

Using outbreak data analysis for source attribution of human salmonellosis and campylobacteriosis in Europe

Sara M. Pires¹, Håkan Vigre¹, Pia Makela², Tine M. Hald¹

¹National Food Institute, Technical University of Denmark, Lyngby, Denmark

²Zoonosis Unit, European Food Safety Authority, Parma, Italy

1. Introduction

Salmonella spp. and *Campylobacter spp.* are the most important 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. We applied an analysis of data from outbreak investigations to attribute human salmonellosis and campylobacteriosis in European countries.

2. Material and methods

European salmonellosis and campylobacteriosis data from 2005 and 2006 were supplied by the European Food Safety Authority (EFSA), which is responsible for the collection and analysis of national data from all the member states (EFSA, 2006;EFSA, 2007b). In 2005, 173,379 human cases of salmonellosis and 198,178 of campylobacteriosis were reported; in 2006, 165,023 laboratory-confirmed *Salmonella* infections and 178,276 *Campylobacter* cases were registered. Reporting of foodborne outbreaks has been mandatory for the European Member States (MS) since 2005. An outbreak is defined as (1) an incidence, observed under given circumstances, of two or more human cases of the same disease, or (2) a situation in which the observed number of cases exceeds the expected number and where the cases are linked (or are probably linked) to the same food source (Anonymous, 2009). Countries are requested to provide all outbreak-related information available. Data received were generally complete and of high quality, but data completeness differed between MS. In the two year period, 6,537 outbreaks of salmonellosis involving 48,565 patients, and 894 outbreaks of campylobacteriosis corresponding to 3,782 illnesses were reported.

Outbreaks were classified as general or household outbreaks, accordingly to the setting of the outbreak. Reported outbreaks associated with traveling abroad were analyzed separately and were not attributed to any of the specific sources. Food items implicated in the outbreaks were categorized using a hierarchical scheme. Foods that contained only one commodity (e.g. steak contains beef) were considered “simple foods”, while foods containing ingredients belonging to different categories (e.g. meatloaf contains beef, egg, bread, and spices) were considered “complex foods”. Each implicated food was assigned to one or more mutually exclusive food categories, according to its ingredients. For outbreaks caused by complex foods for which ingredients were unavailable, an ingredient list was obtained by a review of recipes on the World Wide Web, as described by Painter *et al.* (in preparation): the top three recipes from a Google search were selected. Non-reported sources of infection were classified as *unknown*.

For simple-food outbreaks, all illnesses were attributed to a single food category. For complex-food outbreaks, illnesses were partitioned to each implicated category relative to the proportion

of illnesses attributed to each of the categories in outbreaks caused by simple foods. As a result, illnesses in an outbreak due to a complex food were only attributed to categories that had been implicated in at least one outbreak due to a simple food. The total number of illnesses caused by each category in simple and complex food outbreaks was then summed, and the proportion of illnesses attributed to each source was estimated on the basis of the total number of illnesses analyzed. The proportion of reported human illnesses attributable to specific sources was estimated both on the basis of the number of reported outbreaks of salmonellosis and campylobacteriosis and on the number of ill people reported in the outbreaks. The first analysis was performed to explore potential overestimations of the proportion of disease attributed to sources that caused large outbreaks, e.g. waterborne outbreaks. To obtain confidence limits of the proportion of cases and outbreaks attributed to specific sources, bootstrap re-sampling of the original data was used to generate the bootstrap distribution of the parameter of interest.

The attribution estimates (in %) based on the number of outbreaks was multiplied with the total number of sporadic cases reported in EU to estimate the number of sporadic cases by source. The number of reported outbreak-related cases was then added to the output of this analysis, either to the specific sources implicated in the outbreaks or to “outbreaks with unknown source”. The underlying assumption of this final step is that each outbreak contributes with one case to the total number of sporadic cases. To account for potential regional differences within Europe, separate analyses for the 4 United Nations regions were performed.

