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ORIGINAL PAPER

Outbreaks of Norovirus and Acute Gastroenteritis Associated with British Columbia Oysters, 2016–2017

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Abstract

Two outbreaks of norovirus and acute gastroenteritis took place in Canada between November 2016 and April 2017. Both outbreaks were linked to oysters from British Columbia (BC) coastal waters. This paper describes the multi-agency investigations to identify the source and control the outbreak. Public health officials conducted interviews to determine case exposures. Traceback was conducted by collecting oyster tags from restaurants and analyzing them to determine the most common farms. Oyster samples were collected from case homes, restaurants, and harvest sites and tested for the presence of norovirus. Potential environmental pollution sources were investigated to identify the source of the outbreak. Four hundred and 49 cases were identified as part of the two outbreak waves. The oysters were traced to various geographically dispersed farms in BC coastal waters. Twelve farms were closed as a result of the investigations. No environmental pollution sources could be identified as the cause of the outbreak. Similarities in the timeframe, genotype, and geographic distribution of identified oyster farms indicate that they may have been one continuous event. Genotype data indicate that human sewage contamination was the likely cause of the outbreak, although no pollution source was identified.

Keywords Norovirus · Oysters · Outbreak · Foodborne

Background

Norovirus is the most common enteric pathogen in Canada, and accounts for an estimated 1 million cases of foodborne illness nationally (Thomas et al. 2013). It can be transmitted via fecally contaminated food or water, person-to-person contact, aerosolized particles from vomitus, and fomites, causing acute gastrointestinal symptoms (vomiting, diarrhea, nausea) that last for 24–72 h (Karst 2010).

As oysters are a water-filtering organism, norovirus-contaminated waters can cause the virus to bio-accumulate in their digestive tissue (Le Guyader et al. 2006b; Schwab et al. 1998; Tian et al. 2007). Oysters are sometimes consumed raw, and therefore have been the cause of multiple norovirus outbreaks in Canada and internationally, including both localized, point source outbreaks (Le Guyader et al. 2006a; Alfano-Sobsey et al. 2012; McIntyre et al. 2012; Dam Rasmussen et al. 2016), and outbreaks associated with widespread contamination (David et al. 2007; Westrell et al. 2010).

In British Columbia (BC), Ontario, and Alberta, public health surveillance is in place to detect norovirus outbreaks, particularly those that occur in institutions. However, foodborne-related norovirus outbreaks are unlikely to be laboratory-confirmed since the majority of cases recover before seeking medical care. This is due to the short duration of illness. As a result, in Ontario and Alberta foodborne illnesses involving this pathogen are reported and investigated

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on a complaint basis, while routine surveillance for illnesses associated with shellfish consumption is conducted in BC.

In November 2016, 12 complaints of gastrointestinal illness with oyster consumption within 36 h prior to onset were reported to one health authority within a single day. Investigation of these events revealed that the illnesses stemmed from a single event as well as restaurants located in a small community in BC (wave 1). As the initial investigation concluded, gastroenteritis related to oyster consumption continued to be reported, resulting in the initiation of a second, national investigation (wave 2). This paper describes the multi-agency investigations that lead to the detection of 449 cases of norovirus and acute gastroenteritis associated with BC oysters over a 5-month period, and resulted in the closure of 12 oyster farms along the BC coast.

Methods

Case Finding and Data Collection

Individuals reporting illness to local public health authorities following oyster consumption in BC, AB, and ON were interviewed using a standard questionnaire that asked about demographics, clinical information, travel, seafood exposure history, and ill dining partners. This work was not submitted for an ethics review as it was conducted for the purpose of outbreak investigation and control. Questionnaires were sent for centralized analysis to the BC Centre for Disease Control (BCCDC) during wave 1 and the Public Health Agency of Canada (PHAC) during wave 2. For the first wave of the outbreak, cases were defined as residents or visitors of Community Z with acute gastroenteritis (vomiting and/or diarrhea) within 48 h of exposure to oysters on or after Nov 17, 2016. For the second wave, cases were defined as residents or visitors to Canada with laboratory-confirmed norovirus infection or acute gastroenteritis (vomiting and/or diarrhea) within 48 h after exposure to oysters. In both investigations, cases were excluded if they had contact with another case during their exposure period.

Epidemiological, laboratory, and traceback data were entered into a linelist using Microsoft Excel and descriptive statistics were generated for demographics, clinical information, laboratory results, and oyster exposures. For both waves, exposure analysis was done at the cluster level, defined as one or more individual(s) consuming oysters from the same place at the same time. The onset date for the cluster was classified as the earliest symptom onset date among the cases in that cluster.

