylobacteriosis were calculated by conditional logistic regression.

RESULTS: The risk of campylobacteriosis was reduced 1 month after exposure to macrolides (OR, 0.72; 95% confidence interval [CI], 0.56–0.92). Macrolide exposure 1 month to 2 years before infection was associated with an increased risk of a Campylobacter diagnosis (OR, 1.5; 95% CI, 1.4–1.6). A history of fluoroquinolone use was also associated with increased risk (OR, 2.5; 95% CI, 1.8–3.5). This risk was higher for resistant isolates than for susceptible ones.

CONCLUSIONS: Treatment with macrolides may protect against Campylobacter infection for a limited period of time, possibly due to the antibacterial effects of the drug or its metabolites. Fluoroquinolone treatment confers increased risk, probably due to a combination of competitive and selective effects, similar to what has been observed for nontyphoid Salmonella infection.
Association Between Antimicrobial Resistance in Escherichia coli Isolates from Food Animals and Blood Stream Isolates from Humans in Europe: An Ecological Study

Background: In addition to medical antimicrobial usage, the use of antimicrobials in food animals contributes to the occurrence of resistance among some bacterial species isolated from infections in humans. Recently, several studies have indicated that a large proportion of Escherichia coli causing infections in humans, especially those resistant to antimicrobials, have an animal origin.

Methods: We analyzed the correlation between the prevalence of antimicrobial resistance in E. coli isolates from blood stream infections in humans and in E. coli isolates from poultry, pigs, and cattle between 2005 and 2008 for 11 countries, using available surveillance data. We also assessed the correlation between human antimicrobial usage and the occurrence of resistance in E. coli isolates from blood stream infections.

Results: Strong and significant correlations between prevalences of resistance to ampicillin (r=0.94), aminoglycosides (r=0.72), third-generation cephalosporins (r=0.76), and fluoroquinolones (r=0.68) were observed for human and poultry E. coli isolates. Similar significant correlations were observed for ampicillin (r=0.91), aminoglycosides (r=0.73), and fluoroquinolone resistance (r=0.74) in pig and human isolates. In cattle isolates, only ampicillin resistance (r=0.72) was significantly correlated to human isolates. When usage of antimicrobials in humans was analyzed with antimicrobial resistance among human isolates, only correlations between fluoroquinolones (r=0.90) and third-generation cephalosporins (r=0.75) were significant.

Conclusions: Resistance in E. coli isolates from food animals (especially poultry and pigs) was highly correlated with resistance in isolates from humans. This supports the hypothesis that a large proportion of resistant E. coli isolates causing blood stream infections in people may be derived from food sources.

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Authors: Vieira, A. (Intern), Collignon, P. (Ekstern), Aarestrup, F. M. (Intern), McEwen, S. A. (Ekstern), Hendriksen, R. S. (Intern), Hald, T. (Intern), Wegener, H. C. (Intern)
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Web of Science (2015): Impact factor 2.27
This assessment relates the percentage of broiler-associated human salmonellosis cases to different Salmonella prevalences in broiler flocks in the European Union. It considers the contribution and relevance of different Salmonella serovars found in broilers to human salmonellosis. The model developed to provide quantitative estimates, which is based on the microbial-subtyping approach, considers 22 Member States, four animal-food sources of Salmonella (broilers, laying hens, pigs and turkeys) and 23 Salmonella serovars. The model (called the 'Broiler Target Salmonella Attribution Model' or BT-SAM model) employs data from the EU Baseline Surveys and EU statutory monitoring on Salmonella in animal-food sources, data on incidence of human salmonellosis and food availability data. It is estimated that around 2.4%, 65%, 28% and 4.5% of the human salmonellosis cases are attributable to broilers, laying hens (eggs), pigs and turkeys respectively. Of the broiler-associated human salmonellosis cases, around 42% and 23% are estimated to be due to the serovars Salmonella Enteritidis and Salmonella Infantis respectively, while other serovars individually contributed less than 5%. Different scenarios are presented showing changes in the percentage of broiler-associated human salmonellosis cases under different prevalences of Salmonella in broiler flocks. Compared to 2006, the 2009 Salmonella in broiler flocks prevalence has achieved a reduction of 69% in the number of broiler-associated human salmonellosis cases. When comparing the results of the adjusted prevalences for Salmonella Enteritidis and Salmonella Typhimurium as reported in 2009 with a theoretical combined prevalence of 1% for these two serovars, the difference between the percentages of broiler-associated cases is small. However, when adjusting the combined prevalence of all serovars to 1%, a large reduction in the percentage of broiler-associated cases compared to the one achieved with the two previous
EFSA’s Scientific Panel on Biological Hazards (BIOHAZ) was asked for a scientific opinion on two alternative methods for processing Category (Cat) 2 Animal By-Products (ABP). The material to be treated consists of poultry manure, straw and dead-on-farm poultry; this implies that the animals died due to a disease, which in most cases was not properly diagnosed. The proposed processes are composting methods to be used on-farm. The first method is a continuous open system where composting is done under roof in piles separated by wooden partition walls. The piles are processed without enforced aeration. The second method is a discontinuous closed system consisting of two different types of containers (Box-Compost®) coupled with a device for conditioning temperature and humidity during composting (Compostronic®). The end-product obtained is intended to be used as an organic fertiliser. According to the legislation in force, before being used as an organic fertiliser, Cat. 2 material should be treated with a sterilisation process (i.e. 133°C / 20 min / 3 bars / 50 mm particle size). The BIOHAZ Panel concluded that the identification and characterisation of the risk material was not properly addressed in the application and a comprehensive list of possible hazards was not provided. No experimental validation with representative test-organisms under practical conditions was done. Because of a lack of information in the report, it was not possible to determine the degree of risk reduction of pathogenic bacterial, viral and parasitological agents achieved by the processes. Moreover, the proposed alternative method cannot be considered equivalent to the sterilisation process defined in the current legislation.
EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on On-site treatment of pig carcasses

EFSA's Scientific Panel on Biological Hazards (BIOHAZ) was asked for a scientific opinion on an alternative method for processing Category (Cat) 2 Animal By-Products (ABP). The materials to be treated are placentas and fallen pigs; this implies that the animals died due to a disease, which in most cases was not properly diagnosed. The target parameters are: i) particle size less than 150 mm and ii) heating for 10 – 12 hours at 100°C. The end-product obtained is mixed with pig slurry and used as an organic fertiliser. According to the legislation in force, before being used as an organic fertiliser, Cat. 2 material should be treated with a sterilisation process (i.e. 133°C / 20 min / 3 bars / 50 mm particle size). The most resistant hazards identified by the applicant as target to demonstrate the risk reduction are spores of pathogenic clostridia. Due to uncertainty on the cause of the animals’ death, the presence of more resistant hazards cannot be considered negligible. The sterilisation process defined in the current legislation is able to minimise the risks due to unidentified agents, such as Bacillus anthracis and TSE agents. The BIOHAZ Panel concluded that the process proposed was not properly validated experimentally under real scale conditions. In theory, it should permit a high degree of reduction of spores of pathogenic clostridia but because of several uncertainties (i.e. water evaporation, fat protective effect and particle size) it is not certain that the values of the parameters used in the theoretical calculations would apply in practice. Moreover, the proposed alternative method cannot be considered equivalent to the sterilisation process defined in the current legislation. This would be particularly relevant in the case of extremely heat resistant spores being present in the material to be treated.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on Scientific Opinion on risk based control of biogenic amine formation in fermented foods

A qualitative risk assessment of biogenic amines (BA) in fermented foods was conducted, using data from the scientific literature, as well as from European Union-related surveys, reports and consumption data. Histamine and tyramine are considered as the most toxic and food safety relevant, and fermented foods are of particular BA concern due to associated intensive microbial activity and potential for BA formation. Based on mean content in foods and consumer exposure data, fermented food categories were ranked in respect to histamine and tyramine, but presently available information was insufficient to conduct quantitative risk assessment of BA, individually and in combination(s). Regarding BA risk mitigation options, particularly relevant are hygienic measures to minimize the occurrence of BA-producing microorganisms in raw material, additional microbial controls and use of BA-nonproducing starter cultures. Based on limited published
information, no adverse health effects were observed after exposure to following BA levels in food (per person per meal): a) 50 mg histamine for healthy individuals, but below detectable limits for those with histamine intolerance; b) 600 mg tyramine for healthy individuals not taking monoamino oxidase inhibitor (MAOI) drugs, but 50 mg for those taking third generation MAOI drugs or 6 mg for those taking classical MAOI drugs; and c) for putrescine and cadaverine, the information was insufficient in that respect. Presently, only high-performance liquid chromatography (HPLC)-based methods enable simultaneous and high sensitivity quantification of all BA in foods, hence are best suited for monitoring and control purposes. Monitoring of BA concentrations in fermented foods during the production process and along the food chain would be beneficial for controls and further knowledge. Further research on BA in fermented foods is needed; particularly on toxicity and associated concentrations, production process-based control measures, further process hygiene and/or food safety criteria development, and validation of analysis methods.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on the maintenance of the list of QPS biological agents intentionally added to food and feed (2011 update)
EFSA is requested to assess the safety of a broad range of biological agents (including microorganisms and viruses) in the context of notifications for market authorisation as sources of food and feed additives, enzymes and plant protection products. The qualified presumption of safety (QPS) assessment was developed by EFSA for its own use to provide a generic risk assessment approach applicable across EFSA’s scientific Panels, for biological agents notified for intentional use in the whole food chain. The safety of unambiguously defined biological agents at the highest taxonomic unit that is appropriate for the purpose for which an application is intended and the completeness of the body of knowledge are assessed. Identified safety concerns for a taxonomic unit are where sensible reflected as ‘qualifications’ when a recommendation for the QPS list is given. The list of QPS recommended biological agents is reviewed and updated annually. Therefore, the only valid list is the one in the most recent scientific opinion. The 2011 update reviews microorganisms previously assessed including bacteria, yeasts, filamentous fungi and viruses used for plant protection purposes and confirms the previous recommendations. The anamorph yeast form Phaffia rhodozyma of Xanthophyllomyces dendrorhous was included on the QPS list and to the qualification for yeasts ‘absence of resistance to antimycotics used for medical treatment of yeast infections’, the sentence was added that ‘in the case of Saccharomyces cerevisiae this qualification applies for yeast strains able to grow above 37 °C’. The body of knowledge of filamentous fungi and enterococci was updated and their ineligibility for the QPS list confirmed.

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EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on the public health risks of bacterial strains producing extended-spectrum β-lactamases and/or AmpC β-lactamases in food and food-producing animals

The potential contribution of food-producing animals or foods to public health risks by ESBL and/or AmpC-producing bacteria is related to specific plasmid-mediated ESBL and/or AmpC genes encoded by a number of organisms. The predominant ESBL families encountered are CTX-M, TEM, and SHV; the predominant AmpC-family is CMY. The most common genes associated with this resistance in animals are blaCTX-M-1 (the most commonly identified ESBL), and blaCTX-M-14, followed by blaTEM-52 and blaSHV-12. Among the genes encoding AmpC-type β-lactamases, blaCMY-2 is the most common. The bacterial species most commonly identified with these genes are Escherichia coli and non-typhoidal Salmonella. ESBL/AmpC transmission is mainly driven by integrons, insertion sequences, transposons and plasmids, some of which are homologous in isolates from both food-production animals and humans. Cefotaxime is used as the drug of choice for optimum detection of blaESBL and/or blaAmpC genes. The preferred method for isolation of ESBL- and/or AmpC-producers is screening on selective agar preceded by selective enrichment in a broth. The establishment of risk factors for occurrence of ESBL/AmpC-producing bacteria is particularly complicated by the data unavailability or lack of its accuracy. The use of antimicrobials is a risk factor for the selection and spread of resistant clones, resistance genes and plasmids. Since most ESBL- and AmpC-producing strains carry additional resistances to other commonly-used veterinary drugs, generic antimicrobial use is a risk factor for ESBL/AmpC and it is not restricted specifically to the use of cephalosporins. An additional risk factor is extensive trade of animals in EU MS. There are no data on the comparative efficiency of individual control options in reducing public health risks caused by ESBL and/or AmpC-producing bacteria related to food-producing animals. Prioritisation is complex, but it is considered that a highly effective control option would be to stop all uses of cephalosporins/systemically active 3rd/4th generation cephalosporins, or to restrict their use (use only allowed under specific circumstances). As co-resistance is an important issue, it is also of high priority to decrease the total antimicrobial use in animal production in the EU.

