Ministry for Primary Industries
Manatū Ahu Matua

Use of epidemiological evidence in investigations of foodborne disease outbreaks

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Scientific Interpretive Summary

This SIS is prepared by MPI risk assessors to provide context to the following report for MPI risk managers and external readers

Use of epidemiological evidence in investigations of foodborne disease outbreaks

Thorough investigations of foodborne disease outbreaks aim to identify the food item(s) involved, the microorganism/pathogen that caused the disease, and other contributing factors (e.g. food preparation and handling). This information is used to control and reduce the risks of further disease cases.

Detecting the same strain of a particular pathogenic microorganism in a suspected food or its component and in stool samples from ill people involved in an outbreak provides strong evidence that the consumed food has caused people to get sick. Such definitive microbiological evidence not always available during investigations of foodborne illness outbreaks or sporadic cases. Nevertheless, robust association of the consumption of a particular food to an outbreak can be established using evidence such as descriptive or analytical epidemiological information.

However, use of epidemiological evidence is complex and often not fully understood by the media and general public. As a consequence, the high value given to epidemiological evidence in risk assessments in the absence of positive microbiological test results is often questioned. In contrast, negative tests results are often considered by the general public as an insurance of food safety.

The project “Use of epidemiological evidence in investigations of foodborne disease outbreaks” was undertaken by Massey University to help understanding on how epidemiological methods are used for detecting and investigating foodborne disease outbreaks. It describes criteria for identifying suspected food items, and demonstrates how these criteria work using examples of foodborne disease outbreak investigations in New Zealand.

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Use of epidemiological evidence in investigations of foodborne disease outbreaks

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Executive summary

The use of epidemiological evidence in disease outbreak investigations is complex and often poorly understood by the media and the general public. This report provides a summary on how epidemiological methods are used for detecting and investigating foodborne disease outbreaks. It explains descriptive, analytical and laboratory methods, describes criteria for identifying suspected food items, and demonstrates these in examples of foodborne disease outbreak investigations in New Zealand. Two key messages can be drawn from this report: (1) it is possible to classify an outbreak as very likely to be foodborne based on well-presented descriptive epidemiological data alone; and (2) the limitations around food testing mean that a negative pathogen test does not mean that food is safe.

1 Background and rationale

A wide range of microorganisms such as bacteria, viruses, and parasites can cause food-associated diseases in humans, which can occur as outbreaks or sporadic cases. An outbreak can be described as a localised increase in numbers of sick people (e.g. in a town, a school, or a community) over a specific time period, whereas a sporadic case is not linked to others and thus not part of an outbreak.

Thorough investigations of foodborne disease outbreaks aim to identify the food item(s) involved, the microorganism/pathogen that caused the disease, and other contributing factors (e.g. food preparation and handling). This information is used to control and reduce the risks of further disease cases. In addition, investigations of foodborne disease outbreaks provide valuable information, which is used to improve food safety.

Detecting the same strain of a particular microorganism/pathogen in a suspected food item (ideally unopened) and in stool samples from ill people involved in an outbreak provides strong evidence that the consumed food has caused people to get sick. Because it is not always possible to provide this causal link, epidemiological studies are commonly used to identify an association between the consumption of a particular food item and an outbreak case.

The use of epidemiological evidence in foodborne outbreak investigations is complex and often poorly understood by the media and the general public. Quite often, when there are no laboratory tests of food items, the use of epidemiological evidence is questioned, while in contrast to this, negative test results are often considered as an assurance of food safety.

This report provides clarification on how methods, principally epidemiological, are used for detecting and investigating foodborne outbreaks, and describes criteria for identifying suspected food items in foodborne outbreak investigations.

2 Introduction

2.1 Outline of report

The content of this report is presented in three main sections:

Section 3: Methods used in detecting and investigating foodborne disease outbreaks.

Section 4: Recommended criteria for identifying food implicated in investigations of foodborne disease outbreaks.

Section 5: Examples of foodborne outbreak investigations specific to New Zealand.

A large variety of food-associated pathogens such as bacteria, viruses, and parasites can cause foodborne diseases in humans. These pathogens can come from animals or humans. The examples of foodborne outbreak investigations in this report are limited to pathogens that are of greatest public health importance in New Zealand (e.g. *Campylobacter* spp., *Salmonella* spp., Shiga toxin-producing *Escherichia coli* (STEC), and *Yersinia* spp.).

2.2 Approach

The report draws information from websites and work of national and international organisations such as the Institute of Environmental Science and Research (ESR, New Zealand) [1], Ministry of Health (MoH, New Zealand) [2], *m*EpiLab (Massey University, Palmerston North, New Zealand), the World Health Organisation (WHO) [3], the European Food Safety Authority (EFSA) [4], the European Centre for Disease Prevention and Control (ECDC) [5], and the Centres for Disease Control and Prevention (CDC) [6]. Where appropriate in the report, the authors also used published literature as references. Key terms and definitions are provided in the Glossary at the end of the report.

3 Epidemiological methods

A range of methods are used in detecting and investigating foodborne disease outbreaks. These are explained and discussed in the following sections:

Section 3.1: Methods for detecting when foodborne disease outbreaks/sporadic cases occur.

