Source attribution of foodborne diseases

Foodborne diseases can be caused by a variety of hazards, of foods, and even non-food sources. Determining the sources of foodborne illness is an important part of identifying the most appropriate measures to improve food safety. To be able to intervene in the food production chain – from the farms and production fields to our tables - risk managers need to know where to focus and allocate resources.

Source attribution of foodborne illnesses is the process of estimating the most important sources responsible for specific foodborne illnesses. We use data from public health surveillance and monitoring of animals and foods to partition cases of different foodborne illnesses to animal, food and environmental sources.

How do we know which foods are more important?

Several approaches to attribute foodborne diseases to sources have been developed in the last years. The most commonly used are hazard- occurrence analysis, like models that use microbial subtyping surveillance data on humans and/or animals in mathematical and risk assessment models; and epidemiological methods, mostly analysis of outbreak data or case-control studies of sporadic infections. Other approaches include intervention studies, expert elicitations, and methods that integrate some of these approaches.

The usefulness of each method to attribute disease caused by a foodborne hazard depends on the public health question being addressed, on the data requirements, on advantages and limitations of the method, and on the data availability to apply these models.
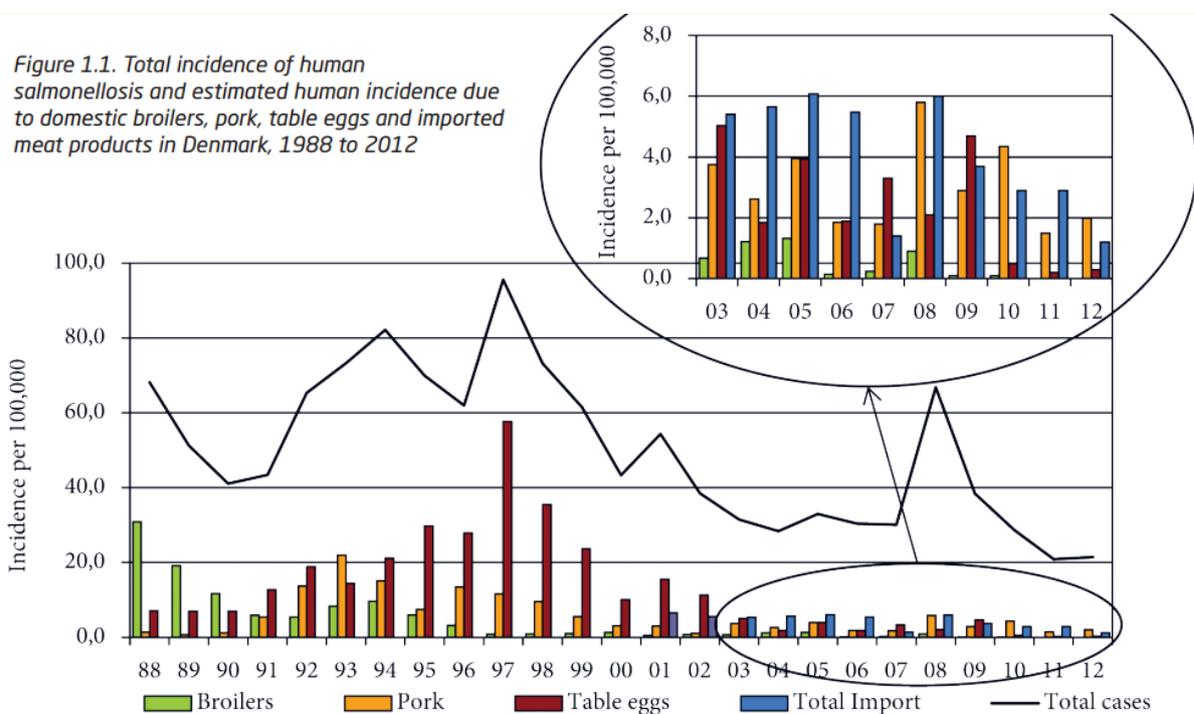
What are we doing about it?

Identifying the sources of salmonellosis in Denmark – a success story

Salmonella has been among the most important foodborne pathogens in Denmark in the last decades. The incidence of salmonellosis in the country reached a peak in the late 90's and has since then decreased sharply, reaching to figures lower than the European average. Identifying the causative food sources and prioritizing interventions has been crucial to reduce the burden of foodborne salmonellosis in the population.

To assist these risk management strategies, the National Food Institute routinely applies a source attribution model to estimate the contribution of the major animal-food sources to human infections o**f Salmonella (**see abstract of the article "A Bayesian approach to quantify the contribution of animal-food sources to human salmonellosis" at NCBI webpage**)**. The principle of the method is to compare the number of human cases caused by different Salmonella sero- and phage types with the distribution of the same subtypes isolated from the various animal-food sources. Antimicrobial resistance profiles of *Salmonella typhimurium* isolates are also included to further distinguish between similar phage types found in animals, food and humans.

Since the model was first implemented in 1995, it has evolved from being purely deterministic to becoming a stochastic model, built under a Bayesian framework. In 2008, a new methodological development was introduced in the model **(**see abstract of the article Assessing the differences in public health impact of salmonella subtypes using a bayesian microbial subtyping approach for source attribution at NCBI webpage**)**, which applies data from multiple years thereby improving the robustness and accurateness of the results without compromising their comparability with estimates from previous years.

Because we have applied this model for several years now, we are able to monitor trends and assess the effect of implemented interventions. These results are also used to revise our food safety measures if needed.

Figure 1.1. Total incidence of human salmonellosis and estimated human incidence due to domestic broilers, pork, table eggs and imported meat products in Denmark, 1988 to 2012

Source: Danish Zoonosis Centre, National Food Institute

Source attribution perspectives

In recent years, our Salmonella source attribution model (also known as the Hald model) has been adapted by several research groups, both for Salmonella and for other pathogens. The success of the Danish Salmonella interventions based on attribution estimates and epidemiological evidence has inspired other countries to collect the best surveillance data and analyse them with the same purpose. This dissemination has also allowed for the development of methodologies and for the investigation of the use of increasingly available molecular data, opening new doors for the development of source attribution models.

In parallel, analyses of data from outbreak investigations have also been extensively applied to attribute foodborne diseases at the national and international level. These studies require the availability of considerable amount of data on outbreaks caused by each pathogen, and thus is more suitable for source attribution in large countries or at international level, i.e. grouping a number of countries in a region.

[Read more on Burden of food-associated diseases in Denmark](#)

Recent publications

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Pires SM, Hald T. Assessing the differences in public health impact of salmonella subtypes using a bayesian microbial subtyping approach for source attribution. Foodborne Pathog Dis. 2010 Feb;7(2):143-51. doi: 10.1089/fpd.2009.0369. PubMed PMID: 19877767.

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