3. Results

We estimated that the most important sources of human 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%). Source attribution estimates differed when the analysis was performed stratifying by European regions. Results suggest that eggs were the most important source of outbreak-associated salmonellosis in Eastern and Western Europe, that chicken was the most important source in Northern Europe, and that the majority of the salmonellosis cases were attributable to meat and poultry-meat in the south of Europe. No outbreak-related salmonellosis were associated with international travel in Southern and Eastern Europe. For *Campylobacter*, around 5% of the cases in Northern Europe were attributed to drinking water, but no cases were attributed to this source in other regions. In Southern Europe, the majority of the cases were attributed to meat and chicken, and travel was the single most important cause of campylobacteriosis in Eastern Europe.

A total of 82,539 cases of salmonellosis were attributed to the consumption of eggs, 38,772 cases to meat and poultry-meat, and 8,124 cases were associated with international travel. 177,135 cases could not be attributed to any source. From the 376,454 *Campylobacter* infections reported, 39,225 were attributed to chicken and 46,530 could be attributed to poultry-meats (including chicken, turkey and other poultry). In total, 97,277 infections were attributed to meat and poultry products.

4. Discussion

Overall, results suggested that the consumption of eggs is the most important source of human salmonellosis, and that chicken most important source of human campylobacteriosis. These

observations go in line with previous source attribution estimates (see e.g. Hald et al, 2004; Stafford et al., 2008; Sheppard et al., 2009).

Attribution of human illness to specific sources differed substantially according to European region. These differences may reflect differences in consumption habits in the different countries, differences in the prevalence of the pathogens in the investigated sources, differences in the data quality and availability, or differences in risk perception among outbreak investigators. In addition, foodborne outbreak investigations and reporting systems are not harmonised within the EU, and thus differences in numbers and types of reported outbreaks and causative agents do not necessarily reflect different levels of food safety between MS.

The comparison between the attribution analyses performed by the number of ill people implicated in reported outbreaks and by the number of outbreaks suggests that the first may lead to an overestimation of the importance of the sources to the overall burden of disease. This can happen when the data is sparse and if some of the reported outbreaks are very large. In our analysis, this revealed to be important for the attribution of campylobacteriosis, for which the number of reported outbreaks was low and where the dimension of the outbreaks varied considerably. Our estimates suggest that an analysis conducted by the number of outbreaks is more suitable to assist attribution of human illness to specific sources, corresponding to a better representation of overall exposures in the population.

The categorization of foods often varies depending on the source of the data. The lack of harmonization of food categories makes it difficult to compare and/or combine outbreak data, as well as to generalize the use of this approach. In addition, the data was combined from many different countries using various reporting schemes. Furthermore, the level of evidence utilized to report the source of the outbreaks varied; some countries reported outbreaks on the basis of laboratory evidence, whereas others reported on the basis of epidemiological evidence alone.

To identify sources and evaluate trends of foodborne disease, it is important to distinguish between sporadic cases and cases associated with an outbreak. In some circumstances, cases classified as sporadic may belong to undetected outbreaks. The relative contribution of each food type to sporadic and outbreak associated disease may differ, and extrapolation of the outbreak experience to sporadic disease should be done with care. Certain vehicles may be more likely to be implicated in outbreaks than others (Batz et al., 2005), especially if investigators preferentially collect data on the types of food perceived as high risk, or when laboratory methods vary in sensitivity according to food type. A systematic vehicle detection bias might underestimate the contribution and risks attributable to foods less commonly implicated in outbreak investigations, e.g., salad items, fruit, or background ingredients such as herbs and spices.

We conclude that the presented source attribution method is a useful tool for the estimation of the importance of different sources for foodborne disease. Also, outbreak data is frequently the only available national data for the attribution of human illness, and in most cases the only evidence of which specific sources are causing disease. The successful use of this approach requires a substantial amount of data, and thus could not be applied individually to data from countries with few reported outbreaks. Still, we encourage countries with available data to apply

this approach and, when appropriate, to other pathogens. Results are found to be useful when prioritizing food safety measures and public health intervention strategies.

References

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