Section 3.2: Descriptive outbreak investigations.

Section 3.3: Analytical outbreak investigations.

Section 3.4: Common laboratory techniques used in foodborne outbreak investigations.

Section 3.5: Limitations of food testing used in foodborne outbreak investigations.

3.1 Detecting foodborne disease outbreaks/sporadic cases

3.1.1 Epidemiologic surveillance systems

Epidemiologic surveillance systems are structures to facilitate the collection, analysis, and interpretation of health and other data on a local, regional, and national level. Surveillance systems monitor patterns and trends of disease as they occur over space and time, detect outbreaks, and guide prevention efforts. As part of a surveillance

system, disease notification, laboratory reporting/surveillance, and an effective reporting system are essential for the rapid detection of foodborne outbreaks and sporadic cases. Surveillance serves as an early warning system for public health emergencies.

Disease notification

New Zealand has a long standing disease notification system, where doctors and other health care providers are required to report cases suspected of having a notifiable disease to public health authorities (e.g. medical officers of health and local authorities). Major foodborne diseases, such as salmonellosis, campylobacteriosis, or listeriosis, are designated as notifiable diseases. A list of notifiable diseases in New Zealand is available on the Ministry of Health's website [7].

Doctors usually diagnose a notifiable disease based on the clinical symptoms they see in the ill person and submit samples (e.g. stool or blood) for laboratory testing to confirm their diagnosis. It is well known in New Zealand [8, 9] (and overseas) that a large number of cases with foodborne disease are unreported as they do not seek medical advice, or are undiagnosed due to not showing clinical symptoms specific for a foodborne disease. Further reasons for underreporting are: doctors not requesting a stool sample from patients, patients not submitting a requested stool sample, and submitted stool samples not testing positive in the laboratory. From all the cases of notifiable diseases that occur in the community, only a very small fraction of cases is reported, as illustrated in a 'disease pyramid' (Figure 1).

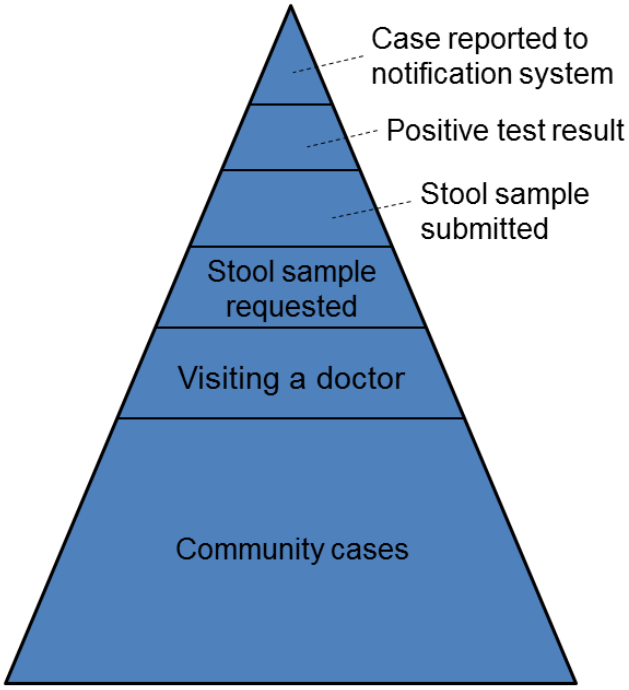

Figure 1: Disease pyramid illustrating how only a small fraction of cases with notifiable diseases that occur in the community are reported in the end (adapted from [10]).

The time elapsed from eating a potentially contaminated food item until both clinical diagnosis and positive laboratory result can vary considerably. This is mostly due to the variable incubation period of disease-causing pathogens, which refers to the time from ingesting a contaminated food item until the onset of clinical symptoms of disease. Some foodborne diseases have very long incubation periods (e.g. 3–70 days for listeriosis) compared to others (e.g. 1–10 days for campylobacteriosis). Furthermore, cases with foodborne disease may not seek medical advice immediately after first signs of disease and diagnostic tests in laboratories also require some time, adding to the elapsed time until a case of notifiable disease is confirmed.

Laboratory-based surveillance

Laboratory-based surveillance is applied to a wide range of infectious diseases important to the public. Laboratory-based surveillance systems analyse laboratory results and data from patients with confirmed infectious diseases. These systems identify trends of diseases as they occur over time and detect and confirm outbreaks (e.g. foodborne outbreaks). Most commonly, clinical laboratories such as laboratories of public hospitals, national reference centres/laboratories, and community diagnostic laboratories participate in laboratory-based surveillance systems.

Laboratory-based surveillance is led by the Institute of Environmental Science and Research (ESR). Diagnostic laboratories throughout New Zealand refer appropriate samples to national reference laboratories at ESR to identify and specify pathogens.

Currently important microorganisms under laboratory-based surveillance in New Zealand are listed on ESR's website [11].

