CHAPTER

4

Foodborne Illness Surveillance and Outbreak Detection

CHAPTER SUMMARY POINTS

- Two general methods are used to detect most outbreaks: pathogen-specific surveillance and complaint systems.
- Recent technology changes have altered foodborne illness surveillance, including culture-independent diagnostic testing (CIDT) and whole-genome sequencing (WGS).
  - Molecular multitarget CIDTs that can detect up to 22 pathogens in an hour are replacing enteric pathogen culture in many clinical laboratories, shifting the burden of isolating bacteria for subtype and other characterization to public health laboratories.
  - WGS offers major improvements over traditional subtyping methods but currently takes longer than pulsed-field gel electrophoresis to complete, leading to potential delays in identification of clusters.
- The usefulness of consumer complaint systems to identify outbreaks is based either on: 1) the ability of groups with a common exposure to self-identify illness and link it to the exposure; or 2) the ability of the complaint system to independently link multiple independent complaints to a common source.
  - To complement the review of individual complaints and patterns of complaints detected through the foodborne illness complaint system, communicable disease surveillance staff should conduct standard interviews for foodborne illness detected through pathogen-specific surveillance (e.g., *Salmonella* and Shiga toxin–producing *Escherichia coli*).
  - Regardless of who receives the complaint or how the complaint is received (phone, online), the complaint should be evaluated for the likelihood of a foodborne illness or outbreak associated with the establishment that is the subject of the complainant or other establishments identified in the food history.

URLs in this chapter are valid as of August 13, 2019.

4.0 Introduction

4.0.1 Foodborne illness surveillance identifies clusters of illness that may be caused by a common food source. This chapter reviews major features, strengths, and limitations of surveillance methods and provides recommendations for increasing the effectiveness of each. In practice, detecting individual foodborne illness outbreaks involves multiple approaches. However, in general, two methods are used to detect most outbreaks: pathogen-specific surveillance and complaint systems (Table 4.1). A third method, syndromic surveillance, is used in some jurisdictions, but its role in detecting foodborne illness outbreaks is limited.

- **Pathogen-specific surveillance:** Healthcare providers and laboratorians report individual cases of illness when selected pathogens, such as *Salmonella enterica* and *Escherichia coli* O157:H7, or specific clinical syndromes, such as hemolytic uremic syndrome and botulism, are identified. Public health professionals gather exposure information through interviews with case-patients.
- **Complaint systems:** Healthcare providers or the public identify and report suspected illness clusters (group notifications) or individual complaints. Exposure information is acquired by interviews with ill people.
- **Syndromic surveillance:** This surveillance method generally involves systematic (usually automated) gathering of data on nonspecific health indicators that might reflect increases in illness, such as purchase of loperamide (an antidiarrheal agent), visits to emergency departments for diarrheal complaints, or calls to poison control hotlines. Exposure information is not routinely collected.

Although these methods are presented separately for descriptive purposes, they are most effective when used together and integrated with food, veterinary, and environmental monitoring programs (Chapters 4 and 5). The range of possible food vehicles detectable through foodborne illness surveillance includes all food or other substances contaminated at any link in the chain from production to ingestion. Foodborne illness surveillance complements regulatory and commercial monitoring programs by providing primary feedback on the effectiveness of prevention programs.

4.0.2 This chapter highlights how recent technology changes have altered foodborne illness surveillance; including the use of culture-independent diagnostic testing (CIDT) and whole-genome sequencing (WGS). Molecular multitarget CIDTs can detect up to 22 pathogens in an hour, which makes them very attractive for clinical laboratories (*1*). Molecular multitarget CIDTs are replacing enteric pathogen culture in many clinical laboratories. The use of CIDTs in clinical laboratories shifts the burden of isolating bacteria for subtype and other characterization to public health laboratories (PHLs). Another major change is the advancement of WGS at PHLs. WGS has replaced traditional methods used at PHLs, such as serotyping and subtyping by pulsed-field gel electrophoresis (PFGE), for the primary foodborne pathogens under routine surveillance.

Table 4.1. Comparison of Foodborne Illness Surveillance Systems

FUNCTIONAL CHARACTERISTIC OF METHOD	SURVEILLANCE METHOD			
	PATHOGEN-SPECIFIC	COMPLAINT		SYNDROMIC
		GROUP NOTIFICATION	INDIVIDUAL COMPLAINT	
Inherent speed of outbreak detection	Relatively slow	Fast	Fast	Variable*
Sensitivity to widespread, low-level contamination events (best practices used)	High	Intermediate	Intermediate	Low†
Types of outbreaks (etiology) that method can potentially detect	Limited to clinically suspected or laboratory-confirmed diseases under surveillance	Any‡	Any, although effectiveness limited to agents with short incubation periods‡	Limited to syndromes (or indicators) under surveillance
Initial outbreak signal (at public health level)	Cluster of cases in space or time with common agent	Report of group illnesses recognized by healthcare provider, laboratory, or the public	Multiple independent reports with common exposures in space or time or unique clinical presentation recognized by the agency receiving the reports	Trend in health indicator different from expected, space/time clusters of diagnosed cases
No. cases needed to create initial signal	Low to moderate	Low	Low to moderate	High§
Signal-to-noise ratio	High¶ (after interview of case-patients and collection of appropriate food history). Even higher when combined with subtyping	High¶ (after interview of case-patients and collection of appropriate food history)	Low to moderate (after interview of case-patients and collection of appropriate food history)	Low**

* An advantage in speed is limited mainly to nonspecific health indicators (preclinical and clinical prediagnostic data). Data must be analyzed, and a follow-up investigation is required, including comparison with standard surveillance, before public health action can be taken.

† Sensitivity is higher for rare, specific syndromes, such as botulism-like syndrome.

‡ Although outbreaks can be detected without an identified etiology, linking multiple outbreaks to a common source may require agent information.

§ The number of cases needed to create a meaningful signal is related to the specificity of the indicator. Indicators that offer an advantage in speed also tend to have low specificity.