Traceback

Local public health authorities visited restaurant and retail locations reported by cases to obtain oyster tags. Oyster tags contain information about the oyster's farm of origin and harvest date, and are usually retained by restaurants and retailers for 90 days, as advised by the Food Retail and Food Services Code (FPT Food Safety Committee 2016). The tag information was sent to the Canadian Food Inspection Agency (CFIA) for verification and traceback, and to BCCDC (wave 1) and PHAC (wave 2) for centralized analysis of oyster farms and harvest dates. Based on the tag information, clusters were classified as single exposure if they were associated with oysters from one farm, and multiple exposure if they were associated with oysters from multiple farms.

Laboratory Investigation

Clinical specimens were sent to provincial laboratories for norovirus detection and genotyping. Clinical stool/vomitus samples were tested using a nucleic acid amplification test that detected norovirus genogroup I (GI) and genogroup II (GII). Norovirus-positive samples were genotyped by Sanger sequencing of the capsid region and compared to reference sequences using an automated pipeline in Galaxy. Some samples were further characterized by Sanger sequencing of the polymerase region to detect recombinant strains. Sequence alignment and phylogenetic analysis was performed using Geneious software 9.0.4. Phylogenetic trees were constructed with Tamura-Nei model and neighbor-joining method using the same reference sequences in Galaxy.

In order to determine if the strains circulating in the community during the same timeframe were similar to the strains causing the oyster outbreak, genotypes from oyster outbreak cases from BC were compared to those from community outbreaks that took place in BC during the same time period of November 2016–May 2017. In BC, only norovirus cases associated with outbreaks are routinely sequenced. For community outbreaks, a single case representing each detectable norovirus genotype(s) is sequenced per outbreak and is thought to be representative of the other cases.

Oyster samples obtained from harvest sites, processors, consumer homes, and food establishments were sent to CFIA laboratories, where they were tested for the presumptive presence of norovirus according to the International Standard ISO 15216-1 for the determination of norovirus in food using real-time RT-PCR (International Organization for Standardization 2013). Any samples reported as presumptive positive for norovirus GI or GII were submitted for confirmation testing by cloning and Sanger Sequencing of the amplicon. Samples taken from harvest sites were further tested for *Escherichia coli* according to the Health Canada method MFHPB-19 (Health Canada 2002) and male-specific coliphage (MSC) according to the method by Cabelli (1998).

Food Safety/Environmental Investigation

Local public health authorities inspected restaurant and retail locations reported by cases to review food handling and safety practices, assess potential onsite sources of contamination, identify any ill food handlers, determine if a persistent risk existed and take mitigating action if warranted, collect any leftover oysters from same batch/lot if possible, and obtain oyster tags for traceback purposes.

CFIA initiated a food safety investigation with implicated shellfish processors and harvesters. They also collected oyster shellstock samples from implicated oyster farms. CFIA recommended farm closures to Department of Fisheries and Oceans based on sampling results and the following information from the epidemiological analysis: number of single-exposure clusters implicating each farm, recentness of the clusters, clinical and/or food specimen results, and whether multi-exposure clusters could be explained by previous farm closures.

Environment and climate change Canada (ECCC) reviewed potential pollution sources nearby the affected oyster farms. This included visiting sites and reviewing records to identify the presence of nearby septic systems, marine vessel activity, wildlife activity, wastewater treatment plants, unscheduled sewage spills or discharges, rainfall, and water quality samples.

Results

Wave 1

Epidemiological Investigation

On November 22, 2016, several reports of acute gastrointestinal illness were reported in a small community on Vancouver Island following the consumption of raw oysters at a local oyster festival event. The oyster festival was held on November 18 and 19 and served mostly raw and some cooked oysters to over 500 participants. Oysters were also served at local restaurants during the same time period (November 16–26, 2016). Over 11,000 oysters were served during the festival.

The investigation identified 117 cases with symptom onset between Nov 17 and 28, 2016 (Fig. 1). All cases consumed oysters and all cases with information available ($n = 107$) consumed raw oysters, and some also had cooked oysters. Eighty-three cases consumed oysters at a single venue prior to onset: the oyster festival ($n = 66$), Restaurant 1 between November 16 and 26 ($n = 16$) or