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EFSA Panels on Biological Hazards (BIOHAZ), on Contaminants in the Food Chain (CONTAM), and on Animal Health and Welfare (AHAW); Scientific Opinion on the public health hazards to be covered by inspection of meat (swine).

A qualitative risk assessment identified Salmonella spp., Yersinia enterocolitica, Toxoplasma gondii and Trichinella spp. as the most relevant biological hazards in the context of meat inspection of swine. A comprehensive pork carcass safety assurance is the only way to ensure their effective control. This requires setting targets to be achieved in/on chilled carcasses, which also informs what has to be achieved earlier in the food chain. Improved Food Chain Information (FCI) enables risk-differentiation of pig batches (hazard-related) and abattoirs (process hygiene-related). Risk reduction measures at abattoir level are focused on prevention of microbial contamination through technology- and process hygiene-based measures (GMP/GHP- and HACCP-based), including omitting palpation/incision during post-mortem inspection in routine slaughter, as well as hazard reduction/inactivation meat treatments if necessary. At farm level, risk reduction measures are based on herd health programmes, closed breeding pyramids and GHP/GFP. Chemical substances listed in Council Directive 96/23/EC were ranked into four categories. Dioxins, dioxin-like polychlorinated biphenyls and chloramphenicol were ranked as being of high potential concern. However, chemical substances in pork are unlikely to pose an immediate or short term health risk for consumers. Opportunities for risk-based inspection strategies by means of differentiated sampling plans taking into account FCI were identified. Regular update of sampling programmes and inclusion of inspection criteria for the identification of illicit use of substances were also recommended. Meat inspection is a key component of the overall surveillance system for pig health and welfare but information is currently under-utilised. The changes proposed to the pig meat inspection system will lead to some reduction in the detection probability of diseases and welfare conditions. The difference is likely to be minimal for diseases/conditions that affect several organs. To mitigate the reduced detection probability, palpation and/or incision should be conducted as a follow-up to visual inspection whenever abnormalities are seen.

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Estimation of the relative contribution of different food and animal sources to human Salmonella infections in the European Union

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Authors: Pires, S. M. (Intern), de Knegt, L. (Intern), Hald, T. (Intern)
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European Food Safety Authority; Analysis of the baseline survey of Salmonella in holdings with breeding pigs, in the EU, 2008; Part B: Analysis of factors potentially associated with Salmonella pen positivity

A European Union-wide Salmonella baseline survey was conducted in 2008 in holdings with breeding pigs. A total of 1,609 randomly selected holdings housing and selling mainly breeding pigs (breeding holdings) and 3,508 holdings housing commercial breeding pigs and mainly selling pigs for fattening or slaughter (production holdings) were sampled. In each selected holding, pooled fresh faecal samples were collected from 10 randomly chosen pens of breeding pigs over six months of age, representing the different stages of the breeding herd, and examined for the presence of Salmonella. Analyses at country-level demonstrated a strong positive association between the prevalence of Salmonella-positive breeding holdings and the prevalence of Salmonella-positive production holdings, suggesting a vertical dissemination of Salmonella between the holdings. Based on the combined results from breeding and production holdings, multivariable regression analysis showed that the odds of Salmonella-positive pens with pigs increased with the number of breeding pigs in the holding and with the following pen-level factors: flooring systems other than slatted floors or solid floors with straw, presence of maiden gilts, number of pigs per pen, feed of commercial compound origin or pelleted feed. A tendency towards some Member State group-specific Salmonella serovars was identified, but spatial distribution of other serovars was heterogeneous. S. Typhimurium and S. Derby were widespread and dominant in the EU, in both breeding and production holdings. However, many other serovars were relatively prevalent in Western EU Member States. A complementary within-holding prevalence study indicated that, due to a non-perfect diagnostic test sensitivity, the observed EU-level prevalence of Salmonella-positive holdings with breeding pigs was roughly 80% of the estimated true EU-level prevalence. But this proportion varied between Member States.

Risk assessment of antimicrobial usage in Danish pig production on the human exposure to antimicrobial resistant bacteria from pork
During the last decades, bacteria with resistance to all commonly used antimicrobial agents have been detected, thereby posing a major threat to public health. In worst case, infections with resistant bacteria can lead to treatment failure and death of humans. The evolution of bacteria resistant to antimicrobials are influenced by the use of antimicrobial agents, and the prudence of antimicrobial use have been emphasized since the Swann report in 1969 recommended that antibiotics used in human medicine should not be used as growth promoters in food-producing animals. In 2007, the World Health Organisation (WHO) pronounced a list of the antimicrobial classes critically important for the treatment of infectious diseases in humans. On this list occurred among others the third and fourth generation cephalosporins. Cephalosporins have been used increasingly worldwide throughout the recent years to treat various infections in veterinary and human medicine and the occurrence of resistance to this antimicrobial class have been detected with increasing frequency.

The purpose of this thesis was to perform a quantitative assessment of the association between the use of antimicrobial agents for treatment of slaughter pigs and the occurrence of extended-spectrum cephalosporinases (ESC) producing E. coli in pigs and pork. The thesis addresses this purpose by estimating the effect of the antimicrobial usage on the occurrence of resistance. And by using the obtained results in a risk assessment model where the human exposure to cephalosporin resistance from pork purchased in retail shops was assessed using different scenarios for the amount of antimicrobial used in the primary production. Also, farm-related factors affecting the antimicrobial usage were investigated as a part of this thesis.

The thesis addresses this in the following sections:

Objective 1: Estimating the association between antimicrobial usage and the detection of ESC producing E. coli
Objective 2: Quantifying the effect of antimicrobial usage on the proportion of ESC producing E. coli
Exposure: Assessing the human exposure to ESC producing E. coli through the purchase of pork chops
Objective 3: Identification of management factors in the Danish finishing pig production important for antimicrobial usage

In Objective 1, the occurrence (presence/non-presence) of ESC producing E. coli in samples from healthy pigs at slaughter was investigated using selective agar plates supplemented with ceftriaxone. The occurrence of ESC producing E. coli was used as the outcome in the data analysis, where the effect of using cephalosporins, extended spectrum penicillins and tetracyclines was estimated using regression analysis.

In Objective 2, the samples collected for Objective 1 were diluted in 10 fold and spread on selective plates in two set of triplicates (one set containing three MacConkey agar plates, and one set containing three MacConkey agar plates supplemented with ceftriaxone). This provided quantitative data for the ESC producing E. coli and total concentration of E. coli in each sample. The proportion of ESC producing E. coli was thereafter estimated using a Poisson regression adjusting for applied dilution factor. The resistance proportion was subsequently used as outcome in a regression model to estimate the effect of the antimicrobial usage on the proportion of ESC producing E. coli.

The prevalence, concentration and proportion of ESC producing E. coli obtained in Objective 1 and Objective 2 was used as input in a human exposure assessment model. In Objective 2, a significant effect on the resistance proportion was found from the quantitative use of tetracyclines one year prior to the sampling date. This effect was used in the exposure assessment model. This model also used data from additional sources to estimate the human exposure to ESC producing E. coli from the purchase of Danish pork chops. By using the ESC producing E. coli prevalence of 41 % (obtained in Objective 1), the resulting prevalence in pork chops was found to vary from 19.70 % to 21.80 %. The prevalence of ESC producing E. coli was increasing as the usage of tetracyclines increased. However, this prevalence was found in pork chops originating from the study population, which was chosen based on their usage of cephalosporin.

In an attempt to check the validity of the model, the data from a national survey was used as input. This survey also used selective enrichment, but did not estimate the concentration of E. coli or the proportion of ESC producing E. coli, therefore the prevalence obtained from the healthy pigs at slaughter was used as input in the model, whereas the remaining steps of the model were not changed. The resulting effect on the estimated prevalence of ESC producing E. coli in 100,000 pork chops was compared to the observed prevalence from the national survey. This analysis estimated the prevalence to 5.3 % ESC producing E. coli, which is 2.6 times higher than the observed prevalence on 2 %. However, the data from the national survey was obtained at retail, whereas the model was not considering the growth or inactivation taking place under the transport and storage of the meat.

In Objective 3, the risk factors for a high usage of tetracycline were investigated by assessing the effect of tetracycline usage on the occurrence of tetracycline resistance in pigs originating from three different production types. The effect of the tetracycline usage and the effect of the production type was estimated using logistic regression. The results of this objective showed a highly significant effect of the production type, where the organic production had significantly lower occurrence of tetracycline resistance, and also had a much lower average usage of tetracycline. No significant difference in the tetracycline resistance could be found between the conventional and free range productions. When estimating the effect of the tetracycline usage in general using all the production types, a significant effect on the occurrence of resistance was found on the quantitative usage of tetracycline.

Data in this study unfortunately did not have enough power to point out single factors within the production types that could be responsible for the size of the tetracycline usage.

The overall conclusion of this thesis is that there is a significant effect of the quantitative antimicrobial usage (i.e. the amount of antimicrobial used) on the occurrence of ESC producing E. coli. A high antimicrobial usage gives an increased prevalence of resistance, but also an increased proportion of resistance. Furthermore, the occurrence of cephalosporin resistance appears to be influenced by a generic use of antimicrobial agents rather than the effect of a single antimicrobial class. The exposure assessment indicate that human exposure to ESC producing E. coli is to some degree affected by the generic use of antimicrobial agents in the primary pig production. However, this thesis also found big differences in the occurrence of resistance and antimicrobial usage, when comparing conventional and free range production to organic
There seems to be a huge potential to lower the generic antimicrobial usage in the conventional and free range productions. Future studies evaluating the effect of specific risk factors in the organic production could lead to useful recommendations on how to lower the antimicrobial usage in the other production types. However, welfare issues need to be investigated to rule out the possibility of untreated diseases in the organic production.

**General information**
State: Published
Organisations: National Food Institute
Authors: Struve, T. (Intern), Hald, T. (Intern), Emborg, H. (Intern), Aarestrup, F. M. (Intern)
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Original language: English
Main Research Area: Technical/natural sciences

Salmonella Source Attribution in Japan by a Microbiological Subtyping Approach
In order to estimate the number of human Salmonella infections attributable to each of major animal-food source, and help identifying the best Salmonella intervention strategies, a microbial subtyping approach for source attribution was applied. We adapted a Bayesian model that attributes illnesses to specific sources and allows for the estimation of the differences in the ability of Salmonella subtypes and food types to result in reported salmonellosis. The number of human cases caused by different Salmonella subtypes is estimated as a function of the prevalence of these subtypes in the animal-food sources, subtype-related factors, and source-related factors. National-surveillance serotyping data from 1998 to 2007 were applied to the model. Results suggested that the relative contribution of the sources to salmonellosis varied during the 10 year period, and that eggs are the most important source of disease, being responsible for over 50 % of the cases in most years. Broilers followed in importance in 1999, 2000, 2001, 2002 and 2005, while swine was the second most important source in 2000, 2004 and 2007. Salmonella was seldom isolated from cattle and few cases were attributed to this source. The proportion of cases attributed to an unknown source varied substantially between years. We conclude that this is valid approach to attribute salmonellosis in Japan, and that and improved dataset would substantially improve results. This is the first indication of the relative contribution of different foods for human salmonellosis, and results may be used for further research, risk management and public health strategies.

