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Attributing human foodborne illness to food sources and water in Latin America and the Caribbean using data from outbreak investigations

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ABSTRACT

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.

1. Introduction

Foodborne pathogens have been recognized as an important public health issue in many countries for decades. They are responsible for a substantial burden of disease in the developed world, but it is expected that the public health, social and economic impact are even larger in developing countries (Schlundt et al., 2004). Though foodborne outbreaks receive the most media and political attention, the main part of the burden of foodborne diseases consists of sporadic cases. Thus far, few countries have implemented surveillance of sporadic cases of foodborne disease, particularly in the developing world, where the majority of reported human cases are associated with foodborne outbreaks.

Since the beginning of 1990s, the Pan-American Health Organization/World Health Organization (PAHO/WHO) developed a strategy to work with Member States to build national capacity for foodborne disease surveillance, in response to the growing incidence of foodborne diseases. Nevertheless, deficiencies in foodborne disease surveillance coverage persist throughout the region, and few cases and outbreaks are detected and reported. From 1993 to 2010, PAHO's regional information system received reports of outbreaks from 22 countries of the region. From the 9180 reported outbreaks in which an etiological agent was identified, 69% were caused by bacteria, 9.7% by viruses, 9.5% by marine toxins, 2.5% by chemical contaminants, 1.8% by parasites and, 0.5% by vegetal toxins (http://ww3.panaftosa.org.br/

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sirveta/). The incidence of illnesses caused by microorganisms that are principally foodborne, such as *Salmonella* spp. and *Campylobacter* spp., continued to increase considerably in many countries. Moreover, new and serious hazards have emerged in the food chain, such as infections from enterohemorrhagic *Escherichia coli* (Rivas et al., 2008).

Outbreak investigations are critical means of identifying new agents and new vehicles, as well as maintaining awareness of contemporary problems. Prompt and thorough investigation of foodborne outbreaks is particularly useful for a timely identification of etiologic agents, sources and vehicles, and allows for the prevention of further cases by identifying and eliminating the source of infection (Havelaar et al., 2007). As opposed to data from sporadic disease surveillance, data from foodborne-outbreak investigations are frequently available, both in developed and developing countries. In the absence of other evidence, outbreak data are fundamental source of information to inform food safety policies as well as to indicate the importance of foodborne pathogens and food sources for human disease in a population, i.e. source attribution. The use of outbreak data for source attribution implies the assumption that food and water sources causing outbreaks are the same sources causing sporadic illnesses in the population. Limitations of the method have been discussed in Pires et al. (2010).

To prioritize food safety interventions, it is essential to identify the most important sources of human illness, the available options for mitigation and their associated costs. A variety of methods to attribute human foodborne illnesses to the responsible sources has been developed during recent years (Pires et al., 2009), e.g. microbiological approaches (e.g. Hald et al., 2004; Mullner et al., 2009), epidemiological approaches (e.g. Pires et al., 2010), expert solicitation approaches (e.g. Havelaar et al., 2008) and intervention studies (Stern et al., 2003). The epidemiological approaches include analysis of data from outbreak investigations, which utilizes readily available data from outbreak surveillance to estimate the relative contribution of different foods for human disease.

A simple summarization of results of outbreak investigations can be useful for identifying the most common food vehicles involved in outbreaks and thus identifying the most important reported sources for human illness (e.g. EFSA, 2010). However, often the implicated food is a “complex” food, i.e. containing several food items and ingredients, where in principle any of them could be the specific source of the outbreak. We describe a method based on outbreak data that is able to consider complex foods to attribute human foodborne illnesses to specific sources in Latin America and the Caribbean.

2. Material and methods

2.1. Data included in the model

The Ministries of Health of each country within Latin America and the Caribbean are responsible for the collection of data from outbreak investigations, which are compiled under the Regional Information System on foodborne diseases surveillance, SIRVETA. Data from foodborne outbreak investigations were obtained from this regional system for this study (http://ww3.panaftosa.org.br/sirveta/).

Data were organized so that each reported outbreak corresponded to one observation in the final data set. Each observation contained information on the year of occurrence, country, etiology, number of ill people and fatalities associated with the outbreak, location of the outbreak, and implicated source. For uncompleted fields, the parameter was included as *unknown*.

The data covered the period from 1993 to 2010. Data reporting was irregular over the years, with no countries providing data every year. Reported hazards included bacteria, chemicals, parasites and fungi. In this study, we (1) analysed all bacterial pathogens together, and (2) focused on important bacterial pathogens separately. The selection of pathogens was based on the frequency of reporting and/or severity of disease; remaining hazards were not considered in the analyses. For the specific models, bacterial pathogens were selected on the basis of their public health importance and on the number of outbreaks reported in the study period. Specific source attribution analyses were done for *Salmonella* spp., *Escherichia coli, Shigella* spp. *Clostridium botulinum, Clostridium perfringens, Bacillus cereus, Staphylococcus* and *Vibrio cholerae*.

2.2. Method

The applied method was based on Pires et al. (2010), modified and applied to the bacterial pathogens listed above. The principle is to attribute human illnesses to food sources on the basis of the number of outbreaks that were caused by each of these foods. For this purpose, implicated foods are 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). The ingredients that constitute the complex foods are designated through defined criteria.

2.2.1. Food categorization

Food items were categorized using a hierarchical classification scheme (Fig. 1), adapted from Painter et al. (2009). All foods were divided in three main groups (i.e. land animals, plant and seafood), which were sub-divided in more specific food categories. Foods that contained only one category (e.g. steak contains beef; salad contains only vegetables, even though it may contain multiple types of vegetables) were considered “simple foods”, while foods containing ingredients belonging to different categories (e.g. tiramisù contains eggs, dairy products, grains and sugar) were considered “complex foods”. Each implicated food was therefore assigned to one or more mutually exclusive food categories, according to its ingredients. The ingredient list for reported complex foods was obtained by a review of recipes on the World Wide Web, as described by Painter et al. (2009).

With the exception of bottled water, water is not considered food according to the definition of *Codex Alimentarius* (www.codexalimentarius.net). Since none of the reported outbreaks implicated bottled water as the source during the study period, water was included as a separate source in this study (i.e. not included in the food categorisation scheme).

2.2.2. Location

Outbreaks were classified as general outbreaks or household outbreaks, depending on the location of the outbreak. The location can refer to where exposure took place (e.g. restaurant, institution) or where the food was produced or commercialized (e.g. retail). Household outbreaks correspond to all outbreaks that occurred in private homes, whereas the category general outbreaks includes all outbreaks that occurred outside private homes, e.g. restaurants and cafés, institutions (e.g. schools, nursery homes), hotels, retail, catering establishments, food producers, slaughterhouses or farms. Due to absence of information, no distinction between point-source (i.e. a common meal) and generalized/diffused (i.e. independent cases) outbreaks was made.

2.2.3. Model overview

The model parameters are described in Table 1. The proportion of disease that can be attributed to each food source was estimated based on the number of simple-food outbreaks caused by that source, on the ingredients (food categories) composing complex-foods, and on the probability that each of these categories were the cause of the complex-foods outbreaks. For each causative agent, the data from simple-food outbreaks were summarized, and the proportion of outbreaks caused by each category was used to define the distribution representing the probability that an outbreak i was caused by source j (P_j). This probability was estimated per source using information from all countries and the whole study period. For the calculation of the