Reporting system

A national reporting system and surveillance database are essential to prevent and control notifiable diseases effectively. ESR operates – on behalf of the Ministry of Health (MoH) – a national surveillance database called 'EpiSurv' [12], where data are stored electronically. Public Health Units (PHUs) across New Zealand use EpiSurv to record data from cases of notifiable and other diseases (e.g. demographic, clinical, and exposure data of cases) as soon as cases are notified. Clinical laboratories use EpiSurv to message PHUs the laboratory confirmation of a notifiable disease. New Zealand's surveillance system for notifiable diseases is shown in Figure 2.

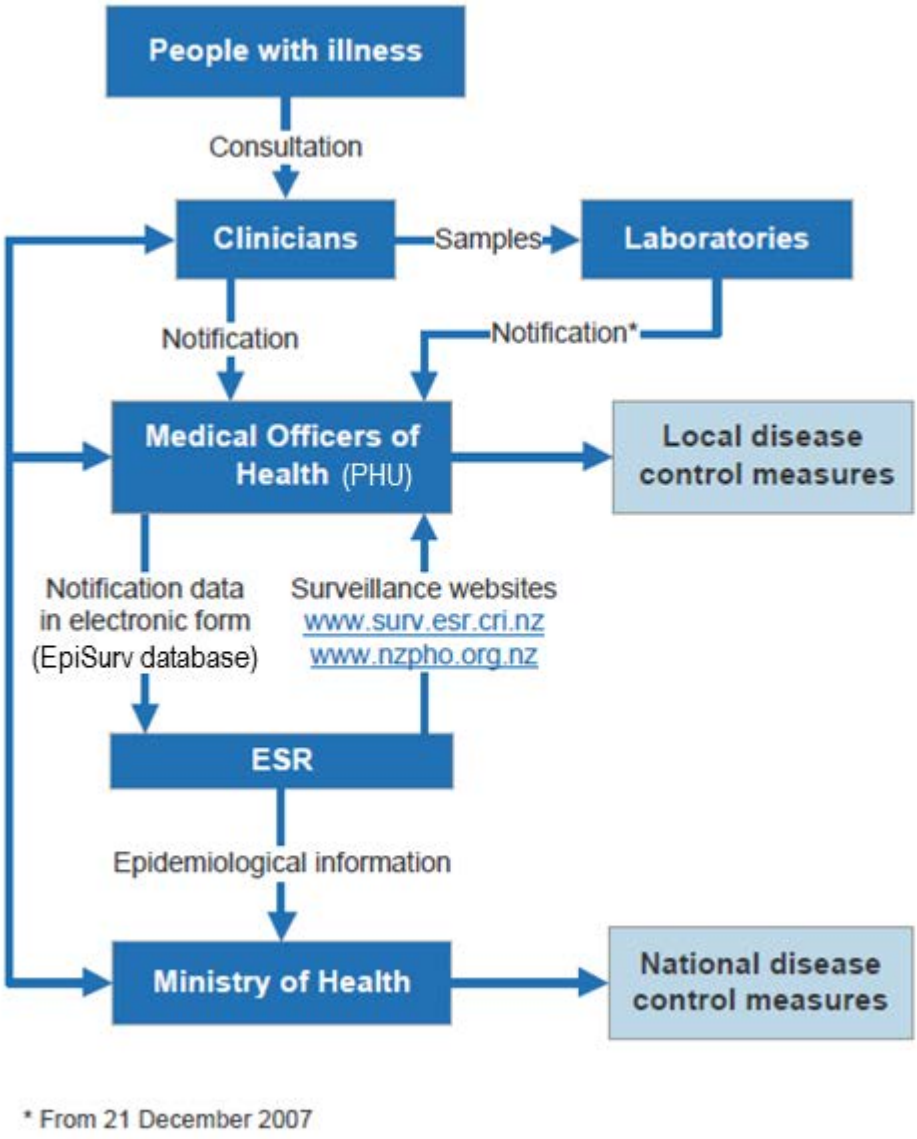

Figure 2: Notifiable disease surveillance system in New Zealand (sourced from [13]).

3.1.2 Detection of cluster of cases/a suspected outbreak

As surveillance systems continuously gather data on diseases (including foodborne), health officials are informed of the expected number of illnesses in a given area over a given time. If the number of cases with the same disease is larger than normally expected, health officials undertake initial investigations and assess whether this is indicative of an outbreak. When the cases are linked by time and a given area, but have no common source of infection, it is called a cluster of cases. However, if two or more cases with the same disease are linked to a common source, for example, have consumed the same contaminated food or drink, or have experienced the same exposure at a common event, it is defined as an outbreak [14]. Before confirming an outbreak, health officials have to verify that the diagnosis and reporting of cases is accurate and that the reported cases reflect a true increase of disease.

3.2 Descriptive outbreak investigations

Once an outbreak is confirmed, health officials collect important data from cases on 'person', 'place'[1], and 'time' – the three standard descriptive epidemiological parameters – to characterise the outbreak. They analyse the data, develop hypotheses about the possible source(s) of infection and may design preliminary control measures (providing that there is sufficient information) to prevent further cases. If required, data collected are used for further analytical outbreak investigations (see Section 3.3).