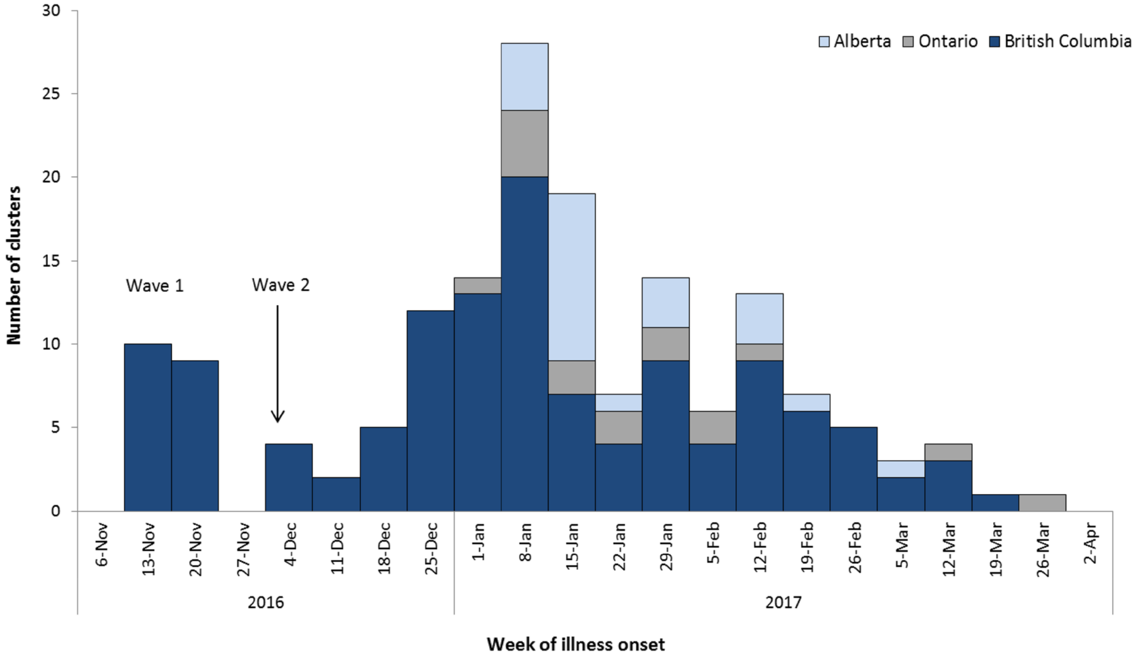

Fig. 1 Number of clusters of norovirus infection or acute gastroenteritis by week of illness onset, oyster outbreak, Canada, 2016–2017 ($n = 164$)

Restaurant 2 on November 18 ($n=1$). Remaining cases ($n=34$) reported consuming oysters at multiple venues; each reported at least one of the three venues listed above.

Cases were grouped into 19 clusters. Cases who consumed at multiple venues were classified using the following hierarchy to determine the most likely place of exposure: festival, Restaurant 1, Restaurant 2, other. Cases who consumed oysters at the festival were divided into two clusters (Nov 18 and Nov 19 events).

Festival attendees consumed oysters from multiple farms and were not able to identify which oysters they consumed. Only clusters exposed to oysters at restaurants could be linked to specific oyster farms and harvest dates. Five clusters had a single oyster exposure; they consumed raw oysters from Farm A (harvested Nov 14 and 23) at Restaurant 1. No other farms or venues were identified in single-exposure clusters. Farm A provided oysters from a different harvest date (Nov 15) to the festival. Oysters from Farm A were definitely or potentially consumed by 18 (95%) clusters. The remaining cluster may have consumed oysters from Farms B, C, or D at Restaurant 2.

Traceback

One distributor provided all raw oysters to the oyster festival from six different farms (Farms A, B, D, and 3 others) harvested from November 13 to 18. All raw oysters were processed by Processor X.

Oysters available on the dates clusters dined at local restaurants all traced back to Processor X. Restaurant 1 received oysters from Farms A, B, and C. Restaurant 2 received oysters from Farms B, C, and D. All farms were in Pacific Fishery Management Areas 13 and 24 off the BC coast (Fig. 2).

Laboratory Investigation

Six cases had laboratory confirmation of norovirus infection, all of whom attended the oyster festival. Genotyping was available for five of these cases. Three were GI.6a and two were GI.2, and sequences were indistinguishable within each genotype (Table 1; Fig. 3).

Oysters were tested from one festival leftover sample from Farm D, one Restaurant 1 leftover sample from Farm