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Czech National Institute of Public Health
Authors: Toyofuku, H. (Ekstern), Pires, S. M. (Intern), Hald, T. (Intern)
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Scopus rating (2017): CiteScore 2.04 SJR 0.957 SNIP 0.853
Web of Science (2017): Impact factor 2.649
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.67 SJR 0.818 SNIP 0.699
Web of Science (2016): Impact factor 2.252
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.204 SNIP 1.034 CiteScore 1.8
A European Union-wide baseline survey on Campylobacter in broiler batches and on Campylobacter and Salmonella on broiler carcasses was carried out in 2008. A total of 10,132 broiler batches were sampled from 561 slaughterhouses in 26 European Union Member States and two countries not belonging to the European Union. From each randomly selected batch the caecal contents of 10 slaughtered broilers were collected, pooled and examined for Campylobacter. From the same batch one carcass was collected after chilling and the neck skin together with the breast skin was examined for the presence of Campylobacter and Salmonella, in addition to the determination of the Campylobacter counts. Campylobacter was detected in pooled caecal contents of broilers and on broiler carcasses in all participating countries. At Community level the prevalence of Campylobacter-colonised broiler batches was 71.2% and that of Campylobacter-contaminated broiler carcasses was 75.8%. The Member State prevalence varied from 2.0% to 100.0% and from 4.9% to 100.0%, for caecal contents and carcasses, respectively. The results of the counts of Campylobacter on broiler carcasses showed substantial variation among the countries in contamination levels. About two-thirds of the Campylobacter isolates from the pooled caecal contents as well as from the broiler carcasses were identified as Campylobacter jejuni, while one-third was Campylobacter coli. Twenty-two Member States and one non-Member State isolated Salmonella on the broiler carcasses, with a Community prevalence of 15.6%. This prevalence varied widely among the Member States, from 0.0% to 26.6%. However, one Member State had an exceptionally high prevalence of 85.6% with the majority of isolates being S. Infantis. The Community prevalence of Salmonella Enteritidis or Salmonella Typhimurium-contaminated broiler carcasses was 3.6%. Salmonella Infantis and Salmonella Enteritidis were the two most frequently isolated serovars on broiler carcasses in the EU and accounted for about one-third and one-sixth of the Salmonella isolates, respectively.

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Authors: EFSA publication
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Publication date: 2010
Assessing the Differences in Public Health Impact of Salmonella Subtypes Using a Bayesian Microbial Subtyping Approach for Source Attribution

Salmonella is a major cause of human gastroenteritis worldwide. To prioritize interventions and assess the effectiveness of efforts to reduce illness, it is important to attribute salmonellosis to the responsible sources. Studies have suggested that some Salmonella subtypes have a higher health impact than others. Likewise, some food sources appear to have a higher impact than others. Knowledge of variability in the impact of subtypes and sources may provide valuable added information for research, risk management, and public health strategies. We developed a Bayesian model that attributes illness to specific sources and allows for a better estimation of the differences in the ability of Salmonella subtypes and food types to result in reported salmonellosis. The model accommodates data for multiple years and is based on the Danish Salmonella surveillance. The number of sporadic cases caused by different Salmonella subtypes is estimated as a function of the prevalence of these subtypes in the animal-food sources, the amount of food consumed, subtype-related factors, and source-related factors. Our results showed relative differences between Salmonella subtypes in their ability to cause disease. These differences presumably represent multiple factors, such as differences in survivability through the food chain and/or pathogenicity. The relative importance of the source-dependent factors varied considerably over the years, reflecting, among others, variability in the surveillance programs for the different animal sources. The presented model requires estimation of fewer parameters than a previously developed model, and thus allows for a better estimation of these factors to result in reported human disease. In addition, a comparison of the results of the same model using different sets of typing data revealed that the model can be applied to data with less discriminatory power, which is the only data available in many countries. In conclusion, the model allows for the estimation of relative differences between Salmonella subtypes and sources, providing results that will benefit future risk assessment or risk ranking purposes.
EFSA Panel on Biological Hazards; Scientific Opinion on a Quantitative Microbiological Risk Assessment of Salmonella in slaughter and breeder pigs

This Quantitative Microbiological Risk Assessment (QMRA) represents a major step forward in terms of modelling Salmonella in pigs from farm to consumption as it takes into account the variability between and within EU Member States (MSs). Around 10-20% of human Salmonella infections in EU may be attributable to the pig reservoir as a whole. From the QMRA analysis it appears that an 80% or 90% reduction of lymph node prevalence should result in a comparable reduction in the number of human cases attributable to pig meat products. Theoretically, according to the QMRA the following scenarios appear possible (a) by ensuring that breeder pigs are Salmonella-free a reduction of 70-80% in high prevalence MSs and 10-20% in low prevalence MSs can be foreseen; (b) by feeding only Salmonella-free feedstuffs, a reduction of 10-20% in high prevalence MSs and 60-70% in low prevalence MSs can be foreseen; and (c) by preventing infection from external sources of Salmonella (i.e. rodents and birds) a reduction of 10-20% in slaughter pig lymph node prevalence can be foreseen in both high and low prevalence MSs. A hierarchy of control measures is suggested - a high prevalence in breeder pigs needs to be addressed first, followed by control of feed and then control of environmental contamination. Also according to the QMRA, for each MS, a reduction of two logs (99%) of Salmonella numbers on
contaminated carcasses would result in more than 90% reduction of the number of human salmonellosis cases attributable to pig meat consumption. The control of Salmonella in pig reservoir in the EU is a reasonable objective. The EU Salmonella control strategy in pigs should be continuously evaluated to identify possible improvements.

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### Integrated Approaches for the Public Health Prioritization of Foodborne and Zoonotic Pathogens

To address the persistent problems of foodborne and zoonotic disease, public health officials worldwide face difficult choices about how to best allocate limited resources and target interventions to reduce morbidity and mortality. Data-driven approaches to informing these decisions have been developed in a number of countries. Integrated comparative frameworks generally share three methodological components: estimating incidence of acute illnesses, chronic sequelae, and mortality; attributing pathogen-specific illnesses to foods; and calculating integrated measures of disease burden such as cost of illness, willingness to pay, and health-adjusted life years (HALYs). To discuss the similarities and differences in these approaches, to seek consensus on principles, and to improve international collaboration, the E.U. MED-VET-NET and the U.S.-based Food Safety Research Consortium organized an international conference convened in Berlin, Germany, on July 19-21, 2006. This article draws in part on the deliberations of the conference and discusses general principles, data needs, methodological issues and challenges, and future research needs pertinent to objective data-driven analyses and their potential use for priority setting of foodborne and zoonotic pathogens in public health policy.

**General information**

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Institute of Public Health and the Environment, University of Florida, Federal Institute for Risk Assessment, George Washington University
Authors: Mangen, M. (Ekstern), Batz, M. (Ekstern), Kassbohrer, A. (Ekstern), Hald, T. (Intern), Morris, G. (Ekstern), Taylor, M. (Ekstern), Havelaar, A. (Ekstern)
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Quantitative Microbiological Risk Assessment on Salmonella in Slaughter and Breeder pigs: Final Report
Project developed on the procurement project CFP/EFSA/BIOHAZ/2007/01

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Salmonellaforekomsten i danske svin stiger

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Baggesen, D. L. (Intern), Aabo, S. (Intern), Hald, T. (Intern)
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Scientific Opinion on a quantitative estimation of the public health impact of setting a new target for the reduction of Salmonella in laying hens

Public health risks of Salmonella infection in laying hens (Gallus gallus) can be associated with exposure through four different pathways: internally contaminated table eggs, externally contaminated table eggs, egg products and meat from spent hens. In relation to eggs, Salmonella Enteritidis is by far the serovar most frequently associated with human illness, and exposure through eggs that are internally contaminated with this serovar has a higher public health significance than exposure to externally contaminated eggs. A mathematical model, using reported field data from two EU Member States (MSs), suggests a linear relationship between the investigated scenarios of flock prevalence for Salmonella Enteritidis and the number of contaminated eggs that would be laid. However, the absolute public health impact of the assessed flock prevalence scenarios is highly uncertain due to lack of data on the number of contaminated eggs produced by infected flocks and on the true number of egg-related human salmonellosis cases. It is suggested that public health benefits, similar to those obtained reaching lower Salmonella flock prevalences, may be achieved by implementing controls based on more sensitive sampling protocols. Diversion of eggs from flocks that are tested positive in the EU Salmonella control programme to the production of egg products subjected to heat treatment may lead to increased health risks as heat
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Section of Fur Animal Diseases and Wildlife, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
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Scientific Opinion on the maintenance of the list of QPS biological agents intentionally added to food and feed (2010 update): EFSA on Biological Hazards (BIOHAZ)

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Authors: EFSA Publication
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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.
Attributing the Human Disease Burden of Foodborne Infections to Specific Sources

Foodborne diseases are an important cause of human illness worldwide. Humans acquire these infections from a variety of sources and routes of transmission. Many efforts have been made in the last decades to prevent and control foodborne diseases, particularly foodborne zoonoses. However, information on the impact of these interventions is limited. To identify and prioritize successful food safety interventions, it is important to attribute the burden of human illness to the specific sources. Defining scientific concepts and harmonizing terminology for “source attribution” is essential for understanding and improving attribution methodologies and for sharing knowledge within the scientific community. We propose harmonized nomenclature, and describe the various approaches for human illness source attribution and their usefulness to address specific public health questions.
Source attribution of human salmonellosis and campylobacteriosis using a systematic review of studies of sporadic infections

Salmonella spp. and Campylobacter spp. are widespread and important causes of human illness worldwide. Disease is most frequently associated with foodborne transmission, but other routes of exposure, such as direct contact with live...
animals and person-to-person transmission, are recognized. Identifying the most important sources of human disease is essential for prioritizing food safety interventions and setting public health goals. Numerous case-control studies of sporadic infections of salmonellosis and campylobacteriosis have been published. These studies investigate a variety of potential risk factors for disease, and often use different methodologies and settings. Systematic reviews (SR) consist of a formal process for literature review focused on a specific research question, and include the identification of relevant literature, quality assessment of relevant studies, summarization or statistical analysis of data, and conclusions. With the objective of identifying the most important risk factors for human sporadic salmonellosis and campylobacteriosis, we performed a SR of case-control studies and meta-analysis of the obtained results. From 1,295 identified references, 132 passed the relevance screening, 73 passed the quality assessment stage, and data was extracted from 72. Of these studies, 34 investigated risk factors for human salmonellosis and 37 focused on campylobacteriosis. Heterogeneity between the studies and possible sources of bias were assessed. Information on exposures of cases and controls, and estimated odds ratios for investigated risk factors were recovered and analyzed with the purpose of assisting attribution of human disease. The most significant results were illustrated using forest plots.