¶ A high signal-to-noise ratio means that even a small number of cases stand out against a quiet background. A low ratio means a cluster of cases or events is difficult to perceive because it is lost in the many other similar cases or events happening simultaneously—similar to a weak radio signal lost in static noise. The signal-to-noise ratio for syndromic surveillance is lowest for nonspecific health indicators, such as loperamide use or visits to the emergency department with diarrheal disease complaints. The ratio increases with increasing specificity of agent or syndrome information. For highly specific, rare syndromes, such as botulism-like syndrome, the signal-to-noise ratio would approach that of pathogen-specific surveillance.

**Exposure histories are not typically obtained.

4.1 Pathogen-Specific Surveillance

4.1.1 The purpose of pathogen-specific surveillance is to systematically collect, analyze, and disseminate information about laboratory-confirmed illnesses or well-defined syndromes as part of prevention and control activities. Surveillance for typhoid fever began in 1912 and was extended to all *Salmonella* spp. in 1942. National serotype-based surveillance of *Salmonella* began in 1963, making it one of the oldest pathogen-specific surveillance programs and the oldest PHL subtype-based surveillance system. The usefulness of pathogen-specific surveillance is related to the specificity with which agents are classified (i.e., use of subtyping and method), enabling grouping of individual cases of illness with other cases most likely to share a common food source or other exposure. The utility of bacterial surveillance increased during the 1990s with the development of PulseNet and molecular subtyping of selected foodborne pathogens, including *Salmonella*, Shiga toxin–producing *E. coli* (STEC) O157:H7, *Shigella*, and *Listeria*. Additional gains in usefulness are anticipated with the adoption of WGS in 2019.

4.1.2 Most illnesses included under pathogen-specific surveillance are reportable (i.e., notifiable) diseases. State or local health agencies establish criteria for voluntary or mandatory reporting of infectious illnesses, including those that might be foodborne (Box 4.1). These criteria describe the illnesses to report, to whom, how, and in what timeframe. For this type of surveillance, illnesses are defined by specific laboratory findings or by well-defined syndromes, such as hemolytic uremic syndrome.

- **Illnesses are reported primarily by laboratories, medical staff (e.g., physicians, infection-control practitioners, medical records clerks), or both.** Reports can be automatically generated from an electronic medical record or laboratory information system or reported through a secure website. Legacy systems, such as telephone, mail, or fax reporting, also are used but are slower and more labor intensive and error prone.
- **Isolates or other clinical materials are forwarded from clinical laboratories serving primary healthcare facilities to PHLs** for confirmation and further characterization, as required by state laws or regulations or as requested by the local jurisdiction.

  Molecular multitarget CIDTs are replacing enteric pathogen culture in many clinical laboratories. Many clinical laboratories that perform enteric pathogen detection using CIDTs do not culture the pathogens identified by the CIDT. Instead, the clinical laboratory sends the specimen to the PHL to perform culture to obtain an isolate for further testing, which is important for foodborne disease surveillance.

  It is imperative that clinical laboratories send the specimens in a transport media (e.g.,

Box 4.1. Selected Nationally Notifiable Diseases that Can be Foodborne

- Anthrax (gastrointestinal)
- Botulism, foodborne
- Campylobacterosis
- Cholera
- Cryptosporidiosis
- Cyclosporiasis
- Giardiasis
- Hemolytic uremic syndrome, postdiarrheal
- Hepatitis A virus infection
- Listeriosis
- Salmonellosis
- Shiga toxin–producing *Escherichia coli* infection
- Shigellosis
- Trichinellosis (trichinosis)
- Typhoid fever
- *Vibrio* infection

In addition, the following are nationally notifiable:

- Foodborne illness outbreaks
- Waterborne illness outbreaks

Source: Centers for Disease Control and Prevention. Nationally Notifiable Infectious Diseases. United States 2018. Historical. https://wwwn.cdc.gov/nndss/conditions/notifiable/2018

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Cary Blair) to PHLs immediately to improve the chances of isolating the pathogen. Immediate transport of specimens also helps identify potential clusters as soon as possible. The Association of Public Health Laboratories has produced guidelines for specimen submission for optimal isolate recovery from specimens that test positive for pathogens by CIDTs (*2*).

4.1.3 Laboratory staff record receipt of samples at the PHL and enter sample information into the laboratory information management system, or LIMS. This process facilitates downstream information sharing with investigation partners. Patient information submitted with the sample may be provided to the epidemiology department for comparison with information from cases already reported and to enable reconciliation of case reports and laboratory samples and identification of previously unreported cases.

- If CIDTs have been used to detect the pathogen in the clinical laboratory, and a specimen is submitted, the PHL attempts to isolate that pathogen.
- Once the isolated pathogen is identified, it is further characterized (e.g., by serotyping, virulence assays, molecular subtyping, or antimicrobial susceptibility tests).
- WGS and PFGE (if conducted at the state level) data, along with accompanying metadata, are uploaded to local and national PulseNet databases. Consolidated daily reports, such as subtype frequency reports, often are used to facilitate cluster recognition. These reports may be automatically generated by laboratory or epidemiology information systems, extracted from the PulseNet database, or extracted from the System for Enteric Disease Response, Investigation and Coordination (SEDRIC).
- Specimen data (including detailed subtyping results) are uploaded to national surveillance systems, such as Laboratory-based Enteric-Diseases Surveillance).
- PHLs issue reports either singly or in groups to the epidemiology department either through electronic systems such as laboratory information management system submission to the epidemiology database or manual entry. Reports also may be issued to submitters as permitted by local policies.
- Rapid identification of clusters in the laboratory and communication of the cluster to foodborne illness epidemiologists is vital to outbreak detection. Case cluster data are enhanced by inclusion of information about matching isolates or outbreaks through PulseNet from other jurisdictions and by matching isolates from food, animal, or environmental monitoring tests that provide information for hypothesis generation.

4.1.4 WGS has replaced traditional methods used at PHLs, such as serotyping using antiserum and subtyping PFGE. PFGE has been the predominant subtyping method for PulseNet since its inception in 1996, but was replaced by WGS in 2019 (*3*).