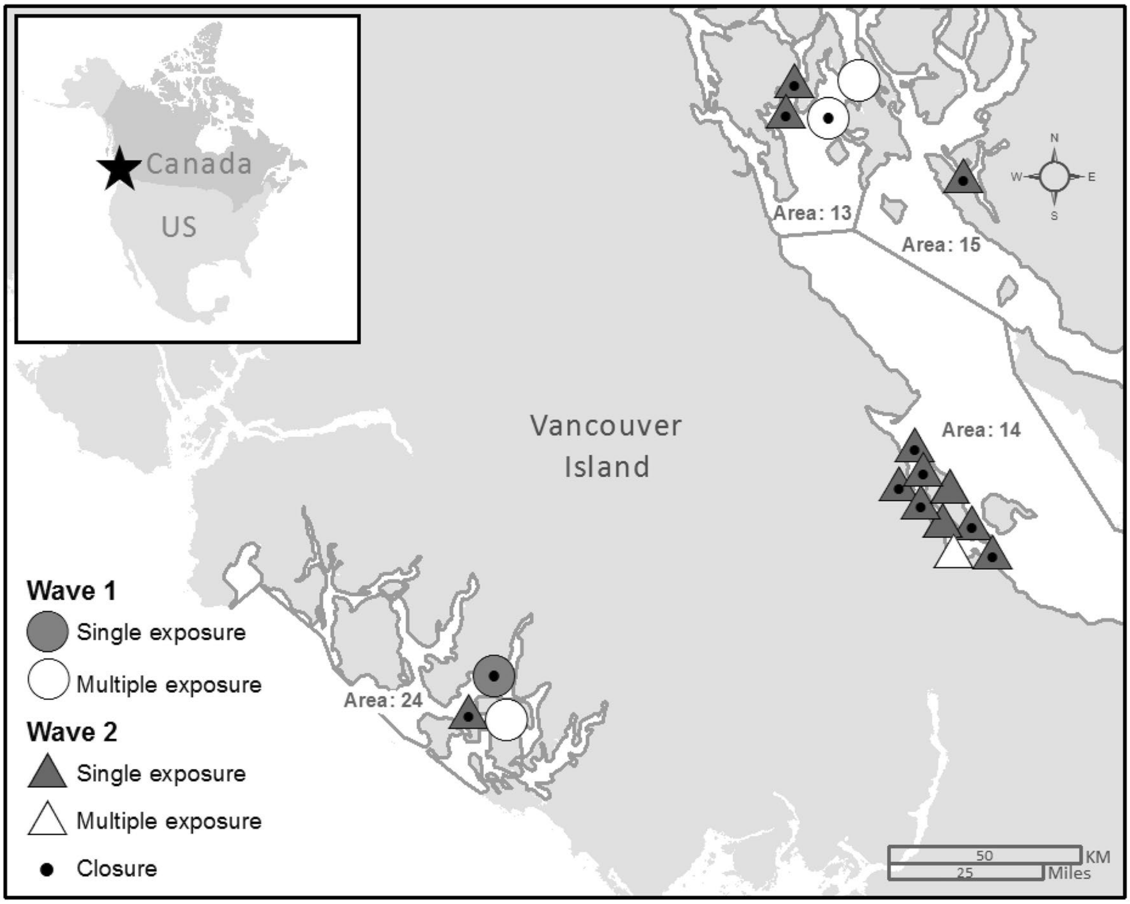

Fig. 2 Map of oyster farms by clusters associated, outbreak wave, and closure status, BC, Canada, 2016–2017

Table 1 Norovirus genotyping results from oyster outbreak waves 1 and 2 and BC community outbreaks, Canada, November 2016–April 2017

Genotypes	Clinical specimens from wave 1	BC clinical specimens from wave 2	ON and AB clinical specimens from wave 2	Community outbreaks in BC (Nov 2016–Apr 2017)
Genogroup I	6	10	1	6
GI.2	2	7	1	0
GI.3b	0	0	0	1
GI.6a	3	1	0	3
GI.9	0	0	0	2
GI untypeable	1	2	0	0
Genogroup II	0	8	4	49
GII.2	0	6	0	15
GII.3c	0	0	1	0
GII.4	0	0	1	24
GII.17	0	2	2	9
GII.6b	0	0	0	1
Coinfections*	0	2	0	0
GI.2 and GII.2	0	2	0	0

*Both strains isolated from single case

C, two harvest-area samples from Farms A and C, and two Processor X samples from Farms A and B. The Restaurant 1 sample from Farm C, processor sample from Farm A, and two harvest-area samples from Farms A and C tested positive for norovirus GI (Table 2).

Food Safety/Environmental Investigation

An inspection of the food premises participating in the oyster festival did not find concerns with any of the food premises with the exception of a single ill food handler. This one ill food handler could not explain all of the cases of illness; only five cases reported eating at this venue.

An inspection of the implicated Processor X did not find any concerns with control measure implementation, food handling, employee hygiene, or plant sanitation. Interviews with the shellfish harvesters did not identify any hygiene or sanitation issues.

Samples were taken at four farms in total. Both Farms A and C, which tested positive for norovirus at harvest, were closed on December 15 and 23, respectively.

Wave 2

Epidemiological Investigation

Investigation of the second wave of the outbreak found 331 cases that met the case definition in BC ($n = 230$), AB ($n = 42$), and ON ($n = 59$) with symptom onset dates ranging from Dec 6, 2016 to Mar 26, 2017 (Fig. 1). The 331 cases comprised 145 clusters (BC = 106, AB = 23, ON = 16), which formed the basis for the traceback data analysis. Oyster preparation details were available for 137 clusters. 108 clusters (78.8%) reported consuming raw oysters only, 11 (8.0%) reported consuming both raw and cooked oysters, and 18 (13.1%) reported consuming only undercooked or cooked oysters (including pan-fried, deep-fried, and broiled).