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Coutinho Calado Domingues, A. R. (Intern), Pires, S. M. (Intern), Hald, T. (Intern)
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Main Research Area: Technical/natural sciences
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The effects, costs and benefits of salmonella control in the Danish table-egg sector

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
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Pages: 828-836
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Main Research Area: Technical/natural sciences

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Attributing the human disease burden of foodborne infections to specific sources

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Pires, S. M. (Intern), Evers, E. G. (Ekstern), van Pelt, W. (Ekstern), Ayers, T. (Ekstern), Scallan, E. (Ekstern), Angulo, F. J. (Ekstern), Havelaar, A. (Ekstern), Hald, T. (Intern)
Publication date: 2008

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Title of host publication: Food Micro 2008
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Estimating differences in public health impact between Salmonella subtypes and food sources

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Pires, S. M. (Intern), Hald, T. (Intern)
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EU-wide baseline studies: achievements and difficulties faced

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Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hald, T. (Intern)
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Scopus rating (2017): CiteScore 6.67 SJR 2.344 SNIP 2.444
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Scopus rating (2016): CiteScore 6 SJR 2.357 SNIP 2.775
Web of Science (2016): Impact factor 5.191
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.232 SNIP 2.626 CiteScore 5.51
Web of Science (2015): Impact factor 5.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.173 SNIP 2.767 CiteScore 5.17
Web of Science (2014): Impact factor 4.651
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.216 SNIP 2.653 CiteScore 4.83
Web of Science (2013): Impact factor 4.651
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.048 SNIP 2.417 CiteScore 3.91
Web of Science (2012): Impact factor 4.135
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.897 SNIP 2.675 CiteScore 3.81
Web of Science (2011): Impact factor 3.672
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.763 SNIP 2.508
Web of Science (2010): Impact factor 3.71
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.187 SNIP 2.567
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.75 SNIP 2.321
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.682 SNIP 2.279
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.17 SNIP 2.065
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.041 SNIP 1.948
Scopus rating (2004): SJR 1.069 SNIP 1.948
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.74 SNIP 1.479
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.882 SNIP 1.55
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.97 SNIP 1.52
Scopus rating (2000): SJR 1.207 SNIP 1.906
Scopus rating (1999): SJR 1.085 SNIP 1.605
New strategies for the use of microbiological examinations in food control in Denmark
The development of the use of microbiological examinations in Danish food control is described. At the end of the millennium an increased number of cases of food-borne disease caused by zoonotic microorganisms necessitated a new strategy. The developments of international concepts and risk analyses procedures have been valuable guides on this route. The organisation of the Danish control structure is described, as well as a summary of the experiences with the new strategy that have been gathered until now.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Authors: Andersen, J. K. (Intern), Hald, T. (Intern), Nielsen, N. L. (Ekstern), Sporon Fiedler, C. (Ekstern), Nørrung, B. (Intern)
Pages: 273-277
Publication date: 2007
Main Research Area: Technical/natural sciences

Published information
Journal: Food Control
Volume: 18
Issue number: 3
The attribution of human infections with antimicrobial resistant Salmonella bacteria in Denmark to sources of animal origin

Based on the Danish Salmonella surveillance in 2000-2001, we developed a mathematical model for quantifying the contribution of each major animal-food sources to human salmonellosis caused by antimicrobial resistant bacteria. Domestic food products accounted for 53.1% of all cases, mainly caused by table eggs (37.6%). A large proportion (19%) of cases were travel related, while 18% could not be associated with any source. Imported food products accounted for 9.5% of all cases; the most important source being imported chicken. Multidrug and quinolone resistance was rarely found in cases acquired from Danish food, but was common in cases related to imported products (49.7% and 35.6% of attributable cases) and travelling (26.5% and 38.3% of attributable cases). For most serovars, the quinolone-resistant isolates were found to be associated with relatively more human infections than that of resistant isolates, which in turn was higher than that of susceptible isolates. This may be due to quinolone-resistant isolates having a higher ability to survive food processing and/or cause disease. This study showed domestic food to be the most important source of Salmonella infections in Denmark, but infections with multidrug- and quinolone-resistant isolates were more commonly caused by imported food products and travelling, emphasizing the need for a global perspective on food safety and antimicrobial usage.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hald, T. (Intern), Lo Fo Wong, D. M. A. (Ekstern), Aarestrup, F. M. (Intern)
Pages: 313-326
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Foodborne Pathogens and Disease
Volume: 4
Issue number: 3
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.016 SJR 1.063 CiteScore 2.47
Web of Science (2017): Impact factor 2.476
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
Web of Science (2016): Impact factor 2.12
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.064 SNIP 1.035 CiteScore 2.41
Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.953 SNIP 1.051 CiteScore 2.16
Web of Science (2014): Impact factor 1.905
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.184 SNIP 1.129 CiteScore 2.41
Web of Science (2013): Impact factor 2.092
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.185 SNIP 1.144 CiteScore 2.55
Web of Science (2012): Impact factor 2.283
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Towards an integrated approach in supporting microbiological food safety decisions

Decisions on food safety involve consideration of a wide range of concerns including the public health impact of foodborne illness, the economic importance of the agricultural sector and the food industry, and the effectiveness and efficiency of interventions. To support such decisions, we propose an integrated scientific approach combining veterinary and medical epidemiology, risk assessment for the farm-to-fork food chain as well as agricultural and health economy. Scientific advice is relevant in all stages of the policy cycle: to assess the magnitude of the food safety problem, to define the priorities for action, to establish the causes for the problem, to choose between different control options, to define targets along the food chain and to measure success.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Pages: 103-117
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Zoonoses and Public Health
Volume: 54
Issue number: 3-4
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): Impact factor 2.688
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): Impact factor 2.323
380,000 syge af fødevarebårne infektioner i EU

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Helwigh, B. (Intern), Hald, T. (Intern), Borck, B. (Intern), Wong, D. L. F. (Intern)

Original language: English
food safety, economics, epidemiology, risk assessment, decision making
Source: orbit
Source-ID: 214347
Publication: Research - peer-review › Journal article – Annual report year: 2007
Human health impact of Salmonella contamination in imported soybean products: A semiquantitative risk assessment

The objectives of our study were to estimate the number of reported cases of human salmonellosis in Denmark that can be attributed to the occurrence of Salmonella in soy-based animal feed and to assess whether certain serotypes can be considered of less importance to human health. The assessment was based on a comparison of Salmonella serotypes isolated from feedstuffs, swine, cattle, and humans, primarily collected through the Danish Salmonella surveillance programs, supplemented with international data sources. The results are presented in three different forms: a qualitative assessment of all serotypes isolated from animal feed and/or food-producing animals based on their detection in humans; a semiquantitative ranking of serotypes by the apparent differences in their public health impact; and an estimate of the number of reported cases of human salmonellosis that can be attributed to the occurrence of Salmonella in soy-based animal feed. Salmonella isolates included in this study belonged to 91 distinct serotypes. Of the 82 serotypes found in both production animals and humans, 45 were also found in feed. In the period from 1999 to 2003, 14.4% of reported human infections were caused by serotypes also isolated from animal feed. Based on a modified version of a previously published risk model, we estimated that up to 1.7% of the total number of reported human cases and 2.1% of domestically acquired infections in the period 1999-2003 could be attributed to feedborne serotypes acquired through the consumption of Danish pork and beef. We concluded that more than 90% of serotypes have the potential, if they occur in feedstuffs, for infecting humans via production animals or foods of animal origin.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hald, T. (Intern), Wingstrand, A. (Intern), Brondsted, T. (Ekstern), Wong, D. L. F. (Intern)
Pages: 422-431
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Foodborne Pathogens and Disease
Volume: 3
Issue number: 4
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.016 SJR 1.063 CiteScore 2.47
Web of Science (2017): Impact factor 2.476
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
Web of Science (2016): Impact factor 2.12
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.064 SNIP 1.035 CiteScore 2.41
Web of Science (2015): Impact factor 2.27
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.953 SNIP 1.051 CiteScore 2.16
Web of Science (2014): Impact factor 1.905
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.184 SNIP 1.129 CiteScore 2.41
Web of Science (2013): Impact factor 2.092
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.185 SNIP 1.144 CiteScore 2.55
Preliminary Report: Analysis of the baseline study on the prevalence of Salmonella in laying hen flocks of Gallus gallus

This is a preliminary report on the analysis of the Community-wide baseline study to estimate the prevalence of Salmonella in laying hen flocks. It is being published pending the full analysis of the entire dataset from the baseline study. The report contains the elements necessary for the establishment of the Community target for reduction of Salmonella in laying hens in accordance with Article 4 of Regulation No 2160/2003 of the European Parliament and of the Council on the control of salmonella and other specified food-borne zoonotic agents. Although the final report will not be published until October 2006, key data such as the prevalence levels of salmonella in laying hens is not foreseen to change significantly with the publication of the final report which will contain the full analyses and results from the study. As the European Commission intends to set targets prior to publication of the final report, EFSA is publishing the preliminary analysis in keeping with its policy of openness and transparency.

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: EFSA publication
Number of pages: 71
Publication date: 2006

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Place of publication: Parma, Italy
Publisher: European Food Safety Authority
Original language: English

Series: The EFSA Journal
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Number: 81
ISSN: 1830-5458
Main Research Area: Technical/natural sciences
Electronic versions:
jun06 BS layers.pdf
DOIs:
10.2903/j.efsa.2006.81r
Links:
Salmonella contamination in soya-based animal feed: a food safety issue?

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Number of pages: 355
Publication date: 2006

Host publication information
Title of host publication: Proceedings of the 11. Symposium of the International Society for Veterinary Epidemiology and Economics, Cairns, Australia: ISVEE 11
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 238743
Publication: Research › Article in proceedings – Annual report year: 2006

Salmonella contamination in soya-based animal feed - a food safety issue?

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Publication date: 2006
Event: Abstract from The International Symposium on Veterinary Epidemiology and Economics, Cairns, Australia, .
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 247937
Publication: Research › Conference abstract for conference – Annual report year: 2006

The Attribution of Animal-food Sources to Human Salmonellosis

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Authors: Hald, T. (Intern), Wong, D. L. F. (Intern), Wegener, H. C. (Intern)
Publication date: 2006
Event: Poster session presented at 5th International Conference on Emerging Infectious Diseases, Atlanta, GA, United States.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 245419
Publication: Research › Poster – Annual report year: 2006

The development of generic risk modules to respond promptly to food safety issues

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Communications and Management Secretariat
Authors: Wong, D. L. F. (Intern), Pires, S. M. (Intern), Hald, T. (Intern), Wingstrand, A. (Intern), Andersen, J. S. (Ekstern), Wegener, H. C. (Intern)
Publication date: 2006
Event: Abstract from The International Symposium on Veterinary Epidemiology and Economics, Cairns, Australia, .
Main Research Area: Technical/natural sciences
Source: orbit
The effects, costs and benefits of Salmonella surveillance in the Danish table-egg sector

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Pires, S. M. (Intern), Hald, T. (Intern)
Publication date: 2006

Host publication information
Title of host publication: Symposia proceedings : the complete archive of ISVEE proceedings
Publisher: Frenchs Forests
Main Research Area: Technical/natural sciences
Links:
http://www.worldcat.org/oclc/123486398
Source: orbit
Source-ID: 239309
Publication: Research › Article in proceedings – Annual report year: 2006

Annual Report on Zoonoses in Denmark 2004

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: Helwigh, B. (Intern), Borck Høg, B. (Intern), Hald, T. (Intern), Sørensen, P. C. (Ekstern), Ethelberg, S. (Ekstern)
Number of pages: 40
Publication date: 2005

Publication information
Publisher: Danish Zoonosis Centre
Original language: English
Main Research Area: Technical/natural sciences

Bibliographical note
ISSN: 0909-4172
Publication: Research - peer-review › Report – Annual report year: 2005

Antibiotikaresistens og salmonellabakterier fra danske og udenlandske kilder

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
A Bayesian approach to quantify the contribution of animal-food sources to human salmonellosis