- WGS data generated from isolates are analyzed to compare isolate relatedness (Figure 4.1). Generally, this comparison is done using the complementary approaches of high-quality single-nucleotide polymorphism (hqSNP) analysis and core or whole-genome multilocus sequence typing (cg/wgMLST). hqSNP analysis identifies differences in single base pairs between closely related isolates, whereas cg/wgMLST analysis relies on a database of all potential genes, or loci, for a particular enteric pathogen. cgMLST looks at those genes in common between all isolates being compared and primarily is used for surveillance and outbreak detection, whereas wgMLST looks at both the genes in common and those that represent the diversity of the strains and is used to further characterize isolates that are

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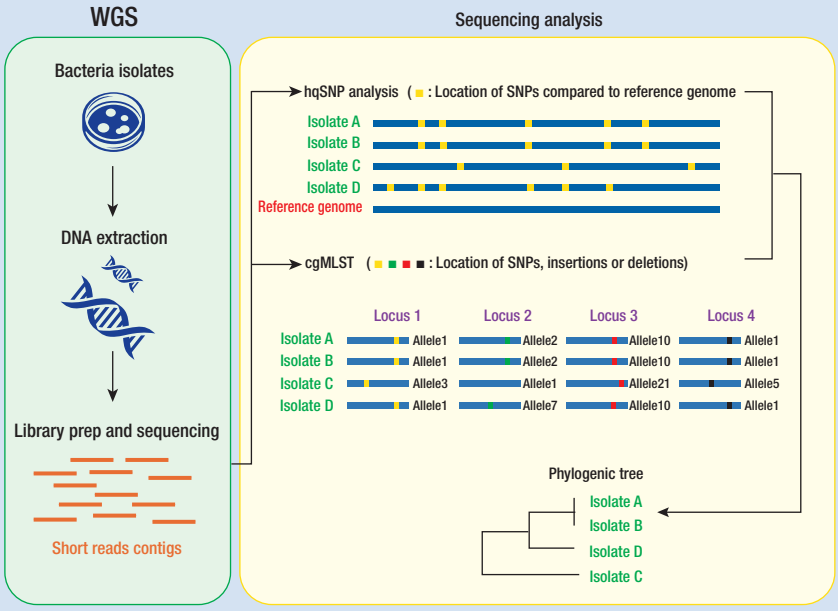
Figure 4.1. Depiction of Whole-Genome Sequencing (WGS) and Sequencing Analysis.

WGS starts with extracted DNA from isolated bacteria. Library preparation is then performed by sequencing, which creates millions of short reads. The reads are combined to create long strands of DNA. DNA from one bacterium can be compared with others using the complementary approaches of high-quality single-nucleotide polymorphism (hqSNP) analysis and core genome multilocus sequence typing (cgMLST). hqSNP analysis identifies differences in single base pairs among closely related isolates, and the cgMLST analysis relies on a database of all potential genes, or loci, for a particular enteric pathogen. Both approaches identify differences between compared isolates and can be used to assign a threshold of genetic relatedness between isolates: for hqSNP isolates, it is a number of SNP, or base pair, differences; and for cgMLST, it is the number of allele, or gene, differences. A phylogenetic tree can be used to visualize the genetic differences using either SNP-based testing or cgMLST.



related and part of a cluster. Both of these approaches identify differences between compared isolates and can be used to assign a threshold of genetic relatedness between isolates. For hqSNP isolates, the threshold of relatedness is a number of SNP, or base pair, differences; for cg/wgMLST it is the number of allele, or gene, differences. Both methods can produce a phylogenetic tree, which aids in interpretation of results.

- Several "rules of thumb" based on the number of allele differences have been developed to help define a cluster by WGS. These rules vary by pathogen and mode of transmission.

Generally, PulseNet uses a definition of at least 3 cases within a 60-day window with 0–10 allele differences, where at least 2 of the cases differ by 5 or fewer alleles, for *Salmonella* and STEC. PHLs may consider a narrower definition (such as 0–5 alleles) to reduce the number of clusters that need to be investigated and to focus investigation resources. Similar to PFGE, there can be common sequence types or rare sequence types, which should be considered during cluster investigations. In addition, if the outbreak occurs over a long period or is zoonotic, more allele differences are detected than in an outbreak representing

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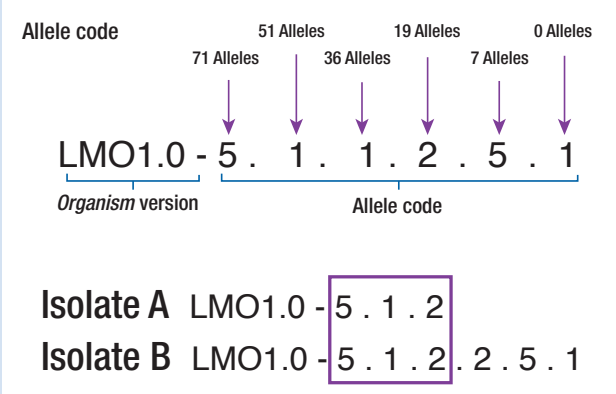
a point source contamination event. When an outbreak source is contaminated with multiple diverse sequence types, known as a polyclonal outbreak, sequence data may be used to identify multiple independent clusters, which can then be used to identify the polyclonal outbreak. One strategy is to use a narrow cluster definition to identify clusters. That strategy will reduce the number of misclassified cases and will increase the measure of association. Once an outbreak is identified, the cluster definition can be expanded to identify addition cases that were missed because of the initial stringent cluster definition.

- cgMLST analyses are built from a stable database of genes so a pattern name, or allele code, can be assigned to the sequence data (Figure 4.2). Allele codes are built from a single linkage tree of all isolates for an organism, and cutoffs are set along certain points, which represent percentage similarity cutoffs, along the tree that produce a stable nomenclature and provide enough resolution to identify potential outbreak clusters. Using the allele code, which is a string of 5–7 numbers, similar to a ZIP code, closely related isolates can be identified and historic frequencies can be tracked. Each shared number along the allele code indicates the genetic relatedness of the isolates. For example, isolates A and B that have the same allele code, 1.1.1.1.1, are closely genetically related; a new isolate, isolate C, that has allele code 1.1.1.1.2 is more closely related than isolate D, with allele code 1.1.1.2.2. Additionally, the allele code can be used to identify clusters and combined with other information predicted from the WGS data, including virulence, serotype, and predicted antibiotic resistance, can be used to prioritize cluster follow-up as part of the triage process. A recent review provides additional information on use and interpretation of WGS data for surveillance (*3*).
- WGS data can be used to identify an organism, predict serotype and antibiotic resistance, and identify virulence genes. There are several tools for conducting these analyses, including tools available through the PulseNet database system.
- Although WGS offers major improvements over traditional subtyping methods and enables PHLs to have more efficient workflows, some challenges exist to using this technology in public health practice. WGS takes longer than PFGE to complete (a minimum of 4 days for WGS vs. 1 day for PFGE). In addition, if WGS replaces

Figure 4.2. Depiction of Allele Code Assembly.