3.2.1 Case definition

After the first cases are recognised, health officials need to identify more cases to help understand the size, timing, severity, and potential source(s) of a foodborne disease outbreak. For this purpose, they develop a case definition to describe precisely which ill person will be considered as part of an outbreak. A case definition may include information on the clinical symptoms of disease a person shows, the laboratory findings of submitted samples (if known), the geographical/residential area of an ill person, and a defined period of time (e.g. last two weeks in September 2015).

Health officials also use the case definition to search for more outbreak-related cases in surveillance and laboratory reports and contact doctors, clinics, hospitals, and health officials in surrounding areas to watch for similar cases, which could be outbreak-related. This approach is called 'enhanced surveillance'.

3.2.2 Interviews and questionnaires

To investigate foodborne disease outbreaks, health officials interview cases in a systematic way using standardised questionnaires. Irrespective of the disease under investigation, they collect data on the cases' identity (e.g. name, contact details) and

[1] 'Place' refers to geographical data (e.g. residence), which enables to describe the extent and pattern of an outbreak.

demography (e.g. sex, age, date of birth, ethnicity, occupation, residence), and clinical information (e.g. manifestation of disease, meeting the case definition).

Furthermore, to identify the source(s) of a foodborne outbreak, health officials collect information from cases on food-related and personal risk factors, which are tailored to the specific disease under investigation (e.g. detailed history of food consumed, exposure to implicated food within incubation period (see Figure 3)). A risk factor can be described as an attribute or exposure of an individual that changes the risk of developing disease or injury.

At the initial stage of a foodborne outbreak investigation, health officials need to consider a large number of different food items as potential sources of infection. However, as more and more cases are interviewed, health officials may be able to create a short list of common food items that were eaten by an appreciable number of cases in the days/weeks before getting sick. This helps to generate hypotheses about the likely source(s) of infection, as food items consumed by none or only a very few cases are less likely to be a source.

One of the major challenges in foodborne outbreak investigations is that cases often cannot remember in detail the food or the ingredients of food items they consumed before becoming ill. Often a long period of time has elapsed until a case of notified disease is confirmed and thus investigated.

3.2.3 Epidemic curves

To illustrate the progression/dynamics of a foodborne outbreak, health officials draw an epidemic curve, which is a two-dimensional bar graph or histogram that shows the number of cases by date/time of disease onset (Figure 3).

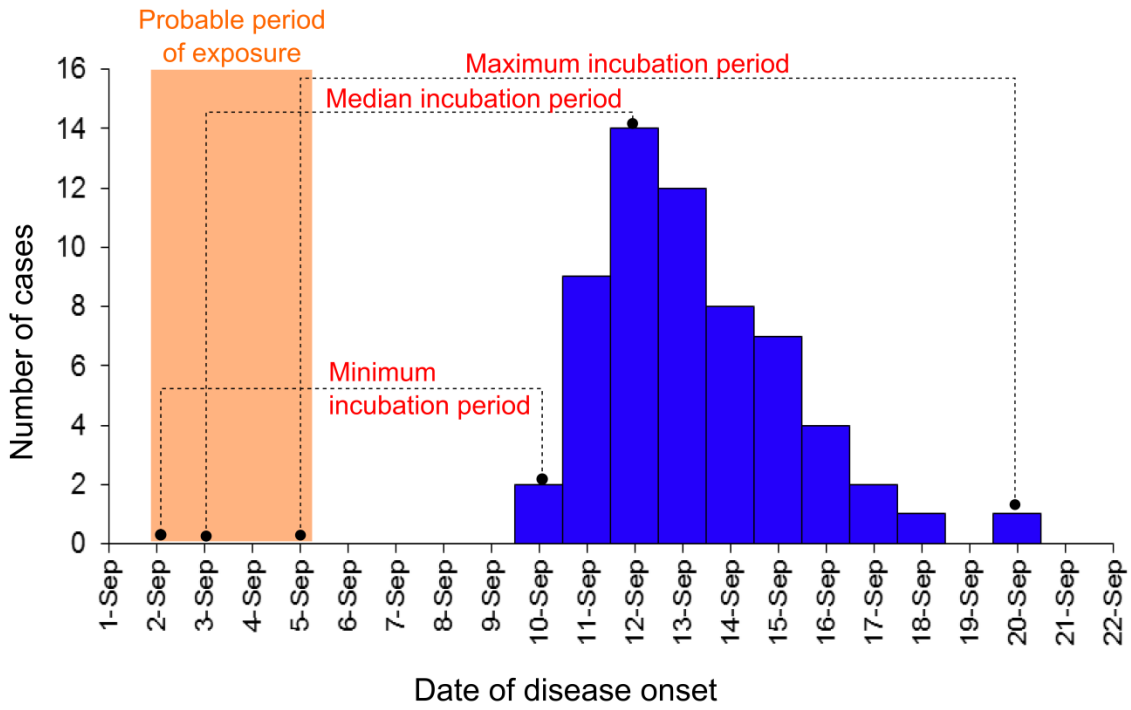

Figure 3: Example of an epidemic curve of a foodborne outbreak illustrating the use of a known pathogen and incubation period to identify a probable period of exposure. This pathogen has a minimum, median, and maximum incubation periods of 8, 9 and 15 days respectively.