Traceback

Tag information obtained from the restaurants and grocery locations was obtained for 122 of 145 clusters (84.1%). Of these 122 clusters, 109 (89.3%) had exposure to BC oysters only, 12 (9.8%) had exposure to both BC and non-BC oysters, and one (0.8%) had exposure to non-BC oysters only.

Sixty-nine (56.5%) clusters were classified as multiple exposure, and 53 (43.4%) clusters were classified as single exposure. These single-exposure clusters were associated with 22 different oyster farms along the BC coast. Most single-exposure clusters were associated with oyster farms located in harvest area 14, with farms in areas 13, 15, and 24 also identified (Fig. 2). Areas 13 and 24 were common to wave 1 of the outbreak, but none of the same farms were identified, likely due to the fact that the two farm closures from wave 1 remained in effect during outbreak wave 2.

Laboratory Investigation

Twenty-five cases from 20 clusters had laboratory confirmation of norovirus infection (Fig. 3). Eleven cases had GI (genotypes GI.2 and GI.6), and 12 had GII (genotypes GII.17, GII.2, GII.3, and GII.4). Two cases had coinfections of GI.2/GII.2. All samples within a genotype were

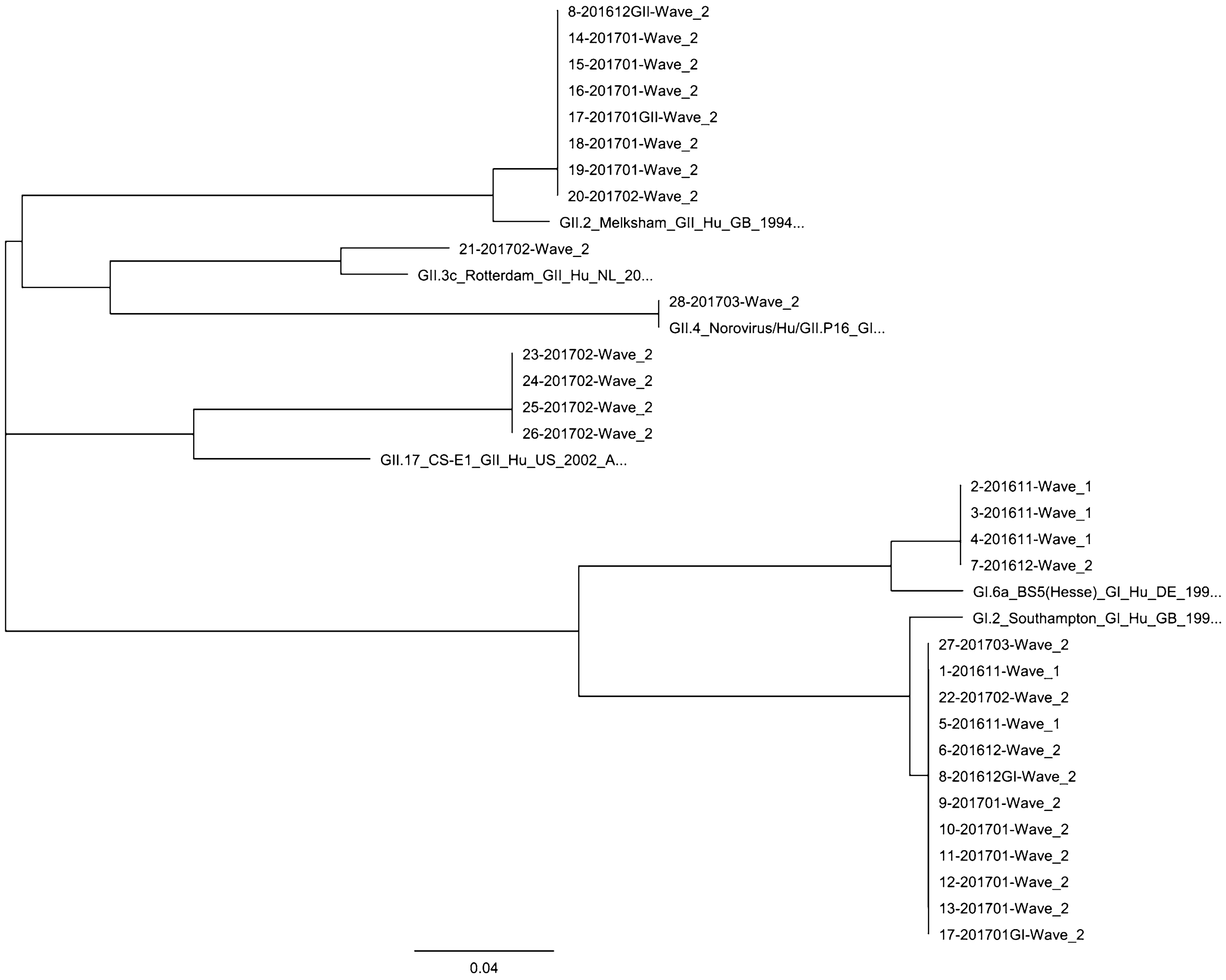

Fig. 3 Phylogenetic tree of clinical specimens and reference strains in outbreak waves 1 and 2, Canada, 2016–2017