Nomenclature is organism-specific with different thresholds for the digits. Organism-specific allele codes are built from a string of 5–7 numbers, similar to a ZIP code. Each shared number along the allele code indicates the genetic relatedness of the isolates. When sequences have partial names, they are singletons in clusters below their last digit. For example, isolates A and B are *Listeria monocytogenes* isolates that are approximately within 36 and 19 alleles of each other.



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traditional serotyping methods, identification of clusters using serotype is delayed. PHLs need to perform WGS in a timely manner to ensure clusters are identified as soon as possible, which can be difficult to do in a cost-efficient manner if the testing level of a jurisdiction is low.

4.1.5 Case-patients are usually interviewed one or more times about potential exposures and additional clinical and demographic information. Routine collection of detailed exposure information as soon as possible after reporting (either CIDT- or culture-positive result) maximizes exposure recall, provides a basis for rapid cluster investigation, is critical to the environmental investigation, and is strongly recommended for high-consequence enteric pathogens, such as STEC O157:H7, *Salmonella*, and *Listeria monocytogenes*.

- The scope of routine interviews varies by jurisdiction, agent, and type of test result. Initial interviews typically cover basic descriptive information and exposures of local importance, such as attendance at a childcare facility, occupation as a food worker, and medical follow-up information. Whereas many local agencies collect information about a limited set of high-risk exposures, where resources are limited, detailed exposure interviews might be conducted only when clusters are investigated or outbreaks are recognized (Chapter 5).

Information the public health agency receives through multiple avenues, including basic clinical and demographic data from individual case-patients of specific laboratory-confirmed illness or well-defined syndromes, is reconciled and linked with case isolates or other clinical materials received in the PHL. Reconciled case reports are forwarded to higher jurisdictional levels (local health agency to state agency, state agency to federal agency) by a variety of mechanisms. In general, records are redacted (stripped of individual identifiers) when they are sent outside the reporting states.

4.1.6 Initial cluster identification and cluster assessment might occur as two processes conducted, respectively, by the laboratory and epidemiology departments or might occur as a single process within epidemiology. Agent, time, and place are examined individually and in combination to identify possibly significant clusters or trends. This is the critical first step in hypothesis generation. Clusters of unusual exposures, exposure frequencies, demographic distributions (e.g., predominance of cases in a particular age group), or connection to food, animal, or environmental monitoring studies might be identified. Clusters of cases are examined as a group and, if a common exposure seems likely, are investigated further (Chapter 5). In some jurisdictions, cluster detection and triage are a laboratory function (see section 4.2.5).

- A cluster is defined as two or more cases of disease linked by place, time, pathogen subtype, or other characteristic. Isolates closely related by genetic subtyping are more likely to share a common source than isolates that are not closely related by genetic subtyping.
- Clusters may be more or less recognizable and more or less actionable. This chapter focuses on case clusters and outbreaks, but for some high-consequence agents or syndromes (e.g., botulism or paralytic shellfish poisoning), even a single case might merit a prompt and aggressive public health response.
- Clusters are common and pursuing them all with equal vigor is not practical or productive. Laboratory staff often identify clusters when they detect an increase of a specific subtype or serotype. Incoming surveillance data are evaluated for unusual case counts based on historical frequencies

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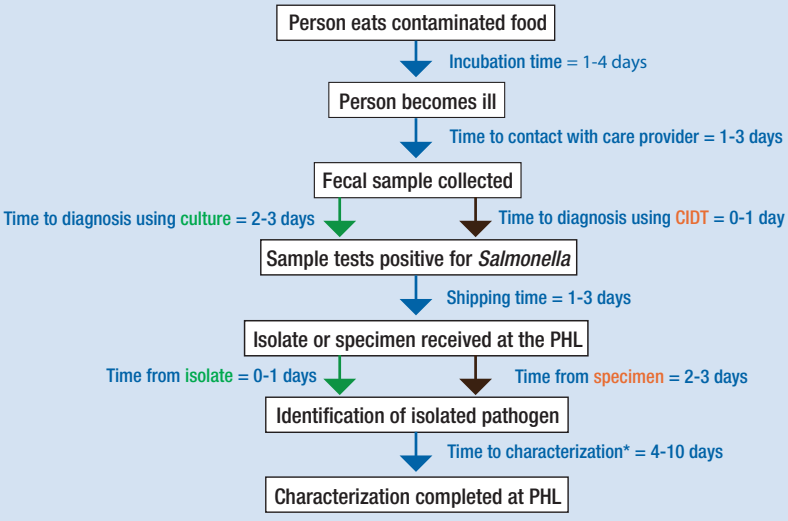
(accounting for seasonality), the severity of disease, and molecular matches between human cases and food or animal monitoring samples. In general, cases clustered over a relatively short period are more likely to indicate an outbreak. The time window used to delimit clusters varies by agent. For example, a wider window is used to evaluate clustering of listeriosis cases than to evaluate salmonellosis cases because of differences in the natural history of each disease.

- Although cluster recognition software packages, such as SaTScan™, cumulative summary (cusum) outbreak detection algorithms, and query algorithms in the System for Enteric Disease Response, Investigation and Coordination have been developed, none have yet been validated for broad-based enteric disease data. The decision to report or pursue a cluster is an important part of the outbreak detection process but not one that is easily distilled into simple best practices. For many organisms, clusters identified by WGS are more indicative of a close genetic relationship and epidemiologic relatedness than are clusters identified by PFGE. An increase in frequency of a strain is only one indication of a potentially significant cluster. Furthermore, absence of an increase in case numbers from expected values does not rule out significance.