An epidemic curve provides health officials with important information on the characteristics of an outbreak as the shape of the curve is determined by the pattern of disease spread, the period of time over which people are exposed, and the incubation periods for the disease. Disease-causing pathogens have characteristic incubation periods, which are commonly presented as a range (minimum to maximum) and median (e.g. for STEC 2–10 days; median 2–3 days) [15, 16]. The median incubation period is the middle value of all individual incubation periods, from the shortest (minimum) to the longest (maximum).

When seeking to identify a probably food vehicle the most likely scenario is that the pathogen was identified and this information can be used to identify when people were most likely exposed. If there is a well-defined peak to the epidemic curve the median incubation period can be counted backwards from that peak to identify the most likely time of exposure. The minimum and maximum incubation periods of the pathogen counted backwards from the first and last cases of the outbreak, respectively, identify a window around the most likely exposure time. For example in Figure 3 this was 2 - 5 September. This facilitates the identification of the vehicle of the outbreak.

Conversely, if the timing of the presumed exposure is known but pathogen unknown, then health officials can use this information and the epidemic curve to estimate the

incubation period of the disease (e.g. a group of people get sick nine days after attending the same wedding). This can help with the identification of the pathogen that caused disease in people.

Well described epidemiological data on person, place, and time of outbreak-associated cases can sometimes provide sufficient epidemiological evidence to identify a suspected food item as the source of infection, without conducting further outbreak investigations as described in Section 3.3.

3.3 Analytical outbreak investigations

Health officials may use analytical epidemiological studies to test their hypotheses about the suspected source(s) of infection in a foodborne outbreak. The most common types of analytical studies they use are 'case-control'[2] and 'cohort studies'[3], which involve a comparison group of healthy people to demonstrate associations between the consumption of a suspected food item and disease in cases. These associations are computed using equations and data on what cases and healthy controls (people without the disease) have eaten. It is therefore important during interviews that people remember what food items they have consumed before becoming ill, as this lack of recall can affect the findings of the analytical studies (resulting in weak or no associations). Furthermore, the elapsed time from eating a contaminated food item until confirmation of a case with notifiable disease adds to the difficulty with recalling what has been eaten.

To support their hypotheses, health officials also use food testing to analyse implicated food for the presence of foodborne pathogens. If pathogens are detected, then they are compared to the pathogens previously identified in stool samples from cases. If the pathogens match, this can provide convincing evidence that the implicated food was the source of infection. Limitations of food testing are discussed in Section 3.5.

Despite all efforts of foodborne outbreak investigations, it is common that analytical studies cannot always find associations between the consumption of an implicated food and outbreak-cases. This can be due to many different reasons, for example:

- An outbreak remained undetected for a long period of time, after which a full investigation was no longer possible.
- After initial investigation, health officials could not generate any hypotheses about the suspected source(s) of infection and therefore no analytical study was conducted.

[2] A case-control study involves a comparison of frequency of exposures among cases (persons with the disease) to frequency of exposures among controls (persons without the disease).

[3] A cohort study involves the monitoring of exposed and non-exposed groups over time to enable the comparison of disease rates over a specified period of time.

- Particularly for foodborne diseases with long incubation periods, outbreak-cases could not remember what food items they consumed before becoming ill (e.g. listeriosis has an incubation period of 3–70 (median 21) days).

- An analytical study was unable to identify an implicated food as the number of cases was too small, or the cases and controls were equally exposed (lack of non-exposed cases or controls), or because multiple food items were contaminated.

- The food testing could not detect the causal pathogen associated with the outbreak, or food testing was not conducted as no food samples were available for testing.

Even without an association or an identified source of infection, a disease outbreak can still be classified as very likely to be foodborne based on well-presented descriptive epidemiological data (see Section 3.2).

3.4 Laboratory methods used in outbreak investigations

If the same pathogens are identified in stool samples of outbreak-cases and the implicated food then this can provide the link between human illness and the source of infection in outbreak investigations. It is important, however, to demonstrate that the detected pathogens match and differentiate outbreak-associated pathogens from those not related to the outbreak.

To compare the detected pathogens, various laboratory typing methods are applied to describe the pathogen in more detail (e.g. the pathogens are the same species but of different type or subtype). Pathogens that are indistinguishable or closely related by typing may be considered epidemiologically-related strains and therefore more likely to have originated from the same source than those that are distinguishable by typing.

Most commonly used typing/subtyping methods in foodborne outbreak investigations are:

- *Serotyping*. This very common method characterises pathogens based on their surface structures or metabolism. For example, pathogens such as *Salmonella* spp. and STEC can be subtyped into numerous serotypes (e.g. STEC O157:H7, STEC O26:H11, etc.), however serotyping is not always possible as some pathogens cannot be serotyped. The Enteric Reference Laboratory (ERL) at ESR provides serotyping of *Salmonella* spp., *Escherichia coli* spp., *Shigella* spp. and *Campylobacter jejuni*.

- *Phage typing*. A widely used typing method applied to identify subtypes of *Salmonella* spp. This method is based on the susceptibility of *Salmonella* spp. to specific bacteriophages, which are viruses that infect bacteria and cause them to die. ERL provides phage typing of *Salmonella* spp.