Based on the data from the integrated Danish Salmonella surveillance in 1999, we developed a mathematical model for quantifying the contribution of each of the major animal-food sources to human salmonellosis. The model was set up to calculate the number of domestic and sporadic cases caused by different Salmonella sero and phage types as a function of the prevalence of these Salmonella types in the animal-food sources and the amount of food source consumed. A multiparameter prior accounting for the presumed but unknown differences between serotypes and food sources with respect to causing human salmonellosis was also included. The joint posterior distribution was estimated by fitting the model to the reported number of domestic and sporadic cases per Salmonella type in a Bayesian framework using Markov Chain Monte Carlo simulation. The number of domestic and sporadic cases was obtained by subtracting the estimated number of travel- and outbreak-associated cases from the total number of reported cases, i.e., the observed data. The most important food sources were found to be table eggs and domestically produced pork comprising 47.1% (95% CI: 43.3-50.8%) and 9% (95% CI: 7.8-10.4%) of the cases, respectively. Taken together, imported foods were estimated to account for 11.8% (95% CI: 5.0-19.0%) of the cases. Other food sources considered had only a minor impact, whereas 25% of the cases could not be associated with any source. This approach of quantifying the contribution of the various sources to human salmonellosis has proved to be a valuable tool in risk management in Denmark and provides an example of how to integrate quantitative risk assessment and zoonotic disease surveillance.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Authors: Hald, T. (Intern), Vose, D. (Ekstern), Wegener, H. C. (Intern), Koupeev, T. (Ekstern)
Pages: 255-269
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Risk Analysis
Volume: 24
Issue number: 1
ISSN (Print): 0272-4332
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.381 SJR 1.01 CiteScore 2.43
Web of Science (2017): Impact factor 2.898
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.21 SJR 1.12 SNIP 1.485
Web of Science (2016): Impact factor 2.518
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.334 SNIP 1.495 CiteScore 2.51
Web of Science (2015): Impact factor 2.225
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.331 SNIP 1.588 CiteScore 2.2
Web of Science (2014): Impact factor 2.502
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.067 SNIP 1.595 CiteScore 2.1
Web of Science (2013): Impact factor 1.974
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
Web of Science (2012): Impact factor 2.278
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.735 SNIP 1.693 CiteScore 2.15
Web of Science (2011): Impact factor 2.366
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): Impact factor 2.096
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
Scopus rating (2003): SJR 0.65 SNIP 1.318
Scopus rating (2002): SJR 0.59 SNIP 1.245
Scopus rating (2001): SJR 0.759 SNIP 1.732
Scopus rating (2000): SJR 0.763 SNIP 1.468
Scopus rating (1999): SJR 0.799 SNIP 1.506

Original language: English
Source: orbit
Source-ID: 237661
Estimating the number of undetected multi-resistant Salmonella Typhimurium DT104 infected pig herds in Denmark

In Denmark, the detection of multi-resistant Salmonella Typhimurium DT104 (MRDT104)-infected pig herds relies on the national Salmonella surveillance programme at the farm and slaughterhouse levels of production. With the surveillance sampling protocol and the diagnostic methods currently used, some herds might remain undetected. The number of undetected Danish pig herds infected with MRDT104 in the period 1 August 2001-31 July 2002 was estimated and compared with the number of culture-confirmed detected herds. A flow chart was constructed to illustrate where infected herds will go undetected in the surveillance system and Monte Carlo simulation was used to model the actual number of pig herds infected with MRDT104. We estimated that 52 (90% CI [28, 178]) finisher herds were infected with MRDT104 compared to 23 (44%) detected. Among sow herds with production of weaners or growers, we estimated that 38 (90% CI [23, 74]) were infected with MRDT104 compared to 7 (18%) actually detected. Among breeder and multiplier herds, we estimated that five (90% CI [3, 8]) herds were infected with MRDT104 compared to three (60%) detected. In total, we estimated that 102 pig herds were infected with MRDT104 from 1 August 2001 till 31 July 2002 (90% CI [63, 228]). In comparison, 33 (32%) infected herds were detected in this period. The predicted proportion of undetected herds varied considerably with herd type. We infer that the proportion of detected MRDT104 infected herds depended on the intensity of the combined serological and bacteriological testing.
Principles, application areas and an example of risk assessment conducted at the Danish Institute for Food and Veterinary Research

The Department for Epidemiology and Risk Analysis at the Danish Institute for Food and Veterinary Research (DFVF) is concerned with risk analyses in the areas of food safety, zoo noses, antimicrobial resistance and OIE (World Organisation for Animal Health) list A and B diseases. The DFVF is responsible for the risk assessment component of the risk analysis process and provides advice and support for the risk management and risk communication component, which is generally under the auspices of the Danish Veterinary and Food Administration (DVFA). The paper presents guidelines for the conduct of risk assessments at the DFVF. Important elements of these guidelines are the independence between risk assessment and risk management, the commitment to science-based, transparent and fully documented procedures and adherence to a protocol that regulates the cooperation between DFVF and DVFA. Typical steps of a quantitative risk assessment are the description of the risk scenario, information retrieval, mathematical modelling with stochastic simulation, final risk estimation with a sensitivity analysis and reporting. The procedure is exemplified using a Monte Carlo simulation model for the assessment of the risk of BSE transmission to calves by tallow-based calf milk replacer.

General information
State: Published
Annual Report on Zoonoses in Denmark 2003

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: Borck Høg, B. (Intern), Hald, T. (Intern), Sørensen, P. C. (Ekstern), Ethelberg, S. (Ekstern)
Number of pages: 32
Publication date: 2003

Publication information
Publisher: Ministry of Food, Agriculture and Fisheries
Main Research Area: Technical/natural sciences

Bibliographical note
ISSN: 0909-4172
Publication: Research › Report – Annual report year: 2003

Salmonella Control Programs in Denmark
We describe Salmonella control programs of broiler chickens, layer hens, and pigs in Denmark. Major reductions in the incidence of foodborne human salmonellosis have occurred by integrated control of farms and food processing plants. Disease control has been achieved by monitoring the herds and flocks, eliminating infected animals, and diversifying animals (animals and products are processed differently depending on Salmonella status) and animal food products according to the determined risk. In 2001, the Danish society saved U.S.$25.5 million by controlling Salmonella. The total annual Salmonella control costs in year 2001 were U.S.$14.1 million (U.S.$0.075/kg of pork and U.S.$0.02/kg of broiler or egg). These costs are paid almost exclusively by the industry. The control principles described are applicable to most industrialized countries with modern intensive farming systems.

General information
State: Published
Organisations: Communications and Management Secretariat, National Food Institute, Division of Microbiology and Risk Assessment, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
The occurrence and epidemiology of Salmonella in European pig slaughterhouses

This study was part of an international research project entitled SALINPORK (FAIR CT-950400) initiated in 1996. The objectives were to investigate the occurrence of Salmonella in pig slaughterhouses and to identify risk factors associated with the contamination of pig carcasses. Data was collected from 12 slaughterhouses in five European countries. Isolates were characterized by serotyping, phage typing and antimicrobial susceptibility. In one country, no Salmonella was found. Salmonella was isolated from 5.3% of 3485 samples of pork and from 13.8% of 3573 environmental samples from the seven slaughterhouses in the four remaining countries. The statistical analyses (multi-level logistic regression) indicated that the prevalence was significantly higher during the warmer months and that the environmental contamination increased during the day of slaughter. The polishing (OR 3.74, 95% CI 1.43-9.78) and pluck removal (OR 3.63, 95% CI 1.66-7.96) processes were found to contribute significantly to the total carcass contamination, the latter especially if the scalding water also was contaminated. To reduce carcass contamination, it is recommended to ensure sufficiently high temperatures of scalding water (62 degreesC) and appropriate cleaning and disinfection of the polishing equipment at least once a day in order to reduce the level of carcass contamination and consequently the prevalence of Salmonella in pork.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hald, T. (Intern), Wingstrand, A. (Intern), Swanenburg, M. (Ekstern), von Altrock, A. (Ekstern), Thorberg, B. (Ekstern)
Pages: 1187-1203
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Epidemiology and Infection
Volume: 131
Issue number: 3
ISSN (Print): 0950-2688
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): Impact factor 2.044
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): Impact factor 2.075
Web of Science (2016): Indexed yes
Annual Report on Zoonoses in Denmark 2001

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics
Authors: Hald, T. (Intern), Brøndsted, T. (Ekstern), Dresling, A. (Ekstern), Ethelberg, S. (Ekstern)
Number of pages: 28
Publication date: 2002

Publication information
Publisher: Ministry of Food, Agriculture and Fisheries
Main Research Area: Technical/natural sciences
Bibliographical note
ISSN: 0909-4172

Assessment of the effect of proposed changes to the management of multi-resistant Salmonella Typhimurium DT104 in primary food animal production in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Publication date: 2002

Publication information
Publisher: Dansk Zoonosecenter
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 237016

Epidemiology and control measures for Salmonella in pigs and pork

In order to effectively manage the problem of human salmonellosis attributable to pork and pork products, control measures should be taken simultaneously at all levels of production. These measures require an understanding of the epidemiology of Salmonella within and between links of the production chain. Two major factors of pre-harvest Salmonella epidemiology are the introduction and subsequent transmission of infection within and between herds. Stress imposed by transportation and the associated handling can significantly increase the number of pigs excreting Salmonella upon arrival at the abattoir and during lairage, exposing negative pigs to Salmonella. Positive pigs carry Salmonella on the skin, in the gastro-intestinal system or in the mouth. The (cross-)contamination of carcasses is basically a matter of redistributing the Salmonella bacteria from the positive pigs during the various slaughter processes. Although the manufacturing and retail levels of pork production depend on the quality of raw materials that are delivered, they share the responsibility for the quality and safety of the end products reaching the consumer. At this level and onwards, the three main factors which influence the microbiological quality of meats are handling, time and temperature. (C) 2002 Elsevier Science B.V. All rights reserved.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Authors: Wong, D. L. F. (Intern), Hald, T. (Intern), Wolf, P. J. V. D. (Ekstern), Swanenburg, M. (Ekstern)
Pages: 215-222
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Livestock Production Science
Volume: 76
Trends and seasonal variations in the occurrence of Salmonella in pigs, pork and humans in Denmark, 1995-2000

A mandatory programme monitoring the occurrence of Salmonella in pork at slaughterhouses and a serological monitoring of slaughter-pig herds has been implemented in Denmark since 1993 and 1995, respectively. All results are stored in a central database. From this, aggregated weekly results of serological and bacteriological samples collected in the period between January 1995 and July 2000 were extracted. In addition, the reported weekly incidence of human infections with S. Typhimurium covering the same time period was obtained. The times series were analysed for trends and cyclic variations by seasonal decomposition. The association between the incidence in humans and the prevalence of Salmonella in pigs and pork, and prevailing weather conditions, were analysed by using a general linear (glm) and a general additive model (gam). Explanatory variables were lagged to account for time elapsed between sampling, consumption, incubation period and case registration. The results of the seasonal decomposition showed an overall declining trend in all three time series. All time series exhibited a double peaked annual cycle. The seasonal variation of the prevalence in pork and the human incidence had a very similar course. The variables that were both biologically meaningful and statistically significant in both regression models were the prevalence in pork sampled 4 to 5 weeks before case registration, the seroprevalence, measured as the average prevalence of week 15 to 35 before case registration, and the air temperature lagged at 2 and 3 weeks. Limitations on inferences from overall surveillance data are discussed.
Udbrud med Salmonella Bovismorbificans

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Authors: Schiellerup, P. (Ekstern), Neimann, J. (Ekstern), Hald, T. (Intern), Ethelberg, S. (Ekstern)
Pages: 5683-5683
Publication date: 2001
Annual Report on Zoonoses in Denmark 1999