4.1.7 The timeline for pathogen-specific surveillance covers a series of events from the time a person is infected through the time public health officials determine that person is part of a disease cluster. The time from infection to cluster detection is one of the limiting factors of pathogen-specific surveillance. Minimizing delays by streamlining the individual processes improves the likelihood of overall success. A sample timeline for *Salmonella* case reporting is presented in Figure 4.3.

Figure 4.3. Sample Timeline for *Salmonella* Case Reporting*



*Abbreviations: CIDT, culture-independent diagnostic testing; PFGE, pulsed-field gel electrophoresis; PHL, public health laboratory; WGS, whole-genome sequencing.

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- **Incubation time:** the time from ingestion of a contaminated food to beginning of symptoms. For *Salmonella*, this typically is 1–4 days, sometimes longer. For more information about incubation times (also called incubation periods) of foodborne pathogens see the Outbreaks of Undetermined Etiology (OUE) Agent list from the CIFOR website (https://cifor.us) and the recent analysis of median incubation periods in outbreaks (*4*).
- **Time to contact with healthcare provider or doctor:** the time from the first symptom to medical care (when a fecal sample will ideally be collected for laboratory testing). This time may be an additional 1–3 days, sometimes longer.
- **Time to diagnosis:** the time from provision of a sample to laboratory identification of the agent in the sample as *Salmonella*. CIDT tests often produces same-day results, whereas culture-based diagnostic methods take 2–3 days.
- **Sample/isolate shipping time:** the time required to ship the *Salmonella* isolate or positive specimen from the initial testing laboratory to the public health authorities who will perform serotyping and subtyping. This usually takes 1–3 days or longer, depending on transportation arrangements within a state and distance between the clinical laboratory and the public health department. Diagnostic laboratories are not required by law in many jurisdictions to forward *Salmonella* isolates to PHLs, and not all diagnostic laboratories forward any isolates unless specifically requested to do so. When a laboratory does submit an isolate or specimen to public health, the timeframe for submission is often based on convenience and cost effectiveness rather than public health considerations.
- **Confirming isolated pathogen:** The time after a sample has tested positive for *Salmonella* to isolation and confirmation of *Salmonella*. Specimens identified as *Salmonella* by CIDTs require culture to isolate the organism from clinical samples that were used to perform CIDT, which takes 2–3 days. If culture-based methods are used at the clinical laboratory, the isolated bacteria is confirmed at the PHL, which takes 1 day.
- **Time to pathogen characterization:** The time required for state public health authorities to serotype and to perform subtyping on the *Salmonella* isolate and compare it with the outbreak pattern. Serotyping typically takes 3 working days but can take longer. PFGE can be accomplished in 1 working day (24 hours), whereas WGS can take as little as 4 working days. However, many PHLs have limited staff and space and experience multiple emergencies simultaneously. In practice, serotyping and PFGE or WGS subtyping may take several days to several weeks in extreme cases. Data derived from WGS can be used to determine the serotype and subtype and predict the antibiotic resistance profile of an isolate, thereby streamlining laboratory processes into a single workflow. However, completion of WGS will take longer than traditional workflows. Additionally, most or all PHLs will have to perform some batching to reduce the cost of the sequencing. Batching should be minimized as much as possible, however, because faster turnaround for pathogen characterization is highly desirable.
- The total time from onset of illness to confirmation of the case as part of an outbreak is typically 2–3 weeks.

4.1.8 Routine testing for specific pathogens of food in production is conducted as part of larger food-safety verification programs operated by the Food and Drug Administration (FDA), U.S. Department of Agriculture (USDA), and state agriculture agencies.

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- WGS is routinely performed on food isolates from FDA- and USDA-regulated products as part of the GenomeTrakr program, and the sequence data and limited metadata are uploaded to a genomic database housed at the National Institutes of Health, National Center for Biotechnology Information (NCBI) as well as to PulseNet. On NCBI, GenomeTrakr sequences are compared with sequences from the Centers for Disease Control and Prevention and other federal, academic, and international public health agencies; closely related isolates identified on the NCBI Pathogen Detection Portal (*5*) can be potential leads for cluster sources.
- Incorporating this routine food or animal monitoring or regulatory surveillance test data into the disease surveillance information stream enhances hypothesis generation and improves the sensitivity and timeliness of outbreak detection. In the United States, data streams from human disease surveillance, food-testing programs, environmental sources, and selected live-animal testing are co-mingled in the PulseNet database; however, important product details might not be readily available.

4.1.9 A key strength of pathogen-specific surveillance is its ability to detect widespread disease clusters initially linked only by a common agent. Most national and international foodborne disease outbreaks are detected in this manner.

Combining specific exposure information with case information from clusters recognized though complaints makes pathogen-specific surveillance the most sensitive method for detecting unforeseen problems in food- and water-supply systems caused by the agents under surveillance. The specificity of agent or syndrome information combined with specific exposure information obtained by interviews enables the positive association of small numbers of cases with exposures.

4.1.10 A key limitation of pathogen-specific surveillance is that it works only for diseases detected by routine testing and reported to a public health agency.

- Pathogen-specific surveillance is relatively slow because of the many steps required (Figure 4.1).
- Subtype-specific surveillance requires an isolate, which is challenging because of the use of CIDTs in clinical laboratories.

4.2 Complaint Systems

Consumer complaint systems are an effective surveillance tool for detecting a variety of food-related incidents, including reportable pathogens. Notification or complaint systems are intended to provide agencies with a tool for documenting, evaluating, and responding to reports from the community about possible foodborne disease events. The information maintained in these systems also helps to conduct prevention and control activities.