- *'Polymerase Chain Reaction' (PCR)*. PCR is used in many laboratories in New Zealand. The method differentiates types/subtypes of pathogens based on their genetic content. For example, it can identify the presence/absence of specific

genes, which cause severe disease in humans. PCR can be applied to almost all pathogens and is a cheap and rapid method. However, the method can sometimes provide false results (e.g. not detecting the correct genes, cross-reacting with other genes, or a sample is contaminated with genetic content from other pathogens or the laboratory environment).

- *'Pulsed-Field Gel Electrophoresis' (PFGE).* PFGE can be applied to a variety of clinically important pathogens (e.g. *Salmonella* spp., STEC, *Listeria* spp., *Campylobacter* spp.). PFGE generates distinct 'barcode-like' profiles of pathogens, but is a technically demanding, time-consuming, labour-intensive, and more expensive method compared to PCR. ERL provides PFGE of enteric bacteria.

- *'Multi-Locus Sequence Typing' (MLST)*. MLST is a typing method applied to a variety of pathogens, such as *Campylobacter* spp. and STEC. Similar to PCR, seven to eight specific genes (called 'housekeeping' genes) are multiplied first and then read (called 'sequenced') to determine any genetic variations. The sequence type (ST) of a pathogen is based on the genetic variations of the housekeeping genes. While MLST is a cheap and relatively rapid method, it has the same limitations as PCR.

- *'Whole Genome Sequencing' (WGS).* WGS is a high-resolution typing method, which reads a pathogen's entire genetic content. Over recent years, WGS has become a very powerful epidemiological tool, which will contribute to the accurate detection and investigation of many outbreaks in the future.

3.5 Limitations of food testing

Food items can become contaminated, cross- and re-contaminated with disease-causing pathogens at any point of the production/processing chain, for example at harvest, after processing, during packaging, at distribution and supermarkets, or during food handling and preparation at public places (e.g. restaurants, cafés, events, care homes) or consumers' homes.

Although food testing can be a powerful tool in outbreak investigations, it also poses numerous challenges. For example: suspected food items with a short shelf life such as raw milk are often no longer available for testing at the time of outbreak investigations; the detection of the pathogen in the food item is difficult as its numbers have naturally decreased over time; the pathogen is overgrown by other microorganisms as spoilage of the food item has progressed; or there is no laboratory method available to test for the pathogen in the implicated food. Furthermore, food testing provides insufficient information on the actual safety status of a food item because of the following limitations:

- A test result is affected by the performance of a laboratory method but also the concentration of the pathogen in a food item/sample. The concentration of the pathogen in the sample could be too low to be detected by the laboratory method, providing a false negative test result. Some pathogens could be present in the sample in very low numbers and still be able to cause disease in

humans. Therefore, a negative test result does not necessarily mean that the pathogen was absent and the food item was safe for consumption.

- Pathogens may not be equally spread in a product (likely to happen in a solid product). So, a sample taken from a food product may not contain the pathogen and consequently lead to a false-negative test result. The negative test result provides misleading assurance of food safety, even though the pathogen was present and the product was not safe for consumption.

- The nature of microorganisms/pathogens also has to be considered when applying food testing as some pathogens, particularly those that come from animals, are not constantly present in animals, the environment, or an animal-derived product. This means that pathogens are present in variable and unpredictable concentrations in products, which can affect the outcome of testing. For example, cattle shed STEC irregularly with their manure. Food products such as milk or meat can become contaminated with STEC-containing manure at harvesting (i.e. at milking or slaughter) and are tested positive for STEC. However, when samples of food products are taken a week later, they may be still contaminated with cattle manure but test negative for STEC, as the cattle were not shedding STEC at the time of sampling.

4 Recommended criteria for identifying implicated food

To weigh the strength of epidemiological evidence for identifying an implicated food in foodborne outbreak investigations, a set of criteria are used (Table 1), which has been presented in a previous publication by MPI [17].

Table 1: Set of descriptive criteria used to weigh the strength of epidemiological evidence for identifying an implicated food in a foodborne outbreak investigation – applied to the example of raw milk consumption.

Strength of evidence	Criteria
Suggestive	Consuming/drinking raw milk recorded as a contributing factor.
Medium	Meeting criterion for *Suggestive* above AND the nature of clustering of cases in space and/or time being consistent with transmission of infection from an implicated food (e.g. reports of purchasing raw milk from same supplier in same week).

Strong	EITHER: a) Meeting criteria for *Medium* above AND a pathogen was isolated from an implicated food during the incubation period of at least one outbreak case. OR: b) Meeting criteria for *Medium* above AND a matching pathogen strain was isolated from outbreak cases that has been identified in at least 75% of human cases and showing a food-producing animal reservoir with a probability of at least 60% based on source attribution models[4]. Pathogen strain may include Multi-Locus Sequence Typing (MLST), phage typing, or other within-species typing/subtyping methods.
Very strong	Meeting the criteria for *Strong b)* above AND a matching pathogen strain was isolated from an implicated food during the incubation period of at least one outbreak case. Pathogen strain may include MLST, phage typing, or other within-species typing/subtyping methods.