indistinguishable by genome sequencing. Clinical samples with genotypes GI.2 and GI.6a were collected from both outbreak waves, and were also indistinguishable by genome sequencing between the two waves (Fig. 3).

BC cases accounted for 80% (20/25) of laboratory-confirmed cases. Genotyping results from community norovirus outbreaks in BC that occurred during the same time period as the oyster outbreak show that 10.1% (6/55) of community outbreaks were GI, compared to 55.6% (10/18) in BC oyster outbreak cases (Table 1). Of the GI specimens from the oyster outbreak, 87.5% (7/8) had GI.2, which was not seen in the community outbreaks occurring concurrently. Forty-nine percent (24/49) of community outbreaks had genotype GII.4, which was not seen in the BC oyster outbreak cases. Genotypes GI.6a, GII.2, and GII.17 were seen in both community and oyster outbreak cases. Sequencing results showed that the community and outbreak GI.6a and GII.17 specimens did not match, while the GII.2 specimens showed 100% sequence match (data not shown).

Twenty-six oyster samples were tested representing 13 shellfish farms (Table 2). This included 21 samples taken at the point of harvest representing 12 farms, three samples from restaurant/retail establishments, and two from case homes. Of the 13 farms represented, six tested positive for norovirus on at least one sample, while the others tested negative or inconclusive. Four of the 12 farms sampled at harvest tested positive, one with GI, two with GII, and one with both GI and GII. Both case home samples and one of the restaurant samples tested positive for norovirus, all with GI.

Food Safety/Environmental Investigation

Inspections of restaurant/retail establishments reported by the cases did not identify any contributing factors related to

Table 2 Summary of oyster sampling results and farm closures in outbreak waves 1 and 2, Canada, 2016–2017

Farm ID	Post-harvest samples		Harvest site samples	Closure	# Clusters associated	# Single-exposure clusters associated
	Sample type	Norovirus results	Norovirus results			
Wave 1						
A	Processor X	**Positive, GI**	**Positive, GI**	Yes	18	5
B	Processor X	Negative		No	9	0
C	Restaurant 1	**Positive, GI**	**Positive, GI**	Yes	4	0
D	Festival	Negative		No	3	0
Wave 2						
E	Restaurant	**Positive, GI**	**Positive, GI*** **Positive, GII** Negative	Yes	13	6
F			Negative*[a] **Positive, GII** Negative	Yes	34	8
G			Negative* **Positive GII** Negative	Yes	13	3
H			Negative*[a]	n/a—relays product to farm E		
I			Negative*[a] Negative[a]	Yes	9	4
J			Negative*	Yes	20	2
K			Inconclusive—GII. Negative for GI	No	8	1
L			**Positive, GI**	Yes	3	2
M			Inconclusive—GII. Negative for GI* Negative	Yes	13	2
N	Restaurant	Negative	Inconclusive—GII. Negative for GI Negative[a]	Yes	18	3
O	Case home	**Positive, GI**	Negative	No	8	0
P	Case home	**Positive, GI**	Negative	Yes	4	4
Q				Yes	5	2
R	Restaurant	Negative		No	4	1

Bold text denotes a positive result

*Sample also had elevated MSC levels (> 50 PFU/100 g)

[a] Sample also had unsatisfactory *E. coli* levels (> M in any sample unit or if c is exceeded: $n = 5$, $c = 1$, $m = 230$ MPN/100 g, $M = 330$ MPN/100 g)

the reported illnesses, such as onsite source of contamination or any ill food handlers.

CFIA instituted food safety investigations for the processors associated with each illness report, and did not find any concerns with control measure implementation, food handling, employee hygiene, or plant sanitation at the processing facilities.

Using the epidemiological information and the harvest-area sampling results, CFIA recommended ten farms for closure (Table 2). Four of the closed farms had harvest-area samples that tested positive for norovirus, as well as multiple single-exposure illness clusters associated with them. Four of the closed farms had satisfactory or inconclusive norovirus test results, but were closed based on elevated MSC counts and/or unsatisfactory *E. coli* levels along with multiple associated single-exposure illness clusters. Two farms were closed without unsatisfactory microbiological testing results on the basis of strong epidemiological evidence, specifically multiple associated single-exposure illness clusters.