4.2.1 The usefulness of consumer complaint systems to identify outbreaks is based on 1) the ability of groups with a common exposure to self-identify illness and link it to the exposure or 2) the ability of the complaint system to independently link multiple independent complaints to a common source. Complaints involving multiple households, instances of multiple independent complaints about the same food establishment, reports of clusters of illness, and complaints involving multiple people in the same household that suggest an exposure outside the home often indicate an outbreak and should be evaluated to determine whether

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an investigation is warranted. In the absence of common, suspicious exposures shared by two or more case-patients, complaints of individual illness with nonspecific symptoms—such as diarrhea or vomiting—generally are not worth pursuing. Thus, sufficient exposure information about every independent complaint should be collected because reported exposures might become more significant when also reported by subsequent complainants. Complaint reporting involves passive collection of reports of possible foodborne illness from individuals or groups, such as the following:

- Reports from any individual or group who observes a pattern of illness affecting a group of people, usually after a common exposure: Examples include reports of illness among multiple persons eating at the same restaurant or attending the same event and reports from healthcare providers of unusual patterns of illness, such as multiple patients with bloody diarrhea in a short time span.
- Multiple independent complaints about illness in single persons or households. Group illness and independent complaints can be used together and linked with data obtained through pathogen-specific surveillance. In contrast to pathogen-specific surveillance, complaint reporting does not require identification of a specific agent or syndrome or contact with the healthcare system.

4.2.2 Detection of outbreaks based on multiple individual complaints requires a system for recording complaints and comparing food histories and other exposures reported by individuals. All complaints require some level of follow-up. A telephone caller should be given some expectation for what follow-up is likely. A person sending a complaint by text, email, or online reporting system should be notified the complaint was received.

- Document complaints received by telephone with a standard intake form to record complainant information. Complaints received through other formats may warrant additional follow-up to fully document the complaint.
- Questions should cover name and contact information of the caller, detailed illness information (including exact time of symptom onset and recovery), suspected food product and product packaging information (if applicable), name and location of retail or restaurant establishment, names and contact information of other members of the dining party (if applicable), and all potentially relevant nonfood exposures.
- When illness is limited to a single person or members of a single household, obtain food history for the 3 days before onset that focuses on meals eaten outside of the home. People often identify an incorrect exposure as the cause of their illness, often attributing it to the last thing they ate. However, only one in five complaints with a known etiology is caused by an agent with an incubation period shorter than 24 hours.
  - A food history of at least 3 days before illness onset should be collected for individual complaints because common exposures are the sole mechanism to link cases. A standardized form that includes both food and nonfood exposures is preferred.
  - Complaint systems that rely on Web-based reporting or other means of self-reporting should also ask for a 3-day food history, with emphasis on meals eaten outside the home; and should request contact information in case additional information is needed.
  - Efforts to capture complaints using social media should incorporate a link to online reporting, an online survey, or a phone number to the health department.
  - Given the ubiquity of norovirus infections, pay particular attention to

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exposures in the 24–48 hours before onset whenever norovirus is suspected. As more information about the likely etiologic agent is collected, this approach can be modified.

- The complaint and subsequent interviews can lead to a hypothesis about the pathogen that leads to a different time frame for the exposure history (e.g., vomiting leads to a different hypothesis and exposure history time frame than does bloody diarrhea).

- When illness is reported among members of multiple households, collect information only for meals in common to members of the different households. Attempt to contact and interview ill meal companions reported by the original caller about symptoms and food consumption.
  - Focus interviews on the event shared by members of the group. However, be aware they might have more than one event in common and explore that possibility.
  - Ask about other possible exposures for the interviewee or for others he or she might have contacted, such as childcare attendance, employment as a food worker, or ill family members.
- Enter all information collected into the complaint database. Review interview data regularly to look for trends or commonalities. As part of the review of the data, consider running reports showing frequencies of specific restaurants or other exposures (such as recreational water venues).
- Set up the reporting process so all reports go through one person or one person routinely reviews reports. Centralization of the reporting or review process increases the likelihood that patterns among individual complaints and seemingly unrelated outbreaks will be detected.

4.2.3 To complement the review of individual complaints and patterns of complaints detected through the foodborne illness complaint system, conduct standard interviews for foodborne illness cases detected through pathogen-specific surveillance (e.g., *Salmonella* and STEC). Enter all food establishments at which affected persons reported eating within the 7 days before illness onset into the complaint database. Routinely examine a list of restaurants reported by complainants and case-patients in pathogen-specific surveillance to search for common establishments.

Complaint data and results of pathogen-specific surveillance are much easier to link if complaint systems are centralized at the same jurisdictional level as pathogen-specific disease surveillance. The link of data from pathogen-specific and complaint surveillance systems can occur at the level of the local health agency or between individual city-based environmental health staff and county-based communicable disease program or at the state level. Such a shared/centralized system should enhance the ability of agencies to detect and respond to possible foodborne outbreaks but should not prevent any participating jurisdiction from fulfilling whatever role is required by law or is determined to be necessary to protect health in the jurisdiction's area.

4.2.4 Environmental health assessment and follow-up is generally managed by environmental health staff at local health departments that also license and inspect restaurants and other food-service establishments.

In jurisdictions where visits are not required to every restaurant named in illness complaints, the investigation and control team must decide whether investigation of a commercial food establishment is likely to be beneficial. To make this decision, consider details of the complainant's illness and the foods eaten at the establishment (Box 4.2).

- If communicable disease surveillance staff receive the complaint, they should immedi-

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ately share the complaint information with the responsible environmental health staff.

- Regardless of who receives the complaint or how the complaint is received (e.g., phone, online), the complaint should be evaluated for the likelihood of a foodborne illness or outbreak associated with the establishment that is the subject of the complaint or with other establishments listed in the food history. In addition, environmental health staff should review the establishment's inspection history, contact the establishment's manager, and determine the value of conducting an environmental assessment. Additional steps, such as an inspection, may be unnecessary if the complaint involves only one person (or persons in one household) and the illness reported is inconsistent with an exposure at the restaurant that is the subject of the complaint.
- All jurisdictions should have a process to ensure that complaints outside that jurisdiction are forwarded to the proper authority. This process includes forwarding complaints between local health agencies, between local health agencies and state departments of agriculture or health, and between local health agencies and state agencies and federal agencies: USDA's Food Safety and Inspection Service (USDA-FSIS) for meat, poultry, and egg product–related complaints and FDA for complaints related to other food items.
- Nongovernment complaint systems that do not share all information with the appropriate jurisdiction(s) and that do not have the authority to investigate the complaint (inspect the establishment or conduct an epidemiologic investigation) are not useful if the goal is to protect the public's health. Such systems should clearly state that the complaint is not being filed with an agency that can act on the complaint and should refer the complainant to the appropriate jurisdiction.