Applying the criteria is demonstrated in foodborne outbreak examples presented in Section 5.

5 Examples of foodborne outbreak investigations in New Zealand

In 2014, 109 foodborne outbreaks were reported in New Zealand, of which 35 (32.1%) were caused by enteric pathogens such as *Campylobacter* spp., *Salmonella* spp., *Shigella* spp., STEC, and *Yersinia* spp. [19]. Based on compelling epidemiological evidence, a food source or vehicle of infection could be identified in about a quarter of the reported foodborne outbreaks (27.5%, 30/109). However, sources of infection could be confirmed by microbiological methods in only a very few foodborne outbreaks.

The following New Zealand specific examples of foodborne outbreaks show how epidemiological investigations identified the likely source of infection. Criteria described in Section 4 are applied to demonstrate the strength of epidemiological evidence for identifying the implicated food.

[4] E.g. the asymmetric island model [18].

Example 1 – outbreak associated with eating cooked pork (2015) [20]

In April 2015, a restaurant in Whanganui prepared a celebratory lunch (buffet-style) for a group of 62 people (20–85 years of age, mostly locals). A few days after the function, the local Public Health Centre was informed that some attendees became ill and showed symptoms of gastroenteritis (diarrhoea, abdominal pain, and nausea within 48 hours after the function). As lunch was the only common factor among all ill people, 40 attendees (both ill and not-ill) were interviewed (by phone and in person) and questionnaires were completed (8–10 days after the lunch) to identify a particular food item as the likely source of infection in this foodborne outbreak.

The collected data were analysed in an analytical study. The results revealed that among all the consumed food items cooked pork, followed by roast potatoes, and green salad were closely linked with disease. Laboratory analysis of stool samples from four cases detected *Clostridium perfringens*.

The strength of epidemiological evidence that pork was the likely source of infection in this outbreak was *medium* as an increased number of people became ill after attending a function at a restaurant and eating shared lunch (epidemiological links between 'person', 'place', and 'time'). Although the analytical study was unable to identify cooked pork as the specific source of infection, there was a strong association. In addition, foods of animal protein such as pork are most often implicated in *C. perfringens* outbreaks and the clinical symptoms of disease among outbreak-cases fitted the description of *C. perfringens* infection.

Example 2 – vegetable (lettuce/carrot)-associated outbreak (2014) [19]

A total of 220 cases across 18 District Health Boards (DHBs) in New Zealand were reported in a multi-regional outbreak of gastroenteritis between September and November 2014.

The outbreak was detected in September 2014, when a sharp increase in *Yersinia pseudotuberculosis* notifications above normal levels was observed. Cases occurred nationwide, with a large number reported in Canterbury, Auckland, Wellington and the Bay of Plenty. At initial investigation, PHU staff interviewed the first few cases to generate a hypothesis about the suspected source(s) of infection. The initial analysis indicated that a high number of cases had eaten fresh fruits and vegetables, dairy products, and cold meats (deli meats).

To test the hypothesis, an analytical study was conducted. The results showed that consumption of fresh lettuce and carrots (and combinations of salad mixes) was strongly associated with disease in cases [21]. However, a wide range of other food items were also identified (including tomatoes, avocados, cucumbers, capsicums, apples, oranges, cheese, yoghurt and ice cream [22], but showed weaker associations and could therefore not be entirely discarded as possible sources of the outbreak.

From the data available, it was suspected that the outbreak was probably caused by a single source of contamination (at the grower and/or processor level), which was followed by a nationwide distribution of contaminated fresh produce [22].

Although no specific food item could be identified in this outbreak of yersiniosis, there was *medium* strength of evidence that fresh produce/vegetable was the source of infection. This is because results of the analytical study revealed a high association between consuming lettuce/carrots and the disease in outbreak-cases.

Example 3 – raw milk-associated outbreak (2009) [23]

In August 2009, the Northland PHU was notified of an outbreak of gastroenteritis (vomiting, diarrhoea and abdominal pain) among 14 school children and a parent after visiting a dairy farm near Whangarei as part of a school trip. An outbreak investigation was conducted and all 64 pupils (aged 5–7 years), 25 parents, and three teachers attending the dairy farm visit were interviewed (by phone or in person) about activities on the farm. Stool samples from four cases and three environmental samples collected at the farm (milk samples from vat and calf feeding tank, and potable water) were submitted for laboratory testing.

The analysis of interview data found that all students had touched calves but used hand sanitiser gel before eating their home-prepared lunches at the dairy farm. However, all of the cases had tasted small amounts of raw milk directly from the processing outlet before it entered the milk vat. The attack rate for drinking raw milk among cases was 56%, compared to 1.6% among those that did not drink raw milk; attack rate is a parameter of disease used in outbreak situations. In the laboratory, *Campylobacter* species were detected in both stool samples of cases and milk samples but were found to be different strains based on PFGE typing.