General information
State: Published
Annual Report on Zoonoses in Denmark 1998

General information
State: Published
Organisations: National Food Institute, Danish Veterinary Laboratory
Authors: Hald, T. (Intern), Wegener, H. C. (Forskerdatabase), Jørgensen, B. B. (Ekstern)
Number of pages: 24
Publication date: 1999

Publication information
Publisher: Ministry of Food, Agriculture and Fisheries
Original language: English
Main Research Area: Technical/natural sciences

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ISSN: 0909-4172
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Annual report on zoonoses in denmark 1997

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Communications and Management Secretariat
Authors: Hald, T. (Intern), Wegener, H. C. (Intern), Jørgensen, B. B. (Ekstern)
Number of pages: 20
Publication date: 1997

Publication information
Publisher: Danish Zoonosis Centre
Original language: English
Series: Zoonose-Nyt
ISSN: 0909-4172
Main Research Area: Technical/natural sciences

Bibliographical note
ISSN: 0909-4172
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Publication: Research - peer-review › Report – Annual report year: 1997

Salmonella typhimurium udbrud på Fyn sensommeren 1996: En case-kontrol undersøgelse

General information
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Organisations: Unknown
Authors: Mølbak, K. (Ekstern), Hald, T. (Intern)
Pages: 5372-5377
Publication date: 1997
Main Research Area: Technical/natural sciences

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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
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BFI (2014): BFI-level 1
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BFI (2012): BFI-level 1
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ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.161 SNIP 0.17
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.158 SNIP 0.201
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.158 SNIP 0.173
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.148 SNIP 0.16
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.141 SNIP 0.164
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.145 SNIP 0.179
Scopus rating (2004): SJR 0.17 SNIP 0.209
Scopus rating (2003): SJR 0.144 SNIP 0.182
Scopus rating (2002): SJR 0.141 SNIP 0.145
Scopus rating (2001): SJR 0.145 SNIP 0.187
Scopus rating (2000): SJR 0.139 SNIP 0.19
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Source: orbit
Source-ID: 243567
Publication: Research - peer-review › Journal article – Annual report year: 1997

Annual Report on Zoonoses in Denmark 1996

General information
State: Published
Projects:

Comparison of ADDs used in VetStat with primary data on usage doses obtained at visits in 20 Danish pig herds
Master project
National Food Institute
Research Group for Genomic Epidemiology
Period: 01/08/2016 → 06/01/2017
Number of participants: 1
antimicrobial usage, VetStat, Epidemiology, pigs
Main Supervisor:
Hald, Tine (Intern)
Project

COMPARE WG 1, Task 1.2: Development of a novel approach for food chain risk assessment based on NGS data
National Food Institute
Research Group for Genomic Epidemiology
Period: 01/02/2016 → 31/12/2018
Number of participants: 1
microbial risk assessment, whole genome sequencing, machine learning, listeria
Supervisor:
Hald, Tine (Intern)
Project

Tools for source attribution based on ngs data
National Food Institute
Period: 01/12/2015 → 31/05/2019
Number of participants: 4
PhD Student:
Munck, Nanna Sophia Mucha (Intern)
Supervisor:
de Knegt, Leonardo (Intern)
Leekitcharoenphon, Pimlapas (Intern)
Main Supervisor:
Hald, Tine (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD
Quantification of exposure to AMR through different transmission routes from animals to humans

This project is part of the EU Consortium “Ecology from Farm to Fork Of microbial drug Resistance and Transmission” (EEFORT). Our work package (WP7) will focus on the development of two source attribution approaches for antimicrobial resistance determinants.

The first approach will estimate the relative exposure to AMR determinants through various transmission routes. This comparative exposure assessment model aims at representing the overall EU population by including data from a representative set of countries, and will include farm and retail data from various food transmission routes such as pork, chicken, turkey, veal and fish.

The second model will use a microbial subtyping approach and will be developed to estimate the relative importance of food animals, pets and environmental sources for the exposure to AMR determinants in occupational risk groups constituted by people working in farms and slaughterhouses. The source-attribution model will be based on the comparison of bacterial genetic profiles found in the various sources with the ones found in humans based on DNA sequence data. Sources will include food-production animals (broilers and pigs), environmental routes and direct contact with pets in farms. The output of this model will be the number of humans that have been exposed to AMR determinants through each source.

The EFFORT project will provide scientific evidence and high quality data that will inform decision makers, the scientific community and other stakeholders about the consequences of Anti-Microbial Resistance (AMR) in the food chain, in relation to animal health and welfare, food safety and economic aspects.

Source attribution of antimicrobial resistance determinants.

National Food Institute
Division of Epidemiology and Microbial Genomics
SAFOSO
Utrecht University
Period: 01/01/2015 → 31/12/2019
Number of participants: 1
Antimicrobial resistance, Source-attribution, Risk assessment, whole genome sequencing, qPCR
Project Manager, organisational:
Hald, Tine (Intern)
Project

Global Decision Support Initiative
Holistic approach to decision analysis considering both risk and sustainability

National Food Institute
Research Group for Genomic Epidemiology
Period: 01/01/2015 → …
Number of participants: 1
risk assessment, sustainability assessment, decision support
Acronym: GDSI
Project participant:
Hald, Tine (Intern)
Project

Attribution of human cases of salmonellosis to different animal reservoirs of the food chain in Denmark

In recent history, Salmonella has been the second most common cause of bacterial foodborne infections in Denmark, with 1,136 cases reported in 2013. During the last three decades, broilers, pigs and laying hens have been ascribed the role of main reservoirs for this pathogen in different time periods, thus demanding different control strategies in the food chain. In order to identify the main food-animal sources of human salmonellosis, Denmark has since 1995 relied on the routine application of a source attribution model.

The source attribution model uses a microbial subtyping approach to attribute cases to their animal reservoirs, i.e., it compares the number of human cases caused by different Salmonella subtypes with the distribution of the same subtypes isolated from various food-animal sources, also taking into account the differences in consumption of the meats/eggs included in the model.

The data required for the model are collected through national surveillance and monitoring programs involving food authorities, the food industry and national reference laboratories for animal and human samples, requiring a well-structured network which has been developed during the last two decades.
Traditionally, the model has used data on serotypes, phage types and antimicrobial resistance profiles of Salmonella isolates. Starting in 2014, molecular methods will be used for subtyping of Salmonella Enteritidis and Salmonella Typhimurium.

Results are published yearly in the Annual Report on Zoonoses in Denmark.

EFFORT: Ecology from farm to fork of microbial drug resistance and transmission

EFFORT will study the complex epidemiology and ecology of antimicrobial resistance and the interactions between bacterial communities, commensals and pathogens in animals, the food chain and the environment. This will be conducted by a combination of epidemiological and ecological studies using newly developed molecular and bio-informatics technologies. EFFORT will include an exposure assessment of humans from animal and environmental sources. The ecological studies on isolates will be verified by in vitro and in vivo studies. Moreover, real-life intervention studies will be conducted with the aim to reduce the use of antimicrobials in veterinary practice. Focus will be on understanding the eco-epidemiology of antimicrobial resistance from animal origin and based on this, predicting and limiting the future evolution and exposure to humans of the most clinically important resistance by synthesising different sources of information in our prediction models.

Through its results, the EFFORT research will provide scientific evidence and high quality data that will inform decision makers, the scientific community and other stakeholders about the consequences of AMR in the food chain, in relation to animal health and welfare, food safety and economic aspects. These results can be used to support political decisions and to prioritise risk management options along the food chain.

The epidemiology of zoonotic antimicrobial resistance in animal production
Salmonella source attribution using molecular typing data

The Danish Salmonella source attribution model uses a microbial subtyping approach to attribute cases to their animal reservoirs, i.e., it compares the number of human cases caused by different Salmonella subtypes with the distribution of the same subtypes isolated from various food-animal sources, also taking into account the differences in consumption of the meats/eggs included in the model.

Molecular typing methods are increasingly used to subtype foodborne pathogens isolated through animal, food and public health surveillance. In particular, MLVA (Multiple-Locus Variable number tandem repeat Analysis) is routinely used to subtype Salmonella isolates in Denmark. These methods are expected to replace phenotypic methods in the near future.

Using molecular data for source attribution is challenging for several reasons, mostly related to a difficult balance between specificity of the method and the required discrimination power for source attribution.

The objectives of this project are to evaluate how MLVA-based data performs in different source attribution approaches, to identify the most appropriate method for routine Salmonella source attribution, and to assess the utility of its results for the decision-making process in Denmark.

National Food Institute
Division of Epidemiology and Microbial Genomics
Statens Serum Institut

Period: 01/01/2013 → 31/12/2015
Number of participants: 1
Source-attribution, Risk assessment, molecular typing, MLVA, source-account, Salmonella
Project Manager, organisational:
Hald, Tine (Intern)
Risk based control in pig slaughter
National Food Institute
Period: 01/09/2012 → 30/09/2017
Number of participants: 8
Phd Student:
Bollerslev, Anne Mette (Intern)
Supervisor:
Hald, Tine (Intern)
Hansen, Tina Beck (Intern)
Nauta, Maarten (Intern)
Main Supervisor:
Aabo, Søren (Intern)
Examiner:
Pamp, Sünje Johanna (Intern)
Alban, Lis (Ekstern)
Zutter, Lieven de (Ekstern)

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

Development of a Salmonella source-attribution model for evaluating targets in the turkey meat production
A Salmonella source attribution model based on a microbial-subtyping approach was developed to estimate the public health effect of setting a new target for the reduction of Salmonella in fattening turkey flocks in the European Union. The model considers the quantitative contribution and relevance of different Salmonella serovars found in turkeys to human salmonellosis and includes 25 Member States, four animal-food sources of Salmonella (turkeys, broilers, laying hens and pigs) and 23 Salmonella serovars. This turkey-target Salmonella attribution model (TT-SAM) employs prevalence and serovar distribution data from the EU statutory monitoring and EU-wide Baseline Surveys on Salmonella in animal-food sources, data on incidence and serovar distribution of human salmonellosis, and food availability data.

National Food Institute
Division of Epidemiology and Microbial Genomics
Period: 01/11/2011 → 30/04/2012
Number of participants: 3
Contact person:
Hald, Tine (Intern)
Project participant:
de Knegt, Leonardo (Intern)
Pires, Sara Monteiro (Intern)

The future approach for Salmonella source attribution
Source attribution is the process of determining what proportion of a particular disease is acquired from a given source (e.g. chicken) and through a given pathway (e.g. food or direct animal contact). Source attribution using microbial subtyping to compare isolates from humans with isolates from animals and food sources and a mathematical model that quantifies the human disease burden by comparing these distributions has recently received a considerable amount of attention. In this project, we will provide the foundation for a new concept for Salmonella source attribution based on molecular typing and mathematical modelling. The hypothesis is that we by applying molecular typing methods can obtain an improved and more conclusive identification of sources of human salmonellosis both for sporadic and outbreak-related human cases.

National Food Institute
Statens Serum Institut
Period: 01/01/2010 → 30/11/2012
Number of participants: 1
Project Manager, organisational:
Hald, Tine (Intern)
Global surveillance of Salmonella in animals, food and humans: Identification of major sources and analysis of global trends

The objectives are to provide an overview of Salmonella serovars in different countries and regions, evaluate trends over the years and analyze the worldwide epidemiology of the various serovars. The overall aim is to estimate the attribution of the global burden of human salmonellosis on the various animal-food sources, by: 1) Reviewing the Salmonella serovar distribution in animal reservoirs to obtain the expected distribution and prevalence of Salmonella serovars in different countries, by animal host. 2) Developing a Global Atlas of Food Consumption from several food consumption databases worldwide, which will provide data on the estimated consumption of animal-originated food items in different countries/regions. 3) Use the Global Livestock Production and Health Atlas (GLiPHA) to provide data on global distribution of animal hosts and other possible animal-originated sources of Salmonella contamination. The project is done in close collaboration with WHO, and supports the WHO initiative to estimate the global burden of foodborne disease (FERG).