4.2.5 Collection and testing of clinical specimens and food samples related to group illness. PHL activities are essential for determining etiology, linking separate events during the investigation, and monitoring the efficacy of control measures (Chapters 5 and 6).

Box 4.2. Considerations for Investigating a Commercial Food Establishment

In the following situations, investigation of a named commercial food establishment might be warranted:

- The confirmed diagnosis and/or clinical symptoms are consistent with the foods eaten and the timing of illness onset (e.g., a person in whom salmonellosis is diagnosed reports eating incompletely cooked eggs 2 days before becoming ill).
- The complainant observed specific food-preparation or serving procedures likely to lead to a food safety problem at the establishment.
- Two or more persons with a similar illness or diagnosis implicate a food, meal, or establishment and have no other shared food history or evident source of exposure.

Regular review of individual complaints is critical to recognizing that multiple persons have a similar illness or diagnosis and share a common exposure.

Clues that a follow-up investigation of a food establishment is unlikely to be productive include

- Confirmed diagnoses and/or clinical symptoms that are not consistent with the foods eaten at the establishment and/or the onset of illness (e.g., bloody diarrhea associated with a well-cooked hamburger eaten the night before illness onset).
- Signs and symptoms (or confirmed diagnoses) among affected persons that suggest they might not have the same illness.
- Ill persons who are not able to provide adequate information for investigation, including date and time of illness onset, symptoms, or complete food histories.

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- Because of public health laboratory testing, links may be seen across jurisdictional boundaries and beyond; even national outbreaks may then be detected.
  - For instance, an outbreak associated with a particular restaurant may come to the attention of authorities solely on the basis of a report by a customer who observed illnesses among multiple fellow patrons. Laboratory testing and identification of *Salmonella* Typhimurium can result in refinement of the case definition used in this investigation, in additional testing and restrictions for workers found to be carriers, or in connecting this outbreak with other outbreaks (concurrent or historic) from a contaminated commodity.
- Obtain clinical specimens from at least five members of the ill group. Collect specimens as soon as possible after illness onset, ideally during active illness. For certain etiologies, clinical specimens need to be collected while the patient is still ill (bacterial intoxications); for many etiologies (norovirus, bacterial pathogens) it may be possible to detect pathogens in specimens collected days after illness recovery. Clinical specimens should be tested as soon as possible- some test types such as syndromic panels (commercially available tests that simultaneously tests for common bacterial, viral, and parasitic pathogens) require testing within 4 days of specimen collection for the results to be valid.
  - Because complaint systems are the primary tool for detecting outbreaks caused by pathogens not under surveillance, the clinical presentation and epidemiologic data should direct the testing priorities.
  - A number of references are available to help ascertain the etiology of an outbreak, e.g., CIFOR's Outbreak of Undetermined Etiology agent tables and interactive tool (*6*), Diagnosis and Management of Foodborne Illnesses, A Primer for Physicians and Other Health Care Professionals (*7*), and 2017 Infectious Diseases Society of America Clinical Practice Guidelines for the Diagnosis and Management of Infectious Diarrhea (*8*).
- If the presumed exposure involves food at a catered event, collect and store food from the implicated event, if feasible.
- Conduct all sampling using legally defensible procedures (e.g., chain-of-custody) and using protocols as guided by the laboratory that will conduct the analysis. Samples should be analyzed within 48 hours after receipt; however, generally test the food only after epidemiologic implication or identification of specific food-safety problems through an environmental health assessment. If the epidemiologic investigation is ongoing and a specific food item has not been implicated or is not suspected yet, food should be stored. Consideration include the following:
- Storage under refrigeration can be longer than 48 hours, if necessary, but the length of the storage period is food-dependent. Because certain bacteria (e.g., *Campylobacter jejuni*) die when frozen, affecting laboratory results, immediate examination of samples without freezing is encouraged.
  - Perishable foods should be frozen (−40°C to −80°C).
  - Food samples that are frozen when collected should remain frozen until examined.
  - Food samples can be collected as part of the process of removing suspected food from service.

If food testing is determined to be necessary—for example, if a food has been epidemiologically implicated—official reference testing methods must be used at a minimum for regulated products (e.g., pasteurized eggs or commercially distributed beef).

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Note: Food testing has inherent limitations because most testing is agent-specific, and demonstration of an agent in food is not always possible or necessary before implementation of public health action. Detection of microbes or toxins in food is most important for outbreaks involving preformed toxins, such as enterotoxins of *Staphylococcus aureus* or *Bacillus cereus*, where detection of toxin or toxin-producing organisms in human specimens frequently is problematic. In addition, organisms such as *S. aureus* and *Clostridium perfringens*, which are commonly found in the human intestinal tract, can confound interpretation of culture results.

Furthermore, food-testing results are often difficult to interpret. Samples collected during an investigation might not represent food ingested when the outbreak occurred. Subsequent handling or processing of food might result in the death of microorganisms, multiplication of microorganisms originally present in low levels, or introduction of new contaminants. If the food is not uniformly contaminated, the sample collected might miss the contaminated portion. Finally, because food usually is not sterile, microorganisms can be isolated from samples but not be responsible for the illness under investigation. Thus, food testing should not be routinely undertaken but should instead be based on meaningful associations identified through data analysis of interviews with suspected case-patients or during environmental health assessments at the implicated food-service establishment.

4.2.6 A key strength of complaint systems is their ability to detect outbreaks from any cause, known or unknown. Thus, the complaint system is one of the best methods for detecting nonreportable pathogens and new or reemerging agents. Recent examples include recognition of sapovirus as a significant agent in norovirus-like outbreaks [*9*], identification of *Arcobacter butzleri* as the likely agent in an outbreak of gastroenteritis at an event [*10*], and atypical enteropathogenic *E. coli* at a restaurant (*11*). In one study, consumer complaint surveillance alone led to detection of 79% of confirmed foodborne outbreaks, including most norovirus outbreaks (*12*).