During follow-up review of pollution sources by ECCC, no single pollution source was found that could explain the contamination of all the affected farms.

Discussion

We investigated the largest recorded outbreak of norovirus associated with oysters in Canada. Although it lasted 5 months and contamination was found in multiple geographically dispersed farms, similarities between the two waves in the timeframe, genotypes, and harvest areas identified indicate that this was a single continuous outbreak. The identification of multiple geographically dispersed oyster farms as a source to a norovirus outbreak is an uncommon occurrence, but was previously seen in BC in 2004 (David et al. 2007).

Farm A in area 24 was thought to be the likely source of wave 1 of the outbreak. Although Processor X was common among all clusters, only Farm A was linked to single-exposure clusters. The positive oyster samples from Farm C in area 13 were believed to be a spurious finding at the time, but may have been an early warning of wider contamination. Wave 2 of the outbreak was linked to multiple farms in areas 13 and 24 (Farms I, P, and Q) as well as additional farms in areas 14 and 15.

The case illness onset dates in the two waves were continuous, with just 1 week between the end of wave 1 and the beginning of wave 2. The large number of cases exposed at the festival in wave 1 may have resulted in earlier detection of an otherwise slow start to an ongoing outbreak. Furthermore, oyster farms in area 14, which is the largest producer of BC oysters by volume and was associated with the majority of wave 2 clusters, were closed during parts of November due to excessive rainfall in that area, and not supplying product to the market at that time. Therefore, it is plausible that the farms identified in waves 1 and 2 were contaminated around the same time, but the later detection of clusters associated with wave 2 was a result of product availability.

Harvest-area and clinical specimens from wave 1 were all GI, while in wave 2 they were a mix of GI and GII. The difference in genogroups between the two waves may have been due to contamination containing multiple norovirus strains, or due to different contamination events occurring near each farm. However, there are insufficient data to assess these hypotheses. Two indistinguishable strains (genotypes GI.2 and GI.6a) were identified in both outbreak waves (Fig. 3), suggesting some similarity in source between the two waves.

Norovirus is not nationally reportable at the case level, and as such an increase in cases is unlikely to be detected by enteric surveillance systems. This outbreak was detected in BC where shellfish-related illnesses are reportable to public health authorities. Subsequently, cases were detected in Alberta and Ontario through review of suspected foodborne illness complaint information. It is likely that the cases reported underestimate the true number of illnesses caused by the contaminated oysters, and cases may also have occurred in provinces where shellfish-related illness and norovirus cases are not routinely followed up.

The short duration of norovirus illness means that few cases seek healthcare and submit a sample, and therefore cases are unlikely to be laboratory-confirmed. To compensate for this under-reporting, norovirus-like illness was included in the case definition to capture cases that exhibited clinical symptoms consistent with norovirus infection after consumption of oysters.

Norovirus commonly circulates in the community in the winter months when this outbreak took place, so it is possible that community-acquired cases were captured as part of the outbreak. However, oysters are a relatively rare exposure, with only 1% of Canadians reporting any oyster consumption and 0.4% reporting raw oyster consumption over a 7-day period (Public Health Agency of Canada 2015), and therefore inclusion of oyster exposure in the case definition minimized potential misclassification of community cases into the outbreak.

The proportion of GI strains seen in the oyster outbreak was much higher than in the community outbreaks occurring during the same time period (Table 1), which is consistent with previous findings regarding bivalve mollusks (Verhoef et al. 2010). Oysters contain a ligand homologous to that found in the humans that allows them to selectively bio-accumulate GI strains of norovirus (Le Guyader et al. 2012). Similar to the 2004 BC oyster outbreak associated with norovirus, the clinical specimens in this outbreak primarily had genotype GI.2 (David et al. 2007). This strain was not detected in any community outbreaks during the same time frame, and was previously found to be associated with foodborne outbreaks significantly more often than person-to-person outbreaks (Verhoef et al. 2010). On the other hand, some of the strains found in the oyster outbreak clusters were similar or the same as those circulating in the community. GI.6a and GII.17 community and oyster outbreak strains were different by sequencing, but some oyster outbreak and community GII.2 specimens showed a 100% match in sequencing results. Of note, one oyster outbreak cluster had genotype GII.4, which was the most common community outbreak strain in BC. This case belonged to the only cluster in the outbreak that consumed oysters from a location other than BC and therefore may have been exposed to other sources of oyster contamination or was actually a community case misclassified as an outbreak case. The genotype and sequencing data suggest that the main oyster outbreak strain GI.2 is the one that is typically associated with oyster outbreaks, likely due to its ability to bind to oysters. It also suggests that oyster outbreak strains like GII.2, GI.6a, and GII.17 arose from community sources of contamination (i.e., human sewage contaminating the marine environment). Strains GI.2 and GII.3c, which were not identified in community settings during the same time period, may possibly have occurred due to under-diagnosis of community cases. In BC, only facility and foodborne outbreaks are tested for norovirus; sporadic cases are not.