Division of Microbiology and Risk Assessment
National Food Institute

World Health Organization
Period: 01/04/2009 → 02/03/2012
Number of participants: 5
Project participant:
de Knegt, Leonardo (Intern)
Aarestrup, Frank Møller (Intern)
Pires, Sara Monteiro (Intern)
Lo Wong, Danilo (Ekstern)
Project Manager, organisational:
Hald, Tine (Intern)

Global surveillance of Salmonella in animals, food and humans: Identification of major sources and analysis of global trends

National Food Institute
Period: 01/04/2009 → 29/05/2013
Number of participants: 6
Phd Student:
de Knegt, Leonardo (Intern)
Supervisor:
Pires, Sara Monteiro (Intern)
Main Supervisor:
Hald, Tine (Intern)
Examiner:
Hendriksen, Rene S. (Intern)
Döpfer, Dörte D.V. (Ekstern)
Ricci, Antonia (Ekstern)

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

Analyses of data on Salmonella serovars and phage types derived from animals and food in the European Union

The objective is to analyse in detail Salmonella serovar and phage typing surveillance data as reported under the Directive 2003/99/EC (Zoonoses Directive) and through the completed EU-wide baseline studies. The analysis will focus on the main relevant epidemiological findings based on frequency and spatial distributions of Salmonella serovars and phage types isolated from animals, food, feed and humans in EU. Special attention will be given to analyse the data in order to investigate the contribution of each animal-food source to human salmonellosis i.e. a source attribution analysis. The project is done in close collaboration with the European Food Safety Authority (EFSA).

Division of Microbiology and Risk Assessment
National Food Institute
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
Period: 01/10/2008 → 31/10/2011
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)

Evaluering og optimering af overvågningsprogrammer for antibiotika resistens og antibiotikaforbrug

National Food Institute
Period: 01/10/2008 → 25/04/2012
Number of participants: 7
Phd Student:
Struve, Tina (Intern)
Supervisor:
Aarestrup, Frank Møller (Intern)
Emborg, Hanne-Dorthe (Intern)
Main Supervisor:
Hald, Tine (Intern)
Examiner:
Jensen, Lars Bogø (Intern)
Bækbo, Poul (Ekstern)
Greiner, Matthias (Ekstern)

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

Campylobacter - human eksponering, smittekilde og Bekæmpelsestiltag

National Food Institute
Period: 01/03/2008 → 23/05/2012
Number of participants: 7
Phd Student:
Boysen, Louise (Intern)
Supervisor:
Ethelberg, Steen (Ekstern)
Hald, Tine (Intern)
Main Supervisor:
Rosenquist, Hanne (Intern)
Examiner:
Hansen, Tina Beck (Intern)
Havelaar, Arie Hendrik (Ekstern)
Jørgensen, Frieda (Ekstern)

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

Animal Health and 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)

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**Balancing microbiological safety against other food quality parameters**

The project focuses on microbiological food safety, treating this as one of several consumer-driven quality parameters of animal production. It will provide general policy recommendations for food safety strategies in diversified food production systems in order to support and strengthen a diverse and viable food production. In this project we will assess the level of microbiological food safety in different production systems and study consumers and producers perception of microbiological food safety risks. We will study consumers' valuation of food quality parameters and their willingness to pay for food safety in the context of other quality parameters of animal products. Based upon the results we will investigate strategies for increased microbiological food safety that respect consumer concerns about other food quality parameters as well.

Division of Microbiology and Risk Assessment

National Food Institute

University of Copenhagen

*Period:* 01/04/2005 → 30/11/2009

*Number of participants:* 13

*Acronym:* QUALYSAFE

*Project participant:*

Hald, Tine (Intern)

Korsgaard, Helle Bisgaard (Intern)

Emborg, Hanne-Dorthe (Intern)

Jensen, Vibeke Frekjær (Intern)

Sandøe, Peter (Ekstern)

Korzen-Bohr, Sra (Ekstern)

Christensen, Tove (Ekstern)

Lund, Mogens (Ekstern)

Denver, Sigrid (Ekstern)

Dejgaard, Jørgen (Ekstern)
Balancing microbiological safety against other food quality parameters (QUALYSAFE)
The project focuses on microbiological food safety, treating this as one of several consumer-driven quality parameters of animal production. It will provide general policy recommendations for food safety strategies in diversified food production systems in order to support and strengthen a diverse and viable food production. In this project we will assess the level of microbiological food safety in different production systems and study consumers and producers perception of microbiological food safety risks. We will study consumers' valuation of food quality parameters and their willingness to pay for food safety in the context of other quality parameters of animal products. Based upon the results we will investigate strategies for increased microbiological food safety that respect consumer concerns about other food quality parameters as well.

Division of Microbiology and Risk Assessment

National Food Institute

University of Copenhagen
Period: 01/04/2005 → 31/12/2009
Number of participants: 14
Project participant:
Sandøe, Peter (Ekstern)
Lassen, Jesper (Ekstern)
Korzen-Bohr, Sara (Ekstern)
Christensen, Tove (Ekstern)
Lund, Mogens (Ekstern)
Denver, Sigrid (Ekstern)
Dejgaard, Jørgen (Ekstern)
Lawson, Lartey G. (Ekstern)
Morten Mørkbak (Ekstern)
Hald, Tine (Intern)
Korsgaard, Helle Bisgaard (Intern)
Emborg, Hanne-Dorthe (Intern)
Jensen, Vibeke Frøkjær (Intern)

Project Manager, organisational:
Wingstrand, Anne (Intern)

Activities:

Incorporation of machine learning methods for whole genome sequencing based risk prediction and source attribution: case of Listeria monocytogenes

Period: 26 Sep 2017

Patrick Murigu Kamau Njage (Speaker)
Pimlapas Leekitcharoenphon (Other)
Clémentine Henri (Other)
Sophie Roussel (Guest lecturer)
Rene S. Hendriksen (Other)
Tine Hald (Other)

National Food Institute
Research Group for Genomic Epidemiology

Description
The 10th International Conference on Predictive Modelling in Food., Córdoba, Spain.
Degree of recognition: International
Related organisation

Incorporation of machine learning methods for whole genome sequencing based risk prediction and source attribution: case of Listeria monocytogenes

Njage, P. M. K. (Speaker), Leekitcharoenphon, P. (Other), Clémentine Henri (Other), Sophie Roussel (Guest lecturer), Hendriksen, R. S. (Other), Hald, T. (Other)

26 Sep 2017

Activity: Talks and presentations › Conference presentations

Applying LCA in decision making- the need and the future perspective

Period: 10 May 2017

Yan Dong (Speaker)
Simona Miraglia (Other)
Stefano Manzo (Other)
Stylianos Georgiadis (Other)
Hjalte Jomo Danielsen Sørup (Other)
Elena Boriani (Other)
Tine Hald (Other)
Sebastian Thøns (Other)
Michael Zwicky Hauschild (Other)

Department of Management Engineering
Quantitative Sustainability Assessment
Centre for oil and gas – DTU
Transport DTU
Transport Modelling
Department of Applied Mathematics and Computer Science
Statistics and Data Analysis
Department of Environmental Engineering
Urban Water Systems
National Food Institute
Research Group for Genomic Epidemiology
Department of Civil Engineering
Section for Structural Engineering

Documents:
AbstrApplying LCA in policy decision making_Final

Links:
https://brussels.setac.org/welcome/

Related event

SETAC Europe: 27th Annual Meeting – Environmental Quality Through Transdisciplinary Collaboration
07/05/2017 → 13/07/2017
Brussels, Belgium
Activity: Talks and presentations › Conference presentations

One Health International Summer Course 2017
Period: 8 May 2017 → 18 Aug 2017

Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Panel member)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)
Description
One Health International Summer Course 2017
5-week elearning part + 1-week on campus part, a total of 5 ECTS
Degree of recognition: International

Related event
One Health International Summer Course 2017
08/05/2017 → 18/08/2017
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Applying LCA in decision making - the need and the future perspective
Period: 7 May 2017 → 11 May 2017
Yan Dong (Guest lecturer)
Simona Miraglia (Guest lecturer)
Stefano Manzo (Guest lecturer)
Stylianos Georgiadis (Guest lecturer)
Hjalte Jomo Danielsen Sarup (Guest lecturer)
Elena Boriani (Guest lecturer)
Tine Hald (Guest lecturer)
Sebastian Thöns (Guest lecturer)
Michael Zwicky Hauschild (Guest lecturer)

Department of Management Engineering
Quantitative Sustainability Assessment
Department of Civil Engineering
Transport DTU
Transport Modelling
Department of Applied Mathematics and Computer Science
Statistics and Data Analysis
Department of Environmental Engineering
Urban Water Systems
National Food Institute
Research Group for Genomic Epidemiology
Section for Structural Engineering

Description
There is nowadays a need of including sustainable considerations in the policy and decision making. Sound decision making requires evidence-based support, i.e. decision analysis to help decision makers in identifying the best alternative based on the associated impacts. Decision analysis includes four steps: 1) structure decision problem; 2) assess possible impacts associated with alternatives; 3) determine stakeholder preferences and 4) evaluate alternatives. Decision analysis can be performed applying different tools, such as cost-benefit analysis (CBA), risk assessment, and life cycle assessment (LCA).

LCA is a decision analysis tool that focuses on environmental impacts. One limit is that LCA is based on defined impact categories and therefore does not provide information for those impacts and consequences out of the LCA scope. However, the LCA framework closely follows the decision analysis scheme and has the potential to be integrated with other decision analysis tools to enhance their assessment of environmental impacts.

To understand why LCA is needed in the policy decision context, we looked into the decision support for policy in several
disciplines. Taking sustainable transport policy as an example, the traditional decision analysis tool for choosing the best alternative is CBA. CBA mainly analyses socio-economic impacts, such as travel time savings and costs, while only some environmental impacts are considered; i.e. the damage costs of greenhouse gas emissions, particulate matters, SOx, NOx and noise. Therefore, current transport policy making rarely reflect a full environmental profile of the suggested alternatives. Making decisions based on incomplete information may lead to sub-optimal solutions, especially where the environment is a major concern. There is a growing attention of conducting LCA in transport. Some identified environmental hotspots, such as consumer and household behavior, which may be the focus for future policies. Others assess the environmental impacts associated with building infrastructures and vehicle use. These studies verify that LCA can successfully quantify the environmental profile of alternatives in transport policy, if the relevant physical changes, e.g. vehicle travel distance and new infrastructures, are well-defined. However, before integrating LCA with other decision analysis methods for decision support, the study system, objectives, scopes, evaluation metrics and uncertainty handling need to be aligned.