- For event-related complaints, food items eaten and other exposures are easily determined because items consumed at the event can be identified by menus or other means and specifically included in the interview.
- Complaint surveillance systems are inherently faster than pathogen-specific surveillance because the chain of events related to laboratory testing and reporting is not required. Exposure information gained through patient interviews has the potential for being high quality because patient recall is highest close to the exposure event.
- Because of the relatively limited number of exposures to consider, investigations of event-related notifications can be pivotal to solving widespread outbreaks detected through pathogen-specific surveillance. For example, a norovirus outbreak associated with contaminated imported raspberries used in commercially distributed ice cream was initially identified from complaints as multiple independent outbreaks (*13*). Complaint systems are key in identifying intentional contamination events that would not be detected in pathogen-specific surveillance, for example, an outbreak of methomyl poisoning caused by intentionally contaminated salsa at a restaurant (*14*).

4.2.7 The value of single complaints of possible cases of foodborne disease in detecting outbreaks is limited by a lack of exposure information to link to any other cases and by the lack of specific agent or disease information to exclude unrelated cases. The illness reported by individuals might or might not be foodborne, and illness presentation might or might not be typical.

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- Without a detailed food history (either from the initial report or follow-up interview), surveillance of independent complaints is sensitive only for short incubation (generally chemical- or toxin-mediated) illness or illness with unique symptoms because most people associate illness with the last meal eaten before onset of symptoms, they are likely to be correct only for exposures with short incubation times. This is not a limitation if full interviews are conducted.
- Notification of illness in groups generally is less sensitive to widespread low-level contamination events than is pathogen-specific surveillance because recognition of a person–place–time connection among case-patients by a healthcare provider or member of the community is required.
- These limitations can be minimized by
  - Collecting a food history for the 3 days before illness onset to detect outbreaks caused by etiologic agents with longer incubations than bacterial toxins.
  - Looking for commonalities between the complete food histories for all complaints with case-patient interviews from pathogen-specific surveillance.
  - Promptly forwarding all complaint to the jurisdictions of establishments mentioned in the food histories for prompt follow-up and/or gathering of additional pertinent information.

4.2.8 Improve communication and cooperation among agencies that receive illness complaints. Consumers may submit complaints to multiple organizations and agencies, such as poison control centers, agricultural agencies, facility-licensing agencies, grocery stores, and online platforms and social media sites.

- Identify the agencies/organizations in the community that are likely to receive complaints. Establish regular communication between agencies that receive illness complaints, epidemiology staff, and laboratory staff. Always keep contact information current. Because complaints might be made to multiple agencies, having a robust method of sharing information is important. If possible, set up a database that public health agencies can access and review. Information-sharing is particularly important in adjacent jurisdictions.
- Check complaint information against national databases, such as the USDA-FSIS Consumer Complaint Monitoring System (CCMS) (*15*). Consumers can report complaints to CCMS by contacting the USDA-FSIS Meat and Poultry Hotline (1-888-MPHotline [1-888-674-6854]) or using the USDA-FSIS online complaint reporting system, the Electronic Consumer Complaint Form (https://foodcomplaint.fsis.usda.gov/eccf).

4.2.9 To increase surveillance sensitivity, remove barriers to reporting by making the reporting process as simple as possible for the public. For example, provide one 24/7 toll-free telephone number or an online reporting form. Such systems enable callers to leave information that public health staff can check later.

Promote reporting by routine press releases that educate the public about food safety, and advertise the contact phone number or website for reports of illness. Use a telephone number that easily can be remembered or found online. Train food managers and workers about the importance of reporting unusual patterns of illness among workers or customers and Food Code requirements for disease reporting (*16*). Communicate the value of such reporting, not just to protect public health, but also to protect food establishments from unfounded allegations of foodborne illness.

4.3 Syndromic Surveillance

The concept of syndromic surveillance was developed in the 1990s and expanded after the 2001 postal system anthrax attacks in an attempt to improve readiness for bioterrorism.

The utility of syndromic surveillance for nonspecific health indicators for foodborne illness surveillance and outbreak investigation is very limited. In theory, the electronic collection of such indicators could permit rapid detection of major trends, including outbreaks. In practice, the right mix of sensitivity and specificity has proven difficult to find, and the utility of such systems might be marginal. Surveillance for highly specific syndromes, such as hemolytic uremic syndrome or botulism, is a critical public health function.

- Some groups (e.g., public health agencies, academic researchers, nongovernment organizations) monitor social media to identify potential outbreaks. The effectiveness of the use of social media tools to identify outbreaks is still being evaluated but may be useful to enhance traditional complaint systems.
- In theory, syndromic surveillance can be used as a tool to identify cases during an outbreak of an emerging or rare pathogen before laboratory testing protocols have been put into place or results have been received.
- Syndromic surveillance can help identify general enteric disease trends in a community (e.g., norovirus activity levels) to craft targeted prevention messaging (e.g., remind food-service establishments to exclude ill food-service employees).

Syndromic surveillance typically relies on automated extraction of health information, such as school and work absenteeism, posts or complaints on social media sites, emergency department chief complaint, lab test orders, or hospital discharge codes (ICD-10). Epidemiology or emergency preparedness groups evaluate alerts triggered by the syndromic surveillance system, and interview case-patients to determine whether the alert represents a true outbreak.

4.3.1 Potential strengths of syndromic surveillance include the use of nonspecific health indicators to identify clusters of disease before definitive diagnosis and reporting.

- Syndromic surveillance may be able to detect large undiagnosed events, such as an increase in gastrointestinal illness among persons of all ages consistent with norovirus or an increase in diarrheal illness among young children consistent with rotavirus, and it may be helpful for monitoring health status after a natural disaster, if other surveillance systems are temporarily unavailable.

4.3.2 The lack of specificity for most syndromic surveillance indicators in the area of foodborne disease is a limitation that makes for an unfavorable signal-to-noise ratio, meaning that only the largest events would be detected, and many false-positive signals would be expected.

- Responding to false-positive signals substantially drains an agency's resources.
- Syndromic surveillance cannot replace routine surveillance.

The ultimate measure of success for any surveillance system is outbreaks detected. Because the usefulness of syndromic surveillance for detecting foodborne disease events is limited, additional investment would compete for resources with under-resourced standard surveillance systems; therefore, it should be used only under very special circumstances when routine surveillance is not possible.

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