Twelve oyster farms were closed throughout the two investigations through a process that took into account epidemiological information and harvest-area sample results. The median time from reporting of the first cluster to public health to closure of each farm was 72 days. In order to reduce the time from illness to closure and prevent additional illnesses from occurring, BCCDC used outbreak data to propose criteria for oyster farm closures based on illness clusters alone. In December 2017, the Canadian Shellfish Sanitation Program, a federal program that governs safety of shellfish meant for consumption, incorporated such criteria to temporarily close farms pending environmental investigation and positive laboratory samples. The closures would be enacted in the event of two single-exposure clusters within 21 days, one single-exposure cluster and two multiple-exposure clusters within 21 days, or a single-exposure cluster comprised of a large number of illnesses resulting from a specific harvest date for a public or private event (such as in the case of wave 1). In this outbreak, the use of these criteria would have closed 14 farms, reduced the median time between reporting of the first cluster to public health and closure to 11 days, and averted 27 clusters of illness.

The majority of cases in this outbreak reported exposure to raw oysters. However, 18 clusters (13.1%) in wave 2 reported exposure to cooked or undercooked oysters, including pan-fried, deep-fried, or broiled oysters. In order to better understand the risk of cooked or undercooked oysters, a cohort study was conducted on a cluster from wave 2 associated with an event where barbecued oysters were served. The cohort was comprised of six ill and 11 well individuals who were asked about their consumption of food items served at the event. Barbecued oysters were associated with the highest risk of illness, although not statistically significant (RR = 5.50, 95% CI 0.40–90.1) (unpublished data). There have also been previous documented reports of outbreaks associated with cooked or undercooked oysters (Alfano-Sobsey et al. 2012; Webby et al. 2007; Smith et al. 2012). Norovirus can survive in temperatures up to 60 °C, and can survive cooking methods including stewing, frying, baking, and steaming (DiGirolamo et al. 1970; Hewitt and Greening 2006; Kirkland et al. 1996). The inactivation of norovirus during cooking depends on oyster species and size, cooking method and duration, and temperature reached during cooking (Richards et al. 2010). This suggests that cooked or undercooked oysters were a plausible source of infection for some clusters in this outbreak.

Several practices may have led to limited misattribution of farms. On occasion, oysters can be moved between farms or wet stored prior to harvest, but only the last farm where the product was stored for greater than 14 days is recorded on the tags. This practice may have contributed to contamination or, alternatively, led to purging of norovirus. Furthermore, during wave 1, there was an anecdotal report of oysters being hung from a dock in a public harbor prior to consumption by a small group. This practice is not permitted by shellfish regulators and may account for the source of contamination for this lot. Finally, the farms that were identified may in part have reflected the areas producing the most oysters during that time period.

The detection of multiple norovirus genogroups in the oyster samples collected at harvest is consistent with environmental contamination (Le Guyader et al. 2006a; Westrell et al. 2010; Symes et al. 2007). Human sewage contamination of BC coastal waters is the most plausible source of the environmental contamination (McIntyre et al. 2017). Potential sources investigated include sewage system overflows, effluent discharges from metropolitan and local wastewater treatment plants, municipal septic discharges, commercial fishing vessels, and other discharges into the marine environment. Ultimately, no discharge events were identified that could explain the environmental norovirus contamination in all of the geographically dispersed oysters farms, particularly since farms were located on the west and east coasts of Vancouver Island. Other authors have found that environmental factors played a role in norovirus outbreaks, and may have played a role here as well (Wang and Deng 2016).

Public health actions taken during this investigation included public communications by national, provincial, and local health authorities advising the public not to consume raw oysters, education to food premises informing them of the outbreak and advising not to serve raw oysters, enhanced HACCP controls by federally registered processing establishments, and the closure of 12 oyster farms.

Conclusions

The successful management of this outbreak relied on the engagement and collaboration of several different organizations including public health professionals, laboratory experts, food safety experts, shellfish regulators, environmental pollution experts, and the shellfish industry. Future shellfish-related outbreak investigations could be assisted by improvements in national surveillance for shellfish-related illnesses, capacity for more rapid testing and genotyping of oyster samples, and the implementation of illness-based criteria for harvest site closures.

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Compliance with Ethical Standards

Conflict of interest The authors have no conflicts of interest to disclose.

Ethics Approval and Consent to Participate This work was not submitted for an ethics review as it was conducted for the purpose of outbreak investigation and control.

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