Degree of recognition: International
Links:
https://brussels.setac.org/

Related event

SETAC Europe: 27th Annual Meeting – Environmental Quality Through Transdisciplinary Collaboration
07/05/2017 → 13/07/2017
Brussels, Belgium
Activity: Talks and presentations › Conference presentations

Burden of disease of barbecued meat - who's at risk?
Period: 31 Mar 2017
Lea Sletting Jakobsen (Guest lecturer)
Stylianos Georgiadis (Guest lecturer)
Bo Friis Nielsen (Guest lecturer)
Anders Stockmarr (Guest lecturer)
Elena Boriani (Guest lecturer)
Lene Duedahl-Olesen (Guest lecturer)
Tine Hald (Guest lecturer)
Sara Monteiro Pires (Guest lecturer)
National Food Institute
Research Group for Risk-Benefit
Department of Applied Mathematics and Computer Science
Statistics and Data Analysis
Research Group for Genomic Epidemiology
Research Group for Analytical Food Chemistry
Degree of recognition: International

Related external organisation
International Association for Food Protection
6200 Aurora Avenue, IA 50322-2864, Des Moines, United States
Activity: Talks and presentations › Conference presentations

Source attribution: Translating science into public health action
Period: 29 Mar 2017 → 31 Mar 2017
Tine Hald (Keynote speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

Related event
2017 Annual Meeting of SVEPM 2017, 29-31 March, Inverness, Scotland
29/03/2017 → 31/03/2017
Scotland, United Kingdom
Activity: Talks and presentations › Conference presentations

**Burden of disease and source attribution**
Period: 16 Mar 2017
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Teaching vet students at the One Health differentiation
Degree of recognition: Local

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

**Waldemir Santiago Neto**
Start date: 3 Mar 2017 → 15 Sep 2017
Tine Hald (Host)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
External research stay for PhD study
Degree of recognition: International
Activity: Hosting a guest lecturer

**Epidemiology and control of Taenia solium in Africa**
Period: 24 Feb 2017
Tine Hald (External examiner)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
PhD thesis
Degree of recognition: International
Activity: Examinations and supervision › Internal examination

**Descriptive study of antibiotic resistance and resistance determinants in indicator E. coli from Danish and imported meat and Danish animals using whole genome sequencing (WGS) and phenotypic resistance determination**
Period: 21 Feb 2017
Tine Hald (Supervisor)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Supervisor and co-examiner of Master thesis, Master in Food Quality and Safety
Degree of recognition: National
Activity: Examinations and supervision › Supervisor activities

**Master i Fødevarekvalitet og - sikkerhed**
Period: 31 Jan 2017 → 28 Apr 2017
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
Tine Hald responsible for a module on Risk Assessment of Foodborne Hazards (9 ECTS)
Degree of recognition: National

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

Molecular epidemiological studies of Campylobacter isolated from different sources in New Zealand between 2005 and 2015.
Period: 1 Jan 2017 → 4 Mar 2017
Tine Hald (External examiner)
National Food Institute
Research Group for Genomic Epidemiology

Description
PhD thesis
Degree of recognition: International
Activity: Examinations and supervision › Internal examination

Attributing the disease burden to different food groups - will it be easier in the future
Period: 7 Nov 2016
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Related event
New Science for Food Safety: supporting food chain transparency for improved health
07/11/2016 → 10/11/2016
Singapore, Singapore
Activity: Talks and presentations › Conference presentations

Global Surveillance
Period: 29 Sep 2016
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
Taking advantage of developments in genomics and data-sharing
Degree of recognition: National

Related event
XVII SIDILV Congress
28/09/2016 → 29/09/2016
Pacengo di Lazise (VR), Italy
Activity: Talks and presentations › Conference presentations
The Global Burden of Foodborne Disease
Period: 28 Sep 2016
Tine Hald (Keynote speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: National

Related event
XVII SIDILV Congress
28/09/2016 → 29/09/2016
Pacengo di Lazise (VR), Italy
Activity: Talks and presentations › Conference presentations

The Global Burden of Foodborne diseases
Period: 6 Jul 2016
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: Local

Related event
Internal seminar for EFSA staff
06/07/2016 → 06/07/2017
Parma, Italy
Activity: Talks and presentations › Conference presentations

Risk assessment of Salmonella in broiler farms with slaughter and sale at the farm
Period: 1 Jun 2016 → 2 Sep 2016
Tine Hald (Consultant)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: National

Related external organisation
Danish Veterinary and Food Administration
Mørkhøj Bygade 19, 2860, Søborg, Denmark
Activity: Public and private sector consultancy › Consultancy

University of Edinburgh
Period: 12 May 2016 → 27 May 2016
Tine Hald (Visiting researcher)
National Food Institute
Research Group for Genomic Epidemiology
Activity: Visiting an external institution › Visiting another research institution

One Health International Summer Course 2016
Period: 9 May 2016 → 23 Aug 2016
Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Organizer)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)
**Description**
One Health International Summer Course 2016

5-week elearning part + 1-week on campus part, a total of 5 ECTS
Degree of recognition: International

**Related event**

One Health International Summer Course 2016  
09/05/2016 → 23/08/2016  
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

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**Impact of Antimicrobial Usage in Food Production**
Period: 27 Apr 2016  
Tine Hald (Speaker)
National Food Institute  
Research Group for Genomic Epidemiology

**Description**
Presentation given for the Food Forum  
Degree of recognition: International

**Related external organisation**
The National Academies of Science, Engineering and Medicine  
500 fifth street, Washington DC, United States
Activity: Talks and presentations › Conference presentations

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World Health Organization's estimates of the relative contributions of food to the burden of disease due to selected foodborne hazards: a structured expert elicitation

Period: 11 Apr 2016  
Tine Hald (Speaker)
National Food Institute  
Research Group for Genomic Epidemiology

**Related event**

Food Safety and Food Security Workshop: COST meeting, IS1304, Network on Structured Expert Elicitation  
11/04/2016 → 13/04/2016  
Dubrovnik, Croatia
Activity: Talks and presentations › Conference presentations

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Trace back and trace forward in foodborne outbreak investigations
Period: 15 Mar 2016  
Tine Hald (Lecturer)
National Food Institute  
Research Group for Genomic Epidemiology
Degree of recognition: International

**Related event**

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SVEPM: Annual meeting 2016: Held a workshop on outbreak investigation
15/03/2016 → 18/03/2016
Elsinore, Denmark
Activity: Talks and presentations › Conference presentations

The Global Burden of Foodborne Disease
Period: 20 Jan 2016
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: Local

Related event

Internal meeting for FVST staff
20/01/2016 → 20/01/2016
Glostrup, Denmark
Activity: Talks and presentations › Conference presentations

Source Attribution Estimates of the Relative Contributions to the Burden of Disease due to selected Foodborne Hazards: a WHO Expert Elicitation
Period: 15 Dec 2015 → 16 Dec 2015
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology

Description
FERG symposium, held in Amsterdam
Degree of recognition: International
Documents:
FERGsyrniumabstractbook

Related external organisation

World Health organization and RIVM (National Institute for Public Health)
Royal Netherlands Academy of Arts and Sciences, Amsterdam, Netherlands
Activity: Talks and presentations › Conference presentations

Estimates of the relative contributions to the burden of disease due to selected foodborne hazards: A World Health Organization Expert Elicitation
Period: 5 Nov 2015
Tine Hald (Speaker)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Documents:
Abstract EE FERG ISVEE 2015 submitted new

Related event

14th International Symposium on Veterinary Epidemiology and Economics
03/11/2015 → 07/11/2015
Mérida, Yucatan, Mexico
Activity: Talks and presentations › Conference presentations

Better Training for Safer Food - Risk Analysis
Period: 3 May 2015 → 5 May 2015
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Tutor at course

**Related external organisation**

**BTSF, Tallin**
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Emmanuel de-Graft Johnson Owusu-Ansah**
Start date: 17 Apr 2015 → 15 Oct 2015
Tine Hald (Host)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International
Activity: Hosting a guest lecturer

**One Health International Summer Course 2015**
Period: 13 Apr 2015 → 21 Aug 2015
Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Organizer)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)
National Food Institute
Research Group for Genomic Epidemiology
National Veterinary Institute
Virology

**Description**
One Health International Summer Course 2015

6-week elearning part + 2 week on campus part, a total of 5 ECTS
Degree of recognition: International

**Related event**

**One Health International Summer Course 2015**
13/04/2015 → 21/08/2015
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Master i Fødevarekvalitet og -sikkerhed**
Period: 1 Jan 2015 → 20 Dec 2015
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

**Description**
Tine Hald responsible for a module on Risk Assessment of Foodborne Hazards (9 ECTS) and a module on Foodborne Outbreak Investigation (4 ECTS)
Degree of recognition: National

**Related external organisation**
Master i Fødevarekvalitet og -sikkerhed
Period: 1 Jan 2012 → 20 Dec 2012
Tine Hald (Lecturer)
National Food Institute
Research Group for Genomic Epidemiology

Description
Tine Hald responsible for a module on Risk Assessment of Foodborne Hazards (9 ECTS) and a module on Foodborne Outbreak Investigation (4 ECTS)
Degree of recognition: National

Related external organisation

EFSA expert panel on Biological Hazard (External organisation)
Period: 1 Jun 2009 → 1 Jun 2015
Tine Hald (Participant)
National Food Institute
Research Group for Genomic Epidemiology
Degree of recognition: International

Related external organisation

EFSA expert panel on Biological Hazard
European Food Safety Authority, Parma, Italy
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

The effects, costs and benefits of Salmonella surveillance in Danish table-egg sector
Tine Hald (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: PromSTAP Workshop ‘Science meets Policy’, Hilversum, the Netherlands

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

WHO-FERG Foodborne Disease Burden Epidemiology Reference Group (External organisation)
Period: 1 Jan 2007 → …
Tine Hald (Participant)
National Food Institute
Research Group for Genomic Epidemiology

Description
Core member of the WHO's Foodborne Disease Burden Epidemiology Reference Group (FERG)
Degree of recognition: International
Related external organisation

WHO-FERG Foodborne Disease Burden Epidemiology Reference Group
World Health Organization, Geneva, Switzerland
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

The development of generic risk modules to respond promptly to food safety issues
Period: 1 Jan 2006 → 1 Feb 2006
Tine Hald (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: International Symposium on Veterinary Epidemiology and Economics, Cairns, Australia

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

The application of risk assessment in food safety
Period: 1 Jan 2003 → 1 Feb 2003
Tine Hald (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: V Congresso Nazionale Società Italiana di Diagnostica di Laboratorio Veterinaria, Pisa, Italy

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Pre-harvest control of salmonella in broilers, layers and swine – results, public health effects and cost effectiveness
Period: 1 Jan 2000 → 1 Feb 2000
Tine Hald (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Int Conf Emerg Infect Dis, Atlanta, GA, USA

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Press clippings:

Salmonella i fjerkrae
Tine Hald
15/01/2014
National Food Institute, Division of Epidemiology and Microbial Genomics

Media contribution (1)

Salmonella i fjerkrae
Salmonellakontrol i fjerkræ i Danmark
Tine Hald
08/02/2012
National Food Institute, Division of Epidemiology and Microbial Genomics

De danske succes'er i relation til salmonellabekæmpelse
Tine Hald
27/09/2010
National Food Institute, Division of Microbiology and Risk Assessment

Forholdsregler for at undgå fødevarebårne infektioner på ferie i udlandet
Tine Hald
06/07/2010
National Food Institute, Division of Microbiology and Risk Assessment

Salmonella i avis- og opformeringsbesætninger
Tine Hald
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment
Salmonella i udenlandsk og dansk fjærkrækød
Tine Hald
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Salmonella i udenlandsk og dansk fjærkrækød
01/01/2010
Print
Tine Hald
National Food Institute, Division of Microbiology and Risk Assessment
Press / Media

Fødevarebårne infektioner
Tine Hald
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Fødevarebårne infektioner
01/01/2010
Print
Tine Hald
National Food Institute, Division of Microbiology and Risk Assessment
Press / Media

Salmonella i avis- og omformeringsbesætninger
Tine Hald
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Salmonella i avis- og omformeringsbesætninger
01/01/2010
Print
Tine Hald
National Food Institute, Division of Microbiology and Risk Assessment
Press / Media

Baggrund for kritisk eftersyn
Tine Hald
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Baggrund for kritisk eftersyn
01/01/2010
TÆNK, Print
Tine Hald
National Food Institute, Division of Microbiology and Risk Assessment
Press / Media

Smittekilderregnskabet 2007
Tine Hald
01/01/2009
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)