The epidemiological and laboratory findings in this investigation provided *strong* evidence that raw milk was the source of infection in this outbreak of campylobacteriosis. This is because (i) the attack rate for drinking raw milk was very high for cases compared to non-drinkers of raw milk, and (ii) *Campylobacter* strains (although different strains) were detected in both stool and milk samples. Although different *Campylobacter* strains were found in stool and milk samples, it is possible that multiple strains of *Campylobacter* were present at the time of the farm visit and when environmental samples were collected 13 days later. It is most likely that the milk was contaminated via cattle manure.

Example 4 – raw flour-associated outbreak (2008) [24]

In October 2008, a cluster of 10 salmonellosis cases caused by *Salmonella* Typhimurium phage type 42 (STM42) was detected in the South Island of New Zealand. As the same phage type was found in raw material of poultry feed 2 months before the first cases, the initial hypothesis was that the cases had consumed chicken or egg products. An outbreak investigation was initiated, a case definition developed,

and cases and healthy controls were interviewed (by phone) about food they had consumed including chicken and eggs.

From October 2008 to January 2009, 67 of 75 notified cases of salmonellosis met the case definition and were part of this outbreak. The cases aged 11 months to 86 years and showed symptoms of gastroenteritis such as diarrhoea, abdominal pain, fever, and vomiting. Most of the outbreak-cases were from the South Island.

Initial investigations revealed that eating uncooked cake or pancake batter was strongly associated with disease in cases, while no association was found with eating chicken or eggs. Based on this, 39 cases and 66 controls were included in an analytical study to test the refined hypothesis that eating raw flour or other baking ingredients was associated with disease in outbreak-cases. The study results indicated that Brand A flour, flour purchased from supermarket A, and plain flour were strongly associated with disease. Flour samples taken from cases' homes, retail premises, and of retrieved product were tested positive for the STM42 outbreak strain.

Epidemiological and laboratory findings in this investigation provided *very strong* evidence that consumption of raw flour (in form of raw baking mixture) was the source of infection in this outbreak of salmonellosis. This is because (i) a high association was found between the consumption of raw baking mixture/raw flour and disease in cases, and (ii) a matching strain of STM42 was detected in samples of flour taken at cases' homes and retail premises.

6 Glossary

Attack rate
Attack rate is a parameter of disease used in outbreak situations. It is defined as the number of cases divided by the number of individuals exposed.

Cluster
An aggregation of disease in space and/or time in numbers that is greater than expected to happen by chance alone [25]. It can also be defined as a group of cases of a particular disease, which are epidemiologically linked by time or place, but not with a common food or other source of infection [26].

Contamination
The presence of a disease-causing pathogen on surfaces of objects or bodies, but also in items or substances including water, milk, and food [27].

Epidemic
The occurrence of illness in a defined community or a region that is clearly above normal expectations and that happens within a specified period [25].

Epidemiology
The study of the occurrence and distribution of health-related events (e.g. outbreaks, diseases, causes of death) in specified populations (e.g. groups of people, a society, local or global population). This includes the study of factors (e.g. biological, behavioural, social, economic) that influence health [25].

EpiSurv
A national notifiable disease surveillance system, which is a collection of data about notifiable diseases and outbreaks reported by public health units (PHUs). EpiSurv is managed by ESR.

Foodborne disease
A disease associated with the consumption of food, containing a specific disease-causing pathogen.

Foodborne disease outbreak
The occurrence of two or more cases of a particular foodborne disease after ingestion of a common food [14].

Gastroenteritis
An inflammation of the stomach and intestines as a result of bacterial or viral infection. Symptoms of gastroenteritis can include vomiting, stomach pain, cramps, and diarrhoea.

Incubation period
The time period between exposure to (initial contact with) a disease-causing pathogen and the onset/appearance of clinical symptoms of disease in a person [27]. Each disease pathogen has a characteristic incubation period.

Infection
The entry and development or multiplication of a disease-causing agent in the body of animals or persons [27].

Outbreak
An outbreak is defined when two or more cases of the same disease are linked to a common source [14]. In foodborne disease outbreaks, the common source can be contaminated food or drink.

Outbreak investigation
Includes all activities to establish the existence of an outbreak, describe the outbreak, and identify the source, transmission mechanism and factors, which may have caused the outbreak.

PHU
There are 12 Public Health Units across the country, covering different districts in the North and South Island of New Zealand. PHUs deliver public health services at the regional level.

Reservoir (of disease-causing pathogens)
Any person, animal, plant, soil or substance, in which a disease-causing pathogen normally lives and multiplies, on which it depends for its survival, and from where it can be transmitted to infect others (e.g. animal, person, plant) [27].

Source attribution model
Statistical method(s) used to estimate the contribution of different sources to the burden of a particular disease in a country.

Source of infection
The person, animal, object or substance, from which a disease-causing pathogen is passed on [27].

Sporadic case
A case of disease, which is epidemiologically not linked to other cases of the same illness, and hence not part of an outbreak [26].

STEC
Shiga-toxin producing *Escherichia coli* (STEC) is a zoonotic pathogen and ruminants, in particular cattle, are recognised as the main reservoir of STEC, shedding the pathogen with their faeces.

Surveillance

The systematic and continuous collection, analysis, and interpretation of data, and the timely dissemination of results for public health action. Surveillance is essential for the planning, implementation and evaluation of public health practice [25].

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